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# Rothamsted Repository Download

**A - Papers appearing in refereed journals**

Mitchell, R. A. C. 2024. Identification of universal grass genes and estimates of their monocot-/ commelinid-/ grass-specificity. *Bioinformatics Advances.* p. vbaf079. https://doi.org/10.1093/bioadv/vbaf079

# all groups in universal_grass_peps database called as monocot- / commelinid- / grass-
# sorted descending values of S  monocot/commelinid/grass

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | specificity | | |
| | non-grass | | non-commelinid | | non-monocot | |
| group_id | S grass | sp of top h | S commeli | sp of top h | S monoco | sp of top h |
| Os08t0528200-01 | 0.74 | Ananas_co | 0.91 | no_hit | 0.91 | no_hit |
| Os01t0210300-01 | 0.57 | Ananas_co | 0.87 | no_hit | 0.87 | no_hit |
| Os04t0258900-01 | 0.87 | Populus_tr | 0.87 | Populus_tr | 0.87 | Populus_tr |
| Os06t0297400-03Zm00 | 0.84 | Dioscorea_ | 0.84 | Dioscorea_ | 0.85 | Actinidia_c |
| Os03t0702900-00 | 0.64 | Ananas_co | 0.83 | no_hit | 0.83 | no_hit |
| Os04t0477100-00 | 0.83 | no_hit | 0.83 | no_hit | 0.83 | no_hit |
| Os03t0727800-01 | 0.82 | Populus_tr | 0.82 | Populus_tr | 0.82 | Populus_tr |
| Zm00001eb246200_P00 | 0.82 | no_hit | 0.82 | no_hit | 0.82 | no_hit |
| Os10t0516900-01 | 0.80 | no_hit | 0.80 | no_hit | 0.80 | no_hit |
| Os10t0522800-01 | 0.23 | Musa_acur | 0.80 | no_hit | 0.80 | no_hit |
| Os02t0160200-01 | 0.46 | Musa_acur | 0.62 | Dioscorea_ | 0.79 | Beta_vulga |
| Os06t0294200-01Zm00 | 0.79 | Dioscorea_ | 0.79 | Dioscorea_ | 0.79 | Actinidia_c |
| Os06t0111100-01 | 0.77 | Ananas_co | 0.79 | Arabidopsi | 0.79 | Arabidopsi |
| Os06t0111200-01 | 0.76 | Ananas_co | 0.77 | Actinidia_c | 0.77 | Actinidia_c |
| Os09t0480600-01 | 0.17 | Ananas_co | 0.76 | no_hit | 0.76 | no_hit |
| Os12t0570500-01 | 0.64 | Ananas_co | 0.74 | Dioscorea_ | 0.76 | Vitis_vinife |
| Os01t0109750-01 | 0.50 | Ananas_co | 0.75 | Capsicum_ | 0.75 | Capsicum_ |
| Os02t0456800-01 | 0.38 | Ananas_co | 0.59 | Dioscorea_ | 0.75 | Pistacia_ve |
| Os06t0535400-01 | 0.75 | Solanum_t | 0.75 | Solanum_t | 0.75 | Solanum_t |
| Os05t0561600-01 | 0.69 | Ananas_co | 0.75 | Solanum_l | 0.75 | Solanum_l |
| Os06t0636800-00 | 0.58 | Ananas_co | 0.75 | no_hit | 0.75 | no_hit |
| Os02t0794400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0397700-01Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0528100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0607100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0838800-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0326000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os11t0214001-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os11t0134500-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0716200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0659600-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0635200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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|---|---|---|---|---|---|---|
| Os03t0165300-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0509700-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0532600-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Zm00001eb312850_P00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0518000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os03t0838100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0275100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0442100-01Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0111800-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0550400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os04t0304200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os12t0561500-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0147900-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0187000-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os04t0653000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0448300-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0256200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0219500-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os05t0540800-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0896400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0578400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0560300-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0596100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0532800-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os11t0490600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os11t0191300-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0842700-03 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0155400-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os11t0568300-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0445800-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0184000-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0529600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0582850-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0209000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0179400-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0467600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0388601-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0641700-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0817000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0748300-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0798100-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0213100-00Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0512100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0573800-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os11t0216000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Zm00001eb140970_P00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0852900-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0545900-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0762400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0297000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0634500-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0561400-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Zm00001eb053840_P00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0498800-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0427100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0343200-01Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0795100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0623400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os07t0530700-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os08t0436200-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os09t0135700-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os03t0809800-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os03t0769700-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os02t0468400-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os02t0771200-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os06t0208200-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os05t0560000-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0570500-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os07t0573000-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os08t0200500-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Zm00001eb130600_P00 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0640200-00Zm00 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os03t0344700-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0939600-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os03t0279600-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os05t0270400-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0158400-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0249100-00 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os02t0302900-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os07t0484300-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0955500-00 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0877400-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os08t0521800-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os10t0320100-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os05t0150400-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os01t0595100-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |
| Os09t0452200-01 | 0.74 no_hit | 0.74 no_hit | 0.74 no_hit |

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| Os07t0695100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0614600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0113650-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0950800-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0607400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0719900-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0371500-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0235200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0601100-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0204400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0878000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0613100-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0588700-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0482300-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0109400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0281000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os03t0229100-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0543200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0577200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0649000-01Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0563400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os09t0451000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0280500-01Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0660700-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0537200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os01t0808400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0516400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0580100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os08t0523200-00Zm00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0568600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os01t0940000-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0105400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0376200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |

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| Os01t0227500-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0825400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Zm00001eb183250_P00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os03t0854200-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0138100-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0515900-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os10t0476600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os05t0535800-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0692300-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0571700-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os02t0731700-02 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0319600-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0567400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os04t0193200-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os09t0507400-01 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os06t0184200-00 | 0.74 | no_hit | 0.74 | no_hit | 0.74 | no_hit |
| Os07t0494900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os11t0706801-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0596200-03 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0768600-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0303700-00Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0899800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os11t0141900-00Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os04t0684200-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os07t0557500-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os12t0193200-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0658400-01 | 0.71 Ananas_co | 0.73 Nymphaea | 0.73 Nymphaea |
| Os03t0660400-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |

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| Os04t0511700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0393700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0552700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0537400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0113100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0293500-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0290500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0123600-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0596500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0726900-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0466700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0619400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0328000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0668300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0285700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0546900-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0103700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0100500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os01t0311500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0724500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0220900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0215300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0612500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb084670_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os11t0146800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0552700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0118800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb131870_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0512100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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|---|---|---|---|---|---|---|
| Os01t0318700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0954900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0147800-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb029740_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0971700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0504900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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|---|---|---|---|---|---|---|
| Os06t0526600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0674300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0448300-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0607200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0548300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0661400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0825800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os12t0244400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0225300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb105090_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0176700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb283310_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0414900-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0770600-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0665500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0290600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0572700-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0409100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0176500-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0372000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os03t0224700-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0133900-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0140400-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os09t0249600-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0714300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0180700-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os03t0778100-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0112101-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os12t0121100-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os04t0507800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os08t0544800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os07t0598700-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0730500-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0672700-02 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os03t0756300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os11t0568700-02 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os03t0674700-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0737900-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0664800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os08t0521200-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0803300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0200300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os03t0773700-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os08t0490300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0472700-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os12t0556100-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |

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| Os02t0830000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0466500-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0290400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0131500-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0376000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0589600-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0708832-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0110100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0807700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb128260_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0462200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0559500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0131600-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb210650_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0150700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0235100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0210100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0563900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0437000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0517900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0437500-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0121800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0744650-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0525200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0145200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0183300-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0101800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0107500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0482100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0581700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb082040_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0710900-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os10t0463800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0321800-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0812100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0701300-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0155200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb312110_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0224500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0521300-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0210900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0116000-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0664200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0201000-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0771500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb431730_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0369700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0513100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0829500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
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| Os09t0111100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0632500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0567500-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0135850-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0605500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0410266-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0571100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0416500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
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| Os04t0488700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0796400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os01t0846300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os04t0403200-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0810300-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os03t0709100-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Zm00001eb193710_P00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os04t0566600-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0290400-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os07t0205000-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0498300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0520100-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os08t0496500-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0552800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0248900-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os07t0546400-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0568000-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0581900-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |

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| Os06t0728902-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0579300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0210800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0487900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0494800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0685900-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0556600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0275100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0523700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0186100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0214800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb421870_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0191000-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0416200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0834300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0415600-00Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0529400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0763900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0183500-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0663100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0236900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0321900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0463300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0415200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0600701-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0143600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0705000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os02t0120500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0110400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0139000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0103100-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0112200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0531200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0233200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0566100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0459700-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0280100-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os04t0600500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0114100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0196800-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0823000-01Zm00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0558100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0548200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0232100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0179300-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0509100-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os08t0512900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb387820_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0578900-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os07t0119800-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0222200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0682100-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |

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| Os11t0128000-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0293300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Zm00001eb283520_P00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os09t0566550-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os11t0139500-02 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os01t0165200-01Zm00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os09t0376600-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os07t0457550-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0184800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os04t0487100-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0100300-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os02t0538700-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0319800-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os06t0554100-00 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |
| Os05t0585800-01 | 0.73 no_hit | 0.73 no_hit | 0.73 no_hit |

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| Os07t0516700-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os03t0823400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0687600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0631600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0171400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0164300-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Zm00001eb394920_P00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0489800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os10t0182000-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0261900-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0829800-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os05t0565701-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os11t0213500-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0224200-00 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0733600-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os12t0189400-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os02t0602100-02 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os01t0908200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os06t0166200-01 | 0.73 | no_hit | 0.73 | no_hit | 0.73 | no_hit |
| Os09t0534000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0307300-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0545100-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0273500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0833400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0554800-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0732200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Zm00001eb169850_P00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0612900-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0349200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0192500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0105900-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0136500-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0416500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0431750-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |

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|---|---|---|---|
| Os03t0281100-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0392300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0386700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0568300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os11t0212100-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os11t0102700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0136200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0752600-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0729300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0923000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0479800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb309040_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0155600-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0192300-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb418150_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0631200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0406800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0116600-00Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0207500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0525000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0831000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb089370_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0661000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os01t0134900-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0564300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os08t0477900-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0569900-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0756400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0663000-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| | | | |
| Os04t0629300-02 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0166500-02 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0775000-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| | | | |
| Os05t0566800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0787000-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0439900-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0816000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0288200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0686400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0945001-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0183800-01 | 0.72 Cynara_car | 0.72 Cynara_car | 0.72 Cynara_car |
| Os05t0568000-02 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0423300-00Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0359000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0656700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os12t0604200-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0307200-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0441400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0100800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb208780_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0293500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0754100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb157880_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0840500-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0472400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0736600-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os09t0453300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0452400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0292100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| | | | |
| Os09t0529300-01 | 0.56 Ananas_co | 0.68 Dioscorea_ | 0.72 Corchorus_ |
| Os12t0431300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os06t0309000-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0786500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0458700-02 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0715200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os12t0534100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0463400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0517000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0122700-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0218100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os08t0531100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0244400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0711100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os09t0497900-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb096170_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os07t0151100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb247120_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os09t0407800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0197100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0385400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0648700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os12t0596300-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb201140_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0465800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0462200-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0579500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os08t0248700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os08t0526500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os05t0597000-00Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|
| Os03t0277500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0545600-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0696900-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb405010_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|---|---|---|
| Os03t0656500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0131700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0213400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os10t0347800-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0520600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0284600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0708800-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0524400-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0304500-00Zm00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0559000-01Zm00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0911000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0478200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0479200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os10t0512100-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0179000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0156000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0794400-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0117600-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Zm00001eb368690_P00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0634000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0497500-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0685700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os10t0109900-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Zm00001eb399930_P00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0511600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |

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|---|---|---|---|---|---|---|
| Os06t0267500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0898800-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0281201-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0540300-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0681950-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0631400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0727000-02 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0256400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0610600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0679000-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0829600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0594500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os11t0207300-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0463600-01 | 0.68 | Ananas_co | 0.72 | Dioscorea_ | 0.72 | Prunus_pe |
| Os09t0536200-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0644100-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0193300-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0907400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0325200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0318700-01Zm00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os12t0565100-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0213300-01 | 0.49 | Ananas_co | 0.64 | Dioscorea_ | 0.72 | Theobrom |
| Os11t0644000-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0521900-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0625800-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0294000-01 | 0.72 | Theobrom | 0.72 | Theobrom | 0.72 | Theobrom |

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|---|---|---|---|
| Os03t0381500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0791366-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os08t0301500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0608200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0217300-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os08t0515000-00Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os12t0605200-01 | 0.36 Ananas_co | 0.66 Dioscorea_ | 0.72 Citrus_cler |
| Os03t0271500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0536700-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0371200-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os02t0689000-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Zm00001eb155470_P00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os10t0150300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os03t0308600-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0680400-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0341300-01Zm00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os09t0482700-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0501800-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os01t0828200-00 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os05t0220100-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os07t0666900-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os06t0593800-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os09t0448500-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |
| Os04t0445300-01 | 0.72 no_hit | 0.72 no_hit | 0.72 no_hit |

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|---|---|---|---|---|---|---|
| Os11t0508600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0915000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0165600-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0684700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0758600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0209100-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0641200-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0654300-01Zm00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0168800-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0613500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0684400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0645600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0642000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0206600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0504400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0593900-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0687200-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os11t0417400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0478600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os01t0637800-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0231950-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0642650-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os09t0438700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0709350-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os05t0335500-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0264300-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0321700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0775700-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0526000-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0409400-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0619800-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os11t0105750-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |

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| Os03t0816500-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os03t0591300-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os02t0594800-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os06t0632400-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os04t0223300-00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0137300-01Zm00 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os07t0298900-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os08t0338600-01 | 0.72 | no_hit | 0.72 | no_hit | 0.72 | no_hit |
| Os12t0424700-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0508300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Zm00001eb363070_P00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0559200-01 | 0.60 | Ananas_co | 0.68 | Dioscorea_ | 0.71 | Solanum_l |
| Os05t0510700-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0767900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0713250-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os12t0102900-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0533150-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0504100-00Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Zm00001eb070600_P00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os07t0296200-01Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0608900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0224100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0493100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0436400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0293400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0381700-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os11t0621500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0527600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0116566-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os12t0187800-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |

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|---|---|---|---|---|---|---|
| Os06t0652100-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0612800-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os07t0409200-01Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Zm00001eb126660_P00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0129000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0528300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0269000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0827600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0326900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0105350-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os12t0623400-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0936100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0569100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0544000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0378900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0523300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os11t0616300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0273200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0560600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0273300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0467400-03 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0132500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0700000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os07t0240600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0596900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Zm00001eb059240_P00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |

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|---|---|---|---|
| Os03t0233300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0151300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os11t0520500-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0924966-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0686700-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0512400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0130300-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os09t0560450-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0545300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os10t0545600-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os11t0703000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0174100-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os12t0630500-01Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0250300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0120100-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0426000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb012890_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os07t0603800-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os12t0614600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |

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|---|---|---|---|---|---|---|
| Os01t0274800-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0373500-01 | 0.64 | Ananas_co | 0.69 | Dioscorea_ | 0.71 | Manihot_e |
| Os05t0489200-01Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Zm00001eb434560_P00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0550400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os07t0609000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0309600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0545400-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0316500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0485400-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0150500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os11t0144900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0124900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0487300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0390900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0560400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0855100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0597200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0251200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os07t0537000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0680600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |

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|---|---|---|---|---|---|---|
| Os03t0753100-01Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0682100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os12t0182500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os11t0587000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0182700-01 | 0.64 | Ananas_co | 0.71 | Theobroma | 0.71 | Theobroma |
| Os09t0541100-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0214900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0610700-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0638800-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0728150-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0747600-02 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0192000-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0172200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0552400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os04t0685400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0508300-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0856000-02 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0629400-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0572900-02 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |

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|---|---|---|---|---|---|---|
| Os03t0834050-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0192100-02 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os06t0714200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0111500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0445600-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0416900-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0154900-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0249100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0203000-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0656201-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0773732-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0453900-01Zm00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0197900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0300700-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os09t0520500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0499100-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0590900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0440100-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0106200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0194350-00 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os05t0551700-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os10t0468500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0386500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0791200-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os01t0617500-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os03t0305500-02 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os02t0265900-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |
| Os08t0421800-01 | 0.71 | no_hit | 0.71 | no_hit | 0.71 | no_hit |

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|---|---|---|---|
| Os06t0139700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0254000-01Zm00 | 0.66 Ananas_co | 0.71 Actinidia_c | 0.71 Actinidia_c |
| Os06t0562700-01Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0103100-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0768700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0167800-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0457800-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb301490_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os07t0571100-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os06t0165800-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0551400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0692600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0124000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0596300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0477700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0195000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0511900-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0369700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os11t0240600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0681000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os07t0694500-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0288925-00Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0411300-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb289700_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0232000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os09t0486500-02 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os10t0360100-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0240600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |

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|---|---|---|---|
| Os03t0398600-00Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0442700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0280400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0588900-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os11t0107600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0207900-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb302740_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0223600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0726600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0356400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0107600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0747700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb406920_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0423100-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os08t0459600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os10t0562000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0122100-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0498000-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os05t0177100-01Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os01t0835700-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os10t0548700-01Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Zm00001eb111000_P00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os07t0664400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0145600-01Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |

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|---|---|---|---|
| Os09t0422500-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0769400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os06t0650300-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os06t0570900-00Zm00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0833600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os03t0825600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0444100-00 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os06t0698900-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0530900-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os07t0158800-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0764400-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os02t0130600-01 | 0.71 no_hit | 0.71 no_hit | 0.71 no_hit |
| Os04t0353000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os10t0512500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0390600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|---|---|---|
| Os05t0551500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0517700-00Zm00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0569000-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0640300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os09t0315100-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0610350-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0636700-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os11t0169400-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os09t0570900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os09t0362900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0861900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0737300-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Zm00001eb096870_P00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0121300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0633700-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os05t0496400-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |

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|---|---|---|---|
| Os09t0299000-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0163400-01 | 0.65 Ananas_co | 0.70 Dioscorea_ | 0.70 Actinidia_c |
| Os07t0259400-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0672500-00Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0246300-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0881300-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0673500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0118000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0137950-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0793000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0608600-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0556600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Zm00001eb189200_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0463000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0237100-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0409100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0772200-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os02t0591600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0729900-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0207200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0535600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os02t0141500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Zm00001eb387450_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Zm00001eb360810_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0297700-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0241700-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os09t0439600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0571900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0914600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os07t0434500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os10t0550000-01 | 0.55 Ananas_co | 0.67 Dioscorea_ | 0.70 Actinidia_c |
| Os11t0183150-00Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0619000-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os06t0622300-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0181400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0144200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os01t0720400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0104400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0305100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0824600-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Zm00001eb400030_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0801901-00Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0108400-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os01t0972200-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0114400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0685900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|---|---|---|
| Os02t0274000-03 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os10t0140300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os05t0499500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0650900-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0663600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0264700-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0265100-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0200200-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0239300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0694500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0184400-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0784900-00Zm00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0476200-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |

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|---|---|---|---|
| Os06t0228200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0284900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0164100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0420800-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os10t0127700-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0754100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0152600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0101800-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0231900-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0686650-00Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0690400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os02t0672400-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0572000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0224900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os02t0758200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0632600-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0314800-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0897100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0188266-00 | 0.48 Ananas_co | 0.70 Ipomoea_t | 0.70 Ipomoea_t |
| Os03t0149100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0338500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os07t0669500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0578300-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0162500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os10t0576600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0557600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0272400-01 | 0.68 Ananas_co | 0.70 Ipomoea_t | 0.70 Ipomoea_t |
| Os09t0423200-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os07t0211500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0654000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0617500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0429500-02Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0683100-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os09t0547200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0653200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os02t0526600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|
| Os03t0389100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0430900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0159000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0410900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0205100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0162800-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0972800-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os03t0169800-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0595500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0183000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0524600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os12t0267900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0179150-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os09t0473966-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Zm00001eb024150_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os10t0532000-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0202500-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0374200-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0554000-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os07t0134200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0567200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0694300-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os06t0108600-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |

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|---|---|---|---|---|---|---|
| Os04t0637300-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0437300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0770000-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0227700-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os05t0417600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0770500-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0733500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0132400-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0583900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0244600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os08t0434000-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0197300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os05t0499400-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0915600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os11t0261600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0772700-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0239700-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os10t0544600-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os11t0700500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0752400-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0209200-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0637900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |

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|---|---|---|---|---|---|---|
| Os09t0242800-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0842500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0110500-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0114900-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os11t0221300-00Zm00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0726400-01 | 0.68 | Musa_acur | 0.70 | Prunus_du | 0.70 | Prunus_du |
| Os05t0356700-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0810800-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0113100-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0585600-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0214900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os11t0610600-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0816200-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os08t0493800-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0623300-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os02t0709600-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0126000-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0431800-00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os12t0174200-01Zm00 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0152800-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os03t0242900-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os12t0239200-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os01t0524500-02 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os06t0714800-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os07t0661400-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |
| Os04t0415000-01 | 0.70 | no_hit | 0.70 | no_hit | 0.70 | no_hit |

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|---|---|---|---|
| Os11t0168000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0682000-01 | 0.69 Dioscorea_ | 0.69 Dioscorea_ | 0.70 Theobroma |
| Os01t0621600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0673000-01Zm00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0221000-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
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| Os02t0699400-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os04t0430600-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0692100-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os05t0295100-02 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| | | | |
| Os03t0716200-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Zm00001eb056980_P00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os11t0472600-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os01t0817650-00 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os08t0157900-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
| Os09t0444700-01 | 0.70 no_hit | 0.70 no_hit | 0.70 no_hit |
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| Os12t0538500-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0146200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0588500-02 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os06t0557100-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0176200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Zm00001eb272150_P00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os04t0105000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0510800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os06t0289900-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0738000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0404800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os11t0139400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0701000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0642900-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0738300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os06t0311600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0730900-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os12t0571000-01Zm00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0689600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0394200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os06t0286228-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os12t0490100-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0752700-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |

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|---|---|---|---|---|---|---|
| Os02t0827200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os09t0491612-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0604200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0436400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0127800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0509300-02 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0695200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os07t0175900-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Zm00001eb040560_P00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Zm00001eb239390_P00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Zm00001eb434530_P00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os05t0374600-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os05t0567200-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0297900-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0279400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0437000-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os08t0467400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0848600-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os08t0554400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0765800-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0719700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os07t0100500-02 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0678100-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os09t0255900-01 | 0.57 | Ananas_co | 0.69 | Corchorus. | 0.69 | Corchorus. |
| Os02t0566700-01 | 0.56 | Ananas_co | 0.69 | Daucus_ca | 0.69 | Daucus_ca |
| Os05t0346800-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os11t0705200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |

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|---|---|---|---|
| Os02t0261000-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os09t0563700-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0129200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0817800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0585900-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0693100-00Zm00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0575500-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0219800-03 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os12t0438300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os04t0548400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os04t0471400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0421800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0930900-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0355200-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0351100-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0486100-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0162836-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Zm00001eb326490_P00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0719000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0618000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0107800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0109501-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os08t0502800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |

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|---|---|---|---|---|---|---|
| Os12t0569200-01 | 0.69 | Glycine_ma | 0.69 | Glycine_ma | 0.69 | Glycine_ma |
| Os04t0532800-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0727000-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0568400-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os10t0553600-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0668900-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0805400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os11t0573200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0698500-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0655800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0781300-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0897300-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os05t0491400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os08t0524800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os12t0577200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0101600-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os12t0634000-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os09t0127700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0827500-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0761300-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os05t0428400-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os07t0641600-02 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0666800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0625900-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os05t0357700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0195800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0604600-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os11t0136800-02Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os08t0510700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0514400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0481900-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0207500-02 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0886500-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os11t0533500-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os08t0111200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Zm00001eb400240_P00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os07t0537500-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0668901-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |

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|---|---|---|---|---|---|---|
| Os03t0190300-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0546400-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os02t0516800-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os07t0495900-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0203800-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0537700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0472200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0594100-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os10t0132300-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os10t0431900-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Zm00001eb240790_P00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0412100-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0716100-01Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0690500-00Zm00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os09t0422600-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os03t0833200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os04t0438700-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0700300-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0848900-01 | 0.53 | Musa_acur | 0.69 | Brassica_ra | 0.69 | Brassica_ra |
| Os02t0320300-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os01t0926200-01 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |
| Os06t0530600-00 | 0.69 | no_hit | 0.69 | no_hit | 0.69 | no_hit |

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|---|---|---|---|
| Os06t0662200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0330300-01 | 0.64 Dioscorea_ | 0.64 Dioscorea_ | 0.69 Corchorus |
| Os01t0740600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os12t0183300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0708600-01Zm00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0757200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0684800-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0491000-01Zm00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0878700-02 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0713600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os03t0650800-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os11t0102900-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Zm00001eb158160_P00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0548100-02 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0644200-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0119300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0850000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os11t0126900-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |

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| Os06t0162600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0426800-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0194300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0490666-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0149500-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Zm00001eb061990_P00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os10t0136500-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0446000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os07t0471300-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os11t0639600-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os08t0520850-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os12t0178633-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os06t0694400-01 | 0.57 Ananas_co | 0.67 Dioscorea_ | 0.69 Vitis_vinife |
| Os01t0859500-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0226600-02 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os08t0107400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |

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| Os07t0184900-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os08t0442400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0730400-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os08t0364900-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0299300-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os02t0661000-00 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os01t0967900-02 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0459000-01 | 0.69 no_hit | 0.69 no_hit | 0.69 no_hit |
| Os05t0406000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0178900-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Zm00001eb061520_P00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0688200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0184000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0656000-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0448700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os04t0563801-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0545300-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0164000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0209800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os08t0492100-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os09t0454300-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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|---|---|---|---|
| Os01t0171000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0271600-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0552500-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0172200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0687300-01Zm00 | 0.55 Ananas_co | 0.66 Dioscorea_ | 0.68 Vitis_vinife |
| Os01t0935000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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|---|---|---|---|
| Os04t0320100-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0701500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0187200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0962200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0148800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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|---|---|---|---|
| Os12t0122000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os12t0540800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0110600-01Zm00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os04t0608300-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0152000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0558500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0132500-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0698200-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0176000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Zm00001eb179280_P00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0125900-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0104500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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| Os10t0405500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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| Os01t0104500-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0324400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0283200-01 | 0.49 | Ananas_co | 0.68 | Prunus_pe | 0.68 | Prunus_pe |
| Os05t0589700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0822400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os06t0226700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0960300-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0448600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0324600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0853800-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0671400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0292000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0193600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Zm00001eb247540_P00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0414700-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0222000-01Zm00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0676600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os06t0238000-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0539900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Zm00001eb306020_P00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0695900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os09t0499400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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| Os02t0754500-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0534000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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| Os06t0697600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0696000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0168500-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0831700-01 | 0.58 | Ananas_co | 0.66 | Dioscorea_ | 0.68 | Vitis_vinife |
| Os03t0720800-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os12t0194600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Zm00001eb311430_P00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0476000-01Zm00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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| Os09t0466400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os11t0643800-01Zm00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os10t0520100-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0607000-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0287800-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0704300-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Zm00001eb209620_P00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0143600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0323000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os09t0332100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0407900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os06t0215100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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|---|---|---|---|---|---|---|
| Os04t0462900-02 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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|---|---|---|---|---|---|---|
| Os03t0758100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0539100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os06t0293500-01 | 0.68 | Theobroma | 0.68 | Theobroma | 0.68 | Theobroma |
| Os01t0303100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0157800-01 | 0.62 | Ananas_co | 0.67 | Dioscorea_ | 0.68 | Theobroma |
| Os02t0602500-02 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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|---|---|---|---|
| Os01t0144300-01 | 0.58 Ananas_co | 0.66 Dioscorea_ | 0.68 Amborella |
| Os06t0249350-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Zm00001eb083520_P00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0150600-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0567900-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0631000-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0361700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0308900-01 | 0.60 Ananas_co | 0.68 Corchorus | 0.68 Corchorus |
| Os01t0588000-01Zm00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0577100-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0432600-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0644100-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os10t0368902-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0687200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0820500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0612300-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0101100-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0132200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os04t0625800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0463401-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0851500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0285300-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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| Os07t0556300-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0646400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0147700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0753150-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0841600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0530300-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0102500-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0495900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0649100-03 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0148900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0874700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0414300-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0451700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0103900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os10t0535800-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0121000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0223900-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os10t0548100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0623200-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0777100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0606050-00 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0736700-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0702100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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|---|---|---|---|
| Os01t0104400-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0510200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0526800-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os04t0614650-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os03t0591600-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0867600-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os11t0593700-01Zm00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0473401-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os12t0479100-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os10t0363100-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0345700-01Zm00 | 0.68 Capsicum_ | 0.68 Capsicum_ | 0.68 Capsicum_ |
| Os03t0267600-01 | 0.55 Ananas_co | 0.62 Dioscorea_ | 0.68 Vitis_vinife |
| Os01t0329800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os12t0465700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0755100-01 | 0.57 Ananas_co | 0.66 Dioscorea_ | 0.68 Prunus_pe |
| Os01t0846450-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0184800-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os10t0481200-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0863400-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0844500-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |

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|---|---|---|---|---|---|---|
| Os03t0430000-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os04t0613800-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os07t0636200-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os03t0836200-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0214400-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os05t0355900-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os02t0552100-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0835600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os08t0433600-01 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |
| Os01t0645400-02 | 0.68 | no_hit | 0.68 | no_hit | 0.68 | no_hit |

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|---|---|---|---|
| Os02t0532500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os09t0456700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os04t0559000-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os10t0563500-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0683900-01 | 0.60 Ananas_co | 0.63 Dioscorea_ | 0.68 Corchorus_ |
| Zm00001eb156640_P00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os06t0115700-02 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os05t0572900-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0664400-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os01t0977100-00 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os07t0688200-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0727700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0766700-01 | 0.68 no_hit | 0.68 no_hit | 0.68 no_hit |
| Os02t0125200-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os05t0421900-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0742000-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0670100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0312100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os03t0260000-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os09t0547300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0962100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0667300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0106400-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |

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|---|---|---|---|---|---|---|
| Os10t0496000-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0286351-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0118300-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0621400-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0626100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0581366-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0179800-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0825700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0379300-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0500700-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0107700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0658700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0643700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0168600-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0565200-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0973000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os12t0274200-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0703300-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0710100-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Zm00001eb000400_P00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0489500-01 | 0.64 | Musa_acur | 0.67 | Prunus_du | 0.67 | Prunus_du |
| Os03t0304100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os10t0518100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0258200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0594600-00 | 0.67 | Solanum_t | 0.67 | Solanum_t | 0.67 | Solanum_t |

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|---|---|---|---|---|---|---|
| Os03t0811800-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0627400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os10t0492900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Zm00001eb015850_P00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0675100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0752800-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0663200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0423000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0149100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0187800-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0648266-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0216500-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0359700-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0346900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |

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| Os02t0658200-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os08t0103000-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os09t0491708-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |

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|---|---|---|---|
| Os11t0102100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0397700-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0523300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0205900-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0437600-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os08t0447300-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os11t0113300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os12t0228350-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os03t0819700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0233900-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0122900-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Zm00001eb372360_P00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0550700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0168600-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0537100-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0117200-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0562300-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0151100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os12t0586300-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0434700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os03t0802700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0704800-00Zm00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0160600-00Zm00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Zm00001eb207400_P00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |

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|---|---|---|---|---|---|---|
| Os06t0717200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0667300-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0158600-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0812000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0770400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0761500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0829600-01 | 0.67 | Corchorus. | 0.67 | Corchorus. | 0.67 | Corchorus. |
| Os03t0188900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0507000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Zm00001eb016770_P00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |

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| Os01t0925000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0896200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0551900-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Zm00001eb064040_P00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0759700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0188200-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0160400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0896300-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0270500-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0573500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0569550-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0619500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0411300-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0581500-01Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Zm00001eb432460_P00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0139500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os11t0506800-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0305800-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os08t0538200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0519100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0186000-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os03t0836300-01 | 0.54 | Ananas_co | 0.67 | Corchorus. | 0.67 | Corchorus. |
| Os08t0521600-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os10t0524600-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0558900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os04t0602400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0204100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0133200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0909400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os08t0438600-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0297800-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |

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| Os04t0555700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Zm00001eb361310_P00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0611100-01Zm00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0463800-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0776400-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os04t0228100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0404300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os10t0496900-02 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os11t0575900-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os12t0623500-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0619800-02 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os01t0786500-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os03t0664600-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os05t0139100-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os08t0120000-05 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |

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|---|---|---|---|---|---|---|
| Os12t0194900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
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| Os01t0224000-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0291700-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0273700-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
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| Os03t0582400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0664400-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| | | | | | | |
| Os01t0312500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0293900-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0572000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os08t0130100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0326850-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0656100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0499301-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0228800-01 | 0.54 | Ananas_co | 0.64 | Dioscorea_ | 0.67 | Prunus_du |
| Os08t0430000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os04t0448000-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os04t0448200-01 | 0.51 | Ananas_co | 0.67 | Daucus_ca | 0.67 | Daucus_ca |
| Os11t0526200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0814900-00Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os08t0384100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| | | | | | | |
| Os12t0472500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0115900-01 | 0.53 | Ananas_co | 0.67 | Cynara_car | 0.67 | Cynara_car |
| Os12t0528000-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0639800-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |

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|---|---|---|---|---|---|---|
| Os09t0116800-00Zm00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0738200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os09t0516200-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os02t0821800-02 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os07t0586600-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os06t0204800-00 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os01t0765500-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |
| Os05t0534100-01 | 0.67 | no_hit | 0.67 | no_hit | 0.67 | no_hit |

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|---|---|---|---|
| Os01t0622300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os03t0798400-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0589000-01Zm00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os08t0521400-03 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0773300-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0242700-00Zm00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os02t0725500-00 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os07t0540366-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os08t0531700-01 | 0.67 no_hit | 0.67 no_hit | 0.67 no_hit |
| Os06t0487900-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0517400-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0594700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0442900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb346560_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb070490_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os01t0957800-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0381000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb024900_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb406800_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0562200-02 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os11t0107000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0542200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0783700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0661700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0656500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0908600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0259900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0667600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0746700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0667100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0530600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os05t0494900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0554100-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0426500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0548800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0412700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os04t0465700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb312330_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os01t0611000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0553500-00Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0277400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0142500-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0672800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os12t0589000-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0497100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0655400-01 | 0.59 Musa_acur | 0.66 Vitis_vinife | 0.66 Vitis_vinife |
| Os04t0506000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0816400-01 | 0.56 Ananas_co | 0.64 Dioscorea_ | 0.66 Pistacia_ve |
| Zm00001eb156230_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0145500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os07t0680400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os01t0922600-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os12t0165900-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0778700-01 | 0.58 Ananas_co | 0.66 Populus_tr | 0.66 Populus_tr |
| Os02t0832150-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0654900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0510700-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0550800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os07t0182900-02 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0595500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0410500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0549600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0238900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0580400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0183800-00Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0460050-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb423130_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0821900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0728500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0103300-01 | 0.36 Ananas_co | 0.66 Phaseolus_ | 0.66 Phaseolus_ |
| Os12t0123800-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0523100-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0634000-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0499900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0708000-01 | 0.66 Ananas_co | 0.66 Gossypium | 0.66 Gossypium |
| Os08t0414200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0464400-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0226900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0270700-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os03t0268200-02 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0526800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0225900-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0431300-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0472700-00 | 0.51 Ananas_co | 0.62 Dioscorea_ | 0.66 Camelina_ |
| Os06t0116500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os11t0247500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0759000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0149900-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0141100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0525800-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0353500-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0518100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0296000-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os11t0592600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0270300-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os11t0278300-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0198300-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0463900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0566800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0147133-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0285700-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0565000-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0335200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0321700-01 | 0.65 Musa_acur | 0.66 Medicago_ | 0.66 Medicago_ |

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|---|---|---|---|---|---|---|
| Os03t0215400-01Zm00 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os01t0218100-01Zm00 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os08t0499000-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os07t0118900-01Zm00 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os01t0144500-00 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os02t0505400-02 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os04t0676700-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os02t0307200-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os01t0709500-03 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os10t0513900-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os03t0298700-01 | 0.61 | Ananas_co | 0.66 | Glycine_ma | 0.66 | Glycine_ma |
| Os01t0351800-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os11t0661200-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os01t0621700-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |
| Os03t0334200-01 | 0.66 | no_hit | 0.66 | no_hit | 0.66 | no_hit |

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|---|---|---|---|
| Zm00001eb218120_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0365200-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0725300-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0199500-01 | 0.65 Musa_acur | 0.66 Phaseolus_ | 0.66 Phaseolus_ |
| Os09t0518200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0367900-02 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0582100-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0675200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb185100_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0753300-00Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0395300-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os06t0275900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0493000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0657400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0722400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os12t0529900-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0349500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0109900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os05t0131000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os03t0675300-01 | 0.43 Ananas_co | 0.66 Vitis_vinife | 0.66 Vitis_vinife |
| Os01t0705700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0817100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0611700-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0167400-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0786900-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb082690_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os04t0675600-01 | 0.25 Ananas_co | 0.49 Dioscorea_ | 0.66 Gossypium |
| Os07t0176600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0463900-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0558600-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0753200-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os08t0496800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0656200-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os12t0530000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os03t0802800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0710500-01Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0677000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0517200-00Zm00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0954500-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0191600-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0684100-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0532900-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0486700-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Zm00001eb369440_P00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os02t0628800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os09t0369500-01 | 0.46 Ananas_co | 0.66 Pistacia_ve | 0.66 Pistacia_ve |
| Os03t0364000-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |

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|---|---|---|---|
| Os04t0569100-02 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os07t0438800-01 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os10t0406900-00 | 0.66 no_hit | 0.66 no_hit | 0.66 no_hit |
| Os01t0812050-00 | 0.61 Ananas_co | 0.66 Theobroma | 0.66 Theobroma |
| Os07t0602200-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0930500-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0727500-02 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os04t0681900-02 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os09t0307800-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Zm00001eb171770_P00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os10t0481450-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os10t0553900-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os06t0145800-00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os11t0587300-00Zm00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os10t0577400-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |

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|---|---|---|---|---|---|---|
| Os11t0639000-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0166800-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os08t0404500-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0106500-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os12t0236500-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0627300-00 | 0.63 | Ananas_co | 0.65 | Beta_vulga | 0.65 | Beta_vulga |
| Os01t0621300-01 | 0.59 | Ananas_co | 0.64 | Dioscorea_ | 0.65 | Actinidia_c |
| Os06t0278000-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os07t0646100-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os06t0498000-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0804900-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0161400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0728700-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0747400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os05t0385400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os09t0491596-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os09t0507200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os08t0366200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0831300-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os06t0283200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os07t0522600-02 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0176100-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |

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|---|---|---|---|---|---|---|
| Os07t0634300-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Zm00001eb311160_P00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os01t0733500-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0649900-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os08t0193900-01Zm00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0208400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os08t0369000-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os07t0516400-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os12t0133900-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0487200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os01t0172300-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Zm00001eb297250_P00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0844850-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os06t0679400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os01t0733200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os07t0588300-00 | 0.50 | Ananas_co | 0.65 | Actinidia_c | 0.65 | Actinidia_c |
| Os05t0440000-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os04t0252200-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os01t0955700-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0122600-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os08t0226400-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os10t0552400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Zm00001eb397390_P00 | 0.52 | Ananas_co | 0.59 | Dioscorea_ | 0.65 | Citrus_cler |

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|---|---|---|---|
| Os01t0602200-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os04t0411200-00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0821800-01Zm00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os12t0267200-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os08t0504000-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os06t0561800-00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os09t0531200-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0739500-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os02t0215000-01Zm00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os05t0481400-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0819800-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os03t0809000-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0878300-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os01t0179300-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os03t0286800-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
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| Os07t0551400-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os03t0658800-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os03t0820700-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os06t0731700-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
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| Os02t0257300-00 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
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| Os04t0101400-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |
| Os05t0116700-01 | 0.54 Ananas_co | 0.61 Dioscorea_ | 0.65 Citrus_cler |
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| Os04t0442300-01 | 0.65 no_hit | 0.65 no_hit | 0.65 no_hit |

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| Os04t0665600-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os07t0247000-02 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os01t0908400-01Zm00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os03t0164800-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0467600-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
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| Os07t0252400-01 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os06t0666500-00 | 0.65 | no_hit | 0.65 | no_hit | 0.65 | no_hit |
| Os02t0752300-01 | 0.65 | Musa_acur | 0.65 | Brassica_na | 0.65 | Brassica_na |
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| Os05t0508500-01 | 0.64 | Dioscorea_ | 0.64 | Dioscorea_ | 0.65 | Corchorus_ |
| Os03t0756700-01 | 0.63 | Musa_acur | 0.64 | Dioscorea_ | 0.65 | Prunus_per |
| Os02t0469000-00 | 0.55 | Ananas_co | 0.65 | Lupinus_ar | 0.65 | Lupinus_ar |
| Os01t0720800-01Zm00 | 0.63 | Musa_acur | 0.65 | Capsicum_ | 0.65 | Capsicum_ |
| Os04t0208600-01 | 0.52 | Ananas_co | 0.65 | Corchorus_ | 0.65 | Corchorus_ |
| Os02t0121800-01 | 0.36 | Ananas_co | 0.64 | Gossypium | 0.64 | Gossypium |
| Os07t0595700-01 | 0.47 | Ananas_co | 0.64 | Theobroma | 0.64 | Theobroma |
| Os07t0472300-01 | 0.52 | Ananas_co | 0.60 | Dioscorea_ | 0.64 | Manihot_es |
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| Os06t0352900-01 | 0.59 | Musa_acur | 0.64 | Citrus_cler | 0.64 | Citrus_cler |
| Os07t0524000-01 | 0.61 | Musa_acur | 0.64 | Corchorus_ | 0.64 | Corchorus_ |
| Os04t0482600-01 | 0.64 | Gossypium | 0.64 | Gossypium | 0.64 | Gossypium |
| Os05t0551100-01 | 0.63 | Musa_acur | 0.64 | Coffea_car | 0.64 | Coffea_car |
| Os01t0572100-01Zm00 | 0.50 | Ananas_co | 0.64 | Ipomoea_t | 0.64 | Ipomoea_t |
| Os02t0178200-00Zm00 | 0.53 | Ananas_co | 0.64 | Corchorus_ | 0.64 | Corchorus_ |
| Os03t0174200-01 | 0.48 | Musa_acur | 0.54 | Dioscorea_ | 0.64 | Gossypium |
| Os01t0885300-01 | 0.54 | Ananas_co | 0.61 | Dioscorea_ | 0.64 | Prunus_avi |

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| Os02t0740500-01 | 0.41 Ananas_co | 0.64 Nymphaea | 0.64 Nymphaea |
| Os03t0770900-01 | 0.52 Ananas_co | 0.63 Coffea_car | 0.63 Coffea_car |
| Zm00001eb099990_P00 | 0.40 Ananas_co | 0.63 Populus_tr | 0.63 Populus_tr |
| Os04t0672200-01 | 0.47 Ananas_co | 0.50 Dioscorea_ | 0.63 Amborella_ |
| Os09t0549600-00 | 0.63 Glycine_m | 0.63 Glycine_m | 0.63 Glycine_m |
| Os08t0550600-01 | 0.57 Ananas_co | 0.62 Dioscorea_ | 0.63 Vitis_vinife |
| Os01t0721000-01Zm00 | 0.59 Musa_acu | 0.63 Populus_tr | 0.63 Populus_tr |
| Os03t0784600-01 | 0.52 Ananas_co | 0.63 Dioscorea_ | 0.63 Populus_tr |
| Os09t0476000-01 | 0.51 Ananas_co | 0.60 Dioscorea_ | 0.63 Vitis_vinife |
| Os05t0366300-01 | 0.44 Musa_acu | 0.54 Dioscorea_ | 0.63 Prunus_avi |
| Os07t0147800-00 | 0.50 Ananas_co | 0.62 Dioscorea_ | 0.63 Citrullus_l |

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| Os07t0603300-01 | 0.58 Musa_acu | 0.63 Theobrom | 0.63 Theobrom |
| Zm00001eb077540_P00 | 0.36 Ananas_co | 0.63 Manihot_e | 0.63 Manihot_e |
| Os09t0133800-01 | 0.55 Ananas_co | 0.58 Dioscorea_ | 0.63 Theobrom |
| Os05t0586400-01 | 0.57 Ananas_co | 0.63 Actinidia_c | 0.63 Actinidia_c |
| Os01t0600300-02 | 0.41 Ananas_co | 0.63 Vitis_vinife | 0.63 Vitis_vinife |

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| Os11t0116900-01Zm00 | 0.63 Glycine_m | 0.63 Glycine_m | 0.63 Glycine_m |
| Zm00001eb152060_P00 | 0.57 Ananas_co | 0.61 Dioscorea_ | 0.62 Pistacia_ve |
| Os03t0762900-01 | 0.57 Ananas_co | 0.58 Dioscorea_ | 0.62 Actinidia_c |

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| Os12t0160400-01 | 0.51 Ananas_co | 0.61 Dioscorea_ | 0.62 Vitis_vinife |
| Os07t0120400-01Zm00 | 0.62 Camelina_ | 0.62 Camelina_ | 0.62 Camelina_ |
| Os07t0250900-01 | 0.57 Ananas_co | 0.62 Cucumis_s | 0.62 Cucumis_s |
| Os02t0574500-01 | 0.58 Musa_acu | 0.61 Dioscorea_ | 0.62 Amborella_ |
| Os03t0387900-01 | 0.54 Ananas_co | 0.62 Vitis_vinife | 0.62 Vitis_vinife |
| Os01t0253200-00 | 0.44 Ananas_co | 0.62 Prunus_pe | 0.62 Prunus_pe |
| Os12t0605300-01 | 0.45 Ananas_co | 0.62 Beta_vulga | 0.62 Beta_vulga |
| Os06t0524300-01 | 0.44 Ananas_co | 0.56 Dioscorea_ | 0.62 Vitis_vinife |
| Os03t0800800-01 | 0.50 Ananas_co | 0.62 Pistacia_ve | 0.62 Pistacia_ve |
| Os09t0284300-01 | 0.61 Ananas_co | 0.62 Medicago_ | 0.62 Medicago_ |
| Zm00001eb364090_P00 | 0.56 Musa_acu | 0.62 Actinidia_c | 0.62 Actinidia_c |
| Os04t0357700-00 | 0.36 Ananas_co | 0.62 Malus_do | 0.62 Malus_do |
| Os03t0193225-01 | 0.59 Dioscorea_ | 0.59 Dioscorea_ | 0.61 Cannabis_ |

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| Os02t0606000-01 | 0.52 Ananas_co | 0.61 Vitis_vinife | 0.61 Vitis_vinife |

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| Os04t0463200-01 | 0.53 Ananas_co | 0.61 Gossypium | 0.61 Gossypium |
| Zm00001eb246290_P00 | 0.40 Ananas_co | 0.60 Dioscorea_ | 0.61 Vitis_vinife |
| Os09t0372900-02 | 0.61 Daucus_ca | 0.61 Daucus_ca | 0.61 Daucus_ca |

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| Os05t0558800-01 | 0.50 Musa_acur | 0.61 Nymphaea | 0.61 Nymphaea |
| Os04t0539100-01 | 0.50 Ananas_co | 0.61 Citrullus_la | 0.61 Citrullus_la |
| Os02t0305600-01 | 0.41 Ananas_co | 0.61 Actinidia_c | 0.61 Actinidia_c |
| Os10t0133166-00 | 0.59 Musa_acur | 0.61 Coffea_car | 0.61 Coffea_car |
| Os04t0655600-01 | 0.44 Ananas_co | 0.56 Dioscorea_ | 0.61 Prunus_avi |
| Os09t0481300-01 | 0.43 Ananas_co | 0.53 Dioscorea_ | 0.61 Manihot_e |
| Os09t0129800-00 | 0.61 Amborella_ | 0.61 Amborella_ | 0.61 Amborella_ |

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| Os06t0571800-02Zm00 | 0.59 Ananas_co | 0.61 Capsicum_ | 0.61 Capsicum_ |
| Os10t0550750-00 | 0.42 Ananas_co | 0.61 Vitis_vinife | 0.61 Vitis_vinife |
| Os02t0258300-01 | 0.40 Ananas_co | 0.54 Dioscorea_ | 0.61 Vitis_vinife |
| Os03t0180300-01 | 0.59 Ananas_co | 0.61 Vitis_vinife | 0.61 Vitis_vinife |

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| Os02t0591500-01 | 0.44 Ananas_co | 0.57 Dioscorea_ | 0.60 Populus_tr |

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| Os02t0537000-01 | 0.56 Musa_acur | 0.60 Rosa_chine | 0.60 Rosa_chine |

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| Os07t0109400-01 | 0.51 Ananas_co | 0.60 Vitis_vinife | 0.60 Vitis_vinife |
| Os06t0120200-01Zm00 | 0.45 Ananas_co | 0.60 Corchorus_ | 0.60 Corchorus_ |
| Os01t0726100-01 | 0.58 Ananas_co | 0.59 Dioscorea_ | 0.60 Actinidia_c |

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| Os03t0183500-01 | 0.58 Ananas_co | 0.60 Manihot_e | 0.60 Manihot_e |
| Os05t0350700-01 | 0.54 Dioscorea_ | 0.54 Dioscorea_ | 0.60 Actinidia_c |
| Os02t0572600-01 | 0.47 Ananas_co | 0.51 Dioscorea_ | 0.60 Actinidia_c |
| Os06t0470000-01 | 0.28 Ananas_co | 0.58 Dioscorea_ | 0.60 Lupinus_ar |

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| Os01t0820700-00 | 0.60 Musa_acur | 0.60 Solanum_t | 0.60 Solanum_t |
| Zm00001eb044090_P00 | 0.34 Ananas_co | 0.44 Dioscorea_ | 0.60 Brassica_n |
| Os01t0845100-01 | 0.37 Ananas_co | 0.49 Dioscorea_ | 0.60 Nicotiana_ |
| Os06t0472700-01Zm00 | 0.60 Arabidopsi | 0.60 Arabidopsi | 0.60 Arabidopsi |
| Os03t0249100-01 | 0.51 Musa_acur | 0.58 Dioscorea_ | 0.60 Brassica_n |
| Os04t0450900-01 | 0.32 Ananas_co | 0.41 Dioscorea_ | 0.60 Actinidia_c |
| Os03t0143700-01 | 0.51 Ananas_co | 0.55 Dioscorea_ | 0.60 Vitis_vinife |
| Os01t0823400-01 | 0.30 Ananas_co | 0.60 Vitis_vinife | 0.60 Vitis_vinife |
| Os02t0120000-01 | 0.52 Ananas_co | 0.57 Dioscorea_ | 0.60 Corchorus_ |

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| Os06t0193400-01 | 0.43 Ananas_co | 0.59 Citrus_cler | 0.59 Citrus_cler |
| Os12t0508200-01 | 0.52 Musa_acur | 0.57 Dioscorea_ | 0.59 Cynara_car |
| Os09t0438100-01 | 0.46 Ananas_co | 0.53 Dioscorea_ | 0.59 Olea_europ |
| Os06t0603300-00 | 0.54 Ananas_co | 0.59 Olea_europ | 0.59 Olea_europ |
| Zm00001eb330260_P00 | 0.48 Ananas_co | 0.59 Amborella_ | 0.59 Amborella_ |
| Os12t0612300-01 | 0.48 Ananas_co | 0.59 Ipomoea_t | 0.59 Ipomoea_t |
| Os12t0119700-01 | 0.41 Ananas_co | 0.45 Dioscorea_ | 0.59 Citrus_cler |
| Os08t0151000-00 | 0.46 Ananas_co | 0.51 Dioscorea_ | 0.59 Prunus_du |
| Zm00001eb028750_P00 | 0.48 Ananas_co | 0.59 Dioscorea_ | 0.59 Actinidia_c |
| Os01t0311700-01 | 0.49 Ananas_co | 0.59 Pistacia_ve | 0.59 Pistacia_ve |
| Os02t0657700-01 | 0.56 Ananas_co | 0.59 Ipomoea_t | 0.59 Ipomoea_t |
| Os05t0443700-01 | 0.51 Dioscorea_ | 0.51 Dioscorea_ | 0.59 Vitis_vinife |
| Os02t0653400-01Zm00 | 0.44 Musa_acur | 0.59 Ipomoea_t | 0.59 Ipomoea_t |
| Os06t0699600-01 | 0.49 Ananas_co | 0.59 Cucumis_s | 0.59 Cucumis_s |
| Os02t0700000-01 | 0.44 Ananas_co | 0.47 Dioscorea_ | 0.59 Vitis_vinife |
| Os03t0765100-01 | 0.44 Ananas_co | 0.50 Dioscorea_ | 0.59 Malus_dom |
| Os08t0529300-00Zm00 | 0.31 Ananas_co | 0.37 Dioscorea_ | 0.59 Citrus_cler |
| Os11t0649600-01 | 0.59 Cynara_car | 0.59 Cynara_car | 0.59 Cynara_car |
| Os08t0553400-00Zm00 | 0.41 Ananas_co | 0.59 Vitis_vinife | 0.59 Vitis_vinife |
| Os07t0674400-01 | 0.40 Ananas_co | 0.59 Cannabis_ | 0.59 Cannabis_ |
| Os04t0671800-01 | 0.41 Ananas_co | 0.57 Dioscorea_ | 0.59 Manihot_e |
| Os06t0105900-01 | 0.49 Musa_acur | 0.55 Dioscorea_ | 0.59 Pistacia_ve |
| Os05t0320500-00 | 0.57 Ananas_co | 0.59 Gossypiur | 0.59 Gossypiur |
| Os09t0488600-00 | 0.44 Ananas_co | 0.55 Dioscorea_ | 0.59 Actinidia_c |
| Os03t0257600-01 | 0.56 Ananas_co | 0.58 Cannabis_ | 0.58 Cannabis_ |

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| Os09t0505100-01 | 0.51 Musa_acur | 0.51 Dioscorea_ | 0.58 Prunus_avi |
| Os08t0532500-01 | 0.51 Ananas_co | 0.58 Manihot_e | 0.58 Manihot_e |

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| Os02t0642600-01 | 0.49 Musa_acur | 0.58 Theobrom | 0.58 Theobrom |
| Os01t0914000-01 | 0.52 Dioscorea_ | 0.52 Dioscorea_ | 0.58 Vitis_vinife |
| Os12t0576300-01 | 0.45 Musa_acur | 0.56 Dioscorea_ | 0.58 Pistacia_ve |

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| Os03t0300400-01 | 0.22 | Ananas_co | 0.39 | Dioscorea_ | 0.58 | Theobrom |
| Os10t0466000-01 | 0.52 | Ananas_co | 0.58 | Prunus_avi | 0.58 | Prunus_avi |
| Os02t0710102-01 | 0.40 | Ananas_co | 0.50 | Dioscorea_ | 0.58 | Vitis_vinife |
| Zm00001eb136860_P00 | 0.51 | Ananas_co | 0.56 | Dioscorea_ | 0.58 | Pistacia_ve |
| Os03t0392400-01 | 0.33 | Ananas_co | 0.58 | Ipomoea_t | 0.58 | Ipomoea_t |
| Os03t0211500-01 | 0.46 | Ananas_co | 0.55 | Dioscorea_ | 0.58 | Actinidia_c |

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| Os01t0726400-01 | 0.16 | Ananas_co | 0.31 | Dioscorea_ | 0.58 | Nymphaea |
| Os03t0283400-01 | 0.50 | Ananas_co | 0.58 | Gossypiu | 0.58 | Gossypiu |
| Os10t0489900-01 | 0.40 | Ananas_co | 0.58 | Actinidia_c | 0.58 | Actinidia_c |
| Os06t0207000-01 | 0.06 | Ananas_co | 0.14 | Dioscorea_ | 0.58 | Arabis_alp |
| Os09t0427125-00 | 0.33 | Ananas_co | 0.58 | Citrullus_l | 0.58 | Citrullus_l |
| Os12t0640500-01 | 0.41 | Ananas_co | 0.57 | Theobrom | 0.57 | Theobrom |
| Os06t0631300-01 | 0.54 | Musa_acu | 0.57 | Actinidia_c | 0.57 | Actinidia_c |

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| Os02t0663100-01 | 0.53 | Musa_acu | 0.57 | Vitis_vinife | 0.57 | Vitis_vinife |
| Os03t0720400-01Zm00 | 0.53 | Musa_acu | 0.57 | Actinidia_c | 0.57 | Actinidia_c |
| Os02t0644500-01 | 0.51 | Musa_acu | 0.57 | Actinidia_c | 0.57 | Actinidia_c |
| Os08t0151700-01 | 0.47 | Ananas_co | 0.57 | Solanum_t | 0.57 | Solanum_t |
| Os01t0830200-01 | 0.37 | Ananas_co | 0.44 | Dioscorea_ | 0.57 | Amborella_ |
| Os06t0143500-00 | 0.24 | Ananas_co | 0.57 | Phaseolus_ | 0.57 | Phaseolus_ |

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| Os10t0577800-01 | 0.38 | Ananas_co | 0.46 | Dioscorea_ | 0.57 | Vitis_vinife |

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| Os01t0593200-01 | 0.52 | Ananas_co | 0.57 | Amborella_ | 0.57 | Amborella_ |
| Os03t0226700-01 | 0.49 | Musa_acu | 0.57 | Vitis_vinife | 0.57 | Vitis_vinife |

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| Os04t0648800-01 | 0.53 Musa_acur | 0.57 Manihot_es | 0.57 Manihot_es |
| Os02t0673500-01 | 0.46 Ananas_co | 0.55 Dioscorea_ | 0.57 Pistacia_ve |
| Os06t0710900-01 | 0.54 Musa_acur | 0.57 Amborella_ | 0.57 Amborella_ |
| Os06t0151100-00Zm00 | 0.23 Ananas_co | 0.57 Prunus_per | 0.57 Prunus_per |
| Os06t0606800-01 | 0.56 Ananas_co | 0.57 Populus_tr | 0.57 Populus_tr |
| Os03t0203000-01 | 0.46 Ananas_co | 0.53 Dioscorea_ | 0.57 Manihot_es |
| Os09t0460100-01 | 0.46 Ananas_co | 0.57 Corchorus_ | 0.57 Corchorus_ |
| Os05t0141500-01 | 0.47 Ananas_co | 0.55 Dioscorea_ | 0.57 Vitis_vinife |
| Os03t0567600-01 | 0.29 Ananas_co | 0.49 Dioscorea_ | 0.57 Actinidia_c |
| Os03t0139200-01 | 0.52 Ananas_co | 0.57 Vitis_vinife | 0.57 Vitis_vinife |
| Os01t0861700-00 | 0.49 Musa_acur | 0.52 Dioscorea_ | 0.56 Pistacia_ve |
| Os09t0309700-01 | 0.56 Rosa_chine | 0.56 Rosa_chine | 0.56 Rosa_chine |
| Os01t0783100-01 | 0.54 Ananas_co | 0.56 Dioscorea_ | 0.56 Citrullus_la |
| Os08t0117800-01 | 0.44 Musa_acur | 0.56 Dioscorea_ | 0.56 Cannabis_s |
| Os11t0170200-01 | 0.44 Ananas_co | 0.50 Dioscorea_ | 0.56 Corchorus_ |
| Os01t0706400-01 | 0.51 Ananas_co | 0.56 Pistacia_ve | 0.56 Pistacia_ve |
| Os01t0224500-01 | 0.32 Ananas_co | 0.43 Dioscorea_ | 0.56 Pistacia_ve |
| Os04t0221600-01 | 0.52 Ananas_co | 0.54 Dioscorea_ | 0.56 Gossypium |
| Zm00001eb248330_P00 | 0.56 Actinidia_c | 0.56 Actinidia_c | 0.56 Actinidia_c |
| Os07t0274300-00 | 0.45 Dioscorea_ | 0.45 Dioscorea_ | 0.56 Pistacia_ve |
| Os05t0466100-01 | 0.49 Musa_acur | 0.56 Solanum_tu | 0.56 Solanum_tu |
| Os05t0531400-01 | 0.37 Ananas_co | 0.54 Dioscorea_ | 0.56 Brassica_ra |
| Os01t0293100-01 | 0.46 Ananas_co | 0.56 Vitis_vinife | 0.56 Vitis_vinife |
| Os03t0651300-01 | 0.52 Musa_acur | 0.56 Prunus_du | 0.56 Prunus_du |
| Os03t0186500-01 | 0.37 Ananas_co | 0.49 Dioscorea_ | 0.56 Citrus_cler |
| Os01t0335700-01 | 0.56 Coffea_car | 0.56 Coffea_car | 0.56 Coffea_car |
| Os03t0728900-00 | 0.46 Ananas_co | 0.54 Dioscorea_ | 0.56 Cannabis_s |
| Os03t0638900-01 | 0.35 Musa_acur | 0.49 Dioscorea_ | 0.56 Actinidia_c |
| Os02t0534700-00 | 0.49 Musa_acur | 0.56 Malus_dom | 0.56 Malus_dom |

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| Os03t0183100-01 | 0.51 Ananas_co | 0.56 Prunus_du | 0.56 Prunus_du |
| Os07t0556000-01 | 0.49 Musa_acur | 0.49 Dioscorea_ | 0.56 Vitis_vinife |

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| Os07t0616000-01 | 0.43 Ananas_co | 0.56 Pistacia_ve | 0.56 Pistacia_ve |

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| Os02t0329800-01 | 0.25 Ananas_co | 0.53 Dioscorea_ | 0.56 Actinidia_c |
| Os11t0229400-01Zm00 | 0.45 Ananas_co | 0.56 Prunus_avi | 0.56 Prunus_avi |
| Os07t0586700-01 | 0.47 Ananas_co | 0.55 Dioscorea_ | 0.56 Cucumis_s |
| Os07t0568900-01 | 0.37 Ananas_co | 0.42 Dioscorea_ | 0.56 Prunus_du |
| Os03t0734100-01Zm00 | 0.54 Ananas_co | 0.56 Vitis_vinife | 0.56 Vitis_vinife |
| Os09t0401900-01 | 0.52 Musa_acur | 0.55 Dioscorea_ | 0.56 Prunus_du |
| Os03t0105800-01 | 0.34 Ananas_co | 0.56 Vitis_vinife | 0.56 Vitis_vinife |
| Os10t0437900-00 | 0.49 Dioscorea_ | 0.49 Dioscorea_ | 0.56 Vitis_vinife |
| Os02t0538900-01 | 0.30 Ananas_co | 0.54 Dioscorea_ | 0.56 Pistacia_ve |
| Os11t0162000-01 | 0.49 Ananas_co | 0.55 Pistacia_ve | 0.55 Pistacia_ve |
| Os02t0697200-01 | 0.46 Ananas_co | 0.55 Malus_don | 0.55 Malus_don |
| Os07t0656300-00 | 0.55 Citrus_cler | 0.55 Citrus_cler | 0.55 Citrus_cler |
| Os06t0702800-01 | 0.38 Ananas_co | 0.50 Dioscorea_ | 0.55 Populus_tr |

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| Os06t0622700-01 | 0.40 Ananas_co | 0.55 Corchorus_ | 0.55 Corchorus_ |
| Os04t0504200-01 | 0.48 Ananas_co | 0.51 Dioscorea_ | 0.55 Ipomoea_t |
| Os01t0246500-01 | 0.37 Ananas_co | 0.53 Dioscorea_ | 0.55 Vitis_vinife |
| Os09t0363500-01 | 0.44 Ananas_co | 0.44 Dioscorea_ | 0.55 Actinidia_c |

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| Os05t0478700-00 | 0.55 Theobrom | 0.55 Theobrom | 0.55 Theobrom |
| Os04t0379600-01 | 0.55 Daucus_ca | 0.55 Daucus_ca | 0.55 Daucus_ca |
| Os01t0725900-01 | 0.37 Ananas_co | 0.52 Dioscorea_ | 0.55 Amborella_ |
| Os02t0572300-00 | 0.54 Ananas_co | 0.55 Dioscorea_ | 0.55 Manihot_e |
| Os11t0269500-00 | 0.52 Musa_acur | 0.55 Gossypiu | 0.55 Gossypiu |
| Os06t0683950-01 | 0.46 Ananas_co | 0.55 Lupinus_a | 0.55 Lupinus_a |
| Zm00001eb079340_P00 | 0.30 Ananas_co | 0.51 Dioscorea_ | 0.55 Vitis_vinife |
| Os07t0106100-01 | 0.46 Ananas_co | 0.54 Dioscorea_ | 0.55 Rosa_chine |
| Os01t0736500-01 | 0.30 Musa_acur | 0.35 Dioscorea_ | 0.55 Coffea_car |

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| Os02t0330200-01 | 0.26 Ananas_co | 0.47 Dioscorea_ | 0.55 Actinidia_c |
| Os01t0935300-02 | 0.55 Coffea_car | 0.55 Coffea_car | 0.55 Coffea_car |

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| Os12t0116700-01 | 0.54 Musa_acur | 0.55 Theobrom | 0.55 Theobrom |
| Os03t0279500-00 | 0.54 Musa_acur | 0.55 Pistacia_ve | 0.55 Pistacia_ve |
| Os01t0631800-01 | 0.55 Rosa_chine | 0.55 Rosa_chine | 0.55 Rosa_chine |

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| Os05t0560200-00 | 0.38 Ananas_co | 0.48 Dioscorea_ | 0.55 Vitis_vinife |
| Os01t0182400-01Zm00 | 0.41 Ananas_co | 0.53 Dioscorea_ | 0.55 Corchorus_ |
| Os03t0312100-00 | 0.55 Ananas_co | 0.55 Daucus_ca | 0.55 Daucus_ca |
| Os02t0833500-01 | 0.44 Ananas_co | 0.50 Dioscorea_ | 0.55 Vitis_vinife |
| Os01t0955600-00Zm00 | 0.34 Musa_acur | 0.55 Glycine_m | 0.55 Glycine_m |

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| Os05t0113500-04 | 0.45 Ananas_co | 0.55 Vitis_vinife | 0.55 Vitis_vinife |
| Os11t0246200-00 | 0.50 Musa_acur | 0.55 Brassica_n | 0.55 Brassica_n |
| Os02t0666900-00 | 0.46 Ananas_co | 0.55 Solanum_t | 0.55 Solanum_t |
| Os05t0584300-01 | 0.40 Ananas_co | 0.54 Dioscorea_ | 0.55 Ipomoea_t |
| Os08t0121800-01Zm00 | 0.55 Manihot_e | 0.55 Manihot_e | 0.55 Manihot_e |
| Os05t0509400-01 | 0.34 Ananas_co | 0.54 Beta_vulga | 0.54 Beta_vulga |
| Os12t0547600-02 | 0.50 Ananas_co | 0.54 Prunus_pe | 0.54 Prunus_pe |

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| Os08t0157600-01 | 0.41 Ananas_co | 0.53 Dioscorea_ | 0.54 Vitis_vinife |
| Os09t0491676-01 | 0.44 Ananas_co | 0.54 Vitis_vinife | 0.54 Vitis_vinife |
| Os05t0495100-01 | 0.44 Musa_acu | 0.54 Actinidia_ | 0.54 Actinidia_ |
| Os10t0414700-01 | 0.54 Manihot_e | 0.54 Manihot_e | 0.54 Manihot_e |

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| Os03t0168400-01 | 0.33 Ananas_co | 0.45 Dioscorea_ | 0.54 Actinidia_ |
| Os06t0130200-01 | 0.49 Ananas_co | 0.54 Corchorus | 0.54 Corchorus |
| Os03t0751600-01 | 0.42 Musa_acu | 0.54 Dioscorea_ | 0.54 Pistacia_ve |
| Os02t0614400-01 | 0.39 Ananas_co | 0.54 Olea_euro | 0.54 Olea_euro |
| Os01t0690200-00 | 0.52 Ananas_co | 0.54 Trifolium_ | 0.54 Trifolium_ |

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| Os05t0140100-01 | 0.53 Ananas_co | 0.54 Manihot_e | 0.54 Manihot_e |
| Os04t0626600-01 | 0.54 Vitis_vinife | 0.54 Vitis_vinife | 0.54 Vitis_vinife |
| Os01t0203800-01 | 0.44 Ananas_co | 0.51 Dioscorea_ | 0.54 Manihot_e |
| Os01t0819000-02 | 0.30 Ananas_co | 0.54 Manihot_e | 0.54 Manihot_e |
| Os02t0230000-01 | 0.46 Dioscorea_ | 0.46 Dioscorea_ | 0.54 Nicotiana_ |
| Os11t0491400-01 | 0.38 Ananas_co | 0.54 Populus_tr | 0.54 Populus_tr |
| Os05t0557500-01 | 0.40 Ananas_co | 0.48 Dioscorea_ | 0.54 Theobrom |

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| Os03t0747100-00 | 0.47 Musa_acu | 0.53 Dioscorea_ | 0.54 Prunus_pe |
| Os08t0276200-01 | 0.30 Ananas_co | 0.35 Dioscorea_ | 0.54 Actinidia_ |
| Os10t0537600-01 | 0.53 Ananas_co | 0.54 Pistacia_ve | 0.54 Pistacia_ve |
| Os09t0499000-01 | 0.42 Musa_acu | 0.54 Malus_do | 0.54 Malus_do |
| Os03t0138500-01 | 0.49 Ananas_co | 0.54 Manihot_e | 0.54 Manihot_e |
| Os10t0414800-01 | 0.38 Ananas_co | 0.49 Dioscorea_ | 0.54 Pistacia_ve |
| Os09t0422000-01Zm00 | 0.37 Ananas_co | 0.46 Dioscorea_ | 0.54 Prunus_du |
| Os04t0599300-01Zm00 | 0.38 Ananas_co | 0.47 Dioscorea_ | 0.54 Amborella_ |
| Os02t0461000-01 | 0.47 Musa_acu | 0.54 Solanum_t | 0.54 Solanum_t |
| Os03t0240400-01 | 0.31 Ananas_co | 0.52 Dioscorea_ | 0.54 Prunus_pe |
| Os03t0705800-00 | 0.39 Musa_acu | 0.48 Dioscorea_ | 0.54 Nymphaea |
| Os06t0661766-00 | 0.42 Ananas_co | 0.51 Dioscorea_ | 0.54 Vitis_vinife |
| Os04t0618600-01 | 0.54 Ipomoea_t | 0.54 Ipomoea_t | 0.54 Ipomoea_t |
| Os05t0535900-01 | 0.39 Ananas_co | 0.44 Dioscorea_ | 0.54 Coffea_ca |
| Os05t0535500-01 | 0.49 Musa_acu | 0.54 Nymphaea | 0.54 Nymphaea |
| Os12t0588800-01 | 0.43 Ananas_co | 0.53 Pistacia_ve | 0.53 Pistacia_ve |
| Os08t0101000-01 | 0.51 Ananas_co | 0.53 Vitis_vinife | 0.53 Vitis_vinife |
| Os06t0707200-01Zm00 | 0.40 Ananas_co | 0.53 Pistacia_ve | 0.53 Pistacia_ve |
| Os02t0241200-00 | 0.40 Ananas_co | 0.42 Dioscorea_ | 0.53 Nymphaea |
| Os12t0158600-00 | 0.33 Ananas_co | 0.53 Cannabis_ | 0.53 Cannabis_ |
| Os08t0516900-01 | 0.37 Ananas_co | 0.53 Malus_do | 0.53 Malus_do |
| Os09t0456100-01 | 0.44 Musa_acu | 0.47 Dioscorea_ | 0.53 Vitis_vinife |
| Os09t0493400-01 | 0.37 Ananas_co | 0.51 Dioscorea_ | 0.53 Nymphaea |
| Os06t0225100-01 | 0.47 Ananas_co | 0.53 Nicotiana_ | 0.53 Nicotiana_ |

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| Os02t0138200-01 | 0.45 Musa_acur | 0.53 Vitis_vinife | 0.53 Vitis_vinife |
| Zm00001eb140390_P00 | 0.41 Ananas_co | 0.49 Dioscorea_ | 0.53 Vitis_vinife |
| Os04t0586000-00 | 0.44 Ananas_co | 0.53 Gossypiur | 0.53 Gossypiur |

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| Os05t0392400-01 | 0.44 Musa_acur | 0.53 Dioscorea_ | 0.53 Actinidia_c |
| Os10t0485500-01 | 0.51 Musa_acur | 0.53 Coffea_car | 0.53 Coffea_car |
| Os04t0557000-01 | 0.53 Cynara_car | 0.53 Cynara_car | 0.53 Cynara_car |
| Zm00001eb191940_P00 | 0.38 Ananas_co | 0.53 Cynara_car | 0.53 Cynara_car |
| Os03t0789200-01 | 0.53 Glycine_ma | 0.53 Glycine_ma | 0.53 Glycine_ma |
| Os04t0380200-01 | 0.53 Rosa_chine | 0.53 Rosa_chine | 0.53 Rosa_chine |

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| Os07t0583700-01 | 0.41 Ananas_co | 0.44 Dioscorea_ | 0.53 Vitis_vinife |
| Os05t0566900-01 | 0.44 Musa_acur | 0.53 Nicotiana_ | 0.53 Nicotiana_ |
| Os06t0244100-01 | 0.38 Ananas_co | 0.53 Pistacia_ve | 0.53 Pistacia_ve |
| Os11t0654800-01Zm00 | 0.51 Ananas_co | 0.53 Prunus_du | 0.53 Prunus_du |
| Os07t0481400-01 | 0.35 Ananas_co | 0.46 Dioscorea_ | 0.53 Vitis_vinife |
| Zm00001eb421370_P00 | 0.38 Ananas_co | 0.53 Vitis_vinife | 0.53 Vitis_vinife |
| Os01t0698100-01 | 0.39 Musa_acur | 0.51 Dioscorea_ | 0.53 Nymphaea |

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| Os01t0821600-01Zm00 | 0.52 Ananas_co | 0.53 Actinidia_c | 0.53 Actinidia_c |
| Os03t0747200-01 | 0.41 Ananas_co | 0.53 Pistacia_ve | 0.53 Pistacia_ve |
| Os02t0148000-01 | 0.44 Ananas_co | 0.53 Malus_don | 0.53 Malus_don |
| Os12t0592300-00Zm00 | 0.44 Ananas_co | 0.50 Dioscorea_ | 0.53 Populus_tr |
| Os01t0663800-01 | 0.45 Musa_acur | 0.53 Citrus_cler | 0.53 Citrus_cler |
| Os11t0424400-01 | 0.53 Beta_vulga | 0.53 Beta_vulga | 0.53 Beta_vulga |
| Os07t0176200-01 | 0.43 Ananas_co | 0.51 Dioscorea_ | 0.53 Theobrom |
| Os03t0184100-01 | 0.46 Ananas_co | 0.53 Glycine_ma | 0.53 Glycine_ma |
| Os01t0179000-01 | 0.21 Ananas_co | 0.49 Dioscorea_ | 0.53 Vitis_vinife |
| Os01t0875700-01 | 0.30 Ananas_co | 0.33 Dioscorea_ | 0.53 Amborella_ |

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| Os05t0154600-01 | 0.53 Pistacia_ve | 0.53 Pistacia_ve | 0.53 Pistacia_ve |
| Os08t0356500-01Zm00 | 0.40 Ananas_co | 0.52 Manihot_es | 0.52 Manihot_es |
| Os07t0419800-01 | 0.52 Dioscorea_ | 0.52 Dioscorea_ | 0.52 Nicotiana_ |
| Zm00001eb191410_P00 | 0.28 Ananas_co | 0.52 Amborella_ | 0.52 Amborella_ |
| Os01t0261100-01 | 0.38 Ananas_co | 0.52 Corchorus_ | 0.52 Corchorus_ |
| Os12t0159000-01 | 0.49 Ananas_co | 0.52 Trifolium_ | 0.52 Trifolium_ |

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| Os02t0822400-01 | 0.41 Ananas_co | 0.51 Dioscorea_ | 0.52 Vitis_vinife |
| Os11t0673000-00 | 0.52 Nymphaea | 0.52 Nymphaea | 0.52 Nymphaea |
| Os02t0735800-01 | 0.52 Nymphaea | 0.52 Nymphaea | 0.52 Nymphaea |

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| Os06t0689600-01 | 0.50 Ananas_co | 0.52 Camelina_ | 0.52 Camelina_ |
| Os03t0274700-01 | 0.47 Ananas_co | 0.50 Dioscorea_ | 0.52 Gossypiu |

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| Os07t0683900-01 | 0.52 Selaginella | 0.52 Selaginella | 0.52 Selaginella |
| Os12t0438400-01 | 0.52 Nymphaea | 0.52 Nymphaea | 0.52 Nymphaea |
| Os07t0414000-01 | 0.30 Musa_acur | 0.36 Dioscorea_ | 0.52 Prunus_du |

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| Os12t0572800-01 | 0.38 Ananas_co | 0.52 Theobrom | 0.52 Theobrom |

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| Os01t0852400-00 | 0.41 Ananas_co | 0.48 Dioscorea_ | 0.52 Manihot_e |
| Os01t0675500-01 | 0.39 Ananas_co | 0.50 Dioscorea_ | 0.52 Amborella_ |

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| Os10t0567000-01 | 0.42 Ananas_co | 0.43 Dioscorea_ | 0.52 Populus_tr |
| Os04t0433900-00 | 0.40 Ananas_co | 0.52 Actinidia_ | 0.52 Actinidia_ |
| Os03t0253500-00 | 0.40 Ananas_co | 0.52 Helianthus | 0.52 Helianthus |
| Os05t0492200-01 | 0.33 Musa_acur | 0.52 Vitis_vinife | 0.52 Vitis_vinife |
| Os01t0651500-00 | 0.43 Musa_acur | 0.52 Cannabis_ | 0.52 Cannabis_ |
| Os01t0235700-01 | 0.39 Ananas_co | 0.52 Vitis_vinife | 0.52 Vitis_vinife |
| Os11t0479100-00Zm00 | 0.37 Musa_acur | 0.37 Dioscorea_ | 0.52 Populus_tr |
| Os04t0111900-01Zm00 | 0.37 Ananas_co | 0.52 Vitis_vinife | 0.52 Vitis_vinife |
| Os04t0405700-00 | 0.48 Ananas_co | 0.49 Dioscorea_ | 0.52 Populus_tr |
| Os03t0578200-01 | 0.52 Medicago_ | 0.52 Medicago_ | 0.52 Medicago_ |
| Os06t0206100-01 | 0.42 Ananas_co | 0.52 Glycine_m | 0.52 Glycine_m |
| Os06t0648500-01 | 0.51 Dioscorea_ | 0.51 Dioscorea_ | 0.52 Malus_do |

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| Os07t0193200-00 | 0.25 Ananas_co | 0.52 Theobrom | 0.52 Theobrom |

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| Os01t0854500-01 | 0.29 Ananas_co | 0.52 Glycine_m | 0.52 Glycine_m |
| Os01t0541600-01 | 0.44 Ananas_co | 0.52 Prunus_avi | 0.52 Prunus_avi |
| Os05t0200700-01 | 0.38 Ananas_co | 0.48 Dioscorea_ | 0.52 Cannabis_ |
| Os05t0513300-00 | 0.43 Musa_acu | 0.52 Manihot_e | 0.52 Manihot_e |
| Os03t0707300-01 | 0.40 Musa_acu | 0.48 Dioscorea_ | 0.52 Manihot_e |
| Os05t0391600-01 | 0.43 Ananas_co | 0.48 Dioscorea_ | 0.52 Nymphaea |
| Zm00001eb019260_P00 | 0.44 Ananas_co | 0.48 Dioscorea_ | 0.52 Citrus_cle |

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| Os02t0152900-01 | 0.46 Dioscorea_ | 0.46 Dioscorea_ | 0.52 Arabidopsi |
| Os10t0556100-01Zm00 | 0.37 Ananas_co | 0.52 Actinidia_c | 0.52 Actinidia_c |
| Os01t0852500-01 | 0.37 Ananas_co | 0.52 Prunus_avi | 0.52 Prunus_avi |
| Zm00001eb410560_P00 | 0.50 Ananas_co | 0.52 Amborella_ | 0.52 Amborella_ |

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| Os11t0601700-01 | 0.41 Ananas_co | 0.48 Dioscorea_ | 0.52 Pistacia_ve |
| Os09t0570100-01 | 0.28 Ananas_co | 0.52 Manihot_e | 0.52 Manihot_e |
| Os06t0589500-01 | 0.39 Ananas_co | 0.52 Actinidia_c | 0.52 Actinidia_c |
| Zm00001eb350990_P00 | 0.48 Ananas_co | 0.52 Vitis_vinife | 0.52 Vitis_vinife |
| Os01t0195400-00 | 0.51 Musa_acu | 0.51 Glycine_m | 0.51 Glycine_m |
| Os05t0564000-00 | 0.35 Ananas_co | 0.51 Manihot_e | 0.51 Manihot_e |
| Os02t0617100-01 | 0.44 Ananas_co | 0.49 Dioscorea_ | 0.51 Vitis_vinife |
| Os04t0638100-01 | 0.37 Ananas_co | 0.42 Dioscorea_ | 0.51 Amborella_ |
| Os02t0705600-01 | 0.36 Ananas_co | 0.42 Dioscorea_ | 0.51 Manihot_e |
| Os03t0198300-01Zm00 | 0.43 Musa_acu | 0.51 Dioscorea_ | 0.51 Pistacia_ve |
| Os03t0371600-00 | 0.39 Ananas_co | 0.51 Cynara_ca | 0.51 Cynara_ca |
| Os03t0199500-01 | 0.51 Ipomoea_t | 0.51 Ipomoea_t | 0.51 Ipomoea_t |

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| Os04t0620200-01 | 0.47 Ananas_co | 0.51 Actinidia_c | 0.51 Actinidia_c |
| Os03t0138900-01 | 0.50 Ananas_co | 0.51 Actinidia_c | 0.51 Actinidia_c |
| Os03t0187100-00 | 0.45 Musa_acur | 0.48 Dioscorea_ | 0.51 Vitis_vinife |
| Os01t0107000-02 | 0.47 Musa_acur | 0.51 Actinidia_c | 0.51 Actinidia_c |
| Os02t0100200-01 | 0.32 Ananas_co | 0.51 Vitis_vinife | 0.51 Vitis_vinife |
| Os02t0671300-01 | 0.51 Ananas_co | 0.51 Glycine_ma | 0.51 Glycine_ma |
| Os03t0766500-01 | 0.51 Theobroma | 0.51 Theobroma | 0.51 Theobroma |
| Os04t0585700-01 | 0.51 Corchorus_ | 0.51 Corchorus_ | 0.51 Corchorus_ |

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| Os06t0659100-00 | 0.48 Musa_acur | 0.48 Dioscorea_ | 0.51 Arabidopsi |

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| Os03t0741400-01 | 0.43 Ananas_co | 0.49 Dioscorea_ | 0.51 Manihot_es |
| Os03t0741600-00 | 0.33 Ananas_co | 0.49 Dioscorea_ | 0.51 Nymphaea |
| Os02t0654600-00 | 0.46 Musa_acur | 0.48 Dioscorea_ | 0.51 Ipomoea_t |
| Os05t0120800-01 | 0.44 Musa_acur | 0.51 Actinidia_c | 0.51 Actinidia_c |
| Os03t0274300-01 | 0.44 Ananas_co | 0.48 Dioscorea_ | 0.51 Vitis_vinife |
| Os02t0175900-01 | 0.51 Theobroma | 0.51 Theobroma | 0.51 Theobroma |
| Os05t0569300-01 | 0.43 Ananas_co | 0.51 Gossypium | 0.51 Gossypium |
| Os09t0272000-01 | 0.48 Ananas_co | 0.51 Coffea_car | 0.51 Coffea_car |
| Os03t0799100-01 | 0.36 Ananas_co | 0.49 Dioscorea_ | 0.51 Prunus_per |
| Os01t0919500-01 | 0.37 Musa_acur | 0.51 Helianthus | 0.51 Helianthus |
| Os07t0112700-01 | 0.35 Musa_acur | 0.45 Dioscorea_ | 0.51 Cannabis_s |
| Os09t0416600-02 | 0.32 Musa_acur | 0.51 Manihot_es | 0.51 Manihot_es |

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| Os07t0498800-01 | 0.37 Ananas_co | 0.42 Dioscorea_ | 0.51 Populus_tr |
| Os07t0695400-01 | 0.39 Ananas_co | 0.50 Dioscorea_ | 0.51 Theobroma |
| Os03t0336000-01 | 0.33 Ananas_co | 0.51 Actinidia_c | 0.51 Actinidia_c |

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| Os05t0411600-01 | 0.46 Ananas_co | 0.51 Coffea_ca | 0.51 Coffea_ca |
| Os02t0798600-01 | 0.48 Ananas_co | 0.51 Prunus_pe | 0.51 Prunus_pe |
| Os09t0298700-01 | 0.42 Musa_acu | 0.51 Pistacia_ve | 0.51 Pistacia_ve |
| Os02t0221100-00Zm00 | 0.44 Musa_acu | 0.51 Prunus_pe | 0.51 Prunus_pe |
| Os03t0342100-01 | 0.39 Ananas_co | 0.51 Helianthus | 0.51 Helianthus |
| Os08t0167400-00 | 0.37 Ananas_co | 0.50 Dioscorea_ | 0.51 Theobrom |
| Os02t0132200-00 | 0.42 Musa_acu | 0.46 Dioscorea_ | 0.51 Vitis_vinife |
| Zm00001eb349390_P00 | 0.42 Musa_acu | 0.51 Vitis_vinife | 0.51 Vitis_vinife |
| Os01t0696000-02 | 0.47 Musa_acu | 0.51 Solanum_t | 0.51 Solanum_t |
| Os09t0509300-01 | 0.51 Citrullus_l | 0.51 Citrullus_l | 0.51 Citrullus_l |
| Os04t0580500-01 | 0.46 Musa_acu | 0.50 Dioscorea_ | 0.51 Capsicum_ |
| Os03t0224200-01 | 0.43 Ananas_co | 0.50 Dioscorea_ | 0.51 Vitis_vinife |
| Os09t0306650-01 | 0.35 Ananas_co | 0.51 Actinidia_c | 0.51 Actinidia_c |
| Zm00001eb404180_P00 | 0.49 Musa_acu | 0.51 Coffea_ca | 0.51 Coffea_ca |
| Os04t0650366-00Zm00 | 0.51 Coffea_ca | 0.51 Coffea_ca | 0.51 Coffea_ca |
| Os08t0105000-01 | 0.33 Musa_acu | 0.34 Dioscorea_ | 0.51 Theobrom |
| Os01t0306400-01 | 0.41 Ananas_co | 0.50 Vigna_ang | 0.50 Vigna_ang |
| Os01t0605650-01 | 0.36 Ananas_co | 0.50 Dioscorea_ | 0.50 Manihot_e |
| Os01t0830500-01 | 0.39 Musa_acu | 0.49 Dioscorea_ | 0.50 Actinidia_c |
| Os09t0493700-01 | 0.44 Musa_acu | 0.46 Dioscorea_ | 0.50 Gossypiu |
| Os03t0107400-01Zm00 | 0.22 Ananas_co | 0.50 Pistacia_ve | 0.50 Pistacia_ve |
| Os01t0647000-01 | 0.39 Musa_acu | 0.50 Coffea_ca | 0.50 Coffea_ca |
| Os07t0637200-01Zm00 | 0.37 Ananas_co | 0.48 Dioscorea_ | 0.50 Rosa_chine |
| Os03t0355700-00 | 0.37 Ananas_co | 0.50 Vitis_vinife | 0.50 Vitis_vinife |
| Os05t0299200-00 | 0.39 Ananas_co | 0.50 Brassica_n | 0.50 Brassica_n |

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| Os04t0541700-02 | 0.46 | Ananas_co | 0.50 | Manihot_e | 0.50 | Manihot_e |
| Os03t0768900-00 | 0.41 | Ananas_co | 0.50 | Manihot_e | 0.50 | Manihot_e |

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| Os02t0181300-01 | 0.37 | Ananas_co | 0.50 | Vigna_ang | 0.50 | Vigna_ang |
| Os09t0371700-01 | 0.45 | Musa_acur | 0.50 | Malus_don | 0.50 | Malus_don |
| Os02t0601800-01 | 0.46 | Ananas_co | 0.50 | Amborella_ | 0.50 | Amborella_ |
| Os07t0574100-00 | 0.18 | Ananas_co | 0.50 | Marchantia | 0.50 | Marchantia |
| Os04t0649200-01 | 0.40 | Ananas_co | 0.50 | Vitis_vinife | 0.50 | Vitis_vinife |

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| Os03t0741100-01 | 0.35 | Ananas_co | 0.50 | Amborella_ | 0.50 | Amborella_ |

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| Os01t0575200-01 | 0.43 | Ananas_co | 0.50 | Actinidia_c | 0.50 | Actinidia_c |
| Os05t0589200-01 | 0.45 | Musa_acur | 0.50 | Amborella_ | 0.50 | Amborella_ |
| Os05t0131900-01 | 0.41 | Musa_acur | 0.50 | Actinidia_c | 0.50 | Actinidia_c |
| Os03t0849800-01 | 0.34 | Ananas_co | 0.50 | Coffea_car | 0.50 | Coffea_car |
| Os09t0525400-01 | 0.45 | Musa_acur | 0.50 | Nymphaea | 0.50 | Nymphaea |

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| Os02t0244100-01 | 0.39 | Musa_acur | 0.46 | Dioscorea_ | 0.50 | Pistacia_ve |
| Os05t0581800-01 | 0.45 | Musa_acur | 0.50 | Vitis_vinife | 0.50 | Vitis_vinife |
| Zm00001eb353850_P00 | 0.48 | Ananas_co | 0.50 | Ipomoea_t | 0.50 | Ipomoea_t |
| Os01t0615200-01 | 0.08 | Ananas_co | 0.50 | Vitis_vinife | 0.50 | Vitis_vinife |
| Os01t0143800-01 | 0.47 | Musa_acur | 0.50 | Cucumis_s | 0.50 | Cucumis_s |

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| Os11t0157600-01 | 0.31 Ananas_co | 0.43 Dioscorea_ | 0.50 Nymphaea |
| Os07t0549100-01 | 0.33 Ananas_co | 0.50 Olea_europ | 0.50 Olea_europ |
| Os02t0454500-01 | 0.34 Ananas_co | 0.50 Malus_dom | 0.50 Malus_dom |
| Os09t0560000-01 | 0.39 Ananas_co | 0.43 Dioscorea_ | 0.50 Vitis_vinife |
| Os07t0673700-01 | 0.38 Musa_acur | 0.50 Medicago_ | 0.50 Medicago_ |
| Os04t0493300-01 | 0.36 Ananas_co | 0.50 Dioscorea_ | 0.50 Vitis_vinife |
| Os06t0157000-01 | 0.27 Ananas_co | 0.50 Coffea_car | 0.50 Coffea_car |
| Os04t0105200-01 | 0.40 Ananas_co | 0.50 Medicago_ | 0.50 Medicago_ |

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| Os01t0904700-01 | 0.33 Ananas_co | 0.50 Vitis_vinife | 0.50 Vitis_vinife |
| Os04t0412800-01 | 0.40 Ananas_co | 0.50 Malus_dom | 0.50 Malus_dom |
| Os01t0665300-02 | 0.48 Ananas_co | 0.50 Nicotiana_a | 0.50 Nicotiana_a |
| Os07t0631700-01 | 0.50 Manihot_es | 0.50 Manihot_es | 0.50 Manihot_es |
| Os05t0185800-01 | 0.37 Ananas_co | 0.45 Dioscorea_ | 0.50 Amborella_ |
| Os03t0160200-01 | 0.43 Ananas_co | 0.43 Dioscorea_ | 0.50 Helianthus |
| Os03t0123200-01 | 0.27 Ananas_co | 0.32 Dioscorea_ | 0.50 Marchantia |
| Os01t0744200-01 | 0.43 Musa_acur | 0.50 Actinidia_c | 0.50 Actinidia_c |
| Os05t0409000-01 | 0.44 Musa_acur | 0.50 Coffea_car | 0.50 Coffea_car |

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| Os03t0230300-01 | 0.37 Ananas_co | 0.50 Actinidia_c | 0.50 Actinidia_c |

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| Os02t0135500-02 | 0.32 Ananas_co | 0.50 Pistacia_ve | 0.50 Pistacia_ve |
| Os11t0158500-01 | 0.37 Ananas_co | 0.47 Dioscorea_ | 0.49 Vitis_vinife |
| Os06t0525200-00 | 0.49 Daucus_ca | 0.49 Daucus_ca | 0.49 Daucus_ca |

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| Os09t0392100-01 | 0.27 Ananas_co | 0.40 Dioscorea_ | 0.49 Theobroma |
| Os02t0527300-01Zm00 | 0.46 Ananas_co | 0.49 Amborella_ | 0.49 Amborella_ |
| Os04t0416700-01 | 0.46 Ananas_co | 0.48 Dioscorea_ | 0.49 Nicotiana_a |
| Os02t0831100-01 | 0.44 Ananas_co | 0.49 Dioscorea_ | 0.49 Nymphaea |
| Os04t0153000-00Zm00 | 0.47 Ananas_co | 0.49 Prunus_du | 0.49 Prunus_du |
| Os01t0566800-00 | 0.45 Ananas_co | 0.49 Citrullus_la | 0.49 Citrullus_la |
| Os02t0208600-01 | 0.40 Ananas_co | 0.49 Theobroma | 0.49 Theobroma |
| Zm00001eb191660_P00 | 0.41 Ananas_co | 0.45 Dioscorea_ | 0.49 Theobroma |
| Os05t0499600-01 | 0.36 Dioscorea_ | 0.36 Dioscorea_ | 0.49 Pistacia_ve |

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| Os08t0152500-01 | 0.33 Ananas_co | 0.42 Dioscorea_ | 0.49 Vitis_vinife |
| Os06t0156600-01 | 0.28 Ananas_co | 0.49 Citrus_cle | 0.49 Citrus_cle |
| Os01t0834100-01 | 0.41 Musa_acu | 0.49 Amborella | 0.49 Amborella |
| Os11t0634200-01 | 0.45 Musa_acu | 0.49 Dioscorea_ | 0.49 Helianthus |
| Os06t0507900-01 | 0.41 Ananas_co | 0.44 Dioscorea_ | 0.49 Vitis_vinife |
| Os04t0580300-01 | 0.39 Musa_acu | 0.49 Capsicum_ | 0.49 Capsicum_ |
| Os05t0360400-01 | 0.35 Ananas_co | 0.49 Camelina_ | 0.49 Camelina_ |
| Os08t0187700-01 | 0.39 Ananas_co | 0.44 Dioscorea_ | 0.49 Amborella |
| Os06t0618700-01 | 0.49 Nicotiana_ | 0.49 Nicotiana_ | 0.49 Nicotiana_ |
| Os02t0127600-00 | 0.27 Ananas_co | 0.49 Vitis_vinife | 0.49 Vitis_vinife |
| Os01t0167900-01 | 0.34 Ananas_co | 0.49 Pistacia_ve | 0.49 Pistacia_ve |

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| Os09t0474000-01 | 0.36 Ananas_co | 0.48 Dioscorea_ | 0.49 Actinidia_c |
| Os01t0918100-01 | 0.38 Ananas_co | 0.49 Citrullus_l | 0.49 Citrullus_l |

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| Os06t0707000-00 | 0.48 Ananas_co | 0.49 Pistacia_ve | 0.49 Pistacia_ve |
| Os06t0604600-01 | 0.36 Ananas_co | 0.49 Coffea_ca | 0.49 Coffea_ca |
| Os09t0504700-01 | 0.37 Ananas_co | 0.49 Vitis_vinife | 0.49 Vitis_vinife |
| Os05t0153300-00Zm00 | 0.33 Musa_acu | 0.49 Amborella | 0.49 Amborella |
| Os08t0561600-01 | 0.30 Ananas_co | 0.49 Pistacia_ve | 0.49 Pistacia_ve |
| Os09t0544700-00 | 0.39 Musa_acu | 0.49 Prunus_avi | 0.49 Prunus_avi |
| Os06t0284800-01 | 0.33 Ananas_co | 0.46 Dioscorea_ | 0.49 Populus_tr |
| Os09t0417500-01 | 0.49 Pistacia_ve | 0.49 Pistacia_ve | 0.49 Pistacia_ve |
| Os08t0536100-03 | 0.40 Ananas_co | 0.49 Vitis_vinife | 0.49 Vitis_vinife |
| Os03t0123800-01 | 0.23 Ananas_co | 0.49 Nicotiana_ | 0.49 Nicotiana_ |
| Os07t0124600-01 | 0.42 Ananas_co | 0.49 Nymphaea | 0.49 Nymphaea |
| Os01t0614500-01 | 0.43 Ananas_co | 0.49 Malus_do | 0.49 Malus_do |
| Os07t0123100-00 | 0.42 Ananas_co | 0.49 Helianthus | 0.49 Helianthus |

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| Os07t0568700-02 | 0.42 Musa_acu | 0.49 Cannabis_ | 0.49 Cannabis_ |
| Os03t0725100-01 | 0.40 Ananas_co | 0.48 Dioscorea_ | 0.49 Manihot_e |
| Os12t0169100-01 | 0.39 Ananas_co | 0.47 Dioscorea_ | 0.49 Vitis_vinife |
| Os02t0161200-01 | 0.35 Musa_acu | 0.49 Actinidia_c | 0.49 Actinidia_c |
| Os07t0647400-00 | 0.42 Musa_acu | 0.46 Dioscorea_ | 0.49 Cucumis_ |

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| Os04t0631600-01 | 0.45 | Musa_acu | 0.48 | Dioscorea_ | 0.49 | Vitis_vinife |
| Os06t0115200-01 | 0.29 | Ananas_co | 0.35 | Dioscorea_ | 0.49 | Manihot_e |
| Os01t0952800-01 | 0.43 | Ananas_co | 0.49 | Vitis_vinife | 0.49 | Vitis_vinife |
| Os11t0148700-01 | 0.37 | Ananas_co | 0.49 | Actinidia_c | 0.49 | Actinidia_c |
| Os02t0667600-03 | 0.38 | Ananas_co | 0.49 | Prunus_pe | 0.49 | Prunus_pe |
| Os04t0415200-01 | 0.29 | Ananas_co | 0.47 | Dioscorea_ | 0.49 | Daucus_ca |
| Os08t0515700-01 | 0.33 | Ananas_co | 0.46 | Dioscorea_ | 0.49 | Citrus_cle |
| Os03t0854800-03 | 0.28 | Ananas_co | 0.34 | Dioscorea_ | 0.49 | Capsicum_ |
| Os08t0224200-01 | 0.44 | Ananas_co | 0.49 | Prunus_pe | 0.49 | Prunus_pe |
| Os05t0488800-01 | 0.49 | Theobrom | 0.49 | Theobrom | 0.49 | Theobrom |
| Os02t0715300-01 | 0.31 | Ananas_co | 0.39 | Dioscorea_ | 0.49 | Cucumis_s |
| Os03t0253600-01 | 0.31 | Ananas_co | 0.49 | Cucumis_s | 0.49 | Cucumis_s |
| Os09t0511300-00 | 0.48 | Ananas_co | 0.48 | Pistacia_ve | 0.48 | Pistacia_ve |
| Os07t0588200-01 | 0.47 | Dioscorea_ | 0.47 | Dioscorea_ | 0.48 | Gossypiu |
| Zm00001eb199550_P00 | 0.39 | Ananas_co | 0.45 | Dioscorea_ | 0.48 | Pistacia_ve |
| Os04t0493100-01 | 0.34 | Ananas_co | 0.48 | Gossypiu | 0.48 | Gossypiu |
| Os12t0574800-02 | 0.40 | Ananas_co | 0.46 | Dioscorea_ | 0.48 | Rosa_chine |
| Os02t0661300-01 | 0.47 | Ananas_co | 0.48 | Rosa_chine | 0.48 | Rosa_chine |
| Os01t0676900-01 | 0.42 | Ananas_co | 0.47 | Dioscorea_ | 0.48 | Olea_euro |
| Os05t0101200-01 | 0.46 | Ananas_co | 0.47 | Dioscorea_ | 0.48 | Manihot_e |
| Os01t0727100-01 | 0.32 | Ananas_co | 0.44 | Dioscorea_ | 0.48 | Prunus_pe |
| Os03t0168300-01 | 0.45 | Musa_acu | 0.48 | Actinidia_c | 0.48 | Actinidia_c |
| Os07t0592300-01 | 0.39 | Musa_acu | 0.45 | Dioscorea_ | 0.48 | Vitis_vinife |

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| Os01t0259900-00 | 0.32 Ananas_co | 0.48 Vitis_vinife | 0.48 Vitis_vinife |
| Os06t0267600-01Zm00 | 0.28 Ananas_co | 0.42 Dioscorea_ | 0.48 Vitis_vinife |

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| Os07t0628500-01 | 0.37 Ananas_co | 0.48 Nymphaea | 0.48 Nymphaea |
| Os03t0825500-01 | 0.48 Cannabis_ | 0.48 Cannabis_ | 0.48 Cannabis_ |
| Os01t0301000-01 | 0.32 Ananas_co | 0.48 Dioscorea_ | 0.48 Malus_do |

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| Os02t0152500-01 | 0.35 Ananas_co | 0.35 Dioscorea_ | 0.48 Prunus_avi |
| Os03t0336700-01 | 0.42 Ananas_co | 0.48 Rosa_chine | 0.48 Rosa_chine |
| Os06t0356800-01 | 0.48 Solanum_t | 0.48 Solanum_t | 0.48 Solanum_t |
| Os02t0193300-01 | 0.46 Ananas_co | 0.48 Nicotiana_ | 0.48 Nicotiana_ |
| Os03t0264600-00 | 0.42 Ananas_co | 0.48 Cannabis_ | 0.48 Cannabis_ |
| Os10t0495000-01Zm00 | 0.39 Musa_acu | 0.42 Dioscorea_ | 0.48 Vitis_vinife |
| Os07t0631300-01 | 0.44 Ananas_co | 0.48 Daucus_ca | 0.48 Daucus_ca |
| Os06t0646400-01 | 0.45 Ananas_co | 0.47 Dioscorea_ | 0.48 Vitis_vinife |

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| Os11t0499600-01 | 0.24 Ananas_co | 0.48 Amborella_ | 0.48 Amborella_ |
| Os02t0709100-01 | 0.32 Musa_acu | 0.48 Amborella_ | 0.48 Amborella_ |
| Os02t0666600-01 | 0.36 Ananas_co | 0.47 Dioscorea_ | 0.48 Medicago_ |
| Os03t0838500-01 | 0.47 Musa_acu | 0.48 Manihot_e | 0.48 Manihot_e |
| Os01t0180300-01 | 0.34 Ananas_co | 0.44 Dioscorea_ | 0.48 Theobrom |
| Os03t0239400-01 | 0.48 Amborella_ | 0.48 Amborella_ | 0.48 Amborella_ |
| Os11t0195800-01 | 0.44 Dioscorea_ | 0.44 Dioscorea_ | 0.48 Theobrom |

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| Os08t0242800-01 | 0.46 Musa_acur | 0.48 Malus_don | 0.48 Malus_don |
| Os02t0647300-01Zm00 | 0.48 Citrus_cler | 0.48 Citrus_cler | 0.48 Citrus_cler |

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| Os03t0180800-01 | 0.44 Musa_acur | 0.48 Medicago_ | 0.48 Medicago_ |
| Zm00001eb012870_P00 | 0.31 Ananas_co | 0.48 Pistacia_ve | 0.48 Pistacia_ve |
| Os10t0469700-01 | 0.38 Ananas_co | 0.46 Dioscorea_ | 0.48 Theobrom |
| Os10t0476900-01 | 0.48 Gossypiur | 0.48 Gossypiur | 0.48 Gossypiur |

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| Os06t0693700-02 | 0.45 Dioscorea_ | 0.45 Dioscorea_ | 0.48 Prunus_du |
| Os12t0594300-00 | 0.42 Ananas_co | 0.45 Dioscorea_ | 0.48 Corchorus_ |
| Os04t0394300-01 | 0.39 Ananas_co | 0.48 Malus_don | 0.48 Malus_don |
| Os04t0683900-01 | 0.48 Populus_tr | 0.48 Populus_tr | 0.48 Populus_tr |
| Os04t0376400-01 | 0.39 Musa_acur | 0.40 Dioscorea_ | 0.48 Nymphaea |

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| Os07t0553400-01 | 0.48 Brassica_na | 0.48 Brassica_na | 0.48 Brassica_na |
| Os02t0168300-01 | 0.46 Ananas_co | 0.48 Vitis_vinife | 0.48 Vitis_vinife |
| Os04t0625900-01 | 0.43 Ananas_co | 0.48 Vitis_vinife | 0.48 Vitis_vinife |

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| Os11t0544700-01 | 0.31 Musa_acur | 0.37 Dioscorea_ | 0.48 Amborella_ |
| Os06t0550800-00 | 0.48 Malus_don | 0.48 Malus_don | 0.48 Malus_don |
| Os02t0815100-01 | 0.30 Ananas_co | 0.48 Nicotiana_ | 0.48 Nicotiana_ |
| Os09t0509400-01 | 0.39 Ananas_co | 0.46 Dioscorea_ | 0.48 Prunus_avi |
| Os02t0814600-01 | 0.34 Ananas_co | 0.48 Nymphaea | 0.48 Nymphaea |

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| Os07t0561300-01 | 0.41 | Musa_acur | 0.45 | Dioscorea_ | 0.48 | Rosa_chin |
| Os07t0419200-01 | 0.48 | Populus_tr | 0.48 | Populus_tr | 0.48 | Populus_tr |
| Os08t0520400-01 | 0.37 | Ananas_co | 0.48 | Coffea_car | 0.48 | Coffea_car |
| Os01t0118700-01 | 0.32 | Ananas_co | 0.48 | Pistacia_ve | 0.48 | Pistacia_ve |
| Os11t0206200-01 | 0.39 | Ananas_co | 0.47 | Dioscorea_ | 0.48 | Beta_vulga |
| Os02t0822000-01 | 0.31 | Musa_acur | 0.48 | Pistacia_ve | 0.48 | Pistacia_ve |
| Os01t0229500-01 | 0.44 | Dioscorea_ | 0.44 | Dioscorea_ | 0.48 | Amborella |
| Os03t0177000-01 | 0.37 | Ananas_co | 0.48 | Amborella | 0.48 | Amborella |
| Os09t0545000-01 | 0.41 | Ananas_co | 0.48 | Vitis_vinife | 0.48 | Vitis_vinife |
| Os11t0615100-01 | 0.32 | Ananas_co | 0.47 | Actinidia_ | 0.47 | Actinidia_ |
| Zm00001eb051330_P00 | 0.43 | Ananas_co | 0.46 | Dioscorea_ | 0.47 | Theobrom |
| Os07t0467500-01 | 0.43 | Musa_acur | 0.47 | Nymphaea | 0.47 | Nymphaea |
| Os05t0115100-02 | 0.42 | Ananas_co | 0.47 | Vitis_vinife | 0.47 | Vitis_vinife |
| Zm00001eb337940_P00 | 0.31 | Ananas_co | 0.43 | Dioscorea_ | 0.47 | Vitis_vinife |
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| Os02t0250400-03 | 0.22 | Ananas_co | 0.47 | Prunus_pe | 0.47 | Prunus_pe |
| Os09t0566100-01 | 0.35 | Ananas_co | 0.44 | Dioscorea_ | 0.47 | Rosa_chin |
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| Os08t0266700-01 | 0.31 | Ananas_co | 0.47 | Theobrom | 0.47 | Theobrom |
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| Os08t0536300-01 | 0.34 | Ananas_co | 0.47 | Ipomoea_t | 0.47 | Ipomoea_t |
| Os06t0531900-01 | 0.24 | Ananas_co | 0.47 | Dioscorea_ | 0.47 | Amborella |

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| Os09t0549450-00 | 0.44 Ananas_co | 0.45 Dioscorea_ | 0.47 Corchorus_ |
| Os11t0214400-01Zm00 | 0.19 Ananas_co | 0.47 Arabidopsi | 0.47 Arabidopsi |
| Os02t0659500-01 | 0.47 Rosa_chine | 0.47 Rosa_chine | 0.47 Rosa_chine |
| Os03t0680800-02 | 0.30 Ananas_co | 0.46 Dioscorea_ | 0.47 Pistacia_ve |
| Os07t0506600-01 | 0.36 Ananas_co | 0.44 Dioscorea_ | 0.47 Vitis_vinife |
| Os07t0588000-01 | 0.28 Musa_acur | 0.39 Dioscorea_ | 0.47 Ipomoea_t |
| Os04t0611200-01 | 0.33 Ananas_co | 0.46 Dioscorea_ | 0.47 Vitis_vinife |
| Os02t0208900-01 | 0.32 Ananas_co | 0.47 Dioscorea_ | 0.47 Theobroma |
| Os04t0687300-01 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.47 Corchorus_ |
| Os02t0593700-01 | 0.43 Dioscorea_ | 0.43 Dioscorea_ | 0.47 Coffea_car |
| Os05t0466200-01 | 0.30 Ananas_co | 0.47 Vitis_vinife | 0.47 Vitis_vinife |
| Os05t0209600-01 | 0.25 Ananas_co | 0.47 Ipomoea_t | 0.47 Ipomoea_t |
| Os04t0592400-01 | 0.37 Dioscorea_ | 0.37 Dioscorea_ | 0.47 Prunus_avi |
| Os01t0949060-01 | 0.34 Ananas_co | 0.44 Dioscorea_ | 0.47 Vitis_vinife |
| Os04t0166400-01 | 0.36 Ananas_co | 0.41 Dioscorea_ | 0.47 Theobroma |
| Os12t0624800-01 | 0.42 Dioscorea_ | 0.42 Dioscorea_ | 0.47 Corchorus_ |
| Os01t0641800-00 | 0.42 Ananas_co | 0.47 Brassica_na | 0.47 Brassica_na |

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| Os06t0544100-01 | 0.44 Ananas_co | 0.47 Cannabis_ | 0.47 Cannabis_ |
| Os06t0183100-01 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.47 Ipomoea_t |
| Os01t0229200-01 | 0.38 Ananas_co | 0.41 Dioscorea_ | 0.47 Gossypiu |
| Os01t0232200-00 | 0.44 Musa_acu | 0.47 Gossypiu | 0.47 Gossypiu |
| Os01t0246100-01 | 0.43 Musa_acu | 0.47 Nicotiana_ | 0.47 Nicotiana_ |
| Os04t0585900-01 | 0.47 Cucumis_ | 0.47 Cucumis_ | 0.47 Cucumis_ |
| Os06t0537600-01 | 0.44 Ananas_co | 0.47 Lupinus_a | 0.47 Lupinus_a |
| Zm00001eb239400_P00 | 0.42 Ananas_co | 0.47 Populus_tr | 0.47 Populus_tr |
| Os01t0261200-01 | 0.28 Ananas_co | 0.41 Dioscorea_ | 0.47 Nymphaea |
| Os03t0198600-01 | 0.35 Ananas_co | 0.47 Ipomoea_t | 0.47 Ipomoea_t |
| Os03t0708700-00 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.47 Amborella |
| Os01t0794100-01 | 0.47 Ipomoea_t | 0.47 Ipomoea_t | 0.47 Ipomoea_t |
| Os07t0587200-01Zm00 | 0.38 Musa_acu | 0.44 Dioscorea_ | 0.47 Gossypiu |
| Os12t0236700-01 | 0.40 Ananas_co | 0.47 Amborella | 0.47 Amborella |
| Os04t0571200-01 | 0.31 Musa_acu | 0.47 Nymphaea | 0.47 Nymphaea |
| Os02t0776700-01 | 0.37 Ananas_co | 0.43 Dioscorea_ | 0.47 Prunus_du |
| Os08t0412700-01Zm00 | 0.37 Ananas_co | 0.47 Vitis_vinife | 0.47 Vitis_vinife |
| Os03t0192300-00 | 0.43 Ananas_co | 0.47 Vitis_vinife | 0.47 Vitis_vinife |
| Os01t0862600-01 | 0.47 Actinidia_ | 0.47 Actinidia_ | 0.47 Actinidia_ |

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| Os07t0615200-01 | 0.43 Musa_acur | 0.47 Actinidia_c | 0.47 Actinidia_c |
| Os07t0686400-00 | 0.28 Ananas_co | 0.42 Dioscorea_ | 0.47 Prunus_per |
| Os06t0275700-01 | 0.47 Theobrom | 0.47 Theobrom | 0.47 Theobrom |

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| Os03t0833300-02 | 0.39 Ananas_co | 0.47 Manihot_e | 0.47 Manihot_e |
| Zm00001eb039600_P00 | 0.40 Musa_acur | 0.47 Vigna_ang | 0.47 Vigna_ang |
| Os03t0206900-01 | 0.44 Musa_acur | 0.47 Citrus_cler | 0.47 Citrus_cler |

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| Os06t0643000-01 | 0.36 Ananas_co | 0.47 Dioscorea_ | 0.47 Citrus_cler |
| Os01t0289100-00 | 0.38 Ananas_co | 0.47 Citrullus_la | 0.47 Citrullus_la |
| Os10t0155200-00 | 0.47 Nicotiana_ | 0.47 Nicotiana_ | 0.47 Nicotiana_ |
| Os03t0118900-01 | 0.26 Ananas_co | 0.37 Dioscorea_ | 0.47 Citrus_cler |
| Zm00001eb344230_P00 | 0.35 Ananas_co | 0.47 Populus_tr | 0.47 Populus_tr |
| Os07t0642600-01 | 0.41 Ananas_co | 0.47 Citrus_cler | 0.47 Citrus_cler |
| Os02t0248200-00Zm00 | 0.43 Ananas_co | 0.47 Arabidopsi | 0.47 Arabidopsi |
| Os05t0132400-01 | 0.12 Ananas_co | 0.20 Dioscorea_ | 0.47 Prunus_avi |
| Os03t0271600-01 | 0.45 Dioscorea_ | 0.45 Dioscorea_ | 0.47 Vitis_vinife |
| Os01t0679000-01 | 0.36 Ananas_co | 0.47 Vitis_vinife | 0.47 Vitis_vinife |

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| Os01t0914400-01 | 0.42 Ananas_co | 0.46 Prunus_avi | 0.46 Prunus_avi |
| Os03t0130700-01 | 0.34 Ananas_co | 0.44 Dioscorea_ | 0.46 Vitis_vinife |
| Os06t0671150-00 | 0.40 Ananas_co | 0.46 Coffea_car | 0.46 Coffea_car |
| Os07t0137900-01Zm00 | 0.36 Ananas_co | 0.46 Dioscorea_ | 0.46 Corchorus_ |
| Os07t0270800-00Zm00 | 0.39 Ananas_co | 0.43 Dioscorea_ | 0.46 Prunus_per |
| Os10t0438300-00 | 0.34 Ananas_co | 0.46 Dioscorea_ | 0.46 Prunus_du |

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|---|---|---|---|---|---|---|
| Os02t0682300-01 | 0.30 | Musa_acur | 0.38 | Dioscorea_ | 0.46 | Prunus_per |
| Os07t0525100-01 | 0.42 | Ananas_co | 0.46 | Vitis_vinife | 0.46 | Vitis_vinife |
| Os02t0703300-01 | 0.27 | Ananas_co | 0.42 | Dioscorea_ | 0.46 | Actinidia_c |
| Os09t0306400-01 | 0.45 | Ananas_co | 0.46 | Lupinus_ar | 0.46 | Lupinus_ar |
| Os09t0298500-01Zm00 | 0.39 | Ananas_co | 0.46 | Populus_tr | 0.46 | Populus_tr |
| Os04t0510500-01 | 0.42 | Musa_acur | 0.46 | Lupinus_ar | 0.46 | Lupinus_ar |
| Os02t0633100-02 | 0.33 | Ananas_co | 0.42 | Dioscorea_ | 0.46 | Vitis_vinife |
| Os02t0121900-01 | 0.32 | Musa_acur | 0.36 | Dioscorea_ | 0.46 | Vitis_vinife |
| Os04t0425100-01 | 0.44 | Ananas_co | 0.46 | Dioscorea_ | 0.46 | Citrullus_la |
| Os06t0595800-01 | 0.10 | Ananas_co | 0.44 | Dioscorea_ | 0.46 | Vitis_vinife |
| Os06t0594600-01 | 0.08 | Ananas_co | 0.40 | Dioscorea_ | 0.46 | Vitis_vinife |
| Os03t0665200-01 | 0.45 | Ananas_co | 0.46 | Dioscorea_ | 0.46 | Theobroma |
| Os06t0724200-01 | 0.43 | Musa_acur | 0.46 | Actinidia_c | 0.46 | Actinidia_c |
| Os12t0480200-01 | 0.34 | Ananas_co | 0.46 | Pistacia_ve | 0.46 | Pistacia_ve |
| Os04t0185100-01 | 0.26 | Ananas_co | 0.39 | Dioscorea_ | 0.46 | Ipomoea_t |
| Os04t0541900-00 | 0.35 | Ananas_co | 0.44 | Dioscorea_ | 0.46 | Vitis_vinife |
| Os04t0664400-02 | 0.35 | Ananas_co | 0.41 | Dioscorea_ | 0.46 | Cucumis_s |
| Os07t0185300-01 | 0.46 | Dioscorea_ | 0.46 | Dioscorea_ | 0.46 | Beta_vulga |
| Os04t0608400-01 | 0.30 | Ananas_co | 0.44 | Dioscorea_ | 0.46 | Corchorus_ |
| Os03t0233800-01 | 0.36 | Ananas_co | 0.46 | Dioscorea_ | 0.46 | Pistacia_ve |
| Os06t0531600-01 | 0.18 | Ananas_co | 0.46 | Prunus_per | 0.46 | Prunus_per |
| Os05t0488600-01 | 0.40 | Ananas_co | 0.46 | Theobroma | 0.46 | Theobroma |
| Os05t0559600-01 | 0.36 | Ananas_co | 0.46 | Amborella_ | 0.46 | Amborella_ |
| Os01t0939300-01 | 0.41 | Ananas_co | 0.46 | Actinidia_c | 0.46 | Actinidia_c |
| Os06t0298400-01 | 0.35 | Ananas_co | 0.46 | Malus_dom | 0.46 | Malus_dom |

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| Os01t0749300-01 | 0.32 | Ananas_co | 0.45 | Dioscorea_ | 0.46 | Actinidia_c |

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| Os09t0470500-01 | 0.37 | Musa_acum | 0.40 | Dioscorea_ | 0.46 | Pistacia_ve |
| Os09t0474100-01 | 0.42 | Ananas_co | 0.46 | Pistacia_ve | 0.46 | Pistacia_ve |
| Os01t0818100-00 | 0.40 | Ananas_co | 0.46 | Vitis_vinife | 0.46 | Vitis_vinife |

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| Os02t0762600-01 | 0.32 | Ananas_co | 0.43 | Dioscorea_ | 0.46 | Lupinus_an |
| Os03t0765500-00 | 0.43 | Dioscorea_ | 0.43 | Dioscorea_ | 0.46 | Olea_europ |
| Os04t0382800-00 | 0.43 | Dioscorea_ | 0.43 | Dioscorea_ | 0.46 | Pistacia_ve |

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| Os01t0193900-01 | 0.46 | Manihot_es | 0.46 | Manihot_es | 0.46 | Manihot_es |

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| Os02t0649300-01 | 0.44 | Ananas_co | 0.46 | Populus_tr | 0.46 | Populus_tr |
| Os02t0689500-01 | 0.43 | Ananas_co | 0.46 | Gossypium | 0.46 | Gossypium |
| Os07t0568500-01 | 0.30 | Ananas_co | 0.46 | Pistacia_ve | 0.46 | Pistacia_ve |

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| Os11t0615200-01Zm00 | 0.33 | Musa_acum | 0.46 | Pistacia_ve | 0.46 | Pistacia_ve |
| Os11t0120200-01 | 0.33 | Ananas_co | 0.41 | Dioscorea_ | 0.46 | Corchorus_ |
| Os12t0157700-00 | 0.46 | Cucumis_s | 0.46 | Cucumis_s | 0.46 | Cucumis_s |
| Os03t0370250-01 | 0.37 | Ananas_co | 0.46 | Coffea_car | 0.46 | Coffea_car |

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| Os02t0104800-01 | 0.36 Ananas_co | 0.46 Amborella | 0.46 Amborella |
| Os09t0439800-01 | 0.45 Ananas_co | 0.46 Manihot_e | 0.46 Manihot_e |
| Os01t0204000-01 | 0.30 Ananas_co | 0.40 Dioscorea_ | 0.46 Prunus_pe |
| Os03t0136800-01 | 0.33 Ananas_co | 0.40 Dioscorea_ | 0.46 Vitis_vinife |
| Os03t0169600-01 | 0.46 Manihot_e | 0.46 Manihot_e | 0.46 Manihot_e |
| Os02t0150700-01 | 0.36 Musa_acu | 0.46 Nymphaea | 0.46 Nymphaea |
| Os08t0120200-01 | 0.41 Ananas_co | 0.46 Vitis_vinife | 0.46 Vitis_vinife |
| Zm00001eb227010_P00 | 0.28 Ananas_co | 0.46 Selaginella | 0.46 Selaginella |
| Os06t0695600-01 | 0.39 Musa_acu | 0.46 Corchorus | 0.46 Corchorus |
| Os03t0353500-01 | 0.27 Ananas_co | 0.40 Dioscorea_ | 0.46 Nicotiana_ |
| Os02t0767000-01 | 0.32 Musa_acu | 0.35 Dioscorea_ | 0.46 Theobrom |
| Os08t0379000-01Zm00 | 0.39 Ananas_co | 0.43 Dioscorea_ | 0.46 Vitis_vinife |
| Os02t0326200-00 | 0.43 Ananas_co | 0.45 Dioscorea_ | 0.46 Prunus_pe |
| Os01t0853000-01 | 0.32 Ananas_co | 0.46 Populus_tr | 0.46 Populus_tr |
| Os07t0588400-00 | 0.44 Ananas_co | 0.46 Dioscorea_ | 0.46 Olea_euro |
| Os11t0629550-00 | 0.46 Populus_tr | 0.46 Populus_tr | 0.46 Populus_tr |

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| Os01t0730700-01 | 0.32 Ananas_co | 0.45 Dioscorea_ | 0.46 Corchorus |
| Os06t0300700-01 | 0.37 Ananas_co | 0.39 Dioscorea_ | 0.46 Actinidia_c |
| Os02t0805700-01 | 0.23 Ananas_co | 0.46 Corchorus | 0.46 Corchorus |

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| Os11t0195500-01 | 0.31 Ananas_co | 0.46 Prunus_du | 0.46 Prunus_du |
| Os01t0765300-01 | 0.39 Ananas_co | 0.46 Prunus_pe | 0.46 Prunus_pe |
| Os01t0194000-01 | 0.32 Ananas_co | 0.41 Dioscorea_ | 0.46 Ipomoea_t |
| Os05t0181200-01 | 0.41 Ananas_co | 0.45 Dioscorea_ | 0.46 Populus_tr |
| Os02t0704600-01 | 0.39 Ananas_co | 0.46 Citrullus_l | 0.46 Citrullus_l |
| Os01t0692300-01 | 0.34 Ananas_co | 0.46 Manihot_e | 0.46 Manihot_e |
| Os08t0378800-01 | 0.38 Ananas_co | 0.46 Vigna_ang | 0.46 Vigna_ang |
| Os04t0562800-00 | 0.33 Ananas_co | 0.39 Dioscorea_ | 0.46 Prunus_avi |
| Os06t0530200-01 | 0.34 Musa_acur | 0.38 Dioscorea_ | 0.46 Gossypium |
| Zm00001eb174530_P00 | 0.34 Ananas_co | 0.40 Dioscorea_ | 0.46 Vitis_vinife |
| Os09t0346400-01 | 0.44 Ananas_co | 0.45 Cucumis_s | 0.45 Cucumis_s |

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| Os01t0185300-01 | 0.04 Ananas_co | 0.39 Dioscorea_ | 0.45 Lupinus_a |

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| Os01t0177400-01 | 0.39 Ananas_co | 0.45 Ipomoea_t | 0.45 Ipomoea_t |
| Os01t0969000-01 | 0.43 Musa_acur | 0.45 Citrus_cler | 0.45 Citrus_cler |
| Os07t0538700-01Zm00 | 0.42 Ananas_co | 0.43 Dioscorea_ | 0.45 Populus_tr |
| Os03t0122100-00 | 0.37 Musa_acur | 0.45 Nymphaea | 0.45 Nymphaea |
| Os12t0594200-00 | 0.44 Dioscorea_ | 0.44 Dioscorea_ | 0.45 Actinidia_c |

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| Os10t0195600-01 | 0.45 Coffea_car | 0.45 Coffea_car | 0.45 Coffea_car |
| Os08t0541500-01 | 0.32 Musa_acur | 0.45 Ipomoea_t | 0.45 Ipomoea_t |
| Os12t0596900-01 | 0.29 Ananas_co | 0.41 Dioscorea_ | 0.45 Trifolium_ |

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| Os03t0174900-01 | 0.27 Ananas_co | 0.37 Dioscorea_ | 0.45 Actinidia_ |
| Os01t0118400-01 | 0.29 Ananas_co | 0.40 Dioscorea_ | 0.45 Actinidia_ |

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| Os10t0562100-01Zm00 | 0.38 Musa_acur | 0.39 Dioscorea_ | 0.45 Ipomoea_t |
| Os06t0173000-00 | 0.45 Populus_tr | 0.45 Populus_tr | 0.45 Populus_tr |
| Os05t0180400-01 | 0.34 Ananas_co | 0.43 Dioscorea_ | 0.45 Theobrom |
| Os05t0510300-01 | 0.34 Musa_acur | 0.44 Dioscorea_ | 0.45 Pistacia_ve |
| Os05t0372200-00Zm00 | 0.40 Ananas_co | 0.45 Vitis_vinife | 0.45 Vitis_vinife |
| Os07t0531700-01 | 0.32 Ananas_co | 0.37 Dioscorea_ | 0.45 Corchorus |

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| Os09t0522200-01 | 0.39 Ananas_co | 0.44 Dioscorea_ | 0.45 Ipomoea_t |

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| Os03t0329900-01 | 0.39 Ananas_co | 0.45 Manihot_e | 0.45 Manihot_e |

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| Os06t0183200-01 | 0.33 Ananas_co | 0.44 Dioscorea_ | 0.45 Vitis_vinife |
| Os12t0189900-01 | 0.29 Ananas_co | 0.37 Dioscorea_ | 0.45 Prunus_pe |
| Os02t0768750-00 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.45 Theobrom |
| Os03t0701600-01 | 0.34 Ananas_co | 0.45 Vitis_vinife | 0.45 Vitis_vinife |
| Os02t0135600-01 | 0.31 Ananas_co | 0.33 Dioscorea_ | 0.45 Vitis_vinife |
| Os01t0625300-01 | 0.40 Ananas_co | 0.45 Prunus_pe | 0.45 Prunus_pe |
| Os05t0409300-01 | 0.45 Gossypiu | 0.45 Gossypiu | 0.45 Gossypiu |
| Os06t0164000-01 | 0.36 Ananas_co | 0.39 Dioscorea_ | 0.45 Coffea_car |
| Os04t0465500-02 | 0.35 Ananas_co | 0.45 Prunus_avi | 0.45 Prunus_avi |
| Os03t0723400-01 | 0.45 Pistacia_ve | 0.45 Pistacia_ve | 0.45 Pistacia_ve |
| Os08t0374200-01 | 0.30 Ananas_co | 0.45 Coffea_car | 0.45 Coffea_car |
| Os03t0120200-01 | 0.41 Ananas_co | 0.45 Theobrom | 0.45 Theobrom |

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| Os09t0459200-01 | 0.29 | Ananas_co | 0.36 | Dioscorea_ | 0.45 | Gossypium |
| Os05t0363500-01 | 0.28 | Ananas_co | 0.37 | Dioscorea_ | 0.45 | Vitis_vinife |
| Os08t0278100-01 | 0.30 | Ananas_co | 0.45 | Amborella_ | 0.45 | Amborella_ |
| Os03t0816800-01 | 0.43 | Musa_acur | 0.45 | Coffea_car | 0.45 | Coffea_car |
| Os03t0228500-01 | 0.34 | Musa_acur | 0.45 | Gossypium | 0.45 | Gossypium |
| Os01t0886000-01 | 0.42 | Musa_acur | 0.44 | Dioscorea_ | 0.45 | Coffea_car |

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| Os02t0266800-01Zm00 | 0.27 | Ananas_co | 0.45 | Coffea_car | 0.45 | Coffea_car |
| Os05t0526700-01 | 0.24 | Musa_acur | 0.29 | Dioscorea_ | 0.45 | Rosa_chine |
| Zm00001eb230680_P00 | 0.45 | Vigna_radi | 0.45 | Vigna_radi | 0.45 | Vigna_radi |
| Os02t0775300-01 | 0.42 | Ananas_co | 0.42 | Dioscorea_ | 0.45 | Phaseolus_ |
| Zm00001eb376990_P00 | 0.31 | Ananas_co | 0.36 | Dioscorea_ | 0.45 | Pistacia_ve |
| Os01t0877500-01 | 0.30 | Ananas_co | 0.42 | Dioscorea_ | 0.45 | Vitis_vinife |
| Zm00001eb119980_P00 | 0.39 | Musa_acur | 0.45 | Glycine_ma | 0.45 | Glycine_ma |
| Os01t0119100-00 | 0.35 | Ananas_co | 0.42 | Dioscorea_ | 0.45 | Actinidia_c |
| Os01t0934300-02 | 0.37 | Ananas_co | 0.45 | Prunus_per | 0.45 | Prunus_per |
| Os02t0723300-01 | 0.32 | Ananas_co | 0.41 | Dioscorea_ | 0.45 | Manihot_es |
| Os03t0710600-01 | 0.32 | Ananas_co | 0.41 | Dioscorea_ | 0.45 | Coffea_car |
| Os02t0509600-01 | 0.36 | Ananas_co | 0.43 | Dioscorea_ | 0.45 | Coffea_car |
| Os02t0654400-01 | 0.37 | Ananas_co | 0.39 | Dioscorea_ | 0.45 | Pistacia_ve |
| Os04t0544400-00 | 0.41 | Dioscorea_ | 0.41 | Dioscorea_ | 0.45 | Vitis_vinife |
| Os02t0164600-01 | 0.26 | Ananas_co | 0.38 | Dioscorea_ | 0.45 | Olea_europ |
| Os06t0480000-01 | 0.27 | Ananas_co | 0.34 | Dioscorea_ | 0.45 | Manihot_es |

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| Os01t0236700-01 | 0.38 | Ananas_co | 0.45 | Corchorus_ | 0.45 | Corchorus_ |
| Os03t0148000-01 | 0.32 | Ananas_co | 0.45 | Actinidia_c | 0.45 | Actinidia_c |
| Os06t0149500-01 | 0.21 | Ananas_co | 0.45 | Populus_tr | 0.45 | Populus_tr |
| Os03t0764600-01 | 0.41 | Musa_acur | 0.43 | Dioscorea_ | 0.45 | Corchorus_ |

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| Os11t0303600-01 | 0.39 | Ananas_co | 0.45 | Manihot_es | 0.45 | Manihot_es |
| Zm00001eb161010_P00 | 0.35 | Musa_acur | 0.45 | Corchorus_ | 0.45 | Corchorus_ |

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| Os02t0805250-01 | 0.41 Ananas_co | 0.43 Dioscorea_ | 0.45 Manihot_es |
| Os03t0811500-01 | 0.41 Dioscorea_ | 0.41 Dioscorea_ | 0.45 Pistacia_ve |
| Os04t0625000-01 | 0.35 Ananas_co | 0.41 Dioscorea_ | 0.45 Manihot_es |
| Os03t0736200-00 | 0.37 Musa_acur | 0.42 Dioscorea_ | 0.45 Citrus_cler |
| Os08t0506700-01 | 0.26 Ananas_co | 0.42 Dioscorea_ | 0.45 Corchorus_ |
| Os05t0367900-01 | 0.36 Musa_acur | 0.38 Dioscorea_ | 0.45 Manihot_es |
| Os05t0526300-02 | 0.45 Amborella_ | 0.45 Amborella_ | 0.45 Amborella_ |
| Os07t0585000-01 | 0.37 Ananas_co | 0.45 Populus_tr | 0.45 Populus_tr |
| Os04t0116900-00Zm00 | 0.45 Vitis_vinife | 0.45 Vitis_vinife | 0.45 Vitis_vinife |
| Os04t0584500-01Zm00 | 0.39 Ananas_co | 0.45 Actinidia_c | 0.45 Actinidia_c |
| Os03t0206400-02 | 0.43 Musa_acur | 0.44 Dioscorea_ | 0.45 Actinidia_c |
| Os11t0104300-01 | 0.41 Musa_acur | 0.42 Dioscorea_ | 0.45 Actinidia_c |
| Os12t0618600-01 | 0.28 Ananas_co | 0.35 Dioscorea_ | 0.45 Citrus_cler |
| Os02t0317300-01 | 0.35 Ananas_co | 0.45 Vitis_vinife | 0.45 Vitis_vinife |
| Os02t0718000-01 | 0.40 Ananas_co | 0.45 Vigna_angu | 0.45 Vigna_angu |
| Os07t0683600-00 | 0.41 Ananas_co | 0.43 Dioscorea_ | 0.45 Physcomitr |
| Os05t0586900-01 | 0.36 Ananas_co | 0.38 Dioscorea_ | 0.44 Theobroma |
| Os02t0669900-01 | 0.32 Ananas_co | 0.35 Dioscorea_ | 0.44 Phaseolus_ |
| Os03t0681900-01 | 0.32 Musa_acur | 0.44 Nymphaea | 0.44 Nymphaea |
| Os10t0198600-01 | 0.43 Ananas_co | 0.44 Pistacia_ve | 0.44 Pistacia_ve |
| Os01t0937100-01 | 0.33 Ananas_co | 0.44 Coffea_car | 0.44 Coffea_car |
| Os04t0423600-01 | 0.29 Ananas_co | 0.40 Dioscorea_ | 0.44 Prunus_du |
| Os03t0270500-01 | 0.24 Ananas_co | 0.35 Dioscorea_ | 0.44 Actinidia_c |

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| Os04t0690300-01 | 0.31 Ananas_co | 0.44 Manihot_e | 0.44 Manihot_e |
| Os07t0542900-00 | 0.44 Brassica_n | 0.44 Brassica_n | 0.44 Brassica_n |
| Os04t0243700-01 | 0.32 Ananas_co | 0.44 Amborella | 0.44 Amborella |
| Os10t0457400-01 | 0.44 Dioscorea_ | 0.44 Dioscorea_ | 0.44 Theobrom |
| Zm00001eb142600_P00 | 0.44 Camelina_ | 0.44 Camelina_ | 0.44 Camelina_ |
| Os07t0107100-01 | 0.31 Ananas_co | 0.44 Arabidopsi | 0.44 Arabidopsi |
| Os03t0660500-00 | 0.37 Musa_acur | 0.44 Solanum_t | 0.44 Solanum_t |
| Os04t0447900-00 | 0.36 Ananas_co | 0.44 Rosa_chine | 0.44 Rosa_chine |
| Os02t0186400-01 | 0.29 Ananas_co | 0.44 Prunus_du | 0.44 Prunus_du |
| Os01t0927300-01 | 0.24 Ananas_co | 0.44 Beta_vulga | 0.44 Beta_vulga |

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| Os01t0159800-02 | 0.31 Ananas_co | 0.37 Dioscorea_ | 0.44 Cucumis_n |
| Os01t0634900-00 | 0.28 Ananas_co | 0.44 Actinidia_c | 0.44 Actinidia_c |
| Os05t0499800-01Zm00 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.44 Pistacia_ve |

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| Os02t0685200-01 | 0.35 Ananas_co | 0.44 Vitis_vinife | 0.44 Vitis_vinife |
| Os03t0257500-01 | 0.38 Ananas_co | 0.44 Prunus_du | 0.44 Prunus_du |
| Os02t0131700-00 | 0.34 Ananas_co | 0.44 Citrus_cler | 0.44 Citrus_cler |
| Os12t0554500-00 | 0.27 Ananas_co | 0.44 Gossypiu | 0.44 Gossypiu |
| Os03t0648600-00 | 0.38 Musa_acur | 0.44 Glycine_ma | 0.44 Glycine_ma |
| Os10t0487300-01 | 0.21 Ananas_co | 0.44 Manihot_e | 0.44 Manihot_e |
| Os11t0140100-02 | 0.41 Dioscorea_ | 0.41 Dioscorea_ | 0.44 Citrus_cler |
| Os05t0295900-01 | 0.39 Ananas_co | 0.44 Coffea_car | 0.44 Coffea_car |

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| Os07t0471000-01 | 0.32 Ananas_co | 0.44 Vitis_vinife | 0.44 Vitis_vinife |
| Os05t0179300-01 | 0.10 Ananas_co | 0.40 Dioscorea_ | 0.44 Vitis_vinife |
| Os01t0649200-01 | 0.41 Ananas_co | 0.44 Coffea_car | 0.44 Coffea_car |
| Os03t0399000-01 | 0.30 Ananas_co | 0.44 Cannabis_ | 0.44 Cannabis_ |
| Os02t0727300-01 | 0.44 Theobrom | 0.44 Theobrom | 0.44 Theobrom |
| Os02t0123400-01 | 0.31 Ananas_co | 0.39 Dioscorea_ | 0.44 Actinidia_c |

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| Os02t0705500-01 | 0.43 Musa_acur | 0.44 Prunus_pe | 0.44 Prunus_pe |

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| Os07t0551700-01 | 0.44 Brassica_n | 0.44 Brassica_n | 0.44 Brassica_n |
| Os05t0188600-02 | 0.35 Dioscorea_ | 0.35 Dioscorea_ | 0.44 Vitis_vinife |

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| Os07t0247100-01 | 0.38 Musa_acu | 0.44 Vitis_vinife | 0.44 Vitis_vinife |
| Os03t0263800-01 | 0.36 Musa_acu | 0.42 Dioscorea_ | 0.44 Solanum_t |
| Os11t0620500-01 | 0.44 Cannabis_ | 0.44 Cannabis_ | 0.44 Cannabis_ |
| Os06t0717600-01 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.44 Actinidia_ |

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| Os03t0796900-01 | 0.39 Ananas_co | 0.40 Dioscorea_ | 0.44 Solanum_t |
| Zm00001eb381960_P00 | 0.24 Ananas_co | 0.44 Daucus_ca | 0.44 Daucus_ca |

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| Os03t0131100-01 | 0.28 Ananas_co | 0.39 Dioscorea_ | 0.44 Vitis_vinife |
| Os03t0723600-01 | 0.32 Ananas_co | 0.39 Dioscorea_ | 0.44 Helianthus |
| Os03t0577100-01 | 0.17 Ananas_co | 0.44 Pistacia_ve | 0.44 Pistacia_ve |
| Os04t0417800-01 | 0.31 Ananas_co | 0.34 Dioscorea_ | 0.44 Populus_tr |

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| Os02t0104200-01 | 0.35 Ananas_co | 0.44 Dioscorea_ | 0.44 Cannabis_ |
| Os02t0636600-00 | 0.34 Ananas_co | 0.44 Theobrom | 0.44 Theobrom |
| Os08t0417100-01Zm00 | 0.26 Ananas_co | 0.44 Ipomoea_t | 0.44 Ipomoea_t |
| Os01t0920100-01 | 0.36 Ananas_co | 0.43 Dioscorea_ | 0.44 Cucumis_ |
| Os02t0820400-01 | 0.17 Ananas_co | 0.40 Dioscorea_ | 0.44 Vitis_vinife |
| Os09t0110200-01 | 0.31 Ananas_co | 0.35 Dioscorea_ | 0.44 Amborella_ |
| Os11t0644700-01 | 0.32 Ananas_co | 0.44 Vigna_radi | 0.44 Vigna_radi |
| Os04t0600400-01 | 0.24 Ananas_co | 0.44 Populus_tr | 0.44 Populus_tr |
| Os02t0567000-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.44 Theobrom |
| Os07t0586800-01 | 0.44 Vitis_vinife | 0.44 Vitis_vinife | 0.44 Vitis_vinife |

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| Os08t0121900-01 | 0.33 | Ananas_co | 0.44 | Vitis_vinife | 0.44 | Vitis_vinife |
| Os04t0613300-01 | 0.41 | Musa_acur | 0.44 | Vitis_vinife | 0.44 | Vitis_vinife |
| Os10t0564200-01 | 0.38 | Musa_acur | 0.44 | Ipomoea_t | 0.44 | Ipomoea_t |

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| Os09t0517600-01 | 0.44 | Glycine_ma | 0.44 | Glycine_ma | 0.44 | Glycine_ma |
| Os06t0199200-01 | 0.35 | Ananas_co | 0.44 | Pistacia_ve | 0.44 | Pistacia_ve |
| Os05t0554500-01 | 0.32 | Ananas_co | 0.44 | Prunus_du | 0.44 | Prunus_du |
| Os07t0679700-01 | 0.26 | Ananas_co | 0.44 | Vitis_vinife | 0.44 | Vitis_vinife |
| Os07t0524900-01 | 0.32 | Ananas_co | 0.44 | Rosa_chine | 0.44 | Rosa_chine |
| Os03t0861100-01 | 0.36 | Ananas_co | 0.44 | Vitis_vinife | 0.44 | Vitis_vinife |
| Os07t0533800-01Zm00 | 0.38 | Ananas_co | 0.42 | Dioscorea_ | 0.44 | Actinidia_c |
| Os03t0130500-01 | 0.34 | Ananas_co | 0.35 | Dioscorea_ | 0.44 | Manihot_es |
| Os04t0623100-01 | 0.41 | Musa_acur | 0.43 | Dioscorea_ | 0.44 | Lupinus_ar |
| Os02t0824300-01 | 0.40 | Musa_acur | 0.43 | Pistacia_ve | 0.43 | Pistacia_ve |
| Os09t0454200-01 | 0.31 | Ananas_co | 0.43 | Theobroma | 0.43 | Theobroma |
| Os03t0187400-01 | 0.35 | Musa_acur | 0.43 | Populus_tr | 0.43 | Populus_tr |
| Os08t0506400-01 | 0.23 | Ananas_co | 0.43 | Coffea_car | 0.43 | Coffea_car |

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| Os09t0550000-01 | 0.36 | Ananas_co | 0.37 | Dioscorea_ | 0.43 | Manihot_es |
| Os01t0957900-01 | 0.32 | Ananas_co | 0.43 | Rosa_chine | 0.43 | Rosa_chine |
| Os06t0669275-00 | 0.33 | Ananas_co | 0.42 | Dioscorea_ | 0.43 | Actinidia_c |
| Os03t0858200-01 | 0.43 | Malus_dom | 0.43 | Malus_dom | 0.43 | Malus_dom |
| Zm00001eb187750_P00 | 0.39 | Dioscorea_ | 0.39 | Dioscorea_ | 0.43 | Prunus_avi |
| Os07t0495300-00 | 0.34 | Ananas_co | 0.43 | Citrus_cler | 0.43 | Citrus_cler |
| Os02t0114600-01 | 0.30 | Musa_acur | 0.43 | Vitis_vinife | 0.43 | Vitis_vinife |
| Os03t0765200-02 | 0.38 | Ananas_co | 0.39 | Dioscorea_ | 0.43 | Prunus_per |
| Os03t0830900-01 | 0.30 | Ananas_co | 0.43 | Gossypium | 0.43 | Gossypium |
| Os08t0519800-02 | 0.33 | Ananas_co | 0.38 | Dioscorea_ | 0.43 | Vitis_vinife |

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| Os11t0629300-01 | 0.32 | Ananas_co | 0.43 | Malus_dom | 0.43 | Malus_dom |
| Os03t0669600-01 | 0.41 | Ananas_co | 0.43 | Manihot_es | 0.43 | Manihot_es |
| Os11t0677500-00 | 0.38 | Ananas_co | 0.39 | Dioscorea_ | 0.43 | Vitis_vinife |

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| Os07t0507700-01 | 0.35 | Ananas_co | 0.42 | Dioscorea_ | 0.43 | Actinidia_c |
| Os03t0203100-01 | 0.28 | Ananas_co | 0.39 | Dioscorea_ | 0.43 | Vitis_vinife |
| Os07t0658100-01 | 0.35 | Ananas_co | 0.43 | Populus_tr | 0.43 | Populus_tr |
| Os10t0390100-02 | 0.33 | Ananas_co | 0.43 | Vitis_vinife | 0.43 | Vitis_vinife |

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| Os07t0644100-01 | 0.36 Musa_acur | 0.41 Dioscorea_ | 0.43 Beta_vulga |
| Os01t0976500-01 | 0.28 Ananas_co | 0.39 Dioscorea_ | 0.43 Theobroma |
| Os11t0580000-01 | 0.24 Ananas_co | 0.36 Dioscorea_ | 0.43 Actinidia_c |
| Os02t0638400-01 | 0.41 Musa_acur | 0.43 Amborella_ | 0.43 Amborella_ |
| Os09t0508200-01 | 0.30 Ananas_co | 0.34 Dioscorea_ | 0.43 Prunus_du |
| Os01t0764000-01 | 0.24 Ananas_co | 0.43 Pistacia_ve | 0.43 Pistacia_ve |

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| Os05t0455200-01 | 0.25 Ananas_co | 0.43 Vitis_vinife | 0.43 Vitis_vinife |
| Os03t0818000-00 | 0.43 Actinidia_c | 0.43 Actinidia_c | 0.43 Actinidia_c |
| Os01t0111200-01 | 0.32 Musa_acur | 0.39 Dioscorea_ | 0.43 Prunus_du |

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| Os01t0780400-02 | 0.29 Ananas_co | 0.37 Dioscorea_ | 0.43 Actinidia_c |
| Os06t0656800-01Zm00 | 0.40 Musa_acur | 0.43 Cucumis_s | 0.43 Cucumis_s |
| Os03t0162500-01 | 0.38 Musa_acur | 0.40 Dioscorea_ | 0.43 Nymphaea |
| Os05t0552200-01 | 0.28 Ananas_co | 0.43 Amborella_ | 0.43 Amborella_ |
| Os02t0700300-01 | 0.38 Ananas_co | 0.43 Actinidia_c | 0.43 Actinidia_c |
| Os12t0162500-01 | 0.40 Musa_acur | 0.43 Actinidia_c | 0.43 Actinidia_c |

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| Zm00001eb424740_P00 | 0.36 | Ananas_co | 0.41 | Dioscorea_ | 0.43 | Vitis_vinife |
| Os01t0168100-01 | 0.34 | Ananas_co | 0.43 | Populus_tr | 0.43 | Populus_tr |
| Os03t0383800-02 | 0.37 | Ananas_co | 0.43 | Populus_tr | 0.43 | Populus_tr |
| Os11t0600500-00 | 0.41 | Ananas_co | 0.43 | Arabidopsi | 0.43 | Arabidopsi |
| Os08t0543900-00Zm00 | 0.36 | Musa_acu | 0.41 | Dioscorea_ | 0.43 | Gossypiu |

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| Os01t0897800-01 | 0.25 | Ananas_co | 0.35 | Dioscorea_ | 0.43 | Manihot_e |

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| Os12t0151500-01 | 0.40 | Dioscorea_ | 0.40 | Dioscorea_ | 0.43 | Malus_do |
| Os09t0484300-01 | 0.37 | Ananas_co | 0.38 | Dioscorea_ | 0.43 | Vigna_radi |
| Os02t0823300-01 | 0.42 | Musa_acu | 0.43 | Theobrom | 0.43 | Theobrom |
| Zm00001eb357210_P00 | 0.37 | Ananas_co | 0.43 | Cannabis_ | 0.43 | Cannabis_ |
| Os08t0461800-01Zm00 | 0.43 | Citrus_cle | 0.43 | Citrus_cle | 0.43 | Citrus_cle |
| Os09t0360400-01 | 0.34 | Ananas_co | 0.43 | Vitis_vinife | 0.43 | Vitis_vinife |

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| Os04t0495800-01 | 0.36 | Ananas_co | 0.41 | Dioscorea_ | 0.43 | Theobrom |
| Os06t0244700-01 | 0.38 | Ananas_co | 0.43 | Glycine_m | 0.43 | Glycine_m |
| Os03t0221800-01 | 0.35 | Ananas_co | 0.40 | Dioscorea_ | 0.43 | Prunus_pe |
| Os03t0178500-01 | 0.28 | Ananas_co | 0.43 | Daucus_ca | 0.43 | Daucus_ca |

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| Os05t0270200-01 | 0.23 | Ananas_co | 0.43 | Citrullus_l | 0.43 | Citrullus_l |
| Os01t0235350-00 | 0.26 | Ananas_co | 0.43 | Vitis_vinife | 0.43 | Vitis_vinife |
| Os03t0127600-01 | 0.30 | Musa_acu | 0.43 | Actinidia_c | 0.43 | Actinidia_c |
| Os11t0293300-01 | 0.29 | Ananas_co | 0.42 | Dioscorea_ | 0.43 | Nicotiana_ |
| Os01t0168800-01 | 0.29 | Musa_acu | 0.43 | Glycine_m | 0.43 | Glycine_m |
| Os09t0501600-01 | 0.31 | Ananas_co | 0.40 | Dioscorea_ | 0.43 | Nymphaea |
| Os05t0389600-01 | 0.28 | Ananas_co | 0.42 | Dioscorea_ | 0.43 | Malus_do |
| Os08t0110300-01 | 0.13 | Musa_acu | 0.42 | Dioscorea_ | 0.43 | Prunus_avi |
| Os07t0423000-01 | 0.43 | Pistacia_ve | 0.43 | Pistacia_ve | 0.43 | Pistacia_ve |

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| Os09t0323100-01 | 0.33 Ananas_co | 0.40 Dioscorea_ | 0.43 Prunus_du |
| Os08t0518100-01 | 0.38 Ananas_co | 0.43 Solanum_l | 0.43 Solanum_l |
| Zm00001eb280970_P00 | 0.28 Ananas_co | 0.43 Lupinus_a | 0.43 Lupinus_a |
| Os04t0599900-01 | 0.33 Ananas_co | 0.43 Nicotiana_ | 0.43 Nicotiana_ |
| Os01t0715900-01 | 0.27 Ananas_co | 0.43 Beta_vulga | 0.43 Beta_vulga |
| Os02t0690600-01 | 0.34 Ananas_co | 0.43 Prunus_avi | 0.43 Prunus_avi |
| Os02t0751300-01 | 0.31 Ananas_co | 0.38 Dioscorea_ | 0.43 Malus_do |
| Zm00001eb058370_P00 | 0.41 Ananas_co | 0.43 Prunus_du | 0.43 Prunus_du |
| Os02t0742000-01 | 0.38 Dioscorea_ | 0.38 Dioscorea_ | 0.43 Vitis_vinife |
| Os05t0207200-00 | 0.27 Ananas_co | 0.33 Dioscorea_ | 0.43 Prunus_pe |
| Os09t0516500-00 | 0.28 Ananas_co | 0.43 Vigna_radi | 0.43 Vigna_radi |
| Os06t0155300-01 | 0.39 Ananas_co | 0.43 Populus_tr | 0.43 Populus_tr |
| Os08t0543400-01 | 0.27 Ananas_co | 0.35 Dioscorea_ | 0.43 Rosa_chin |
| Os10t0391100-01 | 0.30 Musa_acu | 0.30 Dioscorea_ | 0.43 Citrus_cle |
| Os01t0753000-01 | 0.37 Ananas_co | 0.40 Dioscorea_ | 0.43 Prunus_du |

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| Os05t0403600-01 | 0.30 Ananas_co | 0.43 Rosa_chine | 0.43 Rosa_chine |
| Os07t0475700-01 | 0.38 Ananas_co | 0.42 Dioscorea_ | 0.43 Ipomoea_t |
| Os08t0528800-01 | 0.29 Ananas_co | 0.35 Dioscorea_ | 0.43 Manihot_e |
| Os08t0439900-01 | 0.27 Ananas_co | 0.35 Dioscorea_ | 0.43 Theobrom |
| Os10t0500600-01 | 0.22 Ananas_co | 0.33 Dioscorea_ | 0.42 Theobrom |
| Os03t0284900-01 | 0.32 Ananas_co | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Zm00001eb119510_P00 | 0.33 Ananas_co | 0.42 Prunus_avi | 0.42 Prunus_avi |
| Os06t0213400-01Zm00 | 0.39 Musa_acu | 0.42 Nymphaea | 0.42 Nymphaea |
| Os06t0107600-01 | 0.35 Musa_acu | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os01t0772500-01 | 0.36 Ananas_co | 0.39 Dioscorea_ | 0.42 Populus_tr |

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| Os04t0564600-01Zm00 | 0.42 Musa_acu | 0.42 Coffea_ca | 0.42 Coffea_ca |
| Os07t0612400-01 | 0.27 Musa_acu | 0.42 Nymphaea | 0.42 Nymphaea |
| Os01t0286000-01 | 0.28 Ananas_co | 0.42 Manihot_e | 0.42 Manihot_e |
| Os03t0200200-01 | 0.32 Ananas_co | 0.42 Prunus_du | 0.42 Prunus_du |
| Os10t0531900-01 | 0.25 Ananas_co | 0.40 Dioscorea_ | 0.42 Brassica_r |
| Os06t0589600-01 | 0.29 Ananas_co | 0.33 Dioscorea_ | 0.42 Vitis_vinife |
| Os02t0555100-01 | 0.20 Ananas_co | 0.42 Coffea_ca | 0.42 Coffea_ca |
| Os08t0118900-01 | 0.28 Musa_acu | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os03t0326300-01 | 0.22 Ananas_co | 0.42 Corchorus | 0.42 Corchorus |
| Os10t0494000-01 | 0.23 Ananas_co | 0.37 Dioscorea_ | 0.42 Amborella |
| Os06t0677500-01 | 0.27 Ananas_co | 0.37 Dioscorea_ | 0.42 Vitis_vinife |
| Os12t0209300-00 | 0.26 Ananas_co | 0.34 Dioscorea_ | 0.42 Actinidia_ |

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| Os06t0703900-01 | 0.27 Ananas_co | 0.42 Populus_tr | 0.42 Populus_tr |
| Os06t0651900-01 | 0.30 Ananas_co | 0.42 Olea_euro | 0.42 Olea_euro |

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| Os07t0500300-01Zm00 | 0.42 Musa_acu | 0.42 Prunus_du | 0.42 Prunus_du |
| Os07t0631000-01 | 0.34 Musa_acu | 0.42 Gossypiu | 0.42 Gossypiu |
| Os09t0378700-00Zm00 | 0.34 Ananas_co | 0.42 Theobrom | 0.42 Theobrom |
| Os05t0425000-00 | 0.28 Ananas_co | 0.41 Dioscorea_ | 0.42 Manihot_e |

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| Os03t0575200-01 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.42 Populus_tr |
| Os02t0661600-00 | 0.33 Musa_acu | 0.42 Populus_tr | 0.42 Populus_tr |

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| Os01t0226200-00 | 0.41 Musa_acu | 0.42 Actinidia_ | 0.42 Actinidia_ |
| Os04t0103300-01 | 0.22 Ananas_co | 0.42 Rosa_chine | 0.42 Rosa_chine |
| Os08t0567000-01 | 0.28 Ananas_co | 0.40 Dioscorea_ | 0.42 Manihot_e |
| Os01t0347100-01 | 0.33 Musa_acu | 0.42 Actinidia_ | 0.42 Actinidia_ |
| Os03t0124300-01 | 0.31 Ananas_co | 0.42 Camelina_ | 0.42 Camelina_ |
| Os10t0485100-01Zm00 | 0.27 Ananas_co | 0.42 Amborella_ | 0.42 Amborella_ |
| Os01t0235400-02 | 0.32 Ananas_co | 0.42 Theobrom | 0.42 Theobrom |
| Os03t0134900-01 | 0.31 Musa_acu | 0.33 Dioscorea_ | 0.42 Vitis_vinife |
| Os01t0555100-01 | 0.17 Musa_acu | 0.42 Theobrom | 0.42 Theobrom |
| Os07t0623100-01 | 0.28 Ananas_co | 0.37 Dioscorea_ | 0.42 Theobrom |
| Os07t0107300-01 | 0.32 Ananas_co | 0.42 Cannabis_ | 0.42 Cannabis_ |
| Os01t0802700-01 | 0.28 Ananas_co | 0.42 Trifolium_ | 0.42 Trifolium_ |
| Zm00001eb241100_P00 | 0.37 Ananas_co | 0.42 Theobrom | 0.42 Theobrom |
| Os07t0622900-01 | 0.26 Ananas_co | 0.42 Pistacia_ve | 0.42 Pistacia_ve |
| Os08t0402600-01 | 0.26 Ananas_co | 0.38 Dioscorea_ | 0.42 Actinidia_ |
| Os12t0636200-01 | 0.24 Ananas_co | 0.39 Dioscorea_ | 0.42 Theobrom |
| Os03t0786600-01 | 0.28 Ananas_co | 0.31 Dioscorea_ | 0.42 Malus_do |
| Os12t0613000-01 | 0.39 Ananas_co | 0.42 Amborella_ | 0.42 Amborella_ |
| Os06t0101000-01 | 0.31 Ananas_co | 0.42 Ipomoea_t | 0.42 Ipomoea_t |
| Os01t0203300-01 | 0.32 Ananas_co | 0.38 Dioscorea_ | 0.42 Vitis_vinife |
| Zm00001eb269020_P00 | 0.34 Ananas_co | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os03t0110500-01 | 0.21 Musa_acu | 0.42 Daucus_ca | 0.42 Daucus_ca |
| Os05t0121500-01 | 0.18 Ananas_co | 0.42 Malus_do | 0.42 Malus_do |
| Os11t0218000-01 | 0.38 Ananas_co | 0.42 Theobrom | 0.42 Theobrom |
| Os04t0606000-01Zm00 | 0.29 Musa_acu | 0.38 Dioscorea_ | 0.42 Pistacia_ve |
| Os04t0552700-01 | 0.41 Musa_acu | 0.42 Gossypiu | 0.42 Gossypiu |
| Os04t0594100-01 | 0.33 Ananas_co | 0.42 Vigna_radi | 0.42 Vigna_radi |
| Os07t0548900-01 | 0.29 Ananas_co | 0.42 Manihot_e | 0.42 Manihot_e |

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| Os05t0570900-00 | 0.28 Ananas_co | 0.42 Prunus_pe | 0.42 Prunus_pe |
| Os07t0615000-01 | 0.26 Musa_acu | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os01t0506100-01Zm00 | 0.24 Ananas_co | 0.42 Rosa_chine | 0.42 Rosa_chine |
| Os03t0241900-02 | 0.42 Cannabis_ | 0.42 Cannabis_ | 0.42 Cannabis_ |
| Os03t0205400-00 | 0.39 Ananas_co | 0.40 Dioscorea_ | 0.42 Actinidia_c |
| Os03t0167000-01 | 0.35 Ananas_co | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os01t0788700-00 | 0.36 Ananas_co | 0.42 Camelina_ | 0.42 Camelina_ |
| Os10t0575950-01 | 0.34 Ananas_co | 0.39 Dioscorea_ | 0.42 Actinidia_c |
| Os06t0663500-00Zm00 | 0.31 Ananas_co | 0.36 Dioscorea_ | 0.42 Manihot_e |
| Os06t0489200-01 | 0.35 Ananas_co | 0.39 Dioscorea_ | 0.42 Vitis_vinife |
| Os06t0605900-01 | 0.28 Ananas_co | 0.42 Manihot_e | 0.42 Manihot_e |
| Os03t0441000-01Zm00 | 0.37 Ananas_co | 0.42 Vitis_vinife | 0.42 Vitis_vinife |
| Os05t0275600-02 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.42 Prunus_pe |
| Os09t0532400-01 | 0.29 Ananas_co | 0.42 Actinidia_c | 0.42 Actinidia_c |
| Os03t0609500-01 | 0.38 Musa_acu | 0.42 Brassica_ra | 0.42 Brassica_ra |
| Os03t0686900-01 | 0.41 Ananas_co | 0.42 Citrus_cler | 0.42 Citrus_cler |
| Os04t0470300-01 | 0.28 Ananas_co | 0.42 Prunus_du | 0.42 Prunus_du |
| Os12t0456100-00 | 0.32 Ananas_co | 0.42 Prunus_pe | 0.42 Prunus_pe |
| Os03t0203800-01 | 0.34 Ananas_co | 0.42 Pistacia_ve | 0.42 Pistacia_ve |
| Os02t0720900-01 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.42 Nymphaea |
| Os04t0480100-01 | 0.30 Ananas_co | 0.36 Dioscorea_ | 0.42 Actinidia_c |

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| Os03t0764300-01 | 0.28 Ananas_co | 0.34 Dioscorea_ | 0.42 Vitis_vinife |

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| Os03t0782500-01 | 0.37 Musa_acur | 0.42 Populus_tr | 0.42 Populus_tr |
| Os05t0472300-01 | 0.30 Ananas_co | 0.42 Coffea_car | 0.42 Coffea_car |
| Os04t0463000-01 | 0.39 Dioscorea_ | 0.39 Dioscorea_ | 0.42 Pistacia_ve |
| Os09t0548200-01 | 0.26 Ananas_co | 0.42 Rosa_chine | 0.42 Rosa_chine |
| Os07t0617100-01 | 0.34 Musa_acur | 0.42 Cannabis_ | 0.42 Cannabis_ |

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| Os10t0180800-01Zm00 | 0.31 Musa_acur | 0.42 Actinidia_c | 0.42 Actinidia_c |
| Os04t0472500-00 | 0.37 Musa_acur | 0.42 Brassica_na | 0.42 Brassica_na |
| Os02t0732200-01 | 0.27 Ananas_co | 0.35 Dioscorea_ | 0.42 Vigna_angu |
| Os01t0925700-01 | 0.34 Ananas_co | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os06t0113900-01 | 0.28 Ananas_co | 0.41 Capsicum_ | 0.41 Capsicum_ |
| Os08t0430100-01 | 0.28 Ananas_co | 0.41 Dioscorea_ | 0.41 Actinidia_c |

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| Os06t0649000-01 | 0.24 Ananas_co | 0.39 Dioscorea_ | 0.41 Trifolium_ |
| Os09t0560400-01 | 0.35 Musa_acur | 0.40 Dioscorea_ | 0.41 Coffea_car |

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| Os07t0685000-02 | 0.35 Dioscorea_ | 0.35 Dioscorea_ | 0.41 Nymphaea |
| Os01t0100600-01 | 0.35 Ananas_co | 0.40 Dioscorea_ | 0.41 Prunus_avi |
| Os03t0191200-01 | 0.38 Dioscorea_ | 0.38 Dioscorea_ | 0.41 Gossypium |
| Os09t0528200-01 | 0.33 Ananas_co | 0.41 Solanum_t | 0.41 Solanum_t |
| Os10t0375700-01 | 0.25 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os05t0397900-01 | 0.20 Ananas_co | 0.26 Dioscorea_ | 0.41 Actinidia_c |

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|---|---|---|---|
| Os03t0777600-01 | 0.28 Ananas_co | 0.41 Populus_tr | 0.41 Populus_tr |
| Os03t0204100-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.41 Olea_euro |
| Os01t0923600-02 | 0.36 Ananas_co | 0.41 Nymphaea | 0.41 Nymphaea |
| Os11t0294600-01 | 0.29 Ananas_co | 0.41 Glycine_m | 0.41 Glycine_m |
| Os03t0796600-01 | 0.37 Musa_acur | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os09t0516300-01 | 0.40 Ananas_co | 0.41 Malus_dor | 0.41 Malus_dor |
| Os07t0524400-00 | 0.41 Ipomoea_t | 0.41 Ipomoea_t | 0.41 Ipomoea_t |
| Os03t0696300-01 | 0.36 Musa_acur | 0.40 Dioscorea_ | 0.41 Amborella |
| Os09t0456800-01 | 0.27 Ananas_co | 0.36 Dioscorea_ | 0.41 Nymphaea |
| Os03t0294100-00 | 0.32 Ananas_co | 0.41 Theobrom | 0.41 Theobrom |
| Os05t0180700-01 | 0.31 Ananas_co | 0.41 Camelina_ | 0.41 Camelina_ |
| Os02t0127900-01 | 0.28 Ananas_co | 0.41 Camelina_ | 0.41 Camelina_ |
| Os09t0527700-01 | 0.38 Ananas_co | 0.41 Helianthus | 0.41 Helianthus |
| Os08t0160500-01 | 0.41 Dioscorea_ | 0.41 Dioscorea_ | 0.41 Helianthus |
| Os01t0928300-01 | 0.27 Ananas_co | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os05t0556400-01 | 0.27 Ananas_co | 0.41 Amborella | 0.41 Amborella |
| Os09t0382400-01 | 0.41 Ipomoea_t | 0.41 Ipomoea_t | 0.41 Ipomoea_t |
| Os02t0459600-00 | 0.38 Ananas_co | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os05t0381500-01Zm00 | 0.36 Ananas_co | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os06t0710500-01 | 0.28 Ananas_co | 0.41 Phaseolus_ | 0.41 Phaseolus_ |
| Os03t0725800-01 | 0.37 Musa_acur | 0.41 Theobrom | 0.41 Theobrom |

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|---|---|---|---|
| Os11t0176100-01 | 0.36 Ananas_co | 0.41 Beta_vulga | 0.41 Beta_vulga |
| Os01t0778100-01 | 0.39 Ananas_co | 0.41 Solanum_t | 0.41 Solanum_t |
| Os01t0921100-01 | 0.17 Ananas_co | 0.41 Coffea_car | 0.41 Coffea_car |
| Os01t0859300-01 | 0.41 Brassica_n | 0.41 Brassica_n | 0.41 Brassica_n |
| Os01t0219200-01 | 0.39 Musa_acur | 0.41 Olea_euro | 0.41 Olea_euro |
| Os01t0579800-01 | 0.23 Ananas_co | 0.41 Nicotiana_ | 0.41 Nicotiana_ |
| Os06t0314000-01Zm00 | 0.39 Ananas_co | 0.41 Dioscorea_ | 0.41 Nicotiana_ |
| Os09t0458700-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.41 Rosa_chine |
| Os01t0696100-00 | 0.39 Musa_acur | 0.41 Citrus_cler | 0.41 Citrus_cler |
| Os01t0829900-01 | 0.35 Ananas_co | 0.41 Medicago_ | 0.41 Medicago_ |
| Os01t0639200-01 | 0.12 Ananas_co | 0.25 Dioscorea_ | 0.41 Theobrom |
| Os05t0210100-01 | 0.37 Ananas_co | 0.41 Dioscorea_ | 0.41 Olea_euro |
| Os06t0115400-01 | 0.38 Ananas_co | 0.41 Prunus_pe | 0.41 Prunus_pe |
| Os05t0519200-02 | 0.37 Ananas_co | 0.40 Dioscorea_ | 0.41 Malus_dom |
| Os01t0977600-02 | 0.26 Ananas_co | 0.39 Dioscorea_ | 0.41 Amborella_ |
| Os03t0232400-00 | 0.41 Pistacia_ve | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os12t0580500-01 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.41 Corchorus_ |
| Os04t0590900-01 | 0.35 Musa_acur | 0.39 Dioscorea_ | 0.41 Corchorus_ |
| Zm00001eb065330_P00 | 0.41 Theobrom | 0.41 Theobrom | 0.41 Theobrom |
| Os03t0191700-01 | 0.37 Musa_acur | 0.40 Dioscorea_ | 0.41 Pistacia_ve |
| Os03t0372700-02 | 0.34 Musa_acur | 0.41 Vigna_ang | 0.41 Vigna_ang |
| Os05t0566300-01 | 0.29 Ananas_co | 0.41 Rosa_chine | 0.41 Rosa_chine |

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|---|---|---|---|
| Os01t0652800-01 | 0.38 Musa_acur | 0.41 Theobrom | 0.41 Theobrom |
| Os03t0287800-00 | 0.34 Ananas_co | 0.41 Corchorus | 0.41 Corchorus |
| Os08t0564800-01 | 0.29 Musa_acur | 0.41 Citrus_cler | 0.41 Citrus_cler |
| Os01t0960000-01Zm00 | 0.32 Ananas_co | 0.41 Olea_euro | 0.41 Olea_euro |
| Os04t0431100-01 | 0.32 Ananas_co | 0.41 Gossypiur | 0.41 Gossypiur |
| Os03t0853700-01 | 0.28 Ananas_co | 0.41 Cucumis_n | 0.41 Cucumis_n |

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|---|---|---|---|
| Os08t0535200-01 | 0.39 Musa_acur | 0.40 Dioscorea_ | 0.41 Cannabis_ |
| Os01t0769000-01Zm00 | 0.34 Ananas_co | 0.36 Dioscorea_ | 0.41 Cucumis_s |
| Os03t0140700-01 | 0.33 Ananas_co | 0.41 Trifolium_ | 0.41 Trifolium_ |
| Os02t0480900-01 | 0.33 Ananas_co | 0.39 Dioscorea_ | 0.41 Corchorus |

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| Os05t0537100-00 | 0.24 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os01t0505700-01 | 0.29 Musa_acur | 0.41 Populus_tr | 0.41 Populus_tr |
| Os08t0113800-01 | 0.28 Musa_acur | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os03t0831000-00 | 0.33 Ananas_co | 0.36 Dioscorea_ | 0.41 Malus_don |
| Os01t0254200-01 | 0.32 Ananas_co | 0.41 Capsicum_ | 0.41 Capsicum_ |
| Os07t0122400-01 | 0.33 Ananas_co | 0.36 Dioscorea_ | 0.41 Malus_don |
| Os03t0717200-00 | 0.32 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os02t0135700-01 | 0.32 Musa_acur | 0.35 Dioscorea_ | 0.41 Actinidia_c |

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| Os05t0482400-01 | 0.32 Ananas_co | 0.38 Dioscorea_ | 0.41 Gossypium |
| Os01t0842200-01 | 0.41 Citrus_cler | 0.41 Citrus_cler | 0.41 Citrus_cler |
| Zm00001eb282510_P00 | 0.36 Ananas_co | 0.41 Helianthus | 0.41 Helianthus |
| Os03t0777500-01 | 0.32 Ananas_co | 0.41 Gossypium | 0.41 Gossypium |
| Os09t0556800-01 | 0.39 Musa_acur | 0.41 Manihot_e | 0.41 Manihot_e |

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|---|---|---|---|
| Os09t0510500-01 | 0.41 Solanum_t | 0.41 Solanum_t | 0.41 Solanum_t |
| Os06t0311000-00 | 0.30 Ananas_co | 0.40 Dioscorea_ | 0.41 Pistacia_ve |

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| Os03t0647600-01 | 0.24 Ananas_co | 0.32 Dioscorea_ | 0.41 Populus_tr |
| Os01t0633000-01 | 0.41 Manihot_e | 0.41 Manihot_e | 0.41 Manihot_e |
| Os06t0129800-00 | 0.34 Ananas_co | 0.41 Pistacia_ve | 0.41 Pistacia_ve |
| Os01t0800600-00 | 0.39 Ananas_co | 0.41 Amborella_ | 0.41 Amborella_ |
| Os08t0295100-00 | 0.31 Ananas_co | 0.41 Actinidia_c | 0.41 Actinidia_c |
| Os07t0511000-01 | 0.30 Ananas_co | 0.41 Amborella_ | 0.41 Amborella_ |

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|---|---|---|---|
| Os04t0452500-00Zm00 | 0.19 Ananas_co | 0.36 Dioscorea_ | 0.41 Theobroma |
| Zm00001eb002930_P00 | 0.28 Ananas_co | 0.41 Prunus_per | 0.41 Prunus_per |
| Os12t0209700-01 | 0.34 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os06t0253600-00 | 0.26 Ananas_co | 0.35 Dioscorea_ | 0.41 Vitis_vinife |

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| Os05t0136900-01 | 0.12 Ananas_co | 0.39 Dioscorea_ | 0.41 Vitis_vinife |
| Os03t0260432-01 | 0.41 Gossypium | 0.41 Gossypium | 0.41 Gossypium |
| Os07t0158300-01 | 0.41 Arabidopsi | 0.41 Arabidopsi | 0.41 Arabidopsi |

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| Os03t0241100-01 | 0.35 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os02t0692000-01 | 0.37 Musa_acur | 0.39 Dioscorea_ | 0.41 Theobroma |
| Os02t0192100-01 | 0.33 Ananas_co | 0.41 Corchorus_ | 0.41 Corchorus_ |
| Os03t0319100-01 | 0.37 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os10t0178500-01 | 0.31 Ananas_co | 0.41 Arabis_alpi | 0.41 Arabis_alp |
| Os06t0227250-00 | 0.29 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os02t0611400-01 | 0.24 Ananas_co | 0.41 Prunus_per | 0.41 Prunus_per |
| Os12t0533600-01 | 0.33 Musa_acur | 0.41 Corchorus_ | 0.41 Corchorus_ |
| Os08t0110500-01 | 0.39 Ananas_co | 0.40 Dioscorea_ | 0.41 Theobroma |
| Os04t0538800-01 | 0.28 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os03t0263300-01 | 0.35 Musa_acur | 0.41 Citrus_cler | 0.41 Citrus_cler |
| Os02t0700700-01 | 0.33 Musa_acur | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os04t0583200-01 | 0.41 Manihot_es | 0.41 Manihot_es | 0.41 Manihot_es |
| Os04t0165300-01 | 0.31 Ananas_co | 0.41 Amborella_ | 0.41 Amborella_ |
| Os08t0508700-01 | 0.28 Musa_acur | 0.41 Amborella_ | 0.41 Amborella_ |
| Os06t0674800-01 | 0.30 Ananas_co | 0.41 Rosa_chine | 0.41 Rosa_chine |
| Os02t0633900-00 | 0.41 Coffea_car | 0.41 Coffea_car | 0.41 Coffea_car |
| Os04t0526800-01 | 0.31 Ananas_co | 0.41 Theobroma | 0.41 Theobroma |
| Os05t0372800-01 | 0.35 Dioscorea_ | 0.35 Dioscorea_ | 0.41 Pistacia_ve |
| Os08t0531600-01 | 0.30 Musa_acur | 0.32 Dioscorea_ | 0.41 Nymphaea |
| Os03t0809300-01 | 0.35 Musa_acur | 0.37 Dioscorea_ | 0.41 Amborella_ |
| Os03t0246500-01 | 0.24 Ananas_co | 0.38 Dioscorea_ | 0.41 Vitis_vinife |
| Os01t0100500-01 | 0.28 Ananas_co | 0.35 Dioscorea_ | 0.41 Prunus_per |
| Os03t0711100-01 | 0.37 Musa_acur | 0.41 Theobroma | 0.41 Theobroma |
| Os11t0306400-01Zm00 | 0.36 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os10t0578500-00 | 0.20 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os05t0122600-01 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.41 Lupinus_ar |

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| Os02t0782500-01 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.41 Glycine_ma |
| Os07t0593000-01 | 0.35 Ananas_co | 0.41 Rosa_chine | 0.41 Rosa_chine |
| Os08t0320300-01 | 0.39 Ananas_co | 0.39 Dioscorea_ | 0.41 Populus_tr |
| Os03t0249700-01 | 0.35 Musa_acum | 0.41 Populus_tr | 0.41 Populus_tr |
| Os07t0605800-01 | 0.41 Gossypium | 0.41 Gossypium | 0.41 Gossypium |
| Os09t0334500-01 | 0.36 Ananas_co | 0.41 Vitis_vinife | 0.41 Vitis_vinife |
| Os08t0321000-01 | 0.36 Musa_acum | 0.41 Cucumis_s | 0.41 Cucumis_s |
| Os08t0530066-00 | 0.26 Ananas_co | 0.41 Nicotiana_a | 0.41 Nicotiana_a |
| Os08t0428900-01 | 0.38 Ananas_co | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os01t0883200-01 | 0.25 Musa_acum | 0.33 Dioscorea_ | 0.40 Manihot_es |
| Os06t0675200-01 | 0.40 Populus_tr | 0.40 Populus_tr | 0.40 Populus_tr |
| Os03t0564600-01 | 0.35 Musa_acum | 0.40 Dioscorea_ | 0.40 Pistacia_ve |
| Os01t0232400-01 | 0.34 Ananas_co | 0.38 Dioscorea_ | 0.40 Vitis_vinife |
| Os12t0624900-01Zm00 | 0.40 Musa_acum | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os05t0278500-01 | 0.17 Musa_acum | 0.39 Dioscorea_ | 0.40 Theobroma |
| Os09t0442400-01 | 0.24 Ananas_co | 0.33 Dioscorea_ | 0.40 Nymphaea |
| Os09t0487900-01 | 0.27 Ananas_co | 0.40 Corchorus_ | 0.40 Corchorus_ |
| Os03t0750900-00 | 0.40 Actinidia_c | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os09t0123100-01 | 0.29 Ananas_co | 0.40 Vitis_vinife | 0.40 Vitis_vinife |
| Os01t0645000-01 | 0.32 Musa_acum | 0.40 Populus_tr | 0.40 Populus_tr |
| Os06t0203600-01Zm00 | 0.27 Ananas_co | 0.33 Dioscorea_ | 0.40 Theobroma |
| Os05t0117864-01 | 0.36 Dioscorea_ | 0.36 Dioscorea_ | 0.40 Vitis_vinife |
| Os02t0805800-01 | 0.34 Ananas_co | 0.39 Dioscorea_ | 0.40 Manihot_es |
| Os02t0115600-01 | 0.34 Ananas_co | 0.40 Manihot_es | 0.40 Manihot_es |
| Os02t0633200-01 | 0.24 Ananas_co | 0.40 Theobroma | 0.40 Theobroma |
| Os07t0105600-01 | 0.40 Helianthus | 0.40 Helianthus | 0.40 Helianthus |
| Os02t0702600-01 | 0.24 Ananas_co | 0.27 Dioscorea_ | 0.40 Vitis_vinife |

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| Os07t0586900-01 | 0.24 Musa_acur | 0.40 Capsicum_ | 0.40 Capsicum_ |
| Os06t0661700-01 | 0.35 Dioscorea_ | 0.35 Dioscorea_ | 0.40 Pistacia_ve |
| Os09t0573200-01 | 0.32 Musa_acur | 0.37 Dioscorea_ | 0.40 Theobrom |
| Os01t0585600-01 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.40 Vitis_vinife |
| Os04t0201200-01 | 0.40 Musa_acur | 0.40 Populus_tr | 0.40 Populus_tr |
| Os01t0603300-01 | 0.39 Ananas_co | 0.40 Coffea_car | 0.40 Coffea_car |
| Os04t0450500-01Zm00 | 0.40 Dioscorea_ | 0.40 Dioscorea_ | 0.40 Prunus_du |

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| Os08t0441300-01 | 0.40 Trifolium_ | 0.40 Trifolium_ | 0.40 Trifolium_ |
| Os09t0361700-02 | 0.30 Musa_acur | 0.40 Theobrom | 0.40 Theobrom |
| Os02t0605500-01 | 0.30 Ananas_co | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os02t0224300-01 | 0.31 Musa_acur | 0.40 Dioscorea_ | 0.40 Nymphaea |
| Os08t0416800-01 | 0.40 Gossypiur | 0.40 Gossypiur | 0.40 Gossypiur |

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| Os01t0971100-01 | 0.40 Daucus_ca | 0.40 Daucus_ca | 0.40 Daucus_ca |
| Os04t0388500-01 | 0.30 Musa_acur | 0.40 Nymphaea | 0.40 Nymphaea |
| Os01t0617800-01 | 0.29 Ananas_co | 0.40 Citrus_cler | 0.40 Citrus_cler |
| Os04t0463700-01 | 0.29 Ananas_co | 0.38 Dioscorea_ | 0.40 Nicotiana_ |
| Os09t0453400-01 | 0.35 Ananas_co | 0.37 Dioscorea_ | 0.40 Prunus_per |
| Os05t0199100-01 | 0.38 Musa_acur | 0.40 Nicotiana_ | 0.40 Nicotiana_ |
| Os09t0363700-01 | 0.24 Ananas_co | 0.40 Vitis_vinife | 0.40 Vitis_vinife |
| Os07t0408100-01 | 0.39 Dioscorea_ | 0.39 Dioscorea_ | 0.40 Coffea_car |
| Zm00001eb202650_P00 | 0.20 Ananas_co | 0.35 Dioscorea_ | 0.40 Vitis_vinife |
| Zm00001eb254040_P00 | 0.30 Ananas_co | 0.40 Malus_dom | 0.40 Malus_dom |
| Os01t0708700-01 | 0.31 Ananas_co | 0.38 Dioscorea_ | 0.40 Manihot_e |
| Os02t0717900-01Zm00 | 0.23 Ananas_co | 0.40 Theobrom | 0.40 Theobrom |
| Os07t0607300-01 | 0.23 Ananas_co | 0.33 Dioscorea_ | 0.40 Corchorus |

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| Os02t0234300-01 | 0.29 Ananas_co | 0.40 Manihot_e | 0.40 Manihot_e |
| Os03t0769500-01 | 0.29 Ananas_co | 0.40 Olea_euro | 0.40 Olea_euro |
| Os05t0122400-00 | 0.31 Ananas_co | 0.38 Dioscorea_ | 0.40 Theobrom |

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| Os06t0675600-01 | 0.34 Ananas_co | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os01t0559200-01 | 0.30 Ananas_co | 0.40 Corchorus | 0.40 Corchorus |
| Os06t0601000-01 | 0.31 Ananas_co | 0.40 Vitis_vinife | 0.40 Vitis_vinife |

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| Os08t0509600-01 | 0.31 Ananas_co | 0.40 Rosa_chine | 0.40 Rosa_chine |
| Os03t0684100-01 | 0.23 Ananas_co | 0.40 Corchorus | 0.40 Corchorus |
| Os04t0403400-01 | 0.29 Ananas_co | 0.40 Vitis_vinife | 0.40 Vitis_vinife |

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|---|---|---|---|---|---|---|
| Os01t0771200-01 | 0.28 | Musa_acur | 0.40 | Dioscorea_ | 0.40 | Amborella_ |
| Os01t0753500-01 | 0.37 | Ananas_co | 0.40 | Theobrom | 0.40 | Theobrom |
| Os03t0205300-00 | 0.35 | Musa_acur | 0.40 | Pistacia_ve | 0.40 | Pistacia_ve |
| Os12t0514900-01 | 0.35 | Ananas_co | 0.40 | Actinidia_c | 0.40 | Actinidia_c |
| Os03t0669800-01 | 0.31 | Ananas_co | 0.40 | Solanum_t | 0.40 | Solanum_t |
| Os11t0150450-01 | 0.40 | Musa_acur | 0.40 | Manihot_e | 0.40 | Manihot_e |
| Os04t0593400-00 | 0.32 | Ananas_co | 0.38 | Dioscorea_ | 0.40 | Vigna_ang |
| Os03t0241600-01 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.40 | Prunus_pe |
| Os08t0475400-02 | 0.27 | Ananas_co | 0.40 | Actinidia_c | 0.40 | Actinidia_c |
| Os03t0744300-01 | 0.30 | Ananas_co | 0.33 | Dioscorea_ | 0.40 | Populus_tr |
| Os07t0105800-00 | 0.24 | Ananas_co | 0.40 | Gossypiu | 0.40 | Gossypiu |
| Os11t0550900-01 | 0.38 | Ananas_co | 0.40 | Prunus_pe | 0.40 | Prunus_pe |
| Os01t0169500-01 | 0.30 | Ananas_co | 0.40 | Pistacia_ve | 0.40 | Pistacia_ve |
| Os09t0491532-01 | 0.31 | Musa_acur | 0.37 | Dioscorea_ | 0.40 | Theobrom |
| Os03t0325600-01 | 0.36 | Ananas_co | 0.40 | Manihot_e | 0.40 | Manihot_e |
| Os11t0182400-01 | 0.23 | Ananas_co | 0.40 | Vitis_vinif | 0.40 | Vitis_vinif |
| Os04t0282200-01 | 0.26 | Ananas_co | 0.40 | Rosa_chin | 0.40 | Rosa_chin |
| Os02t0643200-01 | 0.30 | Ananas_co | 0.39 | Dioscorea_ | 0.40 | Vitis_vinif |
| Zm00001eb149030_P00 | 0.36 | Musa_acur | 0.40 | Theobrom | 0.40 | Theobrom |
| Os01t0615300-01 | -0.03 | Ananas_co | 0.38 | Dioscorea_ | 0.40 | Populus_tr |
| Zm00001eb200440_P00 | 0.40 | Citrullus_l | 0.40 | Citrullus_l | 0.40 | Citrullus_l |
| Os03t0269900-01 | 0.26 | Ananas_co | 0.29 | Dioscorea_ | 0.40 | Nicotiana_ |
| Os01t0102600-01 | 0.37 | Ananas_co | 0.40 | Gossypiu | 0.40 | Gossypiu |
| Os01t0208400-01 | 0.33 | Ananas_co | 0.40 | Actinidia_c | 0.40 | Actinidia_c |

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| Os07t0622700-01 | 0.29 Ananas_co | 0.37 Dioscorea_ | 0.40 Trifolium_p |
| Os05t0462600-01 | 0.33 Ananas_co | 0.38 Dioscorea_ | 0.40 Amborella_ |
| Os05t0557100-01 | 0.19 Ananas_co | 0.33 Dioscorea_ | 0.40 Olea_europ |
| Os08t0508600-01 | 0.30 Ananas_co | 0.33 Dioscorea_ | 0.40 Citrus_cler |
| Os08t0127600-01 | 0.39 Musa_acur | 0.40 Malus_dom | 0.40 Malus_dom |

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| Os01t0734800-01 | 0.34 Ananas_co | 0.36 Dioscorea_ | 0.40 Vitis_vinife |
| Os10t0506800-01 | 0.30 Ananas_co | 0.40 Amborella_ | 0.40 Amborella_ |
| Os01t0151900-01 | 0.25 Ananas_co | 0.34 Dioscorea_ | 0.40 Daucus_ca |
| Os07t0626500-01 | 0.30 Ananas_co | 0.36 Dioscorea_ | 0.40 Vitis_vinife |
| Os04t0564700-01 | 0.32 Ananas_co | 0.40 Manihot_es | 0.40 Manihot_es |
| Os12t0490000-01 | 0.33 Ananas_co | 0.40 Medicago_ | 0.40 Medicago_ |
| Os06t0181200-01 | 0.29 Ananas_co | 0.37 Dioscorea_ | 0.40 Citrus_cler |
| Os01t0551800-01 | 0.25 Ananas_co | 0.36 Dioscorea_ | 0.40 Populus_tr |
| Os04t0480300-01 | 0.23 Ananas_co | 0.31 Dioscorea_ | 0.40 Manihot_es |
| Os06t0342500-01 | 0.27 Ananas_co | 0.40 Vitis_vinife | 0.40 Vitis_vinife |
| Os06t0728600-00 | 0.29 Ananas_co | 0.40 Ipomoea_t | 0.40 Ipomoea_t |
| Os01t0633400-01 | 0.28 Ananas_co | 0.40 Actinidia_c | 0.40 Actinidia_c |
| Os03t0807400-01 | 0.30 Ananas_co | 0.38 Dioscorea_ | 0.40 Gossypium |
| Os02t0786200-01 | 0.31 Dioscorea_ | 0.31 Dioscorea_ | 0.40 Theobroma |
| Os01t0148000-00 | 0.23 Ananas_co | 0.34 Dioscorea_ | 0.40 Theobroma |
| Os02t0827500-01 | 0.26 Ananas_co | 0.34 Dioscorea_ | 0.40 Manihot_es |
| Os02t0128400-01 | 0.32 Ananas_co | 0.40 Theobroma | 0.40 Theobroma |
| Os12t0493900-01 | 0.37 Musa_acur | 0.40 Gossypium | 0.40 Gossypium |
| Os07t0512100-01 | 0.34 Musa_acur | 0.40 Malus_dom | 0.40 Malus_dom |

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| Os09t0439200-01 | 0.33 Musa_acur | 0.40 Gossypium | 0.40 Gossypium |
| Zm00001eb045730_P00 | 0.20 Ananas_co | 0.39 Corchorus_ | 0.39 Corchorus_ |
| Zm00001eb430030_P00 | 0.39 Malus_dom | 0.39 Malus_dom | 0.39 Malus_dom |
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| Os03t0102700-01 | 0.27 Ananas_co | 0.39 Actinidia_c | 0.39 Actinidia_c |

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| Os01t0547600-01 | 0.33 | Musa_acu | 0.39 | Vitis_vinife | 0.39 | Vitis_vinife |
| Os06t0185500-00 | 0.10 | Ananas_co | 0.31 | Dioscorea_ | 0.39 | Ipomoea_t |
| Os01t0329900-01Zm00 | 0.35 | Ananas_co | 0.39 | Ipomoea_t | 0.39 | Ipomoea_t |
| Os01t0268900-01 | 0.36 | Ananas_co | 0.39 | Beta_vulga | 0.39 | Beta_vulga |
| Os04t0513000-01 | 0.26 | Ananas_co | 0.39 | Dioscorea_ | 0.39 | Nymphaea |
| Os05t0134300-01 | 0.27 | Ananas_co | 0.39 | Gossypiu | 0.39 | Gossypiu |
| Os01t0679900-01 | 0.30 | Musa_acu | 0.38 | Dioscorea_ | 0.39 | Nymphaea |
| Os11t0199700-02 | 0.39 | Prunus_du | 0.39 | Prunus_du | 0.39 | Prunus_du |
| Os03t0587200-01 | 0.30 | Ananas_co | 0.39 | Manihot_e | 0.39 | Manihot_e |
| Os12t0263100-01 | 0.39 | Musa_acu | 0.39 | Prunus_pe | 0.39 | Prunus_pe |
| Os12t0147500-01 | 0.39 | Pistacia_ve | 0.39 | Pistacia_ve | 0.39 | Pistacia_ve |
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| Os01t0890900-00 | 0.21 | Ananas_co | 0.30 | Dioscorea_ | 0.39 | Actinidia_ |
| Os02t0518500-00 | 0.28 | Ananas_co | 0.39 | Manihot_e | 0.39 | Manihot_e |
| Os02t0505500-01 | 0.27 | Ananas_co | 0.35 | Dioscorea_ | 0.39 | Pistacia_ve |
| Os03t0692700-01 | 0.34 | Ananas_co | 0.39 | Solanum_t | 0.39 | Solanum_t |
| Os05t0123200-01 | 0.29 | Musa_acu | 0.38 | Dioscorea_ | 0.39 | Vitis_vinife |
| Os08t0543050-00Zm00 | 0.33 | Dioscorea_ | 0.33 | Dioscorea_ | 0.39 | Populus_tr |
| Os07t0531500-01 | 0.33 | Musa_acu | 0.39 | Gossypiu | 0.39 | Gossypiu |
| Os11t0156000-01 | 0.35 | Musa_acu | 0.39 | Prunus_du | 0.39 | Prunus_du |
| Os03t0282900-01 | 0.34 | Musa_acu | 0.39 | Manihot_e | 0.39 | Manihot_e |
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| Os04t0253000-01 | 0.39 | Coffea_ca | 0.39 | Coffea_ca | 0.39 | Coffea_ca |
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| Os03t0327600-01Zm00 | 0.37 | Ananas_co | 0.39 | Selaginella | 0.39 | Selaginella |

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| Os06t0127800-01 | 0.31 Ananas_co | 0.34 Dioscorea_ | 0.39 Vitis_vinife |
| Os05t0382600-02 | 0.15 Ananas_co | 0.34 Dioscorea_ | 0.39 Prunus_avi |
| Os11t0237700-01Zm00 | 0.32 Musa_acur | 0.39 Cynara_car | 0.39 Cynara_car |
| Os03t0119966-01 | 0.26 Ananas_co | 0.39 Vitis_vinife | 0.39 Vitis_vinife |
| Os05t0490000-01 | 0.26 Ananas_co | 0.39 Actinidia_c | 0.39 Actinidia_c |

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| Os03t0133400-01 | 0.31 Ananas_co | 0.39 Prunus_pe | 0.39 Prunus_pe |
| Os05t0156200-01 | 0.34 Musa_acu | 0.39 Vitis_vinife | 0.39 Vitis_vinife |
| Os02t0658000-01 | 0.27 Musa_acu | 0.37 Dioscorea_ | 0.39 Gossypiu |
| Os04t0218900-01 | 0.32 Ananas_co | 0.39 Glycine_m | 0.39 Glycine_m |
| Os03t0304500-01 | 0.35 Musa_acu | 0.39 Theobrom | 0.39 Theobrom |
| Os09t0431200-01 | 0.23 Ananas_co | 0.35 Dioscorea_ | 0.39 Vitis_vinife |
| Os02t0186700-01 | 0.30 Ananas_co | 0.39 Prunus_pe | 0.39 Prunus_pe |

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| Os07t0566500-01Zm00 | 0.37 Musa_acu | 0.39 Prunus_du | 0.39 Prunus_du |
| Os05t0457700-01 | 0.24 Ananas_co | 0.39 Corchorus | 0.39 Corchorus |

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| Os03t0215200-01 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.39 Theobrom |
| Os04t0598000-01 | 0.35 Ananas_co | 0.39 Actinidia_c | 0.39 Actinidia_c |
| Os03t0853900-01 | 0.23 Ananas_co | 0.30 Dioscorea_ | 0.39 Populus_tr |

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| Os09t0363100-01 | 0.30 Ananas_co | 0.39 Prunus_du | 0.39 Prunus_du |

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| Os03t0144000-02 | 0.31 Ananas_co | 0.38 Dioscorea_ | 0.39 Populus_tr |
| Os05t0290300-00 | 0.35 Musa_acu | 0.39 Populus_tr | 0.39 Populus_tr |

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| Os06t0125800-01 | 0.38 Musa_acu | 0.39 Nymphaea | 0.39 Nymphaea |

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| Os02t0124700-01 | 0.30 Ananas_co | 0.39 Pistacia_ve | 0.39 Pistacia_ve |
| Os01t0144600-01 | 0.26 Ananas_co | 0.39 Vitis_vinife | 0.39 Vitis_vinife |
| Os05t0196500-01 | 0.34 Ananas_co | 0.37 Dioscorea_ | 0.39 Phaseolus_ |
| Os03t0773300-01 | 0.30 Ananas_co | 0.39 Brassica_n | 0.39 Brassica_n |
| Os10t0484400-02 | 0.27 Ananas_co | 0.39 Brassica_r | 0.39 Brassica_r |
| Os11t0160550-00 | 0.33 Ananas_co | 0.39 Populus_tr | 0.39 Populus_tr |
| Os01t0767600-01 | 0.27 Musa_acu | 0.29 Dioscorea_ | 0.39 Brassica_n |
| Os04t0495400-01 | 0.28 Musa_acu | 0.39 Nicotiana_ | 0.39 Nicotiana_ |
| Zm00001eb307020_P00 | 0.31 Ananas_co | 0.34 Dioscorea_ | 0.39 Actinidia_c |
| Os01t0233000-01 | 0.39 Musa_acu | 0.39 Manihot_e | 0.39 Manihot_e |
| Os02t0200900-01 | 0.28 Ananas_co | 0.39 Populus_tr | 0.39 Populus_tr |
| Os06t0167400-01 | 0.25 Ananas_co | 0.35 Dioscorea_ | 0.39 Actinidia_c |
| Zm00001eb009880_P00 | 0.35 Ananas_co | 0.37 Dioscorea_ | 0.39 Manihot_e |
| Os03t0238800-01 | 0.34 Ananas_co | 0.38 Dioscorea_ | 0.39 Prunus_pe |
| Os08t0190700-00 | 0.28 Ananas_co | 0.35 Dioscorea_ | 0.39 Actinidia_c |
| Os09t0455900-01Zm00 | 0.35 Ananas_co | 0.39 Vitis_vinife | 0.39 Vitis_vinife |
| Zm00001eb151550_P00 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.39 Manihot_e |
| Os01t0108800-01 | 0.29 Ananas_co | 0.39 Capsicum_ | 0.39 Capsicum_ |
| Os02t0616100-01 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.39 Actinidia_c |
| Os05t0497700-01 | 0.28 Musa_acu | 0.34 Dioscorea_ | 0.39 Vitis_vinife |
| Os01t0375100-01 | 0.27 Ananas_co | 0.39 Citrus_cle | 0.39 Citrus_cle |
| Os04t0206600-01 | 0.39 Nicotiana_ | 0.39 Nicotiana_ | 0.39 Nicotiana_ |
| Os10t0577600-01 | 0.35 Ananas_co | 0.36 Dioscorea_ | 0.39 Prunus_avi |
| Os03t0271100-01 | 0.39 Populus_tr | 0.39 Populus_tr | 0.39 Populus_tr |
| Os03t0598700-01 | 0.34 Ananas_co | 0.39 Solanum_l | 0.39 Solanum_l |
| Os08t0129600-01 | 0.30 Ananas_co | 0.39 Prunus_du | 0.39 Prunus_du |
| Os07t0569500-01 | 0.39 Populus_tr | 0.39 Populus_tr | 0.39 Populus_tr |
| Os01t0956200-01 | 0.30 Ananas_co | 0.36 Dioscorea_ | 0.39 Phaseolus_ |

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| Os05t0115800-01 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.39 Theobrom |
| Os01t0793800-01 | 0.36 Dioscorea_ | 0.36 Dioscorea_ | 0.39 Medicago_ |
| Os03t0645000-00 | 0.36 Ananas_co | 0.39 Capsicum_ | 0.39 Capsicum_ |
| Os03t0178300-01 | 0.22 Ananas_co | 0.39 Nymphaea | 0.39 Nymphaea |
| Os08t0108700-00 | 0.22 Ananas_co | 0.39 Theobrom | 0.39 Theobrom |
| Os09t0329000-00 | 0.39 Pistacia_ve | 0.39 Pistacia_ve | 0.39 Pistacia_ve |
| Os01t0973200-00 | 0.23 Ananas_co | 0.39 Actinidia_c | 0.39 Actinidia_c |
| Os06t0694600-00 | 0.17 Ananas_co | 0.33 Dioscorea_ | 0.39 Actinidia_c |
| Os05t0447700-01 | 0.35 Ananas_co | 0.37 Dioscorea_ | 0.39 Actinidia_c |
| Os07t0481100-01 | 0.31 Ananas_co | 0.36 Dioscorea_ | 0.39 Manihot_e |
| Os10t0560000-01 | 0.21 Musa_acu | 0.32 Dioscorea_ | 0.39 Malus_do |
| Os06t0713000-01 | 0.32 Musa_acu | 0.39 Gossypiu | 0.39 Gossypiu |

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| Os10t0548600-01 | 0.30 Ananas_co | 0.39 Actinidia_c | 0.39 Actinidia_c |
| Os12t0638600-01 | 0.26 Ananas_co | 0.33 Dioscorea_ | 0.39 Vitis_vinife |

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| Os05t0398000-01 | 0.35 Musa_acu | 0.37 Dioscorea_ | 0.39 Olea_euro |
| Os03t0672700-01 | 0.31 Ananas_co | 0.39 Gossypiu | 0.39 Gossypiu |
| Os07t0290200-01 | 0.24 Ananas_co | 0.39 Gossypiu | 0.39 Gossypiu |
| Os04t0386900-01 | 0.38 Ananas_co | 0.39 Vitis_vinife | 0.39 Vitis_vinife |
| Os05t0558000-01 | 0.35 Musa_acu | 0.39 Arabidopsi | 0.39 Arabidopsi |
| Os07t0115500-01Zm00 | 0.33 Ananas_co | 0.39 Theobrom | 0.39 Theobrom |
| Os01t0701700-01 | 0.19 Ananas_co | 0.35 Dioscorea_ | 0.39 Phaseolus_ |
| Os01t0711200-01 | 0.32 Ananas_co | 0.39 Manihot_e | 0.39 Manihot_e |
| Os02t0121700-01Zm00 | 0.27 Ananas_co | 0.39 Manihot_e | 0.39 Manihot_e |
| Os03t0861900-01 | 0.26 Ananas_co | 0.39 Vitis_vinife | 0.39 Vitis_vinife |

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| Os04t0597300-01 | 0.37 Ananas_co | 0.39 Rosa_chine | 0.39 Rosa_chine |
| Os03t0340700-01 | 0.39 Manihot_e | 0.39 Manihot_e | 0.39 Manihot_e |
| Os02t0601700-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.39 Vitis_vinife |
| Os11t0130100-01 | 0.31 Musa_acu | 0.35 Dioscorea_ | 0.39 Theobrom |

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| Os03t0824100-01 | 0.29 | Ananas_co | 0.39 | Actinidia_c | 0.39 | Actinidia_c |
| Os04t0678300-01 | 0.34 | Musa_acur | 0.34 | Dioscorea_ | 0.39 | Phaseolus_ |
| Os06t0716000-01 | 0.23 | Ananas_co | 0.39 | Theobroma | 0.39 | Theobroma |
| Os01t0129500-02 | 0.29 | Ananas_co | 0.38 | Populus_tr | 0.38 | Populus_tr |
| Os03t0151600-02 | 0.23 | Ananas_co | 0.38 | Capsicum_ | 0.38 | Capsicum_ |
| Os02t0653900-03 | 0.29 | Ananas_co | 0.38 | Citrullus_la | 0.38 | Citrullus_la |
| Os06t0691600-01Zm00 | 0.31 | Ananas_co | 0.38 | Olea_europ | 0.38 | Olea_europ |
| Os02t0831400-01 | 0.16 | Musa_acur | 0.18 | Dioscorea_ | 0.38 | Cynara_car |
| Os02t0631200-01 | 0.22 | Ananas_co | 0.31 | Dioscorea_ | 0.38 | Corchorus_ |

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| Os03t0180900-01 | 0.32 | Musa_acur | 0.36 | Dioscorea_ | 0.38 | Actinidia_c |
| Os09t0452400-01 | 0.26 | Ananas_co | 0.38 | Beta_vulga | 0.38 | Beta_vulga |

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| Os04t0649400-01Zm00 | 0.34 | Musa_acur | 0.38 | Rosa_chine | 0.38 | Rosa_chine |
| Os03t0111800-01 | 0.31 | Musa_acur | 0.35 | Dioscorea_ | 0.38 | Vitis_vinife |
| Os07t0592000-01 | 0.38 | Cynara_car | 0.38 | Cynara_car | 0.38 | Cynara_car |
| Os06t0677000-01 | 0.32 | Ananas_co | 0.38 | Dioscorea_ | 0.38 | Glycine_ma |
| Os07t0681500-01 | 0.25 | Ananas_co | 0.32 | Dioscorea_ | 0.38 | Vitis_vinife |
| Os02t0132600-02 | 0.29 | Ananas_co | 0.38 | Actinidia_c | 0.38 | Actinidia_c |
| Os02t0153000-01 | 0.26 | Ananas_co | 0.38 | Vitis_vinife | 0.38 | Vitis_vinife |
| Os02t0515000-02 | 0.31 | Ananas_co | 0.38 | Populus_tr | 0.38 | Populus_tr |
| Os06t0594400-02 | 0.37 | Musa_acur | 0.38 | Vitis_vinife | 0.38 | Vitis_vinife |
| Os03t0271300-01 | 0.31 | Ananas_co | 0.38 | Malus_dom | 0.38 | Malus_dom |
| Os03t0396900-02Zm00 | 0.31 | Ananas_co | 0.38 | Theobroma | 0.38 | Theobroma |
| Os03t0853500-00 | 0.33 | Musa_acur | 0.38 | Corchorus_ | 0.38 | Corchorus_ |
| Os02t0829100-01 | 0.27 | Musa_acur | 0.30 | Dioscorea_ | 0.38 | Amborella_ |
| Os01t0194200-01 | 0.36 | Dioscorea_ | 0.36 | Dioscorea_ | 0.38 | Vitis_vinife |
| Os03t0149400-01 | 0.25 | Ananas_co | 0.32 | Dioscorea_ | 0.38 | Vitis_vinife |
| Os03t0151400-01 | 0.29 | Ananas_co | 0.38 | Theobroma | 0.38 | Theobroma |
| Zm00001eb410330_P00 | 0.38 | Dioscorea_ | 0.38 | Dioscorea_ | 0.38 | Corchorus_ |
| Os06t0212600-00 | 0.35 | Ananas_co | 0.36 | Dioscorea_ | 0.38 | Gossypium |
| Os03t0719000-01 | 0.36 | Musa_acur | 0.38 | Dioscorea_ | 0.38 | Corchorus_ |
| Os02t0702500-01 | 0.29 | Ananas_co | 0.38 | Corchorus_ | 0.38 | Corchorus_ |
| Os01t0855200-01 | 0.35 | Ananas_co | 0.38 | Dioscorea_ | 0.38 | Actinidia_c |

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| Os03t0131900-01 | 0.21 | Ananas_co | 0.38 | Prunus_pe | 0.38 | Prunus_pe |
| Os01t0176500-01Zm00 | 0.23 | Ananas_co | 0.38 | Prunus_du | 0.38 | Prunus_du |
| Os03t0633900-01 | 0.38 | Ananas_co | 0.38 | Pistacia_ve | 0.38 | Pistacia_ve |
| Os09t0525500-01 | 0.33 | Ananas_co | 0.38 | Cannabis_ | 0.38 | Cannabis_ |
| Os05t0585400-01 | 0.32 | Ananas_co | 0.38 | Actinidia_ | 0.38 | Actinidia_ |
| Os01t0622700-01 | 0.30 | Ananas_co | 0.38 | Solanum_l | 0.38 | Solanum_l |
| Os03t0854300-01 | 0.28 | Ananas_co | 0.29 | Dioscorea_ | 0.38 | Populus_tr |
| Os02t0174800-01 | 0.37 | Ananas_co | 0.38 | Solanum_l | 0.38 | Solanum_l |
| Os03t0692400-01 | 0.37 | Ananas_co | 0.38 | Pistacia_ve | 0.38 | Pistacia_ve |
| Zm00001eb061370_P00 | 0.29 | Ananas_co | 0.36 | Dioscorea_ | 0.38 | Prunus_du |
| Os04t0648500-01 | 0.21 | Ananas_co | 0.38 | Amborella | 0.38 | Amborella |
| Os04t0505700-01 | 0.26 | Ananas_co | 0.34 | Dioscorea_ | 0.38 | Populus_tr |
| Os10t0442700-01 | 0.27 | Ananas_co | 0.38 | Gossypiu | 0.38 | Gossypiu |
| Os03t0278500-01 | 0.35 | Ananas_co | 0.38 | Corchorus | 0.38 | Corchorus |
| Os09t0380200-01 | 0.32 | Ananas_co | 0.38 | Cannabis_ | 0.38 | Cannabis_ |
| Os09t0347800-01 | 0.26 | Ananas_co | 0.38 | Vitis_vinife | 0.38 | Vitis_vinife |
| Os01t0193500-00 | 0.29 | Ananas_co | 0.38 | Coffea_ca | 0.38 | Coffea_ca |
| Os02t0747600-01 | 0.33 | Ananas_co | 0.38 | Cannabis_ | 0.38 | Cannabis_ |
| Os01t0166800-01 | 0.26 | Ananas_co | 0.36 | Dioscorea_ | 0.38 | Actinidia_ |
| Os05t0176700-01 | 0.33 | Ananas_co | 0.38 | Cynara_ca | 0.38 | Cynara_ca |

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| Os06t0126500-01 | 0.32 Musa_acur | 0.36 Dioscorea_ | 0.38 Gossypiur |
| Os12t0193100-01 | 0.32 Ananas_co | 0.38 Prunus_pe | 0.38 Prunus_pe |
| Os03t0288800-01 | 0.27 Musa_acur | 0.32 Dioscorea_ | 0.38 Corchorus_ |

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| Os03t0308200-01 | 0.20 Ananas_co | 0.35 Dioscorea_ | 0.38 Vitis_vinife |
| Os02t0132100-00 | 0.29 Ananas_co | 0.37 Dioscorea_ | 0.38 Vitis_vinife |
| Os02t0614200-01 | 0.27 Ananas_co | 0.38 Rosa_chine | 0.38 Rosa_chine |

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| Os03t0225500-01 | 0.30 Ananas_co | 0.32 Dioscorea_ | 0.38 Actinidia_c |
| Os01t0258700-01 | 0.35 Musa_acur | 0.38 Daucus_ca | 0.38 Daucus_ca |
| Os04t0498900-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.38 Vitis_vinife |
| Os03t0734900-00 | 0.27 Dioscorea_ | 0.27 Dioscorea_ | 0.38 Gossypiur |
| Os01t0705300-01 | 0.37 Musa_acur | 0.38 Nymphaea | 0.38 Nymphaea |
| Os05t0542800-02 | 0.38 Theobrom | 0.38 Theobrom | 0.38 Theobrom |

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| Os02t0707200-00 | 0.38 Theobrom | 0.38 Theobrom | 0.38 Theobrom |

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| Os08t0536800-01 | 0.36 Ananas_co | 0.37 Dioscorea_ | 0.38 Vitis_vinife |

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| Os03t0729500-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.38 Vitis_vinife |
| Os02t0711100-01 | 0.30 Musa_acur | 0.38 Manihot_e | 0.38 Manihot_e |
| Os02t0739900-01 | 0.31 Ananas_co | 0.38 Glycine_ma | 0.38 Glycine_ma |
| Os04t0650600-01 | 0.33 Musa_acur | 0.34 Dioscorea_ | 0.38 Pistacia_ve |
| Os06t0192400-01Zm00 | 0.23 Ananas_co | 0.38 Cannabis_ | 0.38 Cannabis_ |
| Os02t0684900-01 | 0.30 Ananas_co | 0.35 Dioscorea_ | 0.38 Actinidia_ |
| Os06t0185800-01 | 0.28 Ananas_co | 0.31 Dioscorea_ | 0.38 Vitis_vinife |
| Os12t0233600-01 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.38 Vitis_vinife |
| Os03t0302500-01 | 0.36 Musa_acur | 0.38 Amborella_ | 0.38 Amborella_ |
| Os03t0320000-01 | 0.23 Ananas_co | 0.38 Vitis_vinife | 0.38 Vitis_vinife |

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| Os01t0699600-01 | 0.35 Ananas_co | 0.38 Nymphaea | 0.38 Nymphaea |
| Os03t0201700-01 | 0.31 Ananas_co | 0.37 Dioscorea_ | 0.38 Cannabis_ |
| Os07t0520400-01 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.38 Vitis_vinife |

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| Os11t0183900-01 | 0.28 Musa_acur | 0.38 Coffea_car | 0.38 Coffea_car |
| Os04t0629500-01 | 0.35 Musa_acur | 0.38 Citrus_cler | 0.38 Citrus_cler |
| Os03t0215700-01 | 0.38 Vitis_vinife | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os06t0198700-01 | 0.26 Ananas_co | 0.38 Coffea_car | 0.38 Coffea_car |
| Os02t0633066-00Zm00 | 0.31 Musa_acur | 0.38 Cucumis_ | 0.38 Cucumis_ |

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| Os03t0332100-00 | 0.28 Musa_acur | 0.38 Theobrom | 0.38 Theobrom |
| Os06t0656300-01 | 0.19 Musa_acur | 0.38 Trifolium_ | 0.38 Trifolium_ |
| Os06t0245900-01 | 0.27 Ananas_co | 0.38 Populus_tr | 0.38 Populus_tr |
| Os01t0740400-01 | 0.33 Musa_acur | 0.38 Pistacia_ve | 0.38 Pistacia_ve |
| Os01t0599900-00 | 0.38 Prunus_avi | 0.38 Prunus_avi | 0.38 Prunus_avi |
| Os03t0341200-00 | 0.25 Ananas_co | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os06t0332400-01 | 0.32 Ananas_co | 0.34 Dioscorea_ | 0.38 Pistacia_ve |
| Os06t0694200-01 | 0.31 Ananas_co | 0.34 Dioscorea_ | 0.38 Actinidia_ |
| Zm00001eb126330_P00 | 0.09 Ananas_co | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os12t0224400-01 | 0.38 Coffea_car | 0.38 Coffea_car | 0.38 Coffea_car |

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| Os11t0220400-01Zm00 | 0.31 Ananas_co | 0.38 Actinidia_c | 0.38 Actinidia_c |
| Os04t0612900-01 | 0.28 Musa_acur | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os11t0266800-01 | 0.28 Ananas_co | 0.38 Nicotiana_ | 0.38 Nicotiana_ |
| Os02t0110000-01Zm00 | 0.32 Ananas_co | 0.38 Prunus_avi | 0.38 Prunus_avi |
| Os02t0637800-02 | 0.27 Ananas_co | 0.31 Dioscorea_ | 0.38 Prunus_du |
| Os04t0544100-01 | 0.25 Ananas_co | 0.37 Dioscorea_ | 0.38 Rosa_chine |
| Os02t0782100-01 | 0.25 Ananas_co | 0.36 Dioscorea_ | 0.38 Manihot_e |
| Os04t0522800-01 | 0.27 Ananas_co | 0.38 Prunus_du | 0.38 Prunus_du |
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| Os10t0555900-02Zm00 | 0.29 Ananas_co | 0.38 Actinidia_c | 0.38 Actinidia_c |
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| Os07t0613300-01 | 0.26 Ananas_co | 0.31 Dioscorea_ | 0.38 Manihot_e |
| Os09t0539400-00 | 0.27 Ananas_co | 0.35 Dioscorea_ | 0.38 Populus_tr |
| Os03t0584400-01 | 0.29 Ananas_co | 0.33 Dioscorea_ | 0.38 Ipomoea_t |
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| Os10t0402200-01 | 0.32 Ananas_co | 0.38 Populus_tr | 0.38 Populus_tr |
| Os01t0838600-00 | 0.35 Ananas_co | 0.38 Ipomoea_t | 0.38 Ipomoea_t |
| Os02t0179800-00 | 0.27 Ananas_co | 0.37 Dioscorea_ | 0.38 Corchorus_ |
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| Os12t0223300-01 | 0.19 Ananas_co | 0.25 Dioscorea_ | 0.38 Amborella_ |
| Zm00001eb056540_P00 | 0.30 Ananas_co | 0.38 Theobrom | 0.38 Theobrom |
| Os08t0112800-01 | 0.06 Ananas_co | 0.38 Amborella_ | 0.38 Amborella_ |
| Os02t0648100-01 | 0.27 Musa_acur | 0.37 Dioscorea_ | 0.38 Nymphaea |
| Os02t0806600-01 | 0.33 Ananas_co | 0.38 Prunus_avi | 0.38 Prunus_avi |
| Os04t0501200-01 | 0.33 Ananas_co | 0.36 Dioscorea_ | 0.38 Gossypiu |
| Os04t0606800-01 | 0.32 Ananas_co | 0.38 Cynara_ca | 0.38 Cynara_ca |
| Zm00001eb145720_P00 | 0.25 Ananas_co | 0.33 Dioscorea_ | 0.38 Prunus_pe |
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| Os03t0820400-01 | 0.35 Ananas_co | 0.38 Prunus_avi | 0.38 Prunus_avi |
| Os04t0410400-01 | 0.33 Ananas_co | 0.38 Prunus_pe | 0.38 Prunus_pe |
| Os02t0722800-01 | 0.27 Ananas_co | 0.38 Dioscorea_ | 0.38 Vitis_vinife |
| Os04t0510600-01 | 0.30 Musa_acur | 0.38 Actinidia_c | 0.38 Actinidia_c |
| Os04t0418100-00 | 0.22 Ananas_co | 0.38 Manihot_e | 0.38 Manihot_e |

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| Os03t0160100-01 | 0.24 Ananas_co | 0.35 Dioscorea_ | 0.38 Vitis_vinife |
| Os03t0247900-01 | 0.32 Musa_acu | 0.36 Dioscorea_ | 0.38 Vitis_vinife |
| Os03t0798200-01 | 0.36 Ananas_co | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os01t0829100-01Zm00 | 0.20 Musa_acu | 0.38 Populus_tr | 0.38 Populus_tr |
| Os01t0389700-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.38 Amborella_ |
| Zm00001eb291820_P00 | 0.30 Ananas_co | 0.33 Dioscorea_ | 0.38 Actinidia_ |
| Os02t0745300-00 | 0.32 Ananas_co | 0.38 Manihot_e | 0.38 Manihot_e |
| Os06t0324400-01 | 0.38 Solanum_l | 0.38 Solanum_l | 0.38 Solanum_l |
| Os02t0676500-00 | 0.30 Ananas_co | 0.38 Theobrom | 0.38 Theobrom |
| Zm00001eb063610_P00 | 0.29 Ananas_co | 0.38 Nicotiana_ | 0.38 Nicotiana_ |
| Os05t0337400-01 | 0.37 Ananas_co | 0.38 Populus_tr | 0.38 Populus_tr |
| Os04t0585600-01 | 0.32 Ananas_co | 0.35 Dioscorea_ | 0.38 Nymphaea |
| Os09t0413100-01 | 0.26 Ananas_co | 0.38 Vitis_vinife | 0.38 Vitis_vinife |
| Os10t0508700-01 | 0.36 Musa_acu | 0.38 Theobrom | 0.38 Theobrom |
| Zm00001eb419470_P00 | 0.28 Ananas_co | 0.32 Dioscorea_ | 0.38 Pistacia_ve |

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| Os07t0620800-01 | 0.32 Musa_acur | 0.32 Dioscorea_ | 0.37 Amborella_ |
| Os05t0147300-00 | 0.34 Musa_acur | 0.37 Actinidia_c | 0.37 Actinidia_c |
| Os01t0907200-00Zm00 | 0.35 Musa_acur | 0.37 Olea_europ | 0.37 Olea_europ |

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| Os01t0264000-01 | 0.31 Dioscorea_ | 0.31 Dioscorea_ | 0.37 Nymphaea |

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| Os03t0177300-01 | 0.29 Ananas_co | 0.35 Dioscorea_ | 0.37 Glycine_ma |
| Os06t0535300-01 | 0.25 Ananas_co | 0.37 Citrus_cler | 0.37 Citrus_cler |

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| Os10t0562700-01 | 0.33 Musa_acur | 0.33 Dioscorea_ | 0.37 Gossypium |
| Os09t0525600-01 | 0.30 Ananas_co | 0.37 Manihot_es | 0.37 Manihot_es |
| Os06t0574400-01 | 0.26 Ananas_co | 0.31 Dioscorea_ | 0.37 Vitis_vinife |
| Os08t0377500-01 | 0.20 Ananas_co | 0.37 Coffea_car | 0.37 Coffea_car |
| Os07t0134600-01 | 0.31 Ananas_co | 0.37 Amborella_ | 0.37 Amborella_ |
| Os02t0620100-01 | 0.36 Musa_acur | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os12t0610800-01 | 0.22 Ananas_co | 0.35 Dioscorea_ | 0.37 Vitis_vinife |
| Os10t0485300-01 | 0.27 Ananas_co | 0.37 Dioscorea_ | 0.37 Nymphaea |
| Os08t0468400-01Zm00 | 0.26 Ananas_co | 0.27 Dioscorea_ | 0.37 Actinidia_c |
| Os03t0178200-01 | 0.33 Ananas_co | 0.37 Citrullus_la | 0.37 Citrullus_la |

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| Os12t0567300-00 | 0.37 Vitis_vinife | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os07t0584900-01 | 0.30 Ananas_co | 0.37 Manihot_es | 0.37 Manihot_es |
| Os10t0574500-00 | 0.28 Ananas_co | 0.37 Theobroma | 0.37 Theobroma |
| Os01t0805500-00 | 0.34 Ananas_co | 0.37 Theobroma | 0.37 Theobroma |
| Os03t0678400-01 | 0.27 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os10t0181200-01 | 0.29 Ananas_co | 0.36 Dioscorea_ | 0.37 Amborella_ |
| Os09t0370000-00 | 0.29 Ananas_co | 0.37 Camelina_s | 0.37 Camelina_s |
| Os09t0536000-01 | 0.33 Musa_acur | 0.37 Prunus_per | 0.37 Prunus_per |

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| Os04t0476700-01Zm00 | 0.31 Ananas_co | 0.37 Actinidia_c | 0.37 Actinidia_c |

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| Os03t0327100-01 | 0.34 | Ananas_co | 0.37 | Gossypiu | 0.37 | Gossypiu |
| Zm00001eb101040_P00 | 0.17 | Musa_acur | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os11t0104800-01 | 0.31 | Ananas_co | 0.37 | Dioscorea_ | 0.37 | Glycine_ma |
| Os10t0497000-01 | 0.30 | Ananas_co | 0.32 | Dioscorea_ | 0.37 | Vitis_vinife |
| Os02t0679200-01 | 0.29 | Musa_acur | 0.32 | Dioscorea_ | 0.37 | Actinidia_c |
| Os03t0731100-01 | 0.25 | Ananas_co | 0.37 | Capsicum_ | 0.37 | Capsicum_ |

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| Os09t0512700-01 | 0.28 | Ananas_co | 0.37 | Manihot_e | 0.37 | Manihot_e |
| Os03t0251700-00 | 0.37 | Citrus_cler | 0.37 | Citrus_cler | 0.37 | Citrus_cler |
| Os03t0654500-01 | 0.26 | Ananas_co | 0.32 | Dioscorea_ | 0.37 | Vitis_vinife |
| Os02t0529900-01 | 0.25 | Ananas_co | 0.37 | Pistacia_ve | 0.37 | Pistacia_ve |
| Os02t0604100-01 | 0.32 | Musa_acur | 0.37 | Actinidia_c | 0.37 | Actinidia_c |
| Os04t0683600-01 | 0.25 | Ananas_co | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os01t0729400-01 | 0.32 | Ananas_co | 0.35 | Dioscorea_ | 0.37 | Nicotiana_ |

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| Os02t0743500-02 | 0.37 | Musa_acur | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os10t0560500-01Zm00 | 0.24 | Ananas_co | 0.32 | Dioscorea_ | 0.37 | Pistacia_ve |

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| Os12t0163200-01 | 0.24 | Ananas_co | 0.37 | Citrus_cler | 0.37 | Citrus_cler |

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| Os02t0721800-01 | 0.27 | Musa_acur | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os03t0275400-01 | 0.18 | Musa_acur | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os01t0125900-01Zm00 | 0.24 | Ananas_co | 0.32 | Dioscorea_ | 0.37 | Actinidia_c |
| Os02t0218400-01 | 0.32 | Ananas_co | 0.36 | Dioscorea_ | 0.37 | Theobrom |
| Os03t0248000-02 | 0.30 | Ananas_co | 0.37 | Manihot_e | 0.37 | Manihot_e |
| Os03t0712200-01 | 0.34 | Ananas_co | 0.36 | Dioscorea_ | 0.37 | Prunus_per |
| Os07t0137000-01 | 0.30 | Ananas_co | 0.37 | Coffea_car | 0.37 | Coffea_car |
| Os04t0584800-01 | 0.22 | Ananas_co | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Os11t0521000-01 | 0.14 | Ananas_co | 0.28 | Dioscorea_ | 0.37 | Citrullus_la |
| Os03t0174800-01 | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife | 0.37 | Vitis_vinife |
| Zm00001eb364640_P00 | 0.29 | Ananas_co | 0.33 | Dioscorea_ | 0.37 | Nicotiana_ |
| Os07t0682400-01 | 0.23 | Ananas_co | 0.29 | Dioscorea_ | 0.37 | Vitis_vinife |
| Os03t0395300-01Zm00 | 0.32 | Ananas_co | 0.36 | Dioscorea_ | 0.37 | Prunus_avi |
| Os12t0541000-01 | 0.37 | Musa_acur | 0.37 | Medicago_ | 0.37 | Medicago_ |
| Os02t0125000-01 | 0.35 | Ananas_co | 0.37 | Gossypiu | 0.37 | Gossypiu |

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| Os05t0515700-01 | 0.32 Ananas_co | 0.35 Dioscorea_ | 0.37 Rosa_chine |
| Os01t0182832-00 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.37 Pistacia_ve |
| Os01t0672400-01 | 0.37 Musa_acur | 0.37 Rosa_chine | 0.37 Rosa_chine |
| Os09t0558200-01 | 0.35 Musa_acur | 0.37 Nymphaea | 0.37 Nymphaea |

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| Os01t0777300-00 | 0.34 Musa_acur | 0.35 Dioscorea_ | 0.37 Manihot_e |

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| Os02t0730700-02 | 0.20 Ananas_co | 0.37 Nymphaea | 0.37 Nymphaea |

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| Os05t0497600-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.37 Coffea_car |
| Os09t0557400-01 | 0.19 Ananas_co | 0.32 Dioscorea_ | 0.37 Cucumis_n |
| Os06t0103200-01 | 0.30 Ananas_co | 0.33 Dioscorea_ | 0.37 Vigna_ang |
| Os03t0115400-01 | 0.30 Ananas_co | 0.36 Dioscorea_ | 0.37 Corchorus_ |
| Os01t0205200-01 | 0.31 Ananas_co | 0.35 Dioscorea_ | 0.37 Vitis_vinife |
| Os06t0111700-01Zm00 | 0.26 Musa_acur | 0.28 Dioscorea_ | 0.37 Pistacia_ve |
| Zm00001eb096360_P00 | 0.35 Dioscorea_ | 0.35 Dioscorea_ | 0.37 Vigna_ang |
| Os01t0388700-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.37 Amborella_ |
| Os10t0495500-01 | 0.30 Ananas_co | 0.31 Dioscorea_ | 0.37 Citrus_cler |
| Os02t0516600-01 | 0.29 Ananas_co | 0.35 Dioscorea_ | 0.37 Gossypium |

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| Os05t0571000-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.37 Amborella_ |
| Os04t0628200-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.37 Populus_tr |
| Os03t0699100-01 | 0.30 Musa_acur | 0.37 Prunus_avi | 0.37 Prunus_avi |
| Os02t0194600-00 | 0.28 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os06t0255100-01 | 0.27 Musa_acur | 0.27 Dioscorea_ | 0.37 Beta_vulga |
| Os01t0832900-01 | 0.13 Ananas_co | 0.29 Dioscorea_ | 0.37 Vitis_vinife |

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| Os07t0516300-01 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.37 Cynara_car |
| Os07t0644600-01 | 0.31 Musa_acur | 0.37 Amborella_ | 0.37 Amborella_ |
| Os03t0192600-02 | 0.25 Ananas_co | 0.37 Amborella_ | 0.37 Amborella_ |
| Os10t0499400-01 | 0.26 Musa_acur | 0.37 Citrus_cler | 0.37 Citrus_cler |
| Zm00001eb248470_P00 | 0.31 Musa_acur | 0.37 Pistacia_ve | 0.37 Pistacia_ve |
| Zm00001eb433700_P00 | 0.27 Musa_acur | 0.32 Dioscorea_ | 0.37 Vitis_vinife |
| Os07t0446100-01 | 0.21 Musa_acur | 0.37 Malus_don | 0.37 Malus_don |
| Os03t0207200-01 | 0.24 Musa_acur | 0.33 Dioscorea_ | 0.37 Populus_tr |
| Os06t0574200-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.37 Citrus_cler |

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| Os01t0169400-01Zm00 | 0.37 Ananas_co | 0.37 Populus_tr | 0.37 Populus_tr |
| Os09t0520100-01Zm00 | 0.23 Musa_acur | 0.29 Dioscorea_ | 0.37 Cucumis_n |
| Os07t0607500-01 | 0.34 Ananas_co | 0.37 Manihot_e | 0.37 Manihot_e |
| Os05t0409800-00Zm00 | 0.22 Ananas_co | 0.29 Dioscorea_ | 0.37 Theobrom |
| Os09t0103700-01Zm00 | 0.28 Ananas_co | 0.37 Prunus_du | 0.37 Prunus_du |
| Os04t0591000-01Zm00 | 0.32 Musa_acur | 0.35 Dioscorea_ | 0.37 Corchorus |
| Os04t0438300-01 | 0.27 Ananas_co | 0.37 Cannabis_ | 0.37 Cannabis_ |

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| Os05t0408200-01 | 0.32 Musa_acur | 0.33 Dioscorea_ | 0.37 Vitis_vinife |
| Os03t0849900-01 | 0.30 Ananas_co | 0.37 Coffea_car | 0.37 Coffea_car |
| Os09t0433700-01 | 0.29 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os10t0487400-01 | 0.31 Ananas_co | 0.37 Coffea_car | 0.37 Coffea_car |
| Os05t0417200-01 | 0.27 Ananas_co | 0.37 Medicago_ | 0.37 Medicago_ |

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| Os05t0527100-00Zm00 | 0.30 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os03t0708900-01 | 0.21 Ananas_co | 0.37 Theobrom | 0.37 Theobrom |
| Os05t0471000-01 | 0.32 Musa_acur | 0.33 Dioscorea_ | 0.37 Vitis_vinife |
| Os04t0589900-01 | 0.24 Ananas_co | 0.31 Dioscorea_ | 0.37 Pistacia_ve |
| Os02t0739700-01 | 0.21 Ananas_co | 0.37 Populus_tr | 0.37 Populus_tr |
| Os08t0169700-01 | 0.23 Ananas_co | 0.29 Dioscorea_ | 0.37 Actinidia_c |
| Os12t0197400-01 | 0.30 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os07t0224900-02 | 0.25 Ananas_co | 0.29 Dioscorea_ | 0.37 Actinidia_c |
| Os01t0938600-01 | 0.22 Musa_acur | 0.37 Pistacia_ve | 0.37 Pistacia_ve |

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| Os02t0170300-01 | 0.22 Ananas_co | 0.35 Dioscorea_ | 0.37 Amborella |
| Os03t0640000-00 | 0.24 Ananas_co | 0.37 Glycine_ma | 0.37 Glycine_ma |
| Os02t0259100-02 | 0.37 Vitis_vinife | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os01t0688600-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.37 Trifolium_ |
| Os02t0301800-02Zm00 | 0.36 Musa_acur | 0.37 Populus_tr | 0.37 Populus_tr |
| Os01t0968600-00 | 0.27 Musa_acur | 0.36 Dioscorea_ | 0.37 Manihot_e |
| Os11t0683600-00 | 0.28 Ananas_co | 0.37 Manihot_e | 0.37 Manihot_e |
| Os12t0626300-01 | 0.19 Ananas_co | 0.37 Theobrom | 0.37 Theobrom |
| Os10t0494500-01 | 0.37 Vitis_vinife | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os08t0417000-01Zm00 | 0.17 Ananas_co | 0.37 Vitis_vinife | 0.37 Vitis_vinife |
| Os08t0305300-01 | 0.23 Ananas_co | 0.31 Dioscorea_ | 0.37 Prunus_avi |
| Os01t0966400-01 | 0.24 Ananas_co | 0.37 Citrus_cler | 0.37 Citrus_cler |
| Os08t0447200-01 | 0.31 Ananas_co | 0.37 Actinidia_c | 0.37 Actinidia_c |
| Os01t0786900-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.37 Vitis_vinife |
| Os01t0567400-00 | 0.37 Actinidia_c | 0.37 Actinidia_c | 0.37 Actinidia_c |

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| Os07t0173200-02 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.36 Rosa_chine |
| Os03t0837800-01 | 0.30 Ananas_co | 0.36 Amborella_ | 0.36 Amborella_ |
| Os08t0135300-01 | 0.22 Ananas_co | 0.36 Malus_dom | 0.36 Malus_dom |
| Os05t0209400-01 | 0.36 Vigna_radi | 0.36 Vigna_radi | 0.36 Vigna_radi |
| Os05t0182100-01 | 0.32 Ananas_co | 0.36 Populus_tr | 0.36 Populus_tr |
| Os12t0601800-01 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.36 Nymphaea |
| Os03t0700800-01 | 0.22 Ananas_co | 0.32 Dioscorea_ | 0.36 Vitis_vinife |
| Os10t0350500-01 | 0.31 Musa_acun | 0.32 Dioscorea_ | 0.36 Pistacia_ve |
| Os02t0800100-01 | 0.26 Ananas_co | 0.36 Beta_vulga | 0.36 Beta_vulga |
| Os06t0130600-01 | 0.31 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os06t0644800-01 | 0.25 Ananas_co | 0.36 Gossypium | 0.36 Gossypium |
| Os01t0816000-00 | 0.31 Musa_acun | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os04t0475500-01 | 0.24 Ananas_co | 0.27 Dioscorea_ | 0.36 Gossypium |
| Os10t0351500-01 | 0.15 Ananas_co | 0.36 Manihot_es | 0.36 Manihot_es |
| Os08t0386900-01 | 0.21 Ananas_co | 0.36 Theobroma | 0.36 Theobroma |
| Os02t0668500-02 | 0.24 Ananas_co | 0.30 Dioscorea_ | 0.36 Rosa_chine |
| Os10t0508600-01 | 0.31 Ananas_co | 0.36 Prunus_du | 0.36 Prunus_du |
| Os12t0533500-01 | 0.28 Musa_acun | 0.28 Dioscorea_ | 0.36 Pistacia_ve |
| Os02t0114700-01 | 0.31 Musa_acun | 0.36 Theobroma | 0.36 Theobroma |
| Os03t0254400-01 | 0.26 Ananas_co | 0.36 Actinidia_c | 0.36 Actinidia_c |
| Os05t0126200-01 | 0.31 Musa_acun | 0.34 Dioscorea_ | 0.36 Capsicum_ |
| Os05t0210400-00 | 0.35 Ananas_co | 0.36 Amborella_ | 0.36 Amborella_ |
| Os05t0550600-02 | 0.36 Ananas_co | 0.36 Beta_vulga | 0.36 Beta_vulga |
| Os01t0200500-01 | 0.31 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os06t0223700-01 | 0.28 Musa_acun | 0.36 Nymphaea | 0.36 Nymphaea |
| Os12t0538100-01 | 0.29 Musa_acun | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os04t0534300-01 | 0.32 Musa_acun | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os01t0629400-01 | 0.32 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |

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| Os01t0589700-01 | 0.25 Ananas_co | 0.36 Prunus_pe | 0.36 Prunus_pe |
| Os03t0648300-01Zm00 | 0.31 Ananas_co | 0.36 Gossypiu | 0.36 Gossypiu |
| Os01t0736600-01 | 0.34 Ananas_co | 0.36 Arabis_alpi | 0.36 Arabis_alp |
| Os03t0646200-01 | 0.23 Ananas_co | 0.36 Nymphaea | 0.36 Nymphaea |
| Os07t0150500-01 | 0.22 Ananas_co | 0.34 Dioscorea_ | 0.36 Vitis_vinife |
| Os01t0607300-01 | 0.25 Ananas_co | 0.36 Prunus_avi | 0.36 Prunus_avi |
| Os01t0187900-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.36 Ipomoea_t |

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| Os03t0733600-01 | 0.23 Musa_acu | 0.33 Dioscorea_ | 0.36 Nymphaea |
| Os08t0230500-01 | 0.25 Ananas_co | 0.27 Dioscorea_ | 0.36 Gossypiu |
| Os09t0498600-01 | 0.35 Ananas_co | 0.36 Prunus_avi | 0.36 Prunus_avi |
| Os03t0338600-01 | 0.29 Ananas_co | 0.36 Actinidia_ | 0.36 Actinidia_ |
| Os10t0532100-01 | 0.30 Ananas_co | 0.35 Dioscorea_ | 0.36 Manihot_e |
| Os09t0410700-00 | 0.32 Ananas_co | 0.36 Prunus_du | 0.36 Prunus_du |
| Os10t0577000-02 | 0.25 Ananas_co | 0.32 Dioscorea_ | 0.36 Pistacia_ve |

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| Os02t0652000-01 | 0.22 Ananas_co | 0.33 Dioscorea_ | 0.36 Ipomoea_t |
| Os06t0351500-01 | 0.32 Ananas_co | 0.36 Theobrom | 0.36 Theobrom |
| Os05t0404600-01 | 0.23 Ananas_co | 0.36 Actinidia_ | 0.36 Actinidia_ |
| Zm00001eb019630_P00 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.36 Olea_euro |

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| Os10t0480500-01 | 0.31 | Ananas_co | 0.32 | Dioscorea_ | 0.36 | Malus_do |
| Os06t0152200-01 | 0.24 | Ananas_co | 0.36 | Ipomoea_t | 0.36 | Ipomoea_t |
| Os12t0488800-01 | 0.21 | Ananas_co | 0.31 | Dioscorea_ | 0.36 | Populus_tr |
| Os09t0275400-01 | 0.32 | Ananas_co | 0.36 | Manihot_e | 0.36 | Manihot_e |

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| Os06t0176300-00Zm00 | 0.23 | Ananas_co | 0.33 | Dioscorea_ | 0.36 | Theobrom |
| Os02t0767100-01 | 0.27 | Ananas_co | 0.36 | Dioscorea_ | 0.36 | Vitis_vinife |
| Os10t0358700-01 | 0.21 | Ananas_co | 0.29 | Dioscorea_ | 0.36 | Actinidia_ |
| Os04t0584900-01 | 0.30 | Ananas_co | 0.36 | Vitis_vinife | 0.36 | Vitis_vinife |
| Os03t0106500-01 | 0.29 | Ananas_co | 0.36 | Theobrom | 0.36 | Theobrom |
| Os01t0881400-00 | 0.30 | Musa_acu | 0.36 | Pistacia_ve | 0.36 | Pistacia_ve |

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| Os10t0389200-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.36 | Pistacia_ve |

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| Os11t0544600-01 | 0.30 | Ananas_co | 0.30 | Dioscorea_ | 0.36 | Manihot_e |
| Os06t0603400-02 | 0.32 | Musa_acu | 0.36 | Populus_tr | 0.36 | Populus_tr |
| Os03t0197000-01 | 0.25 | Ananas_co | 0.31 | Dioscorea_ | 0.36 | Corchorus |
| Os06t0692600-01 | 0.36 | Theobrom | 0.36 | Theobrom | 0.36 | Theobrom |
| Os10t0534700-01 | 0.31 | Ananas_co | 0.36 | Cannabis_ | 0.36 | Cannabis_ |
| Os02t0234200-01 | 0.26 | Ananas_co | 0.29 | Dioscorea_ | 0.36 | Vitis_vinife |
| Os06t0638500-00 | 0.21 | Ananas_co | 0.32 | Dioscorea_ | 0.36 | Malus_do |
| Os06t0521300-00 | 0.30 | Musa_acu | 0.36 | Vitis_vinife | 0.36 | Vitis_vinife |
| Os05t0592300-01 | 0.27 | Ananas_co | 0.34 | Dioscorea_ | 0.36 | Vitis_vinife |
| Os03t0325500-01 | 0.31 | Musa_acu | 0.35 | Dioscorea_ | 0.36 | Theobrom |
| Os03t0356526-00 | 0.31 | Musa_acu | 0.36 | Citrus_cle | 0.36 | Citrus_cle |
| Os04t0344100-01Zm00 | 0.26 | Ananas_co | 0.36 | Prunus_du | 0.36 | Prunus_du |
| Os01t0195200-01 | 0.24 | Ananas_co | 0.34 | Dioscorea_ | 0.36 | Theobrom |
| Os01t0589500-01 | 0.27 | Musa_acu | 0.36 | Nicotiana_ | 0.36 | Nicotiana_ |
| Os07t0602900-01 | 0.28 | Musa_acu | 0.34 | Dioscorea_ | 0.36 | Gossypiu |
| Os01t0704200-01 | 0.30 | Musa_acu | 0.36 | Vitis_vinife | 0.36 | Vitis_vinife |
| Os02t0726400-01 | 0.18 | Ananas_co | 0.36 | Vitis_vinife | 0.36 | Vitis_vinife |
| Os03t0233000-01 | 0.29 | Ananas_co | 0.36 | Actinidia_ | 0.36 | Actinidia_ |
| Os01t0702400-01Zm00 | 0.26 | Ananas_co | 0.36 | Actinidia_ | 0.36 | Actinidia_ |
| Os11t0167300-01 | 0.25 | Ananas_co | 0.31 | Dioscorea_ | 0.36 | Theobrom |
| Os06t0711700-00 | 0.27 | Ananas_co | 0.35 | Dioscorea_ | 0.36 | Cucumis_ |
| Os09t0370200-01 | 0.19 | Ananas_co | 0.36 | Citrus_cle | 0.36 | Citrus_cle |
| Os05t0497675-01 | 0.28 | Ananas_co | 0.36 | Manihot_e | 0.36 | Manihot_e |
| Os02t0557100-01 | 0.27 | Ananas_co | 0.36 | Citrus_cle | 0.36 | Citrus_cle |
| Os02t0204500-01Zm00 | 0.31 | Ananas_co | 0.36 | Beta_vulga | 0.36 | Beta_vulga |
| Os07t0619100-01 | 0.30 | Ananas_co | 0.36 | Prunus_du | 0.36 | Prunus_du |
| Os02t0672100-01 | 0.36 | Dioscorea_ | 0.36 | Dioscorea_ | 0.36 | Vitis_vinife |

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| Os03t0797600-01 | 0.22 Ananas_co | 0.30 Dioscorea_ | 0.36 Vitis_vinife |

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| Os07t0614400-01Zm00 | 0.30 Musa_acu | 0.36 Actinidia_ | 0.36 Actinidia_ |
| Os10t0513300-01 | 0.32 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os11t0124900-01Zm00 | 0.28 Ananas_co | 0.34 Dioscorea_ | 0.36 Trifolium_ |

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| Os05t0530400-01 | 0.22 Ananas_co | 0.35 Dioscorea_ | 0.36 Actinidia_ |
| Os11t0207100-01 | 0.30 Musa_acu | 0.36 Prunus_du | 0.36 Prunus_du |
| Os01t0618700-01 | 0.35 Ananas_co | 0.36 Theobrom | 0.36 Theobrom |

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| Os01t0230200-01 | 0.36 Corchorus | 0.36 Corchorus | 0.36 Corchorus |
| Os05t0210500-00 | 0.30 Musa_acu | 0.36 Manihot_e | 0.36 Manihot_e |
| Os05t0100900-01 | 0.29 Musa_acu | 0.36 Prunus_pe | 0.36 Prunus_pe |

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| Os03t0362500-00Zm00 | 0.30 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os05t0312500-01 | 0.25 Ananas_co | 0.29 Dioscorea_ | 0.36 Cynara_ca |
| Os01t0172900-00 | 0.29 Ananas_co | 0.36 Citrus_cle | 0.36 Citrus_cle |
| Os09t0542800-01 | 0.21 Musa_acu | 0.28 Dioscorea_ | 0.36 Brassica_n |
| Os02t0193500-01 | 0.29 Ananas_co | 0.36 Citrus_cle | 0.36 Citrus_cle |
| Os02t0762200-01 | 0.30 Ananas_co | 0.34 Dioscorea_ | 0.36 Rosa_chine |
| Zm00001eb405720_P00 | 0.22 Ananas_co | 0.31 Dioscorea_ | 0.36 Citrus_cle |
| Os05t0169400-01 | 0.29 Musa_acu | 0.36 Vitis_vinife | 0.36 Vitis_vinife |

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| Os04t0544200-01 | 0.23 Ananas_co | 0.34 Dioscorea_ | 0.36 Ipomoea_t |
| Os10t0516200-00 | 0.26 Musa_acu | 0.34 Dioscorea_ | 0.36 Prunus_pe |
| Os12t0159600-01 | 0.21 Ananas_co | 0.32 Dioscorea_ | 0.36 Nicotiana_ |
| Os05t0380900-01 | 0.16 Ananas_co | 0.34 Dioscorea_ | 0.36 Daucus_ca |

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| Os07t0552800-01 | 0.36 Nymphaea | 0.36 Nymphaea | 0.36 Nymphaea |
| Os06t0184866-01 | 0.25 Ananas_co | 0.35 Dioscorea_ | 0.36 Coffea_ca |
| Os10t0122300-00Zm00 | 0.31 Ananas_co | 0.36 Rosa_chine | 0.36 Rosa_chine |
| Os01t0735900-01 | 0.26 Ananas_co | 0.33 Dioscorea_ | 0.36 Olea_euro |
| Os02t0293800-02 | 0.30 Ananas_co | 0.36 Dioscorea_ | 0.36 Pistacia_ve |

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| Os06t0681300-02Zm00 | 0.28 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os02t0241100-01 | 0.31 Ananas_co | 0.36 Prunus_avi | 0.36 Prunus_avi |
| Os05t0151300-01 | 0.26 Ananas_co | 0.36 Nicotiana_ | 0.36 Nicotiana_ |
| Os07t0501700-01 | 0.34 Musa_acur | 0.34 Dioscorea_ | 0.36 Malus_do |
| Os07t0123300-01 | 0.22 Ananas_co | 0.36 Actinidia_c | 0.36 Actinidia_c |
| Os04t0617600-01 | 0.25 Ananas_co | 0.33 Dioscorea_ | 0.36 Actinidia_c |
| Os01t0595201-00 | 0.27 Musa_acur | 0.35 Dioscorea_ | 0.36 Theobrom |

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| Os05t0580500-01 | 0.22 Musa_acur | 0.22 Dioscorea_ | 0.36 Populus_tr |
| Os05t0559000-01 | 0.26 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |

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| Os04t0382200-01 | 0.29 Musa_acur | 0.34 Dioscorea_ | 0.36 Vitis_vinife |
| Os05t0475700-01 | 0.21 Ananas_co | 0.34 Dioscorea_ | 0.36 Malus_do |
| Os02t0158600-01 | 0.34 Ananas_co | 0.35 Dioscorea_ | 0.36 Gossypiu |

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| Os03t0795900-01 | 0.31 Ananas_co | 0.34 Dioscorea_ | 0.36 Corchorus |

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| Os03t0301200-01 | 0.27 Ananas_co | 0.36 Nymphaea | 0.36 Nymphaea |
| Os03t0616500-00 | 0.26 Ananas_co | 0.33 Dioscorea_ | 0.36 Populus_tr |
| Os05t0133900-02 | 0.23 Ananas_co | 0.31 Dioscorea_ | 0.36 Prunus_du |
| Os10t0510500-01 | 0.20 Ananas_co | 0.36 Gossypiu | 0.36 Gossypiu |
| Os02t0150900-01 | 0.29 Musa_acur | 0.31 Dioscorea_ | 0.36 Malus_do |

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| Os02t0611200-01 | 0.16 Musa_acur | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os07t0489950-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.36 Vitis_vinife |
| Os10t0579800-01 | 0.19 Ananas_co | 0.36 Manihot_e | 0.36 Manihot_e |
| Os09t0123300-01 | 0.23 Ananas_co | 0.36 Dioscorea_ | 0.36 Vitis_vinife |

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| Zm00001eb314550_P00 | 0.24 Ananas_co | 0.33 Dioscorea_ | 0.36 Vitis_vinife |
| Os03t0295600-01 | 0.24 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |

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| Os01t0614900-01 | 0.35 Ananas_co | 0.36 Vitis_vinife | 0.36 Vitis_vinife |
| Os12t0561200-01 | 0.34 Musa_acur | 0.34 Dioscorea_ | 0.36 Actinidia_c |
| Os05t0557200-01 | 0.26 Ananas_co | 0.36 Prunus_per | 0.36 Prunus_per |
| Os10t0510300-01 | 0.33 Ananas_co | 0.36 Nymphaea | 0.36 Nymphaea |
| Os05t0151100-00 | 0.31 Ananas_co | 0.32 Dioscorea_ | 0.36 Actinidia_c |
| Os07t0668700-01 | 0.29 Musa_acur | 0.33 Dioscorea_ | 0.36 Theobroma |
| Os03t0819400-01 | 0.33 Musa_acur | 0.36 Gossypium | 0.36 Gossypium |
| Os08t0262500-01 | 0.26 Ananas_co | 0.36 Populus_tr | 0.36 Populus_tr |
| Os10t0443000-00 | 0.19 Ananas_co | 0.29 Dioscorea_ | 0.36 Vitis_vinife |
| Os03t0232200-01 | 0.36 Pistacia_ve | 0.36 Pistacia_ve | 0.36 Pistacia_ve |
| Os03t0135100-01 | 0.27 Musa_acur | 0.28 Dioscorea_ | 0.36 Theobroma |
| Os01t0777000-00 | 0.22 Ananas_co | 0.23 Dioscorea_ | 0.36 Citrus_cler |

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| Os11t0621300-00 | 0.28 Ananas_co | 0.34 Dioscorea_ | 0.36 Prunus_du |
| Os07t0223700-00 | 0.23 Musa_acur | 0.33 Dioscorea_ | 0.36 Vitis_vinife |
| Os09t0458900-01 | 0.13 Musa_acur | 0.31 Dioscorea_ | 0.36 Ipomoea_t |
| Os09t0462200-01 | 0.29 Musa_acur | 0.36 Prunus_per | 0.36 Prunus_per |
| Os07t0667100-00 | 0.28 Ananas_co | 0.36 Malus_dom | 0.36 Malus_dom |
| Os02t0670400-01 | 0.35 Musa_acur | 0.36 Nymphaea | 0.36 Nymphaea |
| Os01t0908500-01 | 0.25 Ananas_co | 0.26 Dioscorea_ | 0.36 Actinidia_c |

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| Os09t0456200-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.36 Manihot_es |
| Os05t0534000-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.36 Citrus_cler |
| Os02t0180400-00 | 0.26 Musa_acur | 0.34 Dioscorea_ | 0.36 Coffea_car |
| Os04t0640800-01 | 0.29 Musa_acur | 0.36 Coffea_car | 0.36 Coffea_car |

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| Os01t0745700-01Zm00 | 0.36 Nicotiana_ | 0.36 Nicotiana_ | 0.36 Nicotiana_ |
| Os09t0413300-00 | 0.22 Ananas_co | 0.31 Dioscorea_ | 0.36 Prunus_pe |
| Os06t0176700-01Zm00 | 0.16 Ananas_co | 0.32 Dioscorea_ | 0.35 Pistacia_ve |
| Os06t0663900-03 | 0.25 Ananas_co | 0.33 Dioscorea_ | 0.35 Vitis_vinife |
| Os03t0262300-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.35 Prunus_du |
| Os05t0559900-01 | 0.32 Ananas_co | 0.35 Dioscorea_ | 0.35 Actinidia_c |
| Os10t0324900-01 | 0.32 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os12t0600200-03 | 0.32 Ananas_co | 0.35 Solanum_t | 0.35 Solanum_t |
| Os02t0636700-01 | 0.29 Ananas_co | 0.35 Gossypiu | 0.35 Gossypiu |
| Os05t0352700-00Zm00 | 0.24 Musa_acu | 0.34 Dioscorea_ | 0.35 Vitis_vinife |
| Os12t0548200-02 | 0.27 Musa_acu | 0.33 Dioscorea_ | 0.35 Nicotiana_ |
| Os12t0502700-01Zm00 | 0.29 Ananas_co | 0.35 Prunus_pe | 0.35 Prunus_pe |
| Os02t0244300-01 | 0.21 Ananas_co | 0.32 Dioscorea_ | 0.35 Prunus_du |
| Os02t0704500-01 | 0.35 Prunus_pe | 0.35 Prunus_pe | 0.35 Prunus_pe |
| Os06t0712300-01 | 0.31 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os01t0766600-01 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.35 Theobrom |
| Os04t0548700-01Zm00 | 0.35 Corchorus | 0.35 Corchorus | 0.35 Corchorus |
| Os01t0605100-01 | 0.14 Ananas_co | 0.28 Dioscorea_ | 0.35 Prunus_du |

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| Os01t0158900-01 | 0.25 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os12t0613600-01 | 0.29 Ananas_co | 0.32 Dioscorea_ | 0.35 Malus_dom |
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| Os03t0191000-01 | 0.25 Ananas_co | 0.32 Dioscorea_ | 0.35 Actinidia_c |
| Os02t0720600-01Zm00 | 0.23 Ananas_co | 0.35 Olea_euro | 0.35 Olea_euro |
| Os03t0659900-01 | 0.26 Ananas_co | 0.35 Pistacia_ve | 0.35 Pistacia_ve |
| Os12t0464400-01 | 0.31 Ananas_co | 0.35 Prunus_pe | 0.35 Prunus_pe |
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| Os05t0426200-02 | 0.30 Musa_acu | 0.35 Manihot_e | 0.35 Manihot_e |
| Os06t0725100-01 | 0.31 Ananas_co | 0.33 Dioscorea_ | 0.35 Cynara_ca |
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| Os07t0692600-01 | 0.21 Ananas_co | 0.28 Dioscorea_ | 0.35 Pistacia_ve |
| Os08t0243900-01 | 0.22 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
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| Os01t0826400-01 | 0.35 Glycine_m | 0.35 Glycine_m | 0.35 Glycine_m |
| Os02t0658500-01 | 0.21 Ananas_co | 0.25 Dioscorea_ | 0.35 Gossypiu |
| Os07t0598500-01 | 0.22 Ananas_co | 0.30 Dioscorea_ | 0.35 Manihot_e |
| Os02t0768000-01 | 0.32 Ananas_co | 0.35 Amborella_ | 0.35 Amborella_ |
| Os11t0293900-01Zm00 | 0.21 Ananas_co | 0.35 Dioscorea_ | 0.35 Actinidia_c |
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| Os02t0116600-01 | 0.23 Ananas_co | 0.35 Amborella_ | 0.35 Amborella_ |
| Os02t0621500-01 | 0.21 Musa_acu | 0.35 Beta_vulga | 0.35 Beta_vulga |
| Os06t0308800-01 | 0.29 Ananas_co | 0.32 Dioscorea_ | 0.35 Rosa_chin |
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| Os02t0139400-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.35 Vitis_vinife |

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| Os05t0410200-01 | 0.25 | Musa_acu | 0.28 | Dioscorea_ | 0.35 | Daucus_ca |
| Os02t0619600-01 | 0.30 | Dioscorea_ | 0.30 | Dioscorea_ | 0.35 | Vitis_vinife |
| Os03t0260100-01 | 0.21 | Ananas_co | 0.35 | Amborella_ | 0.35 | Amborella_ |
| Os10t0114500-01 | 0.33 | Musa_acu | 0.35 | Cannabis_ | 0.35 | Cannabis_ |
| Os03t0140100-01 | 0.23 | Ananas_co | 0.35 | Dioscorea_ | 0.35 | Pistacia_ve |
| Os12t0610600-01 | 0.35 | Musa_acu | 0.35 | Trifolium_ | 0.35 | Trifolium_ |
| Os06t0332700-00 | 0.34 | Dioscorea_ | 0.34 | Dioscorea_ | 0.35 | Pistacia_ve |
| Os02t0690500-01 | 0.28 | Ananas_co | 0.35 | Nicotiana_ | 0.35 | Nicotiana_ |
| Zm00001eb337900_P00 | 0.24 | Musa_acu | 0.35 | Amborella_ | 0.35 | Amborella_ |
| Os06t0495700-00 | 0.28 | Musa_acu | 0.35 | Pistacia_ve | 0.35 | Pistacia_ve |
| Os11t0163500-01 | 0.24 | Ananas_co | 0.34 | Dioscorea_ | 0.35 | Vitis_vinife |
| Os01t0927500-01 | 0.22 | Ananas_co | 0.30 | Dioscorea_ | 0.35 | Vitis_vinife |
| Os05t0496000-01 | 0.33 | Ananas_co | 0.35 | Amborella_ | 0.35 | Amborella_ |
| Os06t0184900-01 | 0.12 | Ananas_co | 0.14 | Dioscorea_ | 0.35 | Ipomoea_t |
| Os09t0511600-01 | 0.29 | Ananas_co | 0.35 | Amborella_ | 0.35 | Amborella_ |
| Os08t0237000-01Zm00 | 0.35 | Beta_vulga | 0.35 | Beta_vulga | 0.35 | Beta_vulga |
| Os12t0562300-01 | 0.10 | Ananas_co | 0.35 | Pistacia_ve | 0.35 | Pistacia_ve |
| Zm00001eb004590_P00 | 0.22 | Ananas_co | 0.35 | Prunus_avi | 0.35 | Prunus_avi |
| Os10t0465000-01 | 0.20 | Ananas_co | 0.35 | Citrus_cle | 0.35 | Citrus_cle |
| Os11t0148600-01 | 0.22 | Ananas_co | 0.26 | Dioscorea_ | 0.35 | Vigna_ang |
| Os12t0574000-01 | 0.26 | Ananas_co | 0.35 | Pistacia_ve | 0.35 | Pistacia_ve |
| Zm00001eb100880_P00 | 0.35 | Ipomoea_t | 0.35 | Ipomoea_t | 0.35 | Ipomoea_t |
| Os02t0656200-01 | 0.27 | Ananas_co | 0.31 | Dioscorea_ | 0.35 | Actinidia_c |

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| Os06t0708200-01 | 0.35 Theobrom | 0.35 Theobrom | 0.35 Theobrom |
| Os07t0585700-01 | 0.34 Musa_acu | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os03t0197800-00 | 0.34 Musa_acu | 0.35 Glycine_m | 0.35 Glycine_m |
| Os08t0360300-00 | 0.35 Citrus_cle | 0.35 Citrus_cle | 0.35 Citrus_cle |
| Os02t0818000-01 | 0.29 Musa_acu | 0.32 Dioscorea_ | 0.35 Amborella_ |
| Os03t0245800-02 | 0.35 Solanum_l | 0.35 Solanum_l | 0.35 Solanum_l |
| Zm00001eb257360_P00 | 0.31 Musa_acu | 0.32 Dioscorea_ | 0.35 Theobrom |
| Os06t0214800-01 | 0.35 Actinidia_c | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os01t0719600-01 | 0.15 Ananas_co | 0.34 Dioscorea_ | 0.35 Actinidia_c |
| Os02t0566400-01 | 0.27 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os11t0492800-00Zm00 | 0.30 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os06t0499000-01 | 0.24 Ananas_co | 0.35 Manihot_e | 0.35 Manihot_e |
| Os04t0615700-01 | 0.35 Prunus_du | 0.35 Prunus_du | 0.35 Prunus_du |
| Os01t0260100-01 | 0.25 Ananas_co | 0.35 Corchorus | 0.35 Corchorus |
| Os09t0494300-02 | 0.26 Ananas_co | 0.35 Dioscorea_ | 0.35 Vitis_vinife |
| Os04t0540200-01 | 0.24 Ananas_co | 0.35 Gossypiu | 0.35 Gossypiu |
| Os04t0378200-01 | 0.30 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os05t0512000-01 | 0.28 Musa_acu | 0.32 Dioscorea_ | 0.35 Vitis_vinife |

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| Os04t0597600-01 | 0.20 Ananas_co | 0.35 Rosa_chine | 0.35 Rosa_chine |
| Os03t0314400-01 | 0.29 Ananas_co | 0.33 Dioscorea_ | 0.35 Pistacia_ve |
| Os02t0582200-01 | 0.26 Musa_acur | 0.35 Pistacia_ve | 0.35 Pistacia_ve |

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| Os04t0613000-01 | 0.27 Ananas_co | 0.35 Prunus_du | 0.35 Prunus_du |
| Os10t0492400-01 | 0.24 Ananas_co | 0.35 Populus_tr | 0.35 Populus_tr |
| Zm00001eb227020_P00 | 0.32 Musa_acur | 0.34 Dioscorea_ | 0.35 Vitis_vinife |
| Os12t0114200-01 | 0.26 Ananas_co | 0.35 Dioscorea_ | 0.35 Prunus_du |
| Zm00001eb347360_P00 | 0.23 Ananas_co | 0.30 Dioscorea_ | 0.35 Manihot_e |
| Os11t0279750-00 | 0.35 Phaseolus_ | 0.35 Phaseolus_ | 0.35 Phaseolus_ |
| Os02t0717700-01 | 0.26 Ananas_co | 0.35 Nymphaea | 0.35 Nymphaea |
| Os01t0215700-01 | 0.28 Ananas_co | 0.33 Dioscorea_ | 0.35 Prunus_pe |
| Os02t0219900-01 | 0.24 Ananas_co | 0.33 Dioscorea_ | 0.35 Vitis_vinife |
| Os08t0113200-01 | 0.19 Ananas_co | 0.28 Dioscorea_ | 0.35 Solanum_l |

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| Os02t0576600-01 | 0.27 Ananas_co | 0.29 Dioscorea_ | 0.35 Arabidopsi |
| Os10t0438500-01 | 0.28 Ananas_co | 0.34 Dioscorea_ | 0.35 Ipomoea_t |
| Os04t0663700-01 | 0.24 Ananas_co | 0.28 Dioscorea_ | 0.35 Corchorus |

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| Os04t0645100-01 | 0.33 Musa_acur | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os01t0351300-01 | 0.34 Musa_acur | 0.35 Theobroma | 0.35 Theobroma |
| Os11t0155100-01 | 0.19 Ananas_co | 0.35 Theobroma | 0.35 Theobroma |
| Os03t0804200-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.35 Actinidia_c |
| Os02t0771800-01 | 0.23 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |

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| Os05t0489700-01 | 0.30 Ananas_co | 0.35 Rosa_chine | 0.35 Rosa_chine |

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| Os10t0492200-01 | 0.08 Ananas_co | 0.35 Pistacia_ve | 0.35 Pistacia_ve |
| Os04t0456900-00 | 0.31 Ananas_co | 0.35 Ipomoea_t | 0.35 Ipomoea_t |

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| Os02t0714500-02 | 0.26 Ananas_co | 0.30 Dioscorea_ | 0.35 Vitis_vinife |
| Os03t0179700-00 | 0.15 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os03t0306100-00 | 0.32 Ananas_co | 0.35 Citrullus_la | 0.35 Citrullus_la |
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| Os12t0163600-01 | 0.34 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
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| Os04t0347800-01 | 0.28 Ananas_co | 0.28 Dioscorea_ | 0.35 Malus_dom |
| Os03t0765900-01 | 0.32 Ananas_co | 0.35 Ipomoea_t | 0.35 Ipomoea_t |
| Os09t0314300-02 | 0.26 Musa_acum | 0.32 Dioscorea_ | 0.35 Actinidia_c |
| Zm00001eb202020_P00 | 0.24 Ananas_co | 0.35 Manihot_e | 0.35 Manihot_e |

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| Os12t0593000-01Zm00 | 0.27 Ananas_co | 0.33 Dioscorea_ | 0.35 Vitis_vinife |
| Os03t0435200-01Zm00 | 0.27 Ananas_co | 0.35 Populus_tr | 0.35 Populus_tr |
| Os02t0122400-01 | 0.28 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os04t0544500-01 | 0.27 Ananas_co | 0.32 Dioscorea_ | 0.35 Corchorus_ |
| Os01t0304300-01 | 0.27 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os02t0625100-00 | 0.22 Ananas_co | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os01t0966700-01 | 0.26 Musa_acum | 0.35 Nicotiana_ | 0.35 Nicotiana_ |
| Os02t0116800-01 | 0.31 Ananas_co | 0.35 Theobroma | 0.35 Theobroma |
| Os03t0740800-01 | 0.26 Musa_acum | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os03t0120400-01 | 0.20 Ananas_co | 0.35 Rosa_chine | 0.35 Rosa_chine |
| Os04t0679100-01 | 0.35 Glycine_ma | 0.35 Glycine_ma | 0.35 Glycine_ma |

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| Os08t0115200-01 | 0.18 | Ananas_co | 0.35 | Vitis_vinife | 0.35 | Vitis_vinife |
| Zm00001eb165410_P00 | 0.23 | Ananas_co | 0.26 | Dioscorea_ | 0.35 | Helianthus |
| Os03t0386800-01 | 0.34 | Ananas_co | 0.35 | Vitis_vinife | 0.35 | Vitis_vinife |
| Os07t0656100-01 | 0.32 | Ananas_co | 0.35 | Cannabis_ | 0.35 | Cannabis_ |

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| Os03t0135700-01 | 0.34 | Musa_acu | 0.35 | Ipomoea_t | 0.35 | Ipomoea_t |
| Os05t0430800-01 | 0.27 | Ananas_co | 0.31 | Dioscorea_ | 0.35 | Actinidia_c |

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| Os02t0710300-01 | 0.29 | Ananas_co | 0.35 | Prunus_du | 0.35 | Prunus_du |
| Os02t0661800-01 | 0.34 | Ananas_co | 0.35 | Vitis_vinife | 0.35 | Vitis_vinife |

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| Os05t0474400-01 | 0.28 | Ananas_co | 0.35 | Malus_do | 0.35 | Malus_do |

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| Os06t0196700-02 | 0.34 | Dioscorea_ | 0.34 | Dioscorea_ | 0.35 | Vitis_vinife |
| Os02t0772500-01 | 0.23 | Ananas_co | 0.28 | Dioscorea_ | 0.35 | Cucumis_s |
| Os03t0227400-01 | 0.31 | Ananas_co | 0.31 | Dioscorea_ | 0.35 | Malus_do |

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| Os03t0229500-00 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.35 Manihot_e |
| Os09t0563250-01 | 0.27 Ananas_co | 0.29 Dioscorea_ | 0.35 Vitis_vinife |

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| Os01t0788800-01 | 0.35 Nicotiana_ | 0.35 Nicotiana_ | 0.35 Nicotiana_ |

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| Os04t0467901-01 | 0.35 Theobrom | 0.35 Theobrom | 0.35 Theobrom |
| Os06t0244200-00Zm00 | 0.35 Actinidia_ | 0.35 Actinidia_ | 0.35 Actinidia_ |
| Os01t0901900-01 | 0.28 Ananas_co | 0.35 Gossypiu | 0.35 Gossypiu |
| Os03t0237500-01 | 0.34 Dioscorea_ | 0.34 Dioscorea_ | 0.35 Solanum_t |

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| Os10t0419300-01 | 0.29 Ananas_co | 0.30 Dioscorea_ | 0.35 Vigna_ang |
| Zm00001eb375410_P00 | 0.35 Vitis_vinife | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os05t0508400-01 | 0.26 Ananas_co | 0.30 Dioscorea_ | 0.35 Amborella_ |
| Os10t0546200-00Zm00 | 0.29 Ananas_co | 0.35 Lupinus_a | 0.35 Lupinus_a |

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| Os01t0517500-01 | 0.35 Nymphaea | 0.35 Nymphaea | 0.35 Nymphaea |
| Os09t0526600-02Zm00 | 0.35 Ipomoea_t | 0.35 Ipomoea_t | 0.35 Ipomoea_t |

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| Os01t0937050-01 | 0.19 Ananas_co | 0.35 Coffea_car | 0.35 Coffea_car |

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| Os09t0562600-01Zm00 | 0.35 Vitis_vinife | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os09t0482000-01 | 0.35 Manihot_e | 0.35 Manihot_e | 0.35 Manihot_e |
| Os07t0643100-01 | 0.24 Ananas_co | 0.33 Dioscorea_ | 0.35 Prunus_per |
| Os05t0491500-01 | 0.35 Prunus_du | 0.35 Prunus_du | 0.35 Prunus_du |
| Os11t0491500-00 | 0.35 Corchorus_ | 0.35 Corchorus_ | 0.35 Corchorus_ |
| Os03t0283300-01 | 0.29 Ananas_co | 0.35 Nicotiana_ | 0.35 Nicotiana_ |
| Os02t0565600-01 | 0.31 Musa_acur | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os03t0217000-01 | 0.33 Musa_acur | 0.35 Helianthus | 0.35 Helianthus |
| Os04t0440100-01 | 0.33 Musa_acur | 0.35 Vitis_vinife | 0.35 Vitis_vinife |

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| Os10t0421800-01 | 0.26 Ananas_co | 0.29 Dioscorea_ | 0.35 Theobrom |
| Os01t0723100-01 | 0.19 Musa_acur | 0.35 Vitis_vinife | 0.35 Vitis_vinife |

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| Os03t0140200-01 | 0.21 Ananas_co | 0.35 Dioscorea_ | 0.35 Pistacia_ve |
| Os05t0500500-01 | 0.24 Musa_acur | 0.35 Vitis_vinife | 0.35 Vitis_vinife |
| Os04t0532100-01Zm00 | 0.34 Musa_acur | 0.35 Helianthus | 0.35 Helianthus |
| Os04t0403701-01 | 0.25 Ananas_co | 0.34 Dioscorea_ | 0.35 Vitis_vinife |
| Os12t0177500-01 | 0.20 Ananas_co | 0.35 Actinidia_c | 0.35 Actinidia_c |
| Os03t0685100-01 | 0.29 Musa_acur | 0.31 Dioscorea_ | 0.34 Medicago_ |
| Os12t0527800-01 | 0.26 Musa_acur | 0.34 Corchorus_ | 0.34 Corchorus_ |
| Os12t0620600-01 | 0.31 Ananas_co | 0.34 Corchorus_ | 0.34 Corchorus_ |
| Os06t0101300-01 | 0.34 Actinidia_c | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os04t0677400-02 | 0.22 Ananas_co | 0.32 Dioscorea_ | 0.34 Vitis_vinife |
| Os01t0180600-01 | 0.27 Ananas_co | 0.34 Theobrom | 0.34 Theobrom |
| Os02t0818800-01 | 0.34 Pistacia_ve | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os01t0815800-01 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.34 Vitis_vinife |
| Os01t0144700-01 | 0.30 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |

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| Os12t0534200-01 | 0.27 Ananas_co | 0.34 Manihot_es | 0.34 Manihot_es |
| Os12t0498400-01 | 0.24 Ananas_co | 0.32 Dioscorea_ | 0.34 Citrus_cler |
| Os04t0483200-01 | 0.22 Ananas_co | 0.32 Dioscorea_ | 0.34 Prunus_per |

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| Os02t0810200-01 | 0.24 Ananas_co | 0.30 Dioscorea_ | 0.34 Vitis_vinife |
| Os08t0543600-01 | 0.26 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |

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| Os02t0590800-00 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.34 Theobroma |
| Os09t0514900-01 | 0.22 Ananas_co | 0.34 Amborella_ | 0.34 Amborella_ |
| Os04t0110500-02 | 0.20 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Zm00001eb417780_P00 | 0.25 Ananas_co | 0.34 Helianthus | 0.34 Helianthus |
| Os04t0388800-01 | 0.25 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os09t0461900-01 | 0.32 Musa_acur | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os02t0753500-01 | 0.22 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os01t0754000-01 | 0.31 Musa_acur | 0.34 Cynara_car | 0.34 Cynara_car |
| Os08t0266600-01 | 0.23 Ananas_co | 0.32 Dioscorea_ | 0.34 Actinidia_c |
| Os09t0542200-01 | 0.22 Ananas_co | 0.32 Dioscorea_ | 0.34 Populus_tr |
| Os01t0865400-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.34 Actinidia_c |
| Os04t0669100-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.34 Prunus_per |
| Os07t0584500-01 | 0.34 Vigna_angu | 0.34 Vigna_angu | 0.34 Vigna_angu |
| Os05t0163900-01 | 0.26 Ananas_co | 0.30 Dioscorea_ | 0.34 Actinidia_c |
| Os01t0170100-01 | 0.26 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |

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| Os08t0137400-01 | 0.34 Musa_acur | 0.34 Ipomoea_t | 0.34 Ipomoea_t |
| Zm00001eb157300_P00 | 0.25 Ananas_co | 0.34 Corchorus_ | 0.34 Corchorus_ |
| Os03t0324800-01 | 0.34 Ipomoea_t | 0.34 Ipomoea_t | 0.34 Ipomoea_t |
| Os09t0540500-01 | 0.30 Ananas_co | 0.34 Beta_vulga | 0.34 Beta_vulga |
| Os02t0717200-00 | 0.34 Citrullus_la | 0.34 Citrullus_la | 0.34 Citrullus_la |
| Os07t0177100-01 | 0.24 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os02t0130300-02 | 0.34 Amborella_ | 0.34 Amborella_ | 0.34 Amborella_ |
| Os01t0901000-01 | 0.30 Ananas_co | 0.33 Dioscorea_ | 0.34 Vitis_vinife |
| Os04t0667900-01 | 0.30 Ananas_co | 0.34 Theobroma | 0.34 Theobroma |
| Os10t0484300-01 | 0.24 Ananas_co | 0.34 Manihot_es | 0.34 Manihot_es |
| Os01t0121300-01 | 0.31 Dioscorea_ | 0.31 Dioscorea_ | 0.34 Amborella_ |
| Os10t0555600-01Zm00 | 0.22 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os03t0750800-01 | 0.19 Dioscorea_ | 0.19 Dioscorea_ | 0.34 Amborella_ |
| Os04t0485200-01 | 0.29 Musa_acur | 0.34 Dioscorea_ | 0.34 Capsicum_ |

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| Os05t0490700-01 | 0.18 Ananas_co | 0.21 Dioscorea_ | 0.34 Theobroma |
| Os03t0342900-02 | 0.28 Musa_acur | 0.34 Olea_europ | 0.34 Olea_europ |

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| Os03t0225200-01 | 0.28 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os05t0466900-01 | 0.15 Ananas_co | 0.26 Dioscorea_ | 0.34 Glycine_ma |
| Os04t0517000-01 | 0.25 Musa_acur | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os07t0692200-00 | 0.25 Musa_acur | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os08t0112500-01 | 0.19 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os03t0313300-01 | 0.28 Musa_acur | 0.32 Dioscorea_ | 0.34 Coffea_car |
| Os03t0399532-00Zm00 | 0.34 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os08t0261100-01 | 0.31 Musa_acur | 0.34 Lupinus_ar | 0.34 Lupinus_ar |
| Os11t0187100-00 | 0.26 Ananas_co | 0.31 Dioscorea_ | 0.34 Nymphaea |
| Os01t0174100-01 | 0.14 Ananas_co | 0.21 Dioscorea_ | 0.34 Citrus_cler |
| Os03t0844000-01 | 0.15 Ananas_co | 0.21 Dioscorea_ | 0.34 Nymphaea |
| Os07t0264800-01 | 0.34 Citrus_cler | 0.34 Citrus_cler | 0.34 Citrus_cler |
| Os09t0437500-01 | 0.20 Ananas_co | 0.34 Citrus_cler | 0.34 Citrus_cler |
| Os02t0758000-01 | 0.29 Musa_acur | 0.34 Actinidia_c | 0.34 Actinidia_c |

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| Os02t0763000-01 | 0.24 Musa_acur | 0.34 Corchorus_ | 0.34 Corchorus_ |
| Os06t0634100-01 | 0.19 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Zm00001eb364390_P00 | 0.24 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os09t0372400-01 | 0.21 Ananas_co | 0.34 Malus_dom | 0.34 Malus_dom |
| Os04t0430400-01 | 0.29 Ananas_co | 0.33 Dioscorea_ | 0.34 Vitis_vinife |
| Os01t0752600-01 | 0.22 Ananas_co | 0.30 Dioscorea_ | 0.34 Prunus_du |
| Os04t0523000-00 | 0.28 Musa_acur | 0.34 Prunus_avi | 0.34 Prunus_avi |
| Os03t0178400-01 | 0.21 Ananas_co | 0.34 Glycine_ma | 0.34 Glycine_ma |
| Os09t0444900-01 | 0.27 Musa_acur | 0.34 Malus_dom | 0.34 Malus_dom |
| Os06t0118700-01 | 0.25 Ananas_co | 0.34 Dioscorea_ | 0.34 Beta_vulga |
| Os10t0546100-01 | 0.29 Ananas_co | 0.34 Prunus_du | 0.34 Prunus_du |
| Zm00001eb089270_P00 | 0.26 Ananas_co | 0.32 Dioscorea_ | 0.34 Vitis_vinife |
| Os05t0581300-00 | 0.16 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os10t0534900-01 | 0.32 Ananas_co | 0.34 Cucumis_n | 0.34 Cucumis_n |
| Os10t0485000-01 | 0.26 Ananas_co | 0.30 Dioscorea_ | 0.34 Solanum_ly |
| Os07t0566200-01 | 0.24 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os01t0528000-01 | 0.27 Musa_acur | 0.34 Actinidia_c | 0.34 Actinidia_c |

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| Os02t0820900-03 | 0.28 Musa_acur | 0.28 Dioscorea_ | 0.34 Populus_tr |
| Os12t0165600-01 | 0.21 Ananas_co | 0.31 Dioscorea_ | 0.34 Cucumis_n |
| Os01t0968300-01 | 0.17 Ananas_co | 0.34 Prunus_pe | 0.34 Prunus_pe |
| Os01t0134700-01 | 0.27 Musa_acur | 0.34 Lupinus_ar | 0.34 Lupinus_ar |

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| Os02t0245800-01 | 0.27 Ananas_co | 0.30 Dioscorea_ | 0.34 Prunus_pe |
| Os08t0290000-01 | 0.23 Ananas_co | 0.30 Dioscorea_ | 0.34 Vitis_vinife |
| Os09t0504800-01 | 0.26 Ananas_co | 0.34 Corchorus | 0.34 Corchorus |
| Os06t0651100-01Zm00 | 0.27 Ananas_co | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os04t0594400-01 | 0.32 Musa_acu | 0.34 Corchorus | 0.34 Corchorus |
| Os12t0586000-01 | 0.15 Ananas_co | 0.23 Dioscorea_ | 0.34 Actinidia_c |
| Os02t0103200-00 | 0.23 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os03t0701800-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.34 Amborella |
| Zm00001eb202660_P00 | 0.26 Ananas_co | 0.34 Manihot_e | 0.34 Manihot_e |
| Os03t0722100-01 | 0.26 Musa_acu | 0.34 Malus_do | 0.34 Malus_do |
| Os06t0308200-01 | 0.26 Musa_acu | 0.30 Dioscorea_ | 0.34 Pistacia_ve |
| Os06t0297700-01 | 0.27 Dioscorea_ | 0.27 Dioscorea_ | 0.34 Theobrom |
| Os07t0567300-01 | 0.26 Musa_acu | 0.34 Corchorus | 0.34 Corchorus |
| Os05t0515400-01 | 0.30 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os06t0700100-01 | 0.22 Ananas_co | 0.34 Prunus_pe | 0.34 Prunus_pe |
| Os04t0649700-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.34 Corchorus |
| Os01t0825500-01 | 0.19 Ananas_co | 0.31 Dioscorea_ | 0.34 Malus_do |
| Os11t0167200-01 | 0.24 Musa_acu | 0.31 Dioscorea_ | 0.34 Rosa_chine |
| Zm00001eb162330_P00 | 0.28 Musa_acu | 0.34 Malus_do | 0.34 Malus_do |
| Zm00001eb144480_P00 | 0.26 Ananas_co | 0.33 Dioscorea_ | 0.34 Amborella |
| Os02t0331200-01Zm00 | 0.04 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os02t0798700-01 | 0.26 Ananas_co | 0.34 Cannabis_ | 0.34 Cannabis_ |
| Os03t0116800-01 | 0.16 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os02t0137600-01 | 0.34 Actinidia_c | 0.34 Actinidia_c | 0.34 Actinidia_c |
| Os07t0477000-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.34 Pistacia_ve |
| Os02t0763200-01 | 0.30 Ananas_co | 0.32 Dioscorea_ | 0.34 Theobrom |

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| Os03t0172000-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.34 Actinidia_c |
| Os12t0233100-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.34 Vitis_vinife |

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| Os08t0140300-01 | 0.34 Nymphaea | 0.34 Nymphaea | 0.34 Nymphaea |
| Os05t0420200-01 | 0.29 Ananas_co | 0.34 Malus_dom | 0.34 Malus_dom |
| Os09t0447300-01 | 0.25 Ananas_co | 0.34 Prunus_per | 0.34 Prunus_per |
| Os07t0567500-00 | 0.27 Musa_acu | 0.34 Manihot_e | 0.34 Manihot_e |

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| Os01t0965600-01Zm00 | 0.22 | Ananas_co | 0.34 | Rosa_chin | 0.34 | Rosa_chin |
| Os01t0702000-01 | 0.32 | Musa_acur | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife |
| Os04t0547900-01 | 0.32 | Ananas_co | 0.33 | Dioscorea_ | 0.34 | Malus_dor |
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| Os01t0839200-01 | 0.33 | Ananas_co | 0.34 | Prunus_pe | 0.34 | Prunus_pe |
| Os03t0142500-01 | 0.27 | Ananas_co | 0.31 | Dioscorea_ | 0.34 | Prunus_du |
| Os11t0194900-01 | 0.24 | Ananas_co | 0.31 | Dioscorea_ | 0.34 | Gossypiur |
| Os09t0423300-01 | 0.34 | Pistacia_ve | 0.34 | Pistacia_ve | 0.34 | Pistacia_ve |
| Os04t0578700-01 | 0.28 | Ananas_co | 0.34 | Prunus_du | 0.34 | Prunus_du |
| Os09t0506900-01 | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife |
| Os04t0414800-00 | 0.23 | Ananas_co | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife |
| Os11t0602400-01 | 0.34 | Pistacia_ve | 0.34 | Pistacia_ve | 0.34 | Pistacia_ve |
| Os02t0174400-00 | 0.23 | Ananas_co | 0.30 | Dioscorea_ | 0.34 | Prunus_du |
| Os08t0499100-01 | 0.23 | Ananas_co | 0.34 | Citrus_cler | 0.34 | Citrus_cler |
| Os02t0823800-01 | 0.24 | Ananas_co | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife |
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| Os07t0543000-01 | 0.25 | Ananas_co | 0.32 | Dioscorea_ | 0.34 | Populus_tr |
| Os11t0514800-01 | 0.15 | Ananas_co | 0.34 | Corchorus | 0.34 | Corchorus |
| Os01t0183500-01 | 0.30 | Ananas_co | 0.34 | Vitis_vinife | 0.34 | Vitis_vinife |
| Zm00001eb146450_P00 | 0.34 | Beta_vulga | 0.34 | Beta_vulga | 0.34 | Beta_vulga |
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| Os01t0323300-00 | 0.22 | Ananas_co | 0.32 | Dioscorea_ | 0.34 | Beta_vulga |
| Os03t0249300-01 | 0.30 | Ananas_co | 0.34 | Gossypiur | 0.34 | Gossypiur |
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| Os07t0490200-01 | 0.20 | Ananas_co | 0.29 | Dioscorea_ | 0.34 | Pistacia_ve |
| Os01t0272700-00 | 0.27 | Musa_acur | 0.34 | Theobrom | 0.34 | Theobrom |
| Os08t0117900-01 | 0.25 | Musa_acur | 0.27 | Dioscorea_ | 0.34 | Coffea_car |
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| Os05t0556800-01 | 0.24 | Ananas_co | 0.34 | Capsicum_ | 0.34 | Capsicum_ |
| Os05t0419600-01 | 0.26 | Ananas_co | 0.34 | Manihot_e | 0.34 | Manihot_e |

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| Os08t0513700-01 | 0.21 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os06t0304600-02 | 0.16 Ananas_co | 0.18 Dioscorea_ | 0.34 Amborella_ |
| Os04t0376100-01 | 0.25 Ananas_co | 0.34 Corchorus_ | 0.34 Corchorus_ |
| Os06t0710700-01 | 0.12 Ananas_co | 0.32 Dioscorea_ | 0.34 Ipomoea_t |
| Os02t0763900-01Zm00 | 0.32 Ananas_co | 0.33 Dioscorea_ | 0.34 Manihot_e |

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| Os08t0497300-01Zm00 | 0.28 Musa_acu | 0.34 Theobrom | 0.34 Theobrom |
| Os01t0760400-01 | 0.21 Ananas_co | 0.34 Prunus_du | 0.34 Prunus_du |
| Os03t0289200-01 | 0.25 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os04t0609500-00 | 0.26 Ananas_co | 0.34 Camelina_ | 0.34 Camelina_ |
| Os02t0137500-01 | 0.30 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os09t0548400-01 | 0.27 Ananas_co | 0.34 Rosa_chine | 0.34 Rosa_chine |
| Os06t0618300-01 | 0.34 Phaseolus_ | 0.34 Phaseolus_ | 0.34 Phaseolus_ |
| Os06t0624900-01 | 0.29 Ananas_co | 0.32 Dioscorea_ | 0.34 Manihot_e |
| Os03t0212600-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.34 Actinidia_ |

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| Os12t0597700-01 | 0.33 Ananas_co | 0.33 Dioscorea_ | 0.34 Citrus_cle |
| Os03t0835100-00 | 0.28 Ananas_co | 0.34 Pistacia_ve | 0.34 Pistacia_ve |
| Os09t0463300-01 | 0.23 Ananas_co | 0.29 Dioscorea_ | 0.34 Manihot_e |

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| Os07t0508500-01 | 0.24 Ananas_co | 0.30 Dioscorea_ | 0.34 Pistacia_ve |
| Os07t0587500-01 | 0.27 Ananas_co | 0.34 Brassica_ra | 0.34 Brassica_ra |

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| Os09t0538500-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.34 Actinidia_ |

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| Os04t0394500-00 | 0.20 Ananas_co | 0.33 Dioscorea_ | 0.34 Actinidia_ |

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| Os01t0674700-00 | 0.19 Ananas_co | 0.27 Dioscorea_ | 0.34 Rosa_chine |
| Os07t0456700-01 | 0.20 Ananas_co | 0.34 Malus_dom | 0.34 Malus_dom |
| Zm00001eb224850_P00 | 0.21 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |

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| Os04t0574200-01 | 0.24 Ananas_co | 0.28 Dioscorea_ | 0.34 Rosa_chine |
| Os02t0152300-01 | 0.22 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os02t0557300-01 | 0.22 Musa_acum | 0.25 Dioscorea_ | 0.34 Citrus_clem |

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| Os11t0448000-00 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.34 Daucus_ca |
| Os02t0158500-00 | 0.14 Musa_acum | 0.18 Dioscorea_ | 0.34 Nicotiana_ |
| Os08t0125800-01Zm00 | 0.32 Ananas_co | 0.34 Prunus_per | 0.34 Prunus_per |
| Os03t0659300-01 | 0.29 Ananas_co | 0.34 Beta_vulga | 0.34 Beta_vulga |
| Os03t0767700-01 | 0.23 Ananas_co | 0.34 Vitis_vinife | 0.34 Vitis_vinife |

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| Os02t0618200-01 | 0.23 Ananas_co | 0.34 Theobroma | 0.34 Theobroma |
| Zm00001eb061430_P00 | 0.19 Ananas_co | 0.30 Dioscorea_ | 0.34 Vitis_vinife |
| Os11t0610700-01 | 0.24 Ananas_co | 0.29 Dioscorea_ | 0.34 Actinidia_c |
| Os01t0617600-00 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.34 Lupinus_an |
| Os03t0162900-01 | 0.34 Prunus_du | 0.34 Prunus_du | 0.34 Prunus_du |
| Zm00001eb160790_P00 | 0.23 Ananas_co | 0.34 Vigna_angu | 0.34 Vigna_angu |
| Os06t0195600-01 | 0.29 Ananas_co | 0.32 Dioscorea_ | 0.34 Vitis_vinife |
| Os01t0715800-01Zm00 | 0.31 Musa_acum | 0.33 Dioscorea_ | 0.34 Medicago_ |
| Os09t0516700-01 | 0.22 Musa_acum | 0.34 Vitis_vinife | 0.34 Vitis_vinife |
| Os03t0648100-01 | 0.23 Ananas_co | 0.34 Nicotiana_ | 0.34 Nicotiana_ |
| Os09t0450200-01Zm00 | 0.32 Ananas_co | 0.34 Camelina_s | 0.34 Camelina_s |

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| Zm00001eb270150_P00 | 0.28 Ananas_co | 0.34 Malus_do | 0.34 Malus_do |
| Os02t0639000-01 | 0.27 Ananas_co | 0.33 Theobrom | 0.33 Theobrom |
| Os03t0251350-00Zm00 | 0.33 Nicotiana_ | 0.33 Nicotiana_ | 0.33 Nicotiana_ |
| Os02t0816300-01 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.33 Manihot_e |
| Os01t0241100-01 | 0.25 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os02t0282100-01 | 0.29 Ananas_co | 0.33 Arabidopsi | 0.33 Arabidopsi |
| Os08t0542100-01 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.33 Solanum_l |
| Os11t0169100-01 | 0.24 Ananas_co | 0.33 Dioscorea_ | 0.33 Vitis_vinife |
| Os07t0672500-02 | 0.26 Ananas_co | 0.31 Dioscorea_ | 0.33 Citrullus_l |
| Os12t0437800-01 | 0.33 Corchorus | 0.33 Corchorus | 0.33 Corchorus |
| Os04t0530000-01 | 0.33 Vitis_vinife | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os09t0123200-01 | 0.26 Ananas_co | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os02t0813350-01 | 0.30 Musa_acu | 0.33 Actinidia_c | 0.33 Actinidia_c |

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| Os03t0667100-01 | 0.28 | Ananas_co | 0.33 | Dioscorea_ | 0.33 | Vitis_vinif |
| Os04t0655300-01 | 0.25 | Ananas_co | 0.27 | Dioscorea_ | 0.33 | Trifolium_ |
| Os12t0206700-01 | 0.30 | Musa_acu | 0.33 | Cynara_ca | 0.33 | Cynara_ca |
| Os01t0178100-01 | 0.25 | Ananas_co | 0.33 | Nicotiana_ | 0.33 | Nicotiana_ |
| Os03t0286500-01Zm00 | 0.18 | Ananas_co | 0.30 | Dioscorea_ | 0.33 | Rosa_chin |
| Os01t0178700-01 | 0.30 | Ananas_co | 0.30 | Dioscorea_ | 0.33 | Vitis_vinif |
| Zm00001eb053760_P00 | 0.29 | Ananas_co | 0.33 | Pistacia_ve | 0.33 | Pistacia_ve |
| Os04t0586200-01 | 0.33 | Nicotiana_ | 0.33 | Nicotiana_ | 0.33 | Nicotiana_ |
| Os02t0769900-01 | 0.27 | Ananas_co | 0.33 | Citrullus_l | 0.33 | Citrullus_l |
| Os05t0279400-01 | 0.26 | Ananas_co | 0.30 | Dioscorea_ | 0.33 | Corchorus_ |

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| Os07t0497100-01Zm00 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.33 Prunus_per |

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| Os09t0524800-01 | 0.29 Musa_acum | 0.33 Gossypium | 0.33 Gossypium |
| Os09t0570200-01 | 0.26 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os03t0343300-01 | 0.28 Musa_acum | 0.33 Olea_europ | 0.33 Olea_europ |

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| Os11t0679700-01 | 0.24 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os01t0627400-01 | 0.23 Musa_acum | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os01t0833100-01 | 0.29 Musa_acum | 0.32 Dioscorea_ | 0.33 Coffea_car |
| Zm00001eb420510_P00 | 0.33 Theobroma | 0.33 Theobroma | 0.33 Theobroma |
| Os03t0849700-01 | 0.23 Ananas_co | 0.28 Dioscorea_ | 0.33 Vitis_vinife |

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| Os07t0119000-01 | 0.20 Ananas_co | 0.28 Dioscorea_ | 0.33 Vitis_vinife |
| Os03t0787200-01 | 0.27 Ananas_co | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os12t0609800-01 | 0.21 Ananas_co | 0.28 Dioscorea_ | 0.33 Prunus_avi |

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| Os01t0764700-01 | 0.24 | Ananas_co | 0.27 | Dioscorea_ | 0.33 | Amborella_ |
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| Os03t0388900-01 | 0.25 | Musa_acur | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os03t0775600-02 | 0.19 | Ananas_co | 0.25 | Dioscorea_ | 0.33 | Nicotiana_ |
| Os02t0784900-01 | 0.22 | Musa_acur | 0.33 | Malus_don | 0.33 | Malus_don |
| Os01t0894700-01 | 0.33 | Nymphaea | 0.33 | Nymphaea | 0.33 | Nymphaea |
| Os08t0500800-01 | 0.24 | Ananas_co | 0.33 | Pistacia_ve | 0.33 | Pistacia_ve |
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| Os07t0563300-01 | 0.23 | Musa_acur | 0.25 | Dioscorea_ | 0.33 | Prunus_pe |
| Os01t0871500-01 | 0.25 | Ananas_co | 0.27 | Dioscorea_ | 0.33 | Prunus_avi |
| Os08t0282500-01 | 0.27 | Ananas_co | 0.30 | Dioscorea_ | 0.33 | Coffea_car |
| Os04t0458600-01 | 0.19 | Ananas_co | 0.32 | Dioscorea_ | 0.33 | Amborella_ |
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| Os01t0714800-01 | 0.22 | Ananas_co | 0.33 | Cucumis_s | 0.33 | Cucumis_s |
| Os03t0237600-02 | 0.29 | Musa_acur | 0.30 | Dioscorea_ | 0.33 | Manihot_e |
| Os07t0642800-01 | 0.24 | Ananas_co | 0.33 | Amborella_ | 0.33 | Amborella_ |
| Zm00001eb307130_P00 | 0.30 | Dioscorea_ | 0.30 | Dioscorea_ | 0.33 | Populus_tr |
| Zm00001eb057430_P00 | 0.27 | Ananas_co | 0.33 | Prunus_du | 0.33 | Prunus_du |
| Os05t0164900-01 | 0.26 | Musa_acur | 0.32 | Dioscorea_ | 0.33 | Gossypiu |
| Os03t0728100-01 | 0.19 | Ananas_co | 0.33 | Prunus_pe | 0.33 | Prunus_pe |
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| Os10t0564000-01 | 0.33 | Ananas_co | 0.33 | Actinidia_c | 0.33 | Actinidia_c |
| Os03t0366900-01 | 0.25 | Musa_acur | 0.33 | Capsicum_ | 0.33 | Capsicum_ |
| Os03t0100500-01 | 0.29 | Ananas_co | 0.33 | Populus_tr | 0.33 | Populus_tr |
| Os07t0186500-01Zm00 | 0.07 | Ananas_co | 0.33 | Manihot_e | 0.33 | Manihot_e |
| Os02t0515200-01 | 0.28 | Ananas_co | 0.33 | Prunus_avi | 0.33 | Prunus_avi |

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| Os01t0757200-01Zm00 | 0.27 Musa_acu | 0.30 Dioscorea_ | 0.33 Glycine_ma |
| Os03t0211600-01 | 0.24 Ananas_co | 0.30 Dioscorea_ | 0.33 Corchorus_ |
| Os02t0796400-00 | 0.22 Ananas_co | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os11t0141500-00 | 0.32 Ananas_co | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os07t0159700-00 | 0.20 Ananas_co | 0.25 Dioscorea_ | 0.33 Citrus_cle |
| Os03t0108600-01 | 0.33 Dioscorea_ | 0.33 Dioscorea_ | 0.33 Beta_vulga |
| Os04t0129200-00 | 0.27 Ananas_co | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os03t0330000-01 | 0.18 Ananas_co | 0.28 Dioscorea_ | 0.33 Trifolium_ |
| Os06t0301100-01 | 0.22 Ananas_co | 0.33 Prunus_du | 0.33 Prunus_du |
| Zm00001eb411070_P00 | 0.24 Ananas_co | 0.33 Amborella_ | 0.33 Amborella_ |
| Os01t0747400-01 | 0.27 Ananas_co | 0.32 Dioscorea_ | 0.33 Corchorus_ |
| Os05t0590300-01 | 0.27 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os06t0225800-01Zm00 | 0.17 Ananas_co | 0.24 Dioscorea_ | 0.33 Nymphaea |
| Os01t0805400-01Zm00 | 0.29 Ananas_co | 0.33 Manihot_e | 0.33 Manihot_e |
| Os11t0448400-02 | 0.33 Pistacia_ve | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os04t0619600-01 | 0.19 Ananas_co | 0.29 Dioscorea_ | 0.33 Pistacia_ve |
| Os07t0102500-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.33 Citrus_cle |
| Os08t0128200-01 | 0.26 Musa_acu | 0.33 Theobrom | 0.33 Theobrom |
| Os01t0235800-01 | 0.22 Ananas_co | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os10t0101200-01 | 0.24 Musa_acu | 0.31 Dioscorea_ | 0.33 Manihot_e |
| Os04t0551600-01 | 0.32 Ananas_co | 0.33 Phaseolus_ | 0.33 Phaseolus_ |
| Os10t0485600-01 | 0.20 Ananas_co | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os08t0414500-00Zm00 | 0.26 Ananas_co | 0.33 Gossypiu | 0.33 Gossypiu |
| Os10t0543800-00 | 0.21 Dioscorea_ | 0.21 Dioscorea_ | 0.33 Vitis_vinife |

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| Os08t0559900-01 | 0.22 | Ananas_co | 0.33 | Ipomoea_t | 0.33 | Ipomoea_t |
| Os06t0590700-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.33 | Populus_tr |
| Os11t0490100-01 | 0.25 | Musa_acu | 0.33 | Brassica_n | 0.33 | Brassica_n |
| Os08t0557800-01 | 0.22 | Musa_acu | 0.33 | Amborella | 0.33 | Amborella |
| Os01t0703300-01 | 0.32 | Musa_acu | 0.33 | Gossypiu | 0.33 | Gossypiu |
| Os09t0489500-02 | 0.33 | Gossypiu | 0.33 | Gossypiu | 0.33 | Gossypiu |
| Os03t0649000-01 | 0.29 | Ananas_co | 0.33 | Theobrom | 0.33 | Theobrom |
| Os08t0377400-01 | 0.25 | Ananas_co | 0.33 | Malus_do | 0.33 | Malus_do |
| Os02t0137100-01 | 0.26 | Musa_acu | 0.33 | Citrus_cler | 0.33 | Citrus_cler |
| Os10t0471400-01 | 0.23 | Ananas_co | 0.33 | Nymphaea | 0.33 | Nymphaea |
| Os07t0507200-01 | 0.22 | Ananas_co | 0.33 | Dioscorea_ | 0.33 | Nicotiana_ |
| Os04t0480650-00 | 0.27 | Ananas_co | 0.33 | Vigna_ang | 0.33 | Vigna_ang |
| Os06t0264200-00 | 0.32 | Ananas_co | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os11t0704600-01 | 0.33 | Corchorus | 0.33 | Corchorus | 0.33 | Corchorus |
| Os06t0611400-01 | 0.30 | Dioscorea_ | 0.30 | Dioscorea_ | 0.33 | Amborella |
| Os04t0408600-01 | 0.22 | Ananas_co | 0.33 | Prunus_du | 0.33 | Prunus_du |
| Os06t0331300-01 | 0.19 | Ananas_co | 0.33 | Prunus_pe | 0.33 | Prunus_pe |
| Os05t0473500-01 | 0.20 | Ananas_co | 0.33 | Prunus_avi | 0.33 | Prunus_avi |
| Os05t0304100-01 | 0.32 | Dioscorea_ | 0.32 | Dioscorea_ | 0.33 | Citrus_cler |
| Os09t0349100-00 | 0.26 | Ananas_co | 0.33 | Cucumis_ | 0.33 | Cucumis_ |
| Os03t0381000-01 | 0.21 | Ananas_co | 0.33 | Amborella | 0.33 | Amborella |
| Os08t0102700-01 | 0.28 | Ananas_co | 0.33 | Daucus_ca | 0.33 | Daucus_ca |
| Os12t0612400-01 | 0.31 | Musa_acu | 0.33 | Citrus_cler | 0.33 | Citrus_cler |
| Os06t0239700-01 | 0.23 | Ananas_co | 0.32 | Dioscorea_ | 0.33 | Nicotiana_ |
| Os02t0740700-01 | 0.13 | Ananas_co | 0.33 | Trifolium_ | 0.33 | Trifolium_ |
| Os12t0588900-01 | 0.17 | Ananas_co | 0.26 | Dioscorea_ | 0.33 | Vitis_vinife |
| Os06t0498500-01 | 0.22 | Ananas_co | 0.30 | Dioscorea_ | 0.33 | Prunus_pe |

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| Os03t0858600-01 | 0.33 | Cannabis_ | 0.33 | Cannabis_ | 0.33 | Cannabis_ |
| Os10t0561900-01 | 0.22 | Ananas_co | 0.28 | Dioscorea_ | 0.33 | Solanum_l |
| Os04t0589700-01 | 0.28 | Ananas_co | 0.33 | Prunus_avi | 0.33 | Prunus_avi |
| Os02t0745400-01 | 0.22 | Ananas_co | 0.33 | Brassica_n | 0.33 | Brassica_n |
| Os12t0498500-01 | 0.25 | Ananas_co | 0.33 | Amborella_ | 0.33 | Amborella_ |
| Os08t0266200-01 | 0.20 | Ananas_co | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os07t0471100-01 | 0.29 | Musa_acur | 0.33 | Medicago_ | 0.33 | Medicago_ |
| Os03t0283500-01 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.33 | Cucumis_n |

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| Os03t0807200-01 | 0.22 | Musa_acur | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os03t0277100-01 | 0.29 | Dioscorea_ | 0.29 | Dioscorea_ | 0.33 | Vitis_vinife |

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| Os08t0502000-01 | 0.29 | Musa_acur | 0.33 | Citrus_cler | 0.33 | Citrus_cler |
| Os01t0805000-01 | 0.29 | Ananas_co | 0.33 | Amborella_ | 0.33 | Amborella_ |
| Zm00001eb293740_P00 | 0.30 | Ananas_co | 0.33 | Beta_vulga | 0.33 | Beta_vulga |
| Os02t0813600-01 | 0.28 | Ananas_co | 0.33 | Daucus_ca | 0.33 | Daucus_ca |

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|---|---|---|---|---|---|---|
| Os01t0851000-01 | 0.30 | Ananas_co | 0.33 | Prunus_du | 0.33 | Prunus_du |
| Os12t0594950-01 | 0.32 | Ananas_co | 0.33 | Ipomoea_t | 0.33 | Ipomoea_t |
| Os04t0350300-00 | 0.30 | Musa_acur | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os01t0787600-01 | 0.29 | Musa_acur | 0.33 | Helianthus | 0.33 | Helianthus |
| Os03t0832500-01 | 0.23 | Ananas_co | 0.33 | Theobrom | 0.33 | Theobrom |
| Os02t0295700-01Zm00 | 0.33 | Musa_acur | 0.33 | Manihot_e | 0.33 | Manihot_e |

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| Os01t0610300-01 | 0.25 | Ananas_co | 0.33 | Amborella_ | 0.33 | Amborella_ |

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| Os10t0524500-01 | 0.28 Ananas_co | 0.32 Dioscorea_ | 0.33 Amborella |
| Os11t0265600-00 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.33 Vitis_vinife |

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| Os04t0489800-01 | 0.32 Ananas_co | 0.33 Manihot_e | 0.33 Manihot_e |
| Os03t0116300-01Zm00 | 0.15 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os02t0557000-01 | 0.28 Ananas_co | 0.33 Glycine_m | 0.33 Glycine_m |
| Os07t0644200-01 | 0.25 Musa_acu | 0.30 Dioscorea_ | 0.33 Vitis_vinife |
| Os01t0607900-01 | 0.27 Ananas_co | 0.33 Ipomoea_t | 0.33 Ipomoea_t |
| Os10t0559800-01 | 0.25 Ananas_co | 0.33 Pistacia_ve | 0.33 Pistacia_ve |
| Os06t0708700-01 | 0.26 Ananas_co | 0.32 Dioscorea_ | 0.33 Populus_tr |
| Os04t0564500-01 | 0.28 Musa_acu | 0.33 Prunus_pe | 0.33 Prunus_pe |
| Os06t0186600-02 | 0.26 Ananas_co | 0.32 Dioscorea_ | 0.33 Theobrom |
| Os04t0278000-01 | 0.20 Musa_acu | 0.33 Cannabis_ | 0.33 Cannabis_ |
| Zm00001eb302210_P00 | 0.20 Musa_acu | 0.33 Populus_tr | 0.33 Populus_tr |
| Zm00001eb315840_P00 | 0.28 Musa_acu | 0.32 Dioscorea_ | 0.33 Vitis_vinife |

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| Os01t0580500-01 | 0.26 Musa_acu | 0.33 Gossypiu | 0.33 Gossypiu |
| Os07t0169600-01Zm00 | 0.16 Ananas_co | 0.33 Gossypiu | 0.33 Gossypiu |
| Os03t0627500-01 | 0.27 Musa_acu | 0.33 Actinidia_ | 0.33 Actinidia_ |
| Os03t0452300-01 | 0.29 Ananas_co | 0.33 Amborella | 0.33 Amborella |
| Os03t0370400-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.33 Manihot_e |
| Os01t0309900-01 | 0.33 Cannabis_ | 0.33 Cannabis_ | 0.33 Cannabis_ |
| Os04t0662700-02 | 0.21 Ananas_co | 0.33 Rosa_chine | 0.33 Rosa_chine |
| Os05t0541700-01 | 0.21 Dioscorea_ | 0.21 Dioscorea_ | 0.33 Cucumis_ |
| Os04t0462600-01 | 0.20 Ananas_co | 0.23 Dioscorea_ | 0.33 Amborella |
| Os05t0524500-01Zm00 | 0.09 Ananas_co | 0.33 Citrus_cle | 0.33 Citrus_cle |

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| Os06t0115600-01 | 0.30 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |

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| Os03t0793700-01 | 0.22 Ananas_co | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os03t0336200-01 | 0.24 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os05t0442000-00 | 0.27 Musa_acu | 0.32 Dioscorea_ | 0.33 Manihot_e |
| Os02t0499000-01 | 0.25 Musa_acu | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os12t0158800-01 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.33 Vitis_vinife |
| Os03t0125300-01 | 0.32 Musa_acu | 0.33 Manihot_e | 0.33 Manihot_e |
| Os05t0389000-02 | 0.20 Ananas_co | 0.22 Dioscorea_ | 0.33 Phaseolus_ |
| Os01t0764300-01 | 0.19 Ananas_co | 0.24 Dioscorea_ | 0.33 Citrullus_l |
| Os03t0804100-00 | 0.27 Musa_acu | 0.29 Dioscorea_ | 0.33 Manihot_e |
| Os05t0541100-01 | 0.24 Ananas_co | 0.32 Dioscorea_ | 0.33 Vitis_vinife |
| Os04t0616000-01 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.33 Theobrom |
| Os04t0587500-01 | 0.26 Ananas_co | 0.29 Dioscorea_ | 0.33 Ipomoea_t |
| Os12t0610500-01 | 0.24 Ananas_co | 0.33 Vitis_vinife | 0.33 Vitis_vinife |
| Os01t0529800-01 | 0.33 Actinidia_c | 0.33 Actinidia_c | 0.33 Actinidia_c |
| Os05t0443900-01 | 0.31 Musa_acu | 0.33 Prunus_du | 0.33 Prunus_du |
| Os12t0608900-00Zm00 | 0.33 Phaseolus_ | 0.33 Phaseolus_ | 0.33 Phaseolus_ |
| Os04t0667400-01 | 0.28 Ananas_co | 0.33 Populus_tr | 0.33 Populus_tr |

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| Os01t0913100-01Zm00 | 0.26 | Ananas_co | 0.33 | Capsicum_ | 0.33 | Capsicum_ |
| Os01t0633200-01 | 0.17 | Ananas_co | 0.21 | Dioscorea_ | 0.33 | Manihot_e |
| Os10t0163370-01 | 0.32 | Musa_acu | 0.33 | Ipomoea_t | 0.33 | Ipomoea_t |
| Os10t0181700-01 | 0.21 | Ananas_co | 0.25 | Dioscorea_ | 0.33 | Actinidia_ |

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| Os03t0650900-01 | 0.22 | Ananas_co | 0.33 | Pistacia_ve | 0.33 | Pistacia_ve |
| Os05t0375600-00 | 0.24 | Ananas_co | 0.33 | Pistacia_ve | 0.33 | Pistacia_ve |

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| Os07t0580900-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.33 | Populus_tr |
| Os06t0692800-01 | 0.21 | Ananas_co | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os07t0445600-01 | 0.22 | Ananas_co | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os07t0490600-02 | 0.15 | Musa_acu | 0.16 | Dioscorea_ | 0.33 | Cannabis_ |
| Os06t0618150-00 | 0.22 | Ananas_co | 0.33 | Trifolium_ | 0.33 | Trifolium_ |
| Os07t0491600-01 | 0.27 | Ananas_co | 0.33 | Amborella_ | 0.33 | Amborella_ |
| Os03t0158200-01 | 0.24 | Musa_acu | 0.33 | Solanum_t | 0.33 | Solanum_t |
| Os04t0604800-00 | 0.33 | Beta_vulga | 0.33 | Beta_vulga | 0.33 | Beta_vulga |
| Zm00001eb074280_P00 | 0.25 | Ananas_co | 0.29 | Dioscorea_ | 0.33 | Vitis_vinife |
| Os03t0794000-01 | 0.31 | Ananas_co | 0.33 | Lupinus_a | 0.33 | Lupinus_a |
| Os02t0635700-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.33 | Solanum_t |

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| Os02t0220700-01 | 0.26 | Ananas_co | 0.33 | Vitis_vinife | 0.33 | Vitis_vinife |
| Os10t0162846-00 | 0.20 | Ananas_co | 0.33 | Manihot_e | 0.33 | Manihot_e |
| Os04t0412500-01 | 0.20 | Musa_acu | 0.32 | Nymphaea | 0.32 | Nymphaea |
| Os12t0138800-01 | 0.32 | Citrus_cle | 0.32 | Citrus_cle | 0.32 | Citrus_cle |
| Os01t0799500-01 | 0.29 | Musa_acu | 0.32 | Populus_tr | 0.32 | Populus_tr |
| Zm00001eb229050_P00 | 0.23 | Ananas_co | 0.32 | Actinidia_ | 0.32 | Actinidia_ |
| Os09t0551800-00 | 0.32 | Prunus_du | 0.32 | Prunus_du | 0.32 | Prunus_du |
| Os03t0122000-01 | 0.24 | Ananas_co | 0.32 | Manihot_e | 0.32 | Manihot_e |

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| Os05t0562400-01 | 0.16 | Ananas_co | 0.27 | Dioscorea_ | 0.32 | Populus_tr |
| Os06t0218600-01 | 0.30 | Ananas_co | 0.32 | Manihot_e | 0.32 | Manihot_e |

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| Os11t0592400-00 | 0.28 | Ananas_co | 0.32 | Capsicum_ | 0.32 | Capsicum_ |
| Os09t0426000-01 | 0.25 | Musa_acu | 0.32 | Daucus_ca | 0.32 | Daucus_ca |
| Os03t0268600-01 | 0.30 | Ananas_co | 0.32 | Glycine_ma | 0.32 | Glycine_ma |
| Os05t0127300-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.32 | Prunus_du |
| Os03t0321000-01 | 0.30 | Ananas_co | 0.32 | Dioscorea_ | 0.32 | Citrus_cle |
| Os10t0456400-01 | 0.31 | Ananas_co | 0.32 | Glycine_ma | 0.32 | Glycine_ma |
| Os03t0194500-01 | 0.26 | Ananas_co | 0.32 | Amborella_ | 0.32 | Amborella_ |
| Os12t0566700-01 | 0.24 | Ananas_co | 0.25 | Dioscorea_ | 0.32 | Amborella_ |

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| Os02t0513100-01 | 0.28 | Ananas_co | 0.30 | Dioscorea_ | 0.32 | Amborella_ |
| Os03t0205700-01 | 0.27 | Ananas_co | 0.32 | Cucumis_s | 0.32 | Cucumis_s |
| Os02t0527900-00 | 0.23 | Musa_acur | 0.32 | Cannabis_ | 0.32 | Cannabis_ |
| Os08t0360100-01 | 0.29 | Musa_acur | 0.32 | Actinidia_c | 0.32 | Actinidia_c |
| Os01t0604500-01 | 0.29 | Musa_acur | 0.32 | Gossypium | 0.32 | Gossypium |

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| Os03t0200600-00 | 0.25 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os04t0348100-01 | 0.19 | Ananas_co | 0.32 | Olea_europ | 0.32 | Olea_europ |
| Os05t0123100-01 | 0.18 | Ananas_co | 0.32 | Dioscorea_ | 0.32 | Populus_tr |
| Os03t0756400-01 | 0.26 | Ananas_co | 0.32 | Gossypium | 0.32 | Gossypium |
| Os08t0243100-01 | 0.21 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Populus_tr |
| Os02t0468200-01 | 0.22 | Ananas_co | 0.32 | Olea_europ | 0.32 | Olea_europ |
| Os07t0124800-01 | 0.32 | Pistacia_ve | 0.32 | Pistacia_ve | 0.32 | Pistacia_ve |
| Os08t0535700-00 | 0.30 | Musa_acur | 0.31 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os05t0157100-01 | 0.08 | Ananas_co | 0.12 | Dioscorea_ | 0.32 | Actinidia_c |
| Os04t0602800-01 | 0.23 | Ananas_co | 0.32 | Daucus_ca | 0.32 | Daucus_ca |
| Os06t0259000-01 | 0.32 | Ananas_co | 0.32 | Dioscorea_ | 0.32 | Prunus_du |
| Os02t0221500-01 | 0.22 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Malus_dom |

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| Os11t0521900-02 | 0.26 | Musa_acur | 0.28 | Dioscorea_ | 0.32 | Theobroma |
| Os01t0917200-01 | 0.19 | Ananas_co | 0.24 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os12t0121000-01 | 0.31 | Ananas_co | 0.32 | Dioscorea_ | 0.32 | Gossypium |
| Os09t0323500-01 | 0.22 | Musa_acur | 0.32 | Theobroma | 0.32 | Theobroma |
| Os03t0719500-02 | 0.30 | Musa_acur | 0.32 | Corchorus_ | 0.32 | Corchorus_ |

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| Os02t0745100-01 | 0.21 | Ananas_co | 0.32 | Manihot_es | 0.32 | Manihot_es |

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| Os04t0465600-01 | 0.21 Ananas_co | 0.32 Nicotiana_ | 0.32 Nicotiana_ |
| Os08t0499300-01 | 0.29 Ananas_co | 0.32 Dioscorea_ | 0.32 Ipomoea_t |
| Os06t0693900-00 | 0.30 Ananas_co | 0.32 Nicotiana_ | 0.32 Nicotiana_ |
| Os07t0507300-01Zm00 | 0.27 Ananas_co | 0.31 Dioscorea_ | 0.32 Vitis_vinife |
| Os04t0683500-01Zm00 | 0.24 Ananas_co | 0.32 Corchorus | 0.32 Corchorus |
| Os03t0256800-00 | 0.25 Ananas_co | 0.30 Dioscorea_ | 0.32 Theobrom |
| Os05t0251400-01 | 0.19 Ananas_co | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os04t0541100-01 | 0.32 Prunus_pe | 0.32 Prunus_pe | 0.32 Prunus_pe |
| Os03t0167500-02 | 0.32 Citrus_cler | 0.32 Citrus_cler | 0.32 Citrus_cler |
| Os12t0514000-01 | 0.27 Ananas_co | 0.31 Dioscorea_ | 0.32 Manihot_e |
| Os01t0265800-01 | 0.32 Pistacia_ve | 0.32 Pistacia_ve | 0.32 Pistacia_ve |
| Os03t0186900-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.32 Cannabis_ |
| Os03t0703400-01 | 0.21 Ananas_co | 0.32 Amborella | 0.32 Amborella |
| Os01t0511200-01 | 0.22 Ananas_co | 0.30 Dioscorea_ | 0.32 Beta_vulga |

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| Os10t0509000-01 | 0.32 | Actinidia_c | 0.32 | Actinidia_c | 0.32 | Actinidia_c |
| Os03t0598200-01 | 0.23 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Gossypium |
| Os06t0687600-00 | 0.19 | Musa_acur | 0.22 | Dioscorea_ | 0.32 | Nicotiana_ |
| Os04t0105100-01 | 0.26 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os09t0434200-01 | 0.21 | Ananas_co | 0.22 | Dioscorea_ | 0.32 | Corchorus_ |
| Os04t0689400-01 | 0.24 | Ananas_co | 0.27 | Dioscorea_ | 0.32 | Actinidia_c |
| Os02t0755000-01 | 0.18 | Ananas_co | 0.24 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os12t0180500-00 | 0.26 | Ananas_co | 0.30 | Dioscorea_ | 0.32 | Actinidia_c |
| Os03t0134500-00 | 0.24 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os03t0862100-01 | 0.25 | Ananas_co | 0.29 | Dioscorea_ | 0.32 | Glycine_ma |
| Os06t0151200-01 | 0.29 | Musa_acur | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os01t0813100-01 | 0.30 | Ananas_co | 0.32 | Rosa_chine | 0.32 | Rosa_chine |
| Zm00001eb370340_P00 | 0.14 | Musa_acur | 0.32 | Nymphaea | 0.32 | Nymphaea |

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| Os03t0239200-02 | 0.18 Ananas_co | 0.28 Dioscorea_ | 0.32 Populus_tr |
| Os06t0171700-01Zm00 | 0.24 Musa_acu | 0.32 Coffea_ca | 0.32 Coffea_ca |
| Os06t0306500-00 | 0.26 Ananas_co | 0.32 Manihot_e | 0.32 Manihot_e |
| Zm00001eb359430_P00 | 0.29 Musa_acu | 0.31 Dioscorea_ | 0.32 Citrus_cle |
| Os05t0304600-01 | 0.18 Ananas_co | 0.27 Dioscorea_ | 0.32 Actinidia_ |
| Os03t0806500-01 | 0.23 Ananas_co | 0.28 Dioscorea_ | 0.32 Rosa_chin |
| Os02t0824000-00 | 0.15 Ananas_co | 0.28 Dioscorea_ | 0.32 Pistacia_ve |
| Os03t0734400-01 | 0.22 Ananas_co | 0.27 Dioscorea_ | 0.32 Gossypiu |
| Os04t0508600-01 | 0.20 Ananas_co | 0.32 Manihot_e | 0.32 Manihot_e |

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| Os02t0767400-01 | 0.19 Ananas_co | 0.30 Dioscorea_ | 0.32 Gossypiu |
| Os10t0351700-01 | 0.32 Prunus_du | 0.32 Prunus_du | 0.32 Prunus_du |
| Os03t0828100-02 | 0.32 Cucumis_s | 0.32 Cucumis_s | 0.32 Cucumis_s |
| Os09t0444800-01 | 0.30 Ananas_co | 0.32 Populus_tr | 0.32 Populus_tr |
| Os03t0250200-02 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.32 Cannabis_ |
| Os06t0711800-01 | 0.26 Ananas_co | 0.32 Ipomoea_t | 0.32 Ipomoea_t |
| Os06t0228900-00Zm00 | 0.20 Ananas_co | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os03t0807500-00 | 0.32 Musa_acu | 0.32 Nicotiana_ | 0.32 Nicotiana_ |
| Os02t0126500-01 | 0.29 Ananas_co | 0.32 Ipomoea_t | 0.32 Ipomoea_t |
| Os01t0328900-01 | 0.25 Ananas_co | 0.31 Dioscorea_ | 0.32 Vitis_vinife |
| Os01t0232500-01 | 0.23 Musa_acu | 0.32 Glycine_m | 0.32 Glycine_m |
| Os07t0419000-00 | 0.18 Ananas_co | 0.32 Dioscorea_ | 0.32 Manihot_e |
| Os07t0623600-01 | 0.32 Corchorus | 0.32 Corchorus | 0.32 Corchorus |
| Os05t0453900-00 | 0.14 Dioscorea_ | 0.14 Dioscorea_ | 0.32 Cannabis_ |
| Os06t0171800-01 | 0.25 Ananas_co | 0.30 Dioscorea_ | 0.32 Corchorus |
| Os02t0567800-01 | 0.24 Ananas_co | 0.32 Prunus_pe | 0.32 Prunus_pe |

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| Os01t0209700-01 | 0.26 Ananas_co | 0.29 Dioscorea_ | 0.32 Citrullus_l |
| Os03t0685750-00 | 0.23 Musa_acu | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os06t0643700-01Zm00 | 0.22 Ananas_co | 0.28 Dioscorea_ | 0.32 Nicotiana_ |
| Os01t0830700-01 | 0.18 Ananas_co | 0.30 Dioscorea_ | 0.32 Cannabis_ |
| Os11t0225000-01 | 0.32 Dioscorea_ | 0.32 Dioscorea_ | 0.32 Vigna_ang |
| Os05t0550250-00 | 0.18 Ananas_co | 0.27 Dioscorea_ | 0.32 Nymphaea |
| Os03t0603800-01 | 0.32 Medicago_ | 0.32 Medicago_ | 0.32 Medicago_ |

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| Os10t0472900-01 | 0.30 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
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| Os08t0250900-01 | 0.25 | Ananas_co | 0.32 | Corchorus | 0.32 | Corchorus |
| Os03t0200000-00 | 0.20 | Musa_acur | 0.29 | Dioscorea_ | 0.32 | Manihot_e |
| Zm00001eb119840_P00 | -0.02 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Prunus_pe |
| Os02t0826100-01 | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os02t0168500-01 | 0.26 | Ananas_co | 0.32 | Coffea_car | 0.32 | Coffea_car |
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| Os10t0419200-01 | 0.29 | Musa_acur | 0.31 | Dioscorea_ | 0.32 | Helianthus |
| Os03t0389900-01 | 0.26 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
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| Os09t0567500-01 | 0.22 | Musa_acur | 0.32 | Theobrom | 0.32 | Theobrom |
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| Os03t0158500-01 | 0.32 | Dioscorea_ | 0.32 | Dioscorea_ | 0.32 | Prunus_du |
| Os05t0245300-01 | 0.23 | Ananas_co | 0.32 | Cucumis_ | 0.32 | Cucumis_ |
| Os04t0531700-01 | 0.32 | Rosa_chin | 0.32 | Rosa_chin | 0.32 | Rosa_chin |
| Os02t0633400-01 | 0.18 | Ananas_co | 0.21 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os09t0528800-01 | 0.28 | Ananas_co | 0.32 | Pistacia_ve | 0.32 | Pistacia_ve |
| Os12t0144000-00 | 0.29 | Dioscorea_ | 0.29 | Dioscorea_ | 0.32 | Capsicum_ |
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| Os04t0550400-01 | 0.16 | Ananas_co | 0.27 | Dioscorea_ | 0.32 | Vitis_vinife |
| Os10t0100500-01 | 0.22 | Ananas_co | 0.32 | Manihot_e | 0.32 | Manihot_e |
| Os12t0636000-01Zm00 | 0.21 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os03t0371800-00 | 0.31 | Musa_acur | 0.31 | Dioscorea_ | 0.32 | Ipomoea_t |
| Os08t0375800-01 | 0.17 | Ananas_co | 0.25 | Dioscorea_ | 0.32 | Gossypiu |
| Os01t0771000-01 | 0.27 | Ananas_co | 0.32 | Daucus_ca | 0.32 | Daucus_ca |

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| Os05t0556300-01 | 0.22 | Musa_acur | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os03t0808200-00 | 0.15 | Dioscorea_ | 0.15 | Dioscorea_ | 0.32 | Corchorus |
| Os09t0488800-01 | 0.26 | Ananas_co | 0.32 | Theobrom | 0.32 | Theobrom |

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| Os07t0688100-01 | 0.10 | Ananas_co | 0.26 | Dioscorea_ | 0.32 | Amborella_ |

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| Os06t0141200-01 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.32 | Helianthus |
| Os03t0607200-01 | 0.24 | Ananas_co | 0.30 | Dioscorea_ | 0.32 | Populus_tr |
| Zm00001eb034800_P00 | 0.20 | Ananas_co | 0.30 | Dioscorea_ | 0.32 | Populus_tr |
| Os05t0409100-00 | 0.23 | Ananas_co | 0.32 | Corchorus | 0.32 | Corchorus |
| Os05t0185700-02 | 0.29 | Musa_acur | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os10t0507600-01Zm00 | 0.32 | Beta_vulga | 0.32 | Beta_vulga | 0.32 | Beta_vulga |
| Os07t0510400-01 | 0.32 | Nymphaea | 0.32 | Nymphaea | 0.32 | Nymphaea |

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| Os01t0770200-01 | 0.30 | Ananas_co | 0.31 | Dioscorea_ | 0.32 | Amborella_ |
| Os06t0168000-01 | 0.19 | Ananas_co | 0.32 | Coffea_car | 0.32 | Coffea_car |
| Os02t0143400-00 | 0.28 | Musa_acur | 0.30 | Dioscorea_ | 0.32 | Cannabis_ |
| Os11t0178800-01 | 0.32 | Theobrom | 0.32 | Theobrom | 0.32 | Theobrom |
| Os01t0107900-01 | 0.29 | Ananas_co | 0.32 | Theobrom | 0.32 | Theobrom |
| Os06t0134700-01 | 0.21 | Ananas_co | 0.32 | Citrus_cler | 0.32 | Citrus_cler |
| Os02t0733001-00 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.32 | Populus_tr |

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| Os09t0558300-01 | 0.13 | Ananas_co | 0.29 | Dioscorea_ | 0.32 | Manihot_e |
| Os02t0523300-01 | 0.25 | Ananas_co | 0.32 | Vitis_vinife | 0.32 | Vitis_vinife |
| Os06t0254300-01 | 0.28 | Musa_acur | 0.29 | Dioscorea_ | 0.32 | Prunus_du |
| Os05t0452800-01 | 0.27 | Ananas_co | 0.28 | Dioscorea_ | 0.32 | Amborella_ |

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| Os01t0355900-01 | 0.25 Musa_acu | 0.31 Dioscorea_ | 0.32 Cynara_ca |
| Zm00001eb414530_P00 | 0.24 Ananas_co | 0.32 Solanum_l | 0.32 Solanum_l |

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| Os01t0670800-02 | 0.26 Ananas_co | 0.32 Theobrom | 0.32 Theobrom |
| Os01t0936800-01 | 0.11 Ananas_co | 0.26 Dioscorea_ | 0.32 Vitis_vinife |
| Os01t0207200-01 | 0.24 Ananas_co | 0.32 Amborella | 0.32 Amborella |
| Os06t0198900-01 | 0.25 Musa_acu | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os01t0822200-01 | 0.22 Ananas_co | 0.32 Corchorus | 0.32 Corchorus |

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| Os06t0728000-01 | 0.26 Musa_acu | 0.32 Lupinus_a | 0.32 Lupinus_a |
| Os02t0103500-00 | 0.25 Musa_acu | 0.32 Glycine_m | 0.32 Glycine_m |
| Zm00001eb414950_P00 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.32 Medicago_ |

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| Os02t0673100-01 | 0.17 Ananas_co | 0.32 Pistacia_ve | 0.32 Pistacia_ve |
| Os06t0710300-01 | 0.32 Nymphaea | 0.32 Nymphaea | 0.32 Nymphaea |
| Zm00001eb249870_P00 | 0.22 Ananas_co | 0.32 Actinidia_ | 0.32 Actinidia_ |
| Os05t0432400-02 | 0.24 Ananas_co | 0.32 Ipomoea_t | 0.32 Ipomoea_t |
| Os02t0591900-02 | 0.25 Ananas_co | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os08t0372700-00Zm00 | 0.32 Malus_do | 0.32 Malus_do | 0.32 Malus_do |
| Os07t0461500-00 | 0.30 Ananas_co | 0.32 Theobrom | 0.32 Theobrom |
| Os02t0179000-00 | 0.29 Ananas_co | 0.32 Nymphaea | 0.32 Nymphaea |
| Os09t0248200-01 | 0.21 Musa_acu | 0.24 Dioscorea_ | 0.32 Theobrom |
| Os04t0481000-00 | 0.24 Ananas_co | 0.29 Dioscorea_ | 0.32 Citrus_cle |
| Os08t0267300-00 | 0.25 Ananas_co | 0.29 Dioscorea_ | 0.32 Daucus_ca |
| Os02t0597800-01 | 0.19 Ananas_co | 0.31 Dioscorea_ | 0.32 Prunus_pe |
| Os10t0502100-01 | 0.29 Ananas_co | 0.32 Nicotiana_ | 0.32 Nicotiana_ |

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| Os12t0207000-01 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.32 Populus_tr |
| Os03t0809900-01 | 0.29 Musa_acur | 0.32 Actinidia_c | 0.32 Actinidia_c |
| Os02t0672800-01 | 0.26 Ananas_co | 0.32 Actinidia_c | 0.32 Actinidia_c |
| Os02t0280200-00 | 0.19 Ananas_co | 0.28 Dioscorea_ | 0.32 Actinidia_c |
| Os01t0581400-01 | 0.25 Musa_acur | 0.32 Theobrom | 0.32 Theobrom |
| Os08t0547800-01 | 0.19 Ananas_co | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Zm00001eb084290_P00 | 0.20 Ananas_co | 0.32 Capsicum_ | 0.32 Capsicum_ |
| Os04t0677700-01 | 0.32 Prunus_du | 0.32 Prunus_du | 0.32 Prunus_du |
| Os04t0653600-01 | 0.32 Citrus_cler | 0.32 Citrus_cler | 0.32 Citrus_cler |
| Os09t0103500-01Zm00 | 0.28 Ananas_co | 0.32 Vitis_vinife | 0.32 Vitis_vinife |
| Os02t0734300-01 | 0.26 Ananas_co | 0.32 Populus_tr | 0.32 Populus_tr |
| Os07t0681700-01 | 0.16 Ananas_co | 0.28 Dioscorea_ | 0.32 Citrus_cler |
| Os02t0259600-01 | 0.27 Ananas_co | 0.29 Dioscorea_ | 0.32 Prunus_du |
| Os01t0685900-01 | 0.22 Ananas_co | 0.29 Dioscorea_ | 0.32 Malus_dom |
| Os04t0419550-01 | 0.19 Ananas_co | 0.25 Dioscorea_ | 0.32 Daucus_ca |
| Zm00001eb071830_P00 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.32 Amborella_ |
| Os09t0547100-01Zm00 | 0.27 Ananas_co | 0.32 Ipomoea_t | 0.32 Ipomoea_t |
| Os01t0702700-01 | 0.21 Musa_acur | 0.31 Dioscorea_ | 0.32 Citrus_cler |
| Os12t0527900-01 | 0.23 Ananas_co | 0.32 Pistacia_ve | 0.32 Pistacia_ve |
| Os05t0484800-01 | 0.24 Ananas_co | 0.32 Citrus_cler | 0.32 Citrus_cler |
| Os03t0859100-01 | 0.17 Musa_acur | 0.31 Dioscorea_ | 0.32 Manihot_e |
| Zm00001eb067480_P00 | 0.20 Dioscorea_ | 0.20 Dioscorea_ | 0.32 Rosa_chine |

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| Os03t0752300-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.31 Medicago_ |
| Os10t0580900-01 | 0.29 Musa_acu | 0.31 Theobrom | 0.31 Theobrom |

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| Os07t0548300-01 | 0.23 Musa_acu | 0.31 Corchorus | 0.31 Corchorus |
| Os03t0843400-01 | 0.30 Musa_acu | 0.31 Populus_tr | 0.31 Populus_tr |

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| Os01t0667900-01 | 0.24 Ananas_co | 0.31 Glycine_m | 0.31 Glycine_m |
| Os12t0562100-01 | 0.16 Ananas_co | 0.31 Actinidia_ | 0.31 Actinidia_ |
| Os01t0925200-01 | 0.24 Musa_acu | 0.27 Dioscorea_ | 0.31 Camelina_ |

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| Os04t0301500-01Zm00 | 0.23 Ananas_co | 0.29 Dioscorea_ | 0.31 Nicotiana_ |
| Os09t0535100-01 | 0.24 Ananas_co | 0.31 Cannabis_ | 0.31 Cannabis_ |

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| Os01t0822900-03 | 0.29 Ananas_co | 0.31 Manihot_e | 0.31 Manihot_e |
| Os07t0185700-01 | 0.31 Manihot_e | 0.31 Manihot_e | 0.31 Manihot_e |
| Os01t0556400-01 | 0.31 Prunus_pe | 0.31 Prunus_pe | 0.31 Prunus_pe |
| Os04t0450200-01 | 0.17 Ananas_co | 0.25 Dioscorea_ | 0.31 Malus_do |
| Os03t0131500-01 | 0.27 Ananas_co | 0.31 Populus_tr | 0.31 Populus_tr |

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| Os05t0375400-01 | 0.23 | Ananas_co | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os06t0556600-01 | 0.30 | Musa_acur | 0.31 | Beta_vulga | 0.31 | Beta_vulga |
| Os10t0539700-01 | 0.30 | Ananas_co | 0.31 | Coffea_car | 0.31 | Coffea_car |
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| Os01t0927600-01 | 0.31 | Coffea_car | 0.31 | Coffea_car | 0.31 | Coffea_car |
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| Os03t0393900-01 | 0.27 | Ananas_co | 0.31 | Coffea_car | 0.31 | Coffea_car |
| Os01t0201200-01 | 0.24 | Ananas_co | 0.29 | Dioscorea_ | 0.31 | Corchorus |
| Os03t0300300-01 | 0.22 | Ananas_co | 0.31 | Pistacia_ve | 0.31 | Pistacia_ve |
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| Os09t0280500-01 | 0.30 | Ananas_co | 0.31 | Manihot_e | 0.31 | Manihot_e |
| Os01t0166400-02 | 0.13 | Ananas_co | 0.31 | Actinidia_c | 0.31 | Actinidia_c |
| Os01t0267300-00 | 0.25 | Musa_acur | 0.29 | Dioscorea_ | 0.31 | Prunus_du |
| Os12t0640800-01 | 0.27 | Ananas_co | 0.29 | Dioscorea_ | 0.31 | Amborella |
| Os04t0433600-01 | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os06t0192100-00 | 0.26 | Musa_acur | 0.30 | Dioscorea_ | 0.31 | Citrus_cler |
| Os04t0670000-01 | 0.17 | Musa_acur | 0.24 | Dioscorea_ | 0.31 | Ipomoea_t |
| Os05t0271900-01 | 0.21 | Ananas_co | 0.31 | Malus_dom | 0.31 | Malus_dom |
| Os06t0138200-01 | 0.25 | Ananas_co | 0.28 | Dioscorea_ | 0.31 | Vitis_vinife |
| Os01t0549400-01 | 0.26 | Musa_acur | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
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| Os03t0633800-01 | 0.26 | Ananas_co | 0.30 | Dioscorea_ | 0.31 | Nicotiana_ |
| Os07t0674300-01 | 0.28 | Ananas_co | 0.31 | Corchorus | 0.31 | Corchorus |
| Os04t0624800-01 | 0.28 | Ananas_co | 0.31 | Nymphaea | 0.31 | Nymphaea |
| Os07t0105000-00 | 0.25 | Musa_acur | 0.31 | Theobroma | 0.31 | Theobroma |
| Os01t0242600-01 | 0.25 | Ananas_co | 0.29 | Dioscorea_ | 0.31 | Theobroma |
| Os06t0712400-01 | 0.29 | Ananas_co | 0.31 | Dioscorea_ | 0.31 | Citrus_cler |
| Os09t0514100-02 | 0.23 | Ananas_co | 0.31 | Manihot_e | 0.31 | Manihot_e |
| Os02t0128100-00 | 0.26 | Ananas_co | 0.31 | Ipomoea_t | 0.31 | Ipomoea_t |
| Os09t0382300-00 | 0.23 | Ananas_co | 0.31 | Citrus_cler | 0.31 | Citrus_cler |
| Os07t0563800-02 | 0.23 | Ananas_co | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os01t0700100-01 | 0.27 | Musa_acur | 0.31 | Manihot_e | 0.31 | Manihot_e |
| Os03t0244700-01 | 0.19 | Ananas_co | 0.26 | Dioscorea_ | 0.31 | Cucumis_s |
| Os01t0257400-01 | 0.26 | Ananas_co | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os05t0519300-01Zm00 | 0.17 | Ananas_co | 0.31 | Actinidia_c | 0.31 | Actinidia_c |

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| Os03t0737701-01 | 0.26 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os11t0191400-01 | 0.28 Musa_acur | 0.31 Theobrom | 0.31 Theobrom |

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| Os01t0811300-01 | 0.16 Ananas_co | 0.16 Dioscorea_ | 0.31 Theobrom |
| Os09t0483600-01 | 0.25 Ananas_co | 0.30 Dioscorea_ | 0.31 Actinidia_c |
| Zm00001eb049730_P00 | 0.20 Musa_acur | 0.29 Dioscorea_ | 0.31 Theobrom |
| Os03t0760500-01 | 0.30 Ananas_co | 0.31 Citrus_cler | 0.31 Citrus_cler |
| Os07t0572600-01 | 0.21 Musa_acur | 0.31 Nicotiana_ | 0.31 Nicotiana_ |
| Os07t0662600-01 | 0.24 Ananas_co | 0.31 Pistacia_ve | 0.31 Pistacia_ve |
| Os12t0454600-00 | 0.28 Ananas_co | 0.31 Beta_vulga | 0.31 Beta_vulga |
| Os01t0316100-00 | 0.28 Ananas_co | 0.31 Prunus_avi | 0.31 Prunus_avi |
| Os09t0528000-01 | 0.20 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os03t0828300-01 | 0.31 Vitis_vinife | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os04t0652900-01 | 0.31 Capsicum_ | 0.31 Capsicum_ | 0.31 Capsicum_ |
| Os08t0481000-01Zm00 | 0.17 Ananas_co | 0.23 Dioscorea_ | 0.31 Rosa_chine |
| Os02t0730800-01 | 0.29 Musa_acur | 0.31 Manihot_e | 0.31 Manihot_e |
| Os03t0782900-01 | 0.19 Ananas_co | 0.31 Citrus_cler | 0.31 Citrus_cler |

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| Os09t0518700-01 | 0.21 Ananas_co | 0.31 Actinidia_c | 0.31 Actinidia_c |
| Os12t0552700-01 | 0.15 Ananas_co | 0.24 Dioscorea_ | 0.31 Nymphaea |
| Os02t0608801-00Zm00 | 0.23 Ananas_co | 0.26 Dioscorea_ | 0.31 Actinidia_c |

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| Os09t0454900-01 | 0.18 Ananas_co | 0.27 Dioscorea_ | 0.31 Manihot_e |
| Os10t0477000-01 | 0.14 Ananas_co | 0.29 Dioscorea_ | 0.31 Manihot_e |
| Os02t0754900-01 | 0.20 Ananas_co | 0.31 Rosa_chine | 0.31 Rosa_chine |
| Os07t0204500-01 | 0.12 Ananas_co | 0.31 Prunus_avi | 0.31 Prunus_avi |
| Os09t0482740-01 | 0.22 Musa_acur | 0.31 Amborella_ | 0.31 Amborella_ |
| Os02t0638300-01 | 0.15 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os01t0572300-01 | 0.30 Musa_acur | 0.31 Glycine_m | 0.31 Glycine_m |
| Os12t0428000-01Zm00 | 0.12 Ananas_co | 0.31 Nymphaea | 0.31 Nymphaea |
| Os11t0655800-01 | 0.29 Musa_acur | 0.31 Theobrom | 0.31 Theobrom |

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| Os12t0563200-01 | 0.26 | Musa_acu | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os10t0477200-01 | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os03t0738900-00 | 0.27 | Ananas_co | 0.31 | Capsicum_ | 0.31 | Capsicum_ |
| Os04t0600000-01 | 0.28 | Musa_acu | 0.31 | Actinidia_ | 0.31 | Actinidia_ |
| Os02t0221800-00 | 0.27 | Musa_acu | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os01t0948500-01 | 0.25 | Musa_acu | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os09t0431100-01 | 0.19 | Ananas_co | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |

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| Os07t0503500-01 | 0.31 | Nymphaea | 0.31 | Nymphaea | 0.31 | Nymphaea |
| Os07t0565400-01 | 0.23 | Ananas_co | 0.25 | Dioscorea_ | 0.31 | Rosa_chine |
| Os11t0586001-00 | 0.17 | Ananas_co | 0.31 | Theobrom | 0.31 | Theobrom |
| Os05t0344400-01 | 0.25 | Ananas_co | 0.31 | Populus_tr | 0.31 | Populus_tr |
| Os06t0694100-01 | 0.21 | Musa_acu | 0.31 | Actinidia_ | 0.31 | Actinidia_ |
| Os05t0393100-01 | 0.25 | Musa_acu | 0.28 | Dioscorea_ | 0.31 | Vitis_vinife |
| Os01t0875000-01 | 0.23 | Musa_acu | 0.31 | Lupinus_a | 0.31 | Lupinus_a |
| Os02t0123200-01 | 0.27 | Ananas_co | 0.31 | Actinidia_ | 0.31 | Actinidia_ |
| Os08t0269800-01 | 0.14 | Musa_acu | 0.22 | Dioscorea_ | 0.31 | Corchorus |
| Os08t0489300-01 | 0.25 | Ananas_co | 0.31 | Citrus_cle | 0.31 | Citrus_cle |
| Os06t0677700-00 | 0.23 | Musa_acu | 0.31 | Dioscorea_ | 0.31 | Gossypiu |
| Os09t0424300-01 | 0.10 | Musa_acu | 0.31 | Vitis_vinife | 0.31 | Vitis_vinife |
| Os03t0836500-01 | 0.16 | Ananas_co | 0.31 | Corchorus | 0.31 | Corchorus |

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| Os10t0516800-01 | 0.23 | Ananas_co | 0.28 | Dioscorea_ | 0.31 | Beta_vulga |
| Os03t0216800-01 | 0.29 | Ananas_co | 0.31 | Amborella | 0.31 | Amborella |

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| Os12t0143200-01 | 0.31 | Glycine_m | 0.31 | Glycine_m | 0.31 | Glycine_m |
| Os06t0596300-01 | 0.22 | Ananas_co | 0.25 | Dioscorea_ | 0.31 | Manihot_e |
| Os05t0427900-01 | 0.08 | Ananas_co | 0.16 | Dioscorea_ | 0.31 | Amborella |
| Os03t0298300-01 | 0.25 | Musa_acu | 0.31 | Amborella | 0.31 | Amborella |

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| Os11t0283500-01Zm00 | 0.24 Ananas_co | 0.29 Dioscorea_ | 0.31 Amborella_ |
| Os07t0640000-01 | 0.20 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os02t0712700-01 | 0.22 Ananas_co | 0.31 Prunus_pe | 0.31 Prunus_pe |
| Os08t0326700-00 | 0.28 Ananas_co | 0.31 Theobrom | 0.31 Theobrom |
| Os01t0384300-00 | 0.27 Ananas_co | 0.29 Dioscorea_ | 0.31 Amborella_ |
| Os04t0640600-01 | 0.14 Ananas_co | 0.20 Dioscorea_ | 0.31 Prunus_du |
| Os04t0675400-01 | 0.23 Ananas_co | 0.31 Theobrom | 0.31 Theobrom |
| Os02t0697700-01 | 0.20 Ananas_co | 0.31 Glycine_m | 0.31 Glycine_m |
| Os05t0103500-01 | 0.26 Ananas_co | 0.31 Nicotiana_ | 0.31 Nicotiana_ |
| Os01t0959600-00 | 0.18 Ananas_co | 0.24 Dioscorea_ | 0.31 Vitis_vinife |
| Os04t0584100-01Zm00 | 0.31 Glycine_m | 0.31 Glycine_m | 0.31 Glycine_m |
| Os12t0590900-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.31 Nymphaea |
| Os05t0394200-01 | 0.30 Musa_acu | 0.31 Theobrom | 0.31 Theobrom |
| Os01t0779400-02 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.31 Vitis_vinife |
| Os07t0577300-01 | 0.09 Ananas_co | 0.18 Dioscorea_ | 0.31 Medicago_ |
| Os03t0347500-01 | 0.27 Ananas_co | 0.31 Cannabis_ | 0.31 Cannabis_ |
| Os01t0876400-02 | 0.17 Ananas_co | 0.26 Dioscorea_ | 0.31 Vitis_vinife |
| Os03t0663800-01 | 0.24 Ananas_co | 0.31 Actinidia_c | 0.31 Actinidia_c |
| Os01t0121100-02 | 0.26 Musa_acu | 0.26 Dioscorea_ | 0.31 Theobrom |
| Os03t0243700-01 | 0.17 Ananas_co | 0.29 Dioscorea_ | 0.31 Prunus_avi |
| Os02t0676400-00 | 0.22 Ananas_co | 0.31 Dioscorea_ | 0.31 Gossypiu |
| Os03t0223900-01 | 0.23 Ananas_co | 0.24 Dioscorea_ | 0.31 Malus_do |
| Os04t0528100-01 | 0.29 Dioscorea_ | 0.29 Dioscorea_ | 0.31 Ipomoea_t |
| Os01t0253900-01 | 0.25 Ananas_co | 0.31 Prunus_avi | 0.31 Prunus_avi |
| Os11t0465200-01 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.31 Glycine_m |

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| Os04t0644300-01Zm00 | 0.20 Ananas_co | 0.31 Solanum_l | 0.31 Solanum_l |
| Os10t0375000-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.31 Populus_tr |
| Os03t0259700-01 | 0.23 Musa_acur | 0.28 Dioscorea_ | 0.31 Prunus_du |
| Os05t0432700-01 | 0.25 Ananas_co | 0.31 Capsicum_ | 0.31 Capsicum_ |
| Os04t0497600-01 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.31 Capsicum_ |
| Os01t0280400-00 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.31 Actinidia_c |
| Os08t0152700-01 | 0.29 Musa_acur | 0.31 Helianthus | 0.31 Helianthus |
| Os03t0346700-01 | 0.18 Ananas_co | 0.26 Dioscorea_ | 0.31 Prunus_avi |
| Zm00001eb099000_P00 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.31 Actinidia_c |
| Os07t0661700-01 | 0.27 Musa_acur | 0.31 Phaseolus_ | 0.31 Phaseolus_ |
| Os08t0562500-01 | 0.17 Musa_acur | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os05t0480200-01 | 0.26 Ananas_co | 0.31 Manihot_e | 0.31 Manihot_e |
| Os07t0280200-01 | 0.18 Ananas_co | 0.30 Dioscorea_ | 0.31 Ipomoea_t |
| Os07t0165200-01 | 0.22 Ananas_co | 0.31 Prunus_du | 0.31 Prunus_du |
| Os03t0207800-00 | 0.31 Corchorus | 0.31 Corchorus | 0.31 Corchorus |
| Os04t0116600-01 | 0.31 Coffea_car | 0.31 Coffea_car | 0.31 Coffea_car |
| Os01t0912600-01Zm00 | 0.20 Ananas_co | 0.31 Actinidia_c | 0.31 Actinidia_c |
| Os08t0334900-01 | 0.19 Ananas_co | 0.30 Dioscorea_ | 0.31 Malus_don |
| Os05t0212100-01 | 0.22 Ananas_co | 0.27 Dioscorea_ | 0.31 Actinidia_c |
| Os02t0697500-02 | 0.29 Ananas_co | 0.31 Citrus_cler | 0.31 Citrus_cler |
| Os01t0507700-01 | 0.17 Musa_acur | 0.27 Dioscorea_ | 0.31 Actinidia_c |
| Os07t0287100-01 | 0.18 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os03t0777000-01 | 0.23 Ananas_co | 0.26 Dioscorea_ | 0.31 Vitis_vinife |
| Os04t0491500-02 | 0.18 Ananas_co | 0.20 Dioscorea_ | 0.31 Amborella_ |
| Os04t0581800-01 | 0.22 Musa_acur | 0.31 Brassica_ra | 0.31 Brassica_ra |
| Os02t0133200-01 | 0.23 Ananas_co | 0.30 Dioscorea_ | 0.31 Amborella_ |

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| Os06t0602700-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.31 Beta_vulga |

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| Os05t0198400-01Zm00 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.31 Nymphaea |

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| Os01t0218800-01 | 0.25 Musa_acur | 0.31 Dioscorea_ | 0.31 Vitis_vinife |
| Os05t0576300-01Zm00 | 0.23 Musa_acur | 0.31 Nicotiana_ | 0.31 Nicotiana_ |
| Os03t0816400-02Zm00 | 0.26 Musa_acur | 0.28 Dioscorea_ | 0.31 Theobrom |
| Os09t0116400-01 | 0.20 Dioscorea_ | 0.20 Dioscorea_ | 0.31 Populus_tr |

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| Os04t0671900-01 | 0.17 Ananas_co | 0.27 Dioscorea_ | 0.31 Nicotiana_ |
| Os09t0279100-01 | 0.31 Vitis_vinife | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os10t0544500-01 | 0.25 Ananas_co | 0.31 Manihot_e | 0.31 Manihot_e |
| Os06t0111600-01 | 0.21 Ananas_co | 0.31 Populus_tr | 0.31 Populus_tr |
| Os04t0568800-01 | 0.13 Ananas_co | 0.31 Theobrom | 0.31 Theobrom |
| Os01t0549500-01 | 0.23 Musa_acur | 0.31 Dioscorea_ | 0.31 Prunus_pe |
| Os04t0488000-01 | 0.27 Dioscorea_ | 0.27 Dioscorea_ | 0.31 Helianthus |

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| Os07t0535800-01Zm00 | 0.20 Ananas_co | 0.31 Nymphaea | 0.31 Nymphaea |
| Os03t0288300-01 | 0.16 Ananas_co | 0.21 Dioscorea_ | 0.31 Amborella_ |
| Os06t0639500-01 | 0.15 Ananas_co | 0.31 Populus_tr | 0.31 Populus_tr |
| Os12t0582800-01 | 0.20 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os04t0574600-01 | 0.18 Ananas_co | 0.30 Dioscorea_ | 0.31 Actinidia_ |

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| Os02t0717600-01 | 0.29 Ananas_co | 0.30 Dioscorea_ | 0.31 Theobrom |
| Os12t0508266-01 | 0.27 Musa_acur | 0.27 Dioscorea_ | 0.31 Populus_tr |
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| Os10t0416800-03 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.31 Solanum_t |
| Os05t0446800-01 | 0.26 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
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| Os09t0281900-01 | 0.21 Ananas_co | 0.31 Citrus_cler | 0.31 Citrus_cler |
| Os02t0184400-01 | 0.27 Musa_acur | 0.31 Pistacia_ve | 0.31 Pistacia_ve |
| Os02t0618700-01 | 0.22 Ananas_co | 0.31 Pistacia_ve | 0.31 Pistacia_ve |
| Os06t0687900-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.31 Actinidia_c |
| Os04t0112300-01 | 0.23 Ananas_co | 0.31 Manihot_e | 0.31 Manihot_e |
| Os01t0709400-01 | 0.26 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os03t0212400-01 | 0.24 Ananas_co | 0.31 Vigna_ang | 0.31 Vigna_ang |
| Os05t0468500-01 | 0.28 Ananas_co | 0.28 Dioscorea_ | 0.31 Citrullus_l |
| Os03t0362200-01 | 0.21 Ananas_co | 0.30 Dioscorea_ | 0.31 Corchorus |
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| Os09t0551251-00 | 0.31 Amborella | 0.31 Amborella | 0.31 Amborella |
| Os03t0223000-02 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.31 Nicotiana_ |
| Os03t0262000-01 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.31 Solanum_l |
| Os11t0149200-00Zm00 | 0.31 Corchorus | 0.31 Corchorus | 0.31 Corchorus |
| Os07t0538400-01 | 0.17 Ananas_co | 0.23 Dioscorea_ | 0.31 Manihot_e |
| Os02t0782600-01 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.31 Amborella |
| Os09t0556200-00 | 0.23 Ananas_co | 0.27 Dioscorea_ | 0.31 Actinidia_c |
| Os03t0773000-01 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.31 Theobrom |
| Os10t0407500-00 | 0.25 Ananas_co | 0.31 Vitis_vinife | 0.31 Vitis_vinife |
| Os03t0265900-01 | 0.25 Ananas_co | 0.31 Gossypiu | 0.31 Gossypiu |
| Os05t0405600-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.31 Citrus_cler |
| Os01t0584200-00 | 0.31 Solanum_t | 0.31 Solanum_t | 0.31 Solanum_t |
| Os02t0820300-01 | 0.19 Ananas_co | 0.31 Nymphaea | 0.31 Nymphaea |
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| Os08t0138500-01 | 0.24 Ananas_co | 0.29 Dioscorea_ | 0.31 Glycine_m |
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| Os02t0557500-01 | 0.23 Ananas_co | 0.31 Daucus_ca | 0.31 Daucus_ca |
| Os05t0304900-01 | 0.29 Ananas_co | 0.30 Dioscorea_ | 0.30 Populus_tr |
| Os06t0589300-01 | 0.22 Ananas_co | 0.26 Dioscorea_ | 0.30 Vitis_vinife |
| Os11t0641500-01Zm00 | 0.30 Ipomoea_t | 0.30 Ipomoea_t | 0.30 Ipomoea_t |
| Os08t0505200-01 | 0.19 Ananas_co | 0.30 Dioscorea_ | 0.30 Vitis_vinife |
| Os04t0117300-01 | 0.20 Ananas_co | 0.30 Vitis_vinife | 0.30 Vitis_vinife |
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| Os04t0536300-01 | 0.23 Ananas_co | 0.30 Prunus_pe | 0.30 Prunus_pe |

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| Os01t0927000-01 | 0.30 Gossypiu | 0.30 Gossypiu | 0.30 Gossypiu |
| Os05t0462500-01 | 0.21 Ananas_co | 0.30 Daucus_ca | 0.30 Daucus_ca |

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| Os03t0757500-01 | 0.25 Ananas_co | 0.30 Citrus_cle | 0.30 Citrus_cle |
| Os01t0919600-01 | 0.23 Ananas_co | 0.28 Dioscorea_ | 0.30 Trifolium_ |

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| Os06t0348800-01 | 0.27 Musa_acu | 0.30 Rosa_chin | 0.30 Rosa_chin |
| Os06t0140800-01 | 0.30 Gossypiu | 0.30 Gossypiu | 0.30 Gossypiu |
| Os06t0731400-02 | 0.18 Ananas_co | 0.30 Prunus_avi | 0.30 Prunus_avi |
| Os03t0157700-01 | 0.24 Ananas_co | 0.29 Dioscorea_ | 0.30 Pistacia_ve |
| Os08t0440200-01 | 0.20 Ananas_co | 0.30 Actinidia_ | 0.30 Actinidia_ |
| Os10t0521300-01 | 0.18 Musa_acu | 0.26 Dioscorea_ | 0.30 Beta_vulga |
| Os01t0673800-01 | 0.28 Musa_acu | 0.28 Dioscorea_ | 0.30 Theobrom |
| Os04t0417000-01 | 0.13 Musa_acu | 0.29 Dioscorea_ | 0.30 Citrus_cle |
| Os09t0518500-01 | 0.17 Ananas_co | 0.25 Dioscorea_ | 0.30 Phaseolus_ |
| Os02t0736600-01 | 0.24 Ananas_co | 0.30 Vitis_vinife | 0.30 Vitis_vinife |

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| Os04t0674400-01 | 0.24 Ananas_co | 0.30 Actinidia_ | 0.30 Actinidia_ |
| Os08t0508100-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.30 Theobrom |
| Os05t0106000-01 | 0.28 Musa_acu | 0.30 Beta_vulga | 0.30 Beta_vulga |
| Os02t0719800-02 | 0.26 Ananas_co | 0.27 Dioscorea_ | 0.30 Vitis_vinife |
| Os01t0695600-00 | 0.30 Musa_acu | 0.30 Amborella | 0.30 Amborella |
| Os12t0155200-01 | 0.22 Ananas_co | 0.30 Dioscorea_ | 0.30 Vitis_vinife |
| Os02t0739400-01 | 0.14 Ananas_co | 0.30 Prunus_pe | 0.30 Prunus_pe |

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| Os07t0583200-01 | 0.27 Musa_acur | 0.30 Pistacia_ve | 0.30 Pistacia_ve |
| Os03t0820900-01 | 0.14 Ananas_co | 0.28 Dioscorea_ | 0.30 Actinidia_ |
| Os09t0386600-01 | 0.15 Ananas_co | 0.29 Dioscorea_ | 0.30 Vitis_vinife |
| Os03t0165900-01 | 0.23 Ananas_co | 0.29 Dioscorea_ | 0.30 Citrus_cle |

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| Os03t0133000-01 | 0.25 Musa_acur | 0.26 Dioscorea_ | 0.30 Glycine_m |
| Os07t0558000-01 | 0.18 Ananas_co | 0.30 Gossypiur | 0.30 Gossypiur |
| Os05t0485000-01 | 0.17 Ananas_co | 0.30 Prunus_avi | 0.30 Prunus_avi |
| Os05t0382900-01 | 0.16 Ananas_co | 0.30 Manihot_e | 0.30 Manihot_e |
| Os01t0850400-01 | 0.27 Ananas_co | 0.30 Corchorus_ | 0.30 Corchorus_ |
| Zm00001eb134530_P00 | 0.22 Ananas_co | 0.27 Dioscorea_ | 0.30 Vitis_vinife |
| Os02t0819500-01Zm00 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.30 Phaseolus_ |
| Os01t0894600-01 | 0.20 Ananas_co | 0.30 Amborella_ | 0.30 Amborella_ |

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| Zm00001eb242180_P00 | 0.30 Nymphaea_ | 0.30 Nymphaea | 0.30 Nymphaea |
| Os03t0300600-01 | 0.17 Musa_acur | 0.30 Glycine_m | 0.30 Glycine_m |
| Zm00001eb418060_P00 | 0.17 Ananas_co | 0.30 Malus_dom | 0.30 Malus_dom |
| Os06t0641500-00Zm00 | 0.25 Ananas_co | 0.27 Dioscorea_ | 0.30 Pistacia_ve |
| Os07t0134700-00 | 0.25 Ananas_co | 0.30 Vitis_vinife | 0.30 Vitis_vinife |
| Os06t0634600-01 | 0.20 Ananas_co | 0.27 Dioscorea_ | 0.30 Prunus_avi |
| Os03t0245700-02 | 0.30 Nymphaea_ | 0.30 Nymphaea | 0.30 Nymphaea |
| Os05t0481800-01 | 0.10 Ananas_co | 0.21 Dioscorea_ | 0.30 Actinidia_ |
| Zm00001eb096940_P00 | 0.30 Theobrom | 0.30 Theobrom | 0.30 Theobrom |
| Zm00001eb082660_P00 | 0.26 Musa_acur | 0.30 Malus_dom | 0.30 Malus_dom |

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| Os03t0771100-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.30 Medicago_ |
| Os04t0418000-01 | 0.11 Ananas_co | 0.25 Dioscorea_ | 0.30 Actinidia_ |
| Os12t0563600-03 | 0.28 Ananas_co | 0.30 Nicotiana_ | 0.30 Nicotiana_ |
| Os10t0438800-01 | 0.26 Ananas_co | 0.30 Solanum_l | 0.30 Solanum_l |
| Os01t0879600-00Zm00 | 0.17 Musa_acur | 0.30 Nymphaea | 0.30 Nymphaea |

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| Os03t0309400-01 | 0.20 Ananas_co | 0.30 Glycine_m | 0.30 Glycine_m |

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| Os03t0344300-01 | 0.25 Musa_acur | 0.30 Cucumis_s | 0.30 Cucumis_s |

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| Os04t0601400-01 | 0.21 Musa_acur | 0.30 Amborella_ | 0.30 Amborella_ |
| Os06t0709100-01 | 0.25 Ananas_co | 0.30 Nymphaea | 0.30 Nymphaea |
| Os04t0414300-00 | 0.27 Ananas_co | 0.30 Glycine_ma | 0.30 Glycine_ma |

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| Os03t0437100-01 | 0.30 Vitis_vinife | 0.30 Vitis_vinife | 0.30 Vitis_vinife |
| Os07t0633000-01 | 0.25 Musa_acur | 0.30 Pistacia_ve | 0.30 Pistacia_ve |
| Os03t0335500-01 | 0.23 Ananas_co | 0.27 Dioscorea_ | 0.30 Vitis_vinife |
| Os05t0231700-01 | 0.30 Amborella_ | 0.30 Amborella_ | 0.30 Amborella_ |
| Os01t0933900-01 | 0.13 Ananas_co | 0.30 Malus_dom | 0.30 Malus_dom |
| Os09t0381600-01 | 0.24 Musa_acur | 0.30 Rosa_chine | 0.30 Rosa_chine |
| Os12t0165700-01 | 0.27 Musa_acur | 0.30 Vitis_vinife | 0.30 Vitis_vinife |
| Os07t0560300-01 | 0.26 Ananas_co | 0.30 Corchorus_ | 0.30 Corchorus_ |
| Os06t0112100-01 | 0.22 Ananas_co | 0.26 Dioscorea_ | 0.30 Theobroma |
| Os06t0257600-01 | 0.22 Ananas_co | 0.30 Brassica_ol | 0.30 Brassica_ol |
| Os01t0628700-01 | 0.21 Ananas_co | 0.30 Glycine_ma | 0.30 Glycine_ma |
| Os04t0439100-02Zm00 | 0.20 Ananas_co | 0.26 Dioscorea_ | 0.30 Vitis_vinife |
| Os02t0696500-01 | 0.19 Ananas_co | 0.30 Nymphaea | 0.30 Nymphaea |
| Zm00001eb207560_P00 | 0.20 Ananas_co | 0.28 Dioscorea_ | 0.30 Coffea_car |
| Zm00001eb108910_P00 | 0.30 Coffea_car | 0.30 Coffea_car | 0.30 Coffea_car |
| Os09t0502200-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.30 Nymphaea |

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| Os08t0180300-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.30 Prunus_du |
| Os05t0439300-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.30 Pistacia_ve |
| Os04t0652700-01 | 0.16 Musa_acur | 0.23 Dioscorea_ | 0.30 Manihot_es |
| Os04t0227200-00 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.30 Manihot_es |
| Os06t0717100-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.30 Citrus_cler |
| Zm00001eb040580_P00 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.30 Cucumis_m |
| Os02t0768300-01 | 0.19 Ananas_co | 0.28 Dioscorea_ | 0.30 Populus_tr |

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| Os02t0537500-01 | 0.18 Ananas_co | 0.27 Dioscorea_ | 0.30 Theobroma |
| Os10t0528100-01 | 0.23 Ananas_co | 0.30 Beta_vulga | 0.30 Beta_vulga |
| Os01t0499300-01 | 0.15 Ananas_co | 0.26 Dioscorea_ | 0.30 Gossypium |
| Os07t0538000-01 | 0.30 Dioscorea_ | 0.30 Dioscorea_ | 0.30 Brassica_na |
| Os04t0469400-01 | 0.21 Ananas_co | 0.30 Actinidia_c | 0.30 Actinidia_c |

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| Os02t0757700-01 | 0.15 | Musa_acu | 0.17 | Dioscorea_ | 0.30 | Cannabis_ |
| Os03t0117200-01 | 0.25 | Ananas_co | 0.30 | Prunus_du | 0.30 | Prunus_du |
| Os07t0677900-01 | 0.25 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os08t0492400-01 | 0.23 | Ananas_co | 0.26 | Dioscorea_ | 0.30 | Manihot_e |

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| Os08t0555800-00 | 0.11 | Ananas_co | 0.30 | Glycine_m | 0.30 | Glycine_m |
| Os03t0210400-01 | 0.23 | Musa_acu | 0.25 | Dioscorea_ | 0.30 | Actinidia_c |
| Os09t0497500-01Zm00 | 0.25 | Ananas_co | 0.30 | Amborella_ | 0.30 | Amborella_ |
| Os09t0488700-01 | 0.24 | Musa_acu | 0.26 | Dioscorea_ | 0.30 | Manihot_e |

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| Os11t0267000-02 | 0.30 | Manihot_e | 0.30 | Manihot_e | 0.30 | Manihot_e |
| Os05t0578500-01 | -0.02 | Ananas_co | 0.12 | Dioscorea_ | 0.30 | Theobrom |
| Os01t0906600-01 | 0.20 | Ananas_co | 0.30 | Actinidia_c | 0.30 | Actinidia_c |

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| Os12t0441300-00Zm00 | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os08t0549300-01 | 0.29 | Ananas_co | 0.30 | Ipomoea_t | 0.30 | Ipomoea_t |

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| Os07t0572800-01 | 0.22 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Vigna_ang |
| Os05t0355300-01 | 0.15 | Ananas_co | 0.30 | Helianthus | 0.30 | Helianthus |
| Os07t0166700-01 | 0.17 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os05t0153200-01 | 0.16 | Ananas_co | 0.23 | Dioscorea_ | 0.30 | Cucumis_ |
| Os12t0577100-01 | 0.30 | Nymphaea | 0.30 | Nymphaea | 0.30 | Nymphaea |
| Os09t0381400-01 | 0.29 | Dioscorea_ | 0.29 | Dioscorea_ | 0.30 | Ipomoea_t |
| Os01t0267100-01 | 0.22 | Musa_acu | 0.30 | Olea_euro | 0.30 | Olea_euro |
| Os07t0479100-01 | 0.20 | Ananas_co | 0.22 | Dioscorea_ | 0.30 | Arabidopsi |

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| Os03t0162000-01 | 0.19 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Populus_tr |

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| Os01t0816100-01 | 0.24 | Ananas_co | 0.24 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os09t0439000-00 | 0.25 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Populus_tr |
| Os08t0258200-01 | 0.23 | Ananas_co | 0.29 | Dioscorea_ | 0.30 | Solanum_tı |

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| Os02t0702000-01 | 0.20 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os10t0388200-01 | 0.16 | Musa_acur | 0.22 | Dioscorea_ | 0.30 | Citrus_cler |
| Os09t0375900-01 | 0.30 | Ipomoea_t | 0.30 | Ipomoea_t | 0.30 | Ipomoea_t |
| Os02t0194000-01 | 0.21 | Musa_acur | 0.26 | Dioscorea_ | 0.30 | Citrus_cler |
| Os04t0679200-01 | 0.16 | Ananas_co | 0.23 | Dioscorea_ | 0.30 | Prunus_pei |
| Os04t0472300-01 | 0.15 | Ananas_co | 0.26 | Dioscorea_ | 0.30 | Pistacia_ve |
| Zm00001eb322630_P00 | 0.22 | Ananas_co | 0.25 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os03t0115000-01 | 0.17 | Ananas_co | 0.30 | Malus_dom | 0.30 | Malus_dom |
| Zm00001eb384760_P00 | 0.18 | Ananas_co | 0.30 | Citrus_cler | 0.30 | Citrus_cler |

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| Os06t0683400-02 | 0.21 | Ananas_co | 0.30 | Rosa_chine | 0.30 | Rosa_chine |
| Os08t0450700-01 | 0.25 | Ananas_co | 0.30 | Corchorus_ | 0.30 | Corchorus_ |

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| Os03t0324200-01 | 0.16 | Ananas_co | 0.24 | Dioscorea_ | 0.30 | Citrus_cler |
| Os01t0698200-00 | 0.24 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Rosa_chine |
| Zm00001eb329390_P00 | 0.23 | Ananas_co | 0.30 | Cannabis_s | 0.30 | Cannabis_s |
| Os01t0247900-01Zm00 | 0.23 | Musa_acur | 0.28 | Dioscorea_ | 0.30 | Daucus_ca |
| Os06t0731100-00 | 0.17 | Musa_acur | 0.30 | Gossypium | 0.30 | Gossypium |
| Os02t0733800-01 | 0.28 | Ananas_co | 0.30 | Citrus_cler | 0.30 | Citrus_cler |
| Os04t0492900-03 | 0.25 | Ananas_co | 0.30 | Prunus_du | 0.30 | Prunus_du |
| Os03t0282800-01 | 0.21 | Ananas_co | 0.29 | Dioscorea_ | 0.30 | Theobroma |
| Os01t0874800-03 | 0.25 | Ananas_co | 0.30 | Actinidia_c | 0.30 | Actinidia_c |
| Os05t0389400-01 | 0.23 | Ananas_co | 0.26 | Dioscorea_ | 0.30 | Gossypium |
| Os01t0164400-01 | 0.25 | Dioscorea_ | 0.25 | Dioscorea_ | 0.30 | Populus_tr |
| Os04t0675800-00 | 0.25 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os08t0274700-01 | 0.16 | Ananas_co | 0.22 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os01t0810200-01 | 0.29 | Ananas_co | 0.30 | Citrullus_la | 0.30 | Citrullus_la |
| Os02t0787600-01 | 0.24 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Actinidia_c |
| Os06t0560400-01 | 0.29 | Musa_acur | 0.30 | Vigna_angu | 0.30 | Vigna_angu |
| Os07t0477500-01 | 0.18 | Ananas_co | 0.24 | Dioscorea_ | 0.30 | Manihot_es |
| Os03t0278400-01 | 0.23 | Ananas_co | 0.30 | Rosa_chine | 0.30 | Rosa_chine |
| Os09t0482720-00 | 0.21 | Ananas_co | 0.30 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os06t0234600-01 | 0.11 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Prunus_per |

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| Os02t0809800-01 | 0.21 | Ananas_co | 0.30 | Manihot_es | 0.30 | Manihot_es |
| Os09t0515300-01 | 0.25 | Ananas_co | 0.30 | Actinidia_c | 0.30 | Actinidia_c |
| Os03t0852500-01 | 0.21 | Ananas_co | 0.26 | Dioscorea_ | 0.30 | Populus_tr |
| Os09t0478400-01 | 0.29 | Musa_acur | 0.30 | Cynara_car | 0.30 | Cynara_car |
| Os02t0689200-03 | 0.20 | Ananas_co | 0.24 | Dioscorea_ | 0.30 | Pistacia_ve |
| Os05t0565100-01 | 0.11 | Ananas_co | 0.25 | Dioscorea_ | 0.30 | Amborella_ |
| Os05t0495900-01 | 0.20 | Ananas_co | 0.20 | Dioscorea_ | 0.30 | Theobroma |
| Os02t0781600-00 | 0.15 | Ananas_co | 0.30 | Prunus_avi | 0.30 | Prunus_avi |
| Os02t0819700-01 | 0.29 | Musa_acur | 0.30 | Corchorus_ | 0.30 | Corchorus_ |
| Os02t0796700-01 | 0.24 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os02t0807000-01 | 0.24 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Actinidia_c |
| Os02t0595800-01 | 0.13 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os03t0363800-01 | 0.30 | Amborella_ | 0.30 | Amborella_ | 0.30 | Amborella_ |
| Os04t0508800-01 | 0.26 | Dioscorea_ | 0.26 | Dioscorea_ | 0.30 | Prunus_avi |
| Os01t0256800-01 | 0.24 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Pistacia_ve |

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| Os05t0267800-01 | 0.25 | Ananas_co | 0.30 | Theobrom | 0.30 | Theobrom |
| Os06t0637500-02 | 0.30 | Amborella_ | 0.30 | Amborella_ | 0.30 | Amborella_ |
| Os01t0833800-01 | 0.25 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os03t0746800-01 | 0.25 | Ananas_co | 0.29 | Dioscorea_ | 0.30 | Prunus_du |
| Os05t0459700-01 | 0.22 | Musa_acu | 0.30 | Manihot_e | 0.30 | Manihot_e |
| Os09t0508300-01 | 0.20 | Ananas_co | 0.30 | Citrullus_l | 0.30 | Citrullus_l |
| Os09t0538700-01 | 0.27 | Ananas_co | 0.30 | Manihot_e | 0.30 | Manihot_e |
| Zm00001eb299200_P00 | 0.17 | Ananas_co | 0.30 | Prunus_pe | 0.30 | Prunus_pe |
| Os02t0290300-01 | 0.28 | Musa_acu | 0.30 | Malus_do | 0.30 | Malus_do |
| Os04t0194500-01 | 0.27 | Ananas_co | 0.29 | Dioscorea_ | 0.30 | Populus_tr |
| Os05t0498900-01 | 0.23 | Musa_acu | 0.30 | Populus_tr | 0.30 | Populus_tr |
| Zm00001eb133070_P00 | 0.18 | Ananas_co | 0.30 | Medicago_ | 0.30 | Medicago_ |
| Os04t0644000-01 | 0.23 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Amborella_ |
| Os01t0228400-01 | 0.18 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Malus_do |
| Os06t0586150-00Zm00 | 0.15 | Ananas_co | 0.24 | Dioscorea_ | 0.30 | Manihot_e |
| Os03t0131400-01 | 0.20 | Ananas_co | 0.30 | Theobrom | 0.30 | Theobrom |
| Os11t0534300-01 | 0.29 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os01t0153800-00 | 0.24 | Ananas_co | 0.30 | Malus_do | 0.30 | Malus_do |
| Os03t0727100-01 | 0.23 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os03t0735100-01 | 0.26 | Dioscorea_ | 0.26 | Dioscorea_ | 0.30 | Manihot_e |
| Os04t0661100-00 | 0.30 | Vigna_radi | 0.30 | Vigna_radi | 0.30 | Vigna_radi |
| Os05t0491200-01 | 0.28 | Musa_acu | 0.30 | Gossypiu | 0.30 | Gossypiu |
| Os03t0665800-01 | 0.26 | Ananas_co | 0.29 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os04t0543200-01 | 0.23 | Ananas_co | 0.30 | Amborella_ | 0.30 | Amborella_ |
| Os03t0219400-01 | 0.27 | Ananas_co | 0.30 | Ipomoea_t | 0.30 | Ipomoea_t |
| Os09t0401600-00 | 0.27 | Musa_acu | 0.30 | Nicotiana_ | 0.30 | Nicotiana_ |
| Os03t0778400-00 | 0.20 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os02t0645100-01 | 0.19 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |

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| Os06t0226500-01 | 0.12 | Musa_acur | 0.16 | Dioscorea_ | 0.30 | Helianthus |
| Os02t0141100-00 | 0.27 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os07t0584200-01 | 0.25 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Nicotiana_ |
| Os01t0119000-01 | 0.13 | Ananas_co | 0.28 | Dioscorea_ | 0.30 | Pistacia_ve |
| Os06t0235300-01 | 0.26 | Dioscorea_ | 0.26 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os02t0602400-01 | 0.23 | Ananas_co | 0.25 | Dioscorea_ | 0.30 | Amborella_ |
| Os03t0194600-01Zm00 | 0.18 | Musa_acur | 0.25 | Dioscorea_ | 0.30 | Nymphaea |
| Os10t0400900-01 | 0.22 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Actinidia_ |
| Os11t0657000-01 | 0.25 | Musa_acur | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os07t0517300-01 | 0.19 | Ananas_co | 0.30 | Actinidia_ | 0.30 | Actinidia_ |
| Os01t0889800-01 | 0.26 | Ananas_co | 0.30 | Actinidia_ | 0.30 | Actinidia_ |
| Os04t0563100-00 | 0.28 | Musa_acur | 0.30 | Populus_tr | 0.30 | Populus_tr |
| Os05t0212200-01 | 0.20 | Ananas_co | 0.30 | Theobrom | 0.30 | Theobrom |
| Os01t0748150-01 | 0.29 | Ananas_co | 0.30 | Rosa_chine | 0.30 | Rosa_chine |
| Os07t0657200-01 | 0.19 | Ananas_co | 0.30 | Theobrom | 0.30 | Theobrom |
| Os02t0756100-01 | 0.30 | Nymphaea | 0.30 | Nymphaea | 0.30 | Nymphaea |
| Os03t0748000-01 | 0.28 | Musa_acur | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os06t0232100-02 | 0.29 | Ananas_co | 0.30 | Vitis_vinife | 0.30 | Vitis_vinife |
| Os08t0298700-01 | 0.21 | Musa_acur | 0.30 | Amborella_ | 0.30 | Amborella_ |
| Os08t0175000-00 | 0.21 | Ananas_co | 0.27 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os05t0301600-01 | 0.18 | Ananas_co | 0.25 | Dioscorea_ | 0.30 | Vitis_vinife |
| Os03t0726300-01 | 0.21 | Ananas_co | 0.30 | Amborella_ | 0.30 | Amborella_ |

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| Os09t0431600-00 | 0.20 Ananas_co | 0.26 Dioscorea_ | 0.30 Vitis_vinife |
| Os02t0791300-01 | 0.30 Populus_tr | 0.30 Populus_tr | 0.30 Populus_tr |
| Os03t0855600-01 | 0.21 Dioscorea_ | 0.21 Dioscorea_ | 0.30 Brassica_r |
| Os11t0169600-01 | 0.29 Citrullus_l | 0.29 Citrullus_l | 0.29 Citrullus_l |
| Os07t0509600-01 | 0.22 Ananas_co | 0.28 Dioscorea_ | 0.29 Prunus_du |
| Os04t0320200-01 | 0.19 Ananas_co | 0.27 Dioscorea_ | 0.29 Pistacia_ve |
| Os04t0475600-01 | 0.22 Ananas_co | 0.28 Dioscorea_ | 0.29 Vitis_vinife |
| Os11t0657200-01 | 0.29 Musa_acu | 0.29 Cucumis_s | 0.29 Cucumis_s |
| Os01t0825800-01 | 0.14 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Zm00001eb236170_P00 | 0.29 Amborella_ | 0.29 Amborella_ | 0.29 Amborella_ |
| Os07t0659900-01 | 0.17 Musa_acu | 0.29 Beta_vulga | 0.29 Beta_vulga |
| Os10t0580700-01 | 0.29 Prunus_avi | 0.29 Prunus_avi | 0.29 Prunus_avi |
| Os03t0719400-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.29 Theobrom |
| Os06t0652200-01 | 0.23 Ananas_co | 0.29 Actinidia_ | 0.29 Actinidia_ |
| Os11t0533400-01 | 0.17 Ananas_co | 0.29 Populus_tr | 0.29 Populus_tr |
| Os04t0661300-01Zm00 | 0.19 Musa_acu | 0.25 Dioscorea_ | 0.29 Citrus_cle |
| Os03t0759000-01 | 0.24 Ananas_co | 0.27 Dioscorea_ | 0.29 Theobrom |
| Os09t0554300-01 | 0.15 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os12t0631200-01 | 0.26 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os01t0783600-01 | 0.27 Dioscorea_ | 0.27 Dioscorea_ | 0.29 Prunus_pe |
| Os03t0135400-01 | 0.14 Ananas_co | 0.24 Dioscorea_ | 0.29 Actinidia_ |
| Os07t0687300-01 | 0.24 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os12t0153500-01Zm00 | 0.24 Musa_acu | 0.29 Prunus_du | 0.29 Prunus_du |
| Os07t0299600-01 | 0.12 Musa_acu | 0.15 Dioscorea_ | 0.29 Ipomoea_t |
| Os03t0857600-01 | 0.26 Ananas_co | 0.29 Nymphaea | 0.29 Nymphaea |
| Os05t0402300-02 | 0.22 Musa_acu | 0.24 Dioscorea_ | 0.29 Cannabis_ |
| Os05t0390500-01 | 0.28 Musa_acu | 0.29 Gossypiu | 0.29 Gossypiu |
| Os05t0220600-01 | 0.27 Ananas_co | 0.29 Theobrom | 0.29 Theobrom |
| Os05t0102800-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.29 Vitis_vinife |
| Os08t0335600-01 | 0.15 Ananas_co | 0.29 Cannabis_ | 0.29 Cannabis_ |
| Os06t0545900-01 | 0.25 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os07t0299800-01 | 0.17 Ananas_co | 0.29 Actinidia_ | 0.29 Actinidia_ |
| Os12t0604700-01 | 0.17 Ananas_co | 0.23 Dioscorea_ | 0.29 Vitis_vinife |
| Os02t0114033-00 | 0.26 Ananas_co | 0.28 Dioscorea_ | 0.29 Vitis_vinife |
| Os06t0141700-01 | 0.29 Manihot_e | 0.29 Manihot_e | 0.29 Manihot_e |
| Os04t0223500-01 | 0.17 Ananas_co | 0.29 Prunus_pe | 0.29 Prunus_pe |
| Os09t0460300-01Zm00 | 0.26 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os02t0245000-01 | 0.27 Ananas_co | 0.29 Dioscorea_ | 0.29 Populus_tr |
| Os10t0572000-00 | 0.21 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os07t0111600-01 | 0.26 Ananas_co | 0.29 Beta_vulga | 0.29 Beta_vulga |

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| Os01t0968400-00 | 0.19 Ananas_co | 0.29 Prunus_pe | 0.29 Prunus_pe |
| Os08t0108200-01 | 0.23 Ananas_co | 0.29 Theobrom | 0.29 Theobrom |
| Zm00001eb342390_P00 | 0.26 Musa_acur | 0.29 Citrus_cler | 0.29 Citrus_cler |
| Os03t0168000-01 | 0.26 Ananas_co | 0.29 Nicotiana_ | 0.29 Nicotiana_ |
| Os03t0152900-01 | 0.13 Ananas_co | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os06t0715000-01 | 0.18 Ananas_co | 0.29 Cucumis_s | 0.29 Cucumis_s |
| Os03t0625800-01 | 0.28 Musa_acur | 0.29 Dioscorea_ | 0.29 Amborella_ |

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| Os12t0428600-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.29 Theobrom |
| Os04t0672700-01 | 0.16 Ananas_co | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os12t0271600-01 | 0.14 Ananas_co | 0.23 Dioscorea_ | 0.29 Citrus_cler |
| Os11t0583200-01 | 0.19 Ananas_co | 0.21 Dioscorea_ | 0.29 Manihot_e |

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| Os02t0117500-01 | 0.22 Ananas_co | 0.29 Theobrom | 0.29 Theobrom |

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| Os09t0560900-01 | 0.23 Ananas_co | 0.29 Prunus_du | 0.29 Prunus_du |
| Os06t0109200-01 | 0.22 Musa_acur | 0.29 Glycine_m | 0.29 Glycine_m |

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| Os03t0205000-01 | 0.25 Musa_acur | 0.27 Dioscorea_ | 0.29 Gossypiu |
| Os11t0130300-01 | 0.13 Ananas_co | 0.29 Ipomoea_t | 0.29 Ipomoea_t |
| Os07t0599201-00 | 0.26 Ananas_co | 0.29 Manihot_e | 0.29 Manihot_e |
| Os06t0717900-02 | 0.22 Musa_acur | 0.28 Dioscorea_ | 0.29 Coffea_car |
| Os04t0414700-01 | 0.29 Arabis_alp | 0.29 Arabis_alp | 0.29 Arabis_alp |
| Os12t0109300-01 | 0.23 Ananas_co | 0.26 Dioscorea_ | 0.29 Vitis_vinife |
| Os11t0124500-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.29 Vitis_vinife |
| Os04t0620600-01 | 0.29 Ananas_co | 0.29 Beta_vulga | 0.29 Beta_vulga |
| Os03t0140500-01 | 0.12 Ananas_co | 0.29 Citrus_cler | 0.29 Citrus_cler |
| Os01t0276400-01 | 0.20 Ananas_co | 0.29 Prunus_avi | 0.29 Prunus_avi |
| Os02t0816700-01 | 0.26 Musa_acur | 0.29 Citrus_cler | 0.29 Citrus_cler |

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| Os01t0744000-01 | 0.21 Ananas_co | 0.29 Theobrom | 0.29 Theobrom |
| Os03t0307700-00 | 0.26 Ananas_co | 0.29 Ipomoea_t | 0.29 Ipomoea_t |
| Os02t0655100-01 | 0.21 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os06t0216700-01 | 0.17 Musa_acur | 0.25 Dioscorea_ | 0.29 Amborella |
| Os06t0642900-01 | 0.27 Musa_acur | 0.29 Amborella | 0.29 Amborella |
| Os05t0371600-01 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.29 Citrus_cler |
| Os06t0645800-01 | 0.17 Ananas_co | 0.29 Coffea_car | 0.29 Coffea_car |
| Zm00001eb079320_P00 | 0.23 Musa_acur | 0.28 Dioscorea_ | 0.29 Nicotiana_ |
| Os10t0102400-01 | 0.21 Ananas_co | 0.29 Theobrom | 0.29 Theobrom |
| Os09t0466100-01 | 0.19 Ananas_co | 0.24 Dioscorea_ | 0.29 Vitis_vinife |
| Os02t0751900-01 | 0.17 Ananas_co | 0.29 Nymphaea | 0.29 Nymphaea |
| Os04t0221300-01 | 0.20 Ananas_co | 0.24 Dioscorea_ | 0.29 Actinidia_ |
| Os02t0589400-01 | 0.22 Dioscorea_ | 0.22 Dioscorea_ | 0.29 Olea_euro |
| Os03t0186800-01 | 0.15 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os06t0531400-01 | 0.26 Musa_acur | 0.29 Daucus_ca | 0.29 Daucus_ca |
| Os02t0827900-02 | 0.20 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os04t0545000-01 | 0.28 Dioscorea_ | 0.28 Dioscorea_ | 0.29 Theobrom |
| Os06t0710800-01 | 0.19 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os05t0533100-01 | 0.18 Ananas_co | 0.27 Dioscorea_ | 0.29 Nymphaea |
| Os02t0286200-01 | 0.26 Ananas_co | 0.27 Dioscorea_ | 0.29 Pistacia_ve |
| Os09t0359900-01 | 0.20 Ananas_co | 0.29 Cannabis_ | 0.29 Cannabis_ |
| Os06t0552400-02 | 0.24 Ananas_co | 0.29 Rosa_chine | 0.29 Rosa_chine |
| Os07t0671200-00 | 0.12 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os04t0486800-01 | 0.29 Actinidia_ | 0.29 Actinidia_ | 0.29 Actinidia_ |
| Os07t0563700-01 | 0.21 Ananas_co | 0.28 Dioscorea_ | 0.29 Actinidia_ |
| Os01t0583100-01 | 0.20 Ananas_co | 0.29 Manihot_e | 0.29 Manihot_e |
| Os09t0326100-01 | 0.28 Ananas_co | 0.29 Brassica_n | 0.29 Brassica_n |
| Os01t0803200-01 | 0.29 Cucumis_ | 0.29 Cucumis_ | 0.29 Cucumis_ |
| Os02t0812400-01 | 0.22 Ananas_co | 0.29 Citrus_cler | 0.29 Citrus_cler |
| Os05t0533900-01 | 0.29 Cucumis_ | 0.29 Cucumis_ | 0.29 Cucumis_ |
| Os12t0182800-01 | 0.16 Musa_acur | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os02t0125500-00 | 0.29 Prunus_avi | 0.29 Prunus_avi | 0.29 Prunus_avi |
| Os07t0575900-01 | 0.21 Musa_acur | 0.29 Vitis_vinife | 0.29 Vitis_vinife |

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| Os10t0561200-01 | 0.13 Ananas_co | 0.24 Dioscorea_ | 0.29 Amborella_ |
| Os11t0183700-01 | 0.13 Ananas_co | 0.16 Dioscorea_ | 0.29 Manihot_e |
| Os05t0123300-00 | 0.17 Ananas_co | 0.20 Dioscorea_ | 0.29 Malus_dor |
| Os05t0592100-01 | 0.27 Musa_acur | 0.29 Amborella_ | 0.29 Amborella_ |
| Os02t0559300-02 | 0.16 Ananas_co | 0.29 Amborella_ | 0.29 Amborella_ |
| Os03t0168700-00 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.29 Theobrom |
| Os04t0444800-01 | 0.20 Ananas_co | 0.29 Dioscorea_ | 0.29 Vitis_vinife |
| Os04t0682000-01 | 0.20 Ananas_co | 0.27 Dioscorea_ | 0.29 Amborella_ |
| Os04t0436100-01 | 0.24 Ananas_co | 0.24 Dioscorea_ | 0.29 Actinidia_c |
| Os03t0701200-01Zm00 | 0.22 Musa_acur | 0.27 Dioscorea_ | 0.29 Populus_tr |
| Os02t0170500-01 | 0.25 Ananas_co | 0.29 Nymphaea | 0.29 Nymphaea |
| Os10t0563400-01 | 0.20 Ananas_co | 0.29 Ipomoea_t | 0.29 Ipomoea_t |
| Os03t0294800-01 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.29 Citrus_cler |
| Os04t0414100-01 | 0.25 Ananas_co | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os03t0147400-01 | 0.23 Ananas_co | 0.27 Dioscorea_ | 0.29 Ipomoea_t |
| Os04t0455600-02 | 0.20 Musa_acur | 0.29 Amborella_ | 0.29 Amborella_ |
| Os07t0486500-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.29 Actinidia_c |
| Os04t0306400-01Zm00 | 0.21 Ananas_co | 0.29 Manihot_e | 0.29 Manihot_e |

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| Os01t0784700-00 | 0.17 | Ananas_co | 0.22 | Dioscorea_ | 0.29 | Pistacia_ve |
| Os07t0626300-01 | 0.24 | Ananas_co | 0.28 | Dioscorea_ | 0.29 | Vitis_vinife |

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| Os03t0761100-01 | 0.25 | Dioscorea_ | 0.25 | Dioscorea_ | 0.29 | Pistacia_ve |
| Zm00001eb176980_P00 | 0.20 | Ananas_co | 0.29 | Actinidia_ | 0.29 | Actinidia_ |
| Os02t0791800-01 | 0.19 | Ananas_co | 0.27 | Dioscorea_ | 0.29 | Glycine_m |
| Os03t0797700-01 | 0.17 | Ananas_co | 0.29 | Vitis_vinife | 0.29 | Vitis_vinife |
| Os03t0201600-02 | 0.22 | Ananas_co | 0.29 | Amborella | 0.29 | Amborella |
| Os04t0379300-01 | 0.19 | Ananas_co | 0.29 | Manihot_e | 0.29 | Manihot_e |
| Os06t0660800-01 | 0.22 | Ananas_co | 0.26 | Dioscorea_ | 0.29 | Populus_tr |
| Os06t0193000-01 | 0.18 | Ananas_co | 0.29 | Lupinus_a | 0.29 | Lupinus_a |
| Os05t0363600-01 | 0.22 | Ananas_co | 0.29 | Actinidia_ | 0.29 | Actinidia_ |
| Os01t0504500-02 | 0.25 | Musa_acu | 0.29 | Rosa_chin | 0.29 | Rosa_chin |

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| Os03t0597200-01 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.29 | Citrus_cle |
| Os07t0287400-01 | 0.28 | Dioscorea_ | 0.28 | Dioscorea_ | 0.29 | Rosa_chin |
| Os01t0783400-01 | 0.29 | Vitis_vinife | 0.29 | Vitis_vinife | 0.29 | Vitis_vinife |

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| Os04t0206700-01Zm00 | 0.29 | Nicotiana_ | 0.29 | Nicotiana_ | 0.29 | Nicotiana_ |

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| Os05t0449500-01 | 0.23 | Ananas_co | 0.27 | Dioscorea_ | 0.29 | Amborella_ |
| Os04t0453266-00 | 0.21 | Ananas_co | 0.25 | Dioscorea_ | 0.29 | Amborella_ |

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| Os10t0575600-01 | 0.28 Musa_acur | 0.29 Vitis_vinife | 0.29 Vitis_vinife |

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| Os02t0153400-01 | 0.29 Theobrom | 0.29 Theobrom | 0.29 Theobrom |
| Os03t0801700-01 | 0.12 Ananas_co | 0.22 Dioscorea_ | 0.29 Amborella_ |
| Os06t0268800-01 | 0.21 Ananas_co | 0.29 Amborella_ | 0.29 Amborella_ |
| Os03t0210800-01 | 0.19 Ananas_co | 0.29 Prunus_pe | 0.29 Prunus_pe |
| Os01t0794400-01 | 0.21 Ananas_co | 0.29 Dioscorea_ | 0.29 Amborella_ |
| Os11t0482400-01 | 0.19 Ananas_co | 0.23 Dioscorea_ | 0.29 Rosa_chine |

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| Os04t0541500-01 | 0.20 Ananas_co | 0.22 Dioscorea_ | 0.29 Beta_vulga |
| Os08t0495500-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.29 Glycine_m |
| Zm00001eb330680_P00 | 0.20 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os04t0636100-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.29 Corchorus_ |
| Os03t0632800-01Zm00 | 0.25 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os05t0583950-00 | 0.22 Ananas_co | 0.29 Prunus_avi | 0.29 Prunus_avi |
| Os07t0670000-01 | 0.16 Ananas_co | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os02t0706900-00 | 0.24 Musa_acur | 0.26 Dioscorea_ | 0.29 Nicotiana_ |
| Os12t0557800-01 | 0.20 Ananas_co | 0.24 Dioscorea_ | 0.29 Vitis_vinife |
| Zm00001eb002810_P00 | 0.18 Ananas_co | 0.29 Ipomoea_t | 0.29 Ipomoea_t |

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| Os10t0548900-01 | 0.25 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |

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| Os06t0602500-01Zm00 | 0.22 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os01t0873100-01 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.29 Populus_tr |
| Os08t0565700-01 | 0.24 Ananas_co | 0.27 Dioscorea_ | 0.29 Cucumis_m |
| Os09t0490200-01 | 0.17 Musa_acur | 0.29 Amborella_ | 0.29 Amborella_ |
| Os08t0476400-01 | 0.19 Musa_acur | 0.28 Dioscorea_ | 0.29 Nicotiana_ |
| Os05t0200280-01 | 0.17 Ananas_co | 0.29 Coffea_car | 0.29 Coffea_car |

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| Os01t0921200-01 | 0.16 Ananas_co | 0.25 Dioscorea_ | 0.29 Manihot_e |
| Zm00001eb306350_P00 | 0.27 Ananas_co | 0.29 Manihot_e | 0.29 Manihot_e |
| Os08t0260000-01 | 0.14 Ananas_co | 0.29 Corchorus_ | 0.29 Corchorus_ |

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| Os01t0169800-01 | 0.21 | Musa_acur | 0.29 | Vitis_vinife | 0.29 | Vitis_vinife |
| Os07t0189700-01 | 0.29 | Nymphaea_ | 0.29 | Nymphaea | 0.29 | Nymphaea |
| Os03t0164700-01 | 0.22 | Ananas_co | 0.29 | Citrus_cler | 0.29 | Citrus_cler |
| Os03t0194900-01 | 0.24 | Musa_acur | 0.25 | Dioscorea_ | 0.29 | Nymphaea |

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| Os10t0579600-01 | 0.07 | Ananas_co | 0.27 | Dioscorea_ | 0.29 | Populus_tr |
| Os01t0958400-02 | 0.21 | Ananas_co | 0.25 | Dioscorea_ | 0.29 | Ipomoea_t |

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| Os04t0692200-01 | 0.29 | Rosa_chine | 0.29 | Rosa_chine | 0.29 | Rosa_chine |
| Os01t0505500-00 | 0.18 | Musa_acur | 0.29 | Prunus_avi | 0.29 | Prunus_avi |
| Os04t0436800-01 | 0.18 | Ananas_co | 0.24 | Dioscorea_ | 0.29 | Vitis_vinife |
| Os11t0118600-01 | 0.23 | Musa_acur | 0.25 | Dioscorea_ | 0.29 | Populus_tr |
| Os04t0677800-02 | 0.20 | Ananas_co | 0.29 | Prunus_avi | 0.29 | Prunus_avi |
| Os06t0253100-01 | 0.20 | Musa_acur | 0.29 | Populus_tr | 0.29 | Populus_tr |

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| Os02t0180700-01 | 0.26 Musa_acur | 0.29 Populus_tr | 0.29 Populus_tr |
| Zm00001eb147010_P00 | 0.15 Ananas_co | 0.29 Citrus_cler | 0.29 Citrus_cler |
| Os11t0125500-01 | 0.18 Ananas_co | 0.22 Dioscorea_ | 0.29 Pistacia_ve |
| Os02t0670900-02 | 0.25 Ananas_co | 0.27 Dioscorea_ | 0.29 Nicotiana_ |
| Os01t0746200-01 | 0.28 Musa_acur | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os07t0588100-00 | 0.16 Ananas_co | 0.20 Dioscorea_ | 0.29 Vitis_vinife |
| Os01t0841700-01 | 0.07 Ananas_co | 0.22 Dioscorea_ | 0.29 Vitis_vinife |
| Os01t0973300-01 | 0.20 Ananas_co | 0.28 Dioscorea_ | 0.29 Theobroma |
| Os12t0456200-01 | 0.20 Ananas_co | 0.23 Dioscorea_ | 0.29 Camelina_ |
| Os10t0506000-00 | 0.18 Ananas_co | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os01t0869000-01Zm00 | 0.19 Ananas_co | 0.28 Dioscorea_ | 0.29 Vitis_vinife |
| Os09t0423500-01Zm00 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.29 Vitis_vinife |
| Os04t0270200-01 | 0.18 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os05t0560100-01 | 0.27 Ananas_co | 0.29 Coffea_car | 0.29 Coffea_car |
| Os01t0623200-01 | 0.22 Ananas_co | 0.28 Dioscorea_ | 0.29 Vitis_vinife |
| Os01t0307500-01 | 0.25 Ananas_co | 0.29 Populus_tr | 0.29 Populus_tr |
| Os12t0291000-00 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.29 Actinidia_c |
| Os04t0395900-01 | 0.22 Ananas_co | 0.27 Dioscorea_ | 0.29 Manihot_e |

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| Os04t0182200-01 | 0.08 Ananas_co | 0.29 Nicotiana_ | 0.29 Nicotiana_ |
| Os02t0631100-01 | 0.13 Ananas_co | 0.29 Malus_dom | 0.29 Malus_dom |
| Os03t0275500-01 | 0.21 Ananas_co | 0.29 Corchorus_ | 0.29 Corchorus_ |
| Os05t0537400-00 | 0.27 Ananas_co | 0.29 Populus_tr | 0.29 Populus_tr |
| Os01t0133900-00 | 0.20 Ananas_co | 0.24 Dioscorea_ | 0.29 Vitis_vinife |
| Os09t0293500-01 | 0.22 Dioscorea_ | 0.22 Dioscorea_ | 0.29 Theobroma |
| Os02t0793200-01 | 0.17 Ananas_co | 0.29 Corchorus_ | 0.29 Corchorus_ |
| Os09t0440200-01 | 0.21 Ananas_co | 0.29 Populus_tr | 0.29 Populus_tr |
| Os04t0209300-01 | 0.26 Ananas_co | 0.26 Dioscorea_ | 0.29 Nicotiana_ |
| Os01t0850200-00 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.29 Amborella_ |
| Os09t0442600-01 | 0.22 Ananas_co | 0.26 Dioscorea_ | 0.29 Malus_dom |
| Os09t0463600-02 | 0.17 Ananas_co | 0.29 Cynara_car | 0.29 Cynara_car |
| Os02t0227200-01 | 0.15 Musa_acum | 0.22 Dioscorea_ | 0.29 Beta_vulga |
| Os09t0555400-01 | 0.22 Ananas_co | 0.29 Prunus_per | 0.29 Prunus_per |

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| Os06t0275000-01 | 0.29 Prunus_du | 0.29 Prunus_du | 0.29 Prunus_du |
| Os02t0729400-01 | 0.23 Musa_acu | 0.26 Dioscorea_ | 0.29 Malus_do |
| Os02t0741500-01 | 0.16 Ananas_co | 0.29 Vitis_vinife | 0.29 Vitis_vinife |
| Os08t0520200-01 | 0.29 Pistacia_ve | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Zm00001eb428400_P00 | 0.18 Ananas_co | 0.25 Dioscorea_ | 0.29 Vitis_vinife |
| Os07t0203300-01 | 0.26 Musa_acu | 0.29 Pistacia_ve | 0.29 Pistacia_ve |
| Os02t0119300-01 | 0.28 Musa_acu | 0.29 Citrus_cle | 0.29 Citrus_cle |
| Os05t0126800-01 | 0.28 Manihot_e | 0.28 Manihot_e | 0.28 Manihot_e |
| Os01t0926800-01 | 0.20 Ananas_co | 0.28 Dioscorea_ | 0.28 Amborella_ |
| Os03t0758700-01 | 0.21 Musa_acu | 0.28 Theobrom | 0.28 Theobrom |
| Os01t0805100-01 | 0.26 Musa_acu | 0.28 Brassica_n | 0.28 Brassica_n |
| Os01t0186200-01 | 0.18 Ananas_co | 0.28 Rosa_chin | 0.28 Rosa_chin |
| Os08t0446200-01 | 0.22 Dioscorea_ | 0.22 Dioscorea_ | 0.28 Actinidia_ |

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| Os03t0259100-01 | 0.21 Musa_acur | 0.28 Actinidia_c | 0.28 Actinidia_c |
| Os08t0109000-01 | 0.19 Ananas_co | 0.23 Dioscorea_ | 0.28 Vitis_vinife |
| Os06t0681700-01 | 0.18 Ananas_co | 0.23 Dioscorea_ | 0.28 Coffea_car |
| Os11t0297800-01 | 0.22 Ananas_co | 0.28 Actinidia_c | 0.28 Actinidia_c |
| Os10t0493800-01 | 0.22 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |
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| Os02t0110400-01 | 0.10 Ananas_co | 0.17 Dioscorea_ | 0.28 Vitis_vinife |
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| Os01t0612600-01 | 0.20 Ananas_co | 0.25 Dioscorea_ | 0.28 Brassica_n |
| Os06t0506100-01 | 0.15 Ananas_co | 0.25 Dioscorea_ | 0.28 Pistacia_ve |
| Os09t0524300-00 | 0.21 Ananas_co | 0.27 Dioscorea_ | 0.28 Vitis_vinife |
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| Os01t0251000-01 | 0.16 Musa_acur | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
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| Os03t0299200-01 | 0.26 Ananas_co | 0.28 Malus_dom | 0.28 Malus_dom |
| Os09t0267400-01 | 0.07 Ananas_co | 0.28 Nymphaea | 0.28 Nymphaea |
| Os08t0546400-01 | 0.19 Ananas_co | 0.27 Dioscorea_ | 0.28 Pistacia_ve |
| Os06t0192900-01 | 0.25 Musa_acur | 0.28 Citrus_cler | 0.28 Citrus_cler |
| Os02t0103900-01 | 0.12 Ananas_co | 0.27 Dioscorea_ | 0.28 Pistacia_ve |
| Os03t0205800-00 | 0.15 Ananas_co | 0.25 Dioscorea_ | 0.28 Cannabis_ |
| Os05t0132000-00 | 0.20 Ananas_co | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
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| Os12t0507300-00 | 0.23 Ananas_co | 0.28 Ipomoea_t | 0.28 Ipomoea_t |
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| Os03t0296800-01 | 0.23 Ananas_co | 0.24 Dioscorea_ | 0.28 Theobroma |
| Os02t0751100-01 | 0.20 Ananas_co | 0.28 Actinidia_c | 0.28 Actinidia_c |
| Os06t0127200-01 | 0.22 Musa_acur | 0.28 Phaseolus_ | 0.28 Phaseolus_ |
| Os06t0334400-01 | 0.22 Ananas_co | 0.28 Pistacia_ve | 0.28 Pistacia_ve |
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| Os07t0545800-01 | 0.15 Ananas_co | 0.21 Dioscorea_ | 0.28 Vitis_vinife |
| Os08t0416400-01 | 0.20 Ananas_co | 0.28 Amborella_ | 0.28 Amborella_ |
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| Os03t0201500-01 | 0.28 Citrus_cler | 0.28 Citrus_cler | 0.28 Citrus_cler |

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| Os07t0694400-01 | 0.25 | Musa_acur | 0.28 | Manihot_e | 0.28 | Manihot_e |
| Os03t0159200-01 | 0.23 | Musa_acur | 0.26 | Dioscorea_ | 0.28 | Nymphaea |
| Os05t0148700-01 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os12t0583900-02 | 0.20 | Ananas_co | 0.28 | Coffea_car | 0.28 | Coffea_car |
| Os09t0315800-01 | 0.17 | Ananas_co | 0.28 | Solanum_l | 0.28 | Solanum_l |
| Os01t0819100-01 | 0.19 | Ananas_co | 0.23 | Dioscorea_ | 0.28 | Pistacia_ve |
| Os07t0559400-00 | 0.25 | Musa_acur | 0.28 | Dioscorea_ | 0.28 | Malus_don |

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| Os07t0633600-01 | 0.22 | Musa_acur | 0.28 | Medicago_ | 0.28 | Medicago_ |
| Os10t0195000-01 | 0.21 | Ananas_co | 0.25 | Dioscorea_ | 0.28 | Manihot_e |
| Os02t0652800-01 | 0.22 | Ananas_co | 0.28 | Glycine_m | 0.28 | Glycine_m |

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| Os03t0289800-01 | 0.20 | Ananas_co | 0.28 | Manihot_e | 0.28 | Manihot_e |
| Os12t0563000-00 | 0.19 | Ananas_co | 0.28 | Populus_tr | 0.28 | Populus_tr |
| Os07t0294600-01 | 0.20 | Ananas_co | 0.28 | Actinidia_c | 0.28 | Actinidia_c |
| Os04t0514500-01 | 0.13 | Ananas_co | 0.20 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os05t0188700-01 | 0.23 | Ananas_co | 0.28 | Dioscorea_ | 0.28 | Glycine_m |
| Zm00001eb179460_P00 | 0.17 | Ananas_co | 0.25 | Dioscorea_ | 0.28 | Nicotiana_ |

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| Os05t0595300-02 | 0.14 | Ananas_co | 0.28 | Manihot_e | 0.28 | Manihot_e |
| Os08t0365500-00 | 0.08 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os06t0143400-01 | 0.15 | Ananas_co | 0.21 | Dioscorea_ | 0.28 | Ipomoea_t |
| Os03t0169300-01 | 0.12 | Ananas_co | 0.21 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os03t0849600-01 | 0.17 | Ananas_co | 0.28 | Actinidia_c | 0.28 | Actinidia_c |
| Os01t0756200-01 | 0.24 | Ananas_co | 0.28 | Dioscorea_ | 0.28 | Nymphaea |
| Os03t0377500-01Zm00 | 0.17 | Ananas_co | 0.23 | Dioscorea_ | 0.28 | Citrus_cler |
| Os09t0455400-01 | 0.25 | Ananas_co | 0.28 | Populus_tr | 0.28 | Populus_tr |

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| Os08t0546100-00 | 0.23 | Musa_acur | 0.28 | Glycine_m | 0.28 | Glycine_m |
| Os01t0796700-01 | 0.18 | Ananas_co | 0.20 | Dioscorea_ | 0.28 | Vitis_vinife |

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| Os06t0208800-01 | 0.24 Musa_acur | 0.25 Dioscorea_ | 0.28 Citrus_cler |
| Os03t0634400-01Zm00 | 0.28 Malus_dom | 0.28 Malus_dom | 0.28 Malus_dom |
| Os08t0503200-01 | 0.19 Ananas_co | 0.26 Dioscorea_ | 0.28 Prunus_pe |
| Os03t0643700-01 | 0.24 Ananas_co | 0.28 Actinidia_c | 0.28 Actinidia_c |
| Os02t0661100-01 | 0.28 Ananas_co | 0.28 Cannabis_ | 0.28 Cannabis_ |
| Os07t0105700-01Zm00 | 0.14 Ananas_co | 0.21 Dioscorea_ | 0.28 Vitis_vinife |
| Os02t0740300-01 | 0.16 Ananas_co | 0.28 Dioscorea_ | 0.28 Actinidia_c |
| Os03t0428800-01 | 0.24 Ananas_co | 0.28 Citrus_cler | 0.28 Citrus_cler |
| Os04t0596300-01 | 0.22 Ananas_co | 0.28 Cannabis_ | 0.28 Cannabis_ |
| Os05t0440800-01 | 0.28 Populus_tr | 0.28 Populus_tr | 0.28 Populus_tr |
| Os01t0757800-01 | 0.24 Musa_acur | 0.28 Prunus_du | 0.28 Prunus_du |
| Os03t0795300-01 | 0.18 Ananas_co | 0.28 Coffea_car | 0.28 Coffea_car |
| Os02t0629800-01 | 0.28 Glycine_ma | 0.28 Glycine_ma | 0.28 Glycine_ma |
| Os07t0192900-00 | 0.27 Ananas_co | 0.28 Cannabis_ | 0.28 Cannabis_ |
| Os08t0566000-01 | 0.24 Ananas_co | 0.28 Amborella_ | 0.28 Amborella_ |
| Os02t0822300-00 | 0.15 Ananas_co | 0.27 Dioscorea_ | 0.28 Cannabis_ |
| Os06t0244000-01 | 0.17 Musa_acur | 0.24 Dioscorea_ | 0.28 Pistacia_ve |
| Os12t0560600-01 | 0.21 Ananas_co | 0.28 Citrullus_la | 0.28 Citrullus_la |
| Os03t0712400-02 | 0.27 Dioscorea_ | 0.27 Dioscorea_ | 0.28 Nicotiana_ |
| Os02t0773400-01 | 0.14 Ananas_co | 0.28 Nicotiana_ | 0.28 Nicotiana_ |

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| Os03t0602600-01 | 0.22 Ananas_co | 0.28 Malus_dom | 0.28 Malus_dom |
| Os04t0401700-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.28 Prunus_per |
| Os01t0223000-01Zm00 | 0.23 Ananas_co | 0.28 Amborella_ | 0.28 Amborella_ |
| Os06t0677300-01 | 0.24 Musa_acur | 0.25 Dioscorea_ | 0.28 Vitis_vinife |
| Os01t0214200-01 | 0.25 Musa_acur | 0.28 Ipomoea_t | 0.28 Ipomoea_t |
| Os03t0767600-01 | 0.21 Ananas_co | 0.28 Dioscorea_ | 0.28 Actinidia_c |
| Os01t0550300-02 | 0.24 Ananas_co | 0.28 Citrus_cler | 0.28 Citrus_cler |
| Os06t0539400-01 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.28 Brassica_ol |
| Os03t0160400-01 | 0.17 Ananas_co | 0.22 Dioscorea_ | 0.28 Theobroma |
| Os11t0638900-01 | 0.21 Ananas_co | 0.25 Dioscorea_ | 0.28 Vitis_vinife |
| Os08t0542700-01 | 0.14 Ananas_co | 0.21 Dioscorea_ | 0.28 Phaseolus_ |
| Os01t0321800-01 | 0.22 Musa_acur | 0.24 Dioscorea_ | 0.28 Theobroma |
| Os11t0311300-02 | 0.20 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |
| Os05t0396900-01 | 0.25 Ananas_co | 0.28 Cannabis_ | 0.28 Cannabis_ |
| Os05t0232500-01 | 0.20 Musa_acur | 0.28 Glycine_ma | 0.28 Glycine_ma |
| Os04t0447500-01 | 0.21 Musa_acur | 0.28 Citrus_cler | 0.28 Citrus_cler |
| Os06t0211600-01 | 0.28 Ananas_co | 0.28 Rosa_chine | 0.28 Rosa_chine |
| Os09t0500300-01 | 0.17 Ananas_co | 0.27 Dioscorea_ | 0.28 Amborella_ |
| Os09t0279500-01 | 0.28 Theobroma | 0.28 Theobroma | 0.28 Theobroma |
| Os02t0511500-01 | 0.25 Ananas_co | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
| Os04t0407800-01 | 0.17 Ananas_co | 0.21 Dioscorea_ | 0.28 Glycine_ma |
| Os09t0571500-01 | 0.25 Musa_acur | 0.28 Dioscorea_ | 0.28 Gossypium |
| Os01t0721900-01 | 0.17 Musa_acur | 0.25 Dioscorea_ | 0.28 Nymphaea |
| Os07t0618600-01 | 0.14 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |
| Os10t0555200-01 | 0.27 Musa_acur | 0.28 Pistacia_ve | 0.28 Pistacia_ve |
| Os10t0446200-01 | 0.11 Ananas_co | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
| Os06t0679700-00Zm00 | 0.18 Ananas_co | 0.25 Dioscorea_ | 0.28 Vitis_vinife |
| Os10t0178200-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.28 Nymphaea |
| Os01t0152000-01 | 0.14 Ananas_co | 0.26 Dioscorea_ | 0.28 Populus_tr |
| Os10t0170300-01 | 0.18 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |

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| Os12t0197500-01 | 0.18 | Ananas_co | 0.28 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os02t0168400-01 | 0.11 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os12t0230200-02 | 0.17 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Manihot_e |
| Os01t0248300-00 | 0.22 | Musa_acun | 0.28 | Theobroma | 0.28 | Theobroma |
| Os02t0534400-01 | 0.24 | Musa_acun | 0.28 | Actinidia_c | 0.28 | Actinidia_c |
| Os02t0651000-01 | 0.17 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os03t0378000-01 | 0.19 | Ananas_co | 0.28 | Pistacia_ve | 0.28 | Pistacia_ve |
| Os01t0680900-01 | 0.13 | Ananas_co | 0.28 | Amborella_ | 0.28 | Amborella_ |
| Os01t0272800-01 | 0.16 | Ananas_co | 0.22 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os02t0184500-01 | 0.23 | Musa_acun | 0.28 | Prunus_pe | 0.28 | Prunus_pe |
| Os07t0211900-01 | 0.26 | Ananas_co | 0.28 | Citrus_cler | 0.28 | Citrus_cler |
| Os01t0111100-01 | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os11t0672400-00 | 0.19 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Actinidia_c |
| Os10t0437000-02 | 0.24 | Ananas_co | 0.28 | Gossypiun | 0.28 | Gossypiun |
| Os11t0256100-00 | 0.21 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os04t0641700-00 | 0.28 | Prunus_pe | 0.28 | Prunus_pe | 0.28 | Prunus_pe |
| Os05t0179000-01 | 0.23 | Ananas_co | 0.24 | Dioscorea_ | 0.28 | Corchorus_ |
| Os06t0621900-01 | 0.27 | Musa_acun | 0.28 | Cucumis_n | 0.28 | Cucumis_n |
| Os02t0551900-01 | 0.24 | Musa_acun | 0.28 | Beta_vulga | 0.28 | Beta_vulga |

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| Os01t0853400-01 | 0.22 | Ananas_co | 0.26 | Dioscorea_ | 0.28 | Amborella_ |
| Os06t0555500-01 | 0.22 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Manihot_e |
| Os04t0459800-01 | 0.27 | Ananas_co | 0.28 | Gossypium | 0.28 | Gossypium |
| Os07t0178600-01 | 0.20 | Ananas_co | 0.26 | Dioscorea_ | 0.28 | Corchorus_ |
| Os03t0165600-01Zm00 | 0.26 | Ananas_co | 0.28 | Coffea_car | 0.28 | Coffea_car |
| Os06t0215200-01 | 0.27 | Ananas_co | 0.28 | Gossypium | 0.28 | Gossypium |

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| Os04t0356600-01Zm00 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.28 | Phaseolus_ |
| Os07t0657500-02 | 0.16 | Ananas_co | 0.28 | Cynara_car | 0.28 | Cynara_car |
| Os06t0224200-01 | 0.20 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Gossypium |

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| Os03t0296600-01 | 0.17 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Coffea_car |
| Os10t0165300-01Zm00 | 0.23 | Ananas_co | 0.28 | Solanum_t | 0.28 | Solanum_t |
| Zm00001eb064440_P00 | 0.25 | Dioscorea_ | 0.25 | Dioscorea_ | 0.28 | Prunus_pe |
| Os03t0396200-01Zm00 | 0.19 | Ananas_co | 0.28 | Gossypium | 0.28 | Gossypium |

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| Os03t0215900-01 | 0.25 | Ananas_co | 0.28 | Prunus_pe | 0.28 | Prunus_pe |
| Os09t0445100-00 | 0.18 | Ananas_co | 0.26 | Dioscorea_ | 0.28 | Amborella_ |
| Os03t0769900-01 | 0.23 | Musa_acur | 0.25 | Dioscorea_ | 0.28 | Actinidia_c |
| Os11t0265200-00 | 0.18 | Ananas_co | 0.25 | Dioscorea_ | 0.28 | Citrus_cler |
| Os01t0832200-01 | 0.22 | Musa_acur | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os01t0128400-01 | 0.24 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os07t0564200-01 | 0.19 | Dioscorea_ | 0.19 | Dioscorea_ | 0.28 | Glycine_ma |
| Os10t0396400-01 | 0.19 | Dioscorea_ | 0.19 | Dioscorea_ | 0.28 | Prunus_avi |
| Os07t0661900-01 | 0.20 | Ananas_co | 0.28 | Actinidia_c | 0.28 | Actinidia_c |
| Os01t0521500-01 | 0.21 | Ananas_co | 0.28 | Helianthus | 0.28 | Helianthus |
| Os03t0240500-01 | 0.22 | Musa_acur | 0.26 | Dioscorea_ | 0.28 | Vitis_vinife |

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| Os08t0112300-01Zm00 | 0.28 | Prunus_avi | 0.28 | Prunus_avi | 0.28 | Prunus_avi |
| Os07t0568000-01 | 0.19 | Dioscorea_ | 0.19 | Dioscorea_ | 0.28 | Populus_tr |
| Os04t0458300-01Zm00 | 0.13 | Ananas_co | 0.28 | Amborella_ | 0.28 | Amborella_ |
| Os06t0507400-01 | 0.19 | Ananas_co | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os02t0597700-00 | 0.21 | Musa_acur | 0.25 | Dioscorea_ | 0.28 | Actinidia_c |
| Os04t0573900-01 | 0.19 | Ananas_co | 0.22 | Dioscorea_ | 0.28 | Theobrom |
| Zm00001eb143980_P00 | 0.19 | Ananas_co | 0.27 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os05t0292200-01 | 0.14 | Musa_acur | 0.25 | Dioscorea_ | 0.28 | Manihot_e |
| Os09t0480400-01 | 0.23 | Ananas_co | 0.28 | Dioscorea_ | 0.28 | Nymphaea |
| Os06t0132500-01 | 0.16 | Ananas_co | 0.28 | Nicotiana_ | 0.28 | Nicotiana_ |
| Os01t0883100-01 | 0.22 | Musa_acur | 0.28 | Manihot_e | 0.28 | Manihot_e |
| Os08t0158900-01 | 0.28 | Actinidia_c | 0.28 | Actinidia_c | 0.28 | Actinidia_c |
| Os07t0164500-01 | 0.18 | Ananas_co | 0.24 | Dioscorea_ | 0.28 | Vitis_vinife |
| Os01t0267400-01 | 0.21 | Musa_acur | 0.28 | Nicotiana_ | 0.28 | Nicotiana_ |
| Os05t0113000-01 | 0.12 | Ananas_co | 0.20 | Dioscorea_ | 0.28 | Manihot_e |
| Os11t0242200-00 | 0.18 | Ananas_co | 0.22 | Dioscorea_ | 0.28 | Manihot_e |
| Os01t0731100-01 | 0.22 | Ananas_co | 0.28 | Populus_tr | 0.28 | Populus_tr |
| Os02t0305700-01 | 0.23 | Ananas_co | 0.24 | Dioscorea_ | 0.28 | Citrus_cler |
| Os03t0159900-01 | 0.24 | Ananas_co | 0.28 | Corchorus_ | 0.28 | Corchorus_ |
| Os02t0791700-00 | 0.18 | Ananas_co | 0.28 | Pistacia_ve | 0.28 | Pistacia_ve |
| Os04t0435500-01 | 0.17 | Musa_acur | 0.28 | Vitis_vinife | 0.28 | Vitis_vinife |
| Os03t0618300-01 | 0.18 | Ananas_co | 0.28 | Citrus_cler | 0.28 | Citrus_cler |

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| Os04t0460600-02 | 0.28 Phaseolus_ | 0.28 Phaseolus_ | 0.28 Phaseolus_ |
| Os01t0851400-01 | 0.26 Ananas_co | 0.26 Dioscorea_ | 0.28 Corchorus_ |
| Os04t0107200-01 | 0.23 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |
| Os12t0560500-01 | 0.22 Ananas_co | 0.28 Malus_don | 0.28 Malus_don |
| Os05t0583500-01 | 0.17 Ananas_co | 0.22 Dioscorea_ | 0.28 Theobroma |
| Os01t0717700-01 | 0.19 Ananas_co | 0.28 Citrus_cler | 0.28 Citrus_cler |
| Os04t0503700-01 | 0.14 Ananas_co | 0.28 Vitis_vinife | 0.28 Vitis_vinife |

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| Os05t0169300-01 | 0.21 Musa_acur | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
| Os12t0596101-00 | 0.28 Populus_tr | 0.28 Populus_tr | 0.28 Populus_tr |

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| Os03t0408600-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.28 Populus_tr |
| Os04t0534200-01 | 0.23 Musa_acur | 0.25 Dioscorea_ | 0.28 Actinidia_c |
| Os02t0636300-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.28 Actinidia_c |
| Os09t0555300-00 | 0.21 Ananas_co | 0.28 Actinidia_c | 0.28 Actinidia_c |

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| Os08t0511200-00 | 0.26 | Ananas_co | 0.28 | Populus_tr | 0.28 | Populus_tr |

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| Os08t0498100-01 | 0.26 | Ananas_co | 0.28 | Trifolium_p | 0.28 | Trifolium_p |
| Os07t0145400-01 | 0.16 | Ananas_co | 0.28 | Rosa_chine | 0.28 | Rosa_chine |
| Os11t0151500-01 | 0.27 | Dioscorea_ | 0.27 | Dioscorea_ | 0.28 | Amborella_ |
| Os02t0744100-01 | 0.28 | Citrus_cler | 0.28 | Citrus_cler | 0.28 | Citrus_cler |
| Os01t0748900-01 | 0.22 | Ananas_co | 0.28 | Cucumis_n | 0.28 | Cucumis_n |
| Os09t0420600-01 | 0.20 | Musa_acur | 0.28 | Phaseolus_ | 0.28 | Phaseolus_ |
| Os03t0664700-01 | 0.24 | Musa_acur | 0.25 | Dioscorea_ | 0.28 | Citrus_cler |
| Os09t0498500-00 | 0.23 | Ananas_co | 0.28 | Brassica_na | 0.28 | Brassica_na |

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| Os06t0556000-01 | 0.14 | Ananas_co | 0.19 | Dioscorea_ | 0.28 | Camelina_s |
| Os11t0232100-01 | 0.19 | Ananas_co | 0.26 | Dioscorea_ | 0.28 | Vitis_vinife |
| Zm00001eb177380_P00 | 0.22 | Musa_acur | 0.28 | Nymphaea | 0.28 | Nymphaea |
| Os03t0824200-01 | 0.24 | Musa_acur | 0.28 | Citrullus_la | 0.28 | Citrullus_la |
| Os05t0548200-01 | 0.26 | Ananas_co | 0.28 | Nymphaea | 0.28 | Nymphaea |
| Zm00001eb069710_P00 | 0.25 | Ananas_co | 0.28 | Theobroma | 0.28 | Theobroma |
| Os05t0564800-01 | 0.24 | Ananas_co | 0.28 | Citrus_cler | 0.28 | Citrus_cler |
| Os01t0582400-01Zm00 | 0.18 | Ananas_co | 0.28 | Pistacia_ve | 0.28 | Pistacia_ve |

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| Os01t0126600-01 | 0.10 | Ananas_co | 0.16 | Dioscorea_ | 0.28 | Actinidia_c |
| Os03t0565100-01 | 0.26 | Ananas_co | 0.28 | Cucumis_n | 0.28 | Cucumis_n |
| Os03t0291800-01 | 0.20 | Ananas_co | 0.26 | Dioscorea_ | 0.28 | Rosa_chine |
| Os09t0397400-01 | 0.25 | Musa_acur | 0.28 | Capsicum_ | 0.28 | Capsicum_ |
| Os10t0554100-01 | 0.19 | Ananas_co | 0.25 | Dioscorea_ | 0.28 | Populus_tr |
| Os03t0822300-01 | 0.12 | Ananas_co | 0.22 | Dioscorea_ | 0.28 | Malus_dom |

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| Os04t0348400-01 | 0.12 | Ananas_co | 0.20 | Dioscorea_ | 0.28 | Nymphaea |
| Os06t0559500-01 | 0.19 | Ananas_co | 0.24 | Dioscorea_ | 0.28 | Lupinus_ar |
| Zm00001eb009060_P00 | 0.20 | Ananas_co | 0.28 | Theobroma | 0.28 | Theobroma |

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| Os08t0112700-01 | 0.17 Ananas_co | 0.22 Dioscorea_ | 0.28 Solanum_l |
| Os02t0489500-01 | 0.28 Manihot_e | 0.28 Manihot_e | 0.28 Manihot_e |
| Os10t0520700-01 | 0.19 Musa_acu | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
| Os05t0587100-01 | 0.25 Ananas_co | 0.28 Vitis_vinife | 0.28 Vitis_vinife |
| Os05t0410900-02 | 0.22 Musa_acu | 0.24 Dioscorea_ | 0.28 Theobrom |
| Os05t0390100-01 | 0.19 Ananas_co | 0.28 Theobrom | 0.28 Theobrom |
| Os04t0505400-01 | 0.21 Ananas_co | 0.28 Prunus_du | 0.28 Prunus_du |
| Os03t0422800-01Zm00 | 0.21 Ananas_co | 0.28 Theobrom | 0.28 Theobrom |
| Os09t0521100-01 | 0.26 Dioscorea_ | 0.26 Dioscorea_ | 0.28 Vitis_vinife |
| Os03t0784100-00 | 0.12 Ananas_co | 0.28 Populus_tr | 0.28 Populus_tr |
| Os07t0200000-01 | 0.14 Ananas_co | 0.20 Dioscorea_ | 0.28 Actinidia_ |
| Os04t0615500-01 | 0.15 Ananas_co | 0.28 Helianthus | 0.28 Helianthus |
| Os02t0793000-01 | 0.21 Musa_acu | 0.27 Manihot_e | 0.27 Manihot_e |
| Os01t0550200-00 | 0.18 Musa_acu | 0.24 Dioscorea_ | 0.27 Phaseolus_ |
| Os07t0231400-01 | 0.10 Ananas_co | 0.18 Dioscorea_ | 0.27 Amborella_ |
| Os01t0777200-01 | 0.07 Ananas_co | 0.21 Dioscorea_ | 0.27 Vitis_vinife |
| Os06t0695500-01 | 0.08 Ananas_co | 0.27 Glycine_m | 0.27 Glycine_m |
| Os12t0529400-01 | 0.26 Musa_acu | 0.26 Dioscorea_ | 0.27 Corchorus |
| Os02t0713700-01 | 0.27 Malus_do | 0.27 Malus_do | 0.27 Malus_do |
| Os04t0619900-00 | 0.20 Musa_acu | 0.27 Corchorus | 0.27 Corchorus |
| Zm00001eb232660_P00 | 0.25 Musa_acu | 0.27 Prunus_du | 0.27 Prunus_du |
| Zm00001eb020970_P00 | 0.27 Nicotiana_ | 0.27 Nicotiana_ | 0.27 Nicotiana_ |
| Os02t0642700-01 | 0.27 Prunus_du | 0.27 Prunus_du | 0.27 Prunus_du |
| Os02t0662200-01 | 0.23 Ananas_co | 0.26 Dioscorea_ | 0.27 Prunus_avi |
| Os03t0766900-01 | 0.24 Musa_acu | 0.27 Helianthus | 0.27 Helianthus |
| Os08t0191900-01 | 0.15 Ananas_co | 0.27 Ipomoea_t | 0.27 Ipomoea_t |
| Os01t0871600-01 | 0.19 Ananas_co | 0.26 Dioscorea_ | 0.27 Ipomoea_t |
| Os02t0562300-01 | 0.24 Ananas_co | 0.26 Dioscorea_ | 0.27 Manihot_e |
| Os07t0222800-01Zm00 | 0.27 Cannabis_ | 0.27 Cannabis_ | 0.27 Cannabis_ |
| Os07t0596900-00 | 0.23 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os09t0437400-00 | 0.20 Ananas_co | 0.27 Dioscorea_ | 0.27 Nicotiana_ |

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| Os01t0767900-01 | 0.20 Musa_acu | 0.27 Pistacia_ve | 0.27 Pistacia_ve |

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| Os07t0108900-02 | 0.15 Ananas_co | 0.27 Dioscorea_ | 0.27 Gossypiu |
| Os07t0603900-01 | 0.12 Musa_acu | 0.14 Dioscorea_ | 0.27 Manihot_e |
| Os01t0949800-01 | 0.20 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os08t0379300-01 | 0.18 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os10t0210500-01 | 0.13 Musa_acu | 0.21 Dioscorea_ | 0.27 Vitis_vinife |

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| Os11t0123500-01 | 0.27 Nicotiana_ | 0.27 Nicotiana_ | 0.27 Nicotiana_ |
| Os09t0482660-01 | 0.15 Ananas_co | 0.24 Dioscorea_ | 0.27 Amborella |
| Os01t0925300-01 | 0.21 Ananas_co | 0.27 Prunus_du | 0.27 Prunus_du |
| Os12t0175500-01 | 0.24 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os05t0367100-01 | 0.21 Ananas_co | 0.27 Olea_euro | 0.27 Olea_euro |
| Os11t0248200-01 | 0.11 Ananas_co | 0.16 Dioscorea_ | 0.27 Actinidia_c |
| Os02t0252600-01Zm00 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.27 Medicago_ |
| Os12t0633600-01 | 0.19 Musa_acu | 0.27 Amborella | 0.27 Amborella |
| Os06t0281400-01 | 0.18 Ananas_co | 0.27 Pistacia_ve | 0.27 Pistacia_ve |

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| Os08t0441600-01 | 0.18 Musa_acu | 0.26 Dioscorea_ | 0.27 Cannabis_ |
| Os12t0489300-01 | 0.15 Ananas_co | 0.25 Dioscorea_ | 0.27 Manihot_e |

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| Os07t0170300-01 | 0.25 Musa_acu | 0.27 Prunus_pe | 0.27 Prunus_pe |

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| Os10t0431000-03 | 0.16 Ananas_co | 0.24 Dioscorea_ | 0.27 Actinidia_c |
| Os04t0657900-01 | 0.27 Theobrom | 0.27 Theobrom | 0.27 Theobrom |
| Os10t0529400-01Zm00 | 0.22 Ananas_co | 0.27 Nymphaea | 0.27 Nymphaea |
| Os01t0342800-01 | 0.24 Ananas_co | 0.27 Dioscorea_ | 0.27 Helianthus |

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| Os03t0656900-01 | 0.15 Ananas_co | 0.20 Dioscorea_ | 0.27 Corchorus |

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| Os11t0125900-00 | 0.27 Musa_acum | 0.27 Lupinus_an | 0.27 Lupinus_an |
| Os12t0211400-00 | 0.19 Ananas_co | 0.23 Dioscorea_ | 0.27 Glycine_ma |
| Os03t0857500-01 | 0.18 Ananas_co | 0.27 Helianthus | 0.27 Helianthus |
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| Os07t0643400-01 | 0.19 Ananas_co | 0.27 Glycine_ma | 0.27 Glycine_ma |
| Zm00001eb022650_P00 | 0.21 Ananas_co | 0.25 Dioscorea_ | 0.27 Vitis_vinife |
| Os01t0689800-01 | 0.18 Ananas_co | 0.27 Manihot_es | 0.27 Manihot_es |
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| Os06t0166900-01 | 0.26 Musa_acum | 0.27 Rosa_chine | 0.27 Rosa_chine |
| Os07t0472400-01 | 0.24 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
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| Os01t0267600-01 | 0.22 Ananas_co | 0.27 Glycine_ma | 0.27 Glycine_ma |
| Os01t0194600-02 | 0.12 Ananas_co | 0.27 Helianthus | 0.27 Helianthus |
| Os01t0974500-01 | 0.26 Musa_acum | 0.27 Gossypium | 0.27 Gossypium |
| Os07t0635800-00 | 0.20 Ananas_co | 0.20 Dioscorea_ | 0.27 Pistacia_ve |
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| Os06t0485100-01 | 0.22 Musa_acum | 0.27 Amborella_ | 0.27 Amborella_ |
| Os01t0772150-00 | 0.25 Musa_acum | 0.26 Dioscorea_ | 0.27 Vitis_vinife |
| Zm00001eb085330_P00 | 0.27 Brassica_na | 0.27 Brassica_na | 0.27 Brassica_na |
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| Os04t0581100-01Zm00 | 0.21 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
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| Os03t0820500-01 | 0.27 Prunus_du | 0.27 Prunus_du | 0.27 Prunus_du |
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| Os03t0788200-01 | 0.20 Ananas_co | 0.27 Nicotiana_a | 0.27 Nicotiana_a |
| Os12t0600100-01 | 0.13 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os09t0296400-01 | 0.21 Ananas_co | 0.26 Dioscorea_ | 0.27 Vitis_vinife |
| Zm00001eb000640_P00 | 0.23 Ananas_co | 0.27 Arabidopsi | 0.27 Arabidopsi |
| Zm00001eb176650_P00 | 0.27 Vitis_vinife | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os03t0746600-01 | 0.15 Ananas_co | 0.26 Dioscorea_ | 0.27 Citrus_clem |

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| Os05t0540000-01 | 0.16 | Ananas_co | 0.27 | Nymphaea | 0.27 | Nymphaea |
| Os01t0206300-00 | 0.22 | Ananas_co | 0.27 | Dioscorea_ | 0.27 | Gossypium |
| Os03t0244200-02 | 0.19 | Ananas_co | 0.27 | Vigna_ang | 0.27 | Vigna_ang |
| Os01t0176900-00 | 0.23 | Musa_acu | 0.27 | Olea_euro | 0.27 | Olea_euro |
| Os03t0780200-01 | 0.18 | Ananas_co | 0.27 | Arabidopsi | 0.27 | Arabidopsi |
| Os11t0235750-00 | 0.08 | Ananas_co | 0.21 | Dioscorea_ | 0.27 | Nymphaea |
| Os06t0498900-01 | 0.21 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Nicotiana_ |
| Zm00001eb104120_P00 | 0.22 | Ananas_co | 0.27 | Gossypium | 0.27 | Gossypium |
| Os06t0715500-01 | 0.16 | Ananas_co | 0.27 | Theobrom | 0.27 | Theobrom |

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| Os01t0880200-01 | 0.15 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os10t0489301-00 | 0.27 | Capsicum_ | 0.27 | Capsicum_ | 0.27 | Capsicum_ |

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| Os11t0186900-01 | 0.18 | Ananas_co | 0.26 | Dioscorea_ | 0.27 | Citrullus_l |
| Os03t0142900-01 | 0.19 | Ananas_co | 0.26 | Dioscorea_ | 0.27 | Vitis_vinife |
| Os08t0459300-01 | 0.17 | Ananas_co | 0.22 | Dioscorea_ | 0.27 | Corchorus_ |

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| Os02t0724000-01 | 0.21 | Dioscorea_ | 0.21 | Dioscorea_ | 0.27 | Vitis_vinife |
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| Os04t0588200-00 | 0.24 | Dioscorea_ | 0.24 | Dioscorea_ | 0.27 | Pistacia_ve |
| Os01t0914700-01 | 0.25 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os11t0552600-01Zm00 | 0.16 | Ananas_co | 0.18 | Dioscorea_ | 0.27 | Olea_euro |
| Os10t0541000-01 | 0.27 | Amborella_ | 0.27 | Amborella_ | 0.27 | Amborella_ |
| Os08t0556000-01 | 0.16 | Ananas_co | 0.24 | Dioscorea_ | 0.27 | Prunus_pe |

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| Os11t0580800-01 | 0.18 | Ananas_co | 0.27 | Amborella_ | 0.27 | Amborella_ |
| Os01t0932600-01 | 0.27 | Corchorus_ | 0.27 | Corchorus_ | 0.27 | Corchorus_ |
| Os09t0520300-00 | 0.15 | Ananas_co | 0.27 | Malus_do | 0.27 | Malus_do |
| Os03t0266700-01 | 0.12 | Ananas_co | 0.22 | Dioscorea_ | 0.27 | Cannabis_ |
| Os04t0590200-01 | 0.23 | Ananas_co | 0.27 | Dioscorea_ | 0.27 | Citrus_cle |
| Os11t0111900-01 | 0.18 | Musa_acu | 0.27 | Ipomoea_t | 0.27 | Ipomoea_t |
| Os04t0605300-01 | 0.22 | Musa_acu | 0.27 | Theobrom | 0.27 | Theobrom |
| Os08t0327200-01 | 0.25 | Ananas_co | 0.27 | Theobrom | 0.27 | Theobrom |
| Os03t0254900-02 | 0.14 | Ananas_co | 0.27 | Nicotiana_ | 0.27 | Nicotiana_ |
| Os02t0496100-01 | 0.17 | Ananas_co | 0.21 | Dioscorea_ | 0.27 | Theobrom |
| Os02t0178500-01 | 0.20 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Actinidia_c |
| Os02t0148600-01 | 0.19 | Musa_acu | 0.23 | Dioscorea_ | 0.27 | Vitis_vinife |
| Os03t0707900-01 | 0.17 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os01t0835000-01 | 0.19 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os01t0659900-01 | 0.18 | Ananas_co | 0.27 | Pistacia_ve | 0.27 | Pistacia_ve |
| Os07t0550900-01 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.27 | Populus_tr |

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| Os11t0234200-01 | 0.19 | Ananas_co | 0.24 | Dioscorea_ | 0.27 | Manihot_e |

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| Os10t0483500-01 | 0.07 | Ananas_co | 0.27 | Amborella_ | 0.27 | Amborella_ |
| Os11t0152700-01 | 0.24 | Ananas_co | 0.27 | Prunus_pe | 0.27 | Prunus_pe |
| Os05t0449900-01 | 0.16 | Ananas_co | 0.27 | Dioscorea_ | 0.27 | Nicotiana_ |
| Os05t0109600-01 | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os08t0112400-01 | 0.18 | Ananas_co | 0.27 | Dioscorea_ | 0.27 | Actinidia_c |
| Os05t0567500-01 | 0.27 | Populus_tr | 0.27 | Populus_tr | 0.27 | Populus_tr |
| Os01t0914800-01 | 0.26 | Musa_acur | 0.27 | Populus_tr | 0.27 | Populus_tr |

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| Os12t0613700-01 | 0.25 | Dioscorea_ | 0.25 | Dioscorea_ | 0.27 | Manihot_e |
| Os02t0770100-01 | 0.16 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Gossypium |
| Os08t0542900-01 | 0.20 | Musa_acur | 0.23 | Dioscorea_ | 0.27 | Theobroma |
| Os06t0236300-01 | 0.24 | Musa_acur | 0.27 | Corchorus_ | 0.27 | Corchorus_ |
| Os03t0265200-01 | 0.21 | Ananas_co | 0.27 | Prunus_pe | 0.27 | Prunus_pe |
| Os08t0161900-01 | 0.18 | Ananas_co | 0.27 | Citrus_cler | 0.27 | Citrus_cler |
| Os06t0212500-01Zm00 | 0.27 | Ananas_co | 0.27 | Cannabis_ | 0.27 | Cannabis_ |
| Os07t0408500-01 | 0.24 | Ananas_co | 0.24 | Dioscorea_ | 0.27 | Theobroma |
| Os01t0660800-01 | 0.26 | Ananas_co | 0.27 | Actinidia_c | 0.27 | Actinidia_c |
| Os07t0102100-02 | 0.25 | Dioscorea_ | 0.25 | Dioscorea_ | 0.27 | Populus_tr |
| Os06t0695400-01 | 0.18 | Ananas_co | 0.27 | Helianthus | 0.27 | Helianthus |
| Os03t0742800-01 | 0.20 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Olea_europ |
| Os03t0125700-01 | 0.12 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os09t0394600-01 | 0.24 | Dioscorea_ | 0.24 | Dioscorea_ | 0.27 | Theobroma |
| Zm00001eb382090_P00 | 0.25 | Musa_acur | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |

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| Os12t0502300-01 | 0.20 | Ananas_co | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os01t0248000-01 | 0.25 | Ananas_co | 0.27 | Helianthus | 0.27 | Helianthus |
| Os03t0336600-02 | 0.18 | Ananas_co | 0.27 | Coffea_car | 0.27 | Coffea_car |
| Os11t0705900-01 | 0.27 | Gossypium | 0.27 | Gossypium | 0.27 | Gossypium |
| Os03t0299600-01 | 0.25 | Ananas_co | 0.27 | Gossypium | 0.27 | Gossypium |
| Os06t0109500-01 | 0.17 | Ananas_co | 0.26 | Dioscorea_ | 0.27 | Malus_dom |

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| Os01t0588200-01 | 0.18 | Musa_acur | 0.25 | Dioscorea_ | 0.27 | Coffea_car |

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| Os10t0371000-01 | 0.14 | Musa_acu | 0.18 | Dioscorea_ | 0.27 | Nymphaea |
| Os10t0399700-00 | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os04t0382300-01 | 0.15 | Ananas_co | 0.27 | Rosa_chine | 0.27 | Rosa_chine |
| Os03t0289300-00 | 0.21 | Musa_acu | 0.22 | Dioscorea_ | 0.27 | Vitis_vinife |
| Os07t0573300-01 | 0.25 | Ananas_co | 0.27 | Arabidopsi | 0.27 | Arabidopsi |
| Os12t0484600-02 | 0.11 | Ananas_co | 0.26 | Dioscorea_ | 0.27 | Cynara_ca |
| Os06t0131300-01 | 0.22 | Dioscorea_ | 0.22 | Dioscorea_ | 0.27 | Nicotiana_ |
| Os05t0270000-01 | 0.19 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Citrullus_l |
| Os03t0854500-01 | 0.15 | Ananas_co | 0.23 | Dioscorea_ | 0.27 | Amborella |
| Os08t0479400-01 | 0.17 | Ananas_co | 0.27 | Beta_vulga | 0.27 | Beta_vulga |
| Os10t0521100-01 | 0.26 | Musa_acu | 0.27 | Citrus_cle | 0.27 | Citrus_cle |
| Os08t0192400-00 | 0.25 | Ananas_co | 0.27 | Lupinus_a | 0.27 | Lupinus_a |
| Os02t0193600-01 | 0.22 | Dioscorea_ | 0.22 | Dioscorea_ | 0.27 | Amborella |
| Os10t0479900-01 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.27 | Vitis_vinife |
| Zm00001eb079750_P00 | 0.17 | Ananas_co | 0.27 | Trifolium_ | 0.27 | Trifolium_ |
| Os08t0410500-01 | 0.25 | Musa_acu | 0.27 | Theobrom | 0.27 | Theobrom |
| Os01t0280000-01 | 0.14 | Ananas_co | 0.27 | Nymphaea | 0.27 | Nymphaea |
| Os02t0709800-01 | 0.18 | Ananas_co | 0.27 | Dioscorea_ | 0.27 | Prunus_du |
| Os07t0154400-01 | 0.20 | Ananas_co | 0.27 | Amborella | 0.27 | Amborella |
| Os07t0626800-01 | 0.16 | Musa_acu | 0.19 | Dioscorea_ | 0.27 | Malus_do |
| Zm00001eb202260_P00 | 0.26 | Musa_acu | 0.27 | Actinidia_c | 0.27 | Actinidia_c |
| Os03t0314700-01 | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife | 0.27 | Vitis_vinife |
| Os03t0364500-01 | 0.17 | Ananas_co | 0.27 | Actinidia_c | 0.27 | Actinidia_c |
| Os06t0320100-01 | 0.23 | Musa_acu | 0.27 | Medicago_ | 0.27 | Medicago_ |
| Os09t0453500-01 | 0.19 | Ananas_co | 0.27 | Actinidia_c | 0.27 | Actinidia_c |
| Os09t0542500-00 | 0.13 | Ananas_co | 0.24 | Dioscorea_ | 0.27 | Theobrom |
| Os09t0443500-01 | 0.14 | Ananas_co | 0.18 | Dioscorea_ | 0.27 | Cucumis_s |
| Os02t0106700-01 | 0.27 | Actinidia_c | 0.27 | Actinidia_c | 0.27 | Actinidia_c |
| Os03t0267500-01 | 0.20 | Musa_acu | 0.27 | Prunus_du | 0.27 | Prunus_du |
| Os08t0435800-01 | 0.22 | Dioscorea_ | 0.22 | Dioscorea_ | 0.27 | Medicago_ |

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| Os04t0447100-02 | 0.15 Ananas_co | 0.22 Dioscorea_ | 0.27 Manihot_e |
| Os10t0502900-01 | 0.03 Ananas_co | 0.11 Dioscorea_ | 0.27 Actinidia_c |
| Os12t0171200-01 | 0.14 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os05t0302600-01 | 0.24 Ananas_co | 0.27 Cannabis_ | 0.27 Cannabis_ |
| Os08t0412200-01 | 0.23 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |

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| Os06t0608800-01 | 0.19 Ananas_co | 0.27 Theobrom | 0.27 Theobrom |
| Os02t0119100-01Zm00 | 0.16 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os06t0724500-01 | 0.27 Rosa_chin | 0.27 Rosa_chin | 0.27 Rosa_chin |
| Os07t0170800-01 | 0.20 Ananas_co | 0.25 Dioscorea_ | 0.27 Vitis_vinife |

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| Os02t0301100-01 | 0.15 Ananas_co | 0.23 Dioscorea_ | 0.27 Nymphaea |
| Os12t0638900-01 | 0.20 Musa_acur | 0.23 Dioscorea_ | 0.27 Corchorus_ |

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| Os08t0408200-01 | 0.26 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os10t0504200-01 | 0.15 Musa_acur | 0.24 Dioscorea_ | 0.27 Amborella_ |

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| Os10t0528200-01Zm00 | 0.22 Ananas_co | 0.27 Beta_vulga | 0.27 Beta_vulga |
| Os01t0853700-01 | 0.18 Ananas_co | 0.24 Dioscorea_ | 0.27 Trifolium_ |
| Os02t0677600-01 | 0.26 Musa_acur | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os10t0393800-01Zm00 | 0.26 Musa_acur | 0.27 Coffea_car | 0.27 Coffea_car |
| Os07t0508300-01 | 0.13 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os02t0806700-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.27 Vitis_vinife |
| Zm00001eb381520_P00 | 0.18 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |

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| Os03t0148700-01 | 0.22 Ananas_co | 0.27 Pistacia_ve | 0.27 Pistacia_ve |
| Os01t0894000-01 | 0.15 Ananas_co | 0.27 Manihot_e | 0.27 Manihot_e |
| Os09t0542100-01 | 0.22 Ananas_co | 0.25 Dioscorea_ | 0.27 Amborella_ |
| Os04t0411800-01 | 0.21 Musa_acu | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os01t0704700-01 | 0.23 Musa_acu | 0.27 Actinidia_c | 0.27 Actinidia_c |

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| Os05t0305900-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.27 Populus_tr |
| Os03t0332533-01 | 0.24 Musa_acu | 0.27 Malus_do | 0.27 Malus_do |
| Os08t0369200-01Zm00 | 0.15 Ananas_co | 0.23 Dioscorea_ | 0.27 Actinidia_c |
| Os06t0266400-00Zm00 | 0.27 Prunus_du | 0.27 Prunus_du | 0.27 Prunus_du |

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| Os01t0814300-01 | 0.15 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os04t0461100-01 | 0.27 Citrullus_l | 0.27 Citrullus_l | 0.27 Citrullus_l |
| Os02t0518600-01 | 0.23 Ananas_co | 0.23 Dioscorea_ | 0.27 Pistacia_ve |
| Os03t0710000-01 | 0.22 Ananas_co | 0.27 Malus_do | 0.27 Malus_do |
| Os06t0590600-01 | 0.20 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os01t0261500-02 | 0.21 Ananas_co | 0.27 Theobrom | 0.27 Theobrom |

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| Os02t0325600-01 | 0.27 Manihot_e | 0.27 Manihot_e | 0.27 Manihot_e |
| Os03t0228200-01 | 0.22 Dioscorea_ | 0.22 Dioscorea_ | 0.27 Actinidia_c |
| Os03t0840200-01 | 0.22 Musa_acu | 0.26 Dioscorea_ | 0.27 Vitis_vinife |
| Os06t0622800-01 | 0.20 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |

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| Os06t0162800-01 | 0.26 Musa_acu | 0.27 Amborella_ | 0.27 Amborella_ |
| Os01t0217000-01 | 0.21 Musa_acu | 0.25 Dioscorea_ | 0.27 Citrus_cle |

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| Os04t0631800-00Zm00 | 0.27 Amborella_ | 0.27 Amborella_ | 0.27 Amborella_ |
| Os03t0740700-01 | 0.18 Ananas_co | 0.23 Dioscorea_ | 0.27 Populus_tr |

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| Os06t0144000-01 | 0.27 Populus_tr | 0.27 Populus_tr | 0.27 Populus_tr |
| Os03t0284000-00 | 0.21 Ananas_co | 0.27 Capsicum_ | 0.27 Capsicum_ |
| Os07t0409700-01 | 0.14 Ananas_co | 0.27 Corchorus_ | 0.27 Corchorus_ |
| Os06t0125300-01 | 0.18 Musa_acu | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os02t0193800-01 | 0.19 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |

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| Os06t0663800-01 | 0.23 Ananas_co | 0.27 Pistacia_ve | 0.27 Pistacia_ve |
| Os09t0559800-01 | 0.16 Ananas_co | 0.27 Vitis_vinife | 0.27 Vitis_vinife |
| Os03t0297700-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.27 Ipomoea_t |
| Os07t0596600-02 | 0.19 Ananas_co | 0.23 Dioscorea_ | 0.27 Pistacia_ve |
| Os03t0704400-01 | 0.13 Musa_acur | 0.20 Dioscorea_ | 0.27 Vitis_vinife |
| Os08t0177800-00 | 0.16 Ananas_co | 0.26 Dioscorea_ | 0.27 Phaseolus_ |

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| Os05t0494200-02 | 0.27 Cucumis_n | 0.27 Cucumis_n | 0.27 Cucumis_n |
| Os08t0299200-01 | 0.19 Ananas_co | 0.27 Actinidia_c | 0.27 Actinidia_c |
| Os02t0756800-01 | 0.13 Ananas_co | 0.27 Coffea_car | 0.27 Coffea_car |
| Os09t0525300-01 | 0.15 Ananas_co | 0.25 Dioscorea_ | 0.27 Vitis_vinife |
| Os05t0125400-00 | 0.23 Ananas_co | 0.27 Theobrom | 0.27 Theobrom |

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| Os06t0603600-01 | 0.19 Ananas_co | 0.25 Dioscorea_ | 0.27 Nymphaea |
| Os01t0804900-01 | 0.18 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os12t0231000-01 | 0.19 Ananas_co | 0.21 Dioscorea_ | 0.26 Amborella_ |
| Os07t0436600-00 | 0.17 Ananas_co | 0.25 Dioscorea_ | 0.26 Vitis_vinife |
| Os06t0636700-01Zm00 | 0.11 Ananas_co | 0.23 Dioscorea_ | 0.26 Rosa_chine |
| Os02t0647900-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.26 Capsicum_ |

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| Os03t0610650-01 | 0.18 Ananas_co | 0.24 Dioscorea_ | 0.26 Malus_don |

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| Os02t0738400-01 | 0.17 Ananas_co | 0.19 Dioscorea_ | 0.26 Vitis_vinife |

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| Os07t0630900-02 | 0.17 Ananas_co | 0.26 Nymphaea | 0.26 Nymphaea |
| Zm00001eb166820_P00 | 0.18 Musa_acur | 0.25 Dioscorea_ | 0.26 Actinidia_c |
| Os03t0306200-01 | 0.21 Ananas_co | 0.24 Dioscorea_ | 0.26 Vitis_vinife |
| Os01t0532800-01 | 0.23 Ananas_co | 0.26 Dioscorea_ | 0.26 Vitis_vinife |
| Os10t0422566-01 | 0.13 Ananas_co | 0.21 Dioscorea_ | 0.26 Theobrom |
| Os04t0542900-01 | 0.26 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os12t0565300-01 | 0.17 Ananas_co | 0.26 Amborella_ | 0.26 Amborella_ |

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| Os07t0681300-00 | 0.18 | Musa_acu | 0.26 | Theobrom | 0.26 | Theobrom |
| Os06t0226600-01 | 0.16 | Musa_acu | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os01t0281200-01 | 0.24 | Dioscorea_ | 0.24 | Dioscorea_ | 0.26 | Citrus_cle |
| Os03t0410700-01 | 0.17 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os03t0176900-01 | 0.21 | Musa_acu | 0.26 | Rosa_chine | 0.26 | Rosa_chine |
| Os04t0628000-01 | 0.19 | Ananas_co | 0.22 | Dioscorea_ | 0.26 | Populus_tr |
| Os09t0393200-01 | 0.26 | Ananas_co | 0.26 | Nicotiana_ | 0.26 | Nicotiana_ |
| Os05t0157300-01 | 0.22 | Musa_acu | 0.26 | Dioscorea_ | 0.26 | Cannabis_ |
| Os03t0173900-01 | 0.09 | Dioscorea_ | 0.09 | Dioscorea_ | 0.26 | Manihot_e |
| Os01t0510600-01 | 0.15 | Ananas_co | 0.23 | Dioscorea_ | 0.26 | Manihot_e |
| Os02t0689900-01 | 0.20 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Cannabis_ |
| Zm00001eb055060_P00 | 0.19 | Ananas_co | 0.23 | Dioscorea_ | 0.26 | Prunus_avi |
| Os07t0681100-01 | 0.23 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os09t0327200-00 | 0.17 | Ananas_co | 0.26 | Nymphaea | 0.26 | Nymphaea |
| Os03t0794800-01 | 0.15 | Ananas_co | 0.26 | Prunus_pe | 0.26 | Prunus_pe |
| Os05t0389500-01 | 0.21 | Ananas_co | 0.26 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os02t0464400-01 | 0.17 | Ananas_co | 0.22 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os02t0782200-02 | 0.18 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os03t0793800-01 | 0.26 | Olea_euro | 0.26 | Olea_euro | 0.26 | Olea_euro |
| Os02t0669000-01 | 0.02 | Ananas_co | 0.12 | Dioscorea_ | 0.26 | Amborella |
| Os04t0502800-01 | 0.17 | Ananas_co | 0.20 | Dioscorea_ | 0.26 | Cannabis_ |
| Os02t0290900-00 | 0.17 | Ananas_co | 0.26 | Theobrom | 0.26 | Theobrom |
| Os12t0639100-01 | 0.12 | Ananas_co | 0.23 | Dioscorea_ | 0.26 | Nicotiana_ |
| Os03t0831400-01 | 0.26 | Amborella | 0.26 | Amborella | 0.26 | Amborella |
| Os07t0636900-01 | 0.21 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os03t0277600-01 | 0.16 | Musa_acu | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os02t0821400-01 | 0.26 | Theobrom | 0.26 | Theobrom | 0.26 | Theobrom |
| Os01t0263500-01 | 0.20 | Dioscorea_ | 0.20 | Dioscorea_ | 0.26 | Rosa_chine |
| Os03t0693000-01 | 0.15 | Ananas_co | 0.23 | Dioscorea_ | 0.26 | Manihot_e |
| Zm00001eb232190_P00 | 0.20 | Musa_acu | 0.26 | Amborella | 0.26 | Amborella |
| Os09t0132900-02 | 0.24 | Ananas_co | 0.26 | Corchorus | 0.26 | Corchorus |

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| Os02t0143300-00Zm00 | 0.19 Musa_acur | 0.20 Dioscorea_ | 0.26 Pistacia_ve |
| Os10t0572100-01 | 0.21 Ananas_co | 0.26 Theobroma | 0.26 Theobroma |
| Os08t0323600-02 | 0.21 Ananas_co | 0.24 Dioscorea_ | 0.26 Pistacia_ve |
| Os05t0521300-04 | 0.16 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os03t0635800-01 | 0.13 Ananas_co | 0.22 Dioscorea_ | 0.26 Vitis_vinife |
| Os02t0778500-01 | 0.16 Ananas_co | 0.21 Dioscorea_ | 0.26 Theobroma |
| Zm00001eb119290_P00 | 0.18 Ananas_co | 0.25 Dioscorea_ | 0.26 Actinidia_c |
| Os11t0219000-01Zm00 | 0.17 Ananas_co | 0.26 Rosa_chine | 0.26 Rosa_chine |
| Os02t0625300-00 | 0.20 Musa_acur | 0.23 Dioscorea_ | 0.26 Helianthus |
| Os01t0771100-01 | 0.21 Musa_acur | 0.26 Ipomoea_t | 0.26 Ipomoea_t |
| Os06t0663100-01Zm00 | 0.22 Ananas_co | 0.26 Populus_tr | 0.26 Populus_tr |
| Os01t0178200-00 | 0.24 Musa_acur | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os02t0272300-01 | 0.21 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os09t0543900-01 | 0.26 Nicotiana_ | 0.26 Nicotiana_ | 0.26 Nicotiana_ |
| Os09t0255000-01Zm00 | 0.22 Musa_acur | 0.26 Nymphaea | 0.26 Nymphaea |
| Os08t0104100-01 | 0.22 Ananas_co | 0.26 Glycine_ma | 0.26 Glycine_ma |
| Os06t0297800-01 | 0.17 Ananas_co | 0.21 Dioscorea_ | 0.26 Theobroma |
| Os02t0681100-01 | 0.20 Musa_acur | 0.26 Solanum_t | 0.26 Solanum_t |
| Os05t0134200-01 | 0.21 Musa_acur | 0.23 Dioscorea_ | 0.26 Theobroma |
| Os02t0185300-01Zm00 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.26 Theobroma |
| Os10t0489100-01 | 0.26 Coffea_car | 0.26 Coffea_car | 0.26 Coffea_car |
| Os01t0191300-01 | 0.25 Musa_acur | 0.26 Actinidia_c | 0.26 Actinidia_c |

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| Os03t0693800-00 | 0.26 | Ananas_co | 0.26 | Prunus_du | 0.26 | Prunus_du |
| Os04t0570000-00 | 0.26 | Populus_tr | 0.26 | Populus_tr | 0.26 | Populus_tr |
| Os02t0783100-01 | 0.20 | Ananas_co | 0.26 | Malus_don | 0.26 | Malus_don |
| Zm00001eb237720_P00 | 0.24 | Ananas_co | 0.24 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os09t0383400-01 | 0.24 | Musa_acur | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os12t0540700-01 | 0.06 | Ananas_co | 0.26 | Prunus_pe | 0.26 | Prunus_pe |
| Os06t0678200-01 | 0.18 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Amborella_ |
| Os04t0500700-01 | 0.20 | Ananas_co | 0.24 | Dioscorea_ | 0.26 | Prunus_du |
| Os03t0760600-01 | 0.26 | Musa_acur | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os06t0239500-01 | 0.14 | Ananas_co | 0.20 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os08t0331900-01 | 0.16 | Ananas_co | 0.21 | Dioscorea_ | 0.26 | Manihot_e |
| Os06t0342000-01 | 0.18 | Musa_acur | 0.23 | Dioscorea_ | 0.26 | Phaseolus_ |
| Os09t0464000-01 | 0.13 | Dioscorea_ | 0.13 | Dioscorea_ | 0.26 | Actinidia_c |
| Os01t0840200-01 | 0.22 | Musa_acur | 0.25 | Dioscorea_ | 0.26 | Pistacia_ve |
| Os05t0375100-00 | 0.23 | Musa_acur | 0.26 | Actinidia_c | 0.26 | Actinidia_c |
| Zm00001eb280320_P00 | 0.22 | Ananas_co | 0.26 | Ipomoea_t | 0.26 | Ipomoea_t |
| Os07t0203700-01 | 0.18 | Musa_acur | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os05t0222200-01 | 0.20 | Ananas_co | 0.22 | Dioscorea_ | 0.26 | Populus_tr |
| Os10t0516701-00 | 0.16 | Ananas_co | 0.26 | Corchorus_ | 0.26 | Corchorus_ |
| Os03t0308000-01 | 0.26 | Ananas_co | 0.26 | Rosa_chine | 0.26 | Rosa_chine |

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| Os06t0652000-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.26 Vitis_vinife |
| Os09t0454100-01 | 0.24 Musa_acur | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os04t0490400-01 | 0.25 Ananas_co | 0.26 Manihot_e | 0.26 Manihot_e |
| Os02t0627700-00 | 0.25 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os02t0761200-01 | 0.21 Ananas_co | 0.26 Cannabis_ | 0.26 Cannabis_ |
| Os04t0527800-01 | 0.20 Ananas_co | 0.26 Citrus_cler | 0.26 Citrus_cler |
| Os03t0271400-01 | 0.23 Musa_acur | 0.26 Rosa_chine | 0.26 Rosa_chine |
| Os09t0526800-01 | 0.17 Ananas_co | 0.23 Dioscorea_ | 0.26 Actinidia_c |
| Os01t0814700-01 | 0.20 Musa_acur | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os03t0111100-01 | 0.16 Ananas_co | 0.26 Rosa_chine | 0.26 Rosa_chine |
| Os02t0788500-01 | 0.14 Ananas_co | 0.19 Dioscorea_ | 0.26 Actinidia_c |
| Zm00001eb353990_P00 | 0.20 Ananas_co | 0.25 Dioscorea_ | 0.26 Ipomoea_t |
| Zm00001eb358800_P00 | 0.19 Musa_acur | 0.26 Glycine_ma | 0.26 Glycine_ma |
| Os01t0652100-01Zm00 | 0.19 Musa_acur | 0.26 Nicotiana_ | 0.26 Nicotiana_ |
| Os03t0249200-01 | 0.23 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os03t0699600-01 | 0.19 Ananas_co | 0.21 Dioscorea_ | 0.26 Actinidia_c |
| Os01t0159000-01Zm00 | 0.20 Musa_acur | 0.26 Populus_tr | 0.26 Populus_tr |
| Os01t0674800-01 | 0.16 Ananas_co | 0.26 Amborella_ | 0.26 Amborella_ |
| Os05t0427300-03 | 0.13 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os11t0528300-01 | 0.26 Capsicum_ | 0.26 Capsicum_ | 0.26 Capsicum_ |
| Os04t0670400-02 | 0.26 Corchorus_ | 0.26 Corchorus_ | 0.26 Corchorus_ |
| Os05t0215600-01Zm00 | 0.17 Ananas_co | 0.26 Beta_vulga | 0.26 Beta_vulga |
| Os10t0489000-00 | 0.14 Ananas_co | 0.26 Manihot_e | 0.26 Manihot_e |
| Zm00001eb168670_P00 | 0.11 Ananas_co | 0.26 Manihot_e | 0.26 Manihot_e |
| Os03t0411600-00 | 0.23 Ananas_co | 0.26 Manihot_e | 0.26 Manihot_e |
| Os06t0711600-01 | 0.15 Ananas_co | 0.17 Dioscorea_ | 0.26 Theobroma |
| Os06t0613600-01 | 0.26 Ananas_co | 0.26 Rosa_chine | 0.26 Rosa_chine |
| Os03t0800700-01 | 0.11 Ananas_co | 0.12 Dioscorea_ | 0.26 Rosa_chine |
| Os03t0794300-00 | 0.17 Musa_acur | 0.26 Gossypium | 0.26 Gossypium |
| Os04t0682500-01 | 0.21 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os08t0167000-01 | 0.21 Ananas_co | 0.26 Cucumis_s | 0.26 Cucumis_s |
| Os02t0621800-01 | 0.20 Ananas_co | 0.26 Dioscorea_ | 0.26 Actinidia_c |

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| Os08t0502400-01 | 0.14 Ananas_co | 0.26 Gossypium | 0.26 Gossypium |
| Os07t0564100-01 | 0.26 Nymphaea_ | 0.26 Nymphaea | 0.26 Nymphaea |

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| Os01t0637600-01 | 0.20 Musa_acum | 0.26 Daucus_ca | 0.26 Daucus_ca |
| Os06t0642600-00 | 0.24 Ananas_co | 0.25 Dioscorea_ | 0.26 Citrus_clem |
| Os04t0517500-01 | 0.19 Musa_acum | 0.23 Dioscorea_ | 0.26 Amborella_ |
| Os02t0748100-01 | 0.14 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os01t0730500-01 | 0.22 Ananas_co | 0.26 Pistacia_ve | 0.26 Pistacia_ve |
| Os09t0104300-01 | 0.22 Dioscorea_ | 0.22 Dioscorea_ | 0.26 Manihot_es |

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| Os01t0737800-02 | 0.18 Ananas_co | 0.26 Medicago_ | 0.26 Medicago_ |
| Os03t0781400-01 | 0.22 Ananas_co | 0.26 Glycine_ma | 0.26 Glycine_ma |
| Os02t0736500-01 | 0.16 Ananas_co | 0.26 Gossypium | 0.26 Gossypium |
| Os03t0826300-00 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.26 Manihot_es |
| Os05t0500400-01 | 0.22 Musa_acum | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os03t0200700-01 | 0.19 Musa_acum | 0.26 Actinidia_c | 0.26 Actinidia_c |

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| Os07t0671000-00 | 0.26 Ananas_co | 0.26 Coffea_can | 0.26 Coffea_can |

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| Os01t0798500-02 | 0.21 Ananas_co | 0.26 Citrus_clem | 0.26 Citrus_clem |
| Os03t0775400-01 | 0.18 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |

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| Os03t0657400-00 | 0.20 Ananas_co | 0.26 Manihot_es | 0.26 Manihot_es |
| Os03t0233500-01 | 0.12 Musa_acum | 0.15 Dioscorea_ | 0.26 Gossypium |
| Os07t0621500-01 | 0.17 Ananas_co | 0.22 Dioscorea_ | 0.26 Theobroma |
| Os05t0493600-00 | 0.22 Ananas_co | 0.26 Theobroma | 0.26 Theobroma |
| Os02t0721700-01 | 0.26 Glycine_ma | 0.26 Glycine_ma | 0.26 Glycine_ma |

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| Os09t0508250-00 | 0.22 Musa_acur | 0.22 Dioscorea_ | 0.26 Amborella_ |
| Os04t0281900-01 | 0.22 Ananas_co | 0.26 Cynara_car | 0.26 Cynara_car |

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| Os04t0593500-00 | 0.16 Ananas_co | 0.25 Dioscorea_ | 0.26 Glycine_ma |
| Os02t0695700-01Zm00 | 0.21 Dioscorea_ | 0.21 Dioscorea_ | 0.26 Prunus_per |
| Os05t0366600-01 | 0.15 Ananas_co | 0.21 Dioscorea_ | 0.26 Amborella_ |
| Os01t0259200-02 | 0.26 Nymphaea_ | 0.26 Nymphaea | 0.26 Nymphaea |
| Os06t0238700-00 | 0.22 Musa_acur | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os03t0799500-01 | 0.08 Ananas_co | 0.26 Brassica_na | 0.26 Brassica_na |
| Os03t0759600-00 | 0.12 Ananas_co | 0.26 Prunus_du | 0.26 Prunus_du |
| Os12t0502200-01 | 0.21 Musa_acur | 0.24 Dioscorea_ | 0.26 Vitis_vinife |
| Os06t0531000-00 | 0.26 Vitis_vinife | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os03t0278800-00 | 0.20 Musa_acur | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Zm00001eb000170_P00 | 0.22 Musa_acur | 0.26 Dioscorea_ | 0.26 Actinidia_c |
| Os09t0553900-01 | 0.19 Ananas_co | 0.26 Pistacia_ve | 0.26 Pistacia_ve |
| Os08t0320800-00 | 0.20 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Zm00001eb211510_P00 | 0.17 Ananas_co | 0.26 Nymphaea | 0.26 Nymphaea |
| Os09t0413200-01Zm00 | 0.23 Musa_acur | 0.24 Dioscorea_ | 0.26 Vitis_vinife |
| Os12t0515600-01 | 0.21 Ananas_co | 0.25 Dioscorea_ | 0.26 Manihot_es |
| Os05t0587400-01 | 0.17 Musa_acur | 0.26 Prunus_per | 0.26 Prunus_per |

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| Os07t0562800-01 | 0.23 Ananas_co | 0.26 Amborella_ | 0.26 Amborella_ |
| Os06t0665500-01 | 0.20 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os12t0506400-01 | 0.01 Ananas_co | 0.03 Dioscorea_ | 0.26 Marchantia |
| Os03t0308800-01 | 0.23 Ananas_co | 0.26 Nicotiana_a | 0.26 Nicotiana_a |

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| Os02t0221900-01 | 0.18 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os05t0428100-00 | 0.16 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |

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| Os10t0577700-01 | 0.18 Ananas_co | 0.23 Dioscorea_ | 0.26 Malus_do |
| Os03t0708000-01 | 0.14 Ananas_co | 0.26 Populus_tr | 0.26 Populus_tr |
| Zm00001eb339970_P00 | 0.19 Ananas_co | 0.26 Nymphaea | 0.26 Nymphaea |
| Os05t0480400-01Zm00 | 0.19 Ananas_co | 0.21 Dioscorea_ | 0.26 Vitis_vinife |
| Os08t0512400-02 | 0.23 Ananas_co | 0.26 Theobrom | 0.26 Theobrom |
| Os07t0517800-00 | 0.16 Ananas_co | 0.22 Dioscorea_ | 0.26 Ipomoea_t |
| Os04t0596500-02 | 0.23 Ananas_co | 0.26 Prunus_pe | 0.26 Prunus_pe |
| Os05t0444300-01 | 0.22 Musa_acu | 0.26 Dioscorea_ | 0.26 Vitis_vinife |
| Os03t0586500-01 | 0.25 Musa_acu | 0.26 Daucus_ca | 0.26 Daucus_ca |
| Os07t0101200-01 | 0.17 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os03t0296500-00 | 0.22 Ananas_co | 0.26 Theobrom | 0.26 Theobrom |

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| Os06t0273500-01 | 0.17 Musa_acu | 0.26 Amborella | 0.26 Amborella |
| Os09t0439700-01 | 0.18 Ananas_co | 0.26 Actinidia_c | 0.26 Actinidia_c |

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| Os02t0684150-00 | 0.11 Ananas_co | 0.26 Dioscorea_ | 0.26 Vitis_vinife |
| Os03t0374100-01 | 0.19 Musa_acu | 0.26 Citrus_cle | 0.26 Citrus_cle |

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| Os04t0458900-01 | 0.11 Ananas_co | 0.26 Nymphaea | 0.26 Nymphaea |
| Zm00001eb013150_P00 | 0.13 Ananas_co | 0.26 Manihot_e | 0.26 Manihot_e |

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| Os02t0306401-00 | 0.22 Musa_acu | 0.26 Actinidia_c | 0.26 Actinidia_c |
| Os01t0654400-01 | 0.26 Cucumis_ | 0.26 Cucumis_ | 0.26 Cucumis_ |
| Os09t0407700-01 | 0.18 Ananas_co | 0.26 Citrullus_l | 0.26 Citrullus_l |
| Zm00001eb274760_P00 | 0.12 Ananas_co | 0.25 Dioscorea_ | 0.26 Vitis_vinife |

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| Os01t0360200-01 | 0.26 Theobrom | 0.26 Theobrom | 0.26 Theobrom |
| Os01t0806200-01 | 0.24 Ananas_co | 0.26 Cannabis_ | 0.26 Cannabis_ |
| Os03t0821700-01 | 0.26 Cannabis_ | 0.26 Cannabis_ | 0.26 Cannabis_ |
| Os02t0714300-01 | 0.21 Musa_acu | 0.23 Dioscorea_ | 0.26 Vitis_vinife |
| Os05t0572700-02 | 0.15 Ananas_co | 0.19 Dioscorea_ | 0.26 Citrus_cle |
| Os01t0901600-01Zm00 | 0.26 Pistacia_ve | 0.26 Pistacia_ve | 0.26 Pistacia_ve |
| Os06t0634300-01 | 0.18 Ananas_co | 0.26 Populus_tr | 0.26 Populus_tr |

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| Os03t0821300-01 | 0.26 Vitis_vinife | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os01t0211800-01Zm00 | 0.19 Ananas_co | 0.24 Dioscorea_ | 0.26 Pistacia_ve |
| Os09t0307400-00 | 0.17 Musa_acu | 0.25 Dioscorea_ | 0.26 Glycine_ma |
| Os02t0611800-01 | 0.18 Ananas_co | 0.23 Dioscorea_ | 0.26 Populus_tr |
| Os07t0667400-01 | 0.20 Ananas_co | 0.26 Gossypiu | 0.26 Gossypiu |
| Os03t0407000-01 | 0.13 Ananas_co | 0.26 Nicotiana_ | 0.26 Nicotiana_ |
| Os09t0133000-01Zm00 | 0.17 Musa_acu | 0.23 Dioscorea_ | 0.26 Malus_dom |
| Os03t0626500-00Zm00 | 0.26 Theobrom | 0.26 Theobrom | 0.26 Theobrom |
| Os06t0166000-01 | 0.22 Musa_acu | 0.26 Amborella_ | 0.26 Amborella_ |
| Os03t0850000-01 | 0.22 Musa_acu | 0.26 Cynara_ca | 0.26 Cynara_ca |
| Os02t0326600-01 | 0.20 Ananas_co | 0.23 Dioscorea_ | 0.26 Manihot_e |
| Os10t0442100-00 | 0.17 Ananas_co | 0.26 Prunus_pe | 0.26 Prunus_pe |
| Os10t0558600-00 | 0.18 Ananas_co | 0.26 Actinidia_ | 0.26 Actinidia_ |
| Os12t0241100-01 | 0.26 Manihot_e | 0.26 Manihot_e | 0.26 Manihot_e |
| Os12t0139500-01 | 0.18 Dioscorea_ | 0.18 Dioscorea_ | 0.26 Vitis_vinife |
| Os06t0538900-01 | 0.23 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |
| Os12t0576900-01 | 0.26 Prunus_du | 0.26 Prunus_du | 0.26 Prunus_du |
| Os05t0122800-01 | 0.11 Musa_acu | 0.16 Dioscorea_ | 0.26 Citrus_cle |
| Os07t0693700-01 | 0.14 Ananas_co | 0.26 Vitis_vinife | 0.26 Vitis_vinife |

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| Os03t0101500-01 | 0.19 | Ananas_co | 0.23 | Dioscorea_ | 0.26 | Actinidia_c |
| Os01t0166700-01 | 0.24 | Musa_acu | 0.26 | Theobrom | 0.26 | Theobrom |
| Os11t0116000-01 | 0.25 | Musa_acu | 0.26 | Corchorus | 0.26 | Corchorus |
| Os06t0202900-01 | 0.19 | Ananas_co | 0.26 | Actinidia_c | 0.26 | Actinidia_c |
| Os02t0806000-01 | 0.17 | Musa_acu | 0.22 | Dioscorea_ | 0.26 | Populus_tr |
| Os08t0172200-01 | 0.21 | Ananas_co | 0.22 | Dioscorea_ | 0.26 | Rosa_chine |
| Os02t0556000-00 | 0.21 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os02t0137000-01 | 0.19 | Ananas_co | 0.26 | Corchorus | 0.26 | Corchorus |
| Os03t0356900-01 | 0.19 | Ananas_co | 0.26 | Citrus_cle | 0.26 | Citrus_cle |
| Os04t0510400-01 | 0.24 | Dioscorea_ | 0.24 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os03t0222100-01 | 0.23 | Ananas_co | 0.26 | Rosa_chine | 0.26 | Rosa_chine |
| Os01t0127300-01 | 0.16 | Ananas_co | 0.26 | Cucumis_ | 0.26 | Cucumis_ |
| Os07t0530300-01 | 0.20 | Ananas_co | 0.26 | Citrullus_l | 0.26 | Citrullus_l |
| Os06t0367500-01 | 0.16 | Ananas_co | 0.17 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os09t0132200-01 | 0.23 | Ananas_co | 0.26 | Rosa_chine | 0.26 | Rosa_chine |
| Os03t0676100-00 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.26 | Cucumis_ |
| Os03t0237100-01 | 0.20 | Musa_acu | 0.26 | Gossypiu | 0.26 | Gossypiu |
| Os02t0741700-01 | 0.18 | Musa_acu | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os05t0119600-01 | 0.17 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os02t0767200-01Zm00 | 0.14 | Ananas_co | 0.26 | Manihot_e | 0.26 | Manihot_e |
| Os04t0571600-01 | 0.20 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Prunus_pe |
| Os07t0187400-00 | 0.18 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Gossypiu |

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| Os01t0825000-01 | 0.25 | Ananas_co | 0.26 | Rosa_chine | 0.26 | Rosa_chine |
| Zm00001eb363330_P00 | 0.11 | Ananas_co | 0.17 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os06t0269200-01 | 0.16 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Pistacia_ve |
| Os03t0167400-00Zm00 | 0.15 | Musa_acu | 0.26 | Prunus_du | 0.26 | Prunus_du |
| Os05t0573900-01 | 0.18 | Ananas_co | 0.26 | Gossypiu | 0.26 | Gossypiu |
| Os06t0114650-01Zm00 | 0.12 | Ananas_co | 0.19 | Dioscorea_ | 0.26 | Manihot_e |

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| Os03t0168900-01 | 0.24 | Musa_acu | 0.26 | Brassica_r | 0.26 | Brassica_r |
| Os04t0527000-01 | 0.23 | Ananas_co | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |

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| Os06t0254700-01 | 0.20 | Dioscorea_ | 0.20 | Dioscorea_ | 0.26 | Trifolium_ |
| Os03t0859900-01 | 0.17 | Ananas_co | 0.26 | Actinidia_c | 0.26 | Actinidia_c |
| Os06t0484600-01 | 0.24 | Ananas_co | 0.26 | Medicago_ | 0.26 | Medicago_ |
| Os03t0170300-01 | 0.24 | Musa_acu | 0.26 | Populus_tr | 0.26 | Populus_tr |
| Os01t0876800-00 | 0.13 | Ananas_co | 0.18 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os09t0428900-01 | 0.23 | Musa_acu | 0.25 | Dioscorea_ | 0.26 | Populus_tr |
| Os06t0231400-01 | 0.17 | Ananas_co | 0.26 | Malus_do | 0.26 | Malus_do |

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| Os03t0219100-01 | 0.18 | Musa_acu | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |

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| Os07t0614000-01 | 0.18 | Ananas_co | 0.26 | Cannabis_ | 0.26 | Cannabis_ |
| Os03t0810100-01 | 0.22 | Ananas_co | 0.26 | Corchorus | 0.26 | Corchorus |
| Os12t0156400-01Zm00 | 0.24 | Musa_acu | 0.26 | Populus_tr | 0.26 | Populus_tr |
| Os07t0668900-01 | 0.23 | Ananas_co | 0.26 | Nymphaea | 0.26 | Nymphaea |

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| Os05t0275000-01 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.26 | Vitis_vinife |
| Os02t0761600-01 | 0.23 | Musa_acu | 0.26 | Theobrom | 0.26 | Theobrom |
| Os03t0137400-01 | 0.10 | Ananas_co | 0.16 | Dioscorea_ | 0.26 | Manihot_e |
| Os07t0525400-01 | 0.21 | Ananas_co | 0.22 | Dioscorea_ | 0.26 | Malus_do |

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| Os04t0583500-01 | 0.18 | Musa_acu | 0.26 | Vitis_vinife | 0.26 | Vitis_vinife |
| Os12t0407500-01 | 0.22 | Ananas_co | 0.25 | Dioscorea_ | 0.26 | Corchorus |
| Os07t0572300-01 | 0.24 | Dioscorea_ | 0.24 | Dioscorea_ | 0.26 | Cannabis_ |
| Os03t0317100-01 | 0.26 | Actinidia_c | 0.26 | Actinidia_c | 0.26 | Actinidia_c |
| Os09t0515100-02 | 0.16 | Ananas_co | 0.21 | Dioscorea_ | 0.26 | Amborella_ |

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| Os03t0369100-01 | 0.21 | Ananas_co | 0.26 | Arabidopsi | 0.26 | Arabidopsi |
| Os06t0146400-01 | 0.22 | Ananas_co | 0.25 | Cucumis_ | 0.25 | Cucumis_ |

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| Os05t0586600-01 | 0.22 | Ananas_co | 0.25 | Pistacia_ve | 0.25 | Pistacia_ve |

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| Os11t0199200-01 | 0.25 Dioscorea_ | 0.25 Dioscorea_ | 0.25 Medicago_ |
| Os10t0500500-01 | 0.24 Ananas_co | 0.25 Amborella_ | 0.25 Amborella_ |

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| Os04t0607600-01 | 0.25 Theobrom | 0.25 Theobrom | 0.25 Theobrom |
| Os06t0685300-00 | 0.14 Ananas_co | 0.25 Amborella_ | 0.25 Amborella_ |

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| Os11t0143200-01 | 0.16 Ananas_co | 0.18 Dioscorea_ | 0.25 Prunus_pe |
| Os03t0119000-01Zm00 | 0.20 Ananas_co | 0.25 Manihot_e | 0.25 Manihot_e |

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| Os01t0273800-01 | 0.14 Ananas_co | 0.25 Dioscorea_ | 0.25 Prunus_du |
| Os06t0127500-01Zm00 | 0.17 Musa_acu | 0.25 Theobrom | 0.25 Theobrom |
| Os01t0100100-01 | 0.23 Dioscorea_ | 0.23 Dioscorea_ | 0.25 Populus_tr |
| Os01t0255100-01Zm00 | 0.20 Musa_acu | 0.24 Dioscorea_ | 0.25 Solanum_t |
| Zm00001eb009580_P00 | 0.20 Musa_acu | 0.25 Amborella_ | 0.25 Amborella_ |

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| Os10t0457200-01 | 0.19 Ananas_co | 0.24 Dioscorea_ | 0.25 Coffea_ca |
| Os03t0132200-01 | 0.16 Musa_acu | 0.21 Dioscorea_ | 0.25 Nymphaea |

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| Os02t0752000-01 | 0.20 Ananas_co | 0.25 Dioscorea_ | 0.25 Citrus_cle |
| Os12t0110400-01 | 0.20 Ananas_co | 0.25 Camelina_ | 0.25 Camelina_ |
| Os09t0474800-01 | 0.17 Ananas_co | 0.25 Dioscorea_ | 0.25 Capsicum_ |
| Os04t0539000-01 | 0.18 Musa_acu | 0.25 Glycine_m | 0.25 Glycine_m |
| Os07t0637100-01 | 0.18 Ananas_co | 0.25 Cucumis_ | 0.25 Cucumis_ |

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| Os12t0476200-01 | 0.21 Dioscorea_ | 0.21 Dioscorea_ | 0.25 Amborella_ |
| Os05t0453500-01 | 0.09 Ananas_co | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os11t0264200-01 | 0.19 Musa_acu | 0.25 Rosa_chine | 0.25 Rosa_chine |
| Os08t0427900-01 | 0.18 Musa_acu | 0.25 Citrullus_l | 0.25 Citrullus_l |
| Os04t0571300-01 | 0.13 Ananas_co | 0.23 Dioscorea_ | 0.25 Theobrom |
| Os09t0327300-01 | 0.16 Ananas_co | 0.25 Theobrom | 0.25 Theobrom |
| Os10t0141900-01 | 0.14 Ananas_co | 0.23 Dioscorea_ | 0.25 Populus_tr |

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| Os05t0154700-01 | 0.19 Ananas_co | 0.25 Coffea_ca | 0.25 Coffea_ca |
| Os09t0512800-00 | 0.09 Ananas_co | 0.20 Dioscorea_ | 0.25 Citrus_cle |
| Os03t0376800-01 | 0.16 Ananas_co | 0.25 Dioscorea_ | 0.25 Coffea_ca |
| Os05t0414700-01 | 0.19 Ananas_co | 0.21 Dioscorea_ | 0.25 Vitis_vinife |
| Os05t0298200-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.25 Manihot_e |

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| Os04t0181100-01 | 0.12 Ananas_co | 0.17 Dioscorea_ | 0.25 Vitis_vinife |
| Os01t0920000-01 | 0.19 Ananas_co | 0.22 Dioscorea_ | 0.25 Trifolium_p |

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| Zm00001eb303620_P00 | 0.18 Ananas_co | 0.21 Dioscorea_ | 0.25 Vitis_vinife |
| Os09t0573100-01Zm00 | 0.21 Ananas_co | 0.25 Dioscorea_ | 0.25 Actinidia_c |
| Os01t0266500-01 | 0.20 Musa_acum | 0.25 Dioscorea_ | 0.25 Nymphaea |
| Os06t0698600-01 | 0.23 Musa_acum | 0.24 Dioscorea_ | 0.25 Manihot_es |

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| Os03t0719800-01 | 0.22 Ananas_co | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os07t0108000-01 | 0.16 Ananas_co | 0.25 Rosa_chine | 0.25 Rosa_chine |
| Zm00001eb252440_P00 | 0.18 Musa_acum | 0.25 Amborella_ | 0.25 Amborella_ |

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| Os01t0179400-01 | 0.20 Ananas_co | 0.25 Rosa_chine | 0.25 Rosa_chine |

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| Os02t0753800-01 | 0.19 Ananas_co | 0.23 Dioscorea_ | 0.25 Pistacia_ve |
| Os12t0257600-00Zm00 | 0.25 Pistacia_ve | 0.25 Pistacia_ve | 0.25 Pistacia_ve |
| Zm00001eb208580_P00 | 0.25 Populus_tr | 0.25 Populus_tr | 0.25 Populus_tr |
| Os05t0112900-01 | 0.16 Ananas_co | 0.25 Coffea_car | 0.25 Coffea_car |
| Os02t0550300-00 | 0.18 Ananas_co | 0.25 Nymphaea | 0.25 Nymphaea |
| Os05t0490300-01 | 0.07 Ananas_co | 0.25 Amborella_ | 0.25 Amborella_ |
| Os02t0594700-01 | 0.25 Vitis_vinife | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os08t0520100-01 | 0.11 Ananas_co | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os12t0145900-01 | 0.10 Ananas_co | 0.25 Citrus_clem | 0.25 Citrus_clem |
| Os02t0708400-01 | 0.20 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os05t0459400-01 | 0.19 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os03t0780900-01 | 0.18 Dioscorea_ | 0.18 Dioscorea_ | 0.25 Theobroma |
| Os11t0150400-01Zm00 | 0.25 Pistacia_ve | 0.25 Pistacia_ve | 0.25 Pistacia_ve |
| Os01t0839400-00 | 0.25 Malus_dom | 0.25 Malus_dom | 0.25 Malus_dom |
| Os05t0562200-01 | 0.23 Ananas_co | 0.25 Manihot_es | 0.25 Manihot_es |
| Os06t0715400-01 | 0.23 Ananas_co | 0.25 Coffea_car | 0.25 Coffea_car |
| Os03t0724300-01 | 0.17 Musa_acum | 0.25 Vitis_vinife | 0.25 Vitis_vinife |

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| Os06t0657500-02 | 0.24 Musa_acum | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os01t0134800-01 | 0.22 Ananas_co | 0.24 Dioscorea_ | 0.25 Daucus_ca |
| Os10t0503200-01 | 0.18 Ananas_co | 0.25 Rosa_chine | 0.25 Rosa_chine |

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| Os03t0781100-00 | 0.15 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os03t0345300-01 | 0.16 Ananas_co | 0.22 Dioscorea_ | 0.25 Nymphaea |
| Os10t0420000-01 | 0.21 Musa_acu | 0.22 Dioscorea_ | 0.25 Theobrom |
| Os10t0160100-01 | 0.10 Ananas_co | 0.20 Dioscorea_ | 0.25 Manihot_e |
| Os01t0210500-01Zm00 | 0.20 Ananas_co | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os01t0911200-01 | 0.19 Ananas_co | 0.25 Glycine_m | 0.25 Glycine_m |
| Os04t0451200-01 | 0.19 Ananas_co | 0.25 Theobrom | 0.25 Theobrom |
| Os03t0249500-01 | 0.22 Musa_acu | 0.25 Dioscorea_ | 0.25 Gossypiu |
| Os03t0356484-01 | 0.12 Ananas_co | 0.25 Arabidopsi | 0.25 Arabidopsi |

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| Os01t0799900-01 | 0.22 Ananas_co | 0.25 Corchorus | 0.25 Corchorus |
| Os06t0134900-01 | 0.22 Musa_acu | 0.23 Dioscorea_ | 0.25 Vitis_vinife |
| Os08t0156700-01 | 0.22 Ananas_co | 0.25 Theobrom | 0.25 Theobrom |
| Os08t0116800-01 | 0.22 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Zm00001eb377290_P00 | 0.21 Musa_acu | 0.25 Coffea_ca | 0.25 Coffea_ca |
| Os07t0687500-01 | 0.21 Ananas_co | 0.25 Lupinus_a | 0.25 Lupinus_a |
| Os02t0694201-01 | 0.11 Ananas_co | 0.23 Dioscorea_ | 0.25 Coffea_ca |
| Os01t0142500-01 | 0.20 Ananas_co | 0.24 Dioscorea_ | 0.25 Theobrom |
| Zm00001eb197740_P00 | 0.18 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os04t0639200-01 | 0.18 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os12t0538700-01 | 0.16 Ananas_co | 0.25 Nymphaea | 0.25 Nymphaea |
| Os12t0630700-01 | 0.19 Ananas_co | 0.25 Amborella_ | 0.25 Amborella_ |
| Os09t0346900-01 | 0.24 Dioscorea_ | 0.24 Dioscorea_ | 0.25 Vitis_vinife |
| Zm00001eb089410_P00 | 0.24 Musa_acu | 0.25 Coffea_ca | 0.25 Coffea_ca |
| Os03t0240900-01 | 0.20 Ananas_co | 0.24 Dioscorea_ | 0.25 Vitis_vinife |
| Os03t0374400-01 | 0.16 Ananas_co | 0.25 Manihot_e | 0.25 Manihot_e |
| Os02t0593400-01 | 0.04 Ananas_co | 0.09 Dioscorea_ | 0.25 Coffea_ca |
| Os05t0410800-01 | 0.21 Musa_acu | 0.22 Dioscorea_ | 0.25 Manihot_e |
| Os02t0725100-01 | 0.25 Pistacia_ve | 0.25 Pistacia_ve | 0.25 Pistacia_ve |
| Os02t0556800-01 | 0.24 Musa_acu | 0.25 Lupinus_a | 0.25 Lupinus_a |

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| Os10t0375600-01 | 0.14 Ananas_co | 0.21 Dioscorea_ | 0.25 Actinidia_c |
| Os04t0587400-01 | 0.21 Ananas_co | 0.23 Dioscorea_ | 0.25 Lupinus_a |
| Os03t0786000-01 | 0.22 Musa_acu | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os02t0201900-01 | 0.25 Solanum_t | 0.25 Solanum_t | 0.25 Solanum_t |
| Os03t0182400-01 | 0.23 Musa_acu | 0.25 Citrus_cle | 0.25 Citrus_cle |
| Os06t0622900-01 | 0.25 Vigna_radi | 0.25 Vigna_radi | 0.25 Vigna_radi |
| Os07t0692401-00 | 0.18 Ananas_co | 0.22 Dioscorea_ | 0.25 Actinidia_c |

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| Os04t0574700-01 | 0.15 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os06t0163400-01 | 0.16 Musa_acur | 0.22 Dioscorea_ | 0.25 Populus_tr |
| Os03t0258200-01 | 0.25 Pistacia_ve | 0.25 Pistacia_ve | 0.25 Pistacia_ve |
| Os01t0377700-02 | 0.21 Ananas_co | 0.25 Vigna_radi | 0.25 Vigna_radi |
| Os08t0549200-01 | 0.14 Ananas_co | 0.25 Populus_tr | 0.25 Populus_tr |
| Os06t0656000-00 | 0.15 Ananas_co | 0.20 Dioscorea_ | 0.25 Citrus_cler |
| Os04t0563000-01 | 0.17 Ananas_co | 0.22 Dioscorea_ | 0.25 Actinidia_c |

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| Os04t0413500-01 | 0.23 Musa_acur | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os04t0687800-01 | 0.13 Ananas_co | 0.25 Citrus_cler | 0.25 Citrus_cler |
| Os12t0181900-01 | 0.20 Ananas_co | 0.25 Citrullus_la | 0.25 Citrullus_la |
| Os07t0272400-01 | 0.23 Ananas_co | 0.25 Corchorus_ | 0.25 Corchorus_ |
| Os01t0555300-01 | 0.18 Ananas_co | 0.25 Citrullus_la | 0.25 Citrullus_la |
| Os03t0397300-01 | 0.11 Ananas_co | 0.25 Actinidia_c | 0.25 Actinidia_c |
| Os09t0345700-01 | 0.23 Musa_acur | 0.24 Dioscorea_ | 0.25 Corchorus_ |
| Os03t0737900-01 | 0.16 Ananas_co | 0.25 Vitis_vinife | 0.25 Vitis_vinife |
| Os03t0336500-01 | 0.19 Musa_acur | 0.25 Beta_vulga | 0.25 Beta_vulga |

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| Os07t0680500-01 | 0.23 | Dioscorea_ | 0.23 | Dioscorea_ | 0.25 | Actinidia_c |
| Os01t0730800-01 | 0.17 | Musa_acur | 0.25 | Nymphaea | 0.25 | Nymphaea |
| Os02t0226200-01 | 0.23 | Ananas_co | 0.25 | Gossypium | 0.25 | Gossypium |
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| Os07t0684000-01 | 0.12 | Ananas_co | 0.21 | Dioscorea_ | 0.25 | Citrus_cler |
| Os08t0506000-01 | 0.17 | Ananas_co | 0.22 | Dioscorea_ | 0.25 | Olea_europ |
| Os04t0670800-01 | 0.15 | Ananas_co | 0.22 | Dioscorea_ | 0.25 | Malus_dom |
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| Os10t0553300-01 | 0.21 | Ananas_co | 0.25 | Theobroma | 0.25 | Theobroma |

-specific with added functional annotation

| categorisation using S>0.25 | source | descriptor |
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| grass specific | RAP-DB | [Os] "Phosphatidylcholine (PC):diacylglycerol cholinephosphotransferase, Control of seed saturated triacylglycerol (TAG) levels, Heading date, Flooding resistance (Os06t0607100-01)" |
| grass specific | | |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Calcium-dependent lipid binding annexin, Positive regulation of ABA-dependent drought and osmotic stresses (Os07t0659600-01)" |
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| grass specific | RAP-DB | [Os] "Bell-like homeodomain-containing transcription factor, Secondary cell wall formation (Os03t0165300-01);Homeobox domain containing protein. (Os03t0165300-02);Conserved hypothetical protein. |
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| grass specific | RAP-DB | [Os] "S-Domain kinase-13, Response to Xanthomonas oryzae pv. oryzae in resistant rice genotype (Os03t0838100-01);Serine/threonine protein kinase-related domain containing protein. (Os03t0838100-02);Serine/threonine protein kinase-related domain containing protein. (Os03t0838100- |
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| grass specific | RAP-DB | [Os] "Similar to Nonphototropic hypocotyl protein 1 (EC 2.7.1.37) (Phototropin). (Os04t0304200-01);Rice nonphototropic hypocotyl 1 (NPH1) homologue, Phototropin, Ion homeostasis, Salt stress response |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Jasmonic acid (JA) signalling repressor, Regulation of spikelet development (Os04t0653000-01)" |
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| grass specific | RAP-DB | [Os] "Subunit of SWI2/SNF2-Related 1 Chromatin Remodeling (SWR1) and Nucleosome Acetyltransferase of H4 (NuA4) complexes, Vegetative and reproductive development, GA biosynthesis, Promotion of internode elongation, Pollen germination (Os05t0540800-01);Similar to DNA methyltransferase 1-associated protein 1. (Os05t0540800-02)" |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Regulation of shoot gravitropism and tiller angle, Regulation of polar auxin transport (Os11t0490600-01);Hypothetical conserved gene. (Os11t0490600-02)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Regulation of root hair development (Os06t0184000-01)" |
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| grass specific | RAP-DB | [Os] "Pyruvate kinase, Regulation of seed germination, Glycolytic metabolism and GA/ABA balance, Positive regulation of protein content and negative regulation of total starch content in the grain, Negative regulation of amylose content in the grain (Os11t0216000-01);Similar to Pyruvate kinase. (Os11t0216000-02)" |
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| grass specific | RAP-DB | [Os] "CDK inhibitor (CKI), Seed development (Os02t0762400-01)" |
| grass specific | RAP-DB | [Os] "Ferrochelatase I, Oxyfluorfen herbicide resistance (Os09t0297000- |
| grass specific | RAP-DB | [Os] "Protein kinase-like, Response to drought in tolerant genotypes (Os04t0634500-01)" |
| grass specific | RAP-DB | [Os] "Similar to Transcription factor MYBS3. (Os10t0561400-01);MYB transcription factor, Cold tolerance, Mediation of sugar signaling (Os10t0561400-02);Similar to Myb transcription factor. (Os10t0561400- |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "Homolog of Arabidopsis MOTHER OF FT AND TFL1, Regulation of heading and panicle architecture (Os06t0498800-01)" |
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| grass specific | RAP-DB | [Os] "Protein tyrosine phosphatase, Negative regulation of drought stress response (Os09t0135700-01)" |
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| grass specific | Maizemine | [Zm] Glycerol-3-phosphate dehydrogenase [NAD( )] |
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| grass specific | RAP-DB | [Os] "Protein phosphatase 1 regulatory subunit, Reproductive growth, Regulation of ABA-mediated inhibition of seed germination, ROS homeostasis (Os05t0270400-01)" |
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| grass specific | RAP-DB | [Os] "Flavonoid 3'-hydroxylase, Cytochrome P450 75B3, Flavone C-glycosides biosynthesis (Os10t0320100-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Lysin motif-containing protein, Pattern recognition receptor, Peptidoglycan and chitin perception in innate immunity (Os09t0452200-01);Similar to LysM-domain GPI-anchored protein 1 precursor. Splice isoform 2. (Os09t0452200-02)" |

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| grass specific | RAP-DB | [Os] "Pseudo response regulator, Heading date, Long-day repression (Os07t0695100-01);Similar to Two-component response regulator-like PRR37. (Os07t0695100-02)" |
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| grass specific | RAP-DB | [Os] "LEUNIG-like (LUGL) transcriptional regulator, Regulation of floral organ development (Os01t0607400-01);Similar to STYLOSA protein. (Os01t0607400-02)" |
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| grass specific | RAP-DB | [Os] "cGMP-dependent protein kinase, Mediation of gibberellin signaling, Salt stress response (Os02t0281000-01);Similar to predicted protein. (Os02t0281000-02)" |

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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "ACC oxidase, Ethylene biosynthesis (Os09t0451000-01)" |
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| grass specific | RAP-DB; Knetminer-wheat; Maizemine | [Os] "Cytokinin oxidase/dehydrogenase, Crown root formation (Os01t0940000-01)"; [Zm] Cytokinin dehydrogenase |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "14-3-3 protein, Negative modulation of cell death and disease resistance (Os02t0580300-01);Similar to 14-3-3 protein 6. (Os02t0580300-02);Similar to 14-3-3 protein 6. (Os02t0580300-03);F-box protein, Positive regulator of GA signaling (Os02t0580300-04)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Rac/Rop guanine nucleotide exchange factor, Regulation of immune responses (Os07t0138100-01);Similar to PH domain containing protein. (Os07t0138100-02)" |
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| grass specific | RAP-DB | [Os] "CCT domain domain containing protein. (Os02t0731700-01);CONSTANS (CO)-like protein, Regulation of leaf senescence and drought resistance (Os02t0731700-02)" |
| grass specific | | |
| grass specific | RAP-DB; Maizemine | [Os] "Histidine phosphotransfer protein, Cytokinin signaling and stress response (Os09t0567400-01);Similar to Histidine-containing phosphotransfer protein. (Os09t0567400-02)"; [Zm] Histidine-containing phosphotransfer protein 1 |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to Chloroplast inorganic pyrophosphatase (EC 3.6.1.1). (Os02t0768600-01);Inorganic pyrophosphatase, Member of sPPase, Alkaline tolerance, Osmotic regulatory factor (Os02t0768600-02)" |
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| grass specific | RAP-DB | [Os] "BTB/POX VIRUS AND ZINC FINGER (POZ) domain and ankyrin repeats containing protein, Regulator of proximal-distal patterning of leaves (Os11t0141900-01)" |
| grass specific | RAP-DB | [Os] "Brassinosteroid (BR) signaling kinase, Regulation of BR signaling (Os04t0684200-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Starch-debranching enzyme, Isoamylase, Starch biosynthesis as the ISA1-ISA2 hetero-oligomer in leaf (Os05t0393700-01)"; [Zm] Isoamylase |
| grass specific | RAP-DB | [Os] "UDP-glucosyltransferase, Regulation of endosperm development (Os05t0552700-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Similar to Pyruvate decarboxylase isozyme 2. (Os03t0293500-01);Pyruvate decarboxylase 2, Pyruvate decarboxylase Î±-subunit |
| grass specific | RAP-DB | [Os] "Phosphatidylinositol 3-/4-kinase (PI3/4K) family protein, Ubiquitin-like domain kinase, Control of flowering time (Os02t0290500-01);Similar to phosphatidylinositol 3- and 4-kinase family protein. (Os02t0290500-02)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Receptor-like kinase, Positive regulation of flavonoid metabolism, UV-B tolerance (Os04t0619400-01)" |
| grass specific | RAP-DB | [Os] "DOCK family guanine nucleotide exchange factor, R protein Pit-mediated disease resistance (Os03t0328000-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Meiosis-specific DNA recombinase, Synaptonemal complex (SC) assembly (Os11t0146800-01)" |
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| grass specific | Maizemine | [Zm] 12-oxophytodienoate reductase 1 |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "DEAD-box helicase ATP-binding protein, Response to abiotic stress (salt, dehydration, ABA, blue and red light) (Os06t0526600-01)" |
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| grass specific | RAP-DB | [Os] Lysine and histidine transporter 2 (Os12t0244400-01) |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Class II homeodomain-leucine zipper (HD-ZIP II) protein, HD-ZIP transcription factor, Regulation of tiller angle and shoot gravitropism, Regulation of the local distribution of auxin (Os06t0140400-01);Similar to HAHB-6 (Fragment). (Os06t0140400- |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to Photosystem-1 F subunit. (Os03t0778100-01);Similar to Photosystem-1 F subunit. (Os03t0778100-02);Photosystem-1 F subunit, Modulation of chlorophyll content and photosynthetic electron transportrate, Regulation of plant growth and development |
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| grass specific | RAP-DB | [Os] "DYW-type pentatricopeptide repeat (PPR) protein, Mitochondrial RNA editing, Endosperm development and plant growth (Os01t0737900-01)" |
| grass specific | Knetminer-rice; Knetminer-wheat | |
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| grass specific | Maizemine | [Zm] homeobox-leucine zipper protein ATHB-15-like |
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| grass specific | RAP-DB | [Os] "Influx transporter for Zn and Cd, Zinc/cadmium uptake (Os05t0472700-01)" |
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| grass specific | RAP-DB | [Os] "Î²-Lectin domain protein, Salt stress response (Os04t0110100-01)" |
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| grass specific | Maizemine | [Zm] Cysteine proteinase inhibitor 8 |
| grass specific | RAP-DB | [Os] "P-type cyclin, PHO80 homologous protein, Coordination of phosphate starvation signaling and cell cycle progression under phosphate starvation stress (Os10t0563900-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Flavin monooxygenase-like enzyme , Auxin biosynthesis (Os07t0437000-01)" |
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| grass specific | RAP-DB | [Os] "Homeodomain-leucine zipper (HD-Zip) transcription factor, Regulation of panicle development (Os07t0581700- |
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| grass specific | RAP-DB | [Os] "Domain of unknown function, DUF1338, containing green-plant-unique protein, Regulation of starch synthesis and amyloplast development, Peripheral endosperm development (Os10t0463800-01)" |
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| grass specific | RAP-DB | [Os] "D-type cyclin 3;1, Regulation of branch formation, Maintenance of meristem activity (Os09t0111100-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "AGC kinase, Positive regulation of disease resistance (Os04t0488700-01);Similar to protein kinase KIPK. (Os04t0488700-02)" |
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| grass specific | RAP-DB | [Os] "Clade A type 2C protein phosphatase (PP2C), Negative regulation of drought tolerance through ABA signaling, Regulation of the trade-off between plant growth and drought tolerance (Os01t0846300-01);Similar to protein phosphatase 2C. (Os01t0846300-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Calmodulin isoform, Calmodulin-like protein (Os01t0810300-01)" |
| grass specific | RAP-DB | [Os] "Uclacyanin (UCL), Phytocyanin family protein, Regulation of photosynthesis and grain yield (Os03t0709100-01)" |
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| grass specific | RAP-DB | [Os] "MYB transcription factor, Regulation of organ identity and spikelet determinacy (Os04t0566600-01)" |
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| grass specific | RAP-DB | [Os] "NUCLEAR FACTOR Y (NF-Y) transcription factor, Control of heading date (Os08t0496500-01)" |
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| grass specific | RAP-DB | [Os] "Alpha-expansin, Mediation of the cell extension and growth, Root system architecture (Os01t0248900-01)" |
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| grass specific | RAP-DB | [Os] "Katanin regulatory subunit P80a, Microtubule stabilizer, Root growth via regulating the cell elongation and division (Os10t0494800-01)" |
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| grass specific | RAP-DB | [Os] "P-subfamily pentatricopeptide repeat (PPR) protein, nad5 splicing factor, Regulation of plant growth and pollen development, Splicing of mitochondrial nad5 introns |
| grass specific | RAP-DB; Knetminer-rice | [Os] "bHLH transcription factor, Positive regulation of chilling tolerance, Control of stomatal initiation, Regulation of mature stoma differentiation (Os11t0523700-01)" |
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| grass specific | RAP-DB | [Os] DNA-binding WRKY domain containing protein. (Os05t0321900-01) |
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| grass specific | RAP-DB | [Os] "GIPC glycosyltransferase, Ortholog of AtGMT1, Regulation of plant immunity and heading time |

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| grass specific | RAP-DB; Knetminer-rice | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Tapetum development and degeneration (Os02t0120500-01);Similar to Helix-loop-helix DNA-binding domain containing protein. (Os02t0120500- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Transcription factor, Regulation of Pi signaling and homeostasis, Tolerance to low-Pi stress (Os02t0139000-01)" |
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| grass specific | RAP-DB | [Os] "Disease resistance/zinc finger/chromosome condensation-like region domain containing protein. (Os04t0600500-01);BREVIS RADIX-like protein, Drought and salt stress response (Os04t0600500-02)" |
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| grass specific | RAP-DB | [Os] "Type-1 diacylglycerol acyltransferase, Triacylglycerol accumulation, Storage lipid biosynthesis (Os05t0196800-01)" |
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| grass specific | RAP-DB | [Os] "Tetratricopeptide repeats (TPRs)-containing RNA-binding protein, Broad-spectrum disease resistance (Os10t0548200-01);Hypothetical conserved gene. (Os10t0548200-02);Hypothetical conserved gene. (Os10t0548200-03)" |
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| grass specific | RAP-DB | [Os] "R2R3 MYB domain transcription factor, Target gene of OsmiR159, Positive regulation of BPH resistance (Os03t0578900-01)" |
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| grass specific | RAP-DB | [Os] "Homolog of Arabidopsis FACTOR OF DNA METHYLATION 1, Regulation of floral organ specification and meristem determination (Os02t0293300-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "IQ calmodulin-binding motif family protein, Positive regulator of brassinosteroid signalling, Regulation of grain width and weight (Os05t0187500-01)" |
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| grass specific | RAP-DB | [Os] "KEAP1 ortholog, Regulation of the antioxidant response, Response to abiotic stresses, Plant growth and development (Os01t0165200-01);Similar to KEAP1. (Os01t0165200- |
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| grass specific | RAP-DB | [Os] "Heat shock protein (HSP40), Putative tetratricopeptide repeat(TPR)-containing protein, Growth and development, salt tolerance, abiotic stress tolerance (Os02t0100300-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "C4HC3-type E3 ligase, Broad-spectrum resistance to viral, fungal, and bacterial pathogens (Os06t0554100-01)" |
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| grass specific | Maizemine | [Zm] Pre-mRNA splicing factor SF2 |
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| grass specific | RAP-DB | [Os] "Pentatricopeptide repeat protein, Mitochondrial nad7 transcript editing, Seed development (Os11t0213500-01)" |
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| grass specific | RAP-DB | [Os] "Similar to cDNA clone:J013093F08, full insert sequence. (Os02t0602100-01);CDK (cyclin-dependent kinase) family protein, Positive regulation of defense/stress response (Os02t0602100-02)" |
| grass specific | RAP-DB | [Os] "Member of the Bric-a-Brac/Tramtrack/Broad (BTB) family, BT1/BT2 ortholog, Negative regulation of nitrate uptake and nitrogen use efficiency (Os01t0908200-01)" |
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| grass specific | RAP-DB | [Os] "Type 2C protein phosphatase, Negative regulation of ABA signaling, Response to biotic and abiotic stresses (Os03t0192500-01)" |
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| grass specific | RAP-DB | [Os] "Calcineurin B-like protein (CBL)-interacting protein kinase 17, Grain filling, Regulation of grain development (Os05t0136200-01);Serine/threonine protein kinase domain containing protein. (Os05t0136200-02)" |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Argonaute protein, Reproductive phasiRNA biogenesis and function, Anther development at lower temperatures (Os06t0729300-01);Similar to Protein argonaute 1D. (Os06t0729300-02)" |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Axillary meristem formation (Os01t0831000-01)"; [Zm] Transcription factor LAX PANICLE |
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| grass specific | RAP-DB | [Os] "Similar to H0303G06.18 protein. (Os04t0629300-01);Chromatin remodeling factor 715, Sucrose non-fermenting 2 (Snf2) family protein, Cold stress response, Abscisic acid response, Response to M. oryzae infection (Os04t0629300-02)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] Cold acclimation protein COR413-TM1 (Os05t0566800-01) |
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| grass specific | RAP-DB; Maizemine | [Os] Similar to Leaf angle-associated protein. (Os09t0529300-01);Regulation of tiller angle (Os09t0529300-02); [Zm] Protein TILLER ANGLE CONTROL 1 |
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| grass specific | RAP-DB | [Os] "CC-type glutaredoxin, Panicle development (Os07t0151100-01);Plant-specific CC-type glutaredoxin, Control of meiosis entry in microsporocytes (Os07t0151100-02)" |
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| grass specific | RAP-DB | [Os] "MYELOBLASTOSIS (MYB) transcription factor 36a, Regulation of Casparian strip formation at the root endodermis (Os08t0248700-01)" |
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| grass specific | RAP-DB | [Os] "Orthologue of Arabidopsis MUTE, Basic helix-loop-helix (bHLH) transcription factor, Regulation of stomatal development, Control of guard mother cell fate progression |
| grass specific | RAP-DB | [Os] "Glyoxalase I-3, Seed longevity and vigor, Salt stress tolerance (Os03t0277500-01)" |
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| grass specific | RAP-DB | [Os] "Node-expressed Cd transporter, Putative cation/calcium (Ca) exchanger, Cd accumulation in the grain (Os03t0656500-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "NAC transcription factor, Regulation of secondary wall biosynthesis (Os06t0131700-01);No apical meristem (NAM) protein domain containing protein. (Os06t0131700-02)"; [Zm] Putative NAM (No apical meristem) protein |
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| grass specific | RAP-DB | [Os] "P-type pentatricopeptide repeat (PPR) protein, Mitochondrial RNA splicing and editing, Endosperm development and plant growth (Os07t0179000-01);Pentatricopeptide repeat domain containing protein. (Os07t0179000-02);Pentatricopeptide repeat domain containing protein. |
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| grass specific | Maizemine | [Zm] Twin-arginine translocation protein TatB-like |
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| grass specific | RAP-DB | [Os] "Transcription factor, Response to ethylene stimulus, Wound signaling (Os07t0685700-01)" |
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| grass specific | RAP-DB | [Os] "Similar to NAM1 protein (Fragment). (Os06t0267500-01);Transcription factor SUPPRESSOR OF GAMMA RESPONSE1, Control of DNA damage response and DNA repair, Oxidative stress response (Os06t0267500-02)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Similar to Homeobox protein. (Os03t0727000-01);Knotted1-like homeobox protein, Shoot apical meristem maintenance, Embryogenesis (Os03t0727000-02)"; [Zm] Homeotic protein knotted-1 |
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| grass specific | Maizemine | [Zm] Splicing factor |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Histone lysine demethylase, Stress-responsive H3K27me3(histon H3 lysine 27 trimethylation) demethylation (Os01t0907400-01)" |
| grass specific | RAP-DB | [Os] "Phosphate transporter, Phosphate uptake (Os06t0325200-01)" |
| grass specific | RAP-DB | [Os] "Catharanthus roseus receptor-like kinase1-like kinase, FERONIA-like receptor 3, Receptor-like kinase, Regulation of grain quality, Regulation of redox homeostasis during endosperm development (Os05t0318700-01);Similar to Resistance protein candidate |
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| grass specific | RAP-DB | [Os] "Nuclear factor Y (NF-Y) transcription factor A6, CCAAT box binding factor, Heme-associated protein (HAP)2G (Os07t0608200-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Short vegetative phase (SVP)-group MADS-box protein, Negative regulation of brassinosteroid responses (Os06t0217300-01)" |
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| grass specific | RAP-DB | [Os] "Allantoinase (EC:3.5.2.5), Ureide metabolism, Nitrogen molecular sensor (Os04t0680400-01)" |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "Vacuolar Na+/H+ antiporter, Salt tolerance (Os07t0666900-01);Similar to Sodium/hydrogen exchanger. (Os07t0666900-02)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Transcriptional activator, Regulation of grain shape (Os09t0448500-01)" |
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| grass specific | RAP-DB | [Os] "Sugar transporter, TAL effector-mediated susceptibility to bacterial pathogen (Os11t0508600-01)" |
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| grass specific | RAP-DB | [Os] "RING-H2 type E3 ligase, Drought and salinity tolerance, Regulation of ABA signaling (Os09t0478600-01)" |
| grass specific | RAP-DB | [Os] "MYB transcription factor, Nitrogen uptake and assimilation, Low-nitrogen adaptation (Os01t0637800-01)" |
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| grass specific | RAP-DB | [Os] "Hypothetical conserved gene. (Os03t0816500-01);Rice homolog of E.coli AlkB, DNA 6mA (N6-methyladenine) demethylation |
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| grass specific | RAP-DB | [Os] "No apical meristem (NAM) family protein, Awn development, Regulation of boundary formation, lateral organ separation and floral organ identity (Os02t0594800-01)" |
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| grass specific | RAP-DB | [Os] "Cyclin-dependent kinase F;2, Regulation of grain filling and grain size (Os12t0424700-01)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Fe homeostasis, Regulation of ferric (Strategy II) iron acquisition (Os04t0381700-01)" |
| grass specific | RAP-DB | [Os] "Homologue of Arabidopsis ELF4, Positive regulation of salt tolerance, Regulation of heading date, setting rate and grain size, Regulation of rice circadian clock (Os11t0621500-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Gamma-glutamylcysteine synthetase, Glutathione (GSH) synthesis protein (Os05t0129000-01);Similar to cDNA clone:J033125H02, full insert sequence. (Os05t0129000-02)"; [Zm] Glutamate--cysteine ligase |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "GRAS (GAI-RGA-SCR) plant-specific transcription factor, Maintenance of shoot apical meristem indeterminacy, Regulation of vegetative to reproductive phase change |
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| grass specific | RAP-DB | [Os] Receptor-like cytoplasmic kinase 55 (Os01t0936100-01);Similar to protein kinase family protein. |
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| grass specific | RAP-DB | [Os] "Putrescine hydroxycinnamoyl acyltransferase 4, Hydroxycinnamoylputrescine (HP) biosynthesis, Contribution to defense and cell death (Os09t0544000-01)" |
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| grass specific | RAP-DB | [Os] "Auxin/indoleacetic acid (Aux/IAA) transcription factor, Regulation of salt and drought tolerance (Os05t0523300-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Protein kinase, core domain containing protein. (Os04t0132500-01);Leucine-rich repeat receptor-like kinase, Cold tolerance (Os04t0132500-02)" |
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| grass specific | RAP-DB | [Os] "LysM receptor-like kinase, Arbuscular mycorrhizal (AM) symbiosis (Os03t0233300-01)" |
| grass specific | RAP-DB | [Os] "R2R3-MYB transcription factor, Regulation of leaf shape, cellulose synthesis and mechanical strength (Os08t0151300-01);Myb transcription factor domain containing protein. (Os08t0151300-02)" |
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| grass specific | Knetminer-rice; Knetminer-wheat | |
| grass specific | RAP-DB | [Os] "Bromo-domain-containing protein, Homologous to the Arabidopsis GTE4, Maintenance of root meristem, Cell cycle regulation (Os02t0250300- |
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| grass specific | RAP-DB | [Os] "Nitrate transporter, Regulation of tiller number and grain yield (Os07t0603800-01);Similar to peptide transporter PTR2. (Os07t0603800-02);Nitrate transporter, Regulation of tiller number and grain yield (Os07t0603800-03)" |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat; Maizemine | [Os] "Protein kinase PINOID, Control of polar auxin transport, Regulation of stigma and ovule initiation, Promotion of pistil and stamen development (Os12t0614600-01)"; [Zm] Protein kinase PINOID |

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| grass specific | RAP-DB | [Os] "R2R3-type MYB transcription factor, Sugar partitioning into anther (Os01t0274800-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "F-Box auxin receptor protein, Nuclear protein, Flag leaf inclination, Primary root growth, Crown root initiation, Seed development, Tillering (Os05t0150500-01)" |
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| grass specific | RAP-DB | [Os] "Polygalacturonase, Pectin degrading enzyme, Regulation of intercellular adhesion (Os03t0124900- |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "WRKY transcription factor, Defense response to sheath blight pathogen (Os03t0855100-01)" |
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| grass specific | RAP-DB | [Os] "2-C-methyl-d-erythritol 2,4-cyclodiphosphate synthase, Isoprenoid biosynthesis, Chloroplast development (Os02t0680600-01)" |

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| grass specific | RAP-DB | [Os] "MADS-box transcription factor, Inflorescence and spikelet development (Os03t0753100-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "Î²-carotene isomerase, Strigolactones biosynthesis (Os11t0587000-01);Hypothetical protein. (Os11t0587000-02)" |
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| grass specific | RAP-DB; Maizemine | [Os] "YABBY family transcription factor, Leaf development (Os10t0508300-01)"; [Zm] C2C2-YABBY transcription factor |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Phytosulfokine (PSK) receptor, Regulation of resistance to Xoc (Os02t0629400-01)" |
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| grass specific | RAP-DB | [Os] "Haloacid dehalogenase-like APase, Low-Pi-responsive haloacid dehalogenase (HAD)-like hydrolase, Pi homeostasis (Os03t0834050-01)" |
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| grass specific | RAP-DB | [Os] "ROOT HAIR DEFECTIVE-SIX LIKE (RSL) class I basic helix-loop-helix protein, bHLH transcription factor, Regulation of root hair development |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Homolog of Arabidopsis HY5 transcription factor, Photomorphogenesis, Positive regulation of serotonin biosynthesis, Negative control of UV-B tolerance (Os02t0203000-01)" |
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| grass specific | Maizemine | [Zm] Globulin |
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| grass specific | Knetminer-rice; | [Zm] Adenylate isopentenyltransferase |
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| grass specific | RAP-DB | [Os] N-terminal acetyltransferase A complex auxiliary subunit NAA15 (Os01t0617500-01);Similar to predicted protein. (Os01t0617500-02) |
| grass specific | RAP-DB | [Os] "Argininosuccinate lyase, Root elongation (Os03t0305500-01);Argininosuccinate lyase, Splicing variant with unknown function (Os03t0305500-02)" |
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| grass specific | RAP-DB | [Os] "Xylanase inhibitor, Defense response to pathogen (Os11t0701800-01)" |
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| grass specific | Maizemine | [Zm] Caffeoyl-CoA O-methyltransferase |
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| grass specific | RAP-DB | [Os] "Homeodomain transcription factor, Homeobox protein, Positive regulation of drought response |
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| grass specific | RAP-DB | [Os] "Similar to Type II inositol-1,4,5-trisphosphate 5-phosphatase 12 (EC 3.1.3.36) (At5PTase12) (FRAGILE FIBER3 protein). (Os02t0477700-01);Inositol polyphosphate 5-phosphatase, Development of internode cell-producing intercalary meristem |
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| grass specific | RAP-DB | [Os] "A20/AN1 zinc-finger protein, Response to multiple biotic stresses, Regulation of abiotic stress responses (Os09t0486500-02)" |
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| grass specific | RAP-DB | [Os] "U-box containing E3 ligase, Response to phosphate starvation (Os03t0240600-01)" |

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| grass specific | RAP-DB | [Os] "Leucine-rich repeat receptor-like kinase, Regulation of commissural vein pattern formation (Os08t0442700-01);Similar to predicted protein. (Os08t0442700-02)" |
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| grass specific | RAP-DB | [Os] SUMO protease (Os05t0207900-01);Hypothetical conserved gene. (Os05t0207900-02) |
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| grass specific | RAP-DB | [Os] "Leucine-rich repeat (LRR)-type receptor-like kinase, Regulation of chlorophyll degradation and leaf senescence (Os01t0223600-01)" |
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| grass specific | RAP-DB; Knetminer-wheat; Maizemine | [Os] "12-oxophytodienoate reductase (EC:1.3.1.42), Jasmonic acid (JA) biosynthesis (Os08t0459600-01)"; [Zm] 12-oxophytodienoate reductase 3 |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "CCT domain containing protein, Regulation of heading date (Os01t0835700-01)" |
| grass specific | RAP-DB | [Os] "Receptor-like cytoplasmic kinase, Various stress responses,  Regulation of resistance to bacterial leaf streak (BLS) (Os10t0548700-01);Hypothetical conserved gene. (Os10t0548700-02)" |
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| grass specific | RAP-DB | [Os] "Cellulose synthase A catalytic subunit 9, Cell wall biosynthesis and plant growth (Os09t0422500-01)" |
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| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "Histone H4 acetyltransferase, Regulation of grain weight, yield, and plant biomass (Os06t0650300-01)" |
| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "C2H2 zinc finger protein, Regulation of spikelet development (Os04t0444100-01)" |
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| grass specific | RAP-DB | [Os] "Galacturonosyltransferase-like protein, Glycosyltransferase family 8 (GT8) protein, Salt and cold stress response (Os04t0530900-01);Glycosyl transferase, family 8 protein. (Os04t0530900-02)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "GRAS family nuclear protein, Control of tillering, Regulation of panicle and tiller development, Regulation of axillary meristem (AM) formation (Os06t0610350-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Cyclophilin, Peptidyl-prolyl cis-trans isomerase, Auxin signal transduction, Lateral root initiation, Stress tolerance (Os02t0121300-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Metacaspase 4, Response to abiotic and biotic stresses (Os05t0496400-01)" |

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| grass specific | RAP-DB | [Os] "Similar to CDPK substrate protein 1. (Os09t0299000-01);G2-like family transcription factor, Negative regulation of flowering time (Os09t0299000-02)" |
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| grass specific | RAP-DB | [Os] "CC-NBS-LRR protein, Defense response, Control of crown root development (Os08t0246300-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "AT-hook motif-containing protein, AT-hook DNA-binding protein, Positive regulation of plant immunity in response to M. oryzae infection (Os08t0118000-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "A20/AN1 zinc-finger protein, Stress associated protein, Negative regulation of ABA and water-deficit stress signalling (Os03t0793000-01)" |
| grass specific | RAP-DB | [Os] Similar to Thiosulfate sulfurtransferase (EC 2.8.1.1) (Mercaptopyruvate sulfurtransferase Mst2/Rdh2) (EC 2.8.1.2). (Os12t0608600-01);Sulfurtransferase |
| grass specific | RAP-DB | [Os] "S-Domain receptor like kinase-20, Response to chilling in tolerant rice genotype, Response to Rice Stripe Virus, Response to B. glumae in resistant genotype (Os03t0556600-01)" |

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| grass specific | RAP-DB | [Os] "Chromatin remodeling factor 736, Sucrose non-fermenting 2 (Snf2) family protein, Salt and drought stress response, Response to M. oryzae infection (Os07t0434500-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "AT-rich interaction domain-containing protein, Shoot apical meristem (SAM) development (Os06t0622300-01);Hypothetical conserved gene. (Os06t0622300-02);Similar to DNA-binding protein. (Os06t0622300-03);Similar to DNA-binding protein. (Os06t0622300-04)" |
| grass specific | Maizemine | |
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| grass specific | RAP-DB | [Os] "Phosphate starvation-induced acid phosphatase, Phosphorus metabolism (Os01t0720400-01)" |
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| grass specific | RAP-DB | [Os] "Zinc transporter, Metal-detoxified transporter, ""Detoxification of excess Zn, Cu and Cd"" (Os01t0972200-01)" |
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| grass specific | RAP-DB | [Os] "Similar to Rf2 protein. (Os02t0274000-01);Similar to Rf2 protein. (Os02t0274000-02);Mitochondrial glycine-rich protein, Fertility restoration in LD-CMS (Os02t0274000-03)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Homeobox protein orthologous to Arabidopsis WUS, Initiation of axillary meristem formation (Os04t0663600-01)" |
| grass specific | RAP-DB | [Os] "Cellular retinaldehyde binding/alpha-tocopherol transport family protein. (Os01t0264700-01);Phosphatidylinositol transfer protein, Class III SEC14 protein |
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| grass specific | Maizemine | [Zm] Nucleobase-ascorbate transporter LPE1 |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor 069, Regulation of inflorescence axillary meristem formation during panicle development |
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| grass specific | in_predefined_specific_set | [Os] transporter required to control distribution of Si to leaves and panicle in rice |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "RPD3/HDA1-type histone deacetylase HDA704, Positive regulation of drought and salt tolerance, Control of stomatal aperture and density (Os07t0164100-01)" |
| grass specific | RAP-DB | [Os] Regulation of male gametogenesis during pollen development (Os05t0420800-01) |
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| grass specific | RAP-DB | [Os] WD40 protein (Os07t0572000-01) |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "ASYMMETRIC LEAVES2 (AS2)/LATERAL ORGAN BOUNDARIES (LOB) domain transcription factor, Crown root formation (Os03t0149100-01)"; [Zm] LOB domain-containing protein |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "ERF transcription factor, Mediation of the transition from spikelet to floret meristem, Determination of panicle branching and spikelet formation (Os07t0669500-01)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) protein, Proanthocyanidin synthesis, Regulation of proanthocyanidin pigmentation, (Nipponbare: loss-of-function mutation of Rc) (Os07t0211500-01)" |
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| grass specific | RAP-DB | [Os] "Metacaspase 8, Response to abiotic and biotic stresses (Os03t0389100-01)" |
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| grass specific | RAP-DB | [Os] WRKY1 (WRKY transcription factor 17). (Os01t0972800-01) |
| grass specific | RAP-DB | [Os] "HNH endonuclease domain-containing protein, Early chloroplast development (Os03t0169800-01)" |
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| grass specific | RAP-DB | [Os] S-Domain receptor like protein-1 (Os08t0179150-01) |
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| grass specific | RAP-DB | [Os] "Cytokinin oxidase, Regulation of cytokinin signaling pathway, ""Regulation of tillering, plant height, and panicle size"" (Os05t0374200-01)" |
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| grass specific | RAP-DB | [Os] "Regulation of leaf stomatal development and patterning, Development of root cortical aerenchyma (Os04t0637300-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Cytochrome P450 90B2, Brassinosteroid C-22 hydroxylase, Brassinosteroids biosynthesis (Os03t0227700-01)" |
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| grass specific | RAP-DB | [Os] Similar to WRKY transcription factor 32. (Os02t0770500-00) |
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| grass specific | RAP-DB | [Os] "Magnesium protoporphyrin IX methyltransferase, Light-dependent and photoperiod-regulated chlorophyll synthesis, Light intensity-involved plant growth (Os06t0132400-01)" |
| grass specific | RAP-DB; Knetminer-wheat | [Os] "MYB-related transcription factor, Mediation of response to ABA and drought (Os04t0583900-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] Homologue of FLOC1 (FLO2-interacting cupin domain protein 1) (Os03t0197300-01) |
| grass specific | Maizemine | [Zm] Peroxidase |
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| grass specific | RAP-DB | [Os] "R2R3-MYB transcription factor, Promotion of seed germination under deep-sowing conditions (Os11t0700500-01)" |
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| grass specific | RAP-DB | [Os] "C-type ABC transporter, Cadmium tolerance and accumulation (Os04t0209200-01)" |
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| grass specific | Maizemine | [Zm] Rust resistance kinase Lr10 |
| grass specific | RAP-DB | [Os] "AUX/IAA transcription factor, Development of the dorsal aleurone of early rice grains (Os11t0221300-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Short-chain alcohol dehydrogenase, ABA biosynthesis, Lesion mimic formation, Disease-resistance, Seed dormancy (Os03t0810800-01)" |
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| grass specific | RAP-DB | [Os] "Protein of unknown function DUF617, plant family protein. (Os02t0709600-01);Ortholog of Arabidopsis MIZU-KUSSEI1 (MIZ1), DUF617 domain containing protein, Drought and salt stress tolerance (Os02t0709600-02)" |
| grass specific | RAP-DB | [Os] LIM binding protein domain containing protein. (Os06t0126000-01);SEUSS-LIKE protein (Os06t0126000-02);Hypothetical conserved gene. (Os06t0126000-04);Hypothetical conserved gene. (Os06t0126000-05) |
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| grass specific | RAP-DB | [Os] "Conserved hypothetical protein. (Os01t0524500-01);Transcription factor, Regulation of nutrient mobilization in germination (Os01t0524500-02)" |
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| grass specific | RAP-DB | [Os] Leaf development (Os04t0415000-01) |

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| grass specific | RAP-DB | [Os] "Fertilization barrier 2 protein, Double fertilization (Os11t0168000- |
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| grass specific | RAP-DB | [Os] "Guanosine-tetraphosphate (ppGpp) synthase, RelA/SpoT Homolog 3c (Os02t0699400-01)" |
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| grass specific | RAP-DB | [Os] "PHD-finger transcription factor, Regulation of Ubisch bodies and pollen wall formation (Os03t0716200-01)" |
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| grass specific | RAP-DB | [Os] "RING-finger ubiquitin E3 ligase, Phosphate homeostasis, Positive regulation of Pi accumulation and Pi signaling (Os12t0538500-01)" |
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| grass specific | Knetminer-rice | |
| grass specific | RAP-DB | [Os] "Leucine-rich repeat (LRR) protein, Inhibitor of fungal polygalacturonase, Defence response (Os09t0491612-01)" |
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| grass specific | RAP-DB | [Os] "Rnase III family protein, Shoot apical meristem (SAM) formation and maintenance (Os04t0509300-01);Rnase III family protein, Trans-acting siRNA3 (ta-siRNA)(TAS3) biogenesis (Os04t0509300-02)" |
| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] Similar to WRKY transcription factor 43. (Os05t0567200-00) |
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| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "Bcl-2-associated athanogene (BAG) protein, BAG protein containing a calmodulin-binding domain, Gene regulation and stress responses (Os02t0719700-01)" |
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| grass specific | Knetminer-rice | |

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| grass specific | RAP-DB | [Os] "C2H2 zinc-finger transcription factor, Floral organ identity, Cellular proliferation (Os01t0129200-01)" |
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| grass specific | RAP-DB | [Os] "Homolog of AtSCD1, Clathrin-related vesicular trafficking (Os01t0575500-01)" |
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| grass specific | RAP-DB | [Os] "CO (CONSTANS)-like protein, Zinc finger protein (Os03t0351100-01);Similar to CONSTANS-like protein CO9 (Fragment). (Os03t0351100-02)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Leucine-rich repeat receptor-like kinase, Mn2+/Mg2+-dependent serine/threonine (Ser/Thr) kinase, Ca2+-independent Ser/Thr kinase, Negative regulation of polar auxin transport, Root development (Os05t0486100-01);Hypothetical conserved gene. (Os05t0486100-02)" |
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| grass specific | RAP-DB | [Os] Phytosulfokine (PSK) receptor-like protein (Os07t0107800-01);Hypothetical conserved gene. (Os07t0107800-02) |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Exocyst subunit EXO70 family protein, Positive regulation of disease resistance (Os01t0827500-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Retinoblastoma-related protein, Control of pollen development (Os11t0533500-01);Similar to Retinoblastoma-related protein 2b (Fragment). (Os11t0533500-02)"; [Zm] Retinoblastoma-related protein 2 |
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| grass specific | RAP-DB | [Os] "S-Domain receptor like kinase-2, Response to submergence, Response to bacterial and fungal infection (Os01t0668901-00)" |

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| grass specific | RAP-DB | [Os] "DNA replication helicase 2_4, Salt stress response (Os07t0495900-01);Similar to predicted protein. (Os07t0495900-02);Similar to predicted protein. (Os07t0495900-03);Similar to predicted protein. |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Receptor-like kinase, Heat tolerance (Os06t0203800-01)" |
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| grass specific | RAP-DB | [Os] "Homolog of Arabidopsis BIC1 (Blue-light Inhibitor of Cryptochrome 1), Control of blue light-induced leaf sheath elongation, Regulation of epidermal cell elongation |
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| grass specific | RAP-DB | [Os] "tRNA nucleoside methyltransferase, Methyltransferase for the 2'-O-methyladenosine nucleoside modification, Regulation of salt stress tolerance, ABA hormone |
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| grass specific | RAP-DB | [Os] "Basic leucine zipper (bZIP) transcription factor, Negative regulator of cold and drought stress response (Os06t0662200-01)" |
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| grass specific | Knetminer-rice; Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "NAM/CUC2-like transcription factor 15, Regulation of tolerance to zinc deficiency and cadmium stress (Os07t0684800-01);Similar to NAM / CUC2-like protein. (Os07t0684800- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Amino acid transporter, Regulation of grain protein content and nutritional quality (Os01t0878700-02);Amino acid transporter, transmembrane domain containing |
| grass specific | RAP-DB | [Os] "B3 DNA-binding domain-containing transcription factor, Flowering time regulation, Repression of flowering activator Ehd1 and its downstream genes by binding to the promoter of the Ehd1 gene |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "NAC-domain protein, Drought tolerance (Os11t0126900-01)" |

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| grass specific | | |
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| grass specific | RAP-DB | [Os] "Ankyrin-repeat protein, Herbivore-induced defense response, Blast disease resistance (Os01t0194300-01)" |
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| grass specific | RAP-DB | [Os] "GnK2 domain containing receptor-like kinase-8, Response to chilling stress in tolerant rice genotype Volano, Response to Xanthomonas oryzae pv. oryzae in resistant rice genotype IRBB21 (Os10t0136500-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Argonaute (AGO) protein, Broad-spectrum virus resistance, Male gametophyte development (Os07t0471300-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Ortholog of ZmLG2, bZIP transcriptional factor, Lamina joint positioning and differentiation (Os01t0859500-01)"; [Zm] Transcription factor LG2 |
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| grass specific | RAP-DB | [Os] "ATP-dependent DNA helicase 2 subunit KU70, Maintenance of chromosomal stability, Developmental growth, Telomere length regulation (Os07t0184900-01);Hypothetical conserved gene. (Os07t0184900-02);Similar to Ku70 homolog. (Os07t0184900-03);Hypothetical conserved gene. (Os07t0184900-04)" |
| grass specific | RAP-DB | [Os] "APETALA2/ETHYLENE RESPONSIVE FACTOR (AP2/ERF) transcription factor, Promotion of flowering under long-day (LD) conditions (Os08t0442400-01)" |
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| grass specific | RAP-DB | [Os] MYB3R transcription factor (Os05t0459000-01) |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Small RNA methyltransferase, Small RNA stabilization, Regulation of shoot development (Os07t0164000- |
| grass specific | Maizemine | [Zm] G-box-binding factor 1 |
| grass specific | RAP-DB | [Os] "Class D glycine-rich RNA recognition motif (RRM) containing protein, RNA-binding glycine-rich (RBG) protein, Cold stress tolerance, Regulation of ABA signalling pathway (Os08t0492100-01);Hypothetical conserved gene. (Os08t0492100-02);Paraneoplastic encephalomyelitis antigen family protein. (Os08t0492100- |
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| grass specific | RAP-DB | [Os] BRASSINOSTEROID INSENSITIVE 1 (BRI1)-associated receptor kinase (Os01t0171000-01);Similar to Leucine-rich repeat receptor-like kinase. (Os01t0171000-02) |
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| grass specific | Knetminer-rice | |
| grass specific | RAP-DB | [Os] "Coenzyme F420 hydrogenase/dehydrogenase beta subunit, N-terminal domain containing protein. (Os04t0320100-01);7-hydroxymethyl chlorophyll a reductase, Promotion of chlorophyll degradation, Modulation of cell death signaling (Os04t0320100-02)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Transcription factor, Asymmetric division of the cortex/endodermis progenitor cell in the root, Formation of root endodermis and leaf stomata (Os12t0122000-01)"; [Zm] GRAS domain-containing protein |
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| grass specific | RAP-DB | [Os] "Coiled-coil protein, Homologous chromosome pairing and synapsis in meiosis (Os10t0405500-01)" |

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| grass specific | RAP-DB | [Os] "NAC transcription factor, Regulation of starch and storage protein synthesis (Os01t0104500-01)" |
| grass specific | RAP-DB | [Os] "Secreted protein with a CLE domain, Maintenance of the floral meristem (FM) and the vegetative shoot apical meristem (SAM) (Os02t0324400- |
| grass specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Class-I TCP transcription factor, Water-deficit and salt stress response, Negative regulation of tillering (Os06t0226700-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "OVATE domain-containing protein, Negative modulation of brassinosteroid (BR) response, Modulation of plant architecture |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Homeodomain-leucine zipper (HD-ZIP) transcription factor, Drought tolerance, Lignin biosynthesis, Stomatal closure (Os08t0292000-01);Hypothetical conserved gene. |
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| grass specific | Maizemine | [Zm] Alpha-amylase tetrameric inhibitor subunit CM3 |
| grass specific | RAP-DB | [Os] "HLH (helix-loop-helix) protein, Mediation of defense to brown planthopper (BPH) (Os07t0676600-01)" |
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| grass specific | RAP-DB | [Os] "Putative mitochondrial outer membrane protein 64, Negative regulation of brown planthopper (BPH) and striped stem borer (SSB) resistance, Resistance to both piercing-sucking and chewing insects (Os02t0754500- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "AAA-ATPase family protein, Resistance to blast fungus, Induced by salicylic acid (SA) treatment (Os06t0697600-01)" |
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| grass specific | RAP-DB | [Os] "Zinc finger homeodomain (ZF-HD) class homeobox transcription factor, Rice morphogenesis, Modulation of leaf rolling (Os09t0466400-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Prohibitin, Defense response and/or programmed cell death through the mitochondrial function (Os04t0462900-01);Similar to Prohibitin. (Os04t0462900-02);Similar to prohibitin2. (Os04t0462900-05);Similar to prohibitin2. |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Starch phosphorylase, Alpha-glucan phosphorylase, Starch biosynthesis in rice endosperm at low temperature (Os03t0758100-01)" |
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| grass specific | RAP-DB | [Os] "L-ascorbate oxidase, Cold, salt, drought stress response (Os06t0567900-01)" |
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| grass specific | RAP-DB | [Os] "Putative RING E3 ubiquitin (Ub) ligase, Negative regulator of drought and salt stress responses, Positive factor of cold stress response |
| grass specific | RAP-DB; Knetminer-rice | [Os] "LOB (Lateral Organ Boundaries) domain-like protein, Glume formation (Os02t0820500-01)" |
| grass specific | RAP-DB | [Os] "mRNA cap-binding protein, Rice homolog of a cap-binding protein 20 kD subunit (CBP20), Component of the heterodimeric nuclear cap-binding complex (CBC), Pre-mRNA splicing, mRNA stability and transcription, Regulation of amylose content in rice seeds (Os02t0612300-01)" |
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| grass specific | RAP-DB | [Os] "RNA binding protein, mRNA localization, Regulation of development (Os04t0625800-01);RNA binding protein, mRNA localization, Regulation of development (Os04t0625800-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Homolog of Rad52 (Radiation sensitive 52), Mediation of homologous recombination and DNA repair, (Os03t0851500-01)" |
| grass specific | RAP-DB | [Os] "MYB transcription factor, Regulation of cellulose synthesis, Promotion of nitrogen utilization and biomass production, Secondary cell wall formation (Os01t0285300-01)" |

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| grass specific | RAP-DB | [Os] "Triose phosphate isomerase (EC 5.3.1.1), Abiotic stress response, Response to methylglyoxal (cytotoxin) (Os01t0841600-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to cDNA clone:J023121E19, full insert sequence. (Os04t0649100-01);Pathogenesis-related transcriptional factor and ERF domain containing protein. (Os04t0649100-02);APETALA2 transcription factor, Seed shattering through abscission zone (AZ) |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein, Important roles in rice immunity, Response to M. oryzae infection (Os01t0874700-01);GOLD domain containing protein. (Os01t0874700-02);Similar to patellin-1. |
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| grass specific | RAP-DB | [Os] "Bicyclic triterpene poaceatapetol synthase, Pollen coat formation (Os08t0223900-01)" |
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| grass specific | RAP-DB | [Os] "Heavy metal transporter protein, Regulation of yield and grain Fe-Zn content (Os07t0623200-01);ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter domain containing protein. (Os07t0623200-02);ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter domain containing protein. (Os07t0623200-03)" |
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| grass specific | RAP-DB | [Os] "S-type euonymus-related lectin (EUL), Response to ABA treatment (Os01t0104400-01);Ricin B-related lectin domain containing protein. (Os01t0104400-02);Ricin B-related lectin domain containing protein. (Os01t0104400-03)" |
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| grass specific | RAP-DB | [Os] "Plant-specific protein containing a glutamine-rich region and a conserved motif, Controls of phyllotaxy by affecting cytokinin signaling |
| grass specific | RAP-DB | [Os] "Coiled-coil domain-containing protein, Transcription activator, Pollen wall development, Pollen intine biosynthesis (Os01t0755100-01);Conserved hypothetical protein. (Os01t0755100-02)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Hypothetical conserved gene. (Os01t0846450-01);Homolog of Arabidopsis thaliana HEN1 suppressor 1, Heading date (Os01t0846450-02)" |
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| grass specific | RAP-DB | [Os] "Nuclear envelope membrane protein (NEMP)-domain-containing protein, Regulation of embryo sac development and fertilization (Os03t0430000-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Nuclear protein belonging to the SNF2 subfamily SMARCAL1,  Chromatin remodeler, Regulation of both male and female reproductive development (Os07t0636200-01);Similar to chromatin remodeling complex subunit. (Os07t0636200-02);Similar to chromatin remodeling complex subunit. (Os07t0636200-03)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Pectate lyase-like protein, Pollen development (Os02t0214400-01)" |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Flavin monooxygenase-like enzyme , Auxin biosynthesis (Os01t0645400-01);Flavin monooxygenase-like enzyme , Auxin biosynthesis (Os01t0645400-02)"; [Zm] Flavin-containing monooxygenase |

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| grass specific | RAP-DB; Knetminer-rice | [Os] "Germin-like protein, Fungal blast and bacterial blight resistance (Os02t0532500-01)" |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Regulation of ABA signaling and biosynthesis, Drought resistance (Os02t0766700-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Gibberellin biosynthesis enzyme, Gibberellin 20 oxidase-4, Homologous to OsGA20ox2 (Sd1), GA metabolism, Regulation of panicle length (Os05t0421900-01)" |
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| grass specific | RAP-DB | [Os] "Isoflavone reductase-like protein, Homeostasis of reactive oxygen species (ROS) (Os01t0106400-01)" |

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| grass specific | RAP-DB | [Os] "DNA binding with one finger transcription factor, Intrinsically disordered protein, Thermal stress tolerance (Os10t0496000-02)" |
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| grass specific | RAP-DB | [Os] "Iron regulated bHLH transcription factor, Response to iron deficiency, Regulation of iron homeostasis (Os03t0379300-01);Helix-loop-helix DNA-binding domain containing protein. (Os03t0379300-02);Iron-related transcription factor, Response to iron deficiency, Regulation of iron homeostasis (Os03t0379300-03)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "MADS box transcription factor, Pollen maturation (Os11t0658700-01);MADS domain transcription factor, pollen maturation (Os11t0658700-02)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Chloroplast ribonucleoprotein, Drought and cold stress tolerance, Regulation of chloroplast mRNA stability (Os09t0565200-02)"; [Zm] 31 kDa ribonucleoprotein |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Similar to Protein kinase domain containing protein, expressed. (Os03t0710100-01);Rice HOP2 homolog, Promotion of homologous pairing and synapsis in meiosis, Regulation of crossover maturation (Os03t0710100-02)" |
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| grass specific | RAP-DB | [Os] "Pectin methylesterase, Regulation of diurnal flower opening time, Regulation of the stiffness of the lodicule cell wall (Os07t0675100-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "Similar to Isoform 2 of MADS-box transcription factor 14. (Os03t0752800-01);APETALA1 (AP1)/ FRUITFULL (FUL)-like MADS box transcription factor, Specification of inflorescence meristem identity (Os03t0752800-02)"; [Zm] Fruitful-like MADS-box transcription factor (Fragment) |
| grass specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "AT-hook motif and PPC domain containing protein, Drought tolerance, Regulation of root development under drought condition, Oxidative stress response, Regulation of the content of chlorophyll (Os11t0149100-01)" |
| grass specific | RAP-DB | [Os] "Purine permease, Modulation of cytokinin distribution, Regulation of plant height and grain weight (Os03t0187800-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "WUS-type homenodomain protein, Leaf development (Os11t0102100-01);WUS-type homenodomain protein, Leaf development (Os11t0102100-02)"; [Zm] WUSCHEL-related homeobox 3A |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Leucine-rich repeat receptor kinase, Regulation of floral meristem size (Os06t0717200-01)"; [Zm] THICK TASSEL DWARF1 |
| grass specific | RAP-DB; Knetminer-rice | [Os] "CONSTANS-like transcriptional activator, Negative regulation of flowering (Os07t0667300-01)" |
| grass specific | RAP-DB | [Os] "Similar to OsGA2ox1. (Os05t0158600-01);GA 2-oxidase1, GA metabolism (Os05t0158600-02)" |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "Transcriptional activator of gibberellin-dependent alpha-amylase expression, Regulation of nutrient mobilization in germination (Os01t0812000-01);Myb-like transcription factor, Induction of alpha-amylase in aleurone, Pollen development (Os01t0812000-02);Similar to cDNA clone:J033109N02, full insert sequence. (Os01t0812000-03)" |
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| grass specific | RAP-DB | [Os] "Protein phosphatases type-2C (PP2C) protein phosphatase, Regulation of phosphate homeostasis (Os07t0507000-01)" |
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| grass specific | Knetminer-rice |  |
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| grass specific | RAP-DB | [Os] "Ortholog of Arabidopsis FASCIATA1, Chromatin assembly factor-1 p150 subunit, Meristem maintenance, Regulation of cell-cycle period (Os01t0896300-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "bZIP transcription factor, Regulation of endoplasmic reticulum stress response (Os05t0411300-01);Similar to DNA binding protein. |
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| grass specific | RAP-DB | [Os] "Bcl-2-associated athanogene (BAG) protein, BAG protein containing a calmodulin-binding domain, Gene regulation and stress responses (Os11t0506800-01)" |
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| grass specific | RAP-DB | [Os] "AP2/EREBP family transcription factor, Tolerance to heat and drought stress (Os08t0521600-01)" |
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| grass specific | RAP-DB | [Os] "Nuclear factor Y (NF-Y) transcription factor A11, CCAAT box binding factor, Heme-associated protein, Drought and salt stress |
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| grass specific | RAP-DB | [Os] "Similar to Protochlorophyllide reductase B, chloroplastic. (Os10t0496900-01);NADPH: protochlorophyllide oxidoreductase, Chlorophyll synthesis (Os10t0496900-02)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Typical DNA-binding bHLH protein, Negative regulation of grain length and weight (Os05t0139100-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "Succinate dehydrogenase iron-protein subunit (SDHB). (Os08t0120000-01);Succinate dehydrogenase iron-protein subunit (SDHB). (Os08t0120000-02);Iron-sulfur subunit of succinate dehydrogenase, Leaf senescence, Grain yield (Os08t0120000-04);Ribosomal protein S14 (Os08t0120000-05)"; [Zm] Succinate dehydrogenase [ubiquinone] iron-sulfur subunit |

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| grass specific | RAP-DB | [Os] "Amino acid permease, A member of the amino acid transporter (AAT) family, Regulation of tillering and grain yield, Regulation of neutral amino acid transport (Os12t0194900-01)" |
| grass specific | RAP-DB | [Os] "S-Domain receptor like kinase-48, Response to drought and chilling in tolerant genotypes (Os01t0224000- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "MADS box transcription factor, Regulation of seed size, Heat stress response during reproductive development (Os03t0582400-01)" |
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| grass specific | RAP-DB | [Os] "Pectin methylesterase, Regulation of diurnal flower opening time, Regulation of the stiffness of the lodicule cell wall (Os01t0312500-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Homolog of the Arabidopsis TAPETUM DETERMINANT1 (TPD1) protein, Regulation of early anther cell differentiation (Os12t0472500-01)" |
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| grass specific | RAP-DB | [Os] "MADS-box transcription factor, Regulation of early seed development (Os09t0116800-01)" |
| grass specific | Knetminer-rice; Knetminer-wheat | |
| grass specific | RAP-DB | [Os] "Similar to Transcription factor RF2a. (Os09t0516200-01);bZIP DNA-binding protein, Disease resistance, Vascular development (Os09t0516200- |
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| grass specific | RAP-DB | [Os] "D-cysteine desulfhydrase, H2S biosynthesis (Os02t0773300-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "MADS-box transcription factor, Regulation of floral identity, Regulation of amylose content at high temperature (Os08t0531700-01)" |
| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "SUMO (Small Ubiquitin-like Modifier) Protease, Salt tolerance (Os06t0487900-01);Hypothetical conserved gene. (Os06t0487900-02)"; [Zm] Ubiquitin-like-specific protease 1D |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "ABC transporter, White-brown complex homolog protein, Silicon-promoted formation of Casparian bands in the exodermis (Os10t0442900-01)" |
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| grass specific | RAP-DB | [Os] "Membrane-bound NAC-like transcription factor, Transcriptional repressor, Suppression of flowering (Os08t0562200-02);Hypothetical conserved gene. (Os08t0562200-03)" |
| grass specific | RAP-DB | [Os] "Xylan acetyltransferase, Resistance to bacterial leaf blight disease (Os11t0107000-01)" |
| grass specific | | |
| grass specific | RAP-DB; Maizemine | [Os] "Similar to Lysine ketoglutarate reductase/saccharopine dehydrogenase. (Os02t0783700-01);Lysine ketoglutarate reductase/saccharopine dehydrogenase, Lysine-degrading enzyme in developing grain (Os02t0783700-02)"; [Zm] Lysine- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Transcriptional factor, SBP (SQUAMOSA promoter Binding Protein) DNA binding protein, Control of laminar joint and ligule development (Os04t0656500-01)" |
| grass specific | RAP-DB | [Os] "Proline (Pro) and Î³-aminobutyric acid (GABA) transporter, Stress tolerance, Cadmium stress tolerance (Os01t0908600-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Heavy metal transport/detoxification protein domain containing protein. (Os04t0667600-01);Copper metallochaperone, Heavy metal-transporting ATPase (HMA) isoprenylated plant protein, Delivery of metal micronutrients (Os04t0667600-02)" |
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| grass specific | RAP-DB | [Os] "Poly(ADP-ribose) polymerase, Double-strand break (DSB) repair, Likely to be involved in the Ku-independent alternative non-homologous end-joining pathway (A-NHEJ pathway) (Os02t0530600-01);Similar to Poly. (Os02t0530600-02)" |

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| grass specific | Maizemine | [Zm] Thaumatin |
| grass specific | RAP-DB; Maizemine | [Os] "RNA-dependent RNA polymerase 2, Positive regulation of DNA methylation in stamens and pistils, Biosynthesis of siRNAs, Male and female reproductive development (Os04t0465700-01)"; [Zm] RNA- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "DUF642 domain containing protein, Control of diurnal flower opening time (Os01t0611000-01);Hypothetical conserved gene. |
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| grass specific | Knetminer-rice; Knetminer-wheat | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "WRKY transcription factor, Drought tolerance (Os07t0680400-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "SQUAMOSA promoter-binding-like protein 2, miR156-target gene, Signal transduction induced by hydrogen peroxide (Os01t0922600- |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "DNA methyltransferase, Maintenance of methylation, Gene silencing (Os07t0182900-01);DNA methyltransferase, Maintenance of CpG methylation after DNA replication (Os07t0182900-02);DNA methyltransferase, Maintenance of CpG methylation after DNA replication (Os07t0182900-03);DNA methyltransferase, Maintenance of CpG methylation after DNA replication (Os07t0182900-04);DNA methyltransferase, Maintenance of CpG methylation after DNA replication (Os07t0182900-05);DNA methyltransferase, Maintenance of CpG methylation after DNA replication (Os07t0182900-06)" |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "TCP family transcription factor, Regulation of palea development, Control of floral zygomorphy (Os09t0410500-01)"; [Zm] Retarded palea 1 protein (Fragment) |
| grass specific | RAP-DB; Knetminer-rice | [Os] "bHLH transcription factor, Regulation of early tapetum development, Anther development (Os07t0549600-01)" |
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| grass specific | RAP-DB | [Os] S-Domain receptor like kinase-32 (Os04t0634000-01) |
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| grass specific | RAP-DB | [Os] "As-responsive RING E3 ubiquitin ligase 3, Positive regulation of plant response to arsenate (AsV) stress (Os08t0414200-01)" |
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| grass specific | RAP-DB | [Os] "Membrane-associated kinase-9, Response to submergence (Os07t0141100-01)" |
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| grass specific | RAP-DB | [Os] "Rice ortholog of Arabidopsis TDF1, A member of the R2R3 MYB family, Essential regulator for tapetum programmed cell death, Tapetum development (Os03t0296000-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] Similar to WRKY1 (WRKY transcription factor 17). (Os03t0335200-01) |
| grass specific | RAP-DB; Knetminer-rice | [Os] "WRKY transcription factor, Component in the signal transduction pathways of auxin response, Disease resistance (Os03t0321700-01)" |

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| grass specific | RAP-DB | [Os] "MADS-domain-containing protein, Sexual reproduction (Os03t0215400-01)" |
| grass specific | Knetminer-rice |  |
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| grass specific | RAP-DB | [Os] Component of Exo70 exocyst complex (Os02t0505400-02) |
| grass specific | RAP-DB | [Os] "MYB transcription factor, Drought and salt stress resistance (Os04t0676700-01);Similar to H0101F08.8 protein. (Os04t0676700- |
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| grass specific | RAP-DB | [Os] "UDP:glucose salicylic acid glucosyltransferase, Chemically-induced disease resistance |
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| grass specific | RAP-DB | [Os] "Acetyl-serotonin methyltransferase, Melatonin biosynthesis (Os01t0753300-01)" |
| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "GARP DNA-binding protien, GARP (Golden2, ARR-B and Psr1) transcription factor, Leaf polarity modeling, Regulation of anther dehiscence (Os09t0395300-01)"; [Zm] Putative transcription factor RL9 |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "B-Box domain-containing protein 11, BBX transcription factor, Regulation of spikelet development and yield production (Os04t0493000-01)" |
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| grass specific | RAP-DB | [Os] "Serine/threonine protein kinase, Never-in-mitosis A (NIMA)-related kinase, Pollen germination |
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| grass specific | RAP-DB | [Os] "BURP domain containing protein, Pollen development (Os08t0496800- |
| grass specific | RAP-DB | [Os] "Protein phosphatase 2C family protein, Salinity tolerance in the seedling stage (Os01t0656200-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Extracellular kinase-1, Response to drought in tolerant genotype, Response to submergence, Response to Rice Stripe Virus and R. solani (Os02t0710500-01)" |
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| grass specific | RAP-DB | [Os] "Basic leucine zipper transcription factor 16, bZIP transcription factor 16, Positive regulation of drought resistance (Os02t0191600-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "A member of the Ubiquitin-Like (UBL) Protein subfamily, Defense against rice stripe virus (RSV) infection (Os02t0628800-01)" |
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| grass specific | RAP-DB | [Os] "Similar to OCL1 homeobox protein. (Os04t0569100-01);Homeodomain-leucine zipper IV protein, GL2-type homeobox protein, Transcription factor, Promotion of flowering time preferentially under long days, Positive regulation of cuticular wax biosynthesis, Drought stress response (Os04t0569100-02)" |
| grass specific | RAP-DB | [Os] "MYB-CC family protein, Pi-starvation signaling (Os07t0438800-01);Similar to Phosphate starvation response regulator-like protein. (Os07t0438800-02)" |
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| grass specific | RAP-DB | [Os] "A member of S40 gene family, Leaf senescence (Os01t0727500-02)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to H0124B04.8 protein. (Os04t0681900-01);Acyl-CoA-binding protein , Stress response (Os04t0681900-02)" |
| grass specific | RAP-DB; Maizemine | [Os] "SET domain-containing histone methyltransferase, H3 lysine 36 (H3K36) methylation, Flowering promotion (Os09t0307800-01);Similar to histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20specific. (Os09t0307800-02)"; [Zm] histone-lysine N-methyltransferase ASHH3-like |
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| grass specific | RAP-DB; Maizemine | [Os] "WHIRLY (WHY) family protein, Chloroplast RNA editing and splicing, Early chloroplast development (Os06t0145800-01)"; [Zm] single-stranded DNA-binding protein WHY1 |
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| grass specific | RAP-DB | [Os] "G1-like protein 1, Arabidopsis LSH1 and Oryza G1 (ALOG) gene family protein, Control of inflorescence development, Regulation of inflorescence branching (Os02t0166800- |
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| grass specific | RAP-DB | [Os] "Ribonucleotide reductase, Chloroplast biogenesis (Os02t0804900-01)" |
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| grass specific | RAP-DB | [Os] "MADS-box transcription factor 8, Floral organ determination, Seed germination, ABA signaling and catabolism, Hybrid weakness (Os09t0507200-01)" |
| grass specific | RAP-DB | [Os] "Ortholog of Arabidopsis ELF4, Positive regulation of salt stress (Os08t0366200-01)" |
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| grass specific | RAP-DB | [Os] "Glutamate receptor-like channel, Brassinosteroid (BR)-mediated internode elongation, Root-to-shoot systemic wound signaling (Os07t0522600-01);Similar to Glutamate receptor 3.4 precursor (Ligand-gated ion channel 3.4) (AtGLR4). Splice isoform 2. |
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| grass specific | RAP-DB | [Os] "F-box protein, Regulation of tiller angle and spikelet development (Os04t0208400-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Inactive leucine-rich-repeat receptor-like kinase (LRR-RLK), Leaf angle regulation, Positive regulation of BR signal transduction (Os04t0487200- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Homolog of the Arabidopsis EARLY FLOWERING 3 protein, Photoperiodic flowering, Short-day/long-day promotion (Os06t0142600-01)" |
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| grass specific | Knetminer-wheat | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Heat shock factor, Transcription factor, ABA-mediated salt stress tolerance, Response to osmotic stress (Os01t0733200-01)" |
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| grass specific | RAP-DB | [Os] "CRT-like transporter, Glutathione homeostasis, Arsenic tolerance (Os01t0955700-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "MIKC-type MADS-box protein, Flowering activator, Short-day/long-day promotion of flowering (Os03t0122600-01);Transcription factor, MADS-box domain containing protein. (Os03t0122600-02)"; [Zm] Suppressor of overexpression of CO1 |
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| grass specific | RAP-DB | [Os] "U-box E3 ubiquitin ligase, Drought tolerance (Os10t0552400-01)" |
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| grass specific | RAP-DB | [Os] "Cytochrome P450 monooxygenase, Tolerance to acetolactate synthase-inhibiting herbicides (pseudogene) |
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| grass specific | RAP-DB | [Os] "Universal stress protein, Resistance against M. oryzae (Os07t0551400-01);Similar to USP family protein. (Os07t0551400-02)" |
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| grass specific | RAP-DB | [Os] "Thylakoid rhodanese-like protein, Thylakoid membrane anchor (Os02t0257300-01)" |
| grass specific | in_predefined_specific_set | [Os] production of tricin a secondary metabolite and lignin monomer specific to grasses / monocots |
| grass specific | | |
| grass specific | RAP-DB | [Os] "A-type response regulator, Cytokinin signaling (Os04t0442300-01);A-type response regulator, Cytokinin signaling (Os04t0442300- |

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| grass specific | RAP-DB | [Os] "HTH_MYB-like transcription factor, Positive regulation of leaf inclination (Os04t0665600-01);Splicing variant of REGULATOR OF LEAF INCLINATION 1 (RLI1) containing MYB DNA binding domain, Regulation of brassinolide (BL) biosynthesis and signaling, Regulation of leaf inclination, Modulation of Pi starvation signaling (Os04t0665600-02);Splicing variant of REGULATOR OF LEAF INCLINATION 1 (RLI1) containing both MYB and coiled-coil (CC) domains, Modulation of Pi starvation signaling (Os04t0665600-03)" |
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| grass specific | RAP-DB | [Os] Cellulose synthase A6 (Os07t0252400-01);Similar to Cellulose synthase BoCesA7. (Os07t0252400-02) |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Protein of unknown function DUF594 domain containing protein. (Os05t0508500-01);Thioredoxin protein, Bacterial F-box effector (XopI)-interacting protein, Regulation of rice immunity (Os05t0508500-02)" |
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| grass specific | RAP-DB | [Os] "Photosystem II (PSII) auxiliary protein, Regulation of D1 protein stability of PSII (Os06t0352900-01);Hypothetical conserved gene. (Os06t0352900-02)" |
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| grass specific | RAP-DB | [Os] "TON1 RECRUIT MOTIF (TRM)-containing protein, Regulation of grain size and shape (Os07t0603300-01)" |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor 46, Disease resistance to Magnaporthe oryzae (Os11t0116900-01)" |
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| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "Glycine-rich protein (GRP), Regulation of chloroplast development at early leaf stage (Os02t0606000-01)" |

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| grass specific | Maizemine | [Zm] GTD-binding domain-containing protein |
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| grass specific | RAP-DB | [Os] "Protein of unknown function DUF1675 family protein. (Os05t0558800-01);JAZ-interacting adaptor protein, Negative regulation of OsMYC2-mediated JA signaling (Os05t0558800-02);Similar to UPF0737 |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Similar to GATA transcription factor 20. (Os06t0571800-01);Similar to GATA transcription factor 3 (AtGATA-3). (Os06t0571800-02);GATA-type zinc finger transcription factor, Cold tolerance (Os06t0571800-03)" |
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| grass specific | RAP-DB | [Os] Meiotic processes (Os02t0591500-01) |
| grass specific | RAP-DB | [Os] Pectin methylesterase inhibitor 8 (Os02t0537000-01) |
| grass specific | RAP-DB | [Os] "SLG7-like protein, Regulation of grain shape (Os07t0109400-01)" |
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| grass specific | RAP-DB | [Os] "FCS-like zinc finger (FLZ) protein 10, Submergence response (Os03t0183500-01)" |
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| grass specific | RAP-DB | [Os] DNA-binding WRKY domain containing protein. (Os01t0820700-00) |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Tolerance to phosphate starvation (Os06t0193400-01);Similar to BHLH transcription factor. (Os06t0193400- |
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| grass specific | RAP-DB | [Os] "Deubiquitinase, Regulation of immune response (Os09t0505100-01)" |
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| grass specific | RAP-DB | [Os] "Meiotic component, Regulation of crossover formation (Os02t0642600- |
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| commelinid specific | RAP-DB; Knetminer-rice; Knetminer-wheat; Maizemine | [Os] "Jasmonate inducible pathogenesis-related class 10 protein, Self-defense against biotic and abiotic stresses (Os03t0300400-01)"; [Zm] Pathogenesis-related protein 10 |
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| commelinid specific | RAP-DB | [Os] "MADS box transcription factor, Regulation of floral organ identity (Os01t0726400-01)" |
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| grass specific | RAP-DB | [Os] "GRAS (GAI-RGA-SCR) plant-specific transcription factor, Maintenance of shoot apical meristem indeterminacy, Regulation of vegetative to reproductive phase change (Os02t0663100-01)" |
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| grass specific | RAP-DB | [Os] "Transcription factor binding protein, Poly (ADP-ribose) polymerase (PARP) domain protein, Abiotic stress tolerance, Control of leaf cell fate (Os10t0577800-01);Similar to Poly polymerase catalytic domain containing protein, expressed. (Os10t0577800- |
| grass specific | RAP-DB | [Os] "FCS-like zinc finger (FLZ) protein 2, Submergence response (Os01t0593200-01)" |
| grass specific | | |

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| grass specific | RAP-DB | [Os] "C3HC4 RING domain-containing E3 ubiquitin ligase, Modulation of heading date by physically interacting with Hd1 (Os04t0648800-01);Similar to Zinc finger, C3HC4 type family protein. (Os04t0648800-02)" |
| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) DNA-binding protein, Regulation of metaxylem vessel number and area, Repression of drought-induced metaxylem plasticity (Os02t0673500- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Xylan arabinosyltransferase 3 (Os03t0567600-01);Glycosyltransferase AER61, uncharacterized domain containing protein. (Os03t0567600-02);Similar to Glycosyltransferase. (Os03t0567600-03)" |
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| grass specific | RAP-DB | [Os] "Ethylene response factor, Transcription factor, Negative regulation of ethylene biosynthesis, Drought tolerance (Os09t0309700-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Control of anther cell differentiation, Pollen development (Os01t0293100-01)" |
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| grass specific | RAP-DB | [Os] "DNA-binding protein with a SAP-like domain, Regulation of cell proliferation (Os03t0183100-01);SAP-like protein BP-73 (OsBP-73) (Riaa1). (Os03t0183100-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Transcriptional regulator, Regulation of panicle erectness, panicle length and grain size, Regulation of leaf inclination (Os07t0616000-01);Hypothetical conserved gene. (Os07t0616000-02)" |
| commelinid specific | in_predefined_specific_set | [Os] "implicated in addition of hydroxycinnamoyl-arabinofuranose to xylan, a key feature of grass cell walls" |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "bZIP transcription factor, Endoplasmic reticulum stress response (Os06t0622700-01);Active form of bZIP transcription factor, Endoplasmic reticulum stress response (Os06t0622700-02)" |
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| grass specific | RAP-DB | [Os] Hypothetical conserved gene. (Os05t0478700-00) |
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| grass specific | in_predefined_specific_set | [Os] adds arabinofuranose to xylan to make arabinoxylan |
| grass specific | | |
| grass specific | RAP-DB | [Os] "WRKY transcription factor 64, Specific role in defense signaling in rice during M. grisea interactions, Response to the rice pathogens, Regulation of root elongation under iron excess, Iron stress tolerance (Os12t0116700-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] Similar to tumor-related protein-like. (Os05t0560200-00) |
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| grass specific | RAP-DB | [Os] "Similar to BRI1-KD interacting protein 130. (Os05t0113500-03);BR-INSENSITIVE 1 (BRI1)-interacting protein, Salt tolerance through modulation of ABA synthesis and scavenging ROS (Os05t0113500-04);Similar to BRI1-KD interacting protein 130. (Os05t0113500-05)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "MYB transcription factor, Circadian clock, Tolerance to salinity, osmotic, and drought stresses (Os08t0157600-01);Similar to LHY protein. (Os08t0157600-02)" |
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| grass specific | RAP-DB | [Os] "Hypothetical conserved gene. (Os03t0168400-01);P-type pentatricopeptide repeat (PPR) protein, Maintenance of mitochondrial function and endosperm development, Trans-splicing of the mitochondrial nad1 intron1 (Os03t0168400-02)" |
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| grass specific | RAP-DB | [Os] "R2R3 MYB transcription factor, Regulation of phosphate-starvation responses and root architecture (Os05t0140100-01);Myb transcription factor domain containing protein. (Os05t0140100-02);Myb transcription factor domain containing protein. (Os05t0140100-03)" |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor 82, Response to the rice pathogens, Response to jasmonic acid |
| grass specific | RAP-DB | [Os] DNA replication helicase 2_9 (Os10t0537600-01) |
| grass specific | RAP-DB | [Os] "SnRK1A protein kinase-interacting negative regulator, Repression of sugar/nutrient starvation signaling (Os09t0499000-01)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor, Regulator of tapetal programmed cell death, Male reproductive development |
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| grass specific | Maizemine | |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Positive regulation of deep sowing tolerance, Mesocotyl elongation (Os04t0618600-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "tRNAHis guanylyltransferase, Regulation of auxin signaling in response to high temperature |
| grass specific | | |
| grass specific | RAP-DB | [Os] "ABI3/VP1 transcription factor family protein, Regulation of iron-deficiency response and tolerance (Os08t0101000-01)" |
| grass specific | RAP-DB | [Os] Xylan arabinosyltransferase 4 (Os06t0707200-01) |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "SnRK1A protein kinase-interacting negative regulator, Repression of sugar/nutrient starvation signaling (Os08t0516900-01)" |
| grass specific | RAP-DB | [Os] "Remorin_C-containing protein, Control of panicle length (Os09t0456100-01);Hypothetical conserved gene. (Os09t0456100-02)" |
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| grass specific | RAP-DB | [Os] "Chromatin remodeling factor 742, Sucrose non-fermenting 2 (Snf2) family protein, Salt stress response, Response to M. oryzae infection (Os05t0392400- |
| grass specific | | |
| grass specific | Maizemine | [Zm] Genetic modifier |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor, Regulation of stem elongation and seed development (Os07t0583700-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "WRKY transcription factor, Promotion of phosphate accumulation under Pi-replete conditions (Os01t0821600-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "RING E3 ubiquitin ligase, Target of the M. oryzae effector AvrPiz-t, Component of pathogen-associated molecular pattern-triggered immunity (Os05t0154600-01);Similar to VIP2 protein. (Os05t0154600-02)" |
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| grass specific | RAP-DB | [Os] "NAC family transcription factor like protein, Negative regulation of blast disease resistance (Os02t0822400-01);Similar to NAC-like protein. (Os02t0822400-02)" |
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| grass specific | RAP-DB | [Os] "Response to drought in tolerant genotype Dagad desi, Response to submergence, Response to Xanthomonas oryzae pv. oryzae and B. glumae in resistant genotypes, Response to R. solani in susceptible rice genotype (Os06t0689600-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "D-type euonymus-related lectin (EUL), Response to drought stress and ABA treatment,  Response to biotic treatment (Os07t0683900-01);Similar to Osr40g2 protein (Fragment). (Os07t0683900-02)" |
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| grass specific | RAP-DB | [Os] "RNA-Recognition-Motif (RRM) protein, Regulation of the premeiotic G1/S-phase transition of germ cells (Os12t0572800-01)" |
| grass specific | RAP-DB | [Os] "Homologue of the Arabidopsis OPS (OCTOPUS), Regulation of grain size, Brassinosteroid signaling (Os01t0852400-01)" |
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| grass specific | RAP-DB | [Os] "Fluoride exporter, Fluoride tolerance (Os10t0567000-01);Hypothetical gene. (Os10t0567000-02)" |
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| grass specific | RAP-DB; Maizemine | [Os] "WUSCHEL-type homeobox protein, Specification and maintenance of the stem cells (quiescent center cells) in the root apical meristem (Os01t0854500-01)"; [Zm] Homeobox domain-containing protein |
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| grass specific | RAP-DB | [Os] "Nucleus-encoded chloroplast protein, Chloroplast development, Biogenesis of chloroplast ATP synthase (Os02t0152900-01)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcription factor 061, Regulation of Fe homeostasis (Os11t0601700-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Remorin protein, Grain setting (Os04t0620200-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Squamosa promoter-binding-like protein, Transcription factor, Salt tolerance, Control of trichome formation (Os06t0659100-01)"; [Zm] Squamosa promoter-binding-like protein 10 |
| grass specific | RAP-DB; Maizemine | [Os] Similar to SUSIBA2. (Os03t0741400-01); [Zm] WRKY domain-containing protein |
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| grass specific | RAP-DB | [Os] "Ubiquitin-like domain-containing protein, AvrPi9-interacting protein, Negative regulation of blast disease resistance (Os07t0498800-01);Similar to Calreticulin interacted protein. (Os07t0498800-02);Calreticulin interacting protein, Response to cold stress (Os07t0498800-03)" |
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| grass specific | RAP-DB | [Os] "RNA-binding protein, Modulation of sugar transport (Os09t0298700-01)" |
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| grass specific | RAP-DB | [Os] "Putative member of the hydroxyproline-rich glycoprotein family, Regulation of cell wall extensibility in the root elongation zone |
| grass specific | | |
| grass specific | RAP-DB | [Os] "B-type response regulator, Cytokinin signaling (Os03t0224200-01);B-type response regulator, Cytokinin signaling (Os03t0224200-02);Similar to response regulator 8. |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Homeodomain (PHD) transcriptional regulator, Flowering promoter (Os08t0105000-01);Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os08t0105000-02);Similar to PHD-finger family protein. (Os08t0105000-03)" |
| grass specific | RAP-DB | [Os] "Homolog of Arabidopsis DOG1, Regulation of seed dormancy (Os01t0306400-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] NUE (nitrogen use efficiency)-related transcription factor (Os09t0493700-01) |
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| grass specific | RAP-DB | [Os] "Similar to Homeobox-leucine zipper protein HOX22. (Os04t0541700-01);Homeodomain-leucine zipper (HD-Zip) protein, Transcription factor, ABA-mediated drought and salt tolerance (Os04t0541700-02)" |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-wheat | [Os] "WRKY transcription factor, Defense response (Os02t0181300-01)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor, Drought tolerance (Os03t0741100-01)" |
| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Negative regulation of salt stress (Os01t0575200-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "RING-type E3 ubiquitin ligase, Regulation of grain width and weight (Os02t0244100-01)" |
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| grass specific | RAP-DB; Knetminer-wheat; Maizemine | [Os] "Circadian-associated rice pseudo response regulator, Control of flowering time (Os11t0157600-01)"; [Zm] Two-component response regulator-like APRR9 |
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| grass specific | RAP-DB | [Os] "B-type response regulator, Cytokinin signaling (Os01t0904700-01)" |
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| grass specific | RAP-DB | [Os] "Homologue of SRO (similar to RCD one), Regulation of stomatal closure, Abiotic stress response (Os03t0230300-01);Non-protein coding transcript. (Os03t0230300-02)" |
| grass specific | RAP-DB | [Os] Similar to glycosyltransferase. (Os02t0135500-01);Xylan arabinosyltransferase 5 (Os02t0135500-02) |
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| grass specific | RAP-DB | [Os] "Ortholog of Arabidopsis EDS1, Regulation of rice-pathogen interactions, Disease resistance (Os09t0392100-01)" |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Cold tolerance, Mediation of host susceptibility to disease (Os09t0474000-01)" |
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| grass specific | RAP-DB | [Os] "GT61 glycosyltransferase, Beta-1,2-xylosyltransferase, Xylan xylosyltransferase, Xylan biosynthesis (Os06t0707000-01)" |
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| grass specific | RAP-DB | [Os] "Polygalacturonase-inhibiting protein, Inhibitor of fungal polygalacturonase, Regulation of floral organ number (Os07t0568700-02)" |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Regulation of the salt stress response, Control of flowering (Os04t0631600- |
| grass specific | RAP-DB | [Os] "ER-localized glycosylated membrane protein, Ethylene signaling (Os06t0115200-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Iron-related bHLH transcription factor 2, Tolerance to Fe deficiency, Regulation of Fe uptake from soil, Fe transport during germination, Fe translocation to grain during seed maturation (Os01t0952800-01);Conserved hypothetical protein. (Os01t0952800-02)" |
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| grass specific | RAP-DB | [Os] "Salt-induced RING Finger Protein, Negative regulation of response to salt stress (Os05t0488800-01)" |
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| grass specific | RAP-DB | [Os] "Class I formin protein, Necessary for plant morphology and chloroplast relocation (Os07t0588200-01);Similar to Formin-like protein 13. (Os07t0588200-02)" |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor, Defense response (Os04t0493100-01);Non-protein coding transcript. (Os04t0493100-02)" |
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| grass specific | RAP-DB | [Os] "Homologue of Arabidopsis INP1, Regulation of pollen aperture formation (Os02t0661300-01)" |
| grass specific | Maizemine | [Zm] SPOROCYTELESS-like EAR-containing protein 4 |
| grass specific | RAP-DB | [Os] Peroxisomal membrane protein (Os05t0101200-01) |
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| grass specific | RAP-DB | [Os] Homolog of SAD1 (RNA polymerase I subunit A34.5) (Os01t0259900-00) |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Cold stress response (Os07t0628500-01);Basic helix-loop-helix dimerisation region bHLH domain containing protein. (Os07t0628500-02)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Chromatin remodeling factor, Protein containing PHD domain, FNIII domain and VID domain, Positive regulator of flowering, Regulation of leaf angle (Os02t0152500-01);Non-protein coding transcript. (Os02t0152500-02)" |
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| commelinid specific | RAP-DB | [Os] "Hydroxysteroid dehydrogenase, Cuticle formation, Lipid homeostasis, Submergence tolerance (Os11t0499600-01);Similar to cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase. (Os11t0499600-02)" |
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| grass specific | RAP-DB | [Os] Potential plastid sigma factor of RNA polymerase (Os08t0242800-01);Similar to Sigma factor SIG6. |
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| grass specific | RAP-DB | [Os] "TIFY domain-containing transcriptional regulator, Salt and dehydration stress tolerance (Os03t0180800-01)" |
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| grass specific | RAP-DB | [Os] "Protein of unknown function DUF1644 family protein. (Os06t0693700-01);DUF1644 family member protein, Positive regulation of salt and drought resistance (Os06t0693700-02);Similar to predicted protein. (Os06t0693700-03);Protein of unknown function DUF1644 family protein. |
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| grass specific | RAP-DB | [Os] Cellulose synthase-like protein (Os07t0553400-01) |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Structural homolog of eukaryotic general repressor DrAp1, Repressor (Os11t0544700-01)"; [Zm] Nuclear factor Y subunit C11 |
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| grass specific | RAP-DB | [Os] "F-box containing protein, Salt tolerance (Os07t0561300-01)" |
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| grass specific | Maizemine | [Zm] Growth-regulating factor |
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| commelinid specific | RAP-DB | [Os] "Similar to Esterase. (Os02t0250400-01);Similar to Esterase. (Os02t0250400-02);GDSL esterase, Xylan deacetylation, Control of secondary wall formation and |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Orthologue of yeast Rad21, Pollen development (Os08t0266700-01)" |
| grass specific | RAP-DB | [Os] "CONSTANS-like transcription factor, Rice ortholog of AtCOL15, Floral regulator, Suppression of flowering (Os08t0536300-01)" |
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| grass specific | RAP-DB | [Os] "NLP family transcriptional factor, Promotion of nitrogen use efficiency (NUE), Transactivation of nitrogen assimilation gene OsNiR (Os09t0549450-01)" |
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| grass specific | RAP-DB | [Os] "Cofactor of beta-ketoacyl-CoA synthase, Homolog of Arabidopsis CER2, Leaf cuticular wax synthesis, Very-long-chain fatty acid (VLCFA) elongation (Os04t0611200-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "J-protein of the third category (Hsp40 family), Heat shock protein, DnaJ protein, Molecular chaperone, ABA-mediated antioxidant defense, Response to drought and salt stress (Os04t0687300-01)" |
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| commelinid specific | RAP-DB | [Os] GDSL esterase/lipase protein (Os05t0209600-01) |
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| grass specific | Knetminer-rice | |
| grass specific | RAP-DB | [Os] "B-type response regulator, Cytokinin signaling (Os06t0183100-01);B-type response regulator, Cytokinin signaling (Os06t0183100- |
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| grass specific | RAP-DB | [Os] "NAC transcription factor, Heat stress tolerance (Os01t0261200-01);Similar to NAC domain-containing protein 74. (Os01t0261200-02)" |
| grass specific | RAP-DB | [Os] "Homeodomain-leucine zipper transcription factor, Regulation of panicle exsertion, Negative regulation of sheath blight disease resistance (Os03t0198600-01)" |
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| grass specific | RAP-DB | [Os] "RING H2-type E3 ligase, Salinity tolerance (Os04t0571200-01)" |
| grass specific | RAP-DB | [Os] "Telomere repeat-binding factor like protein, Telomere maintenance, Telomere length homeostasis (Os02t0776700-01);Similar to Single myb histone 6. (Os02t0776700-02);Hypothetical conserved gene. |
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| grass specific | RAP-DB | [Os] "A member of S40 gene family, Leaf senescence (Os01t0862600-01)" |

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| grass specific | RAP-DB | [Os] "JASMONATE ZIMDOMAIN (JAZ) protein, Regulation of coleoptile length under submergence (Os07t0615200-01)" |
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| grass specific | RAP-DB | [Os] "Similar to Squamosa promoter-binding-like protein 6. (Os03t0833300-01);A member of the SPL gene family, Transcriptional repressor of the ER stress sensor IRE1 (Os03t0833300-02);Similar to Squamosa promoter-binding-like protein 6. (Os03t0833300-03);Similar to Squamosa promoter-binding-like protein 6. (Os03t0833300- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Plant-unique phox-homology domain-containing protein, Rab5a effector, Mediation of tethering and membrane fusion of dense vesicles (DVs) with protein storage vacuoles (PSVs) in rice endosperm |
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| grass specific | RAP-DB | [Os] "Orthologue of Arabidopsis EPFL9, Regulation of leaf stomatal density (Os01t0914400-01)" |
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| grass specific | RAP-DB | [Os] "RING-type E3 ligase, Negative regulation of cuticular wax biosynthesis, Drought stress response (Os02t0682300-01)" |
| grass specific | RAP-DB | [Os] "Putative integral membrane protein containing EamA-like transporter family domains, Regulation of intracellular auxin transport |
| grass specific | | |
| grass specific | RAP-DB | [Os] "bZIP transcription factor, Drought and salt tolerance (Os09t0306400-01)" |
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| commelinid specific | in_predefined_specific_set | ["Bd, Zm"] mediates addition of hydroxycinnamates to monolignols leading to commelinid-specific features on lignin |
| commelinid specific | RAP-DB | [Os] "BAHD acyltransferase, Glucuronoarabinoxylan modification in grass cell wall (Os06t0594600-01)" |
| grass specific | RAP-DB | [Os] "FCS-like zinc finger (FLZ) protein 11, Submergence response (Os03t0665200-01)" |
| grass specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Auxin response factor 1. (Os04t0664400-01);Auxin response factor, Transcriptional factor, Transcriptional regulation of plant height and leaf angle (Os04t0664400- |
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| grass specific | RAP-DB | [Os] "Heat shock transcription factor, Cadmium tolerance, Heat stress response (Os01t0749300-01);Heat shock transcription factor, Cadmium tolerance, Heat stress response (Os01t0749300-02)" |
| grass specific | RAP-DB | [Os] "Homeodomain-leucine zipper (HD-Zip) protein, Regulation of gibberellin signaling (Os09t0470500-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "SG1 (SHORT GRAIN1)-related protein, Brassinosteroid signaling, Regulation of seed and panicle development (Os02t0762600-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] ALWAYS EARLY/LIN-9 homologous protein (Os01t0193900-01);ALWAYS EARLY/LIN-9 homologous protein (Os01t0193900-02) |
| grass specific | RAP-DB | [Os] "HD-ZIP I protein, Transcription activator, Stress response, Panicle development (Os02t0649300-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "Control of root system architecture, Drought avoidance (Os09t0439800-01)" |
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| grass specific | RAP-DB | [Os] "Dof (DNA binding with one finger) transcription factor, Regulation of Flowering time, Brassinosteroid (BR) signaling to modulate plant architecture (Os03t0169600-01)" |
| grass specific | RAP-DB | [Os] "RING finger E3 ligase, Regulation of abiotic stress tolerance (Os02t0150700-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "RING E3 ligase, Negative regulator for salt-stress response (Os06t0695600-01)" |
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| grass specific | RAP-DB | [Os] "Root Hair Defective-Six Like (RSL) Class II family of transcription factor, Regulation of root hair development (Os07t0588400-01)" |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor 14, Response to M. oryzae infection (Os01t0730700-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "Rice ortholog of Arabidopsis phytoalexin deficient 4, Positive regulation of defense responses to bacterial pathogens (Os11t0195500-01)" |
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| commelinid specific | in_predefined_specific_set | ["Bd, Os, Sv, Sc"] "implicated in formation of feruloyl-arabinofuranosyl precursor prior to additon to xylan, a key feature of commelinid cell walls" |
| grass specific | RAP-DB; Maizemine | [Os] "GA 3 beta-hydroxylase2, GA metabolism (Os01t0177400-01)"; [Zm] GA 3beta-hydroxylase |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Acyl transferase 1, Bacterial blight resistance, Blast disease resistance, Resistance to both fungal and bacterial pathogens (Os10t0195600-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Similar to RAPB protein. (Os03t0174900-01);NF-YA transcription factor 1, Suppression of jasmonic acid-mediated antiviral defense (Os03t0174900-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "MYB transcription factor, Regulation of Î±-Amylase expression in maintaining sugar homeostatic states (Os10t0562100-01);Similar to Transcription factor MYBS2. |
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| grass specific | RAP-DB | [Os] "Transcription activator, Tolerance to drought, high-salt and cold stresses, Negative regulation of resistance to brown planthopper (BPH) (Os09t0522200-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "MYB-CC family protein, Pi-starvation signaling (Os03t0329900-01)" |
| grass specific | RAP-DB | [Os] "Histidine kinase, Cytokinin signaling (Os06t0183200-01)" |
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| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "Unknown product, Brassinosteroid signaling, Control of organ length (Os09t0459200-01)" |
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| grass specific | RAP-DB | [Os] "bZIP transcriptional activator, Tolerance to salt and drought stresses (Os02t0266800-01)" |
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| grass specific | RAP-DB | [Os] "Nodule inception (NIN) like protein 3, Regulation of nitrogen use efficiency and grain yield under nitrate-sufficient conditions (Os01t0236700-01)" |
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| grass specific | Maizemine | [Zm] Flavonoid O-methyltransferase-like protein |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor, Regulation of grain size (Os02t0805250-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "Basic helix-loop-helix (bHLH) transcription factor, Homolog of Arabidopsis FBH, Control of flowering (Os08t0506700-01)" |
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| grass specific | RAP-DB | [Os] "Substrate of the SCFD3 ubiquitination complex, Repressor of strigolactone (SL) signalling (Os11t0104300-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "NF-YA transcription factor 10, Negative modulation of rice resistance to rice stripe virus (RSV) and southern rice black-streaked dwarf virus (SRBSDV) (Os12t0618600-01)"; [Zm] Nuclear transcription factor Y subunit |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "D-type euonymus-related lectin (EUL), ""Response to salt and drought stress, hormone treatment"",  Response to biotic treatment (Os07t0683600-01)" |
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| grass specific | RAP-DB | [Os] "Similar to DNA binding protein. (Os01t0159800-01);Basic helix-loop-helix (bHLH) transcription factor, Mediation of seed germination, Seedling recovery from salt stress |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "MYB transcription factor, Transcriptional activator in mediating stress and rhythm responsivegene expression (Os02t0685200-01)" |
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| grass specific | RAP-DB | [Os] "Endoplasmic reticulum (ER) stress sensor, Transducer of ER stress, ER stress response (Os07t0471000-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "bHLH transcription factor, Regulation of brassinosteroid signalling, Regulation of leaf angle and grain length (Os02t0705500-01);Helix-loop-helix DNA-binding domain containing protein. (Os02t0705500-02)" |

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| grass specific | RAP-DB | [Os] Cellulose synthase like protein F8 (Os07t0551700-01) |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Chloroplast-localised putative leucine carboxyl methyltransferase (LCMT), O-methyltransferase, Regulation of jasmonate (JA)- and brassinosteroid (BR)-mediated growth and defence responses, Leaf senescence, heading date and grain production via melatonin biosynthesis (Os07t0247100-01)" |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Globulin gene promoter in endosperm (Os03t0796900-01)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "NODULE INCEPTION (NIN)-like protein, Regulation of nitrogen (N) utilization (Os03t0131100-01)" |
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| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Minor quantitative locus (QTL) for heading date, Promotion of heading date under long-day conditions (Os02t0104200-01);Conserved hypothetical protein. (Os02t0104200- |
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| grass specific | RAP-DB | [Os] "Class I formin protein, Regulation of grain size, Control of microtubule and actin filament cytoskeleton systems (Os09t0517600-01)" |
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| grass specific | RAP-DB | [Os] "RING finger E3 ligase, Negative regulation of gamma-ray response (Os11t0629300-01)" |
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| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "Basic leucine zipper transcription factor, Regulation of grain chalkiness, ER homeostasis, Regulation of storage protein and starch biosynthesis (Os07t0644100-01)" |
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| commelinid specific | Maizemine | [Zm] Glutathione transferase |
| grass specific | RAP-DB; Knetminer-rice | [Os] "BELL1-type homeodomain transcription factor, Initiation and maintenance of the shoot apical meristem during embryogenesis, Construction of inflorescence architecture, Modulation of seed shattering (Os05t0455200-01);Similar to QSH-1. (Os05t0455200-02)" |
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| grass specific | RAP-DB | [Os] "Katanin P80 ortholog, Katanin regulatory subunit P80c (Os01t0780400-02)" |
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| commelinid specific | RAP-DB | [Os] "Rice homologue of yeast RAD21, Mitotic chromosome cohesion (Os01t0897800-01);Similar to Rad21/Rec8-like protein. (Os01t0897800-02);Rad21/Rec8 like protein, C-terminal domain containing protein. (Os01t0897800-03);Similar to Rad21/Rec8-like protein. (Os01t0897800-04)" |
| grass specific | RAP-DB | [Os] Sialyltransferase-like protein 2 (Os12t0151500-01) |
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| grass specific | RAP-DB | [Os] "NIN-like protein 2, Nitrate responsive transcript factor, Regulation of ABA content during seed germination under salt stress (Os04t0495800-01);Similar to OSIGBa0159F11.11 protein. (Os04t0495800-02)" |
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| commelinid specific | RAP-DB | [Os] "Sad1/UNC-84 (SUN) domain protein, Promotion of telomere clustering and homologous pairing in meiosis (Os05t0270200-01)" |
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| grass specific | RAP-DB | [Os] "RING finger ubiquitin E3 ligase, Heat tolerance, Modulation of hydrogen peroxide-induced stomatal closure (Os09t0323100-01);Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os09t0323100-02)" |
| grass specific | RAP-DB | [Os] "Microtubule-associated protein, Asymmetric control of cell division during early steps of crown root meristem differentiation (Os08t0518100-01);Hypothetical conserved gene. (Os08t0518100-02)" |
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| grass specific | RAP-DB | [Os] "C2H2-type zinc-finger protein, Drought stress tolerance (Os03t0764100-01)" |
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| grass specific | RAP-DB | [Os] "P-type pentatricopeptide repeat (PPR) protein, Mitochondrial function, Endosperm development (Os05t0207200-01)" |
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| grass specific | RAP-DB | [Os] "Similar to VOZ transcription factor. (Os01t0753000-01);Transcriptional repressor, PAMP-triggered immunity (PTI) and Piz-t-mediated effector-triggered immunity (ETI) |

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| grass specific | RAP-DB; Maizemine | [Os] "High mobility group (HMG) protein, Regulation of drought tolerance (Os04t0564600-01);Similar to H0409D10.9 protein. (Os04t0564600-02)"; [Zm] High mobility group B protein 4 |
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| grass specific | RAP-DB | [Os] "MYB-CC domain containing transcription factor, Positive regulation of Pi-starvation signaling and Pi-homeostasis (Os06t0703900-01);Homeodomain-like containing |
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| grass specific | RAP-DB | [Os] "C2-domain abscisic acid-related protein, CAR protein, Regulation of ABA signaling in seed germination (Os07t0500300-01)" |
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| grass specific | RAP-DB | [Os] "High-affinity potassium transporter, Maintenance of potassium homeostasis, Salt tolerance (Os03t0575200-01)" |
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| grass specific | Knetminer-wheat | |
| commelinid specific | RAP-DB | [Os] "RanBP2-type zinc-finger protein, Magnesium (Mg) homeostasis (Os01t0555100-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Auxin efflux transporter, Regulation of ammonium-induced rice tiller bud elongation (Os01t0802700-01)"; [Zm] Auxin efflux carrier component |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Endoplasmic reticulum (ER) membrane protein, Early tapetum development and meiosis (Os07t0622900-01)" |
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| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Nuclear factor Y (NF-Y) transcription factor A9, CCAAT box binding factor, Heme-associated protein (HAP)2B (Os12t0613000-01)" |
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| grass specific | RAP-DB; Knetminer-wheat | [Os] "MYB transcription factor, Regulation of cellulose biosynthesis during secondary cell wall formation, Negative regulation of root development, Drought resistance |
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| commelinid specific | RAP-DB | [Os] "Pentatricopeptide repeat domain containing protein. (Os01t0506100-01);Pentatricopeptide repeat (PPR) protein, Regulation of salt tolerance (Os01t0506100-02)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "E3 ligase, Resistance to brown planthopper (BPH) (Os06t0605900-01);Leucine-rich repeat, cysteine-containing subtype containing protein. (Os06t0605900-02)" |
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| grass specific | RAP-DB | [Os] "Circadian-associated rice pseudo response regulator, Control of flowering time (Os09t0532400-01);Signal transduction response regulator, receiver region domain containing protein. (Os09t0532400-02)" |
| grass specific | RAP-DB | [Os] "LATERAL ORGAN BOUNDARIES DOMAIN (LBD) protein, Transcriptional activator, Regulation of heading date and yield (Os03t0609500-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "CBM48 domain-containing protein, Compound granule formation and starch synthesis (Os03t0686900-01)" |
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| grass specific | RAP-DB | [Os] "MAPK kinase kinase 18, Ortholog of AtMAPKKK5, Regulation of chitin-induced immune responses (Os03t0764300-01);Truncated mitogen-activated protein kinase kinase kinase 5, Protein lacking an intact serine/threonine protein kinase, catalytic domain (S_TKc domain), Positive regulation of plant height and |
| grass specific | RAP-DB | [Os] "Phytochrome-interacting factor-like bHLH protein, Stress-responsive transcription factor, Regulator of reduced internode elongation under drought conditions (Os03t0782500-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Wall-associated kinase, Negative regulation of rice blast resistance (Os10t0180800-01);Similar to Calcium binding EGF domain containing protein, expressed. (Os10t0180800-02);Hypothetical conserved gene. (Os10t0180800-03)" |
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| commelinid specific | RAP-DB | [Os] "PAMP (pathogen-associated molecular pattern)-responsive transrepressor, Defense response (Os06t0649000-01)" |
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| grass specific | RAP-DB | [Os] Dof transcription factor (Os07t0685000-02) |
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| grass specific | RAP-DB | [Os] "Spen (Split ends)-like protein, Vegetative to reproductive transition (Os09t0516300-01)" |
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| grass specific | RAP-DB; Maizemine | [Os] "Nuclear factor (NF)-YA transcription factor, Response to abscisic acid (Os03t0696300-01);Similar to nuclear transcription factor Y subunit A-1. (Os03t0696300-02)"; [Zm] Nuclear transcription factor Y |
| grass specific | RAP-DB; Knetminer-rice | [Os] B-type heat shock transcription factor (Os09t0456800-01) |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "MLG (mixed-linkage glucan) synthase, Biosynthesis of MLG (cell wall polysaccharide) (Os08t0160500-01);Similar to Cellulose synthase-like CslF6. (Os08t0160500-02)" |
| grass specific |  |  |
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| grass specific | Maizemine | [Zm] Protein PLASTID REDOX INSENSITIVE 2 |
| grass specific | RAP-DB | [Os] "Lectin receptor kinase, Regulation of pollen development, Regulation of pollen aperture formation (Os02t0459600-01)" |
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| grass specific | Knetminer-wheat |  |

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| grass specific | RAP-DB; Knetminer-rice | [Os] "bZIP transcription factor, Stress response and ABA signal transduction, Regulation of plant fertility (Os01t0859300-01);bZIP transcription factor, Stress response and ABA signal transduction, Regulation of plant fertility (Os01t0859300-02)" |
| grass specific | RAP-DB | [Os] "F-box protein, Mediation of bouquet formation, Promotion of homolog pairing, synapsis, and crossover formation in meiosis |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Iron(III)-deoxymugineic acid transporter, Translocation of iron in reproductive organs and phloem in joints (Os01t0829900-01)" |
| moncot specific | RAP-DB | [Os] "Cinnamoyl-CoA reductase-like gene family member, Defense response (Os01t0639200-01)" |
| grass specific | RAP-DB | [Os] "GDSL-type lipase, Regulation of ethylene signaling in rice root (Os05t0210100-01)" |
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| grass specific | Maizemine | [Zm] RimM domain-containing protein |

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| grass specific | RAP-DB | [Os] "Xyloglucan backbone O-acetyltransferase 1, DUF231 protein (Os01t0652800-01);Domain of unknown function DUF231, plant domain containing protein. |
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| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "Sugar transporter, A member of the MtN3 gene family, Host disease-susceptibility gene for bacterial blight (Os08t0535200-01)" |
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| commelinid specific | RAP-DB;<br>Knetminer-rice | [Os] "WRKY transcription factor 7, Response to the rice pathogens (Os05t0537100-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Cytochrome P450 monooxygenase, Gibberellin (GA)-deactivating enzyme, Modulation of internode elongation, Regulation of grain size and flag leaf angle (Os05t0482400-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcriptional activator, Control of leaf angle and grain size (Os09t0510500-01)" |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Nuclear factor Y (NF-Y) transcription factor A3, CCAAT box binding factor, Heme-associated protein (HAP)2H (Os03t0647600-01)" |
| grass specific | | |
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| commelinid specific | RAP-DB; Maizemine | [Os] "Transverse filament (TF) protein, Homolog of Arabidopsis ZYP1, Central element of the synaptonemal complex, Regulation of the number of crossovers during meiosis (Os04t0452500-01)"; [Zm] Synaptonemal complex protein |
| grass specific | | |
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| commelinid specific | in_predefined_specific_set | [Os] mediates addition of hydroxycinnamates to monolignols leading to commelinid-specific features on lignin |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "U-box/ARM repeat E3 ligase, Stress response, Regulation of cell death, Blast disease resistance |
| grass specific | | |
| grass specific | RAP-DB | [Os] "GRAS-domain transcription factor, Strigolactone (SL) biosynthesis (Os03t0263300-01)" |
| grass specific | RAP-DB | [Os] "BREVIS RADIX-like protein, Drought, salt and cold stress response (Os02t0700700-01)" |
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| grass specific | RAP-DB | [Os] "Glucosyltransferases-like GTPase activators and Myotubularin (GRAM) domain-containing protein, Drought and salt tolerance, Regulationof the ABA pathway (Os04t0526800-01)" |
| grass specific | | |
| grass specific | RAP-DB; Maizemine | [Os] "Transcription factor, Positive regulator of cell proliferation, Control of grain size, shape and quality (Os08t0531600-01)"; [Zm] Teosinte glume architecture 1 (Fragment) |
| grass specific | | |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Member of the CONSTANS-like (COL) family, Flowering time repressor (Os03t0711100-01)" |
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| grass specific | RAP-DB | [Os] "C2H2 transcription factor, Cys2/His2 zinc finger protein, Leaf development, Regulation of plant height and internode elongation, Modulation of grain length and pollen viability |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor, Tolerance to phosphate starvation, Regulator of Fe starvation and cold stress (Os09t0334500-01)" |
| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] Regulation of grain length (Os06t0675200-01) |
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| commelinid specific | in_predefined_ specific_set | [Os] mediates addition of hydroxycinnamates to monolignols leading to commelinid-specific features on lignin |
| commelinid specific | RAP-DB | [Os] "Ortholog of Arabidopsis gamete expressed 1 (GEX1), Required for nuclear fusion during reproduction (Os09t0442400-01)" |
| grass specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) transcription factor 130, Drought tolerance (Os09t0487900-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "SHR transcription factor, Formation of root endodermis and leaf stomata, Regulation of the number of cortex cell layers in the root (Os07t0586900-01)" |
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| grass specific | RAP-DB | [Os] "Putative protease inhibitor I family protein, Control of plant architecture, Plant development (Os08t0441300-01)" |
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| grass specific | RAP-DB | [Os] "Drought-induced protein family 19-5, Negative regulation of salt stress tolerance (Os01t0971100-01)" |
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| grass specific | RAP-DB | [Os] "U-Box E3 ubiquitin ligase, Diurnal rhythm regulation, Abiotic stress response (Os02t0234300-01)" |
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| grass specific | RAP-DB | [Os] "NAC transcription factor, Positive regulator of heading and senescence during the reproductive phase (Os06t0675600-01)" |
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| grass specific | RAP-DB | [Os] "Squamosa promter-binding-like transcription activator, Regulation of branching in panicles and vegetative shoots, Semidominant regulator of plant architecture (Os08t0509600-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "XA21 binding protein 24, ATPase, Inhibition of pattern recognition receptor (PRR) -mediated immunity (Os01t0771200-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | Knetminer-rice | |
| grass specific | RAP-DB | [Os] "Squamosa promoter-binding-like protein 17, Transcription factor, Target gene of microRNA156, SBP-box family protein, Modulation of root elongation in response to nitrate supply (Os09t0491532-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to WUSCHEL-related homeobox 6. (Os03t0325600-01);WUSCHEL-related homeobox 6, Transcription factor, Control of tiller angle, Response to gravistimulation (Os03t0325600-02)" |
| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Transcription factor, DNA-binding intermediate protein for SLR1, Modulation of gibberellin signaling pathway, Regulation of plant growth and development (Os02t0643200-01)" |
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| commelinid specific | in_predefined_specific_set | [Bd] "implicated in formation of feruloyl-arabinofuranosyl precursor prior to additon to xylan, a key feature of commelinid cell walls" |
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| grass specific | RAP-DB | [Os] "Flavonoid O-diglucosyltransferase, Uridine diphosphate glycosyltransferase (Os01t0734800-01);UDP-glucuronosyl/UDP-glucosyltransferase family protein. (Os01t0734800-02)" |
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| grass specific | Maizemine | [Zm] Polypeptide |
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| grass specific | RAP-DB; Maizemine | [Os] "Jasmonate ZIM-domain protein, Jasmonate-induced resistance to bacterial blight, Repressor of jasmonic acid signaling (Os09t0439200-01)"; [Zm] Tify domain-containing protein |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] Expansin-B7 (Os03t0102700-01) |

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| grass specific | RAP-DB | [Os] "High-affinity nitrate transporter, Nitrate transport, Auxin signaling (Os01t0547600-01)" |
| commelinid specific | | |
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| grass specific | Maizemine | [Zm] Holliday junction resolvase MOC1 |
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| commelinid specific | RAP-DB; Knetminer-wheat | [Os] "Rice ZIP4 homolog, ZMM protein, Required for homologous chromosome synapsis and crossover formation (Os01t0890900-01)" |
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| grass specific | RAP-DB | [Os] "Histone H1, Tolerance to cold and heat stress (Os04t0253000-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "D-type euonymus-related lectin (EUL), ""Response to salt and drought stress, hormone treatment"", Response to biotic treatment (Os03t0327600-01)" |

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| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "GAI-RGA-SCR (GRAS) family protein, Brassinosteroid signaling (Os06t0127800-01)" |
| commelinid specific | RAP-DB;<br>Knetminer-rice | [Os] "Calcium-binding rice annexin protein, Modulation of ROS production, Mediation of ABA-induced Ca2+ flux (Os05t0382600-02);Annexin family protein. (Os05t0382600-03)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "NAC-domain protein, Resistance to rice dwarf virus, Regulator of jasmonate (JA) signaling (Os03t0119966-01)" |
| grass specific | | |

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| grass specific | RAP-DB | [Os] "Lysine motif (LysM) receptor-like protein (RLP), Chitin oligosaccharide elicitor-binding protein, Perception and transduction of chitin elicitor signal for defense responses (Os03t0133400-01)" |
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| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "NAC transcription factor, Regulation of seed-storage protein content (Os07t0566500-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-wheat; Maizemine | [Os] "Putative transcription factor, Carpel specification, Midrib formation (Os03t0215200-01)"; [Zm] DROOPING LEAF |
| grass specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Chloroplast group IIA intron splicing factor CRS1, Splicing of chloroplast group I and II introns, Chloroplast development |
| grass specific | RAP-DB | [Os] "Conserved hypothetical protein. (Os03t0144000-01);DUF4487 domain containing protein, Regulation of meiotic recombination, Prevention of aberrant meiotic recombination, Regulation of crossover formation |
| grass specific | | |
| grass specific | RAP-DB | [Os] "RING finger protein with E3 ligase activity, Mediation of broad-spectrum disease resistance (Os06t0125800-01)" |

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| grass specific | RAP-DB | [Os] "H3K4-specific demethylase, JmjC domain-containing protein, Control of stem elongation, Control of transposon activity, Panicle development (Os05t0196500-01)" |
| grass specific | Maizemine | [Zm] Putative LRR receptor-like serine/threonine-protein kinase |
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| grass specific | RAP-DB | [Os] "F-box protein, Positive regulation of the resistance to brown planthopper (Os02t0200900-01);Leucine-rich repeat, cysteine-containing containing protein. (Os02t0200900-02)" |
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| commelinid specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "UDP-glucosyltransferase, Detoxification of deoxynivalenol (Os04t0206600-01)" |
| grass specific | RAP-DB | [Os] "H3K9 demethylase, Floral organ development (Os10t0577600-01)" |
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| grass specific | RAP-DB | [Os] Xylan arabinosyltransferase 7 (Os01t0956200-01) |

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| commelinid specific | RAP-DB | [Os] "Mitogen-activated protein kinase (MAPK) phosphatase, Negative regulation of wound responses, Negative regulator of grain size, Positive regulator of grain number (Os05t0115800-01);Similar to MAP kinase phosphatase. (Os05t0115800-02)" |
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| grass specific | Knetminer-rice | |
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| grass specific | in_predefined_specific_set | [Zm] grass-specific beta-expansins evolved to mediate expansion in grass primary cell walls |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Similar to Cyclin-P3-1. (Os05t0398000-01);P-type cyclin, PHO80 homologous protein, Negative regulation of phosphate starvation signaling in root (Os05t0398000-02)" |
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| grass specific | Maizemine | [Zm] Linalool synthase |
| grass specific | | |
| grass specific | RAP-DB | [Os] Similar to WERKY protein (Fragment). (Os04t0597300-01) |
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| grass specific | RAP-DB | [Os] "Pentatricopeptide repeat protein, Regulation of chloroplast development (Os03t0824100-01)" |
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| grass specific | RAP-DB | [Os] "Jasmonate ZIM-domain containing protein, Transcriptional repressor of JA signaling, Regulation of phosphate starvation responses, Pi homeostasis (Os03t0180900-01)" |
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| grass specific | RAP-DB | [Os] "WUSCHEL-related homeobox protein, Meristem maintenance (Os04t0649400-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "A member of gibberellic acid (GA)-stimulated transcript gene family, Regulation of grain size and yield (Os07t0592000-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Patatin-related phospholipase A, Regulation of panicle length, grain shape and grain number per panicle (Os06t0677000-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "F-box E3 ligase, KMD family of F-box protein, Negative regulation of rice blast resistance, Negative regulation of cytokinin signalling (Os06t0594400- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "BREVIS RADIX-like protein, Cold stress response (Os03t0853500-01)" |
| grass specific | RAP-DB | [Os] 32-kDa subunit of replication protein A (Os02t0829100-01) |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Chloroplast signal recognition particle 43 KD protein, Chloroplast development and photosynthesis (Os03t0131900-01)" |
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| grass specific | RAP-DB | [Os] "Chaperone-like protein of protochlorophyllide oxidoreductase (POR), J-like protein, Chloroplast-localized protein containing DUF3353, Regulation of chlorophyll biosynthesis, Chlorophyll and lutein accumulation, Chloroplast development (Os09t0380200-01)" |
| grass specific | RAP-DB; Maizemine | [Os] "Histone acetyltransferase1, Promotion of cell proliferation (Os09t0347800-01)"; [Zm] Histone acetyltransferase |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Bcl-2-associated athanogene (BAG) protein, BAG protein containing a ubiquitin-like (UBL) structure, Plant development (Os06t0126500-01)" |
| grass specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Modulation of leaf rolling, Regulation of abaxial side cell differentiation, Regulation of leaf shape, male fertility and seed size, Positive regulation of heading date (Os03t0308200-01);Similar to ATP-dependent Clp protease proteolytic subunit. (Os03t0308200-02)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Nucleoporin, Common symbiosis signaling (SYM) pathway (Os03t0225500-01);Nucleoporin, Nup133/Nup155-like, N-terminal domain containing protein. |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Transcription factor, Modulation of sugar transport (Os02t0707200-01)" |
| grass specific | RAP-DB | [Os] "Similar to TA1 protein (Fragment). (Os08t0536800-01);Homologue of OsBC1, bHLH transcription factor, Positive regulator in cell elongation of laminar joints and grains, Regulation of leaf angle and grain length |

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| grass specific | RAP-DB | [Os] "Transcription factor, Floral organ development (Os03t0729500-01)" |
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| commelinid specific | Maizemine | [Zm] Hexosyltransferase |
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| grass specific | RAP-DB | [Os] "Mitogen-activated protein kinase kinase kinase (MAPKKK), Negative regulation of seed dormancy (Os01t0699600-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Maizemine | [Os] "Gibberellin 13-oxidase, Cytochrome P450 714B2, Negative regulation of plant growth, GA homeostasis (Os03t0332100-01)"; [Zm] Cytochrome P450 family protein |
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| grass specific | RAP-DB | [Os] Similar to Beta-expansin. (Os10t0555900-01);Beta-expansin 3 (Os10t0555900-02) |
| grass specific | RAP-DB | [Os] "Ortholog of exportin-t, Regulation of tRNA export (Os07t0613300-01);Similar to PAUSED. (Os07t0613300-02);Similar to predicted protein. (Os07t0613300-03)" |
| grass specific | | |
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| grass specific | RAP-DB; Maizemine | [Os] "Origin recognition complex subunit 3, Lateral root development (Os10t0402200-01)"; [Zm] Origin recognition complex subunit 3 |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] CYB5-like heme/steroid binding domain-containing protein (Os12t0223300-01);Similar to Cytochrome b5. (Os12t0223300-02) |
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| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "C2H2-type zinc finger protein, Positive regulation of of ABA catabolism, Salinity and drought tolerance, Seed germination |
| grass specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Mitogen-activated protein kinase kinase kinase (MAPKKK), Disease resistance, Defense/stress response (Os03t0160100-01)" |
| grass specific | RAP-DB | [Os] ACT domain repeat protein 9 (Os03t0247900-01) |
| grass specific | RAP-DB | [Os] "RING Ub E3 ligase, Positive regulator of salt and osmotic stress tolerance (Os03t0798200-01)" |
| commelinid specific | | |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "GATA transcription factor, Zinc finger transcription factor, Regulation of chlorophyll content and senescence (Os03t0831200-01);Hypothetical conserved gene. (Os03t0831200-02)" |
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| grass specific | RAP-DB | [Os] "Dof transcription factor, Promotion of nutrient ion uptake and accumulation (Os01t0264000-01)" |
| grass specific | Knetminer-rice | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "DUF630 and DUF632 domains containing protein, Control of leaf rolling, Regulation of tiller number, Regulation of axillary bud development, Stomatal patterning (Os10t0562700-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] Intracellular Ras-group-related leucinerich repeat protein 3 (Os04t0476700-01) |

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| grass specific | RAP-DB | [Os] "NAC (NAM, ATAF, and CUC2) transcription factor, Drought tolerance, Modulation of lignin accumulation (Os03t0327100-01)" |
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| grass specific | RAP-DB | [Os] "Nucleotide exchange factor of OsBiP1, Regulation of the activity of a major endoplasmic reticulum luminal chaperone, Salt stress response (Os09t0512700-01)" |
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| grass specific | RAP-DB | [Os] "Similar to EDR1. (Os02t0743500-01);MAPK kinase kinase (MAPKKK), Mediation of drought resistance, Regulation of scavenging of ROS (Os02t0743500-02)" |
| commelinid specific | | |
| commelinid specific | Knetminer-rice | |
| grass specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein (Os02t0721800-01)" |
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| grass specific | RAP-DB | [Os] "Transcriptional activator, Target protein of bacterial effector, Xoo virulence, PAMP-triggered immunity (PTI) and Piz-t-mediated effector-triggered immunity (ETI) |
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| grass specific | RAP-DB | [Os] "Exonuclease 1, Cell proliferation, UV-damaged nuclear DNA repair under dark conditions (Os01t0777300-01)" |
| commelinid specific | Knetminer-rice | |
| commelinid specific | RAP-DB | [Os] "Arsenic-induced RING E3 ligase, Abiotic stress response (Os05t0497600-01)" |
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| commelinid specific | RAP-DB | [Os] "SPA ortholog, WD40 repeat-like domain containing protein (Os05t0571000-01);Similar to SPA1 (SUPPRESSOR OF PHYA-105 1); protein binding / signal transducer. (Os05t0571000-02)" |
| grass specific | | |
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| commelinid specific | | |
| grass specific | RAP-DB | [Os] "A member of S40 gene family, Leaf senescence, Response to pathogen infection (Os07t0516300-01)" |
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| commelinid specific | | |
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| grass specific | Maizemine | [Zm] Protection of telomeres protein 1 |
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| grass specific | Knetminer-rice; | [Zm] Ramosa 2 protein (Fragment) |
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| grass specific | RAP-DB | [Os] "Transcription factor, Transcriptional regulation of miR528, Antiviral response, Defense to rice stripe  virus (RSV) (Os05t0408200-01)" |
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| grass specific | RAP-DB | [Os] "UDP-glucosyltransferase, Cold tolerance (wild rice) (Os05t0527100- |
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| commelinid specific | RAP-DB; Maizemine | [Os] "MADS box transcription factor, Regulator of early seed development (Os02t0170300-01)"; [Zm] B-class MADS-box protein PI |
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| grass specific | RAP-DB | [Os] Apyrase 5 (Os10t0350500-01) |
| grass specific | | |
| grass specific | RAP-DB | [Os] "GAGA-binding transcription factor 1, Negative regulation of seedling growth and grain length development, Suppressor of flowering (Os06t0130600- |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Pentatricopeptide repeat (PPR) protein, Early chloroplast development under cold stress (Os04t0475500-01)" |
| commelinid specific | | |
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| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Protein containing PHD domain, FNIII domain and VID domain, Positive regulator of flowering (Os12t0533500-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Patatin-related phospholipase A, Modulation of longitudinal growth of vegetative tissues and seeds (Os03t0254400-01);Similar to patatin-like protein 3. (Os03t0254400-02)" |
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| grass specific | RAP-DB | [Os] "FCS-like zinc finger (FLZ) protein 20, Submergence response (Os06t0223700-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Transcriptional cofactor, Ortholog of Arabidopsis ANGUSTIFOLIA3(AN3), Regulation of stem, leaf and grain size, Positive regulation of cell proliferation (Os03t0733600-01)"; [Zm] GRF1-interacting factor 1 |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "P-type cyclin, PHO80 homologous protein, Coordination of phosphate starvation signaling and cell cycle progression under phosphate starvation stress (Os02t0652000-01)" |
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| grass specific | RAP-DB | [Os] "Double-stranded RNA-binding protein 2, Modulation of leaf rolling by regulating accumulation of microRNAs related to leaf development (Os10t0480500-01)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 5 (Os06t0176300-01)" |
| grass specific | | |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Red chlorophyll catabolite reductase, Leaf senescence, Wound responses (Os10t0389200-01)" |

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| grass specific | RAP-DB | [Os] "CHZ-domain protein, Histone chaperone, Regulation of chromatin dynamics and genome transcription (Os11t0544600-01);Hypothetical conserved gene. (Os11t0544600-02)" |
| grass specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "NHL domain-containing protein, Determination of panicle architecture, grain shape and grain weight (Os02t0234200-01)" |
| commelinid specific | Knetminer-rice; Knetminer-wheat | |
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| grass specific | Knetminer-wheat | |
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| grass specific | Maizemine | [Zm] Protein WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 1 |
| grass specific | RAP-DB; Maizemine | [Os] "C2H2-type zinc finger transcription factor, Promotion of flowering (Os02t0672100-01)"; [Zm] Naked endosperm1 |

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| commelinid specific | RAP-DB | [Os] "Typical bHLH transcription factor, Negative regulation of leaf angle (Os03t0797600-01);Similar to BHLH transcription factor. (Os03t0797600- |
| grass specific | RAP-DB | [Os] "Homolog of DRO1 (DEEPER ROOTING 1), Control of root system architecture, Root gravitropic response (Os07t0614400-01)" |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Heat stress transcription factor, Plant growth and balancing reactive oxygen species (ROS) during biotic and abiotic stress (Os05t0530400-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] Atypical basic helix-loop-helix transcription factor (Os01t0230200-01) |
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| grass specific | Knetminer-wheat; Maizemine | [Zm] Terpene synthase family |
| commelinid specific | | |
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| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "P-type cyclin, PHO80 homologous protein, Coordination of phosphate starvation signaling and cell cycle progression under phosphate starvation stress (Os04t0544200-01)" |
| grass specific | | |
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| grass specific | in_predefined_specific_set | [Os] "makes (1,3;1,4)-beta-glucan, a component of grass cell walls absent in dicots" |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "Similar to 10A19I.14. (Os05t0580500-01);Rice homolog of yeast REC8, OsRad21-4 protein, Meiotic processes (Os05t0580500-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Component of Exo70 exocyst complex, Response to the fungal effector, AVR-Pii, Pii-dependent resistance (Os04t0382200-01)" |
| commelinid specific | | |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Heat stress transcriptioon factor, High-temperature stress tolerance, Tolerance to environmental stresses (Os03t0795900-01)" |
| grass specific | RAP-DB | [Os] "COBRA-Like (COBL) family protein, Glycosyl-phosphatidyl inositol (GPI)-anchor protein, Regulation of stomatal development (Os03t0301200-01);Glycosyl-phosphatidyl inositol-anchored, plant domain containing protein. (Os03t0301200-02)" |
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| commelinid specific | RAP-DB | [Os] "S-adenosylmethionine decarboxylase, Polyamine biosynthesis, Abiotic stress (Os02t0611200-01);Similar to S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) (Induced stolen tip protein TUB13) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain]. (Os02t0611200-02);Similar to S-adenosylmethionine decarboxylase 2. |
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| grass specific | RAP-DB | [Os] "Rice homolog of ATG7, Autophagy-related protein, Autophagy-dependent lipid metabolism in anther development, Autophagy-mediated regulation of starch metabolism during seed maturation (Os01t0614900-01);Similar to autophagy-related 7. (Os01t0614900-02)" |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Glycine-rich domain (GRD)-containing protein, Regulation of cell death and disease resistance (Os11t0621300-01)" |
| commelinid specific | | |
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| grass specific | Maizemine | [Zm] High mobility group B protein 4 |
| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "bZIP transcription factor, Drought tolerance, Regulation of ABA signaling, Seed germination (Os09t0456200-01)" |
| moncot specific | | |
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| grass specific | RAP-DB | [Os] "GATA transcription factor, Negative regulation of heading date, Positive regulation of panicle development and grain number, Regulation of grain size (Os01t0745700-01);Hypothetical conserved gene. |
| commelinid specific | RAP-DB | [Os] "Pentatricopeptide repeat protein, Chloroplast biogenesis (Os09t0413300-01)" |
| commelinid specific | RAP-DB | [Os] "HIS1-like protein, Fe(II)/2-oxoglutarate-dependent oxygenase (Os06t0176700-01)" |
| commelinid specific | | |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Homologue of the human TATA modulatory factor (TMF), Transcription activator, Negative regulation of cold tolerance through modification of cell wall properties (Os05t0559900-01);Similar to SKIP interacting protein 25. (Os05t0559900-02)" |
| grass specific | RAP-DB | [Os] Homolog of Arabidopsis LHP1 (Os10t0324900-01) |
| grass specific | | |
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| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Hypothetical conserved gene. (Os12t0548200-01);Auxilin-like protein, Type III J-protein, Positive regulation of resistance to Xoo, Regulation of cell death (Os12t0548200- |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Ubiquitin-specific protease, Deubiquitination enzyme, Positive regulation of grain width and size (Os02t0244300-01)" |
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| commelinid specific | RAP-DB | [Os] "Ca2+/CaM-associated transcription factor, Negative regulation of thermotolerance (Os03t0191000- |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "NAC transcription factor, Iron homeostasis (Os05t0426200-02)" |
| grass specific | | |
| commelinid specific | RAP-DB;<br>Knetminer-rice | [Os] "Orthologue of the CLASSY1 gene in Arabidopsis, Anaerobic germination, RNA directed DNA methylation (RdDm) pathway, Control for germination and seedling establishment under flooding (Os07t0692600-01)" |
| commelinid specific | | |
| grass specific | RAP-DB;<br>Knetminer-rice | [Os] "WRKY transcription factor, Negative regulation of abscisic acid and gibberellin signaling in aleurone cells (Os01t0826400-01)" |
| moncot specific | | |
| commelinid specific | | |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Basic helix-loop-helix (bHLH) protein, Maintenance of Fe homeostasis (Os02t0116600-01);Helix-loop-helix DNA-binding domain containing protein. (Os02t0116600-02)" |
| commelinid specific | | |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Similar to Squamosa promoter-binding-like protein 3. (Os02t0139400-01);SBP-domain transcription factor, OsmiR156  target  gene, Regulation of crown root development (Os02t0139400-02)" |

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| grass specific | | |
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| commelinid specific | | |
| grass specific | RAP-DB | [Os] GAGA-binding transcription factor 2 (Os10t0114500-01) |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "NAC transcription factor, Negative regulation of drought tolerance (Os12t0610600-01)" |
| grass specific | | |
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| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Trihelix transcription factor, Positive regulation of responses to salt stress, Salinity adaptation |
| commelinid specific | | |
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| moncot specific | | |
| grass specific | RAP-DB | [Os] "Transglucosidase (Os09t0511600-01);Non-protein coding transcript. (Os09t0511600-02);Glycoside hydrolase, family 1 protein. (Os09t0511600-03);Glycoside hydrolase, family 1 protein. |
| grass specific | RAP-DB | [Os] "Xyloglucan endotransglucosylases/hydrolase, Cell wall modification processes during rice growth and development (Os08t0237000-01)" |
| commelinid specific | | |
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| grass specific | | |
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| grass specific | RAP-DB | [Os] "Similar to Ceramide kinase. (Os02t0656200-01);Ceramide kinase, Modulation of cell fate (Os02t0656200-02);Ceramide kinase (Os02t0656200- |

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| grass specific | RAP-DB | [Os] "a member of the TopoVIB-like protein family, Promotion of meiotic DNA double-strand break (DSB) formation (Os06t0708200-01);Hypothetical conserved gene. (Os06t0708200-02);DNA Topoisomerase VI-B Subunit, Meiotic bipolar spindle assembly, Promotion of meiotic DNA double-strand break (DSB) |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Zinc finger protein, Pre-harvest sprouting resistance (Os07t0585700-01)" |
| grass specific | | |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Cystathionine Î²-synthase (CBS) domain containing protein, Resistance to Magnaporthe oryzae (Os02t0818000- |
| grass specific | RAP-DB | [Os] "Chloroplast-localized small heat shock protein, Tolerance against heat and oxidative stress, Salt tolerance germinability (Os03t0245800-02)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "ARGONAUTE (AGO) family protein, Regulation of anther development (Os04t0615700-01)" |
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| commelinid specific | RAP-DB | [Os] "BBX transcription factor, Regulation of heading date (Os04t0540200-01)" |
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| commelinid specific | RAP-DB | [Os] "Nitrate transporter, Regulation of tiller number and grain yield (Os04t0597600-01);Nitrate transporter, Regulation of tiller number and grain yield (Os04t0597600-02)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Zinc transporter, Preferential distribution of Zn to developing tissues (Os04t0613000-01)" |
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| grass specific | RAP-DB | [Os] Sucrose transporter 5 (Os02t0576600-01) |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Tetratricopeptide repeat (TPR) domain containing protein, Grain size and starch quality (Os04t0645100-01);Similar to H0811D08.1 protein. (Os04t0645100-02)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Modulation of the floral transition, Floral repressor (Os05t0489700-01)" |
| commelinid specific | RAP-DB | [Os] Xylan arabinosyltransferase 6 (Os10t0492200-01) |
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| grass specific | RAP-DB | [Os] "Pentatricopeptide repeat protein, Organellar RNA editing (Os12t0163600-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Homologous recombination initiation factor, Meiotic spindle assembly (Os04t0347800-01)" |
| grass specific | | |
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| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to Extra-large G-protein. (Os12t0593000-01);Extra-large GTP-binding protein, Regulation of plant growth, grain filling, panicle architecture, stress tolerance and disease resistance (Os12t0593000-02)" |
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| commelinid specific | RAP-DB | [Os] "Microtubule-localized IQ-domain containing protein, Modulation of microtubule cytoskeleton dynamics, Regulation of grain shape (Os08t0115200-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Basic helix-loop-helix transcription factor, Nucleotide-binding site leucine-rich repeat (NLR) protein-mediated resistance to rice blast disease (Os03t0135700-01);Transcriptional activator Rb homolog (Fragment). (Os03t0135700- |
| grass specific | | |
| grass specific | RAP-DB | [Os] "ROOT HAIR DEFECTIVE-SIX LIKE (RSL) class I basic helix-loop-helix protein, bHLH transcription factor, Regulation of root hair development |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Prenylated Rab acceptor, Rice PRA1 homolog, Rab effector for vacuolar trafficking (Os05t0474400- |
| grass specific | RAP-DB | [Os] "Similar to Auxin response factor 1. (Os06t0196700-01);Auxin response factor, Transcription factor, Cytokinin-mediated inhibition of phosphate transport, Phosphate signaling, Auxin and phosphate starvation response (Os06t0196700-02)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "MATE (multidrug and toxic compounds extrusion) transporter, Regulation of grain size, Modulation of flavonoid and lignin biosynthesis (Os03t0229500-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Similar to Isoform 2 of Homeobox-leucine zipper protein TF1. (Os01t0788800-01);Similar to Isoform 2 of Homeobox-leucine zipper protein TF1. (Os01t0788800-02);Similar to Isoform 2 of Homeobox-leucine zipper protein TF1. (Os01t0788800-03);HD-GL2 family homeobox protein, Early embryo and endosperm development (Os01t0788800-04)" |
| grass specific | RAP-DB | [Os] "Plant-specific kinesin-14, Processive minus-end-directed microtubule motor (Os04t0467901- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Heat stress transcription factor (Os10t0419300-01);Heat stress transcription factor, Splice variant of OsHsfA6a (Os10t0419300-02)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Polygalacturonase, Pectin degrading enzyme, Regulation of intercellular adhesion, Blast disease-resistance (Os01t0517500-01)" |
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| commelinid specific | RAP-DB | [Os] "Homolog of xylanase inhibitor, Chitinase-like protein, Defense response against pathogens, Growth regulation through calcium signaling (Os01t0937050-01)" |
| grass specific | RAP-DB | [Os] "Wall-associated kinase, Positive regulation of rice blast resistance (Os09t0562600-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Pentatricopeptide repeat (PPR) protein, Chloroplast development under cold stress (Os10t0421800-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Similar to Cytochrome P450 86A1 (EC 1.14.-.-) (CYPLXXXVI) (P450-dependent fatty acid omega-hydroxylase). (Os03t0140200-01);Cytochrome P450 family member, Leaf cuticular wax synthesis |
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| commelinid specific | RAP-DB | [Os] "Kinesin-related protein, Regulation of cell division and plant development (Os02t0810200-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] Tubulin complex-related serine/threonine protein kinase (Os02t0590800-01) |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "A member of the uclacyanin family, Target of OsmiR528, Regulation of pollen intine development (Os08t0137400-01);Cupredoxin domain containing protein. |
| commelinid specific | | |
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| moncot specific | | |
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| moncot specific | RAP-DB; Maizemine | [Os] "Rice Su(var)3-9 homolog (SUVH), Histone methyltransferase, Retrotransposon repression (Os05t0490700-01);Hypothetical gene. (Os05t0490700-02)"; [Zm] Histone-lysine N-methyltransferase |
| grass specific | | |

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| grass specific | RAP-DB | [Os] "Meiosis specific cyclin-like protein, Meiotic double-strand break formation (Os03t0225200-01);Similar to cyclin, N-terminal domain containing protein. (Os03t0225200-02)" |
| commelinid specific | | |
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| commelinid specific | | |
| grass specific | Maizemine | [Zm] Heat shock 22 kDa protein |
| commelinid specific | RAP-DB | [Os] "FW2.2-like gene family protein, Regulation of grain width and weight (Os02t0763000-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to Ethylene receptor-like protein 2. (Os02t0820900-01);Similar to Ethylene receptor-like protein 2. (Os02t0820900-02);Ethylene receptor, Ethylene response, Floral transition and starch accumulation (Os02t0820900- |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Inward rectifying shaker-like potassium channel, Negative regulation of OsKAT2 channel activity (Os02t0245800-01)" |
| commelinid specific | RAP-DB | [Os] "Nuclear-localized pentatricopeptide repeat (PPR) protein, Regulation of mitochondrial development and/or functions, Endosperm development (Os08t0290000-01)" |
| grass specific | | |
| grass specific | Maizemine | [Zm] NADPH HC toxin reductase (Fragment) |
| grass specific | | |
| moncot specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Phosphatidylinositol 4-phosphate 5-kinase, Regulation of heading, Regulation of floral induction genes (Os03t0701800-01);Similar to Isoform 2 of Phosphatidylinositol-4-phosphate 5-kinase 1. (Os03t0701800-02)" |
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| commelinid specific | RAP-DB | [Os] "F-box family E3 ubiquitin ligase, Modulation of primary root meristem activity (Os03t0116800-01);Similar to F-box protein. (Os03t0116800-02)" |
| grass specific | | |
| moncot specific | | |
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| grass specific | Knetminer-rice | |
| moncot specific | | |
| grass specific | RAP-DB | [Os] "Aromatic L-amino acid decarboxylase (AADC), Senescence-induced serotonin biosynthesis (Os08t0140300-01)" |
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| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "DUF966 family protein, Abiotic stress response (Os01t0839200-01)" |
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| commelinid specific | Knetminer-rice | |
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| grass specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Basic helix-loop-helix (bHLH) transcription factor 057, Positive regulation of disease resistance, Drought tolerance (Os07t0543000-01);Similar to Helix-loop-helix-like protein (Fragment). (Os07t0543000- |
| commelinid specific | | |
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| commelinid specific | RAP-DB; Maizemine | [Os] "CRM domain-containing protein, Regulation of chloroplast development, Promotion of the splicing of chloroplast group IIA and IIB introns (Os01t0323300-01)"; [Zm] CRS2-associated factor 2 |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Calmodulin (CaM)-binding transcription factor, Negative regulation of defense response (Os07t0490200-01);Similar to CaM-binding transcription factor. (Os07t0490200- |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Purine permease, Transport of cytokinin, Growth and development control (Os05t0556800-01)" |
| grass specific | | |

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| commelinid specific | Knetminer-rice; Knetminer-wheat | |
| moncot specific | | |
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| grass specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein (Os08t0497300-01);Similar to SEC14 cytosolic factor (Secretion factor 14) family protein (Fragment). (Os08t0497300-02);Similar to phosphatidylinositol transporter/ transporter. (Os08t0497300-03)" |
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| grass specific | RAP-DB | [Os] "WRKY transcription factor, Cold tolerance (Os12t0597700-01);Similar to WRKY DNA binding domain containing protein, expressed. (Os12t0597700- |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Ser/Thr kinase, Generation of proper tension between homologous kinetochores (Os07t0508500-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Tetratricopeptide repeat domain-containing protein, Grain fertility (Os09t0538500-01)" |
| commelinid specific | RAP-DB | [Os] "DNA-dependent RNA polymerase III subunit C4, Pollen sterility in an interspecific hybrid (Os04t0394500- |

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| commelinid specific | RAP-DB | [Os] "Chloroplast-targeted pentatricopeptide repeat (PPR) protein, Chloroplast development and photosynthesis at early leaf stage (Os01t0674700-01)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Fasciclin-like arabinogalactan protein, Positive regulation of pollen exine development, Pollen fertility (Os04t0574200-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Transmembrane kinase TMK1, Control of chloroplast development and leaf senescence, Regulation of ROS homeostasis (Os11t0448000-01)" |
| moncot specific | | |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Circadian-associated rice pseudo response regulator, Control of flowering time (Os02t0618200-01)" |
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| commelinid specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "GnK2 domain containing receptor-like kinase-7, Response to chilling in tolerant rice genotype Volano, Response to Xanthomonas oryzae pv. oryzae in resistant rice genotype (Os10t0136400-00)" |
| grass specific | RAP-DB | [Os] "Double stranded RNA binding domain (dsRBD) containing protein, Regulation of stress responses (Os02t0639000-01)" |
| grass specific | RAP-DB | [Os] "NUCLEAR FACTOR Y (NF-Y) transcription factor, Control of heading date (Os03t0251350-01)" |
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| grass specific | RAP-DB | [Os] "Protease inhibitor, MG1 (M. GRAMINICOLA-RESISTANCE GENE 1)-mediated nematode resistance, MG1 is absent from Nipponbare (Susceptible) (Os12t0437800-01)" |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "FCA-like protein, FCA gamma protein, Flowering time related protein involved in autonomous flowering pathway (Os09t0123200-01);Similar to Flowering time control protein isoform OsFCA-1. (Os09t0123200-02)" |
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| grass specific | RAP-DB | [Os] "Rice NPR1 paralog 3, Disease resistance (Os03t0667100-01);Paralog of Non Expressor of PR genes 1 (OsNPR1), Bacterial blight resistance (Os03t0667100-02);Similar to BTB/POZ domain containing protein, expressed. (Os03t0667100-03)" |
| commelinid specific | RAP-DB | [Os] "Response to drought in tolerant rice genotype Nagina 22, Response to submergence in japonica cultivar Taikeng 9, Response to Xanthomonas oryzae pv. oryzae in resistant rice genotype IRBB21 (Os04t0655300-01)" |
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| grass specific | RAP-DB | [Os] "RING-type E3 ubiquitin ligase, Control of innate immunity and broad-spectrum disease resistance (Os05t0279400-01);Zinc finger, RING-type domain containing protein. (Os05t0279400-02)" |

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| grass specific | RAP-DB | [Os] "Chromodomain, helicase/ATPase, and DNA-binding domain (CHD) protein, Chromatin-remodeling factor, Mi-2-like protein, Crown root development, Chloroplast development in adaxial mesophyll, Maintenance of H3K4me3 (Os07t0497100-01)" |
| grass specific | RAP-DB | [Os] "Bcl-2-associated athanogene (BAG) protein, BAG protein containing a ubiquitin-like (UBL) structure, Plant development (Os09t0524800-01);Apoptosis regulator Bcl-2 protein, BAG domain containing protein. (Os09t0524800-02)" |
| grass specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Glycerol-3-phosphate acyltransferase, Anther development, Pollen formation (Os11t0679700-01)" |
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| commelinid specific | RAP-DB | [Os] "MAPK kinase kinase 11, Ortholog of AtMAPKKK5, Regulation of chitin-induced immune responses |
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| commelinid specific | RAP-DB | [Os] "Metacaspase 1, Response to abiotic and biotic stresses (Os03t0388900-01)" |
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| commelinid specific | RAP-DB | [Os] "B3 domain transcriptional repressor, Regulator of seed germination and seedling development (Os07t0563300-01)" |
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| commelinid specific | RAP-DB | [Os] "WRKY transcription factor 26, Response to M. oryzae infection (Os01t0714800-01)" |
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| grass specific | Knetminer-rice; Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "GA 2-oxidase3, GA metabolism (Os01t0757200-01)" |
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| grass specific | RAP-DB | [Os] "DEAD-box RNA helicase, Early chloroplast development under cold stress, Cold tolerance, Defence responses against biotic and abiotic stresses (Os03t0108600-01)" |
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| grass specific | RAP-DB | [Os] "Alpha/beta-hydrolase receptor Dwarf14 family protein, Establishment of arbuscular mycorrhizal (AM) symbiosis (Os05t0590300-01)" |
| moncot specific | RAP-DB | [Os] "Shikimate kinase domain containing protein. (Os06t0225800-01);Shikimate kinase 2, Defense response, Panicle development |
| grass specific | RAP-DB | [Os] Cytokinin glycosyltransferase (Os01t0805400-01) |
| grass specific | Knetminer-rice; Maizemine | [Zm] RNA polymerase sigma factor |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Serine carboxypeptidase, Regulation of grain filling and seed germination (Os10t0101200-01)" |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Dicer-like protein, Phased small RNA biogenesis (Os10t0485600-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "bZIP transcription factor, Tapetum development (Os09t0489500-01);Similar to DNA binding protein. (Os09t0489500-02)" |
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| grass specific | RAP-DB | [Os] "CONSTANS-like protein, Transcription factor, Repression of flowering, Regulation of plant height and grain yield (Os06t0264200-01)" |
| grass specific | RAP-DB | [Os] "Beta-glucanase 2, Resistance to sheath blight by inhibiting the permeability of plasmodesmata (Os11t0704600-01);Similar to Beta-1,3 glucanase precursor (EC 3.2.1.39). (Os11t0704600-02);Glycoside hydrolase, family 17 protein. |
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| commelinid specific | Knetminer-rice | |
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| commelinid specific | RAP-DB | [Os] "Matrix metalloproteinase, Plant development, Symplastic apoplastic transport (Os02t0740700-01)" |
| commelinid specific | RAP-DB | [Os] "Cytosolic tRNA 2-thiolation protein 2, High-temperature tolerance (Os12t0588900-01);Similar to Cytoplasmic tRNA 2-thiolation protein 2. (Os12t0588900-02)" |
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| grass specific | Knetminer-rice | |
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| commelinid specific | RAP-DB | [Os] "DUF1639 domain containing protein, Positive regulation of ABA responses in seed germination, Tolerance to drought stress, ABA-induced antioxidant defense |
| grass specific | | |
| grass specific | RAP-DB | [Os] "N6-adenine methyltransferase-like (MTL) domain-containing protein, Anther development (Os08t0502000- |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Carbohydrate/purine kinase domain containing protein. (Os01t0851000-01);Plastid-encoded RNA polymerase (PEP)-associated protein, Protection of chloroplast development from heat stress, Chloroplast biogenesis and plant |
| grass specific | | |
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| grass specific | Knetminer-rice | |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "A member of the ASI1-AIPP1-EDM2 (AAE) complex, Rice orthologue of Arabidopsis IBM2 protein, Regulation of rice fertility and flowering time, Mediation of alternative polyadenylation, Control of global poly(A) site usage (Os01t0610300-01)" |

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| grass specific | RAP-DB | [Os] "Putative glucose-methanol-choline oxidoreductase, Regulation of tapetum degeneration and pollen exine formation, Anther cuticle formation (Os10t0524500-01)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Armadillo/beta-catenin repeat family protein, Negative regulation of seed shattering, Regulation of endogenous S-nitrosothiol levels (Os04t0489800-01)" |
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| grass specific | RAP-DB | [Os] "ACC oxidase, Ethylene biosynthesis (Os01t0580500-01)" |
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| grass specific | RAP-DB | [Os] "Plant-specific protein with a short C-terminal coiled-coil domain and a functional NLS, Common symbiosis signaling (SYM) pathway (Os06t0115600-01)" |

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| commelinid specific | RAP-DB; Maizemine | [Os] "Cupin domain protein, Regulation of seed vigour (Os03t0793700-01)"; [Zm] Globulin-2 |
| commelinid specific | RAP-DB | [Os] "bZIP DNA-binding protein, Disease resistance, Vascular development (Os03t0336200-01);Transcription factor RF2b. |
| grass specific |  |  |
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| grass specific | RAP-DB | [Os] "E2F-like protein, E2F homolog (Os12t0158800-01)" |
| grass specific |  |  |
| moncot specific | RAP-DB | [Os] "Similar to AP2-1 protein (Fragment). (Os05t0389000-01);AP2/ERF transcription factor, Regulation of cell elongation and proliferation in root meristem, Organ size control, Nitrogen-responsive regulation of tillering (Os05t0389000-02)" |
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| grass specific | RAP-DB | [Os] "Beta-ketoacyl-CoA Synthase, Drought tolerance, Cuticular wax synthesis (Os01t0529800-01)" |
| grass specific | RAP-DB | [Os] "Ortholog of ZmLG2, bZIP transcriptional factor, Lamina joint positioning and differentiation (Os05t0443900-01)" |
| grass specific |  |  |
| grass specific | RAP-DB | [Os] "Melatonin 2-hydroxylase, Control of the melatonin level in plants (Os04t0667400-01)" |

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| grass specific | | |
| moncot specific | Maizemine | [Zm] Factor of DNA methylation 1 |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Ortholog of Arabidopsis NLA (AtNLA), RING-type E3 ubiquitin-ligase (Os03t0650900-01)" |
| commelinid specific | | |
| grass specific | RAP-DB; Maizemine | [Os] Geranylgeranyl diphosphate synthase (Os07t0580900-01);Similar to GGDP synthase. (Os07t0580900-02); [Zm] Geranyl diphosphate synthase large subunit |
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| commelinid specific | Knetminer-rice | |
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| grass specific | RAP-DB; Maizemine | [Os] "CRM domain protein, Splicing of group IIB introns in chloroplast (Os11t0592400-01)"; [Zm] CRM family member |
| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Clade III SWEET transporter, Sucrose transporter, Regulation of sucrose transport in response to drought and salt stress, TAL effector-mediated susceptibility to bacterial pathogen (Os02t0513100-01)" |
| grass specific | | |
| commelinid specific | | |
| grass specific | Maizemine | [Zm] Chloroplast RNA splicing1 |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Tetratricopeptide repeat (TPR) protein, Promotion of heading by regulating florigen transport (Os03t0200600-01)" |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "A member of the RNA Pol II CTD phosphatase-like family, Positive regulation of brassinosteroid signaling (Os11t0521900-01);Similar to NLI interacting factor-like phosphatase family protein, expressed. (Os11t0521900-02);Similar to NLI interacting factor-like phosphatase family protein, expressed. (Os11t0521900-03)" |
| moncot specific | | |
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| commelinid specific | in_predefined_specific_set | [Os] transporter required for active uptake of Si in grasses |

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| commelinid specific | RAP-DB; Maizemine | [Os] "Major latex protein, Bet v1 family protein, Positive regulation of drought and salinity tolerance (Os04t0465600-01)"; [Zm] Major latex protein 22 |
| grass specific | RAP-DB; Knetminer-rice | [Os] "WRKY transcription factor, Disease resistance against X. oryzae, Drought tolerance (Os08t0499300-01);Similar to WRKY transcription factor 42 (Fragment). (Os08t0499300-02)" |
| grass specific | | |
| grass specific | Maizemine | [Zm] germinal center kinase 1 |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "A member of the synaptonemal complex (SC), OmpH/coiled-coil motif-containing protein, Regulation of meiotic double-strand break (DSB) formation and SC assembly, Meiotic recombination (Os05t0251400-01)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "Splicing isoform of OsRMR1 (Os03t0167500-01);Receptor-like membrane Ring-H2 (RMR) protein, Sorting receptor in transporting vicilin-like storage proteins (Os03t0167500- |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "RNA binding protein, RNA metabolism, Regulation of genes important for plant growth and development (Os01t0265800-01);RNA-binding region RNP-1 (RNA recognition motif) domain containing protein. (Os01t0265800-02)" |
| commelinid specific | RAP-DB | [Os] "Aspartic proteinase, Promotion of programmed cell death (Os03t0186900-01)" |
| commelinid specific | RAP-DB | [Os] "MAPK kinase kinase22, Chloroplast development (Os03t0703400-01)" |
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| grass specific | RAP-DB | [Os] "Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os04t0105100-01);RING E3 ligase, Negative regulation of salt stress response (Os04t0105100-02)" |
| moncot specific | RAP-DB | [Os] "RING finger E3 ligase, Ortholog of Arabidopsis ABI3-interacting protein 2 (AIP2), Control of seed germination and stress responses, Regulation of ABA signaling in germinating seed (Os09t0434200-01);Similar to ABI3-interacting protein 2-1 protein. (Os09t0434200-02)" |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Putative methyltransferase, Pectin methyltransferase, Pectin synthesis and methylesterification, Root development, Cellular adhesion, Salt tolerance, Ion homeostasis (Os02t0755000-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "bZIP transcription factor, Modulation of the floral transition, Floral repressor (Os01t0813100-01)" |
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| commelinid specific | RAP-DB; Knetminer-wheat | [Os] "Similar to CONSTANS interacting protein 6. (Os03t0239200-01);PHD-finger (plant homeodomain-finger) protein, Growth regulator, Transcriptional regulator, Regulator of multiple metal transporter genes (Os03t0239200-02);Protein of unknown function DUF1423, plant domain containing protein. (Os03t0239200-03);Protein of unknown function DUF1423, plant domain containing protein. |
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| commelinid specific | RAP-DB | [Os] "S-Domain receptor like kinase-59, Partial S-domain containing protein, Response to submergence (Os02t0767400-01)" |
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| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Gibberellin 2-oxidase 7, GA catabolism (Os01t0209700-01)" |
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| grass specific | RAP-DB | [Os] "Beta-ketoacyl-CoA synthase, Î²-ketoacyl-CoA synthase, Ethylene biosynthesis, Regulation of plant height (Os10t0472900-01)" |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Homologue of the Arabidopsis thaliana Suppressor of MAX2-1, Negative regulation of arbuscular mycorrhizal symbiosis, Control of strigolactone biosynthesis |
| commelinid specific | | |
| commelinid specific | | |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Cys2/His2-type zinc finger transcription factor, Heading date (Os10t0419200-01)" |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Fatty acyl-CoA reductase 1, Primary fatty alcohol biosynthesis, Drought tolerance (Os09t0567500-01);Similar to Fatty acyl coA reductase. (Os09t0567500-02)" |
| grass specific | RAP-DB | [Os] "YT521-B homology (YTH) family protein, N6-methyladenosine (m6A) binding protein, Regulation of plant height (Os03t0158500-01);Similar to YT521-B-like family protein, expressed. (Os03t0158500-02);Similar to YT521-B-like family protein, expressed. (Os03t0158500-03);Similar to YT521-B-like family protein, expressed. (Os03t0158500-04)" |
| commelinid specific | | |
| grass specific | | |
| moncot specific | | |
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| commelinid specific | RAP-DB | [Os] "E3 ligases of H2Bub1, Transcriptional regulation of anther development (Os04t0550400-01)" |
| commelinid specific | | |
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| grass specific | | |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Ortholog of WSD1 (wax ester synthase/diacylglycerol O-acyltransferase in Arabidopsis), Drought tolerance (Os05t0556300-01)" |
| moncot specific | | |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "P-type pentatricopeptide repeat protein, 5'-end processing of mitochondrial nad5 mRNA, Endosperm development (Os07t0688100-01)" |
| grass specific | RAP-DB | [Os] "Putative zinc finger protein, Negative regulation of salt stress response (Os06t0141200-01)" |
| commelinid specific | | |
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| grass specific | | |
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| grass specific | RAP-DB | [Os] "Aromatic L-amino acid decarboxylase (AADC), Conversion of tyrosine into tyramine (Os01t0770200-01)" |
| commelinid specific | | |
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| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Cyclic nucleotide-gated channel protein, Regulation of resistance to rice blast disease (Os09t0558300-01);Similar to cyclic nucleotide-gated ion channel 14. (Os09t0558300-02)" |
| grass specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "SUMO protease, Ortholog of AtEsd4, Flowering time, Plant height (Os01t0355900-01);Splicing variant of OsELS1 (Os01t0355900-02);Splicing variant of OsELS1 (Os01t0355900-03)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Similar to Auxin response factor 2. (Os01t0670800-01);Ortholog of Arabidopsis ETTIN, Awn development (Os01t0670800-02)" |
| commelinid specific | | |
| commelinid specific | | |
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| grass specific | RAP-DB; Maizemine | [Os] High mobility group (HMG) protein (Os06t0728000-01);HMG1 protein (HMGB1). (Os06t0728000-02); [Zm] DNA-binding protein MNB1B |
| grass specific | | |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Aluminum-activated malate transporter, Maintenance of panicle size and grain yield (Os02t0673100-01);Similar to ALMT3. (Os02t0673100-02)" |
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| grass specific | RAP-DB | [Os] "Floral homeotic gene, Ortholog of Arabidopsis STK (SEEDSTICK), Specification of flower organ identity and meristem determinacy |
| grass specific | RAP-DB | [Os] "Core subunit of exon junction complex (EJC), Embryonic organogenesis and development (Os03t0809900-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Katanin P80 ortholog, Katanin regulatory subunit P80b (Os04t0677700-01)" |
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| commelinid specific | | |
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| commelinid specific | RAP-DB; Knetminer-wheat | [Os] "Microtubule-associated protein 65-3.1, MAP65-3 homologue, Phragmoplast microtubule organization in cytokinesis (Os01t0685900-01);Similar to 65kD microtubule associated protein. (Os01t0685900- |
| moncot specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to B0403H10-OSIGBa0105A11.9 protein. (Os04t0600900-01);Transcriptional activator/repressor, Reguration of KNOX gene, Oskn2 (Regulator of meristem function) (Os04t0600900- |
| grass specific | Maizemine | [Zm] SAUR52-auxin-responsive SAUR family member |
| commelinid specific | | |
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| commelinid specific | | |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Similar to H0112G12.13 protein. (Os04t0661600-01);Similar to H0112G12.12 protein. (Os04t0661600-02);Homolog of MoeA, Molybdenum cofactor biosynthesis (Os04t0661600-03);Molybdopterin biosynthesis protein CNX1 (Os04t0661600-04)" |

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| commelinid specific | RAP-DB | [Os] "Two-pore K+ channel family protein, K+ homeostasis (Os03t0752300-01)" |
| grass specific | | |
| commelinid specific | Maizemine | [Zm] Pentatricopeptide repeat-containing protein |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "CC-type glutaredoxin, Homeostatic regulation of nitrogen use, Hormone signaling, Facilitation of iron utilization (Os01t0667900-01)" |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Basic helix-loop-helix transcription activator, Control of disease resistance, Regulation of salicylic acid (SA) and jasmonic acid (JA) signaling (Os04t0301500-01)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Non-specific lipid transfer protein (nsLTP), Regulation of plant height (Os01t0822900-03);Non-protein coding transcript. (Os01t0822900-04)" |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Endo-(1,3;1,4)-Î²-glucanase, ""Response to wounding, methyl jasmonate, abscisicacid and ethephon"" (Os05t0375400-01)" |
| grass specific | | |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Auxin response factor (ARF) family protein, Transcription factor, Negative regulation of grain size and weight (Os01t0927600-01)" |
| grass specific | RAP-DB | [Os] "Pollen-specific phospholipase, Patatin like phospholipase A, Pollen viability (Os03t0393900-01)" |
| commelinid specific | | |
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| grass specific | Knetminer-rice | |
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| grass specific | Maizemine | [Zm] Glycosyltransferase |
| moncot specific | | |
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| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB; Maizemine | [Os] "Myo-inositol kinase, Phytic acid (PA) biosynthesis (Os03t0737701-01)"; [Zm] Inositol 3-kinase |
| grass specific | | |
| moncot specific | RAP-DB; Maizemine | [Os] "DNA methylation reader, Response to salt stress (Os01t0811300-01)"; [Zm] Histone-lysine N-methyltransferase |
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| moncot specific | | |
| grass specific | Maizemine | [Zm] RRM domain-containing protein |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Inositol 1,3,4-trisphosphate 5/6-kinase 6, Phytic acid biosynthesis, Essential for rice growth and reproduction (Os09t0518700-01);Similar to inositol 1, 3, 4-trisphosphate 5/6-kinase family |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "S-Domain receptor like kinase-65, Partial S-domain containing protein, Response to drought and submergence, Target of SUB1A and ERF66 transcription factors, Response to Xanthomonas oryzae pv. oryzae and Rice Stripe Virus (Os09t0454900-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Plastid ribosomal small subunit protein S6, Chloroplast development at low temperature (Os12t0563200-01)" |
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| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Glucosyltransferase, Insect resistance (Os07t0503500-01);UDP-glucuronosyl/UDP-glucosyltransferase domain containing protein. (Os07t0503500-02)" |
| moncot specific | Knetminer-rice | |
| commelinid specific | | |
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| commelinid specific | | |
| commelinid specific | Knetminer-rice | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Long-chain base kinase, Regulation of disease resistance response and programmed cell death (PCD) (Os10t0516800-01);Diacylglycerol kinase, catalytic region domain containing protein. |
| grass specific | | |
| grass specific | RAP-DB; Knetminer-wheat | [Os] "COMPASS-like complex component, Homolog of Arabidopsis ASH2R, Control of floral transition, Regulation of plant growth and development (Os12t0143200-01)" |
| commelinid specific | | |
| moncot specific | | |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] Protein arginine methyltransferase (Os07t0640000-01) |
| commelinid specific | Knetminer-rice | |
| grass specific | | |
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| moncot specific | RAP-DB | [Os] "Shikimate kinase. (Os04t0640600-01);Similar to OSIGBa0138H21-OSIGBa0138E01.13 protein. (Os04t0640600-02);Shikimate kinase 3, Defense response, Panicle development (Os04t0640600-03)" |
| commelinid specific | | |
| commelinid specific | | |
| grass specific | | |
| moncot specific | Maizemine | [Zm] PPR repeat protein-like |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os01t0779400-01);Snf2 family chromatin remodeling ATPase, Chromatin remodeling factor 706, Negative regulation of alkaline tolerance, Salt and drought stress response, Response to M. oryzae |
| moncot specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Sugar transporter SWEET12, Disease susceptibility to Xoo (Os03t0347500-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Globulin 1 (Fragment). (Os03t0663800-01);FLO2-interacting cupin domain protein, Control of seed fertility and seed quality (Os03t0663800-02)" |
| grass specific | | |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "UDP-3-O-N-acetylglucosamine deacetylase, Regulation of cold tolerance (Os03t0223900-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "La protein, RNA-binding protein, Positive regulation of grain size, Pollen development, Rice growth and development (Os04t0497600-01)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "BAHD acyltransferase-like protein, Control of grain size and leaf angle, Regulation of brassinosteroid homeostasis (Os08t0562500-01);Similar to Acyltransferase. (Os08t0562500-02)" |
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| commelinid specific | RAP-DB | [Os] "NAC transcription factor, Positive regulation of resistance to blast and bacterial blight (Os03t0777000-01)" |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein (Os02t0133200-01)" |

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| commelinid specific | RAP-DB | [Os] "Plastid adenine nucleotide uniporter, Chloroplast development at early leaf stage (Os06t0602700-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Plasma membrane Zn transporter of the Zn-regulated, iron-regulated transporter-like protein (ZIP) family (Os05t0198400-01)" |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "TRITHORAX-like protein, Regulation of H3K4 methylation, Regulation of plant height and pollen grain development (Os01t0218800-01);Similar to SET domain protein. (Os01t0218800-02)" |
| commelinid specific | | |
| grass specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Transcription factor, Regulator for phosphate homeostasis, Positive regulation of grain filling and grain size (Os04t0671900-01);Similar to Auxin response factor 12. (Os04t0671900-02);Similar to Auxin response factor 12. (Os04t0671900-03)" |
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| commelinid specific | RAP-DB | [Os] "GnK2 domain containing receptor-like kinase-5, Response to drought, chilling, and submergence in tolerant genotypes (Os07t0535800-01)" |
| moncot specific | | |
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| grass specific | | |
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| grass specific | RAP-DB | [Os] "Class IIIb chitinase, Family 8 of plant pathogenesis-related protein, Defense against pathogenic fungi (Os10t0416800-03)" |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] Mediator subunit 14_2 (Os09t0281900-01);Similar to SWP (STRUWWELPETER). (Os09t0281900-02) |
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| grass specific | RAP-DB | [Os] S-Domain kinase-11 (Os09t0551251-00) |
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| commelinid specific | RAP-DB | [Os] "bHLH transcription factor, Regulation of iron homeostasis (Os08t0138500-01)" |
| commelinid specific | Maizemine | [Zm] Zinc finger CCCH domain-containing protein 5 |
| grass specific | | |
| commelinid specific | | |
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| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Transcription factor with zinc finger domain and helix-loop-helix domain (YABBY domain), Leaf development (Os04t0536300-01)" |

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| grass specific | RAP-DB; Maizemine | [Os] "Histone H3K9-specific methyltransferase, DNA methylation, Transposition of transposable elements, Genome stability (Os01t0927000-01)"; [Zm] Histone-lysine N-methyltransferase H3 lysine-9 specific |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "UDP-glucosyltransferase, Regulation of grain size and abiotic stress tolerance (Os03t0757500-01)" |
| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "GARP transcription factor, Orthologous to maize Golden2-like 1, Regulation of chloroplast development (Os06t0348800-01);Homeodomain-like containing protein. (Os06t0348800-02);Transfactor-like protein. (Os06t0348800-03)"; [Zm] Transcription activator like |
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| commelinid specific | RAP-DB | [Os] "Rice ortholog of yeast Dre2 and human Anamorsin, Regulation of chitin-induced immune responses (Os04t0674400-01)" |
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| grass specific | RAP-DB | [Os] "Mitochondrial transcription termination factor (mTERF) protein, Chloroplastic protein, Chloroplast development, Photosynthesis establishment, Temperature acclimation (Os07t0583200-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "NAC transcription factor, Drought and salt stress tolerance, Modulation of ABA-mediated pathway (Os03t0133000-01)" |
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| grass specific | Knetminer-rice | |
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| grass specific | Knetminer-wheat | |
| commelinid specific | | |
| commelinid specific | Maizemine | [Zm] Glutathione transferase |
| commelinid specific | | |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "MYELOBLASTOSIS (MYB) transcription factor 36c, Regulation of Casparian strip formation at the root endodermis (Os03t0771100-01)" |
| moncot specific | | |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Pectin methyl esterase, Pollen development (Os03t0309400-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "SUMO protease, Panicle architecture and fertility (Os03t0344300-01);Similar to Ulp1 protease family, C-terminal catalytic domain containing protein, expressed. (Os03t0344300-02);Splicing variant of OsFUG1 (Os03t0344300-03);Splicing variant of OsFUG1 (Os03t0344300-04)" |

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| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "C2H2 zinc finger protein, Transcriptional repressor, Drought tolerance, Positive regulation of plant growth and productivity (Os03t0437100-01)" |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "Chromatin remodeling factor 725, Sucrose non-fermenting 2 (Snf2) family protein, RING finger SNF2 ATPase, Salt and drought stress response, Suppression of rice blast resistance (Os08t0180300-01);Hypothetical conserved gene. (Os08t0180300-02);DEAD-like helicase, N-terminal domain containing protein. |
| grass specific | | |
| moncot specific | Knetminer-rice | |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] E2F transcription factor (Os02t0537500-01) |
| commelinid specific | | |
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| moncot specific | | |
| grass specific | Maizemine | [Zm] HTP reductase |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Rice MEI4 (MEIOSIS INHIBITOR 4)/PRD2 (PUTATIVE RECOMBINATION INITIATION DEFECTS 2) homolog, Double-strand break (DSB) formation in meiosis (Os08t0555800-01)" |
| commelinid specific | | |
| grass specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Regulator of the Magnesium-chelatase subunit ChlH activity, Activation of the ChlH subunit of magnesium chelatase, Chlorophyll synthesis (Os11t0267000-02);GUN4-like domain containing protein. |
| moncot specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Acetyl-serotonin methyltransferase, Target of miR1846e (Os12t0441300-01)" |
| grass specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "WNK (With No Lysine) kinase, Ser/thr protein kinase family member, Abiotic stress tolerance, Internal circadian rhythm (Os07t0572800-01);Hypothetical conserved gene. (Os07t0572800-02)" |
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| commelinid specific | RAP-DB | [Os] "Flavin-containing monooxygenase (FMO), Auxin biosynthesis (Os03t0162000-01)" |
| moncot specific | RAP-DB; Maizemine | [Os] "Plant-specific transcription factor, Regulation of hypersensitive response (HR) cell death (Os01t0816100-01)"; [Zm] NAC domain-containing protein |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Pentatricopeptide repeats protein, Splicing of chloroplast mRNA, Regulation of chloroplast development (Os02t0702000-01)" |
| moncot specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Small calcium-binding protein with one EF-hand motif, Positive regulation of osmotic and salt tolerance (Os06t0683400-02)" |
| commelinid specific | | |

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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Transcription factor involved in the ethylene signal transduction pathway, Positive regulator of ethylene response, Wound signaling (Os03t0324200-01);Similar to cDNA clone:J033123C05, full insert sequence. (Os03t0324200-02)" |
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| commelinid specific | Knetminer-rice | |
| moncot specific | | |
| grass specific | | |
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| commelinid specific | Knetminer-rice | |
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| commelinid specific | RAP-DB | [Os] "Phosphate (Pi) transporter, Root-to-shoot Pi transfer (Os02t0809800-01)" |
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| commelinid specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein (Os05t0267800-01)" |
| grass specific | RAP-DB; Knetminer-rice | [Os] "MYB transcription factor, Regulation of leaf senescence (Os06t0637500-02)" |
| grass specific | Knetminer-wheat | |
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| grass specific | RAP-DB | [Os] "WD40 domain containing protein, Transcription activator of WOX11, Regulation of grain width (Os02t0290300-01)" |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Helix-loop-helix protein, Brassinosteroid signaling (Os06t0226500-01)" |
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| grass specific | RAP-DB | [Os] Thylakoid rhodanese-like protein (Os01t0889800-01) |
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| commelinid specific | RAP-DB | [Os] Rice Sec31p homolog (Os07t0657200-01);WD40/YVTN repeat-like domain containing protein. (Os07t0657200-02);Similar to Sec31p. (Os07t0657200-03);Similar to Sec31p. |
| grass specific | RAP-DB | [Os] "Small epidermal patterning factor-like 2 peptide, Regulation of awn development and grain length (Os02t0756100-01)" |
| grass specific | RAP-DB | [Os] "YT521-B homology (YTH) family protein, N6-methyladenosine (m6A) binding protein, Regulation of plant height (Os03t0748000-01);Similar to YT521-B-like family protein, expressed. (Os03t0748000-02)" |
| grass specific | | |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Protein phosphatase 1 regulatory subunit, Reproductive growth, Regulation of ABA-mediated inhibition of seed germination, ROS homeostasis (Os05t0301600-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "2-oxoglutarate-dependent-Fe (II) dioxygenase, Anther dehiscence, Pollen fertility, Seed initiation, Maintenance of auxin homeostasis in reproductive organs (Os04t0475600-01)" |
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| commelinid specific | RAP-DB | [Os] "HECT-domain E3 ubiquitin ligase, Control of panicle size and grain number (Os12t0428600-01);Similar to predicted protein. (Os12t0428600-02)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Glutamate receptor like protein, Mediation of ion uptake (Os02t0117500-01)" |
| commelinid specific | RAP-DB | [Os] "C2H2-type zinc finger transcription factor, Promotion of flowering (Os09t0560900-01);C2H2 zinc finger protein, Transcription factor, Regulation of flowering time |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "CUE (coupling of ubiquitin conjugation to ER degradation) domain-containing protein, Regulation of cell death and defense response (Os03t0205000-01)" |
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| grass specific | RAP-DB | [Os] "Transcriptional repressor for secondary cell wall formation, Repression of rice lignification, Negative regulation of plant height and grain size, Inhibition of gibberellin signaling |
| commelinid specific | RAP-DB | [Os] "Pentatricopeptide repeat (PPR) protein, Intron splicing, Early chloroplast development (Os06t0710800-01)" |
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| commelinid specific | RAP-DB | [Os] "Yeast ELP1-like protein, the largest subunit of Elongator, Leaf development, Meristem function (Os07t0563700-01)" |
| commelinid specific | Knetminer-rice | |
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| grass specific | Maizemine | [Zm] Cysteine proteinase inhibitor |
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| moncot specific | RAP-DB | [Os] "Subunit of SWITCH/SUCROSE NONFERMENTING (SWI/SNF) chromatin remodeling complex, Negative regulation of drought resistance and root growth (Os11t0183700-01);Hypothetical conserved gene. |
| moncot specific | | |
| grass specific | RAP-DB | [Os] "Plastidic caseinolytic protease, Homolog of Arabidopsis ClpR1, Regulation of chloroplast development, Chloroplast RNA editing |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Ferric reductase oxidase, Fe homeostasis, Salt stress response (Os04t0444800-01);Ferric reductase-like transmembrane component family protein. (Os04t0444800-02)" |
| commelinid specific | RAP-DB | [Os] "Cysteine protease, Autophagy associated gene (Os04t0682000-01)" |
| moncot specific | RAP-DB | [Os] "Acyl-CoA thioesterase, Target of miR1432, Regulation of fatty acid metabolism, Grain filling (Os04t0436100-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Nuclear factor Y (NF-Y) transcription factor C1, CCAAT box binding factor, Heme-associated protein 5A (Os02t0170500-01)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Putative citrate transporter, Citrate-metal hydrogen symport (CitMHS) family protein, Citrate transport and distribution during leaf development (Os03t0147400-01);Similar to cDNA clone:J023091E03, full insert sequence. |
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| moncot specific | RAP-DB | [Os] "S-Domain receptor like kinase-3, Response to Xanthomonas oryzae pv. oryzae in resistant rice genotypes, Response to R. solani (Os01t0784700-00)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Protein phosphatase 2C2, Disease resistance (Os03t0761100-01);Splicing variant of protein phosphatase 2C2 (Os03t0761100-02);Protein phosphatase 2C-like protein. |
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| grass specific | RAP-DB | [Os] "Pentatricopeptide repeat protein, Chloroplast development (Os03t0597200-01)" |
| grass specific | | |
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| grass specific | RAP-DB | [Os] "UDP-glucosyltransferase, Salicylic acid (SA) homeostasis, Disease resistance (Os04t0206700-01);UDP-glucuronosyl/UDP-glucosyltransferase family protein. (Os04t0206700-02)" |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Component of the SCF E3 ubiquitin ligase complex, Jasmonate-regulated defense responses, Regulation of leaf senescence (Os05t0449500-01)" |
| moncot specific | | |

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| grass specific | Maizemine | [Zm] Homeobox-leucine zipper protein ROC3 |
| grass specific | RAP-DB | [Os] Leucine-rich repeat receptor-like kinase (Os02t0153400-01) |
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| moncot specific | RAP-DB | [Os] "Long-chain base kinase, Regulation of disease resistance response and programmed cell death (PCD) (Os04t0541500-01)" |
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| grass specific | Maizemine | [Zm] UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2 |
| commelinid specific | RAP-DB | [Os] "S-Domain receptor like kinase-38, Response to drought, chilling and Xanthomonas oryzae pv. oryzae in tolerant rice genotypes, Response to submergence (Os06t0602500-01)" |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Mannosyl-oligosaccharide glucosidase, N-glycan formation, Auxin-mediated root development (Os01t0921200-01)" |
| grass specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Tryptophan aminotransferase, Indole-3-acetic acid (IAA) biosynthesis (Os01t0169800-01)" |
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| commelinid specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Nitrate and peptide transporters family (NPF) member, Regulation of shoot branching and nitrogen utilization efficiency (Os10t0579600-01);Nitrate and peptide transporters family (NPF) member, Regulation of shoot branching and nitrogen utilization efficiency (Os10t0579600- |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Chloroplast nucleoid-associated protein, Chloroplast development, Regulator of plastid-encoded plastid RNA polymerase (PEP) activity (Os04t0692200-01);Non-protein coding transcript. (Os04t0692200-02)" |
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| grass specific | RAP-DB | [Os] "Cinnamoyl-CoA reductase 21, Response to biotic and abiotic stresses (M. grisea and Xoo infections, UV irradiation and high salinity) (Os02t0180700-01)" |
| commelinid specific | RAP-DB | [Os] "R-R-type MYB-like transcription factor, Response to drought stress during reproductive development (Os05t0442400-01)" |
| moncot specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Nucleoporin, Common symbiosis signaling (SYM) pathway (Os01t0746200-01);Similar to Nucleoporin. (Os01t0746200-02)" |
| moncot specific | | |
| moncot specific | RAP-DB; Knetminer-wheat | [Os] "Fungal elicitor-responsive C2-domain protein, Defense signaling (Os01t0841700-01);Fungal elicitor-responsive C2-domain protein, Defense signaling (Os01t0841700-02)" |
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| grass specific | RAP-DB | [Os] "Guanine nucleotide exchange factor for Rho-type GTPase of plant (ROP/Rac), Pollen germination, Pollen tube growth (Os05t0560100-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Na+ transporter, A member of HKT (high-affinity K+ transporter)-type transporters, Regulation of K+/Na+ homeostasis, Salt tolerance (Os01t0307500-01)" |
| commelinid specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Clade A type 2C protein phosphatase, Negative regulation of ABA signaling, Stomatal closure (Os05t0537400-01);Splicing variant of protein phosphatase 2C50 (Os05t0537400-02)" |
| moncot specific | Knetminer-wheat | |
| moncot specific | RAP-DB | [Os] "BR receptor kinase, Brassinosteroid (BR) perception in the root (Os09t0293500-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Guanosine-tetraphosphate (ppGpp) synthase, RelA/SpoT Homolog 3, Chloroplast biogenesis during early leaf development (Os09t0442600-01)" |
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| grass specific | RAP-DB; Knetminer-rice; Maizemine | [Os] "Zinc finger protein, Heading date (Os06t0275000-01)"; [Zm] Homolog of Constans/Heading date 1 |
| commelinid specific | Knetminer-wheat; Maizemine | [Zm] calcium sensing receptor |
| commelinid specific | RAP-DB | [Os] "Ribbon-helix-helix domain containing protein. (Os02t0741500-01);Nuclear-pore anchor protein, Likely homolog of the vertebrate translocated promoter region protein, Panicle development (Os02t0741500-02)" |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein, Important roles in rice immunity, Response to M. oryzae infection |
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| commelinid specific | Knetminer-rice | |
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| moncot specific | RAP-DB | [Os] "Cytosolic pentatricopeptide repeat protein, Regulation of plastid development and programmed cell death (PCD) in the tapetum, Pollen development (Os02t0110400-01)" |
| moncot specific | RAP-DB | [Os] "DUF1644 family protein, Salt tolerance (Os01t0612600-01)" |
| moncot specific | | |
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| commelinid specific | Maizemine | [Zm] Protein TRIGALACTOSYLDIACYLGLYCEROL 4 |
| grass specific | Maizemine | [Zm] Tasselseed2-like short-chain dehydrogenase/reductase (Fragment) |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Similar to WRKY DNA binding domain containing protein, expressed. (Os12t0507300-00)" |
| moncot specific | RAP-DB; Knetminer-rice | [Os] "Mitochondrial Fe transporter, Essential for plant growth and development, Fe homeostasis (Os03t0296800-01);Hypothetical conserved gene. (Os03t0296800-02)" |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "GRAS family protein, N-acetylchitooligosaccharide elicitor-responsive protein, Pathogen-induced defense response (Os07t0545800-01)" |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "Glycosyl hydrolase, GH10 family protein, Modulation of defence response, Contrasting roles in immunity depending on the type of pathogens (hemibiotrophic vs necrotrophic) |

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| commelinid specific | Knetminer-rice | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Leucoanthocyanidin dioxygenase, Cold and salt stress response (Os03t0289800-01)" |
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| commelinid specific | RAP-DB | [Os] "NRR alternative splicing variant, Regulation of root development in response to macronutrient deficiency (Os05t0595300-01);CCT domain-containing protein, Regulator of starch synthesis, Regulation of root development in response to macronutrient deficiency |
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| commelinid specific | RAP-DB | [Os] "Bcl-2-associated athanogene (BAG) protein, BAG protein containing a ubiquitin-like (UBL) structure, Plant development (Os08t0546100-01)" |
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| moncot specific | RAP-DB | [Os] "Lysin motif-containing protein, Pattern recognition receptor, Peptidoglycan and chitin perception in innate immunity (Os06t0208800-01)" |
| grass specific | RAP-DB | [Os] "Calcineurin B-like protein-interacting protein kinase 7, Cold sensing (Os03t0634400-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Trehalose-6-phosphate phosphatase, Trehalose biosynthesis, Chilling tolerance (Os02t0661100-01);Similar to Trehalose-phosphate phosphatase. (Os02t0661100-02)" |
| moncot specific | RAP-DB | [Os] Class-XIV kinesin (Os07t0105700-01) |
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| grass specific | RAP-DB | [Os] "Defensin-like protein, Antimicrobial peptide, Positive regulation of Cd accumulation in rice leaves, Mediation of Cd efflux from cytosol into extracellular spaces via chelation, Pathogen defense |
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| moncot specific | Maizemine | [Zm] Anthranilate O-methyltransferase 1-like |
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| commelinid specific | RAP-DB | [Os] "PfkB family fructokinase, WLP2 paralog, Chloroplast biogenesis and plant growth, Protection of chloroplasts under heat stress (Os03t0602600-01)" |
| moncot specific | RAP-DB | [Os] "Potassium transporter, Potassium mediated growth, Salt tolerance (Os04t0401700-01);Similar to Isoform 2 of Potassium transporter 1. (Os04t0401700-02);Potassium transporter 1 (OsHAK1). Splice isoform 2. (Os04t0401700-03)" |
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| commelinid specific | RAP-DB | [Os] "Similar to Gda-1 protein. (Os01t0550300-01);N-rich protein, Blast disease resistance (Os01t0550300- |
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| moncot specific | RAP-DB | [Os] DNA replication helicase 2_8 (Os03t0160400-01) |
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| commelinid specific | RAP-DB; Maizemine | [Os] "Homolog of Arabidopsis suppressor of gene silencing 3, Cofactor of RNA-dependent RNA polymerase, Defense response to virus (Os12t0197500-01);Similar to Protein SUPPRESSOR OF GENE SILENCING 3 homolog. (Os12t0197500-02);Similar to Protein SUPPRESSOR OF GENE SILENCING 3 homolog. (Os12t0197500-03)"; [Zm] Suppressor of gene silencing |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Similar to Protein kinase-like protein. (Os12t0230200-01);Calcium-dependent protein kinase 29, Regulation of pollen development (Os12t0230200-02)" |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Cell-wall invertase, Sucrose metabolism in the early stages of caryopsis development (Os02t0534400-01)" |
| commelinid specific | Maizemine | [Zm] U6 snRNA phosphodiesterase |
| commelinid specific | RAP-DB | [Os] Apyrase 2 (Os03t0378000-01) |
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| grass specific | RAP-DB | [Os] "bHLH transcription factor, Positive regulation of brassinosteroid signaling and leaf inclination, Regulation of lamina joint bending (Os04t0641700- |
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| commelinid specific | Knetminer-rice | |

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| commelinid specific | RAP-DB;<br>Knetminer-wheat | [Os] "Component of the SCF E3 ubiquitin ligase complex, Jasmonate-regulated defense responses, Promoting leaf senescence (Os01t0853400-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "S-Domain receptor like kinase-25, Response to Xanthomonas oryzae pv. oryzae. (Os04t0356600-01)" |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Fertilization barrier 1 protein, Double fertilization (Os03t0296600- |
| commelinid specific | | |
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| commelinid specific | RAP-DB;<br>Maizemine | [Os] "Plastid-localized pentatricopeptide repeat (PPR) protein, Plant growth and pollen development, RNA editing of chloroplast rps8 mRNA (Os03t0215900-01)"; [Zm] Smr domain-containing protein |
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| grass specific | Knetminer-wheat | |
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| moncot specific | RAP-DB | [Os] "Putative cytochrome P450, CYP704A3, Target gene of miRNA (osa-miRf10422-akr), Control of seed length (Os04t0573900-01);Similar to cDNA clone:001-036-C03, full insert sequence. (Os04t0573900-02);Similar to cytochrome P450. (Os04t0573900- |
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| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] Control of wax biosynthesis (Os06t0132500-01) |
| commelinid specific | RAP-DB; Maizemine | [Os] "Rice PISTILLATA ortholog, MADS-box protein, Lodicule and stamen development (Os01t0883100-01)";<br>[Zm] PISTILLATA-like MADS-box transcription factor (Fragment) |
| grass specific | | |
| moncot specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Similar to H0219H12.10 protein. (Os04t0460600-01);NAC transcription factor, Regulation of shoot branching, plant height and flowering time (Os04t0460600-02)" |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-wheat | [Os] "Tryptophan aminotransferase, Indole-3-acetic acid (IAA) biosynthesis, Grain development (Os05t0169300-01);Similar to Tryptophan aminotransferase. (Os05t0169300-02)" |
| grass specific | | |
| grass specific | RAP-DB | [Os] "GRAS-domain transcription factor, Strigolactone (SL) biosynthesis (Os03t0408600-01)" |
| commelinid specific | | |
| moncot specific | | |
| commelinid specific | | |

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| grass specific | RAP-DB | [Os] "NAC protein, Homolog of Arabidopsis CUC3, Control of meristem/organ boundary specification (Os08t0511200-01)" |
| grass specific | RAP-DB | [Os] O-methyltransferase (Os08t0498100-01) |
| commelinid specific | Knetminer-rice | |
| grass specific | | |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Amino acid permease, Transport of amino acids (Os06t0556000-01)" |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | | |
| grass specific | | |
| grass specific | | |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Paralog of FACTOR OF DNA METHYLATION LIKE 1 (OsFDML1), Regulation of flower development (Os01t0126600-01)" |
| grass specific | | |
| commelinid specific | | |
| grass specific | | |
| moncot specific | | |
| moncot specific | | |
| moncot specific | RAP-DB | [Os] "U-box type E3 ubiquitin ligase, Negative regulation of drought and salinity stress (Os04t0348400-01)" |
| moncot specific | | |
| commelinid specific | | |

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| moncot specific | RAP-DB; Knetminer-rice | [Os] "MADS-box transcription factor, Regulator of both biotic and abiotic stress responses (Os08t0112700-01)" |
| grass specific | | |
| commelinid specific | | |
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| moncot specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB; Maizemine | [Os] "S-Domain receptor like protein-8, Response to drought, Response to chilling in tolerant genotypes (Os03t0422800-01)"; [Zm] Receptor-like serine/threonine-protein kinase |
| grass specific | | |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Guanine nucleotide exchange factor 3, Small GTPase regulator, Regulation of grain size and plant height (Os02t0662200-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "P-type pentatricopeptide repeat protein, Chloroplast RNA splicing, Regulation of chloroplast development under low-temperature conditions (Os08t0191900-01)" |
| commelinid specific | | |
| commelinid specific | | |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "WRKY transcription factor 88, SA-dependent Xa1-mediated resistance to Xoo (Os07t0596900-01)" |
| commelinid specific | | |

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| commelinid specific | Knetminer-rice | |
| commelinid specific | RAP-DB; Knetminer-wheat | [Os] "Similar to MADS-box transcription factor 15. (Os07t0108900-01);APETALA1 (AP1)/ FRUITFULL (FUL)-like MADS box transcription factor, Specification of inflorescence meristem identity, sexual reproduction |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | | |
| grass specific | RAP-DB | [Os] SNF7 paralog (Os11t0123500-01) |
| moncot specific | | |
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| commelinid specific | RAP-DB | [Os] "Chorismate mutase, Resisitance to bacterial leaf blight (BLB) disease (Os08t0441600-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "YT521-B homology (YTH) family protein, N6-methyladenosine (m6A) binding protein, Regulation of plant height (Os07t0170300-01)" |
| moncot specific | RAP-DB | [Os] "Similar to predicted protein. (Os10t0431000-01);Rice homolog of Arabidopsis PQT3 encoding an E3 ubiquitin ligase, Negative regulation of abiotic (oxidative and salt) stress resistance (Os10t0431000-03)" |
| grass specific | | |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "Plastid RNA-binding protein, Regulation of chloroplast RNA metabolism, Early chloroplast development under cold stress (Os03t0656900-01)" |

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| grass specific | | |
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| commelinid specific | Knetminer-rice | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Receptor-like cytoplasmic kinase, Regulation of leaf rolling, Modulation of bulliform cell development (Os06t0166900-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Sad1/UNC-84 (SUN) domain protein, Promotion of telomere clustering and homologous pairing in meiosis (Os01t0267600-01)" |
| commelinid specific | | |
| grass specific | | |
| moncot specific | | |
| commelinid specific | Maizemine | [Zm] SAWADEE domain-containing protein |
| commelinid specific | | |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "Salicylic acid hydroxylase 3, Disease resistance, SA homeostasis (Os04t0581100-01)" |
| grass specific | RAP-DB | [Os] "Actin depolymerizing factor, Actin-binding protein, Abiotic stress response (Os03t0820500-01)" |
| commelinid specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class IV ML protein (Os03t0788200-01)" |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Glycosyltransferase, Plant and endosperm development, Regulation of sphingolipid synthesis (Os05t0540000-01)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Xylan glucuronosyltransferase, Accumulation of cellulose and hemicellulose in the cell wall deposition (Os01t0880200-01);Similar to secondary cell wall-related glycosyltransferase family 8. (Os01t0880200-02);Similar to cDNA clone:J013112C08, full insert sequence. (Os01t0880200-03)" |
| grass specific | | |
| commelinid specific | RAP-DB | [Os] "ACC oxidase, Ethylene biosynthesis (Os11t0186900-01)" |
| commelinid specific | | |
| moncot specific | | |
| moncot specific | RAP-DB; Knetminer-rice | [Os] "CONSTANS-like protein, Heading promotion under long-day condition (Os02t0724000-01)" |
| moncot specific | RAP-DB | [Os] DNA replication helicase 2_1 (Os04t0588200-01) |
| commelinid specific | | |
| moncot specific | | |
| grass specific | Maizemine | [Zm] Barley mlo defense gene |
| moncot specific | | |

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| commelinid specific | Maizemine | [Zm] High chlorophyll fluorescence106c |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Intracellular Ras-group-related leucinerich repeat protein 1 (Os04t0605300-01);Leucine-rich repeat, typical subtype containing protein. (Os04t0605300-02)" |
| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "Kelch-domain-containing F-box protein, Component of an SCF E3 ligase, Regulation of anther and root secondary cell wall thickenings, Regulation of lignification (Os01t0659900-01)" |
| moncot specific | RAP-DB | [Os] "S-Domain receptor like kinase-40, Response to drought stress in tolerant genotypes, Response to Rice Stripe Virus and B. glumae (Os07t0550900- |

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| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Cytokinin oxidase/dehydrogenase 3, Control of panicle architecture and grain number (Os10t0483500-01)" |
| commelinid specific | | |
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| grass specific | RAP-DB; Knetminer-rice | [Os] "Auxin response factor 25, Target gene of miR167d, Regulation of flower opening and stigma size (Os12t0613700-01);Similar to Auxin response factor 25. (Os12t0613700-02)" |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "A2-type cyclin, Stomatal and root development, Required for the asymmetric entry divisions to produce guard mother cell (GMC) at the early stage of stomatal development (Os12t0502300-01)" |
| grass specific | | |
| commelinid specific | | |
| grass specific | Knetminer-rice | |
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| moncot specific | RAP-DB | [Os] "Voltage-dependent anion channel 3, Mitochondrial porin (Os01t0588200-01);Voltage-dependent anion channel. (Os01t0588200-02)" |

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| moncot specific | RAP-DB | [Os] "Extensin-like protein, Lodging resistance, Regulation of cell elongation and cell wall thickening (Os10t0371000-01)" |
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| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Arginine decarboxylase, Chilling stress response (Os06t0131300-01)" |
| moncot specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Zinc-finger homeobox transcription factor, Promotion of root meristem activity, Ethylene biosynthesis (Os08t0479400-01)" |
| grass specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "GTPase-activating protein, Regulation of vesicle trafficking from trans-Golgi network to plasma membrane or central vacuole |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] Lipoate-protein ligase A (Os08t0435800-01) |

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| moncot specific | RAP-DB;<br>Knetminer-rice | [Os] "Similar to Lipoxygenase. (Os04t0447100-01);Type-2 13-lipoxygenase, Control of hull splitting (Os04t0447100-02)" |
| moncot specific | | |
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| commelinid specific | RAP-DB | [Os] "RING-type E3 ubiquitin ligase, Positive regulation of basal resistance against M. oryzae (Os06t0608800-01);Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os06t0608800-02);Similar to Copine-1. (Os06t0608800-03);Zinc finger, RING/FYVE/PHD-type domain containing protein. (Os06t0608800- |
| commelinid specific | | |
| grass specific | | |
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| moncot specific | RAP-DB | [Os] "Ortholog of maize ZmSWEET4c, Hexose transporter, Seed filling (Os02t0301100-01)" |
| moncot specific | | |
| grass specific | RAP-DB | [Os] "WD40 subfamily protein, Salt stress (Os08t0408200-01)" |
| moncot specific | | |
| commelinid specific | Knetminer-rice | |
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| grass specific | RAP-DB | [Os] "Leucine-rich repeat receptor-like kinase, Regulation of salt stress tolerance (Os05t0305900-01);Protein kinase, core domain containing protein. (Os05t0305900-02)" |
| commelinid specific | | |
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| commelinid specific | Maizemine | [Zm] Pentatricopeptide repeat-containing protein |
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| grass specific | RAP-DB | [Os] "Nitrate-inducible and autorepressible transcriptional repressor, Nitrogen response (Os02t0325600-01);Similar to Phosphate starvation response regulator-like protein. (Os02t0325600- |
| moncot specific | | |
| commelinid specific | | |
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| grass specific | in_predefined_specific_set | [Os] specifies spikelet identity in rice inflorescence |
| moncot specific | | |
| grass specific | RAP-DB | [Os] "S-Domain kinase-6, Response to drought in tolerant genotype, Response to Xanthomonas oryzae pv. Oryzae and R. solani. (Os04t0631800-00)" |
| moncot specific | | |
| grass specific | RAP-DB | [Os] "Rice homologue of mammalian X-ray repair cross complementing 1 (XRCC1), DNA repair (Os06t0144000- |
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| grass specific | RAP-DB; Maizemine | [Os] "Similar to Cystatin (Fragment). (Os05t0494200-01);Cysteine proteinase inhibitor (cystatin), Oryzacystatin-II (Os05t0494200-02)"; [Zm] Cysteine proteinase inhibitor |
| commelinid specific | | |
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| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "SPX domain-containing protein, Phosphate (Pi) homeostasis, Negative regulation of leaf inclination (Os06t0603600-01);SPX domain-containing protein, Phosphate (Pi) homeostasis (Os06t0603600-02)" |
| commelinid specific | | |
| moncot specific | | |
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| moncot specific | | |
| moncot specific | Knetminer-rice | |
| moncot specific | RAP-DB | [Os] "Serpin protein, Serine proteinase inhibitor, Negative regulation of pathogen, UV and salt-induced cell death, Regulation of tillering (Os03t0610650-01)" |
| moncot specific | RAP-DB; Knetminer-rice | [Os] "Similar to Histidine kinase. (Os02t0738400-01);Histidine kinase, Cytokinin signaling (Os02t0738400-02)" |
| commelinid specific | RAP-DB | [Os] "Similar to cDNA clone:J013000F18, full insert sequence. (Os07t0630900-01);Cellulose synthase like protein A7 (Os07t0630900-02)" |
| moncot specific | | |
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| commelinid specific | RAP-DB | [Os] "Gibberellin 13-oxidase, Cytochrome P450 714B1, Negative regulation of plant growth, GA homeostasis (Os07t0681300-01)" |
| commelinid specific | | |
| moncot specific | Knetminer-rice | |
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| grass specific | | |
| commelinid specific | | |
| moncot specific | Knetminer-rice; Knetminer-wheat | |
| moncot specific | RAP-DB | [Os] "Homolog of fluorescent (FLU) in Arabidopsis thaliana, Tetratricopeptide repeat (TPR)-containing protein, Regulation of chlorophyll biosynthesis (Os01t0510600-01)" |
| moncot specific | RAP-DB | [Os] "Low-affinity nitrate transporter, Ortholog of Arabidopsis NRT1.5/AtNPF7.3, Mediation of nitrate allocation (Os02t0689900-01)" |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "5'-3' exoribonuclease, Resistant to viral infection (Os03t0794800-01);Hypothetical conserved gene. (Os03t0794800-02)" |
| commelinid specific | | |
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| grass specific | | |
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| commelinid specific | RAP-DB | [Os] "GDSL esterase/lipase protein, Mediation of lipid homeostasis, Anther development, Pollen fertility (Os02t0290900-01)" |
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| moncot specific | Maizemine | [Zm] Protein kinase domain-containing protein |
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| commelinid specific | RAP-DB | [Os] "Guanine nucleotide exchange factor for Rho-type GTPase of plant (ROP/Rac), Pollen germination, Pollen tube growth (Os02t0272300-01)" |
| grass specific | RAP-DB | [Os] "Putrescine hydroxycinnamoyl acyltransferase 3, Hydroxycinnamoylputrescine (HP) biosynthesis, Contribution to defense and cell death (Os09t0543900-01);Transferase family protein. |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "C2 domain-containing protein 49, Cold stress response (Os06t0297800-01);Similar to predicted protein. (Os06t0297800-02)" |
| commelinid specific | | |
| moncot specific | | |
| moncot specific | | |
| grass specific | RAP-DB | [Os] Protein arginine methyltransferase (Os10t0489100-01) |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Similar to NAC-type transcription factor. (Os01t0191300-01);Similar to NAC-type transcription factor. (Os01t0191300-02);NAC transcription factor, Drought resistance (Os01t0191300-03)" |

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| grass specific | RAP-DB | [Os] "Oxalate oxidase 2, Positive regulation of panicle blast resistance (Os03t0693800-01)" |
| grass specific | RAP-DB | [Os] "Cytochrome P450 87A3, Auxin signaling in the regulation of coleoptile growth (Os04t0570000-01)" |
| commelinid specific | | |
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| commelinid specific | | |
| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Solanesyl diphosphate synthase, Supply of solanesyl diphosphate for ubiquinone-9 (UQ-9) biosynthesis in mitochondria (Os06t0678200-01)" |
| moncot specific | | |
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| commelinid specific | RAP-DB | [Os] "Hexokinase 10, Pollen-specific hexokinase (Os05t0375100-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Putative splicing factor 3b subunit 3 (SF3b3), Regulation of cell death and resistance responses (Os07t0203700-01)" |
| moncot specific | | |
| commelinid specific | | |
| grass specific | RAP-DB | [Os] "ER-associated degradation (ERAD)-related E2 ubiquitin conjugating enzyme, Regulation of grain size and weight through the brassinosteroid signaling pathway (Os03t0308000-01)" |

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| moncot specific | RAP-DB; Maizemine | [Os] Similar to T3/T7-like RNA polymerase (Fragment). (Os06t0652000-01);Similar to DNA-directed RNA polymerase. (Os06t0652000-02);Nuclear-encoded plastid RNA polymerase (Os06t0652000-03); [Zm] |
| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Similar to cDNA clone:J023049H21, full insert sequence. |
| commelinid specific | | |
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| commelinid specific | | |
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| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Pre-mRNA splicing factor, Accessory spliceosome protein, Regulation of grain length and panicle architecture (Os06t0711600-01);mRNA splicing factor SYF2 family protein. (Os06t0711600-02)" |
| grass specific | | |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "ABC Transporter, Half-size ATP-binding cassette transporter, Control of long-distance transport of cytokinins from root to shoot, Promotion of grain yield (Os08t0167000-01)" |
| commelinid specific | RAP-DB | [Os] "Glucose-methanol-choline (GMC) oxidoreductase family protein, Hybrid breakdown (HB) (Os02t0621800-01)" |

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| commelinid specific | | |
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| commelinid specific | RAP-DB | [Os] "Peptide deformylase 1B, Development of chloroplast and mitochondria (Os01t0637600-01)" |
| commelinid specific | | |
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| commelinid specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Similar to Farnesyltransferase beta subunit. (Os01t0737800-01);Î²-subunit of farnesyltransferase, Negative regulation of primary root growth under nonstressed conditions, Response to ABA and drought stress (Os01t0737800- |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | | |
| commelinid specific | | |
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| grass specific | RAP-DB | [Os] "Homologue of Arabidopsis FLOWERING PROMOTING FACTOR1 (FPF1), ACE1 homologue, Control of internode elongation during the reproductive phase (Os07t0671000- |
| commelinid specific | RAP-DB | [Os] "Similar to predicted protein. (Os01t0798500-01);Hypothetical chloroplast open reading frame 3 (Ycf3)-interacting protein 1, Thylakoid protein, Saline and alkaline tolerance (Os01t0798500-02)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] Hypothetical conserved gene. (Os03t0657400-00) |
| moncot specific | | |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Sucrose transporter, Member of the clade III SWEET family, Sugar transport-dependent male fertility, Potential bacterial leaf blight susceptibility (Os09t0508250-01);Similar to MTN3. (Os09t0508250- |
| commelinid specific | | |
| commelinid specific | Knetminer-wheat | |
| moncot specific | | |
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| grass specific | | |
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| moncot specific | | |
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| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] Myosin heavy chain class VIII A2 protein (Os07t0562800-01);Similar to Myosin heavy chain class VIII A2 protein. (Os07t0562800-02);Similar to Myosin heavy chain class VIII A2 protein. (Os07t0562800-03);Myosin heavy chain class VIII A1 protein |
| commelinid specific | | |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Cytochrome P450 family member, Homolog of Arabidopsis MORE AXILLARY GROWTH 1 (MAX1), Regulation of tiller number by fertilization (Os02t0221900-01);Similar to Cytochrome P450 monooxygenase. (Os02t0221900-02);Similar to Cytochrome P450 monooxygenase. |
| commelinid specific | | |

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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Shikimate kinase-like 2 protein, Positive regulation of salt and drought tolerance (Os10t0577700-01)" |
| commelinid specific | | |
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| moncot specific | | |
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| grass specific | | |
| commelinid specific | | |
| commelinid specific | Knetminer-rice | |
| commelinid specific | RAP-DB | [Os] "Xyloglucan backbone O-acetyltransferase 4, DUF231 protein (Os06t0273500-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "DNA replication helicase 2_15, Drought and salt stress response (Os02t0684150-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Pectin methylesterase 14, Aluminum-induced inhibition of root elongation (Os04t0458900-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Nicotianamine aminotransferase, Response to iron deficiency, Biosynthesis of mugineic acid family phytosiderophores (Os02t0306401-01)" |
| grass specific | | |
| commelinid specific | | |
| moncot specific | | |

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| grass specific | RAP-DB; Knetminer-rice | [Os] "NADPH oxidase, Disease resistance (Os01t0360200-01);Similar to Respiratory burst oxidase homolog. (Os01t0360200-03)" |
| commelinid specific | | |
| grass specific | | |
| moncot specific | | |
| moncot specific | Knetminer-rice | |
| grass specific | | |
| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice | [Os] "Protein phosphatase 2C, Negative regulation of XA21-mediated innate immune response and cell death (Os03t0821300-01);Similar to Protein phosphatase 2C 35. (Os03t0821300- |
| moncot specific | | |
| commelinid specific | | |
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| grass specific | Maizemine | [Zm] Diacylglycerol kinase |
| moncot specific | | |
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| commelinid specific | Maizemine | [Zm] Adenylate isopentenyltransferase 5 |
| moncot specific | | |
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| moncot specific | | |
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| commelinid specific | Maizemine | [Zm] methylecgonone reductase-like |
| commelinid specific | | |
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| commelinid specific | | |
| moncot specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Lateral organ boundary domain (LBD)-containing protein, LBD transcription factor, Regulation of constitutive aerenchyma and lateral root formation (Os01t0825000-01)" |
| moncot specific | | |
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| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Ribosomal L32-like protein, Aluminum tolerance (Os03t0168900- |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "Caleosin-like peroxygenase, Response to abiotic stress (Os06t0254700-01)" |
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| commelinid specific | RAP-DB | [Os] "Phosphatidylinositol transfer protein, Class III SEC14 protein (Os03t0219100-01)" |

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| commelinid specific | | |
| commelinid specific | Maizemine | [Zm] adenylate isopentenyltransferase 5 |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | Maizemine | [Zm] Pentatricopeptide repeat-containing protein |
| commelinid specific | | |
| moncot specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Expansin, Al-inducible expansin, Root cell elongation (Os04t0583500-01);Similar to Expansin-A10. (Os04t0583500-02)" |
| moncot specific | | |
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| grass specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Lipid transfer protein, Receptor kinase CRINKLY 4 (CR4) interacting protein, Regulation of seed development and germination, Regulation of seed quality (Os03t0369100-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] Similar to SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor. (Os05t0586600-01);Potential plastid sigma factor of RNA polymerase |

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| moncot specific | RAP-DB; Knetminer-wheat | [Os] "Protein disulfide isomerase-like enzyme, Starch synthesis, Maturation of proglutelin in endosperm (Os11t0199200-01);Similar to Protein disulfide isomerase. (Os11t0199200-02)" |
| commelinid specific | | |
| grass specific | RAP-DB; Knetminer-rice; Knetminer-wheat | [Os] "High-affinity K+ transporter (HKT) family protein, Na+ exclusion from leaf blade upon salt stress (Os04t0607600-01)" |
| commelinid specific | | |
| moncot specific | RAP-DB; Knetminer-rice | [Os] "Cytochrome P450 90A3, Maintenance of plant architecture by modulating brassinosteroid biosynthesis (Os11t0143200-01)" |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "YUCCA protein, Indole-3-acetic acid (IAA) biosynthesis, Control of IAA production in developing rice grain (Os01t0273800-01)" |
| commelinid specific | | |
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| moncot specific | RAP-DB | [Os] "Pectate lyase (PEL) precursor, Maintenance of normal cell division, Induction of leaf senescence (Os10t0457200-01)" |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Cellular retinaldehyde-binding/triple function, C-terminal domain containing protein. (Os02t0752000-01);Phosphatidylinositol transfer protein, Class III SEC14 protein |
| commelinid specific | | |
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| moncot specific | RAP-DB; Knetminer-rice | [Os] "Sucrose transporter, TAL effector PthXo2-dependent disease susceptibility to bacterial pathogen (Os12t0476200-01)" |
| commelinid specific | Maizemine | [Zm] Guanylyl cyclase 1 |
| commelinid specific | | |
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| commelinid specific | RAP-DB; Knetminer-rice | [Os] "Kinesin 13 protein, Regulation of grain length and plant height, Negative regulation of the BR signaling (Os05t0154700-01)" |
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| moncot specific | Knetminer-rice; | [Zm] Stress-induced transcription factor NAC1 |
| commelinid specific | | |
| moncot specific | | |
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| commelinid specific | RAP-DB; Maizemine | [Os] "Phytochrome A, Photoreceptor (Os03t0719800-01)"; [Zm] Phytochrome |
| commelinid specific | | |
| commelinid specific | | |
| commelinid specific | RAP-DB | [Os] "Amyloplast-localized protein containing DUF490, Regulation of starch grain sizes (Os01t0179400-01)" |
| moncot specific | RAP-DB; Knetminer-rice; Knetminer-wheat; Maizemine | [Os] "Calcium-binding protein, Annexin, Heat and drought stress tolerance (Os02t0753800-01)"; [Zm] Annexin |
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| commelinid specific | RAP-DB | [Os] "Hypothetical conserved gene. (Os06t0657500-01);AP2/ERF transcription factor (Os06t0657500-02);AP2/ERF transcription factor, Regulation of trichome formation (Os06t0657500-03)" |
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| commelinid specific | RAP-DB | [Os] "Metacaspase 6, Response to abiotic and biotic stresses (Os01t0799900-01)" |
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| moncot specific | RAP-DB | [Os] "Ca2+/CaM-associated transcription factor, SCT1 homologue, Negative regulation of thermotolerance (Os10t0375600-01)" |
| moncot specific | | |
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| commelinid specific | | |
| grass specific | Knetminer-rice | |
| moncot specific | | |

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| commelinid specific | in_predefined_specific_set | [Hv] contains a monocot-specific motif that confers nitrate-sensitivity to guard cell anion channel |
| moncot specific | | |
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| commelinid specific | RAP-DB;<br>Knetminer-rice | [Os] "Cell-wall invertase, Carbon partitioning during early grain filling, Regulation of endosperm development (Os04t0413500-01)" |
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| moncot specific | RAP-DB | [Os] "Similar to ATP binding / DNA binding / helicase/ nucleic acid binding / protein binding / zinc ion binding. (Os07t0680500-01);Chromatin remodeling factor 739, Sucrose non-fermenting 2 (Snf2) family protein, Response to M. oryzae infection (Os07t0680500-02)" |
| commelinid specific | | |
| commelinid specific | | |
| moncot specific | RAP-DB | [Os] "S-type euonymus-related lectin (EUL), ""Response to salt and drought stress, ABA treatment"", Response to biotic treatment (Os07t0684000-01)" |
| moncot specific | | |
| moncot specific | | |
| commelinid specific | RAP-DB | [Os] "Trehalose-6-phosphate phosphatase, Trehalose biosynthesis, Response to chilling stress, Response to abiotic stresses (Os10t0553300-01)" |

from associated publications

| pubs | genesymbols |
|---|---|
| [Os] "Hong J et al. Plant Cell Environ, 46(4):1278-1294 (2023)" | [Os] "OsLP1, PDCT" |
| [Os] PMID:"28107441\| PMID:35643623 | [Os] HTD1\| HTD1 |
| [Os] "Li X et al. Plant Sci, 284:212-220 (2019)"; [Os] PMID:31084874 | [Os] OsANN3; [Os] ANN3 |

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| [Os] "Hirano K et al. Plant Cell Physiol, 54(11):1791-802 (2013)" | [Os] OsBLH6 |
| [Os] "Naithani S et al. PeerJ, 9:e11052 (2021)" | [Os] SDK13 |
| [Os] "Khrueasan N et al. Genes (Basel), 10(10): (2019) \| Kanegae H et al. Plant Cell Physiol, 41(4):415-23 (2000) \| Kasahara M et al. Plant Physiol, 129(2):762-73 (2002)" | [Os] "PHOT2, OsPHOT2, OsNPH1b" |
| [Os] "Cai Q et al. Nat Commun, 5:3476 (2014)" | [Os] "EG2, OsTIFY3, OsJAZ10, OsJAZ 1, OsJAZ1, EG2/OsJAZ1, JAZ1/EG2" |

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| [Os] "Ikram AU et al. Plant Physiol, 188(4):2199-2214 (2022)" | [Os] OsSWC4 |
| [Os] "Li P et al. Cell Res, 17(5):402-10 (2007)"; [Os] PMID:32913047\| PMID:"25028496; [Zm] PMID:24987012 | [Os] "LA1, LAZY1, OsLAZY1, OsLazy1"; [Os] LA1\| LA1 |
| [Os] "Ding W et al. Cell Res, 19(11):1309-11 (2009) \| Moon S et al. Plant Physiol, 179(2):558-568 (2019)" | [Os] OsRHL1 |

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| [Os] "Yang B et al. J Exp Bot, 73(11):3446-3461 (2022) \| Dong N et al. Int J Mol Sci, 23(23): (2022)" | [Os] "OsPK5, OsPK10" |
| [Os] "BarrÃ´co RM et al. Plant Physiol, 142(3):1053-64 (2006)" | [Os] "KRP1, OsiICK1, Orysa;KRP1, OrysaICK1, Orysa;ICK1, CDKI" |
| [Os] "Kiyoon Kang et al. Journal of Plant Biology, 53(4):291-296 (2010)" | [Os] FC1 |
| [Os] "Naithani S et al. PeerJ, 9:e11052 (2021)" | [Os] OsRLCK166 |
| [Os] "Lu CA et al. Plant Cell, 14(8):1963-80 (2002) \| Su CF et al. Plant Physiol, 153(1):145-58 (2010)" | [Os] MYBS3 |
| [Os] "Song S et al. J Exp Bot, 69(18):4283-4293 (2018) \| Chardon F et al. J Mol Evol, 61(5):579-90 (2005)"; [Os] PMID:30671680\| PMID:30671680; [Ta] PMID:"27162497 | [Os] OsMFT1; [Os] MFT\| MFT; [Ta] MFT |

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| [Os] "Liu B et al. Plant Cell Rep, 31(6):1021-32 (2012)" | [Os] OsPFA-DSP1 |
| [Zm] PMID:29990328 | |
| [Os] "Jadoon S et al. Front Plant Sci, 13:990575 (2022)" | [Os] OsINH3 |
| [Os] "Lam PY et al. New Phytol, 223(1):204-219 (2019)" | [Os] "CYP75B3, F3'H" |
| [Os] PMID:36232465\| PMID:36232465 | [Os] null\| null |
| [Os] "Liu B et al. Plant Cell, 24(8):3406-19 (2012)" | [Os] "LYP4, Os-LYP4, OsLYP4" |

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| [Os] "Murakami M et al. Biosci Biotechnol Biochem, 69(2):410-4 (2005) \| Murakami M et al. Plant Cell Physiol, 44(11):1229-36 (2003) \| Koo BH et al. Mol Plant, 6(6):1877-88 (2013)" | [Os] "Hd2, OsPRR37, PRR37, Prr4, OsPRR4, DTH7, OsCCT28, Ghd7.1, EH7-2" |
| [Os] "Yang C et al. Plant Sci, 288:110239 (2019)" | [Os] "OsLUGL, OsKKX" |
| [Os] "Shen Q et al. Plant Cell, 31(12):3073-3091 (2019)" | [Os] OsPKG |

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| [Os] PMID:31552586\| PMID:"19324458\| PMID:"32197452\| PMID:32197452\| PMID:"32916530\| PMID:"32916530\| PMID:32197452\| PMID:"31481833\| PMID:36435087\| PMID:"12920519\| PMID:"26345744\| PMID:"19823935\| PMID:"29617374\| PMID:30778635\| PMID:29617374\| PMID:"31134103 | [Os] OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019\| OSBHLH019 |
| [Os] "Iwai T et al. Plant Physiol, 142(3):1202-15 (2006)" | [Os] "ACO1, OsACO1, ACO" |
| [Os] "Gao S et al. Plant Physiol, 165(3):1035-1046 (2014) \| Hirose N et al. Plant Cell Physiol, 48(3):523-39 (2007)"; [Ta] PMID:"34768924\| PMID:"33923687\| PMID:"34768924\| PMID:22670578\| PMID:22670578\| PMID:24884376; [Zm] PMID:26519657 | [Os] "CKX4, OsCKX4, ckx4, OsSCRM, OsSCRM2, SCRM, SCRM2"; [Ta] CKX1\| CKX1\| CKX1\| CKX1\| CKX1\| CKX1 |

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| [Os] "Manosalva PM et al. Plant J, 68(5):777-87 (2011) \| Sasaki A et al. Science, 299(5614):1896-8 (2003) \| Gomi K et al. Plant J, 37(4):626-34 (2004) \| Chen F et al. DNA Res, 13(2):53-63 (2006)"; [Os] PMID:"26467468 | [Os] "GF14e, GID2, OsGID2"; [Os] GID2 |
| [Os] "Yamaguchi K et al. Plant J, 70(3):389-97 (2012)" | [Os] OsSWAP70B |
| [Os] "Liu J et al. J Exp Bot, 67(19):5785-5798 (2016)" | [Os] "OsK, Ghd2" |
| [Os] "Sun L et al. Plant Physiol, 165(1):335-45 (2014)"; [Zm] PMID:15576555 | [Os] "AHP2, OHP2, HPt, OsAHP2 Hpt3, Ohp2, OsHP1, OsHpt3" |

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| [Os] "Wang B et al. Front Plant Sci, 10:759 (2019)"; [Os] PMID:31244876\| PMID:31244876 | [Os] OsPPa6; [Os] PPa6\| PPa6 |
| [Os] "Toriba T et al. Nat Commun, 10(1):619 (2019) \| Chern M et al. BMC Genomics, 15(1):461 (2014)" | [Os] "OsBOP2, NH5" |
| [Os] "Zhang B et al. Plant Physiol, 170(2):1149-61 (2016) \| Vij S et al. Mol Plant, 1(5):732-50 (2008)" | [Os] OsBSK3 |

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| [Os] "Utsumi Y et al. Plant Physiol, 156(1):61-77 (2011)"; [Zm] PMID:12615940 | [Os] "OsISA2, ISA2" |
| [Os] "Wu Z et al. J Integr Plant Biol, 64(1):135-148 (2022)" | [Os] EDR1 |
| [Os] "Agarwal S et al. Plant Physiol Biochem, 45(9):637-46 (2007) \| Sauter M et al. J Exp Bot, 53(379):2325-31 (2002)" | [Os] "Ospdc2, PDC2" |
| [Os] "Song S et al. Plant Cell, 29(3):491-507 (2017)" | [Os] "OsUbDKÎ³4, OsUbDKg4" |
| [Os] "Zhang F et al. Sci China Life Sci, 65(7):1380-1394 (2022)"; [Os] PMID:35079956 | [Os] OsRLCK160; [Os] OSRLCK160 |
| [Os] "Wang Q et al. Proc Natl Acad Sci U S A, 115(49):E11551-E11560 (2018)" | [Os] OsSPK1 |

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| [Os] "Wang H et al. Plant Physiol, 171(1):230-41 (2016) \| Sakane I et al. Nucleic Acids Res, 36(13):4266-76 (2008)"; [Os] PMID:17562186 | [Os] "RILIM15B, DMC1B, RiLIM15B, OsDMC1B, OsDmc1B, Dmc1B"; [Os] DMC1 |
| [Zm] PMID:16247560 | |
| [Os] PMID:33930508\| PMID:25922483\| PMID:25922483\| PMID:33930508 | [Os] ABC1\| ABC1\| ABC1\| ABC1 |
| [Os] "Macovei A et al. Plant Signal Behav, 7(9):1138-43 (2012)" | [Os] OsABP |
| [Os] "Fan T et al. Plants (Basel), 12(4): (2023)" | [Os] OsLHT2 |

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| [Os] "Hu Y et al. Plant Physiol, 184(3):1424-1437 (2020)"; [Os] PMID:32913047 | [Os] OsHOX28; [Os] OSHOX28 |
| [Os] PMID:31352021 | [Os] SAUR30 |
| [Os] "Ramamoorthy R et al. Plant Cell Rep, 37(2):377-385 (2018)"; [Os] PMID:29149369\| PMID:29149369 | [Os] OsPS1-F; [Os] OSPS1-F\| OSPS1-F |
| [Os] "Yang H et al. J Integr Plant Biol, 65(3):755-771 (2023)" | [Os] DYW3 |
| [Os] PMID:12557686\| PMID:12557686\| PMID:35699777; [Ta] PMID:12557686\| PMID:12557686 | [Os] APL\| APL\| APL; [Ta] APL\| APL |
| [Zm] PMID:16805899 | |
| [Os] "Tan L et al. Plant Physiol, 183(3):1235-1249 (2020)" | [Os] OsZIP5 |

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| [Os] "Ray S et al. Transgenic Res, 21(2):351-66 (2012)" | [Os] BLEC-Str8 |
| [Zm] PMID:15979170 | |
| [Os] "Deng M et al. Plant Mol Biol, 86(6):655-69 (2014) \| Xu L et al. J Integr Plant Biol, 62(7):1017-1033 (2020)" | [Os] OsCYCP4;1 |
| [Os] "Yamamoto Y et al. Plant Physiol, 143(3):1362-71 (2007)"; [Os] PMID:28829777 | [Os] "YUCCA6, OsYUCCA6, OsYUC6"; [Os] YUC3 |
| [Os] "Shao J et al. PLoS One, 13(7):e0199248 (2018)" | [Os] Oshox14 |

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| [Os] "Zhang L et al. J Exp Bot, 67(3):633-47 (2016)" | [Os] "FLO7, Flo7, flo7(t), flo-7" |
| [Os] "Ohyama A et al. J Plant Physiol, 270:153634 (2022)" | [Os] OsCYCD3;1 |
| [Os] "Matsui H et al. Plant Cell Physiol, 51(12):2082-91 (2010) \| Matsui H et al. Plant Cell Physiol, 51(10):1731-44 (2010)"; [Os] PMID:"21051443 | [Os] OsOxi1; [Os] AGC2 |

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| [Os] "Miao J et al. New Phytol, 227(5):1417-1433 (2020) \| Xue T et al. BMC Genomics, 9:550 (2008)" | [Os] OsPP2C09 |
| [Os] "Li DF et al. FEBS Lett, 580(18):4325-31 (2006) \| Dong A et al. Plant Mol Biol, 48(3):203-10 (2002)" | [Os] OsCaM61 |
| [Os] "Zhang JP et al. Plant Physiol, 175(3):1175-1185 (2017)" | [Os] OsUCL8 |
| [Os] "Li YF et al. Plant Physiol, 184(2):988-1003 (2020) \| Ren D et al. Plant Physiol, 184(1):251-265 (2020)" | [Os] "MOF1, MFS2" |
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| [Os] "GarciadeblÃ¡s B et al. Plant J, 34(6):788-801 (2003) \| Suzuki K et al. BMC Plant Biol, 16:22 (2016)"; [Os] PMID:"28582424; [Ta] PMID:"27440547 | [Os] "HKT7, OsHKT7, OsHKT1;4"; [Os] HKT7; [Ta] null |
| [Os] "Zhan H et al. Plant Sci, 325:111482 (2022)"; [Os] PMID:"28061864 | [Os] "OsCPD1, CYP90A3, OsCPD1/CYP90A3"; [Os] CPD |
| [Os] "Abu-Zaitoon YM et al. Physiol Plant, 146(4):487-99 (2012)" | [Os] OsYUC9 |

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| [Os] "Leng Y et al. Plant Physiol, 174(2):1151-1166 (2017)" | [Os] DEL1 |
| [Os] "Pei M et al. Plants (Basel), 12(11): (2023)" | [Os] OsSec14-10 |
| [Os] "Zhou J et al. Plant J, 82(4):632-43 (2015)"; [Os] PMID:"28371825\| PMID:32620100\| PMID:"26991395<br>[Zm] PMID:18074115 | [Os] "SWEET13, OsSWEET13"; [Os] MTN3\| MTN3\| MTN3<br>[Zm] LOC103642433 |
| [Os] "Zhang Y et al. Theor Appl Genet, 135(5):1751-1766 (2022) \| Kitagawa K et al. Plant Cell Physiol, 51(8):1315-29 (2010) \| Wu T et al. Plant Cell Rep, 33(2):235-44 (2014)"; [Os] PMID:25807460\| PMID:36361748\| PMID:"36361748 | [Os] "SRS3, SAR1, SGL, BHS1"; [Os] SRS3\| SRS3\| SRS3 |

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|---|---|
| [Os] PMID:32803271; [Zm] PMID:25937463 | [Os] NAC3 |
| [Os] "Takano M et al. Plant Cell, 17(12):3311-25 (2005) \| Takano M et al. Plant Cell, 13(3):521-34 (2001)"; [Zm] PMID:15280251 | [Os] "PHYA, phyA, PHYA* (phyA), PHYA*, Phya, PHY18, phy 18, OsPHYA"; [Zm] PHYA |
| [Os] "Matsushima R et al. Plant Physiol, 164(2):623-36 (2014)" | [Os] SSG4 |
| [Os] "Singh A et al. FEBS J, 281(3):894-915 (2014) \| Qiao B et al. J Exp Bot, 66(19):5853-66 (2015)"; [Os] PMID:"16551598; [Ta] PMID:27236332\| PMID:32290993\| PMID:"21656015; [Zm] PMID:8938425 | [Os] "ANN2, OsANN2"; [Os] ANN1; [Ta] ANN1\| ANN1\| ANN1 |
| [Os] "Li P et al. Acta Biochim Biophys Sin (Shanghai), 43(9):688-97 (2011) \| Sun W et al. Mol Plant, 10(11):1417-1433 (2017) \| Yilmaz A et al. Plant Physiol, 149(1):171-80 (2009)" | [Os] "OsPLT2, HL6" |

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|---|---|
| [Os] "Huang L et al. Int J Mol Sci, 16(7):16216-41 (2015) \| Wang L et al. J Genet, 93(1):93-102 (2014)" | [Os] OsMC6 |
| [Os] "Kan Y et al. Nat Plants, 8(1):53-67 (2022)" | [Os] SCT2 |
| [Os] PMID:30190374 | [Os] null |

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|---|---|
| [Hv] "Schäfer et al., 2018 https://doi.org/10.1016/j.cub.2018.03.027" | [Hv] SLAC1 |
| [Os] "Cho JI et al. Plant Cell Rep, 24(4):225-36 (2005) \| Wang E et al. Nat Genet, 40(11):1370-4 (2008) \| Wang H et al. Int J Mol Sci, 19(8): (2018)"; [Os] PMID:32886328\| PMID:21805338 | [Os] "GIF1, gif1, CIN2, OsCIN2, OsGIF1, WB1"; [Os] GIF1\| GIF1 |

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|---|---|
| [Os] "Guo M et al. Front Plant Sci, 13:910663 (2022)" | [Os] "OsCHR739, CHR739" |
| [Os] "Lambin J et al. Front Plant Sci, 11:185 (2020)" | [Os] OsEULS2 |
| [Os] "Shima S et al. FEBS J, 274(5):1192-201 (2007)" | [Os] OsTPP2 |

|  | functional annotation |  |
|---|---|---|
| traits | Ensembl_descriptor | biological_ |
|  | Conserved hypothetical protein |  |
|  | Cyclin-like F-box domain containing protein |  |
|  | Similar to OSIGBa0116M22.4 protein |  |
|  | Cyclin-like F-box domain containing protein |  |
|  | Cyclin-like F-box domain containing protein |  |
|  | Similar to F-box domain containing protein |  |
|  | Conserved hypothetical protein |  |
|  | Conserved hypothetical protein |  |
|  | Paired amphipathic helix domain containi | GO:00063 |
|  | Similar to Pollen signalling protein with a | GO:00069 |
|  | Similar to E3 ubiquitin ligase EL5 (EC 6.3. | GO:00165 |
|  | Similar to Translation initiation factor IF- | GO:00064 |
|  | Similar to 30S ribosomal protein S31, chl | GO:00325 |
|  | Similar to phosphatidic acid phosphatase | GO:00066 |
|  | Zinc finger, C2H2 domain containing pro | GO:00100 |
|  | Protein of unknown function DUF2232, membrane d |  |
|  | Hypothetical conserved gene | GO:00065 |
| [Os] tiller number TO:0000346\| spikelet fertility TO:0000180 | WD40 repeat-like domain containing pro | GO:00094 |
|  | IQ calmodulin-binding region domain containing pr |  |
| [Os] root length TO:0000227 | Similar to annexin-like protein RJ4 | GO:00069 |
|  | Protein of unknown function DUF3537 domain conta |  |

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|---|---|---|
| | Conserved hypothetical protein | GO:00063 |
| | Similar to HKT1 (High-affinity potassium | GO:00068 |
| | Zm00001e034146 | GO:00063 |
| [Os] bacterial blight disease resistance (TO:0000175) | Serine/threonine protein kinase-related | GO:00064 |
| | Similar to TA11 protein (Fragment) | GO:00064 |
| | Transferase family protein | |
| | Similar to RING-H2 finger protein ATL5P | |
| [Os] light sensitivity (TO:0000075) \| salt tolerance (TO:0006001) | Similar to Nonphototropic hypocotyl prot | GO:00064 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Peptidase S26A, signal peptidase I domai | GO:00064 |
| | Similar to Cytochrome P450 CYP71K14 | |
| [Os] panicle length (TO:0000040) \| drought tolerance (TO:0000276) \| flower number (TO:0002736) \| root length (TO:0000227) \| abscisic acid sensitivity (TO:0000615) \| spikelet anatomy and morphology trait (TO:0000657) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| cold tolerance (TO:0000303) \| grain weight (TO:0000590) \| grain size (TO:0000397) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| stem length (TO:0000576) \| spikelet fertility | Jasmonic acid (JA) signalling repressor, R | GO:00096 |
| | Similar to glycerol-3-phosphate acyltran | GO:00101 |
| | Similar to Keratinocytes proline-rich prot | GO:00064 |
| | Plant lipid transfer protein/Par allergen f | GO:00068 |

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|---|---|---|
| [Os] tiller number (TO:0000346) \| plant height (TO:0000207) \| internode length (TO:0000145) | Homeodomain-like containing protein | GO:00001 |
| | Similar to JHL23J11.5 protein | |
| | Photosystem II oxygen evolving complex | GO:00097 |
| | Similar to NAC-type transcription factor | GO:00063 |
| | GLE1-like domain containing protein | GO:00064 |
| [Os] tiller angle (TO:0000567) \| plant height (TO:0000207) \| gravity response trait (TO:0002693); [Os] auxin content TO:0002672\| tiller angle TO:0000567 | Regulation of shoot gravitropism and till | GO:00096 |
| | Similar to MEI1 protein | GO:00062 |
| | Similar to predicted protein | GO:00161 |
| | Cell division cycle-associated protein dor | GO:00063 |
| [Os] root development trait (TO:0000656) \| crown root number (TO:0002685) \| abscisic acid content (TO:0002667) \| root hair length | Similar to BHLH transcription factor | GO:00063 |
| | Hypothetical conserved gene | GO:00062 |
| | General substrate transporter family prot | GO:00342 |
| | Hypothetical conserved gene | GO:00068 |
| | Similar to cap-binding protein p28 | GO:00064 |
| | Conserved hypothetical protein | |
| | Similar to predicted protein | GO:00063 |
| | Homeodomain-related domain containin | GO:00063 |
| | Similar to VMP3 protein | |
| | Similar to predicted protein | GO:00093 |
| | Similar to Chaperone protein dnaJ 15 (Pr | GO:00099 |
| | Hypothetical conserved gene | |

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|---|---|---|
| [Os] abscisic acid sensitivity (TO:0000615) \| grain thickness (TO:0000399) \| protein content (TO:0000598) \| grain yield per plant (TO:0000449) \| amylose content (TO:0000196) \| seed viability (TO:0000345) \| sucrose content (TO:0000328) \| fructose content (TO:0006005) \| seed set percent (TO:0000455) \| starch content (TO:0000696) \| total soluble sugar content (TO:0000340) \| germination rate (TO:0000430) \| seedling vigor (TO:0000280) \| glucose content (TO:0000300) \| abscisic acid content (TO:0002667) \| 1000-seed weight | Pyruvate kinase family protein | GO:00060 |
| | Zm00001e018628 | GO:00311 |
| | Pentatricopeptide repeat domain containing protein | |
| | Multi antimicrobial extrusion protein Mat | GO:00068 |
| | CDK inhibitor (CKI), Seed developmen | GO:00070 |
| | Similar to Ferrochelatase | GO:00067 |
| [Os] bacterial blight disease resistance (TO:0000175) \| inflorescence development trait (TO:0000621) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| seed development trait (TO:0000653) | Similar to H0315F07.6 protein | GO:00064 |
| [Os] salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) | Similar to Transcription factor MYBS3 | GO:00001 |
| | Zm00001e005344 | GO:00096 |
| [Os] abscisic acid sensitivity (TO:0000615) \| inflorescence anatomy and morphology trait (TO:0000373) \| days to heading (TO:0000137) \| spikelet number (TO:0000456) \| jasmonic acid sensitivity (TO:0000172); [Os] seed maturation TO:0002661\| seed dormancy TO:0000253; [Ta] seed dormancy TO:0000253 | | |
| | Octicosapeptide/Phox/Bem1p domain containing pr | |
| | Conserved hypothetical protein | GO:00096 |
| | Exonuclease domain containing protein | GO:00007 |

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|---|---|---|
| | Conserved hypothetical protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Protein tyrosine phosphatase, Negative r | GO:00064 |
| | Lipid-binding START domain containing | GO:00159 |
| | Protein of unknown function DUF573 do | GO:00063 |
| | Photosystem I reaction center subunit VI, | GO:00159 |
| | Similar to Dual specificity kinase 1 | GO:00064 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Zm00001e017525 | GO:00429 |
| | Similar to AAA-type ATPase family protein | |
| | Similar to Glycerol-3-phosphate dehydro | GO:00059 |
| [Os] abiotic stress trait (TO:0000168) \| abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| osmotic response sensitivity (TO:0000095) \| pollen fertility (TO:0000421) \| grain number (TO:0002759) \| anther color (TO:0000187) \| proline content (TO:0006002) | Protein phosphatase inhibitor family prot | GO:00325 |
| | Galactose-binding like domain containing protein | |
| | Similar to Expansin-A9 | GO:00096 |
| | Reticulon family protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| | Putative calcium-binding protein CML19 | GO:00197 |
| | Similar to Avr9 elicitor response-like pro | GO:00064 |
| [Os] anthocyanin content (TO:0000071) \| seed development trait (TO:0000653) \| heat tolerance (TO:0000259) | Similar to Flavonoid 3'-monooxygenase ( | GO:00098 |
| [Os] rolled leaf TO:0006064\| leaf rolling TO:0000085 | Double-stranded RNA-binding domain containing p | |
| | Hypothetical conserved gene | GO:00001 |
| [Os] bacterial disease resistance (TO:0000315) \| fungal disease resistance (TO:0000439) | Lysin motif-containing protein, Pattern r | GO:00023 |

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|---|---|---|
| [Os] starch content (TO:0000696) \| days to heading (TO:0000137) \| photoperiod sensitivity (TO:0000229) \| flowering time (TO:0002616) \| panicle length (TO:0000040) \| grain yield (TO:0000396) \| growth and development trait (TO:0000357) \| plant height (TO:0000207) \| filled grain number (TO:0000447) | Pseudo response regulator, Heading date | GO:00001 |
| | Hypothetical conserved gene | GO:00064 |
| | Essential protein Yae1, N-terminal domai | GO:00064 |
| [Os] sterility related trait (TO:0000485) \| inflorescence development trait (TO:0000621) \| auxin content (TO:0002672) \| seed anatomy and morphology trait (TO:0000184) | Similar to STYLOSA protein | |
| | Similar to predicted protein | GO:00066 |
| | Protein of unknown function DUF231 dor | GO:00104 |
| | Similar to Aminoalcoholphosphotransfera | GO:00066 |
| | Conserved hypothetical protein | |
| | Similar to predicted protein | |
| | ABC transporter-like domain containing | GO:00550 |
| | Kelch related domain containing protein | GO:00063 |
| | AUX/IAA protein family protein | GO:00063 |
| [Os] spikelet fertility (TO:0000180) \| seed weight (TO:0000181) \| gibberellic acid sensitivity (TO:0000166) \| salt tolerance (TO:0006001) \| hydrogen peroxide content (TO:0000605) \| germination rate (TO:0000430) \| internode length (TO:0000145) \| grain weight (TO:0000590) \| pollen fertility (TO:0000421) \| plant height (TO:0000207) \| seed set percent (TO:0000455) | RmlC-like jelly roll fold domain containin | GO:00064 |

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|---|---|---|
| [Os] iron concentration TO:0006049\| salt tolerance TO:0006001\| grain shape TO:0002730\| leaf size TO:0002637\| stomatal resistance TO:0000523\| stomatal resistance TO:0000522\| leaf shape TO:0000492\| male sterility TO:0000437\| germination rate TO:0000430\| cold tolerance TO:0000303\| drought tolerance TO:0000276\| seed dormancy TO:0000253\| leaf angle TO:0000206\| genic male sterility TO:0000199\| flag leaf angle TO:0000124\| disease resistance TO:0000112 | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Similar to CDPK substrate protein 1 | GO:00063 |
| | Similar to Rac GTPase activating protein | GO:00071 |
| | Protein of unknown function DUF761, plant family p | |
| [Os] abscisic acid sensitivity (TO:0000615) \| phosphorus sensitivity (TO:0000102) \| heat tolerance (TO:0000259) \| auxin sensitivity (TO:0000163) \| drought tolerance (TO:0000276) \| jasmonic acid | ACC oxidase, Ethylene biosynthesi | |
| | Similar to Myosin XI (Fragment) | GO:00070 |
| | Similar to Calcium-dependent protein ki | GO:00064 |
| | Similar to cDNA clone:006-306-H07, full insert seq | |
| | DTW domain containing protein | GO:00080 |
| [Os] black streak dwarf virus resistance (TO:0000020) \| plant growth hormone sensitivity (TO:0000401) \| nitrogen sensitivity (TO:0000011) \| viral disease resistance (TO:0000148) \| jasmonic acid sensitivity (TO:0000172) \| cytokinin sensitivity (TO:0000167) \| crown root number (TO:0002685) \| root development trait (TO:0000656) \| auxin sensitivity (TO:0000163); [Ta] chlorophyll content TO:0000495\| grain number TO:0002759\| grain weight TO:0000919\| 1000-grain weight TO:0000382\| 1000-grain weight TO:0000533\| grain width TO:0000975 | Cytokinin oxidase/dehydrogenase, Crow | GO:00096 |
| | Similar to B0616E02-H0507E05.3 protei | GO:00550 |
| | Leucine-rich repeat, typical subtype containing prot | |

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|---|---|---|
| | Cytochrome P450 family protein | |
| | Similar to Mitochondrial import inner me | GO:00450 |
| [Os] sheath blight disease resistance (TO:0000255) \| mimic response (TO:0000063) \| viral disease resistance (TO:0000148) \| hydrogen peroxide content (TO:0000605) \| drought tolerance (TO:0000276) \| leaf width (TO:0000370) \| heat tolerance (TO:0000259) \| leaf lamina color (TO:0000299) \| salt tolerance (TO:0006001) \| gibberellic acid sensitivity (TO:0000166) \| plant height (TO:0000207) \| bacterial blight disease resistance (TO:0000175); [Os] disease resistance TO:0000112 | Zm00001e022823 | GO:00097 |
| | Exoribonuclease domain containing prot | GO:00062 |
| | Rac/Rop guanine nucleotide exchange fa | GO:00181 |
| | Similar to heat- and acid-stable phosphoprotein | |
| | Similar to Protein phosphatase 2A 62 kD | GO:00064 |
| | Similar to F14O23.10 protein | GO:00434 |
| | Peptidase C14, ICE, catalytic subunit p20, active site | |
| | Similar to Ethylene-responsive transcripti | GO:00063 |
| [Os] drought tolerance (TO:0000276) \| leaf senescence (TO:0000249) \| iron sensitivity (TO:0000224) \| gibberellic acid sensitivity (TO:0000166) \| jasmonic acid sensitivity (TO:0000172) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) | CCT domain domain containing protein | GO:00063 |
| | Poly(A) polymerase, central domain dom | GO:00063 |
| [Os] osmotic response sensitivity (TO:0000095) \| leaf senescence (TO:0000249) \| plant height (TO:0000207) \| tiller number (TO:0000346) \| ethylene sensitivity (TO:0000173) \| root length (TO:0000227) \| cytokinin sensitivity (TO:0000167) \| fertility related trait (TO:0000420) \| root development trait (TO:0000656) \| salt tolerance | Histidine phosphotransfer protein, Cytok | GO:00001 |
| | Methyl-CpG DNA binding domain containing protei | |
| | Conserved hypothetical protein | |
| | Hypothetical conserved gene | GO:00083 |
| | Conserved hypothetical protein | |

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|---|---|---|
| | Putative cyclin-D7-1 | GO:00000 |
| [Os] plant height (TO:0000207) \| spikelet fertility (TO:0000180) \| proline content (TO:0006002) \| alkali sensitivity (TO:0000481) \| net photosynthetic rate (TO:0001027) \| sugar content (TO:0000333) \| sodium to potassium content ratio (TO:0000525) \| sucrose content (TO:0000328) \| starch content (TO:0000696) \| chlorophyll content (TO:0000495) \| osmotic response sensitivity (TO:0000095) \| amino acid content (TO:0002673) \| grain yield (TO:0000396) \| relative biomass (TO:0000143) \| plant fresh weight (TO:0000442) \| fruit width (TO:0002627); [Os] net photosynthetic rate TO:0001027\| photosynthetic rate TO:0001015 | Similar to Chloroplast inorganic pyrophos | GO:00067 |
| | Pathogenesis-related transcriptional fact | GO:00063 |
| [Os] leaf shape (TO:0000492) \| inflorescence development trait (TO:0000621) | | |
| [Os] sheath blight disease resistance (TO:0000255) \| gibberellic acid sensitivity (TO:0000166) \| blast disease (TO:0000074) \| anatomy and morphology related trait (TO:0000017) \| grain size (TO:0000397) \| grain weight (TO:0000590) \| brassinosteroid sensitivity (TO:0002677) \| UV-B light sensitivity (TO:0000601) \| grain length (TO:0000734) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615) \| auxin sensitivity (TO:0000163) \| inflorescence development trait (TO:0000621) \| bacterial blight disease resistance (TO:0000175) | Brassinosteroid (BR) signaling kinase, Re | GO:00097 |
| | WRC domain containing protein | GO:00331 |
| | Hypothetical conserved gene | GO:00097 |

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|---|---|---|
|  | Similar to OSIGBa0157K09-H0214G12.1 | GO:00071 |
|  | Similar to Isoamylase-type starch debran | GO:00059 |
| [Os] grain length (TO:0000734) \| seed development trait (TO:0000653) \| seed maturation (TO:0002661) \| seed quality (TO:0000162) \| chalky endosperm (TO:0000266) \| grain size (TO:0000397) \| 1000-seed weight (TO:0000382) \| grain thickness (TO:0000399) \| protein content | UDP-glucuronosyl/UDP-glucosyltransferase family p |  |
|  | Similar to receptor-like serine-threonine | GO:00064 |
|  | Protein kinase, catalytic domain domain c | GO:00064 |
| [Os] copper sensitivity (TO:0000021) | Similar to Pyruvate decarboxylase isozyme 2 |  |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Phosphatidylinositol 3-/4-kinase (PI3/4K | GO:00099 |
|  | Hypothetical conserved gene | GO:00068 |
|  | Similar to RING-H2 finger protein ATL3I (YGHL1-C3 |  |
|  | Similar to Ubiquitin ligase protein FANCL | GO:00062 |
|  | Armadillo-type fold domain containing protein |  |
| [Os] cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| osmotic response sensitivity (TO:0000095) \| submergence tolerance (TO:0000524) \| heat tolerance (TO:0000259) \| drought tolerance (TO:0000276) \| inflorescence development trait (TO:0000621) \| seed development trait (TO:0000653); [Os] flavonoid content TO:0000290 | Protein kinase, core domain containing p | GO:00064 |
| [Os] blast disease (TO:0000074) \| grain size (TO:0000397) \| plant height (TO:0000207) \| grain length (TO:0000734) \| grain thickness (TO:0000399) | Dedicator of cytokinesis family protein | GO:00072 |
|  | Lipase, GDSL domain containing protein |  |
|  | Similar to predicted protein | GO:00064 |
|  | Similar to Zinc finger, C3HC4 type family | GO:00065 |
|  | Similar to 60S ribosomal protein L9 (Gibb | GO:00021 |
|  | Regulation of nuclear pre-mRNA protein | GO:00063 |

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|---|---|---|
| | Similar to PHS1 (PROPYZAMIDE-HYPERSEN | GO:00064 |
| | Similar to ABC transporter (PDR5-like) isc | GO:00550 |
| | Prefoldin domain containing protein | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Phospholipase/carboxylesterase domain containing | |
| | Zm00001e008289 | GO:00064 |
| [Os] male sterility (TO:0000437) \| sterility related trait (TO:0000485); [Os] pollen sterility TO:0000053 | Meiosis-specific DNA recombinase, Syna | GO:00007 |
| | Arbuscular mycorrhizal specific marker 2 | GO:00550 |
| | Zm00001e123719 | GO:00066 |
| [Os] grain number TO:0002759\| seed shape TO:0000484\| grain size TO:0000397\| plant height TO:0000207 | Similar to ABC1 protein (Fragment) | GO:00067 |
| | Similar to Nucleoid DNA-binding-like pr | GO:00065 |
| | Hypothetical conserved gene | GO:00063 |
| | Zm00001e003020 | GO:00064 |
| | Streptomyces cyclase/dehydrase family protein | |
| | DEAD-box helicase ATP-binding protein, Response | |
| | NPH3 domain containing protein | GO:00165 |
| | Protein of unknown function DUF751 family protein | |
| | ATPase, AAA-type, core domain containing protein | |
| | Protein kinase, core domain containing p | GO:00064 |
| [Os] cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| jasmonic acid sensitivity (TO:0000172) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | Similar to Lysine and histidine specific tr | GO:00033 |
| | Zm00001e010377 | GO:00064 |
| | Myb-like DNA-binding domain, SHAQKY | GO:00063 |
| | Zm00001e031204 | GO:00157 |
| | Similar to Endonuclease/Exonuclease/ph | GO:00063 |
| | Similar to U-box domain containing prot | GO:00064 |
| | Similar to Dual specificity protein phosph | GO:00439 |
| | Similar to Blue copper-binding protein | GO:00229 |
| | Hypothetical conserved gene | GO:00065 |
| | ATP10 family protein | GO:00336 |
| | Ribosomal protein L22/L17 family protei | GO:00060 |

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|---|---|---|
| | Similar to HSP protein (Fragment) | GO:00063 |
| | Protein of unknown function DUF829, eukaryotic fa | |
| [Os] brassinosteroid sensitivity (TO:0002677) \| auxin content (TO:0002672) \| tiller angle (TO:0000567) \| gravity response trait (TO:0002693) \| salt tolerance (TO:0006001) \| submergence tolerance (TO:0000524); [Os] auxin content | Similar to HAHB-6 (Fragment) | GO:00063 |
| | Similar to small nuclear ribonucleoprotei | GO:00003 |
| [Os] auxin sensitivity TO:0000163 | Auxin responsive SAUR protein family pr | GO:00097 |
| | Hypothetical conserved gene | GO:00063 |
| [Os] plant height (TO:0000207) \| tiller number (TO:0000346) \| grain yield (TO:0000396) \| leaf color (TO:0000326) \| chlorophyll content (TO:0000495) \| photosynthetic ability (TO:0000316); [Os] tiller number TO:0000346\| plant height TO:0000207 | Similar to Photosystem-1 F subunit | GO:00159 |
| | Epsin-like, N-terminal domain containin | GO:00068 |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | UbiE/COQ5 methyltransferase family pro | GO:00322 |
| | PCF2 | GO:00072 |
| | Hypothetical conserved gene | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to Growth-regulating factor 3 | GO:00063 |
| [Os] growth and development trait (TO:0000357) | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] stomatal resistance TO:0000523\| stomatal resistance TO:0000522\| grain size TO:0000397; [Ta] stomatal resistance TO:0000522\| stomatal resistance TO:0000523 | Similar to Phosphate starvation regulator protein (Re | |
| | Similar to Receptor-like protein kinase 1 | GO:00064 |
| | Epsin-like, N-terminal domain containin | GO:00068 |
| | Similar to Homeobox-leucine zipper prot | GO:00063 |
| | Similar to Receptor-like protein kinase 2 | GO:00064 |
| | RNA recognition motif, glycine rich prote | GO:00987 |
| [Os] zinc sensitivity (TO:0000351) | | |

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|---|---|---|
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | CCT domain containing protein | GO:00099 |
| | Ferroporti-1 domain containing protein | GO:00068 |
| | Conserved hypothetical protein | GO:00007 |
| | Similar to arogenate dehydrogenase | GO:00065 |
| [Os] manganese sensitivity (TO:0000073) \| copper sensitivity (TO:0000021) \| salt tolerance | Concanavalin A-like lectin/glucanase dor | GO:00022 |
| | Zm00001e017314 | GO:00063 |
| | 2OG-Fe(II) oxygenase domain containing protein | |
| | Similar to YDG/SRA domain containing p | GO:00165 |
| | Zm00001e011642 | |
| | Cyclin-like F-box domain containing protein | |
| | Similar to predicted protein | |
| | Hypothetical conserved gene | GO:00069 |
| | Cyclin-related 2 domain containing prote | GO:00000 |
| [Os] black streak dwarf virus resistance (TO:0000020) \| auxin content (TO:0002672) \| gravity response trait (TO:0002693); [Os] ethylene sensitivity TO:0000173 | Flavin monooxygenase-like enzyme , Auxin biosynt | |
| | 2 , 3 cyclic phosphodiesterase, plant dor | GO:00091 |
| | Glycosyl transferase, family 14 protein | |
| | Similar to CSLA1-cellulose synthase-like | GO:00715 |
| | Protein of unknown function DUF947 far | GO:00004 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| | Quinoprotein amine dehydrogenase, beta | GO:00082 |
| | Uncharacterised protein family, Shwachm | GO:00422 |
| | LETM1-like domain containing protein | GO:00068 |
| | Homeodomain-leucine zipper (HD-Zip) t | GO:00063 |
| | Zm00001e008026 | GO:00063 |
| | Similar to CCAAT displacement protein-r | GO:00068 |

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|---|---|---|
| | Similar to OSIGBa0097I24.2 protein | GO:00359 |
| | Similar to NHL25 | |
| | Similar to predicted protein | |
| | Zinc finger, PHD-type domain containing protein | |
| | Similar to TCP family transcription factor | |
| | Similar to 60Kd inner membrane protein, | GO:00329 |
| | Similar to UDP-glucose:glycoprotein gluc | GO:00064 |
| | Similar to Isoform 2 of Homeobox protei | GO:00063 |
| | Zm00001e041744 | GO:00160 |
| | Similar to Glutathione S-transferase GST | GO:00067 |
| | Similar to PlCYC4 protein (Fragment) | GO:00063 |
| | Beta-lactamase-like domain containing p | GO:00466 |
| | Cyclin D domain containing protein | GO:00000 |
| | Arf GTPase activating protein family prot | GO:00507 |
| | Protein kinase, catalytic domain domain | GO:00064 |
| | Hypothetical conserved gene | |
| | Tesmin/TSO1-like, CXC domain containi | GO:00063 |
| | Pectin lyase fold/virulence factor domain | GO:00425 |
| | 6-phosphogluconolactonase domain con | GO:00059 |
| [Os] blast disease (TO:0000074); [Os] disease resistance TO:0000112 | Similar to PHY3 | GO:00064 |
| | EMSY N-terminal domain containing protein | |

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|---|---|---|
| [Os] plant height (TO:0000207) \| grain size (TO:0000397) \| grain yield (TO:0000396) \| growth and development trait (TO:0000357) \| stomatal frequency (TO:0000566) \| stem elongation (TO:0006036) \| root development trait (TO:0000656) \| root length (TO:0000227) \| filled grain number (TO:0000447) \| abscisic acid sensitivity (TO:0000615) \| osmotic response sensitivity (TO:0000095) \| grain yield per plant (TO:0000449) \| germination rate (TO:0000430) \| grain weight (TO:0000590) \| drought tolerance (TO:0000276) \| root to shoot ratio (TO:0000278) | Similar to Protein phosphatase 2C | GO:0035 |
| [Os] spikelet fertility (TO:0000180) \| flower organ size (TO:0002600) \| filled grain number (TO:0000447) \| grain yield (TO:0000396) \| anther shape (TO:0000214) \| plant height (TO:0000207) | Uclacyanin (UCL), Phytocyanin family prot | GO:0022 |
| | Zm00001e023820 | |
| [Os] spikelet anatomy and morphology trait (TO:0000657) \| floral organ number (TO:0006038) \| flower development trait (TO:0000622) | Homeodomain-like containing protein | |
| | Ribosomal biogenesis, methyltransferase | GO:0032 |
| | Similar to Cytochrome-C reductase 14 k | GO:0006 |
| | Glycosyltransferase AER61, uncharacterized domain | |
| | Similar to MPPN domain containing prote | GO:0006 |
| [Os] abscisic acid sensitivity (TO:0000615) \| flowering time (TO:0002616) \| drought tolerance (TO:0000276) \| salt tolerance | | |
| [Os] root hair length (TO:0002665) \| lateral root number (TO:0001013) \| root length (TO:0000227) \| plant height (TO:0000207) \| root development trait (TO:0000656) \| salt tolerance (TO:0006001) | Alpha-expansin, Mediation of the cell ex | GO:0009 |
| | NPH3 domain containing protein | GO:0016 |
| | Nonaspanin (TM9SF) family protein | GO:0072 |
| | X8 domain containing protein | |

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|---|---|---|
| | Similar to predicted protein | |
| | NADH:ubiquinone oxidoreductase 17.2 k | GO:0006 |
| | Similar to Sterol glucosyltransferase-like protein (Fr | |
| [Os] root length (TO:0000227) | Katanin regulatory subunit P80a, Microtu | GO:0007 |
| | Similar to Pherophorin-dz1 protein precu | GO:0007 |
| [Os] growth and development trait (TO:0000357) \| pollen fertility (TO:0000421) \| plant height (TO:0000207) \| pollen sterility (TO:0000053) | Pentatricopeptide repeat domain containing protein | |
| [Os] cold tolerance (TO:0000303) \| oligosaccharide content (TO:0006003); [Os] cold tolerance TO:0000303 | Similar to Transcription factor ICE1 (Indu | GO:0006 |
| | Protein kinase, catalytic domain domain | GO:0006 |
| | Lipase, GDSL domain containing protein | |
| | Zm00001e040827 | GO:0006 |
| | Similar to Glucose transporter (Fragment) | GO:0008 |
| | Beta tubulin, autoregulation binding site domain co | |
| | Similar to OO_Ba0013J05-OO_Ba0033A15.30 protei | |
| | X8 domain containing protein | |
| | Hypothetical conserved gene | |
| | Similar to OSIGBa0099L20.2 protein | |
| | SET domain containing protein | GO:0018 |
| [Os] bacterial blight disease resistance (TO:0000175) \| drought tolerance (TO:0000276) \| drought sensitivity (TO:0000188) \| white-backed planthopper resistance (TO:0000205) | DNA-binding WRKY domain containing p | GO:0006 |
| | Ribosomal protein L25/L23 domain cont | GO:0006 |
| | Similar to Jasmonate-induced protein | |
| | Similar to predicted protein | GO:0006 |

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|---|---|---|
| [Os] temperature response trait (TO:0000432); [Os] male sterility TO:0000437 | Basic helix-loop-helix (bHLH) transcripti | GO:00063 |
| | Similar to EMB2773 (EMBRYO DEFECTIVE | GO:00063 |
| [Os] root hair length (TO:0002665) \| herbicide sensitivity (TO:0000058) \| abiotic stress trait (TO:0000168) | Transcription factor, Regulation of Pi sig | GO:00063 |
| | Saposin-like domain containing protein | GO:00065 |
| | WD40 repeat domain containing protein | |
| | Similar to RING-H2 finger protein ATL1R | GO:00165 |
| | RNA recognition motif domain domain c | GO:00104 |
| | Disease resistance/zinc finger/chromosome conden | |
| | Similar to endonuclease/exonuclease/ph | GO:00468 |
| | Similar to Diacylglycerol acylCoA acyltran | GO:00060 |
| | EF hand domain containing protein | |
| [Os] blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) | Tetratricopeptide-like helical domain co | GO:00064 |
| | Similar to Tonoplast membrane integral | GO:00068 |
| | Similar to RAD23 protein, isoform II | GO:00062 |
| | No apical meristem (NAM) protein domai | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to MYB1 | GO:00301 |
| | Protease inhibitor I4, serpin, plant domai | GO:00109 |
| | Similar to nitrate and chloride transporter | |

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|---|---|---|
| | Similar to secondary cell wall-related gly | GO:00064 |
| [Os] floral organ development trait (TO:0006022) \| carpel anatomy and morphology trait (TO:0006012) | Homolog of Arabidopsis FACTOR OF DN | GO:00310 |
| [Os] inflorescence development trait (TO:0000621) \| grain length (TO:0000734) \| heat tolerance (TO:0000259) \| seed development trait (TO:0000653) \| temperature response trait (TO:0000432) \| seed quality (TO:0000162) \| grain weight (TO:0000590) \| chalky endosperm (TO:0000266) \| grain size (TO:0000397) \| seed size (TO:0000391) \| grain shape (TO:0002730) \| yield trait (TO:0000371) \| grain width (TO:0000402); [Os] grain length TO:0002760\| grain shape TO:0002730\| grain width TO:0000975\| grain weight TO:0000919\| grain length TO:0000734\| submergence tolerance TO:0000524\| grain length to width ratio TO:0000411\| grain thickness TO:0000399\| grain size TO:0000397\| seed size TO:0000391\| stigma exsertion TO:0000044 | Zm00001e031222 | |
| | Similar to serine/threonine protein kinas | GO:00064 |
| | Similar to RNA recognition motif family p | GO:00064 |
| [Os] blast disease (TO:0000074) \| abscisic acid sensitivity (TO:0000615) \| growth and development trait (TO:0000357) | | |
| | Tyrosine protein kinase domain containi | GO:00064 |
| | Similar to CAAX amino terminal protease | GO:00164 |
| | Similar to Low-temperature induced protein lt101.1 | |
| | Galactose oxidase/kelch, beta-propeller domain co | |
| [Os] heat tolerance (TO:0000259) \| salt tolerance (TO:0006001) | Heat shock protein (HSP40), Putative tetr | GO:00466 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | Similar to ABC-type Co2+ transport system, permea | |
| [Os] blast disease (TO:0000074) \| viral disease resistance (TO:0000148) \| disease resistance (TO:0000112) \| bacterial blight disease resistance | Hypothetical conserved gene | GO:00165 |
| | Protein of unknown function DUF1221 d | GO:00064 |

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|---|---|---|
| | Similar to Bowman-Birk type trypsin inhib | GO:00065 |
| | Similar to Arginine/serine-rich coiled coi | GO:00003 |
| | Integrator complex, subunit 3 domain containing pr | |
| | Pollen Ole e 1 allergen/extensin domain containing | |
| | Zm00001e038219 | |
| | Similar to Alanyl-tRNA synthetase, mitoc | GO:00064 |
| | Metallophosphoesterase domain containing protein | |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] chalky endosperm (TO:0000266) \| embryo development trait (TO:0000620) \| seed development trait (TO:0000653) \| shrunken endosperm | Pentatricopeptide repeat protein, Mitoch | GO:00094 |
| | Hypothetical conserved gene | GO:00100 |
| | Flavoprotein pyridine nucleotide cytochro | GO:00097 |
| | Similar to Photosystem I reaction centre s | GO:00159 |
| | Similar to cDNA clone:J013093F08, full i | GO:00064 |
| [Os] nitrogen sensitivity (TO:0000011) \| tillering ability (TO:0000329) | Member of the Bric-a-Brac/Tramtrack/Br | GO:00063 |
| | Zinc finger, C2H2-type domain containing protein | |
| | Adipose-regulatory protein, Seipin doma | GO:00066 |
| | Targeting for Xklp2 family protein | GO:00321 |
| | Protein of unknown function DUF1218 family protei | |
| | Heat shock protein DnaJ, N-terminal domain contai | |
| | Similar to ABC transporter (PDR5-like) isolog (PDR1 | |
| | GTP-binding protein, HSR1-related domain containi | |
| | Zm00001e021466 | GO:00065 |
| | Lipase, GDSL domain containing protein | |
| | Similar to AMP deaminase 1 (EC 3.5.4.6) | GO:00061 |
| [Os] abscisic acid sensitivity (TO:0000615) | Sporulation stage II, protein E C-terminal domain co | |
| | NB-ARC domain containing protein | GO:00069 |
| | Conserved hypothetical protein | |
| | Hypothetical conserved gene | GO:00304 |
| | Hypothetical conserved gene | GO:00063 |

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| | Ankyrin repeat containing protein | GO:00353 |
| | Similar to Cyclin-dependent kinase D-1 | GO:00064 |
| | Similar to OSIGBa0148P16.6 protein | |
| | Similar to ZF protein (Fragment) | GO:00511 |
| | Similar to NBS-LRR disease resistance protein family | |
| | Peptidase C48, SUMO/Sentrin/Ubl1 famil | GO:00003 |
| [Os] root length (TO:0000227) \| plant height (TO:0000207) \| salt tolerance (TO:0006001) \| root fresh weight (TO:0000578) \| disease resistance (TO:0000112) \| heat tolerance (TO:0000259) \| drought tolerance (TO:0000276) \| plant dry weight (TO:0000352) | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to predicted protein | GO:00062 |
| [Os] genic male sterility-thermo sensitive (TO:0000067) \| male sterility (TO:0000437) \| cold tolerance (TO:0000303) \| anther shape (TO:0000214) \| stamen anatomy and morphology trait (TO:0000215) \| stamen size (TO:0002601) \| pollen fertility (TO:0000421) \| stamen length (TO:0002609); [Os] male sterility TO:0000437\| panicle number TO:0000152\| panicle length | Similar to AGO1 homologous protein | GO:00310 |
| | Conserved hypothetical protein | |
| | Cyclin-like F-box domain containing protein | |
| | Zm00001e033722 | |
| | ATPase, AAA-type, core domain containing protein | |
| | Zm00001e040430 | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Leucine-rich repeat, N-terminal domain containing | |
| | Similar to TPD1 | GO:00017 |
| [Os] spikelet sterility (TO:0000436) \| grain weight (TO:0000590) \| spikelet weight (TO:0000501) \| spikelet number (TO:0000456) \| grain number (TO:0002759) \| filled grain number (TO:0000447) \| panicle type (TO:0000089) \| panicle number (TO:0000152) \| inflorescence branching (TO:0000050); [Os] meristem identity TO:0006017 | Basic helix-loop-helix (bHLH) transcripti | GO:00072 |
| | Zm00001e118270 | |
| | Uncharacterised protein family UPF0497, trans-me | |

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|---|---|---|
| | (1,4)-beta-xylan endohydrolase, isoenzy | GO:00002 |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | IQ calmodulin-binding region domain containing pr | |
| | Conserved hypothetical protein | |
| | Protein kinase, catalytic domain domain | GO:00064 |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) | Similar to H0303G06.18 protein | GO:00062 |
| | Leucine carboxyl methyltransferase dom | GO:00322 |
| [Os] drought tolerance (TO:0000276);<br>[Os] drought tolerance TO:0000276 | Cold acclimation protein COR413-TM1 | |
| | Allergen V5/Tpx-1 related family protein | GO:00096 |
| | Similar to Translocon Tic40 precursor | GO:00096 |
| | Conserved hypothetical protein | GO:00097 |
| | Similar to RECA3 (RECA HOMOLOG 3); D | GO:00000 |
| | Cyclin-like F-box domain containing protein | |
| | Similar to FAE1 | GO:00066 |
| | Uncharacterised conserved protein UCP022348 dom | |
| | Similar to phosphoinositide binding | GO:00097 |
| | Pentatricopeptide repeat domain contain | GO:00094 |
| | Protein of unknown function DUF623, pl | GO:00458 |
| | Zm00001e025292 | |
| | Similar to Pectate lyase B (Fragment) | GO:00454 |
| | Similar to S1 self-incompatibility locus-l | GO:00002 |
| | Zm00001e020269 | GO:00086 |
| | Conserved hypothetical protein | GO:00708 |
| | Similar to Thioredoxin | GO:00706 |
| | Annexin family protein | |
| | 3'-5' exonuclease domain containing pro | GO:00061 |
| | Hypothetical conserved gene | GO:00064 |
| [Os] culm angle (TO:0000427) \| tiller number (TO:0000346) \| tiller angle (TO:0000567) \| filled grain number (TO:0000447) \| grain yield (TO:0000396) | Similar to Leaf angle-associated protein | GO:00017 |

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| Similar to Glycine-rich protein 2 | GO:00062 |
| Hypothetical conserved gene | GO:00905 |
| Conserved hypothetical protein | |
| Similar to RES protein | |
| DNA/RNA helicase, C-terminal domain containing p | |
| Similar to SET domain protein | GO:00062 |
| MAP65/ASE1 family protein | GO:00002 |
| Pentatricopeptide repeat domain containi | GO:00094 |
| Conserved hypothetical protein | GO:00063 |
| No apical meristem (NAM) protein domai | GO:00063 |
| Zm00001e009494 | GO:00064 |
| CC-type glutaredoxin, Panicle developme | GO:00454 |
| Zm00001e015107 | |
| Pentatricopeptide repeat domain containi | GO:00094 |
| Similar to Sugar transporter protein | GO:00086 |
| Bifunctional inhibitor/plant lipid transfer | GO:00065 |
| DNA repair nuclease, XPF-type/Helicase | GO:00062 |
| Zm00001e024537 | GO:00062 |
| Similar to RbohAp108 | GO:00098 |
| Hypothetical conserved gene | GO:00430 |
| Similar to ribosomal protein L35 containi | GO:00064 |
| Similar to Blind | GO:00301 |
| Similar to SOX-1 protein | |
| Forkhead-associated (FHA) domain doma | GO:00351 |
| Myb-like DNA-binding domain, SHAQKY | GO:00063 |
| Zm00001e039190 | GO:00064 |

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|---|---|---|
| [Os] calcium sensitivity (TO:0000006) \| iron sensitivity (TO:0000224) \| salt tolerance (TO:0006001) \| UV light sensitivity (TO:0000160) \| abscisic acid sensitivity (TO:0000615) \| zinc sensitivity (TO:0000351) \| drought tolerance (TO:0000276) | Node-expressed Cd transporter, Putative | GO:00068 |
| [Os] leaf angle (TO:0000206) \| lignin biosynthesis trait (TO:0000733) \| flower anatomy and morphology trait (TO:0000499) \| lignin content (TO:0000731) \| sugar content (TO:0000333) \| drought tolerance (TO:0000276) | Similar to NAM protein | GO:00063 |
| | Similar to Formin-like protein 4 | GO:00300 |
| | Thioredoxin-like fold domain containing | GO:00551 |
| | Hypothetical conserved gene | GO:00063 |
| | Protein of unknown function DUF568, DOMON-like | |
| | Sas10/Utp3/C1D domain containing prot | GO:00004 |
| | Conserved hypothetical protein | |
| | Similar to Receptor protein kinase-like protein | |
| [Os] cell organelle development trait (TO:0002755) \| growth and development trait (TO:0000357) \| floury endosperm (TO:0000104) | Pentatricopeptide repeat domain containing protein | |
| | Similar to Myb family DNA-binding protein | |
| | Similar to N-acetyltransferase | |
| | Hypothetical conserved gene | GO:00324 |
| | Zm00001e144019 | GO:00517 |
| | Similar to THA4 | GO:00068 |
| | Similar to MYB transcription factor | GO:00301 |
| [Os] salt sensitivity (TO:0000429) \| ethylene sensitivity (TO:0000173) | Transcription factor, Response to ethylen | GO:00098 |
| | Major facilitator superfamily, general sub | GO:00550 |
| | Zm00001e038697 | GO:00063 |

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|---|---|---|
| [Os] seed development trait (TO:0000653) \| embryo development trait (TO:0000620) \| oxidative stress (TO:0002657) | Similar to NAM1 protein (Fragment) | GO:00063 |
| | Conserved hypothetical protein | GO:00430 |
| | Zinc finger, C6HC-type domain containin | GO:00002 |
| | Similar to H0124B04.9 protein | GO:00059 |
| | Six-hairpin glycosidase domain containin | GO:00101 |
| [Os] temperature response trait (TO:0000432) \| leaf shape (TO:0000492) \| leaf sheath length (TO:0002689) \| leaf lamina joint bending (TO:0002688) \| auxin content (TO:0002672) \| leaf angle (TO:0000206) \| filled grain number | Similar to Homeobox protein | GO:00063 |
| | Similar to Dynein light chain 1 protein DL | GO:00070 |
| | Similar to 9G8-like SR protein (RSZp22 s | GO:00003 |
| | Similar to H0801D08.9 protein | GO:00086 |
| | Similar to ARO1-like protein 3 | GO:00071 |
| | Sterile alpha motif homology domain containing pro | |
| [Os] stress trait (TO:0000164) \| bacterial blight disease resistance (TO:0000175) \| jasmonic acid sensitivity (TO:0000172); [Os] meristem | Histone lysine demethylase, Stress-respo | GO:00063 |
| [Os] phosphorus sensitivity (TO:0000102) | Phosphate transporter, Phosphate uptak | GO:00068 |
| | NB-ARC domain containing protein | GO:00069 |
| | Similar to Protein kinase domain containi | GO:00064 |
| | Similar to IQ calmodulin-binding motif family protei | |
| | Plant lipid transfer protein/Par allergen f | GO:00068 |
| | Conserved hypothetical protein | |

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|---|---|---|
| | Conserved hypothetical protein | |
| | Plastocyanin-like domain containing prot | GO:00229 |
| | Similar to Sucrose-phosphate synthase 2 | GO:00059 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| viral disease resistance (TO:0000148) | Similar to CCAAT-binding transcription f | GO:00063 |
| [Os] inflorescence development trait (TO:0000621) \| panicle number (TO:0000152) \| grain size (TO:0000397) \| grain weight (TO:0000590) \| plant height (TO:0000207) \| brassinosteroid sensitivity (TO:0002677); [Os] grain size TO:0000397\| panicle number | | |
| | KIP1-like domain containing protein | |
| | Conserved hypothetical protein | |
| | Similar to Peroxidase 1 | GO:00069 |
| | Similar to Glutathione-S-transferase 19E | GO:00067 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| [Os] nitrogen sensitivity (TO:0000011) | Allantoinase (EC:3.5.2.5), Ureide metabol | GO:00061 |
| | Hypothetical conserved gene | |
| | Per1-like family protein | GO:00065 |
| [Os] relative plant height (TO:0001034) \| relative biomass (TO:0000143) \| drought tolerance (TO:0000276) \| water use efficiency (TO:0001017) \| light intensity sensitivity (TO:0000460) \| salt tolerance (TO:0006001) \| relative yield (TO:0000153) \| sodium to potassium content ratio (TO:0000525); [Os] salt tolerance TO:0006001; [Ta] salt sensitivity TO:0000429 | Vacuolar Na+/H+ antiporter, Salt toleran | GO:00068 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| [Os] chalky endosperm (TO:0000266) \| grain shape (TO:0002730); [Os] grain shape TO:0002730 | Transcriptional activator, Regulation of g | GO:00071 |
| | Pectinesterase inhibitor domain containin | GO:00430 |

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|---|---|---|
| [Os] bacterial blight disease resistance (TO:0000175) \| plant height (TO:0000207) \| auxin sensitivity (TO:0000163) \| gibberellic acid sensitivity (TO:0000166) | Sugar transporter, TAL effector-mediate | GO:00086 |
| | HPP family protein | |
| | Peptidase A1 domain containing protein | GO:00065 |
| [Os] amino acid content TO:0002673\| protein content TO:0000598 | Similar to cationic amino acid transporter | GO:00033 |
| | KIP1-like domain containing protein | |
| | Similar to Transcription factor (Fragment) | GO:00063 |
| | Similar to AG-motif binding protein-3 | GO:00063 |
| | Carboxylesterase, type B family protein | |
| | Uncharacterised protein family UPF0497, trans-mem | |
| | Similar to uncharacterized enzyme involv | GO:00015 |
| | Methyltransferase-related domain contai | GO:00063 |
| | Protein of unknown function DUF581 fam | GO:00063 |
| | Protein phosphatase 2C domain containi | GO:00359 |
| [Os] drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| abscisic acid content (TO:0002667) \| relative water content (TO:0000136) \| plant height (TO:0000207) \| seed size (TO:0000391) \| seed dormancy (TO:0000253) \| gibberellic acid sensitivity (TO:0000166) | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] leaf senescence (TO:0000249) \| tiller number (TO:0000346) \| nitrogen sensitivity (TO:0000011) \| shoot dry weight (TO:0000552) | Similar to Transcription factor (Fragment) | GO:00063 |
| | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Similar to 20 kDa chaperonin, chloroplas | GO:00064 |
| | Hypothetical conserved gene | |
| | Conserved hypothetical protein | GO:00100 |
| | Similar to Serine carboxypeptidase I prec | GO:00065 |
| | Similar to H0502B11.6 protein | |
| | Mitochodrial transcription termination fa | GO:00063 |
| | Similar to H0714H04.3 protein | |
| | Quinonprotein alcohol dehydrogenase-li | GO:00096 |

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|---|---|---|
| | Hypothetical conserved gene | GO:00062 |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| [Os] awn anatomy and morphology trait (TO:0002718) \| awn length (TO:0000072) \| inflorescence development trait (TO:0000621) | No apical meristem (NAM) protein domai | GO:00063 |
| | Similar to Peroxisome type ascorbate per | GO:00003 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to Papain-like cysteine peptidase | GO:00065 |
| | Zm00001e028328 | |
| | Glutaredoxin 2 family protein | GO:00551 |
| | Similar to IBR domain containing protein | GO:00002 |
| | Similar to BRASSINOSTEROID INSENSITIVE | GO:00064 |
| [Os] floral organ identity TO:0006019\| organ identity TO:0006018\| oxidative stress TO:0002657\| male sterility TO:0000437 | | |
| | Similar to Epstein-Barr virus (B95-8 isola | GO:00068 |
| | Protein phosphatase 2C domain containi | GO:00359 |
| | Similar to KI domain interacting kinase 1 | GO:00064 |
| | NAD(P)-binding domain containing prote | GO:00086 |
| | Similar to basic helix-loop-helix family p | GO:00000 |
| [Os] leaf color (TO:0000326) \| growth and development trait (TO:0000357) \| iron sensitivity (TO:0000224) | Similar to OSIGBa0092E09.4 protein | GO:00063 |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Similar to EARLY FLOWERING 4 (Fragment | GO:00096 |
| | Similar to GTP-binding protein (Fragment | GO:00068 |
| | Hypothetical conserved gene | GO:00066 |

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|---|---|---|
| | AT hook, DNA-binding, conserved site d | GO:00062 |
| | Zm00001e017140 | GO:00063 |
| [Os] cold tolerance (TO:0000303) \| copper sensitivity (TO:0000021) | Similar to Gamma-glutamylcysteine synt | GO:00067 |
| [Os] stigma length TO:0011008\| days to heading TO:0000137 | Similar to ABC transporter | GO:00550 |
| | Similar to Hydroxymethylglutaryl-CoA ly | GO:00065 |
| | Protein of unknown function DUF296 do | GO:00063 |
| [Os] abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| sheath blight disease resistance (TO:0000255) \| salt tolerance (TO:0006001) | Conserved hypothetical protein | GO:00070 |
| [Os] blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) | Similar to Protein kinase | GO:00064 |
| | PIG-P domain containing protein | GO:00065 |
| [Os] animal damage resistance (TO:0000054) | Transferase family protein | |
| | Similar to Golgi transport complex protei | GO:00068 |
| | Similar to IAA8 (Fragment) | GO:00063 |
| [Os] lignin content TO:0000731 | Similar to Laccase (EC 1.10.3.2) | GO:00094 |
| | Homeodomain-like containing protein | |
| | Similar to ATPUP3 | GO:00068 |
| [Os] spikelet fertility (TO:0000180) \| pollen fertility (TO:0000421) \| cold tolerance (TO:0000303) \| germinability at low temperature (TO:0000483) \| yield trait (TO:0000371) | Protein kinase, core domain containing p | GO:00064 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | GTP-binding signal recognition particle S | GO:00063 |
| | Zm00001e005854 | GO:00064 |

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|---|---|---|
| [Os] blast disease (TO:0000074) \| lateral root number (TO:0001013) | LysM receptor-like kinase, Arbuscular my | GO:00064 |
| [Os] brittle culm (TO:0000200) \| leaf rolling (TO:0000085) \| gibberellic acid sensitivity (TO:0000166) \| lignin content (TO:0000731) | R2R3-MYB transcription factor, Regulatio | GO:00301 |
| | Conserved hypothetical protein | GO:00009 |
| | Auxin responsive SAUR protein family pr | GO:00097 |
| | Similar to protein binding protein | GO:00165 |
| | Similar to Midline 1 protein (Tripartite m | GO:00007 |
| | Hypothetical conserved gene | |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to transposon protein | GO:00165 |
| | Thaumatin, pathogenesis-related family | GO:00069 |
| | Similar to transferase family protein | |
| [Os] disease resistance TO:0000112; [Ta] disease resistance TO:0000112 | | |
| [Os] drought tolerance (TO:0000276) | Bromodomain containing protein | |
| | Similar to Splicing factor RSZ33 | GO:00003 |
| | MtN3 and saliva related transmembrane | GO:00086 |
| | Zm00001e001270 | GO:00150 |
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| [Os] auxin sensitivity (TO:0000163) \| stamen number (TO:0000225) \| sterility related trait (TO:0000485) \| lodicule number (TO:0006010) \| salt tolerance (TO:0006001) \| anther shape (TO:0000214); [Os] auxin sensitivity TO:0000163; [Ta] drought tolerance TO:0000276 | Serine/threonine protein kinase domain | GO:00064 |

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|---|---|---|
| [Os] pollen fertility (TO:0000421) \| drought tolerance (TO:0000276) \| brassinosteroid sensitivity (TO:0002677) \| starch content (TO:0000696) \| photoperiod sensitivity (TO:0000229) \| genic male sterility-photoperiod sensitive (TO:0000009) \| heat tolerance (TO:0000259) | | |
| | Protein of unknown function DUF594 domain contai | |
| | Zm00001e042021 | GO:0007 |
| | Cupredoxin domain containing protein | GO:0022 |
| | Transcription factor GRAS domain contai | GO:0006 |
| [Os] herbicide sensitivity (TO:0000058) \| auxin sensitivity (TO:0000163) \| ethylene sensitivity (TO:0000173) \| root length (TO:0000227) \| black streak dwarf virus resistance (TO:0000020); [Os] plant height TO:0000207 | F-Box auxin receptor protein, Nuclear pr | GO:0009 |
| | Conserved hypothetical protein | |
| | Pectin lyase fold/virulence factor domain | GO:0005 |
| | Similar to Dual-specificity protein phosp | GO:0006 |
| | Similar to Alpha-L-fucosidase 1 | GO:0005 |
| [Os] bacterial blight disease resistance (TO:0000175) \| sheath blight disease resistance (TO:0000255) \| white-backed planthopper resistance (TO:0000205); [Os] disease resistance | Similar to WRKY transcription factor 12 | GO:0006 |
| | Similar to DNA-binding protein phosphat | GO:0006 |
| | Kelch related domain containing protein | GO:0009 |
| | Similar to Receptor protein kinase | GO:0006 |
| [Os] light sensitivity (TO:0000075) \| UV light sensitivity (TO:0000160) \| chloroplast development trait (TO:0002715) \| carotenoid content (TO:0000496) \| chlorophyll content (TO:0000495) \| chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| leaf color (TO:0000326) | 2-C-methyl-d-erythritol 2,4-cyclodipho | GO:0015 |

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|---|---|---|
| [Os] inflorescence branching (TO:0000050) \| female sterility (TO:0000358) \| grain number (TO:0002759) \| inflorescence development trait (TO:0000621) \| sterile lemma shape (TO:0002726) | | |
| [Os] tiller number (TO:0000346) \| auxin sensitivity (TO:0000163) \| stem length (TO:0000576) \| leaf lamina joint bending (TO:0002688) \| cytokinin sensitivity (TO:0000167) \| panicle number (TO:0000152) \| tillering ability (TO:0000329) \| plant height (TO:0000207) \| nitrogen sensitivity (TO:0000011) \| leaf width (TO:0000370) \| lateral root number (TO:0001013) \| seminal root length (TO:0000586); [Ta] tiller number TO:0000346\| plant height TO:0000207 | beta-carotene isomerase, Strigolactones | GO:00102 |
| | Cupredoxin domain containing protein | GO:00229 |
| | Chlorophyll a/b binding protein domain domain con | |
| | Similar to HVA22F (HVA22-LIKE PROTEIN F) | |
| | Similar to Acetyltransferase, GNAT family | GO:00458 |
| | Polymerase and histidinol phosphatase-li | GO:00062 |
| | DNA/RNA helicase, DEAD/DEAH box type, N-termin | |
| | Similar to OSIGBa0143N19.4 protein | |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| [Os] inflorescence development trait (TO:0000621) | YABBY family transcription factor, Leaf de | GO:00072 |
| | Similar to CDC6 protein | GO:00002 |
| [Os] blast disease (TO:0000074) \| heat tolerance (TO:0000259) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| bacterial leaf streak disease resistance (TO:0000203) \| root development trait (TO:0000656); [Os] drought tolerance TO:0000276\| root length TO:0000227 | Similar to Phytosulfokine receptor precur | GO:00064 |
| | Similar to AT-hook protein 1 | |

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|---|---|---|
| | Haloacid dehalogenase-like APase, Low-Pi-responsi | |
| | Similar to Serine carboxypeptidase family | GO:00065 |
| | Similar to calcium dependent protein kin | GO:00064 |
| [Os] root hair length (TO:0002665) | ROOT HAIR DEFECTIVE-SIX LIKE (RSL) cla | GO:00063 |
| | Similar to oxidoreductase/ transition metal ion bind | |
| | Armadillo-like helical domain containing protein | |
| | Pleckstrin homology-type domain contai | GO:00068 |
| | Serine/threonine protein kinase-related | GO:00064 |
| [Os] amino acid content (TO:0002673) \| hydrogen peroxide content (TO:0000605) \| shoot fresh weight (TO:0000571) \| leaf color (TO:0000326) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| plant growth hormone sensitivity (TO:0000401) \| UV-B light sensitivity (TO:0000601) | Similar to transcription factor HY5 | GO:00063 |
| | Hypothetical conserved gene | GO:19909 |
| | Protein of unknown function DUF623, pla | GO:00458 |
| | Pentatricopeptide repeat domain containing protein | |
| | 26 kDa globulin (Alpha-globulin) | |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | DP TF | GO:00063 |
| | F-box domain, Skp2-like domain contain | GO:00165 |
| [Os] floral organ number TO:0006038\| grain number TO:0002759 | tRNA isopentenyltransferase family prote | GO:00064 |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Similar to Trehalose-6-phosphate phosp | GO:00059 |
| | Ankyrin domain containing protein | |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) | Tetratricopeptide-like helical domain con | GO:00094 |
| [Os] root development trait (TO:0000656) \| root length (TO:0000227) | Argininosuccinate lyase, Root elongatio | GO:00424 |
| | Reticulon family protein | GO:00096 |
| | Similar to Mitogen-activated protein kina | GO:00064 |

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|---|---|---|
| | Glycosyl transferase, family 43 protein | GO:00059 |
| | Protein of unknown function DUF573 dor | GO:00063 |
| | Similar to Chalcone reductase homologue (Fragment | |
| | Similar to Glycerol-3-phosphate acyltran | GO:0010 |
| [Os] blast disease (TO:0000074) | Zm00001e032947 | GO:00059 |
| | Conserved hypothetical protein | GO:00427 |
| | Similar to Caffeoyl-CoA 3-O-methyltrans | GO:00322 |
| | Homeodomain-related domain containing protein | |
| | Uncharacterised conserved protein UCP0 | GO:00442 |
| [Os] drought tolerance (TO:0000276) | Homeodomain-related domain containin | GO:00063 |
| | Cytochrome P450 domain containing protein | |
| [Os] stem length (TO:0000576) \| plant height (TO:0000207) \| temperature response trait (TO:0000432) \| lodging incidence (TO:0000068) \| internode length (TO:0000145) \| flag leaf angle (TO:0000124) \| cold tolerance (TO:0000303) | Similar to Type II inositol-1,4,5-trisphos | GO:00075 |
| | Similar to Vacuolar assembly protein VPS | GO:00066 |
| | Similar to aminoacylase-1 | GO:00065 |
| | Similar to Pentatricopeptide repeat protei | GO:00094 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Uncharacterised protein family UPF0089 | GO:00194 |
| | Similar to PWWP domain containing prote | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to Heat shock transcription factor | GO:00063 |
| [Os] salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| cold tolerance (TO:0000303) \| biotic stress trait (TO:0000179) \| heat tolerance (TO:0000259) \| disease resistance (TO:0000112) \| oxidative stress (TO:0002657) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| submergence tolerance (TO:0000524) | A20/AN1 zinc-finger protein, Response t | GO:00165 |
| | Similar to Sugar transporter protein | GO:00086 |
| | U-box containing E3 ligase, Response to | GO:00165 |

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|---|---|---|
| | Leucine-rich repeat receptor-like kinase, | GO:00064 |
| | Similar to mitochondrial chaperone BCS1 | |
| | Similar to prenylated Rab receptor 2 | GO:00161 |
| | Peptidase C48, SUMO/Sentrin/Ubl1 doma | GO:00065 |
| | Zm00001e134673 | GO:00063 |
| [Os] chlorophyll-b content (TO:0000295) \| leaf senescence (TO:0000249) \| panicle number (TO:0000152) \| spikelet number (TO:0000456) \| chlorophyll-a content | Similar to Pto kinase interactor 1-like pro | GO:00064 |
| | Similar to tic20 protein-related | |
| | Similar to multidrug resistance protein A | GO:00550 |
| | Similar to photosystem II 11 kDa protein- | GO:00102 |
| | Zm00001e039390 | GO:00063 |
| | Monooxygenase, FAD-binding domain containing p | |
| [Os] starch content (TO:0000696) \| blast disease (TO:0000074) \| black streak dwarf virus resistance (TO:0000020) \| abscisic acid sensitivity (TO:0000615) \| brown planthopper resistance (TO:0000424) \| jasmonic acid content (TO:0002668) \| seed anatomy and morphology trait (TO:0000184); [Ta] male sterility TO:0000437\| heat tolerance | 12-oxophytodienoate reductase (EC:1.3. | GO:00066 |
| | Similar to glycoprotein | |
| | Similar to JHL05D22.13 protein | GO:00064 |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616); [Os] oxidative stress TO:0002657 | CCT domain containing protein | GO:00099 |
| [Os] drought tolerance (TO:0000276) \| blast disease (TO:0000074) | | |
| | Zm00001e010927 | GO:00064 |

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|---|---|---|
| [Os] sodium content (TO:0000608) \| proline content (TO:0006002) \| secondary branch number (TO:0000557) \| salt tolerance (TO:0006001) \| nitrogen sensitivity (TO:0000011) \| abiotic stress trait (TO:0000168) \| leaf shattering (TO:0000108) \| root length (TO:0000227) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| tiller number (TO:0000346) \| stem strength (TO:0000051) \| light intensity sensitivity (TO:0000460) \| sugar content (TO:0000333) \| cold tolerance (TO:0000303) \| hydrogen peroxide | Cellulose synthase A catalytic subunit 9, | GO:00098 |
| | BTB/POZ fold domain containing protein | GO:00165 |
| [Os] seed maturation (TO:0002661) \| grain weight (TO:0000590) \| plastochron (TO:0000735) \| grain length (TO:0000734) \| grain size (TO:0000397) \| grain yield (TO:0000396) \| grain width (TO:0000402); [Os] grain weight | Histone H4 acetyltransferase, Regulation of grain we | |
| [Ta] stem elongation TO:0006036\| drought tolerance TO:0000276 | | |
| | Similar to Basic leucine zipper transcripti | GO:00063 |
| | Hypothetical conserved gene | GO:00096 |
| [Os] inflorescence development trait (TO:0000621) \| sterile lemma width (TO:0002727) \| glume length (TO:0020033) \| sterile lemma length (TO:0000240) \| lemma and palea anatomy and morphology trait (TO:0000079) \| lodicule anatomy and morphology trait (TO:0006009) | Hypothetical conserved gene | GO:00063 |
| | Similar to GATA transcription factor 25 | GO:00063 |
| [Os] cold tolerance (TO:0000303) | Glycosyl transferase, family 8 protein | |
| [Os] brittle culm TO:0000200 | Protein of unknown function DUF266, plant family p | |
| | Similar to Galactoside 2-alpha-L-fucosyl | GO:00099 |
| | Conserved hypothetical protein | |
| | Similar to Cation-transporting ATPase | GO:00453 |
| | RNA-binding, CRM domain domain containing prote | |
| | Oligopeptide transporter OPT superfamil | GO:00356 |

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|---|---|---|
| | Similar to Endoribonuclease Dicer homol | GO:00063 |
| [Os] primary branch number (TO:0000547) \| plant height (TO:0000207) \| spikelet weight (TO:0000501) \| inflorescence development trait (TO:0000621) \| root development trait (TO:0000656) \| abscisic acid sensitivity (TO:0000615) \| inflorescence branching (TO:0000050) \| panicle number (TO:0000152) \| gibberellic acid sensitivity (TO:0000166) \| tillering ability (TO:0000329) \| spikelet number (TO:0000456); [Os] stem elongation TO:0006036\| meristem identity TO:0006017\| shoot branching TO:0002639\| tiller number TO:0000346\| plant height TO:0000207; | GRAS family nuclear protein, Control of ti | GO:00063 |
| | IQ calmodulin-binding region domain containing pr | |
| | Similar to Zinc finger, C2H2 type family protein, exp | |
| | Amino acid-binding ACT domain containing protein | |
| | SET domain containing protein | GO:00165 |
| | | |
| | Similar to Phosphoesterase | GO:00062 |
| | Zm00001e009565 | GO:00159 |
| [Os] salt tolerance (TO:0006001) \| chlorophyll content (TO:0000495) \| gravity response trait (TO:0002693) \| auxin sensitivity (TO:0000163) \| heat tolerance (TO:0000259) \| root length (TO:0000227) \| drought tolerance (TO:0000276) \| root development trait (TO:0000656) \| lateral root number (TO:0001013); [Os] fruit size TO:0002625\| seed size TO:0000391\| grass weed TO:0000343 | Cyclophilin, Peptidyl-prolyl cis-trans iso | GO:00004 |
| | Similar to T-cell activation protein phosphatase 2C- | |
| [Os] cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| drought tolerance (TO:0000276) \| bacterial blight disease resistance (TO:0000175) \| abscisic acid sensitivity (TO:0000615) \| heat tolerance (TO:0000259) | | |

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|---|---|---|
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Similar to CDPK substrate protein 1 | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] root meristem development (TO:0002692) \| root development trait (TO:0000656) \| temperature response trait (TO:0000432) \| growth hormone content (TO:0000476) \| jasmonic acid content (TO:0002668) \| vascular tissue related trait (TO:0000470) \| crown root number (TO:0002685) \| shoot development trait (TO:0000654) \| total biomass yield (TO:0000457) \| spikelet number (TO:0000456) \| 1000-dehulled grain weight (TO:0000592) \| grain length (TO:0000734) \| tiller number (TO:0000346) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| bacterial blight disease resistance (TO:0000175) \| vegetative vigor (TO:0000296) \| cold tolerance (TO:0000303) | | |
| | Non-protein coding transcript | GO:00086 |
| | Similar to predicted protein | GO:00311 |
| [Os] drought tolerance (TO:0000276) | Protein of unknown function DUF296 domain contai | |
| | Similar to predicted protein | GO:00064 |
| [Os] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| drought tolerance (TO:0000276) \| stress trait | Zinc finger, AN1-type domain containing protein | |
| | Similar to Thiosulfate sulfurtransferase (EC 2.8.1.1) | |
| [Os] bacterial disease resistance (TO:0000315) \| cold tolerance (TO:0000303) \| viral disease resistance (TO:0000148) | Serine/threonine protein kinase-related | GO:00064 |

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|---|---|---|
| | Similar to Receptor protein kinase-like pr | GO:00064 |
| | RNA recognition motif domain domain c | GO:00064 |
| | Trehalose-6-phosphate phosphatase | GO:00059 |
| | Transcription initiation factor IIF, beta su | GO:00063 |
| | WD40 repeat domain containing protein | |
| | | |
| | Similar to MAP3Ka | GO:00001 |
| | Zinc finger, Tim10/DDP-type family prot | GO:00723 |
| | | |
| | | |
| | Zm00001e028115 | GO:00064 |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | | |
| | Exo70 exocyst complex subunit family pr | GO:00068 |
| | Targeting for Xklp2 family protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | | |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) | Similar to chromatin remodeling complex | GO:00801 |
| | | |
| [Os] cytokinin content (TO:0002660) \| shoot apical meristem development (TO:0006020) \| shoot meristem development (TO:0002638) \| auxin content (TO:0002672) \| drought tolerance (TO:0000276); [Os] shoot meristem development TO:0002638 | | |
| | Similar to barley mlo defense gene homo | GO:00069 |
| | Similar to Pectate lyase homolog (EC 4.2. | GO:00454 |
| | | |
| | | |
| | HAD-superfamily subfamily IB hydrolase, hypothetic | |
| | Similar to IQ calmodulin-binding motif fa | GO:00064 |
| | Similar to Transcription factor IIIB 90 kDa | GO:00063 |
| | Similar to cytokinin-N-glucosyltransferase 1 | |
| | Zm00001e038709 | GO:00100 |
| | | |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | | |
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| [Os] zinc sensitivity (TO:0000351) | Similar to Zinc transporter 2 precursor (Z | GO:00068 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to Receptor-like protein kinase-li | GO:00064 |

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|---|---|---|
| [Os] male fertility restoration trait (TO:0000308) | Similar to Rf2 protein | GO:00096 |
| | Esterase, SGNH hydrolase-type domain c | GO:00066 |
| | Similar to predicted protein | |
| | Conserved hypothetical protein | GO:00420 |
| [Os] pistil anatomy and morphology trait (TO:0000223) \| spikelet number (TO:0000456) \| spikelet fertility (TO:0000180) \| spikelet anatomy and morphology trait (TO:0000657) \| cytokinin content (TO:0002660) \| stamen anatomy and morphology trait (TO:0000215) \| tiller bud dormancy (TO:0000661) \| female sterility (TO:0000358) \| spikelet sterility (TO:0000436) \| tiller number (TO:0000346) \| inflorescence development trait (TO:0000621) \| tillering ability (TO:0000329) \| drought tolerance (TO:0000276) \| auxin sensitivity (TO:0000163) \| panicle number (TO:0000152); [Os] floral organ number TO:0006038\| meristem identity TO:0006017\| tiller angle TO:0000567\| leaf width TO:0000370\| tiller number TO:0000346\| drought tolerance TO:0000276\| root length TO:0000227\| culm number TO:0000027 | Homeobox protein orthologous to Arabi | GO:00198 |
| | Cellular retinaldehyde binding/alpha-toc | GO:00159 |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| | Similar to Permease 1 | GO:00550 |
| | Similar to predicted protein | |
| | Tetratricopeptide TPR-1 domain containi | GO:00063 |

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|---|---|---|
| [Os] sulfur sensitivity (TO:0000007) \| silicon sensitivity (TO:0000031) | Aquaporin NIP III subfamily protein, Aqua | GO:00550 |
| | Similar to OSIGBa0145C02.7 protein | |
| [Os] plant height (TO:0000207) \| cold tolerance (TO:0000303) \| auxin sensitivity (TO:0000163) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276); [Os] salt tolerance TO:0006001\| callus induction TO:0000428 | Histone deacetylase superfamily protein | GO:00001 |
| [Os] pollen fertility (TO:0000421) \| spikelet fertility (TO:0000180) | Regulation of male gametogenesis during pollen de | |
| | Protein of unknown function DUF639 family protein | |
| | Nucleic acid-binding, OB-fold domain containing pr | |
| | Pentatricopeptide repeat domain containing protein | |
| | Protein of unknown function DUF821, CAP10-like fa | |
| | Similar to Calmodulin-binding protein ph | GO:00359 |
| | Sugar transporter, conserved site domain | GO:00064 |
| | WD40 protei | GO:00515 |
| | FAD-dependent glycerol-3-phosphate d | GO:00060 |
| | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Spectrin repeat containing protein | GO:00096 |
| [Os] root number (TO:0000084) \| callus induction (TO:0000428) \| crown root number (TO:0002685) \| root length (TO:0000227); [Os] lateral root number TO:0001013\| crown rootless TO:0000230\| root number TO:0000084 | ASYMMETRIC LEAVES2 (AS2)/LATERAL OR | GO:00097 |
| | Pectinesterase inhibitor domain containin | GO:00430 |

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|---|---|---|
| [Os] vascular bundle number (TO:0000472) \| inflorescence development trait (TO:0000621) \| flower anatomy and morphology trait (TO:0000499) \| panicle number (TO:0000152) \| grain number (TO:0002759) \| inflorescence branching (TO:0000050) \| spikelet number (TO:0000456) \| 1000-dehulled grain weight (TO:0000592) \| grain size (TO:0000397) \| sterile lemma length (TO:0000240) \| grain yield per plant (TO:0000449) \| grain yield (TO:0000396) \| secondary branch number (TO:0000557) \| 1000-seed weight (TO:0000382) \| spikelet anatomy and morphology trait (TO:0000657) \| hydrogen peroxide content (TO:0000605) \| panicle length (TO:0000040) \| grain length (TO:0000734) \| filled grain number (TO:0000447) \| panicle type (TO:0000089) \| panicle shape (TO:0000262) \| lemma length (TO:0000650) \| auxin content (TO:0002672); [Os] floral organ identity TO:0006019\| organ identity TO:0006018\| meristem identity TO:0006017\| grain number | ERF transcription factor, Mediation of the | GO:00063 |
| | Similar to H0404F02.10 protein | GO:00436 |
| | Protein kinase-like domain containing pr | GO:00064 |
| | Tetratricopeptide-like helical domain containing pro | |
| | Ubiquitin-conjugating enzyme/RWD-like domain co | |
| | Conserved hypothetical protein | GO:00094 |
| | Protein kinase, catalytic domain domain c | GO:00064 |
| [Os] pericarp color (TO:0000707) \| seed coat color (TO:0000190) \| endosperm color (TO:0000487) | | |
| | Peptidase C19, ubiquitin carboxyl-termin | GO:00065 |
| | Cyclin, C-terminal domain containing pro | GO:00070 |
| | Protein of unknown function DUF292, eu | GO:00081 |
| | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Peptidase C12, ubiquitin carboxyl-terminal hydrolas | |

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| [Os] sheath blight disease resistance (TO:0000255) \| salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| drought tolerance (TO:0000276) \| bacterial blight disease resistance (TO:0000175) | Peptidase C14, caspase catalytic domain | GO:00065 |
| | TGF-beta receptor, type I/II extracellular | GO:00068 |
| | Phox-associated domain domain containing protein | |
| | Like-Sm ribonucleoprotein, core family p | GO:00003 |
| | NLI interacting factor domain containing protein | |
| | SANT domain, DNA binding domain containing prot | |
| [Os] bacterial blight disease resistance (TO:0000175) | WRKY1 (WRKY transcription factor 17) | GO:00063 |
| [Os] leaf development trait (TO:0000655) \| chloroplast development trait (TO:0002715) \| temperature response trait (TO:0000432) \| leaf color (TO:0000326) \| variegated leaf (TO:0000069) \| chlorophyll content (TO:0000495) | HNH endonuclease domain containing pr | GO:00903 |
| | Similar to GmCK3p (EC 2.7.1.32) (Fragme | GO:00066 |
| | Oligopeptide transporter OPT superfamil | GO:00356 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00063 |
| | Hypothetical conserved gene | GO:00485 |
| | Similar to B-box zinc finger family protei | GO:00063 |
| [Os] auxin sensitivity (TO:0000163) \| tiller number (TO:0000346) \| filled grain number (TO:0000447) \| nitrogen sensitivity (TO:0000011) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| plant growth hormone sensitivity (TO:0000401) \| inflorescence number (TO:0000582) \| cytokinin sensitivity (TO:0000167) \| primary branch number (TO:0000547) | Similar to Cytokinin dehydrogenase 2 | GO:00096 |
| | WD-40 repeat containing protein | GO:00165 |
| | Receptor-like protein kinase 3 | GO:00064 |
| | Uncharacterised protein family UPF0005 | GO:00157 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to Expansin-A17 | GO:00096 |

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|---|---|---|
| [Os] stomatal conductance (TO:0000522) \| water use efficiency (TO:0001017) \| stomatal frequency (TO:0000566) \| heat tolerance (TO:0000259) \| drought tolerance | Similar to predicted protein | GO:00100 |
| [Os] tiller angle TO:0000567 | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Uncharacterised protein family UPF0089 | GO:00194 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| black streak dwarf virus resistance (TO:0000020) | Cytochrome P450 90B2, Brassinosteroid | GO:00066 |
| [Os] white-backed planthopper resistance (TO:0000205) \| bacterial blight disease resistance (TO:0000175) | Similar to WRKY transcription factor 32 | GO:00063 |
| | EF-Hand type domain containing protein | |
| [Os] leaf color (TO:0000326) \| chlorophyll content (TO:0000495) \| light sensitivity (TO:0000075) | Similar to Magnesium-protoporphyrin O- | GO:00159 |
| [Os] cold tolerance (TO:0000303) \| proline content (TO:0006002) \| total soluble sugar content (TO:0000340) \| drought tolerance (TO:0000276); [Ta] disease resistance TO:0000112\| heterosis TO:0000355 | Similar to LHY protein | |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to Cupin family protein, expressed | |
| | Haem peroxidase family protein | GO:00069 |
| | Similar to TA1 protein (Fragment) | GO:00063 |
| | Similar to Subtilisin-like serine proteinas | GO:00065 |
| | Similar to Leucine-rich receptor-like prot | GO:00064 |
| [Os] flooding related trait (TO:0000114) \| mesocotyl length (TO:0000544) \| gibberellic acid sensitivity (TO:0000166) \| relative root length (TO:0000516) \| oxidative stress (TO:0002657) \| relative plant height | Similar to Snapdragon myb protein 305 h | GO:00063 |
| | Hypothetical conserved gene | GO:00064 |
| | Similar to MRP-like ABC transporter | GO:00550 |
| | Similar to Centromere protein-like protein (Fragmen | |

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|---|---|---|
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| | Similar to Laccase (EC 1.10.3.2) | GO:00462 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to LRK14 | GO:00064 |
| [Os] seed development trait (TO:0000653) | | |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF231, pla | GO:00098 |
| [Os] bacterial blight disease resistance (TO:0000175) \| abscisic acid content (TO:0002667) \| drought tolerance (TO:0000276); [Os] seed dormancy TO:0000253 | Short-chain alcohol dehydrogenase, ABA | GO:00065 |
| | Similar to Thymidine kinase | GO:00063 |
| | Conserved hypothetical protein | GO:00063 |
| | FAD-dependent pyridine nucleotide-disu | GO:00196 |
| | Zinc finger, RING-type domain containin | GO:00165 |
| | Lipase, GDSL domain containing protein | |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to Splicing factor SC35 | GO:00003 |
| [Os] disease resistance (TO:0000112) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| osmotic response sensitivity (TO:0000095) \| nutrient sensitivity (TO:0000480) | Protein of unknown function DUF617, pla | GO:00102 |
| [Os] inflorescence development trait (TO:0000621) | LIM binding protein domain containing p | GO:00001 |
| | Similar to SBT2 protein (Subtilisin-like pr | GO:00065 |
| | Conserved hypothetical protein | GO:00436 |
| [Os] drought tolerance (TO:0000276) \| seedling vigor (TO:0000280) \| abiotic stress trait (TO:0000168) \| blast disease (TO:0000074) \| seed dormancy (TO:0000253) | Conserved hypothetical protein | GO:00097 |
| [Os] plant height (TO:0000207) | | |

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|---|---|---|
| [Os] seed set percent (TO:0000455) | Protein of unknown function DUF1278 fa | GO:00095 |
| | Hypothetical conserved gene | |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Aux/IAA_ARF_dimerisation domain conta | GO:00063 |
| [Os] photosynthetic rate (TO:0001015) \| leaf development trait (TO:0000655) \| chloroplast development trait (TO:0002715) | RelA/SpoT protein domain containing pr | GO:00159 |
| | Similar to OSIGBa0160I14.1 protein | |
| | Glutathione S-transferase, C-terminal-li | GO:00067 |
| | Hypothetical conserved gene | GO:00004 |
| [Os] male sterility (TO:0000437) \| anther color (TO:0000187) \| salt tolerance (TO:0006001) \| anther length (TO:0000531) \| pollen free | Zinc finger, PHD-type domain containing protein | |
| | Zm00001e107552 | GO:00063 |
| | Similar to NAM protein | GO:00063 |
| | Similar to mitochondrial carrier-like prot | GO:00157 |
| | Similar to PGPD14 protein | GO:00065 |
| | Similar to Thaumatin-like protein | GO:00069 |
| | Hypothetical conserved gene | GO:00060 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Zm00001e030156 | |
| | Zinc finger, CCCH-type domain containin | GO:00063 |
| | Histone-fold domain containing protein | GO:00063 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | NAD(P)-binding domain containing prote | GO:00066 |
| | Protein of unknown function DUF250 do | GO:00550 |
| | Similar to HEAT repeat family protein, ex | GO:00066 |
| | Nucleic acid-binding, OB-fold domain co | GO:00062 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to Mannan endo-1,4-beta-mann | GO:00081 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to subtilase family protein | GO:00065 |
| | Cupredoxin domain containing protein | GO:00229 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Heat shock protein DnaJ, N-terminal domain contai | |

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|---|---|---|
| [Os] grain size TO:0000397\| tiller number TO:0000346\| root dry weight TO:0000078 | Similar to Sucrose transporter | GO:00096 |
| [Os] bacterial leaf streak disease resistance (TO:0000203) | Leucine-rich repeat (LRR) protein, Inhibitor of funga | |
| | Similar to Xyloglucan endotransglycosyla | GO:00059 |
| | Concanavalin A-like lectin/glucanase dor | GO:00059 |
| [Os] embryo related trait (TO:0000064) \| leaf shape (TO:0000492) \| blast disease (TO:0000074) | Rnase III family protein, Shoot apical mer | GO:00063 |
| [Ta] seed coat color TO:0000190\| seed dormancy TO:0000253 | Similar to P-type R2R3 Myb protein (Frag | GO:00301 |
| | Similar to Inositol-1, 4, 5-trisphosphate | GO:00468 |
| | Zm00001e042018 | |
| [Os] abscisic acid sensitivity (TO:0000615) \| bacterial blight disease resistance (TO:0000175) \| plant growth hormone sensitivity (TO:0000401) \| jasmonic acid sensitivity (TO:0000172) \| drought sensitivity (TO:0000188) \| heat tolerance (TO:0000259) | Similar to WRKY transcription factor 43 | GO:00063 |
| | Similar to laccase 90c | GO:00462 |
| | Major facilitator superfamily antiporter | GO:00550 |
| [Ta] seed size TO:0000391\| grain size TO:0000397\| protein content TO:0000598 | No apical meristem (NAM) protein domai | GO:00063 |
| | Zinc/iron permease family protein | GO:00068 |
| | Similar to NOI protein | |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| | Pyridoxal phosphate-dependent transferase, major | |
| | IQ calmodulin-binding region domain co | GO:00064 |
| | Conserved hypothetical protein | GO:00723 |
| | Protein of unknown function DUF247, plant family p | |
| [Os] disease resistance TO:0000112 | Similar to Scarecrow-like 9 (Fragment) | GO:00063 |

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|---|---|---|
| | Conserved hypothetical protein | |
| | Kelch related domain containing protein | GO:00349 |
| [Os] pistil anatomy and morphology trait (TO:0000223) \| male sterility (TO:0000437) \| stamen anatomy and morphology trait (TO:0000215) \| flower anatomy and morphology trait (TO:0000499) \| lemma and palea anatomy and morphology trait (TO:0000079) \| lodicule anatomy and morphology trait (TO:0006009) | C2H2 zinc-finger transcription factor, Flc | GO:00082 |
| | Protein of unknown function DUF231 dor | GO:19909 |
| | Hypothetical conserved gene | |
| | Similar to predicted protein | GO:00009 |
| | Conserved hypothetical protein | GO:00069 |
| | NB-ARC domain containing protein | GO:00069 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to Short chain alcohol dehydrogenase-like | |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] cold tolerance (TO:0000303) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| gibberellic acid sensitivity (TO:0000166) \| drought tolerance | Similar to CONSTANS-like protein CO9 (Fragment) | |
| [Os] tiller number (TO:0000346) \| plant height (TO:0000207) \| root development trait (TO:0000656) \| auxin sensitivity (TO:0000163) \| auxin content (TO:0002672) \| abscisic acid sensitivity (TO:0000615); [Os] salt tolerance TO:0006001\| plant height TO:0000207 | Leucine-rich repeat receptor-like kinase, | GO:00064 |
| | Similar to Protein kinase domain containi | GO:00064 |
| | Zm00001e035452 | GO:00002 |
| | Exonuclease domain containing protein | GO:00004 |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| blast disease (TO:0000074) \| bacterial leaf streak disease resistance (TO:0000203) \| seed development trait (TO:0000653) | Similar to Phytosulfokine receptor precur | GO:00064 |
| | Hypothetical conserved gene | GO:00063 |
| | SWIB/MDM2 domain containing protein | |

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|---|---|---|
| | Exostosin-like family protein | GO:00064 |
| | Similar to H0211B05.3 protein | |
| | Hypothetical conserved gene | |
| | Similar to Zinc knuckle family protein, expressed | |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to LRR protein | |
| | Similar to TA1 protein (Fragment) | GO:00063 |
| | Conserved hypothetical protein | |
| | Immunoglobulin-like fold domain containing protei | |
| | Conserved hypothetical protein | |
| [Os] hydrogen peroxide content (TO:0000605) \| blast disease (TO:0000074); [Os] disease resistance TO:0000112 | Exo70 exocyst complex subunit family pr | GO:00068 |
| | SAM (and some other nucleotide) binding | GO:00064 |
| | WD40 repeat-like domain containing pro | GO:00063 |
| | Similar to CAAX prenyl protease 2 | GO:00065 |
| | Similar to DNAJ heat shock N-terminal domain-cont | |
| | Homeodomain-like containing protein | |
| | Peptidoglycan binding-like domain conta | GO:00063 |
| | Similar to H0510A06.12 protein | GO:00066 |
| | Hypothetical conserved gene | GO:19909 |
| | Similar to Ribosomal protein L37 | |
| [Os] pollen free (TO:0000245) \| anther color (TO:0000187) \| mitotic cell cycle trait (TO:0000730) \| anther length (TO:0000531) \| sterility related trait (TO:0000485) \| pollen abortion type (TO:0000218) | Similar to Retinoblastoma-related protei | GO:00000 |
| | Beta-glucosidase, GBA2 type domain con | GO:00059 |
| [Os] fungal disease resistance (TO:0000439) \| bacterial disease resistance (TO:0000315) \| submergence tolerance (TO:0000524) | Protein kinase, catalytic domain domain | GO:00064 |

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|---|---|---|
| | Similar to protein binding protein | |
| | Protein of unknown function DUF6, trans | GO:00550 |
| [Os] salt tolerance (TO:0006001) | Similar to low-level beta-amylase 1 | GO:00001 |
| [Os] salt tolerance (TO:0006001) \| seed development trait (TO:0000653) \| heat tolerance (TO:0000259) \| grain length (TO:0000734) \| drought tolerance (TO:0000276) \| panicle size (TO:0006032) \| inflorescence development trait (TO:0000621) \| seed set percent (TO:0000455) \| awn length (TO:0000072) \| plant height (TO:0000207) \| spikelet number (TO:0000456) \| cytokinin content (TO:0002660) \| grain size (TO:0000397); [Os] male sterility | Receptor-like kinase, Heat toleranc | GO:00015 |
| | X8 domain containing protein | |
| | Similar to H0418A01.11 protein | GO:00098 |
| | Crotonase, core domain containing prote | GO:00065 |
| | Similar to Jasmonate-induced protein | |
| | Serine/threonine protein kinase-related | GO:00064 |
| [Os] gibberellic acid content (TO:0002675) \| blue light sensitivity (TO:0000159) \| leaf sheath length (TO:0002689) | Similar to H0717B12.8 protein | GO:00097 |
| | Protein of unknown function DUF566 fam | GO:00070 |
| [Os] proline content (TO:0006002) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| chlorophyll content (TO:0000495) | tRNA nucleoside methyltransferase, Meth | GO:00080 |
| | Similar to Muscleblind-like protein | GO:00003 |
| | Similar to Chalcone isomerase 3 | GO:00066 |
| | Similar to RING-H2 finger protein RHF1a | GO:00165 |

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|---|---|---|
| [Os] temperature response trait (TO:0000432) \| cold tolerance (TO:0000303) | Basic leucine zipper (bZIP) transcription f | GO:00063 |
| | Transferrin receptor-like, dimerisation domain cont | |
| [Os] root hair length TO:0002665\| root hair density TO:0001051; [Ta] water use efficiency TO:0001017\| drought tolerance TO:0000276 | Similar to 3'(2'),5'-bisphosphate nucleoti | GO:00163 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| [Os] zinc sensitivity (TO:0000351) \| relative shoot dry weight (TO:0000636) \| relative root dry weight (TO:0000644) \| root length (TO:0000227) \| submergence tolerance (TO:0000524) | Similar to NAM / CUC2-like protein | GO:00063 |
| [Os] protein content (TO:0000598) \| seed quality (TO:0000162) | Amino acid transporter, transmembrane | GO:00033 |
| [Os] flowering time (TO:0002616) \| flower development trait (TO:0000622) \| days to heading (TO:0000137) | B3 DNA-binding domain-containing tran | GO:00063 |
| | Protein of unknown function DUF593 family protein | |
| | Similar to predicted protein | GO:00064 |
| | Zm00001e020296 | GO:19909 |
| | Similar to VIP1 protein | |
| | Protein of unknown function DUF125, tra | GO:00068 |
| | Homeodomain-related domain containin | GO:00063 |
| [Os] viral disease resistance (TO:0000148) \| salt tolerance (TO:0006001) \| rice grassy stunt 1 and 2 virus resistance (TO:0000213) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| rice ragged stunt virus resistance (TO:0000386) \| black streak dwarf virus resistance (TO:0000020) \| herbicide sensitivity (TO:0000058) \| jasmonic acid sensitivity (TO:0000172); [Os] protein content TO:0000598\| cold tolerance TO:0000303; [Ta] protein | NAC-domain protein, Drought toleranc | GO:00063 |

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|---|---|---|
| | Similar to Ribosomal protein L11 methylt | GO:00068 |
| | Hypothetical conserved gene | |
| [Os] plant height (TO:0000207) \| brown planthopper resistance (TO:0000424) \| bacterial blight disease resistance (TO:0000175) \| mimic response (TO:0000063) \| tiller number (TO:0000346) \| disease resistance (TO:0000112) \| jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074) \| auxin sensitivity (TO:0000163) \| root development trait (TO:0000656) \| seed number (TO:0000445) \| seed weight (TO:0000181) \| plant growth hormone sensitivity (TO:0000401) \| sheath blight disease resistance (TO:0000255) \| abscisic acid sensitivity (TO:0000615) | Ankyrin-repeat protein, Herbivore-induc | GO:00016 |
| | Similar to Barwin-related endoglucanase | |
| [Os] cold tolerance (TO:0000303) \| bacterial blight disease resistance (TO:0000175) | Similar to SRK5 protein (Fragment) | GO:00064 |
| [Os] male sterility (TO:0000437) \| viral disease resistance (TO:0000148) | Similar to Protein argonaute 18 | GO:00310 |
| | NB-ARC domain containing protein | GO:00069 |
| | WD40 repeat domain containing protein | |
| | Similar to Basic leucine zipper protein (Li | GO:00063 |
| | Similar to C4-dicarboxylate transporter/r | GO:00068 |
| | Similar to GDP-mannose transporter | GO:00069 |

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|---|---|---|
| [Os] abiotic stress trait (TO:0000168) \| sterility related trait (TO:0000485) \| growth and development trait (TO:0000357) | ATP-dependent DNA helicase 2 subunit k | GO:00007 |
| [Os] plant height (TO:0000207) \| gibberellic acid content (TO:0002675) \| flowering time (TO:0002616) \| 1000-seed weight (TO:0000382) \| panicle length (TO:0000040) \| days to heading (TO:0000137) | Similar to BABY BOOM | GO:00063 |
| | Six-bladed beta-propeller, TolB-like domain contai | |
| | Hypothetical conserved gene | GO:00101 |
| | Similar to peroxisomal biogenesis factor | GO:00450 |
| | Similar to predicted protein | GO:00065 |
| | Similar to Gag/env/c-myb protein (Fragm | GO:00063 |
| | Conserved hypothetical protein | |
| | PRP38 family protein | GO:00003 |
| | Zm00001e006068 | GO:00064 |
| | NUC156 family protein | GO:00004 |
| | Hypothetical conserved gene | GO:00094 |
| | Similar to H0409D10.4 protein | GO:00159 |
| | Similar to Histone H2A | GO:00063 |
| [Os] bacterial blight disease resistance (TO:0000175); [Os] disease resistance TO:0000112 | Small RNA methyltransferase, Small RNA | GO:00015 |
| | Similar to HALF-1 | GO:00063 |
| [Os] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| root development trait (TO:0000656) \| flowering time (TO:0002616) \| days to heading (TO:0000137) | Paraneoplastic encephalomyelitis antigen | GO:00104 |
| | Cyclin-like F-box domain containing protein | |

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|---|---|---|
| | BRASSINOSTEROID INSENSITIVE 1-associa | GO:00064 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Similar to ROOT HAIRLESS 1 | GO:00420 |
| [Os] plant height TO:0000207 | Zinc finger, C2H2-type domain containin | GO:00063 |
| [Os] herbicide sensitivity (TO:0000058) \| oxidative stress (TO:0002657) \| light intensity sensitivity (TO:0000460) \| leaf necrosis (TO:0000652) \| carotenoid content (TO:0000496) \| leaf senescence (TO:0000249) \| hydrogen peroxide content (TO:0000605) \| chlorophyll content (TO:0000495) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| bacterial blight disease resistance (TO:0000175) \| leaf color (TO:0000326) \| mimic response (TO:0000063) | Coenzyme F420 hydrogenase/dehydroge | GO:00159 |
| | GNS1/SUR4 membrane protein family pr | GO:00066 |
| | Similar to Membrane protein | GO:00066 |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| [Os] stomatal frequency (TO:0000566) | Transcription factor, Asymmetric division | GO:00063 |
| | Galactose oxidase/kelch, beta-propeller | GO:00068 |
| | Auxin responsive SAUR protein domain c | GO:00097 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Protein of unknown function DUF246, pla | GO:00060 |
| | Similar to Homeobox-leucine zipper prot | GO:00063 |
| | Similar to nucleotide binding protein Zm00001e022411 | |
| | Haem peroxidase, plant/fungal/bacterial | GO:00069 |
| | Coiled-coil protein, Homologous chromo | GO:00071 |

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|---|---|---|
| [Os] seed shape (TO:0000484) \| starch content (TO:0000696) \| endosperm storage protein content (TO:0002653) \| protein content (TO:0000598) | No apical meristem (NAM) protein domai | GO:00063 |
| | Secreted protein with a CLE domain, Mai | GO:0007 |
| | Pectinesterase inhibitor domain containin | GO:0043 |
| | Similar to cDNA, clone: J090072P03, full | GO:00064 |
| | Conserved hypothetical protein | GO:0032 |
| [Os] cold tolerance (TO:0000303) \| panicle length (TO:0000040) \| leaf color (TO:0000326) \| leaf angle (TO:0000206) \| plant height (TO:0000207) \| tiller number (TO:0000346) \| tillering ability (TO:0000329) \| nitrogen sensitivity (TO:0000011) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| jasmonic acid sensitivity (TO:0000172); [Os] nitrogen | Similar to PCF1 | GO:00063 |
| | Similar to Glucose inhibited division prot | GO:00020 |
| | ChaC-like protein family protein | GO:00067 |
| [Os] plant height (TO:0000207) \| stem strength (TO:0000051) \| leaf thickness (TO:0000258); [Os] grain shape TO:0002730\| grain size TO:0000397 | OVATE domain-containing protein, Nega | GO:00458 |
| | C2 calcium-dependent membrane targeti | GO:00069 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| [Os] drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| relative water content (TO:0000136) | Homeodomain-leucine zipper (HD-ZIP) transcription | |
| | Similar to Aminoacyl-tRNA synthetase | GO:00063 |
| | Zm00001e015144 | GO:00064 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| brown planthopper resistance (TO:0000424) | Similar to DNA binding protein | GO:00063 |
| | Armadillo-like helical domain containing | GO:00165 |
| | Protein of unknown function DUF1230 family protei | |
| | Zm00001e033374 | GO:0061 |
| | Homeodomain-related domain containing protein | |

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|---|---|---|
| [Os] jasmonic acid content (TO:0002668) \| hydrogen peroxide content (TO:0000605) \| brown planthopper resistance (TO:0000424) \| stem borer resistance (TO:0000454) | Tetratricopeptide-like helical domain con | GO:00066 |
| | Protein of unknown function DUF821, CAP10-like fa | |
| [Os] plant growth hormone sensitivity (TO:0000401) \| blast disease (TO:0000074) | ATPase, AAA-type, core domain containing protein | |
| | Harpin-induced 1 domain containing pro | GO:00092 |
| | WD40 repeat-like domain containing pro | GO:00000 |
| | Similar to MYB transcription factor R2R3 | GO:00063 |
| | Similar to DNA binding protein | GO:00063 |
| | Zm00001e033989 | GO:00090 |
| [Os] lodging incidence (TO:0000068) \| lateral root length (TO:0001012) \| leaf curling (TO:0002681) \| leaf development trait (TO:0000655) | Zinc finger homeodomain (ZF-HD) class | GO:00063 |
| | Cyclin-like F-box domain containing protein | |
| | Putative cyclin-F2-1 | GO:00000 |
| | Similar to Phosphatidic acid phosphatase | GO:00066 |
| | Conserved hypothetical protein | GO:00431 |
| | Similar to Signal recognition particle 68 k | GO:00066 |
| | Conserved hypothetical protein | |
| | Similar to Serine/threonine protein kinas | GO:00064 |
| | Similar to prohibitin2 | GO:00070 |
| [Os] starch grain synthesis (TO:0002658); [Os] seed size TO:0000391 | Similar to Phosphorylase (Fragment) | GO:00059 |
| | Similar to Digalactosyldiacylglycerol synt | GO:00193 |
| | Conserved hypothetical protein | |
| | Similar to Chitinase precursor (EC 3.2.1.1 | GO:00059 |
| | Similar to Pre-mRNA-splicing factor ISY1 | GO:00003 |

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|---|---|---|
| | Conserved hypothetical protein | GO:00097 |
| | Zm00001e008169 | GO:00193 |
| | Transferase family protein | |
| [Os] cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | L-ascorbate oxidase, Cold, salt, drought stress resp | |
| | Similar to H0322F07.6 protein | GO:00717 |
| | Similar to Fip1 motif family protein, expr | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Similar to Beta-keto acyl reductase (Fragment) | |
| | Leucine-rich repeat, N-terminal domain containing | |
| | Pentatricopeptide repeat domain containing protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| [Os] floral organ development trait (TO:0006022) \| sterile lemma length (TO:0000240); [Os] lateral root number TO:0001013\| crown rootless TO:0000230\| root number TO:0000084 | Similar to LOB domain protein 17 | GO:00097 |
| [Os] temperature response trait (TO:0000432) \| osmotic response sensitivity (TO:0000095) \| abscisic acid sensitivity (TO:0000615) \| dull endosperm (TO:0000105) \| salt sensitivity (TO:0000429) \| amylose content (TO:0000196) | Similar to Nuclear cap binding protein su | GO:00003 |
| | Initiation factor 3 family protein | GO:00064 |
| | Similar to RNA Binding Protein 45 | GO:00510 |
| | Homolog of Rad52 (Radiation sensitive 5 | GO:00007 |
| | Myb transcription factor domain containi | GO:00101 |

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|---|---|---|
| | Octicosapeptide/Phox/Bem1p domain containing p | |
| | Transmembrane protein 97, predicted domain cont | |
| | Region of unknown function XH domain | GO:00310 |
| | Optic atrophy 3-like domain containing | GO:00192 |
| | Triose phosphate isomerase (EC 5.3.1.1), | GO:00060 |
| | Exo70 exocyst complex subunit family p | GO:00068 |
| [Os] grain shattering (TO:0000473);<br>[Os] seed shattering TO:0000930\| grain weight TO:0000919\| grain shattering TO:0000473\| plant height TO:0000207\| panicle length TO:0000040 | Similar to cDNA clone:J023121E19, full i | GO:00063 |
| | Similar to Glutathione-S-transferase 19E | GO:00067 |
| | GOLD domain containing protein | GO:00070 |
| | Protein of unknown function DUF1218 family protei | |
| [Os] heat tolerance (TO:0000259) \| humidity related trait (TO:0000441) \| male sterility (TO:0000437) | Similar to Cycloartenol synthase (EC 5.4. | GO:00161 |
| | Similar to DM280 protein | |
| | ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/ | GO:00300 |
| | Conserved hypothetical protein | GO:00071 |
| | Similar to T15D22.3 | |
| | Similar to transcription factor GT-3b | GO:00063 |

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|---|---|---|
| [Os] jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| blast disease (TO:0000074) | | |
| | Probable protein phosphatase 2C 56 | GO:00064 |
| | Similar to OSIGBa0126B18.8 protein | |
| | Protein of unknown function DUF247, plant domain | |
| | Similar to UDP-glucose:sterol glucosyltra | GO:00059 |
| | Hypothetical conserved gene | GO:00068 |
| | Hypothetical conserved gene | GO:00072 |
| | Conserved hypothetical protein | GO:00454 |
| | YT521-B-like protein family protein | GO:00611 |
| [Os] cytokinin sensitivity (TO:0000167) \| phyllotaxy (TO:0006014) | Plant-specific protein containing a glutan | GO:00458 |
| [Os] male sterility (TO:0000437) \| pollen fertility (TO:0000421) | | |
| [Os] flowering time (TO:0002616) \| days to heading (TO:0000137); [Os] leaf width TO:0000370 | | |
| | Thioredoxin fold domain containing prot | GO:00064 |
| | Conserved hypothetical protein | |
| | Hypothetical protein | |
| | Peptidase aspartic, catalytic domain cont | GO:00065 |

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|---|---|---|
| [Os] female sterility (TO:0000358) \| pollen abortion type (TO:0000218) \| spikelet fertility (TO:0000180) \| floral organ development trait (TO:0006022) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| panicle length (TO:0000040) \| panicle color (TO:0000201) \| stamen number (TO:0000225) \| pollen fertility (TO:0000421) \| stamen length (TO:0002609) \| seed set percent (TO:0000455) \| embryo development trait (TO:0000620) \| cytokinin content (TO:0002660) | Twin arginine translocation signal, Tat domain conta | |
| | Methyl-CpG DNA binding domain containing protei | |
| [Os] blast disease (TO:0000074) \| drought tolerance (TO:0000276) \| sterility related trait (TO:0000485) \| salt tolerance (TO:0006001); [Os] grain weight TO:0000919\| grain size TO:0000397 | DEAD-like helicase, N-terminal domain c | GO:00062 |
| | Similar to RNA-binding protein RZ-1 | GO:00094 |
| [Os] male sterility (TO:0000437); [Os] male sterility TO:0000437 | Pectate lyase-like protein, Pollen develop | GO:00454 |
| | Conserved hypothetical protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | AT hook, DNA-binding, conserved site domain cont | |
| | Protein of unknown function DUF962 far | GO:00465 |
| [Os] auxin content (TO:0002672) \| black streak dwarf virus resistance (TO:0000020) \| silicon sensitivity (TO:0000031) \| root number (TO:0000084) \| adventitious root number (TO:0001006) \| root fresh weight (TO:0000578) \| abscisic acid sensitivity (TO:0000615) \| heat tolerance (TO:0000259) \| drought tolerance (TO:0000276); [Os] auxin content TO:0002672\| seed size TO:0000391\| root to shoot ratio TO:0000278\| ethylene sensitivity | Flavin monooxygenase-like enzyme , Au | GO:00098 |

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|---|---|---|
| [Os] jasmonic acid content (TO:0002668) \| salt tolerance (TO:0006001) \| panicle blast disease resistance (TO:0000477) \| bacterial blight disease resistance (TO:0000175) \| jasmonic acid sensitivity (TO:0000172) \| drought tolerance (TO:0000276) \| submergence sensitivity (TO:0000286) \| hydrogen peroxide content (TO:0000605); [Os] seed | Germin-like protein, Fungal blast and bacterial bligh | |
| | Proteinase inhibitor, propeptide domain | GO:00065 |
| | Protein kinase, core domain containing p | GO:00007 |
| | Zm00001e020152 | GO:00063 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to predicted protein | GO:00097 |
| | Similar to Typical P-type R2R3 Myb prote | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| [Os] relative yield (TO:0000153) \| oxidative stress (TO:0002657) \| abiotic stress trait (TO:0000168) \| proline content (TO:0006002) \| sugar content (TO:0000333) \| abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| relative water content (TO:0000136) \| drought tolerance (TO:0000276) \| nitrogen sensitivity (TO:0000011) \| grain yield | bZIP transcription factor, Regulation of A | GO:00063 |
| | Similar to DNA-binding protein | |
| [Os] panicle length (TO:0000040) \| growth and development trait (TO:0000357) \| enzyme activity (TO:0000599) | GA 20-oxidase4, GA metabolis | GO:00094 |
| | tRNA/rRNA methyltransferase, SpoU dom | GO:00001 |
| | Conserved hypothetical protein | GO:00071 |
| | Peptidase C12, ubiquitin carboxyl-terminal hydrolas | |
| | Dynamin family protein | GO:00002 |
| | Protein of unknown function DUF632 do | GO:00712 |
| | Conserved hypothetical protein | |
| [Os] blast disease (TO:0000074) \| abscisic acid sensitivity (TO:0000615) \| oxidative stress (TO:0002657) | Similar to Isoflavone reductase homolog IRL (EC 1.3. | |

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|---|---|---|
| | Zinc finger, Dof-type family protein | GO:00063 |
| | Armadillo-type fold domain containing p | GO:00062 |
| | Similar to predicted protein | |
| | Similar to 50S ribosomal protein L7/L12 | GO:00064 |
| | Zinc finger, C2H2 domain containing pro | GO:00063 |
| | Similar to VHS2 protein (Fragment) | GO:00068 |
| [Os] iron sensitivity (TO:0000224) | | |
| | Hypothetical conserved gene | |
| | Similar to LIMONENE cyclase like protein | GO:00064 |
| [Os] male sterility (TO:0000437) | MADS box transcription factor, Pollen ma | GO:00063 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Similar to 3-glucanase | GO:00059 |
| [Os] cold tolerance (TO:0000303) \| light intensity sensitivity (TO:0000460) \| leaf color (TO:0000326) \| chlorophyll-a content (TO:0000293) \| drought tolerance (TO:0000276) | Similar to Nucleic acid-binding protein p | GO:19012 |
| | HAD-superfamily hydrolase, subfamily IA, variant 3 | |
| | Calponin-like actin-binding domain containing prot | |
| | Zm00001e000040 | |
| | CMP/dCMP deaminase, zinc-binding dom | GO:00021 |
| | RabGAP/TBC domain containing protein | GO:00068 |
| | Similar to high mobility group family | |
| | Similar to F-box domain containing protein | |

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|---|---|---|
| | Ribosomal protein L36 family protein | GO:00064 |
| | Similar to alpha-galactosidase Zm00001e001562 | GO:00059 |
| | Similar to Pectin methylesterase isoform | GO:00425 |
| [Os] flower development trait (TO:0000622) | Similar to Isoform 2 of MADS-box transc | GO:00063 |
| | Similar to Protein kinase APK1B, chloropl | GO:00064 |
| | Cyclin-like F-box domain containing protein | |
| [Os] drought tolerance TO:0000276 | AT-hook motif and PPC domain containing protein, | |
| [Os] leaf length (TO:0000135) \| secondary branch number (TO:0000557) \| primary branch number (TO:0000547) \| leaf sheath length (TO:0002689) \| tiller number (TO:0000346) \| grain size (TO:0000397) \| ethylene sensitivity (TO:0000173) \| auxin sensitivity (TO:0000163) \| abscisic acid sensitivity (TO:0000615) \| jasmonic acid sensitivity (TO:0000172) \| gibberellic acid sensitivity (TO:0000166) \| brassinosteroid sensitivity (TO:0002677) \| inflorescence development trait (TO:0000621) \| grain number (TO:0002759) \| cytokinin sensitivity (TO:0000167) \| panicle length (TO:0000040) \| grain weight (TO:0000590) \| plant height | Protein of unknown function DUF250 dor | GO:00068 |
| [Os] grain length TO:0002760\| grain length TO:0000734\| starch content TO:0000696\| plant height TO:0000207 | Similar to 2-oxo acid dehydrogenase, lip | GO:00063 |
| | Similar to Syntaxin-71 | GO:00068 |
| | Conserved hypothetical protein | GO:00458 |

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|---|---|---|
| | Zinc finger, PHD-type domain containing protein | |
| | Protein of unknown function DUF296 domain contai | |
| [Os] lateral root number (TO:0001013) \| leaf width (TO:0000370) \| gibberellic acid sensitivity (TO:0000166) \| plant height (TO:0000207) \| leaf shape (TO:0000492) \| grain width (TO:0000402) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| tiller number (TO:0000346) \| spikelet anatomy and morphology trait (TO:0000657) \| root development trait (TO:0000656) \| gibberellic acid content (TO:0002675); | WUS-type homenodomain protein, Leaf d | GO:00063 |
| | Similar to DNA binding | GO:00007 |
| | Armadillo-type fold domain containing p | GO:00726 |
| | Mitogen activated protein kinase kinase k | GO:00001 |
| | Similar to serine esterase family protein | GO:00442 |
| | Similar to cDNA clone:J013003E06, full i | GO:00165 |
| | Similar to Dimethyladenosine transferase | GO:00063 |
| | Zm00001e036104 | GO:00063 |
| | Similar to Nucleolar autoantigen-like pro | GO:00004 |
| | Ovarian tumour, otubain domain containi | GO:00165 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Similar to BEL1-type homeodomain prote | GO:00063 |
| | Myb-like DNA-binding domain, SHAQKY | GO:00063 |
| | RH27 helicase (Fragment) | GO:00004 |
| | Zm00001e025158 | GO:00097 |

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|---|---|---|
| [Os] seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| flower anatomy and morphology trait (TO:0000499) \| stamen number (TO:0000225) \| tiller number (TO:0000346) \| internode length (TO:0000145) \| lemma and palea anatomy and morphology trait (TO:0000079) \| seed anatomy and morphology trait (TO:0000184) \| leaf senescence (TO:0000249) \| pistil anatomy and morphology trait (TO:0000223) \| primary branching of inflorescence (TO:0000052); [Os] floral organ number TO:0006038\| tiller | Serine/threonine protein kinase domain c | GO:00064 |
| [Os] flowering time (TO:0002616); [Os] grain number TO:0002759\| plant height TO:0000207\| days to heading TO:0000137 | CONSTANS-like transcriptional activator, Negative r | |
| [Os] salt tolerance (TO:0006001) \| plant height (TO:0000207) \| gibberellic acid sensitivity (TO:0000166) \| plant growth hormone sensitivity (TO:0000401) \| cold tolerance (TO:0000303) | Similar to OsGA2ox1 | GO:00096 |
| [Os] anther length (TO:0000531) \| blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) \| abscisic acid sensitivity (TO:0000615) \| gibberellic acid sensitivity (TO:0000166) \| internode length (TO:0000145) \| male sterility (TO:0000437) \| pollen fertility (TO:0000421) \| germination rate (TO:0000430) \| anther color (TO:0000187) \| leaf shape (TO:0000492) \| drought tolerance (TO:0000276) \| plant growth hormone sensitivity (TO:0000401); [Os] embryoless TO:0000189; [Ta] drought | Transcriptional activator of gibberellin-d | GO:00063 |
| | Cyclin-like F-box domain containing protein | |
| | Similar to Subtilisin-like protease (Fragm | GO:00065 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Similar to HAHB-7 (Fragment) | GO:00063 |
| | Protein phosphatase 2C | GO:00064 |
| | Zm00001e001658 | GO:00064 |

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|---|---|---|
| | ENTH/VHS domain containing protein | GO:00063 |
| [Os] grain shape TO:0002730\| yield trait TO:0000371 | | |
| | Similar to ER33 protein (Fragment) | GO:00063 |
| | Similar to Monosaccharide transporter 3 | GO:00086 |
| | Hypothetical conserved gene | GO:00062 |
| | Similar to Monosaccharide transporter 1 | GO:00086 |
| | Similar to protein kinase | GO:00022 |
| [Os] tiller angle TO:0000567\| plant height TO:0000207 | bZIP transcription factor, Regulation of e | GO:00063 |
| | Zm00001e041815 | GO:00063 |
| | Similar to CONSTANS-like protein CO9 (F | GO:00099 |
| | Similar to BAG domain containing protein | GO:00064 |
| | Galactosyl transferase family protein | GO:00099 |
| | Kelch-type beta propeller domain contai | GO:00063 |
| | Similar to 30S ribosomal protein S31, chl | GO:00325 |
| | Harpin-induced 1 domain containing protein | |
| [Os] grain length (TO:0000734) \| grain weight (TO:0000590) \| grain size (TO:0000397) \| ethylene sensitivity (TO:0000173) \| inflorescence development trait (TO:0000621) \| seed maturation (TO:0002661) \| grain thickness (TO:0000399) | Similar to Dehydration responsive eleme | GO:00063 |
| | Peptidase S8, subtilisin-related domain c | GO:00065 |
| | Similar to Frsb-prov protein | GO:00064 |
| | Similar to Maltose excess protein 1, chlo | GO:00000 |
| | Conserved hypothetical protein | |
| | Similar to Dehydrogenase/reductase SDR | GO:00487 |
| | Exostosin-like family protein | GO:00064 |
| | Similar to GPI-anchored protein | |

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|---|---|---|
| | Similar to Actin-depolymerizing factor (A | GO:00070 |
| | Zm00001e028157 | GO:00065 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] viral disease resistance (TO:0000148) \| jasmonic acid sensitivity (TO:0000172) | Similar to nuclear transcription factor Y s | GO:00063 |
| | Zinc finger, RanBP2-type domain contain | GO:00097 |
| [Os] mimic response (TO:0000063) \| leaf development trait (TO:0000655) \| chlorophyll content (TO:0000495) \| chlorophyll ratio (TO:0000298) \| light sensitivity (TO:0000075) \| leaf color (TO:0000326) \| carotenoid content (TO:0000496) \| leaf lamina color (TO:0000299) \| chloroplast development trait (TO:0002715) | Similar to Protochlorophyllide reductase | GO:00159 |
| | Conserved hypothetical protein | |
| [Os] drought tolerance TO:0000276 | Similar to Cationic amino acid transporte | GO:00033 |
| | Similar to CDPK-related protein kinase | GO:00064 |
| | Similar to early nodulin 20 | GO:00229 |
| | Plant lipid transfer protein/seed storage/trypsin-al | |
| [Os] grain length (TO:0000734) \| shoot habit (TO:0002756) \| light sensitivity (TO:0000075); [Os] drought tolerance TO:0000276\| plant height TO:0000207 | Helix-loop-helix DNA-binding domain c | GO:00063 |
| [Os] panicle length (TO:0000040) \| filled grain number (TO:0000447) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| photosynthetic ability (TO:0000316) \| stomatal conductance (TO:0000522) \| seed fertility (TO:0000639) \| inflorescence development trait (TO:0000621) \| hydrogen peroxide content (TO:0000605) \| seed set percent (TO:0000455) \| panicle size (TO:0006032) \| chloroplast development trait (TO:0002715) \| carotenoid content (TO:0000496) \| chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| photosynthetic rate (TO:0001015) \| grain yield (TO:0000396) \| leaf | Succinate dehydrogenase iron-protein su | GO:00060 |

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|---|---|---|
| [Os] plant height (TO:0000207) \| growth and development trait (TO:0000357) \| proline content (TO:0006002) \| plant fresh weight (TO:0000442) \| shoot fresh weight (TO:0000571) \| amino acid content (TO:0002673) \| total biomass yield (TO:0000457) \| tillering ability (TO:0000329) \| grain yield | Similar to Amino acid carrier (Fragment) | GO:00033 |
| [Os] cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) | Serine/threonine protein kinase-related | GO:00064 |
| | Similar to PTAC16 (PLASTID TRANSCRIPTI | GO:00076 |
| | VHS domain containing protein | GO:00068 |
| | MADS box transcription factor, Regulatio | GO:00063 |
| | HMG-I and HMG-Y, DNA-binding domain containin | |
| | Similar to Pectinesterase | GO:00425 |
| | Similar to FK506-binding protein 39 kDa | |
| | Pathogenesis-related transcriptional fact | GO:00063 |
| [Os] disease resistance TO:0000112 | Zinc finger, LSD1-type domain containing protein | |
| | Yos1-like domain containing protein | GO:00068 |
| | Conserved hypothetical protein | |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to OSIGBa0152K17.7 protein | |
| | Similar to predicted protein | GO:00101 |
| | Double-stranded RNA-binding-like dom | GO:00063 |
| [Os] heat tolerance (TO:0000259) | Homolog of the Arabidopsis TAPETUM D | GO:00017 |
| | EF-HAND 1 domain containing protein | GO:00063 |
| | Hypothetical gene | GO:00065 |

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|---|---|---|
| [Os] seed quality (TO:0000162) \| spikelet sterility (TO:0000436) \| 1000-dehulled grain weight (TO:0000592) \| seed size (TO:0000391) \| seed development trait (TO:0000653) \| protein content (TO:0000598) \| glucose content (TO:0000300) \| fructose content (TO:0006005) \| endosperm storage protein content (TO:0002653) \| starch grain synthesis (TO:0002658) \| seed shape (TO:0000484) | | |
| [Os] nitrogen content TO:0020093\| salt tolerance TO:0006001\| beta-carotene content TO:0002695\| oxidative stress TO:0002657\| photosynthetic rate TO:0001015\| protein content TO:0000598\| root fresh weight TO:0000578\| carotenoid content TO:0000496\| chlorophyll content TO:0000495\| leaf color TO:0000326\| soluble protein content TO:0000325\| cold tolerance TO:0000303\| carbohydrate content TO:0000291\| carotene content TO:0000289\| drought tolerance TO:0000276\| amylose content TO:0000196\| brown rice protein TO:0000138\| disease resistance TO:0000112\| pollen sterility TO:0000053; [Ta] potassium concentration TO:0000513\| lutein content TO:0002701\| protein content TO:0000598\| nitrogen content TO:0020093\| proline content TO:0006002\| amino acid content TO:0002673\| carbon content TO:0000466\| chlorophyll content TO:0000495\| sugar content TO:0000333\| salt tolerance TO:0006001\| oxidative stress TO:0002657\| leaf water potential | Zinc finger, RING/FYVE/PHD-type domain | GO:00165 |
| | Similar to Transcription factor RF2a | GO:00063 |
| | Similar to Fibrillarin-2 | GO:00049 |
| | Conserved hypothetical protein | |
| | Similar to Growth-regulating factor 2 | GO:00063 |

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|---|---|---|
| | Similar to Plastid uroporphyrinogen deca | GO:0006 |
| | Prenylated rab acceptor PRA1 family prot | GO:0016 |
| | Similar to Zn-finger, RanBP-type, containing protein | |
| [Os] salt tolerance (TO:0006001) | Pyridoxal phosphate-dependent deamina | GO:0009 |
| | Cupredoxin domain containing protein | |
| | Similar to kelch repeat-containing protei | GO:0034 |
| [Os] temperature response trait (TO:0000432) \| male sterility (TO:0000437) \| pollen free (TO:0000245) \| inflorescence anatomy and morphology trait (TO:0000373) \| lemma and palea anatomy and morphology trait (TO:0000079) \| lodicule anatomy and morphology trait (TO:0006009) \| flowering time (TO:0002616) \| inflorescence development trait (TO:0000621) \| stamen anatomy and morphology trait (TO:0000215) \| lodicule development trait (TO:0006023) \| carpel anatomy and morphology trait (TO:0006012); [Os] floral organ identity TO:0006019\| organ identity TO:0006018\| amylose content TO:0000196\| spikelet fertility | Similar to MADS-box transcription factor | GO:0006 |
| [Os] abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| oxidative stress (TO:0002657) \| chlorophyll content (TO:0000495) \| germination rate (TO:0000430) \| abscisic acid content (TO:0002667) \| cell growth and development trait (TO:0002686) \| salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| root length (TO:0000227) \| root development trait (TO:0000656) \| cold tolerance (TO:0000303); [Os] salt tolerance TO:0006001\| germination rate | | |
| | IQ motif, EF-hand binding site domain cc | GO:0000 |
| | ABC transporter, White-brown complex homolog pr | |
| | Zm00001e026794 | |
| | Zm00001e006914 | GO:0006 |

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|---|---|---|
| | Similar to DRP3A (DYNAMIN-RELATED PR | GO:00002 |
| | Zm00001e039377 | GO:20006 |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| leaf development trait (TO:0000655) | Membrane-bound NAC-like transcription | GO:00063 |
| [Os] plant height (TO:0000207) | Xylan acetyltransferase, Resistance to ba | GO:00069 |
| | Similar to Resistance gene analog PIC25 ( | GO:00069 |
| [Os] protein content (TO:0000598) \| amino acid content (TO:0002673) | | |
| | Transcriptional factor, SBP (SQUAMOSA promoter Bi | |
| | Amino acid transporter, transmembrane | GO:0003 |
| | Protein of unknown function DUF593 family protein | |
| | Similar to 60S ribosomal protein L18A | |
| | Poly(ADP-ribose) polymerase, regulatory | GO:00063 |

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|---|---|---|
| | SH2 motif domain containing protein | GO:00063 |
| | Similar to Integral membrane protein DU | GO:00550 |
| | Similar to Nectarin 5 (Fragment) | |
| | Thaumatin, pathogenesis-related family | GO:00069 |
| [Os] brassinosteroid content (TO:0002676) \| gibberellic acid content (TO:0002675) | RNA-dependent RNA polymerase, eukary | GO:00011 |
| | Zm00001e034091 | GO:00064 |
| [Os] flowering time (TO:0002616) | | |
| | Membrane bound O-acyl transferase, MB | GO:00066 |
| [Os] drought tolerance TO:0000276;<br>[Ta] root hair length TO:0002665 | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Similar to 1-acyl-sn-glycerol-3-phospha | GO:00066 |
| | Conserved hypothetical protein | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Zm00001e020109 | GO:00064 |
| [Os] bacterial blight disease resistance (TO:0000175) \| cold tolerance (TO:0000303) \| leaf senescence (TO:0000249) \| drought tolerance (TO:0000276) \| heat tolerance (TO:0000259); [Os] disease resistance TO:0000112 | WRKY transcription factor, Drought toler | GO:00063 |
| [Os] tiller number TO:0000346\| plant height TO:0000207 | | |
| | Similar to zinc finger (C3HC4-type RING finger) fam | |
| [Os] oxidative stress TO:0002657 | Similar to CONSTANS-like protein CO6 | GO:00099 |
| | Similar to calcium dependent protein kin | GO:00064 |
| | Major intrinsic protein family protein | GO:00068 |

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|---|---|---|
| [Os] growth and development trait (TO:0000357); [Ta] male sterility TO:0000437 | DNA methyltransferase, Maintenance of r | GO:00063 |
| | Similar to NAD-dependent isocitrate deh | GO:00060 |
| [Os] tillering ability (TO:0000329) \| tiller number (TO:0000346); [Os] tiller number TO:0000346 | TCP family transcription factor, Regulatio | GO:00063 |
| [Os] pollen free (TO:0000245) \| stamen anatomy and morphology trait (TO:0000215); [Os] male sterility TO:0000437 | Similar to Undeveloped tapetum 1 | |
| | Similar to Protein SOF1 | GO:00004 |
| | Dynein light chain, type 1 family protein | GO:00070 |
| | Zm00001e040937 | GO:00063 |
| | Conserved hypothetical protein | |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Similar to Dihydrolipoamide acetyltransfe | GO:00060 |
| | Conserved hypothetical protein | |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Pentatricopeptide repeat domain containing protein | |
| | Phosphatidylinositol 3-/4-kinase, catalyt | GO:00468 |

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|---|---|---|
| | Serine/threonine protein kinase domain c | GO:00004 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| | Similar to MYB transcription factor MYB71 | GO:00301 |
| | Similar to H0305E08.4 protein | GO:00517 |
| | Pleckstrin homology-type domain containing protei | |
| | Putative homeobox-leucine zipper protei | GO:00063 |
| [Os] submergence tolerance (TO:0000524) | Protein kinase, core domain containing p | GO:00064 |
| | Similar to glucan endo-1,3-beta-glucosi | GO:00059 |
| | Protein of unknown function DUF803 fam | GO:00068 |
| | Similar to DNA binding protein | |
| | Targeting for Xklp2 family protein | GO:00002 |
| | Similar to Cationic peroxidase isozyme 4 | GO:00069 |
| | Hypothetical conserved gene | |
| | Bifunctional inhibitor/plant lipid transfer protein/se | |
| | HECT domain containing protein | GO:00002 |
| | Toll-Interleukin receptor domain containi | GO:00071 |
| | Hypothetical conserved gene | |
| [Os] cold tolerance (TO:0000303) \| white-backed planthopper resistance (TO:0000205) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| bacterial blight disease resistance (TO:0000175); [Os] grain size TO:0000397\| seed length TO:0000395\| leaf angle TO:0000206\| seed length TO:0000146\| disease resistance TO:0000112 | Similar to WRKY1 (WRKY transcription fac | GO:00063 |
| [Os] internode length (TO:0000145) \| abscisic acid sensitivity (TO:0000615) \| hydrogen peroxide content (TO:0000605) \| bacterial blight disease resistance (TO:0000175) \| plant height (TO:0000207) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074); [Os] plant height TO:0000207 | Similar to WRKY transcription factor 55 | GO:00063 |

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|---|---|---|
| [Os] panicle type (TO:0000089) \| lemma shape (TO:0000614) \| male sterility (TO:0000437) \| spikelet anatomy and morphology trait (TO:0000657) \| seed set percent (TO:0000455) \| spikelet sterility (TO:0000436) \| flower anatomy and morphology trait (TO:0000499) \| floret anatomy and morphology trait (TO:0000274) \| carpel anatomy and morphology trait (TO:0006012) \| days to flower (TO:0000344) \| glume cover (TO:0001000) \| embryosac abortion (TO:0000416) \| grain thickness (TO:0000399) \| seed length (TO:0000146) \| seed width (TO:0000149) \| seed thickness (TO:0000304) \| 1000-dehulled grain weight (TO:0000592) \| floral organ number (TO:0006038) \| glume number (TO:0006029) \| lemma number (TO:0000208) \| palea number (TO:0000209) \| lodicule number (TO:0006010) \| pistil number (TO:0002659) \| lodicule anatomy and morphology trait (TO:0006009) \| carpel shape (TO:0006037) \| stamen number (TO:0000225) \| lemma and palea anatomy and morphology trait (TO:0000079) \| inflorescence anatomy | | |
| [Os] grain length TO:0002760\| grain length TO:0000734\| grain size TO:0000397\| plant height TO:0000207 | | |
| | Ubiquitin fusion degradation protein UFD | GO:00065 |
| [Os] blast disease (TO:0000074) | Component of Exo70 exocyst comple | GO:0006 |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | Similar to H0101F08.8 protein | GO:00097 |
| | Similar to transducin family protein / WD | GO:00062 |
| | Conserved hypothetical protein | GO:00064 |
| | Cytochrome P450 family protein | |
| | Hypothetical conserved gene | GO:00300 |
| | 2OG-Fe(II) oxygenase domain containing protein | |
| | Heat shock protein DnaJ, N-terminal dom | GO:00068 |
| | Myosin tail 2 domain containing protein | |
| | Protein of unknown function DUF3133 dc | GO:19001 |

<table>
<tr><td></td><td>Zm00001e012352</td><td>GO:00063</td></tr>
<tr><td></td><td>Barwin-related endoglucanase domain c</td><td>GO:00488</td></tr>
<tr><td></td><td>Cyclin-like F-box domain containing protein</td><td></td></tr>
<tr><td></td><td>UDP-glucuronosyl/UDP-glucosyltransferase family p</td><td></td></tr>
<tr><td></td><td>Conserved hypothetical protein</td><td>GO:00097</td></tr>
<tr><td></td><td>Zm00001e023018</td><td></td></tr>
<tr><td>[Os] ethylene sensitivity (TO:0000173) | abscisic acid sensitivity (TO:0000615) | heat tolerance (TO:0000259) | salt tolerance (TO:0006001) | drought tolerance (TO:0000276) | biotic stress trait (TO:0000179) | cold tolerance (TO:0000303) | cytokinin sensitivity (TO:0000167) | jasmonic acid sensitivity (TO:0000172) | auxin sensitivity (TO:0000163) | gibberellic acid sensitivity (TO:0000166)</td><td></td><td></td></tr>
<tr><td>[Os] root development trait (TO:0000656) | leaf rolling (TO:0000085) | photosynthetic ability (TO:0000316) | chlorophyll content (TO:0000495) | leaf development trait (TO:0000655) | root length (TO:0000227) | adventitious root number (TO:0001006) | lateral root length (TO:0001012) | lemma and palea anatomy and morphology trait (TO:0000079) | pollen sterility (TO:0000053) | glume opening (TO:0000474) | seed size (TO:0000391) | seed development trait (TO:0000653) | plant height (TO:0000207); [Os] rolled</td><td>GARP DNA-binding protien, Leaf polarity</td><td>GO:00063</td></tr>
<tr><td></td><td>Forkhead-associated domain containing protein</td><td></td></tr>
<tr><td>[Os] temperature response trait (TO:0000432); [Os] salt tolerance TO:0006001; [Ta] stomatal resistance TO:0000522| stomatal resistance TO:0000523</td><td>Similar to H0425E08.14 protein</td><td>GO:00063</td></tr>
<tr><td></td><td>Glycosyltransferase AER61, uncharacterized domain</td><td></td></tr>
<tr><td></td><td>Similar to AAP7</td><td>GO:00033</td></tr>
<tr><td></td><td>Pleckstrin homology-type domain contai</td><td>GO:00435</td></tr>
<tr><td></td><td>Protein of unknown function DUF247, plant family p</td><td></td></tr>
</table>

| | | |
|---|---|---|
| | Similar to Transcription factor ICE1 (Indu | GO:00063 |
| | TRAM, LAG1 and CLN8 homology domain containin | |
| | Similar to Protein synthesis inhibitor II (E | GO:00069 |
| | Zm00001e008090 | |
| | Hypothetical conserved gene | |
| | Serine/threonine protein kinase, Never-ir | GO:00064 |
| | Similar to RAFTIN1a protein (RAFTIN1a ar | GO:00095 |
| [Os] brown planthopper resistance (TO:0000424) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) | Protein phosphatase 2C family protein | GO:00359 |
| | Similar to Histone H2A | GO:00063 |
| | Conserved hypothetical protein | GO:00063 |
| [Os] submergence tolerance (TO:0000524) \| viral disease resistance (TO:0000148) \| drought tolerance (TO:0000276) \| sheath blight disease resistance (TO:0000255) | | |
| | Protein of unknown function DUF702 fam | GO:00063 |
| | Basic-leucine zipper (bZIP) transcription | GO:00063 |
| | Similar to Thioredoxin-like 1 | GO:00454 |
| | Glycoside hydrolase, family 17 protein | GO:00059 |
| [Os] disease resistance TO:0000112\| blast disease resistance TO:0000074 | Similar to P90 ribosomal S6 kinase | GO:00064 |
| [Os] viral disease resistance (TO:0000148) | Similar to Ubiquitin-like protein 5 (Fragm | GO:00003 |
| | Similar to ubiquitin-like protein | |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) \| embryo related trait (TO:0000064) \| drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) \| leaf shape (TO:0000492) | Similar to OCL1 homeobox protein | GO:00063 |
| [Os] phosphorus sensitivity (TO:0000102) \| root hair length (TO:0002665) \| bacterial blight disease resistance (TO:0000175) \| abiotic stress trait (TO:0000168) | MYB-CC family protein, Pi-starvation sig | GO:00063 |
| | Hypothetical conserved gene | GO:00096 |
| | Similar to HDA1 | GO:00001 |
| [Os] carbon content (TO:0000466) \| chlorophyll content (TO:0000495) \| leaf senescence (TO:0000249) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| grain weight (TO:0000590) \| leaf color (TO:0000326) | | |
| [Os] salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| cold tolerance (TO:0000303) \| drought tolerance (TO:0000276); [Os] grain weight TO:0000919\| protein content TO:0000598\| grain size TO:0000397\| seed dormancy TO:0000253 | Similar to H0124B04.8 protein | |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | SET domain-containing histone methyltr | GO:00063 |
| | Similar to Zinc finger, C3HC4 type family protein, ex | |
| [Os] chlorophyll-a content (TO:0000293) \| chloroplast development trait (TO:0002715) \| carotenoid content (TO:0000496) \| chlorophyll-b content (TO:0000295) \| | Similar to Whirly family nucleic acid bindi | GO:00063 |

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|---|---|---|
| | Similar to Phyb1 | GO:00163 |
| | Protein of unknown function DUF640 dor | GO:00072 |
| | C1-like domain containing protein | |
| | Similar to Aspartyl aminopeptidase-like p | GO:00065 |
| | Similar to H0303G06.2 protein | GO:00100 |
| | Hypothetical conserved gene | GO:19001 |
| | Similar to predicted protein | |
| | Conserved hypothetical protein | GO:00063 |
| | Ribonucleotide reductase, Chloroplast bi | GO:00062 |
| | Similar to IQ calmodulin-binding motif family protei | |
| | Ribosomal RNA-processing protein 7 dor | GO:00000 |
| | Similar to PCF1 | GO:00063 |
| [Os] inflorescence development trait (TO:0000621) \| lemma and palea anatomy and morphology trait (TO:0000079) \| inflorescence anatomy and morphology trait (TO:0000373) \| flower development trait (TO:0000622) \| lodicule anatomy and morphology trait (TO:0006009) \| carpel anatomy and morphology trait (TO:0006012) \| lodicule development trait (TO:0006023) \| flowering time (TO:0002616) \| stamen anatomy and morphology trait (TO:0000215) \| pollen | MADS box protein | GO:00063 |
| | Protein of unknown function DUF1313 fa | GO:00096 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] blast disease (TO:0000074) | Similar to glutamate-gated kainate-type | GO:00068 |
| | Similar to predicted protein | GO:00063 |

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|---|---|---|
| | Similar to Low temperature viability prote | GO:00000 |
| | Zm00001e033963 | GO:00610 |
| | Protein of unknown function DUF579, pla | GO:00098 |
| | Cyclin-like F-box domain containing protein | |
| | Similar to Permease 1 | GO:00550 |
| | Similar to Epa4p | GO:00063 |
| [Os] brassinosteroid sensitivity (TO:0002677) \| grain size (TO:0000397) \| leaf angle (TO:0000206); [Os] tiller angle | Serine/threonine protein kinase domain | GO:00064 |
| [Os] leaf senescence (TO:0000249) \| photoperiod sensitivity (TO:0000229) \| grain weight (TO:0000590) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| grain yield | Zm00001e032561 | GO:20000 |
| [Ta] male sterility TO:0000437 | Similar to Myb-related protein Pp2 | GO:00301 |
| [Os] abiotic stress trait (TO:0000168); [Os] salt tolerance TO:0006001 | Similar to Heat shock transcription factor | GO:00063 |
| | Zinc finger, Dof-type family protein | GO:00063 |
| | Similar to CPSF160; nucleic acid binding | |
| [Os] root length (TO:0000227) \| plant height (TO:0000207) | CRT-like transporter, Glutathione homeostasis, Arse | |
| [Os] crown root number (TO:0002685) \| inflorescence development trait (TO:0000621) \| temperature response trait (TO:0000432) \| male sterility (TO:0000437) \| root development trait (TO:0000656) | MIKC-type MADS-box protein, Flowering | GO:00063 |
| | Hypothetical conserved gene | GO:00096 |
| [Os] drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| salt tolerance (TO:0006001) | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Zm00001e038460 | |

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|---|---|---|
| [Os] herbicide sensitivity (TO:0000058) | Cytochrome P450 monooxygenase, Tolerance to ace | |
| | Cyclopropane-fatty-acyl-phospholipid synthase dor | |
| | Similar to WIP5 protein | GO:00104 |
| | ABC transporter, transmembrane domain | GO:00550 |
| | RNA recognition motif 2 domain containing protein | |
| | Transcriptional factor B3 family protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Plant disease resistance response protein | GO:00096 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to WD and tetratricopeptide repeats protein | |
| [Os] blast disease (TO:0000074) \| salt tolerance (TO:0006001) | | |
| | Cytochrome P450 family protein | GO:00072 |
| | Zinc finger, CCHC-type domain containing protein | |
| | Similar to predicted protein | |
| [Os] jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074) | Rhodanese-like domain containing protein | |
| [Os] lignin biosynthesis trait (TO:0000733) | Flavone synthase II (FNSII), Biosynthesis o | GO:00098 |
| [Os] cytokinin sensitivity (TO:0000167) \| auxin sensitivity (TO:0000163) \| days to heading (TO:0000137) | A-type response regulator, Cytokinin sig | GO:00001 |

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|---|---|---|
| [Os] leaf lamina joint bending (TO:0002688) \| leaf angle (TO:0000206) \| phosphorus sensitivity (TO:0000102) | HTH_MYB-like transcription factor, Positi | GO:00101 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Similar to SKIP interacting protein 8 (Fragment) | |
| | Similar to Cinnamate 4-hydroxylase CYP73 | |
| | Similar to Cellulose synthase-8 | GO:00098 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] bacterial blight disease resistance (TO:0000175) | Protein of unknown function DUF594 domain contai | |
| | Cyclin-like F-box domain containing protein | |
| | Succinate dehydrogenase, cytochrome b | GO:00060 |
| | Hypothetical protein | |
| | Conserved hypothetical protein | |
| [Os] light intensity sensitivity (TO:0000460) \| drought tolerance (TO:0000276) \| hydrogen peroxide content (TO:0000605) \| chloroplast development trait (TO:0002715) \| photosynthetic ability (TO:0000316) | | |
| | Conserved hypothetical protein | GO:00100 |

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|---|---|---|
| | Zm00001e009868 | |
| | Poly(ADP-ribose) polymerase, catalytic region doma | |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Hypothetical conserved gene | GO:00068 |
| | Prefoldin domain containing protein | GO:00104 |
| [Os] grain length to width ratio (TO:0002731) \| grain size (TO:0000397) \| grain length (TO:0000734) \| grain shape (TO:0002730) \| 1000-seed weight (TO:0000382) \| seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| chalky endosperm (TO:0000266) \| seed quality (TO:0000162) \| yield trait | TON1 RECRUIT MOTIF (TRM)-containing | GO:00515 |
| | Zm00001e007598 | GO:00069 |
| | Protein of unknown function DUF3133 dc | GO:19001 |
| [Os] bacterial blight disease resistance (TO:0000175) \| iron sensitivity (TO:0000224) \| UV light sensitivity (TO:0000160) \| insect damage resistance (TO:0000261) | | |
| | Protein of unknown function DUF566 fam | GO:00070 |
| [Ta] ash content TO:0000607 | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | General substrate transporter domain co | GO:00342 |
| | Conserved hypothetical protein | GO:00063 |
| | Similar to pectinesterase inhibitor domain containin | |
| | Tesmin/TSO1-like, CXC domain containi | GO:00063 |
| | Protein of unknown function DUF3133 dc | GO:19001 |
| | Forkhead-associated domain containing | GO:00439 |
| | Zm00001e028424 | |
| | Frigida-like family protein | GO:00099 |
| [Os] chlorophyll content (TO:0000495) \| chloroplast development trait (TO:0002715) | | |

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|---|---|---|
| | Protein of unknown function DUF593 family protein<br>Zm00001e015026<br>Hypothetical conserved gene | GO:00071 |
| [Os] bacterial blight disease resistance (TO:0000175) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) | Protein of unknown function DUF1675 fa | GO:00071 |
| [Os] drought tolerance TO:0000276 | Spectrin repeat containing protein<br>Conserved hypothetical protein<br>Similar to OSIGBa0147J19.13 protein<br>Similar to Rwp34 (Fragment)<br>Conserved hypothetical protein | GO:00717 |
| [Os] abscisic acid sensitivity (TO:0000615) \| cold tolerance (TO:0000303) | | |
| | Zinc finger, FYVE/PHD-type domain cont | GO:19001 |
| | Similar to H0305E08.4 protein | GO:00517 |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Conserved hypothetical protein | GO:00515 |
| | Pollen Ole e 1 allergen and extensin domain contain | |
| [Os] oxygen sensitivity (TO:0000015) \| submergence tolerance (TO:0000524) | | |
| | Glycosyltransferase AER61, uncharacterized domain | |
| [Os] salt tolerance (TO:0006001) | DNA-binding WRKY domain containing p | GO:00063 |
| | Protein of unknown function DUF668 fam | GO:00459 |
| | Hypothetical conserved gene<br>Pentatricopeptide repeat domain containing protein | |

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|---|---|---|
| [Os] abiotic stress trait (TO:0000168) | Similar to Helix-loop-helix protein homo | GO:00063 |
| | Conserved hypothetical protein | |
| | VQ domain containing protein | |
| | Zm00001e035816 | |
| | Similar to Myb-like DNA-binding domain, SHAQKYF | |
| | Zm00001e002906 | |
| | Pectinesterase inhibitor domain containin | GO:00430 |
| | Uncharacterised conserved protein UCP012943 dom | |
| | Syntaxin 6, N-terminal domain containin | GO:00150 |
| | CCT domain containing protein | GO:00063 |
| | Uncharacterised protein family UPF0497, trans-men | |
| | Zinc finger, CCCH-type domain containin | GO:00169 |
| | Hypothetical conserved gene | GO:00081 |
| [Os] chlorophyll-b content (TO:0000295) \| hydrogen peroxide content (TO:0000605) \| blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) \| chloroplast development trait (TO:0002715) \| chlorophyll-a content (TO:0000293) \| chlorophyll content (TO:0000495) \| mimic response (TO:0000063) | Peptidase C19, ubiquitin carboxyl-termin | GO:00065 |
| | Hypothetical conserved gene | GO:00063 |
| [Os] sterility related trait (TO:0000485) | Hypothetical conserved gene | GO:00007 |
| | Conserved hypothetical protein | GO:00083 |

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|---|---|---|
| [Os] jasmonic acid sensitivity (TO:0000172) \| viral disease resistance (TO:0000148) \| sheath blight disease resistance (TO:0000255) \| temperature response trait (TO:0000432) \| black streak dwarf virus resistance (TO:0000020) \| blast disease (TO:0000074); [Os] disease resistance TO:0000112; [Ta] disease resistance TO:0000112 | Pathogen-related protein (JIOsPR10) | GO:00069 |
| | Hypothetical conserved gene | GO:00069 |
| | Heat shock protein DnaJ, N-terminal domain contai | |
| [Os] lemma and palea anatomy and morphology trait (TO:0000079) \| carpel anatomy and morphology trait (TO:0006012) \| fruit structure trait (TO:0002629) \| inflorescence development trait (TO:0000621) | MADS box transcription factor, Regulatio | GO:00063 |
| | Similar to CDT1a protein | GO:00000 |
| | Fumble domain containing protein | GO:00159 |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to Na+/H+ antiporter-like protei | GO:00068 |
| [Os] shoot apical meristem development (TO:0006020) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| vegetative to reproductive phase transition trait (TO:0006021) | GRAS (GAI-RGA-SCR) plant-specific trans | GO:00063 |
| | Autophagy-related protein 13 domain co | GO:00000 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] heat tolerance (TO:0000259) \| salt tolerance (TO:0006001) \| osmotic response sensitivity (TO:0000095) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| oxidative stress (TO:0002657) | Transcription factor binding protein, Poly (ADP-ribo | |
| [Os] submergence tolerance (TO:0000524) \| oxygen sensitivity (TO:0000015) | | |
| | Conserved hypothetical protein | |

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|---|---|---|
| [Os] flowering time (TO:0002616) \| photoperiod sensitivity (TO:0000229) \| days to heading (TO:0000137) | C3HC4 RING domain-containing E3 ubiq | GO:00165 |
| [Os] vascular tissue related trait (TO:0000470) \| drought tolerance (TO:0000276) | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Targeting for Xklp2 family protein | |
| | Similar to somatic embryogenesis related | GO:00001 |
| [Os] lodging incidence (TO:0000068) | Glycosyltransferase AER61, uncharacterized domain | |
| | Ethylene response factor, Transcription f | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| | Cation/H+ exchanger domain containing | GO:00068 |
| | Protein of unknown function DUF292, eu | GO:00081 |
| | Conserved hypothetical protein | GO:00004 |
| | Zinc finger, PHD-type domain containing protein | |
| | Hypothetical conserved gene | |
| [Os] oxidative stress TO:0002657 | CCT domain containing protein | GO:00099 |
| | Pollen Ole e 1 allergen and extensin domain contain | |
| [Os] male sterility type (TO:0000106) \| heat tolerance (TO:0000259) \| anther shape (TO:0000214) \| pollen sterility (TO:0000053) | bHLH transcription factor, Control of ant | GO:00063 |
| | Protein of unknown function DUF580 fa | GO:00550 |
| | Myoactive tetradecapeptides family protein | |
| | NB-ARC domain containing protein | GO:00069 |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | Cyclin-like F-box domain containing pro | GO:00165 |
| | Pectinesterase inhibitor domain containing protein | |

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|---|---|---|
| | SAP-like protein BP-7 | GO:00063 |
| | Cyclin D domain containing protein | GO:00000 |
| [Os] secondary branch number (TO:0000557) \| spikelet fertility (TO:0000180) \| grain width (TO:0000402) \| 1000-seed weight (TO:0000382) \| inflorescence branching (TO:0000050) \| stem strength (TO:0000051) \| grain number (TO:0002759) \| vascular bundle number (TO:0000472) \| plant height (TO:0000207) \| stem thickness (TO:0000339) \| leaf angle (TO:0000206) \| panicle length (TO:0000040) \| grain size (TO:0000397) \| leaf size (TO:0002637) \| lemma and palea anatomy and morphology trait (TO:0000079) \| leaf | | |
| [Os] | Glycosyltransferase, Xylan biosynthesi | |
| | Similar to HRT transcription factor (Fragn | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to ER lumen protein retaining rec | GO:0007 |
| | Heat shock protein Hsp20 domain contai | GO:00094 |
| | Basic-leucine zipper (bZIP) transcription | GO:00063 |
| | Autophagy-related protein 13 domain co | GO:00000 |
| | Conserved hypothetical protein | GO:00063 |
| | Conserved hypothetical protein | GO:00159 |
| [Os] blast disease (TO:0000074) \| temperature response trait (TO:0000432) \| heat tolerance (TO:0000259); [Os] cold tolerance TO:0000303; [Ta] heat tolerance TO:0000259\| root branching | bZIP transcription factor, Endoplasmic re | GO:00063 |
| | Similar to Minus dominance protein | GO:00063 |
| | Conserved hypothetical protein | |

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|---|---|---|
| [Os] drought sensitivity (TO:0000188) \| abscisic acid sensitivity (TO:0000615) \| white-backed planthopper resistance (TO:0000205) \| bacterial blight disease resistance (TO:0000175) \| jasmonic acid sensitivity (TO:0000172) \| plant growth hormone sensitivity | Hypothetical conserved gene | GO:00063 |
| | Defence response, Rin4 domain containing protein | |
| | Similar to arabinogalactan protein | |
| | Similar to RING-H2 finger protein ATL3B | GO:00065 |
| | Similar to HAT family dimerisation domain containin | |
| | Armadillo-like helical domain containing protein | |
| | Zm00001e007784 | GO:00062 |
| | Leucine-rich repeat, SDS22 containing protein | |
| | Similar to harpin-induced protein | |
| [Os] lodging incidence (TO:0000068) \| pesticide sensitivity (TO:0002649) | Glycosyltransferase AER61, uncharacterized domain | |
| | Similar to cullin-1 | GO:00065 |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| iron sensitivity (TO:0000224) \| cold tolerance (TO:0000303) \| bacterial blight disease resistance (TO:0000175) \| heat tolerance (TO:0000259) \| viral disease resistance (TO:0000148) | Similar to WRKY transcription factor 64 | GO:00063 |
| | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to tumor-related protein-like | GO:00063 |
| | Hypothetical conserved gene | GO:00063 |
| | Cation/H+ exchanger domain containing | GO:00068 |
| | Kelch-type beta propeller domain contai | GO:20007 |
| | Zinc finger, RING-type domain containing protein | |
| | Harpin-induced 1 domain containing protein | |
| | Similar to DNA binding protein-like | GO:00063 |
| | Calmodulin binding protein-like domain containing | |

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|---|---|---|
| [Os] blast disease (TO:0000074) \| shoot branching (TO:0002639) \| tillering ability (TO:0000329) \| yield trait (TO:0000371) \| tiller number (TO:0000346) \| seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| nitrogen sensitivity (TO:0000011) \| flowering time (TO:0002616) \| days to heading (TO:0000137); [Ta] disease resistance TO:0000112\| heterosis TO:0000355\| grain size TO:0000397\| grain number TO:0002759\| starch | MYB transcription factor, Circadian cloc | |
| | Zinc finger, C2H2-type domain containin | GO:00002 |
| | K Homology domain containing protein | GO:00104 |
| [Os] growth and development trait (TO:0000357) \| fat and essential oil content (TO:0000604) \| protein content (TO:0000598) \| grain size (TO:0000397) \| floury endosperm (TO:0000104) \| starch grain size (TO:0002655) \| chalky endosperm (TO:0000266) \| grain weight (TO:0000590) \| grain thickness (TO:0000399) \| starch content (TO:0000696) \| starch grain shape (TO:0002656) \| filled grain number (TO:0000447) \| seed color (TO:0000486) \| 1000-seed weight (TO:0000382) \| amylose content | Hypothetical conserved gene | GO:00016 |
| | Cell cycle regulated microtubule associat | GO:00321 |
| | Similar to Circumsporozoite protein | GO:00300 |
| | Peptidase aspartic, active site domain containing pr | |
| | Hypothetical conserved gene | |
| [Os] submergence tolerance (TO:0000524) | R2R3 MYB transcription factor, Regulatio | GO:00101 |
| | Similar to OSIGBa0117N13.2 protein | |
| | Protein of unknown function DUF641, pla | GO:00096 |
| | Conserved hypothetical protein | |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF2921 domain conta | |

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|---|---|---|
| | ERG2/sigma1 receptor-like domain containing prote | |
| [Os] drought tolerance (TO:0000276) | Similar to WRKY transcription factor 44 (V | GO:00063 |
| | Conserved hypothetical protein | GO:00001 |
| [Os] cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| abiotic stress trait (TO:0000168) | | |
| | Conserved hypothetical protein | GO:00071 |
| | Protein of unknown function DUF593 family protein | |
| [Os] temperature response trait (TO:0000432) \| heat tolerance (TO:0000259) \| male sterility (TO:0000437) | | |
| | FAS1 domain domain containing protein | |
| | Conserved hypothetical protein | GO:00011 |
| [Os] gibberellic acid sensitivity (TO:0000166) \| mesocotyl length (TO:0000544) | Similar to Long hypocotyl in far-red 1 (bH | GO:00063 |
| | IQ calmodulin-binding region domain containing pr | |
| | tRNAHis guanylyltransferase domain cont | GO:00064 |
| | Cyclin D domain containing protein | GO:00000 |
| [Os] chlorophyll content (TO:0000495) \| abscisic acid sensitivity (TO:0000615) \| jasmonic acid sensitivity (TO:0000172) \| iron sensitivity (TO:0000224) \| plant height (TO:0000207) | ABI3/VP1 transcription factor family prot | GO:00063 |
| [Os] pesticide sensitivity (TO:0002649) | | |
| [Os] organ identity TO:0006018 | Myb-like DNA-binding domain, SHAQKYF class dom | |
| | TB2/DP1 and HVA22 related protein family protein | |
| [Os] drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| abiotic stress trait (TO:0000168) | | |
| [Os] panicle length (TO:0000040) | | |
| | Mitochodrial transcription termination fa | GO:00063 |

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|---|---|---|
| | RNA recognition motif, RNP-1 domain containing pr | |
| [Os] salt tolerance (TO:0006001) \| blast disease (TO:0000074) | SNF2-related domain containing protein | GO:00801 |
| | Similar to Genetic modifier Zm00001e023650 | GO:00063 |
| | Protein of unknown function DUF593 family protein | |
| [Os] abscisic acid sensitivity (TO:0000615) \| bacterial blight disease resistance (TO:0000175) | WRKY transcription factor 78 | GO:00063 |
| | Similar to TA9 protein (Fragment) | |
| | Tetratricopeptide-like helical domain con | GO:00063 |
| | NB-ARC domain containing protein | GO:00069 |
| | SWAP/Surp domain containing protein | GO:00003 |
| [Os] drought tolerance (TO:0000276) \| oxygen sensitivity (TO:0000015) \| salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| abscisic acid sensitivity (TO:0000615) \| bacterial blight disease resistance (TO:0000175) \| cold tolerance (TO:0000303); [Ta] disease resistance TO:0000112 | | |
| | Protein of unknown function DUF1423, plant domai | |
| | CCT domain containing protein | GO:00063 |
| | Protein of unknown function DUF1296 family protei | |
| | Conserved hypothetical protein | GO:00070 |
| | Tesmin/TSO1-like, CXC domain containi | GO:00063 |
| | Conserved hypothetical protein | GO:00094 |
| | Transferase family protein | |
| | Heat shock protein DnaJ family protein | GO:00064 |
| [Os] sheath blight disease resistance (TO:0000255) \| blast disease (TO:0000074); [Os] disease resistance TO:0000112 | Similar to VIP2 protein | GO:00165 |
| | Zinc finger, RING-type domain containing protein | |
| | Harpin-induced 1 domain containing pro | GO:00985 |

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|---|---|---|
| [Os] drought tolerance (TO:0000276) \| leaf development trait (TO:0000655) \| blast disease (TO:0000074) \| salt tolerance (TO:0006001) | No apical meristem (NAM) protein domai | GO:00063 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| bacterial disease resistance (TO:0000315) \| sheath blight disease resistance (TO:0000255) \| bacterial blight disease resistance (TO:0000175) \| submergence tolerance (TO:0000524) | Hypothetical conserved gene | GO:00064 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| blast disease (TO:0000074) | Ricin B-related lectin domain containing protein | |
| | Transferase domain containing protein | |
| | RNA-Recognition-Motif (RRM) protein, Regulation o | |
| [Os] grain size (TO:0000397) | | |
| | Similar to Glycoprotein-specific UDP-glu | GO:00059 |
| [Os] plant growth hormone sensitivity (TO:0000401) \| nutrient sensitivity (TO:0000480) \| fluorine sensitivity (TO:0000038) \| gibberellic acid sensitivity (TO:0000166) \| abscisic acid sensitivity (TO:0000615) | Camphor resistance CrcB protein family | GO:19034 |
| | Similar to predicted protein | GO:00063 |
| | D111/G-patch domain containing protei | GO:00003 |
| | NB-ARC domain containing protein | GO:00069 |
| | Wax synthase domain containing protein | GO:00066 |
| | Similar to BHLH transcription factor (Frag | GO:00063 |
| | Similar to H0502B11.13 protein | GO:00516 |
| | Similar to Gb protein | |
| | Conserved hypothetical protein | GO:00083 |

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|---|---|---|
|  | Ankyrin repeat containing protein |  |
| [Os] grain size (TO:0000397) \| panicle length (TO:0000040) \| hydrogen peroxide content (TO:0000605) \| osmotic response sensitivity (TO:0000095) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| ethylene sensitivity (TO:0000173) \| yield trait (TO:0000371) \| grain yield (TO:0000396) \| salt tolerance (TO:0006001) \| cytokinin sensitivity (TO:0000167) \| root thickness (TO:0000306) \| plant growth hormone sensitivity (TO:0000401) \| embryo development trait (TO:0000620) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| grain length | Homeobox domain containing protein | GO:00063 |
|  | RNAse P, Rpr2/Rpp21 subunit domain co | GO:00063 |
|  | Conserved hypothetical protein |  |
|  | Glycosyltransferase AER61, uncharacterized domain |  |
| [Os] plant height (TO:0000207) \| tiller number (TO:0000346) \| photosynthetic ability (TO:0000316) \| 1000-dehulled grain weight (TO:0000592) \| leaf color (TO:0000326) \| chlorophyll content (TO:0000495) \| chloroplast development trait (TO:0002715) | Nucleus-encoded chloroplast protein, Ch | GO:00096 |
|  | ELM2 domain containing protein |  |
|  | Zm00001e039720 |  |
| [Os] relative yield (TO:0000153) \| drought tolerance (TO:0000276) \| nitrogen sensitivity (TO:0000011) | Helix-loop-helix DNA-binding domain c | GO:00063 |
|  | Protein kinase, catalytic domain domain | GO:00064 |
|  | Zm00001e027207 |  |
|  | Harpin-induced 1 domain containing protein |  |
|  | Conserved hypothetical protein |  |
|  | Transferase family protein |  |
| [Os] disease resistance TO:0000112 | Armadillo-like helical domain containing | GO:00165 |
| [Os] disease resistance TO:0000112 |  |  |
|  | Conserved hypothetical protein | GO:00096 |

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|---|---|---|
| [Os] glucose content (TO:0000300) \| sugar content (TO:0000333) \| sucrose content (TO:0000328) \| 1000-seed weight (TO:0000382) \| fructose content (TO:0006005) \| seed maturation (TO:0002661) \| grain thickness (TO:0000399) \| starch content (TO:0000696) \| carbohydrate content (TO:0000291); [Os] sugar content TO:0000333 | | |
| | Conserved hypothetical protein | |
| | Similar to peroxin Pex14 | GO:00150 |
| | Steroid nuclear receptor, ligand-binding | GO:00635 |
| | Basic helix-loop-helix dimerisation regio | GO:00635 |
| [Os] rolled leaf TO:0006064 | Similar to Two-component response reg | GO:00635 |
| [Os] sodium concentration (TO:0000526) \| potassium concentration (TO:0000513) \| salt tolerance (TO:0006001) \| potassium content (TO:0000609) \| sodium content (TO:0000608); [Os] leaf trichome density TO:0006066\| salt tolerance TO:0006001\| drought tolerance | Similar to Squamosa-promoter binding protein 1 | |
| [Os] bacterial blight disease resistance (TO:0000175) | Similar to SUSIBA2 | GO:00635 |
| | Prenylated rab acceptor PRA1 family prot | GO:00161 |
| | Domain of unknown function DUF632 do | GO:00712 |
| | Protein of unknown function DUF2870 d | GO:00033 |
| | Similar to Initiator-binding protein | |
| | Mitotic checkpoint protein PRCC, C-terminal domai | |
| | Similar to G-box binding factor 1 | GO:00635 |
| | Similar to WAVE-DAMPENED2 | GO:00022 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Cupredoxin domain containing protein | GO:00229 |
| | Similar to Calreticulin interacted protein | |
| | KIP1-like domain containing protein | |
| | Pentatricopeptide repeat domain containing protein | |

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|---|---|---|
| | Similar to nucleic acid binding protein | |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Hypothetical conserved gene | |
| | Zm00001e027059<br>Similar to Calcium-activated outward-rectifying pot | |
| [Os] lateral root number (TO:0001013) | | |
| [Os] ethylene sensitivity (TO:0000173) \| cytokinin sensitivity (TO:0000167) | B-type response regulator, Cytokinin sig | GO:00001 |
| | Hypothetical conserved gene | GO:00097 |
| [Os] flowering time (TO:0002616) | Homeodomain (PHD) transcriptional regu | GO:00063 |
| | Hypothetical conserved gene | GO:00063 |
| | Zinc finger, C3HC-like domain containing protein | |
| | 2OG-Fe(II) oxygenase domain containing protein | |
| [Os] leaf development trait (TO:0000655) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) \| nitrogen sensitivity | Similar to CUC2 | GO:00063 |
| | Cyclin-like F-box domain containing protein | |
| | Hypothetical conserved gene | |
| | Hypothetical conserved gene | |

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|---|---|---|
| [Os] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| gibberellic acid sensitivity (TO:0000166) \| auxin sensitivity (TO:0000163) \| cold tolerance (TO:0000303) \| relative yield (TO:0000153) \| nitrogen sensitivity (TO:0000011) \| osmotic response sensitivity (TO:0000095) \| drought tolerance (TO:0000276) \| abiotic stress | Similar to Homeobox-leucine zipper prot | GO:00063 |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| bacterial blight disease resistance (TO:0000175) \| white-backed planthopper resistance (TO:0000205); [Ta] drought tolerance TO:0000276 | WRKY transcription factor, Defense respo | GO:00022 |
| | Bromodomain containing protein | |
| | Similar to receptor-kinase isolog | GO:00064 |
| [Os] drought tolerance (TO:0000276) \| gibberellic acid sensitivity (TO:0000166) \| jasmonic acid | Basic helix-loop-helix transcription facto | GO:00063 |
| [Os] abiotic stress trait (TO:0000168) | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | RNA polymerase sigma factor, region 2 d | GO:00063 |
| | Hypothetical conserved gene | |
| | Similar to RING finger protein 13 (C-RZF) | GO:00165 |
| [Os] grain size (TO:0000397) \| grain yield (TO:0000396) \| grain weight (TO:0000590) \| seed size (TO:0000391) \| grain width (TO:0000402); [Ta] seed size TO:0000391\| protein content TO:0000598\| grain length TO:0002760\| grain length TO:0000734\| grain size TO:0000397\| tiller number TO:0000346\| grain width TO:0000975\| spikelet number TO:0000456\| grain | Protein of unknown function DUF1296 family protei | |
| | Zm00001e027477 | |
| | Transferase family protein | |
| | Mitochondrial glycoprotein family protein | GO:00701 |

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|---|---|---|
| [Os] flowering time (TO:0002616) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| spikelet number (TO:0000456); [Ta] grain size TO:0000397\| drought tolerance TO:0000276 | Circadian-associated rice pseudo respon | GO:00001 |
| | Conserved hypothetical protein | |
| | Membrane bound O-acyl transferase, MB | GO:00066 |
| | Armadillo-like helical domain containing protein | |
| | Kelch-type beta propeller domain containing protei | |
| | Similar to H0522A01.11 protein | |
| | Esterase, SGNH hydrolase-type domain containing | |
| [Os] cytokinin sensitivity (TO:0000167) | B-type response regulator, Cytokinin sig | GO:00001 |
| | Thioredoxin fold domain containing prot | GO:00454 |
| | Similar to CTD-phosphatase-like protein | |
| | EF-Hand type domain containing protein | |
| | Conserved hypothetical protein | GO:00096 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | UBA-like domain containing protein | |
| [Os] drought tolerance (TO:0000276) \| oxidative stress (TO:0002657) \| stomatal conductance (TO:0000522) \| hydrogen peroxide content (TO:0000605) | Homologue of SRO (similar to RCD one), Regulation | |
| | Similar to glycosyltransferase | |
| | Basic helix-loop-helix dimerisation regio | GO:00063 |
| [Os] bacterial leaf streak disease resistance (TO:0000203) \| bacterial blight disease resistance (TO:0000175) \| brown planthopper resistance (TO:0000424) \| bacterial disease | Lipase, class 3 family protein | GO:00066 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | Conserved hypothetical protein | GO:00169 |
| | Hypothetical conserved gene | GO:00063 |
| | Transcription elongation factor S-II, cent | GO:00063 |
| | Zm00001e023624 | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |

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|---|---|---|
| | Uncharacterised protein family UPF0402 domain co | |
| | Lipase, GDSL domain containing protein | |
| | GRAS transcription factor domain contain | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | ENTH/VHS domain containing protein | GO:00063 |
| | VQ domain containing protein | |
| | Pentatricopeptide repeat domain containing protein | |
| | KIP1-like domain containing protein | |
| [Os] bacterial blight disease resistance (TO:0000175) \| hydrogen peroxide content (TO:0000605) \| sugar content (TO:0000333) \| grain yield (TO:0000396) \| seed set percent (TO:0000455) \| abscisic acid content (TO:0002667) \| cold tolerance | bZIP transcription factor, Cold tolerance, | GO:00063 |
| | Conserved hypothetical protein | GO:00071 |
| [Os] pesticide sensitivity (TO:0002649) | Glycosyltransferase AER61, uncharacterised domain | |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Protein of unknown function DUF966 fam | GO:00512 |
| | Spectrin repeat containing protein | GO:00104 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to Hydrolase | |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Nucleotide-binding, alpha-beta plait do | GO:00063 |
| [Os] stamen number (TO:0000225) \| bacterial leaf streak disease resistance (TO:0000203) \| lemma number (TO:0000208) \| spikelet anatomy and morphology trait (TO:0000657) \| pistil anatomy and morphology trait (TO:0000223) \| palea number (TO:0000209) | Polygalacturonase-inhibiting protein, Inh | GO:00301 |
| | Conserved hypothetical protein | GO:00063 |
| | Zinc finger, CCCH-type domain containing protein | |
| | BSD domain containing protein | |

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|---|---|---|
| [Os] flowering time (TO:0002616) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) | Basic helix-loop-helix dimerisation region bHLH do | |
| [Os] ethylene sensitivity (TO:0000173) | Quinonprotein alcohol dehydrogenase-like domain | |
| [Os] salt tolerance (TO:0006001) \| copper sensitivity (TO:0000021) \| heat tolerance (TO:0000259) \| gibberellic acid sensitivity (TO:0000166) \| red light sensitivity (TO:0000158) \| iron sensitivity (TO:0000224) \| cold tolerance (TO:0000303); [Os] seed maturation TO:0002661 | Achaete-scute transcription factor relate | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Similar to cDNA clone:002-146-F05, full insert seq | |
| | TB2/DP1 and HVA22 related protein family protein | |
| | Similar to Poly polymerase catalytic domain containi | |
| | Similar to H0702G05.3 protein | |
| [Os] salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) | Salt-induced RING Finger Protein, Negati | GO:00065 |
| | Conserved hypothetical protein | |
| | Actin-binding FH2 domain containing pr | GO:00300 |
| | Zm00001e024354 | GO:00065 |
| [Os] blast disease (TO:0000074) \| brown planthopper resistance (TO:0000424) \| jasmonic acid sensitivity (TO:0000172) \| abiotic stress trait (TO:0000168) \| plant growth hormone sensitivity (TO:0000401) \| | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Conserved hypothetical protein | |
| | Conserved hypothetical protein | GO:00063 |
| | Hypothetical conserved gene | GO:00063 |
| | Peroxisome membrane anchor protein Pe | GO:00150 |
| | Glycosyl transferase, family 8 protein | GO:00454 |
| | Frigida-like family protein | GO:00099 |

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|---|---|---|
| [Os] submergence tolerance (TO:0000524) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| cold tolerance (TO:0000303) | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Transcription antitermination protein, Nu | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] gibberellic acid sensitivity (TO:0000166) \| brassinosteroid sensitivity (TO:0002677) \| filled grain number (TO:0000447) \| primary branch number (TO:0000547) \| panicle size (TO:0006032) \| total biomass yield (TO:0000457) \| auxin sensitivity (TO:0000163) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| leaf angle (TO:0000206) \| abscisic acid sensitivity (TO:0000615) \| secondary branch number (TO:0000557) \| grain yield (TO:0000396); [Os] floral organ number TO:0006038\| grain number | Chromatin remodeling factor, Protein cor | GO:00069 |
| | Similar to Xylanase inhibitor protein I pre | GO:00059 |
| | Similar to Nucleic acid binding protein | |
| | Tyrosine protein kinase domain containi | GO:00064 |
| [Os] brassinosteroid sensitivity (TO:0002677) \| submergence tolerance (TO:0000524) \| internode length (TO:0000145) \| flooding related trait (TO:0000114) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| total fat content (TO:0000602) \| leaf composition trait (TO:0000493) \| plant height (TO:0000207) | Hydroxysteroid dehydrogenase, Cuticle formation, L | |
| | Conserved hypothetical protein | |
| | Harpin-induced 1 domain containing protein | |
| | Similar to Transcription factor HBP-1a(C1 | GO:00063 |
| | Conserved hypothetical protein | GO:00099 |

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|---|---|---|
| | Similar to Sigma factor SIG6 | GO:00063 |
| [Os] plant height (TO:0000207) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074) \| days to heading (TO:0000137) \| cold tolerance (TO:0000303) \| panicle length (TO:0000040) \| flower number (TO:0002736) \| flowering time (TO:0002616) \| root length (TO:0000227) \| viral disease resistance (TO:0000148) \| grain weight (TO:0000590) \| grain size (TO:0000397) \| stem length (TO:0000576) \| spikelet fertility | TIFY domain-containing transcriptional r | GO:00096 |
| | Zm00001e001268 | GO:00104 |
| | Leucine-rich repeat, typical subtype containing prot | |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | Protein of unknown function DUF1644 family protei | |
| | Hypothetical conserved gene | GO:00064 |
| | Similar to H0718E12.5 protein | GO:00468 |
| | Protein of unknown function DUF296 domain contai | |
| | Glycoside hydrolase, family 18, catalytic | GO:00059 |
| | Cellulose synthase-like protei | GO:00098 |
| | Conserved hypothetical protein | GO:00071 |
| | Similar to OSIGBa0148A10.9 protein | GO:00106 |
| [Os] salt tolerance TO:0006001\| drought tolerance TO:0000276 | Repressor protein | GO:00001 |
| | C2 membrane targeting protein domain | GO:00069 |
| | EF-HAND 1 domain containing protein | GO:00069 |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) | Cyclin-like F-box domain containing protein | |
| | Similar to HGA4 | |
| | Mitochodrial transcription termination fa | GO:00063 |
| | Thioesterase superfamily domain containing protein | |
| | Acyl-CoA N-acyltransferase domain containing prot | |
| | Cation/H+ exchanger domain containing | GO:00068 |
| | RNA polymerase I associated factor, A49- | GO:00011 |
| | Zm00001e005099 | |
| | WRC domain containing protein | GO:00063 |
| | Zm00001e025992 | GO:00064 |
| | Similar to Esterase | |
| | ENTH/VHS domain containing protein | GO:00063 |
| | Rad21/Rec8 like protein, C-terminal dom | GO:00063 |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Similar to Hd1 | |
| | Lipase, GDSL domain containing protein | |

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|---|---|---|
| [Os] root fresh weight (TO:0000578) \| root to total biomass ratio (TO:0001019) \| abscisic acid sensitivity (TO:0000615) \| cytokinin sensitivity (TO:0000167) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) \| tiller number (TO:0000346) \| yield trait (TO:0000371) \| total biomass yield (TO:0000457) \| drought tolerance (TO:0000276) \| grain yield per plant (TO:0000449) \| growth and development trait (TO:0000357) \| relative shoot dry weight (TO:0000636) \| relative root dry weight (TO:0000644) \| relative root length (TO:0000516) \| nitrogen sensitivity (TO:0000011) \| shoot fresh weight (TO:0000571) \| root development trait (TO:0000656) \| root number (TO:0000084) \| root length (TO:0000227) \| lateral root length (TO:0001012) \| lateral root number (TO:0001013) \| plant fresh weight | Similar to NIN-like protein 1 | GO:00063 |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| | Similar to cDNA clone:J023038C04, full ir | GO:00063 |
| [Os] genic male sterility (TO:0000199) \| humidity related trait (TO:0000441) | Cofactor of beta-ketoacyl-CoA synthase, Homolog c | |
| | Similar to ZIGA2 protein (Fragment) | GO:00069 |
| | Similar to TA4 protein (Fragment) | |
| | KIP1-like domain containing protein | |
| | Similar to Esterase | |
| | t-snare domain containing protein | GO:00071 |
| | Hypothetical conserved gene | GO:00062 |
| | Similar to OSIGBa0136O08-OSIGBa0153H12.2 prote | |
| | Conserved hypothetical protein | |
| | Similar to Carbonic anhydrase | GO:00069 |

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|---|---|---|
| [Os] sporogenesis TO:0000727\| male sterility TO:0000437 | Tyrosine protein kinase domain containi | GO:00064 |
| | B-type response regulator, Cytokinin sig | GO:00001 |
| | VHS domain containing protein | GO:00068 |
| | WD40 repeat domain containing protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00063 |
| | Zm00001e132280 | GO:00063 |
| [Os] cold tolerance (TO:0000303) \| leaf development trait (TO:0000655) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| heat tolerance (TO:0000259) | No apical meristem (NAM) protein domai | GO:00063 |
| [Os] submergence tolerance (TO:0000524) \| inflorescence exsertion (TO:0001002) \| gibberellic acid content (TO:0002675) | Homeodomain-leucine zipper transcripti | GO:00063 |
| | Protein of unknown function DUF593 domain contai | |
| | Chaperonin Cpn60/TCP-1 family protein | GO:00163 |
| | Similar to OSIGBa0111L12.9 protein | GO:00165 |
| [Os] sterility related trait (TO:0000485) | Similar to Single myb histone 6 | |
| | Hypothetical conserved gene | GO:00512 |
| [Os] leaf senescence (TO:0000249) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) | | |

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|---|---|---|
| [Os] grain number (TO:0002759) \| days to heading (TO:0000137) \| spikelet fertility (TO:0000180) \| grain weight (TO:0000590) \| flag leaf length (TO:0002757) \| jasmonic acid sensitivity (TO:0000172) \| flower number (TO:0002736) \| root length (TO:0000227) \| bacterial disease resistance (TO:0000315) \| stem length (TO:0000576) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| salt tolerance (TO:0006001) | Tify domain containing protein | GO:00096 |
| | Similar to Beta-catenin repeat family prot | GO:00165 |
| | Similar to Squamosa promoter-binding-like protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| [Os] floury endosperm (TO:0000104) \| endosperm color (TO:0000487) \| endosperm storage protein content (TO:0002653) | Phox-like domain containing protein | GO:00150 |
| | Armadillo-type fold domain containing p | GO:00097 |
| | Zm00001e026576 | |
| | Transcription elongation factor, TFIIS/CRSP70, N-te | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | RNA polymerase III Rpc82, C -terminal d | GO:00063 |
| [Os] stomatal frequency (TO:0000566) | Similar to EPIDERMAL PATTERNING FACT | GO:00103 |
| | Auxin responsive SAUR protein family pr | GO:00097 |

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|---|---|---|
| [Os] drought tolerance (TO:0000276) | | |
| | Putative integral membrane protein conta | GO:00550 |
| | Protein of unknown function DUF1218 family protei | |
| [Os] salt tolerance (TO:0006001) \| sugar content (TO:0000333) \| pollen fertility (TO:0000421) \| grain yield (TO:0000396) \| seed set percent (TO:0000455) \| cold tolerance (TO:0000303) \| abscisic acid content (TO:0002667) \| hydrogen peroxide | bZIP transcription factor, Drought and sa | GO:00063 |
| | Similar to OSIGBa0157K09-H0214G12.10 protein | |
| | Hypothetical conserved gene | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00063 |
| ["Bd, Zm"] lignin biosynthesis trait (TO:0000733) | Transferase family protein | |
| | BAHD acyltransferase, Glucuronoarabinoxylan modi | |
| [Os] oxygen sensitivity (TO:0000015) \| submergence tolerance (TO:0000524) | | |
| | Conserved hypothetical protein | |
| | Similar to H0321H01.14 protein | GO:00064 |
| | DNA replication factor CDT1-like domain | GO:00000 |
| | Similar to cysteine-type endopeptidase/ ubiquitin t | |
| [Os] viral disease resistance (TO:0000148); [Os] plant height TO:0000207\| auxin sensitivity TO:0000163 | Auxin response factor 1 | GO:00063 |
| | Protein of unknown function YGGT family | GO:00100 |
| | Nuclear pore complex, nucleoporin 88 d | GO:00000 |
| | Lipase, GDSL domain containing protein | |
| | Similar to Phosphate starvation regulator | GO:00063 |
| | Glycosyl transferase, family 43 protein | GO:00059 |
| | WW/Rsp5/WWP domain containing protein | |

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|---|---|---|
| | Heat shock transcription factor, Cadmiu | GO:00063 |
| [Os] salt tolerance (TO:0006001) \| plant height (TO:0000207) \| tiller number (TO:0000346) | Homeodomain leucine zipper protein | GO:00063 |
| | Similar to TA1 protein (Fragment) | GO:00063 |
| | Hypothetical conserved gene | GO:00069 |
| [Os] spikelet density (TO:0000625) \| leaf angle (TO:0000206) \| brassinosteroid sensitivity (TO:0002677) \| panicle length (TO:0000040) \| seed length (TO:0000146) \| plant height (TO:0000207) \| grain length (TO:0000734) \| internode length (TO:0000145) \| seed development trait (TO:0000653) \| inflorescence | | |
| | Hypothetical conserved gene | GO:00101 |
| | Homeodomain-like domain containing pr | GO:00000 |
| [Os] abiotic stress trait (TO:0000168) \| tiller number (TO:0000346) \| panicle number (TO:0000152) \| heat tolerance (TO:0000259) \| osmotic response sensitivity (TO:0000095) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| relative root length (TO:0000516) \| gibberellic acid sensitivity (TO:0000166) \| auxin sensitivity (TO:0000163) \| osmotic adjustment capacity (TO:0000507) \| relative chlorophyll content (TO:0001016) \| abscisic acid sensitivity | HD-ZIP I protein, Transcription activator, | GO:00063 |
| | Peptidase aspartic, active site domain containing pr | |
| [Os] starch content TO:0000696\| grain size TO:0000397 | | |
| | Protein of unknown function DUF573 fa | GO:00063 |

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|---|---|---|
| | Uncharacterised conserved protein UCP0 | GO:19026 |
| [Os] root anatomy and morphology trait (TO:0000043) \| drought tolerance (TO:0000276) \| gravity response trait (TO:0002693) \| root development trait (TO:0000656) \| relative yield (TO:0000153); [Os] leaf curling TO:0002681\| drought tolerance TO:0000276\| root length TO:0000227\| root dry weight TO:0000078 | Control of root system architecture, Drou | GO:00096 |
| | DNA polymerase subunit Cdc27 domain | GO:00062 |
| | Heat shock protein DnaJ, N-terminal domain contai | |
| [Os] panicle size (TO:0006032) \| drought tolerance (TO:0000276) \| temperature response trait (TO:0000432) \| mineral and ion content related trait (TO:0000465) \| potassium sensitivity (TO:0000008) \| chlorine sensitivity (TO:0000029) \| photosynthetic ability (TO:0000316) \| chlorophyll content (TO:0000495) \| potassium content (TO:0000609) \| leaf number (TO:0000241) \| plant height (TO:0000207) \| light intensity sensitivity (TO:0000460) \| panicle length (TO:0000040) \| panicle weight (TO:0000014) \| shoot weight (TO:0000568) \| growth and development trait (TO:0000357) | Dof (DNA binding with one finger) transc | GO:00063 |
| [Os] salt tolerance (TO:0006001) | Zinc finger, RING-type domain containin | GO:00165 |
| | ATPase, AAA+ type, core domain contain | GO:00062 |
| | Zm00001e013182 | GO:00102 |
| [Os] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| osmotic response | RING E3 ligase, Negative regulator for sal | GO:00165 |
| | Nucleolar protein 12 domain containing | GO:00063 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Conserved hypothetical protein | |
| [Os] root hair length (TO:0002665) | Similar to basic helix-loop-helix protein | GO:00063 |
| | Similar to Disease resistance protein RPM | GO:00069 |

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|---|---|---|
| [Os] bacterial blight disease resistance (TO:0000175) \| blast disease (TO:0000074) \| viral disease resistance (TO:0000148) \| leaf senescence (TO:0000249) \| cold tolerance (TO:0000303) | WRKY transcription factor 14 (WRKY14) | GO:00063 |
| | Protein phosphatase 4 core regulatory su | GO:00064 |
| | Conserved hypothetical protein | |
| [Os] brown planthopper resistance (TO:0000424) \| momilactone A content (TO:0002670) \| jasmonic acid content (TO:0002668) \| jasmonic acid sensitivity (TO:0000172) \| bacterial blight disease resistance (TO:0000175);<br>[Ta] disease resistance TO:0000112 | Hypothetical conserved gene | GO:00016 |
| | RNA recognition motif domain domain containing p | |
| | Similar to Phytochrome P450-like protein | |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF827, pla | GO:00099 |
| | Sterile alpha motif homology 2 domain containing p | |
| | Similar to H0211B05.8 protein | GO:00712 |
| | Zm00001e021905 | |
| | Conserved hypothetical protein | GO:00101 |
| ["Bd, Os, Sv, Sc"] | Transferase family protein | |
| [Os] panicle length (TO:0000040) \| flower anatomy and morphology trait (TO:0000499) \| gibberellic acid sensitivity (TO:0000166) \| brassinosteroid sensitivity (TO:0002677) \| stem length (TO:0000576) \| plant growth hormone sensitivity (TO:0000401) \| plant height (TO:0000207) \| cold tolerance (TO:0000303) \| leaf lamina color (TO:0000299) \| leaf shape (TO:0000492) \| gibberellic acid content (TO:0002675) \| radiation response trait | | |
| | Similar to Chloroplast outer envelope 24 kD protein | |
| | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Hypothetical conserved gene | GO:00066 |

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|---|---|---|
| [Os] mimic response (TO:0000063) \| blast disease (TO:0000074) \| momilactone A content (TO:0002670) \| bacterial blight disease resistance (TO:0000175); [Os] grain size | Transferase family protein | GO:00069 |
|  | Glycosylphosphatidylinositol-mannosyltr | GO:00065 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| viral disease resistance (TO:0000148) | Similar to RAPB protein | GO:00063 |
|  | Similar to HGA6 | GO:00096 |
| [Os] grain weight (TO:0000590) \| grain yield per plant (TO:0000449) \| osmotic response sensitivity (TO:0000095) \| heat tolerance (TO:0000259) \| drought tolerance (TO:0000276) |  |  |
|  | Armadillo-type fold domain containing p | GO:0007 |
|  | Peptidase C19, ubiquitin carboxyl-termin | GO:00065 |
|  | NUC153 domain containing protein | GO:00063 |
| [Os] stress trait (TO:0000164) \| gibberellic acid sensitivity (TO:0000166) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| heat | DRE-binding protein 1A | GO:00063 |
| [Os] root hair length (TO:0002665); [Os] phenol reaction TO:0000062 | MYB-CC family protein, Pi-starvation sigr | GO:00063 |
|  | Histidine kinase, Cytokinin signalin | GO:00001 |
|  | Las1-like family protein | GO:00004 |
|  | Hypothetical conserved gene | GO:00063 |
|  | Similar to Heat shock transcription factor | GO:00063 |
|  | Similar to Cysteine protease inhibitor | GO:00069 |
|  | Zinc finger, MIZ-type domain containing | GO:00169 |
|  | Acyl-CoA N-acyltransferase domain containing prot |  |

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|---|---|---|
| [Os] inflorescence development trait (TO:0000621) \| brassinosteroid sensitivity (TO:0002677) \| grain size (TO:0000397) \| leaf color (TO:0000326) \| leaf angle (TO:0000206) \| plant height (TO:0000207) \| leaf width (TO:0000370) \| panicle length (TO:0000040) \| seed development trait (TO:0000653) \| grain length (TO:0000734) \| seed length (TO:0000146) \| internode length (TO:0000145); [Os] stay green trait | | |
| | Hypothetical conserved gene | GO:00071 |
| | Osteocrin domain containing protein | |
| [Os] hydrogen peroxide content (TO:0000605) \| abscisic acid sensitivity (TO:0000615) \| root development trait (TO:0000656) | | |
| | Harpin-induced 1 domain containing protein | |
| | Zm00001e130155 | GO:00096 |
| | Conserved hypothetical protein | |
| | Zm00001e036499 | |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Zm00001e016462 | |
| | Similar to Glycosyltransferase | |
| | Similar to Flowering-time protein isofor | GO:00102 |
| | Hypothetical conserved gene | GO:00063 |
| | Conserved hypothetical protein | |
| | | |
| | Transcription initiation factor TFIID comp | GO:00063 |
| | Hypothetical conserved gene | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| [Os] nitrogen sensitivity (TO:0000011) \| heat tolerance (TO:0000259) \| cold tolerance (TO:0000303) \| cytokinin sensitivity (TO:0000167) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) | Octicosapeptide/Phox/Bem1p domain co | GO:00063 |
| | Protein of unknown function DUF677 family protein | |
| | Conserved hypothetical protein | |
| | Homeodomain-like containing protein | GO:00063 |
| | | |
| | Similar to Herbicide safener binding prot | GO:00194 |
| | Zm00001e127856 | GO:00458 |

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|---|---|---|
| [Os] grain yield (TO:0000396) \| grain size (TO:0000397) | Basic helix-loop-helix transcription factor, Regulati | |
| | Zinc finger, HIT-type domain containing | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] panicle size (TO:0006032) \| flowering time (TO:0002616) \| grain number (TO:0002759); [Ta] drought tolerance TO:0000276 | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | Similar to F-box domain containing protein | |
| [Os] panicle type (TO:0000089) \| leaf color (TO:0000326) \| shoot anatomy and morphology trait (TO:0000077) \| mesocotyl length (TO:0000544) \| tillering ability (TO:0000329) \| plant growth hormone sensitivity (TO:0000401) \| leaf length (TO:0000135) \| stem length (TO:0000576) \| plant height (TO:0000207) \| tiller number | Substrate of the SCF<sup>D3</sup> ub | GO:00195 |
| [Os] viral disease resistance (TO:0000148) \| drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) | Similar to Transcriptional activator HAP2 | GO:00063 |
| | Cyclin-like F-box domain containing pro | GO:00165 |
| | Conserved hypothetical protein | |
| [Os] bacterial blight disease resistance (TO:0000175) \| blast disease (TO:0000074) \| brown planthopper resistance (TO:0000424) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615) | | |
| | Hypothetical conserved gene | GO:00094 |
| | Similar to H0211B05.8 protein | GO:00712 |
| | Similar to RGP-3 (Fragment) | |
| | Intron-encoded nuclease 2 domain containing prote | |
| | Similar to Xylanase inhibitor precursor (X | GO:00065 |
| | SET domain containing protein | |
| | Protein of unknown function DUF668 fan | GO:00459 |

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|---|---|---|
| | Similar to H0814G11.17 protein | GO:00066 |
| | Similar to blue copper protein | GO:00229 |
| [Os] drought tolerance TO:0000276 | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| | Similar to shugoshin-1 | GO:00160 |
| | Plant disease resistance response protein | GO:00096 |
| | Auxin responsive SAUR protein domain c | GO:00097 |
| | Domain of unknown function DUF623 do | GO:00458 |
| | Spectrin repeat containing protein | GO:00071 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| [Os] abscisic acid content (TO:0002667) \| salt tolerance (TO:0006001) \| abiotic stress trait (TO:0000168) \| chromium sensitivity (TO:0000034) | Similar to DNA binding protein | GO:00063 |
| [Ta] disease resistance TO:0000112\| heterosis TO:0000355 | MYB transcription factor, Transcriptional activator in | |
| | Protein of unknown function DUF292, eu | GO:00081 |
| | Similar to RNA binding protein | |
| | Lipase, class 3 family protein | GO:00066 |
| | Similar to Zinc finger, C3HC4 type family | GO:00165 |
| | Forkhead-associated domain containing | GO:00007 |
| | Similar to mitochondrial glycoprotein | GO:00701 |
| | Conserved hypothetical protein | GO:00063 |
| | Endoplasmic reticulum (ER) stress sensor | GO:00063 |
| | Transferase family protein | |
| | Similar to Esterase | |
| | Pectin lyase fold domain containing prot | GO:00425 |
| | Similar to Beta-catenin repeat family prot | GO:00165 |
| [Os] brassinosteroid sensitivity (TO:0002677) \| gibberellic acid content (TO:0002675) \| cell elongation trait (TO:0002687) \| grain yield (TO:0000396) \| grain size (TO:0000397) \| brassinosteroid content (TO:0002676) \| days to heading (TO:0000137) \| grain shape (TO:0002730) \| leaf development trait (TO:0000655) \| grain length (TO:0000734) \| leaf angle (TO:0000206); [Os] grain shape | Helix-loop-helix DNA-binding domain c | GO:00063 |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) | Similar to Cellulose synthase (Fragment) | GO:00098 |
| | Conserved hypothetical protein | GO:00099 |
| [Os] bacterial blight disease resistance (TO:0000175) \| leaf color (TO:0000326) \| chlorophyll-b content (TO:0000295) \| photosynthetic rate (TO:0001015) \| hydrogen peroxide content (TO:0000605) \| grain yield (TO:0000396) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| momilactone A content (TO:0002670) \| momilactone B content (TO:0002671) \| blast disease (TO:0000074) \| jasmonic acid content (TO:0002668) \| leaf lamina joint bending (TO:0002688) \| mimic response (TO:0000063) \| chlorophyll-a | Chloroplast-localised putative leucine ca | GO:00301 |
| | S-ribonuclease binding protein, SBP1, po | GO:00165 |
| | Tyrosine protein kinase domain containi | GO:00064 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | bZIP transcription factor, Globulin gene p | GO:00063 |
| | Zm00001e036951 | GO:00701 |
| [Os] cytokinin sensitivity (TO:0000167) \| nitrogen sensitivity (TO:0000011) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) | Octicosapeptide/Phox/Bem1p domain co | GO:00063 |
| | Conserved hypothetical protein | GO:00165 |
| | Nuf2 family protein | GO:00070 |
| | WD40 repeat-like domain containing protein | |
| [Os] days to heading (TO:0000137) | | |
| | Transferase family protein | |
| | Pentatricopeptide repeat domain containing protein | |
| | Plant disease resistance response protein | GO:00096 |
| | Peptidase aspartic, catalytic domain containing prot | |

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|---|---|---|
| | Protein of unknown function DUF23 family protein | |
| | Protein of unknown function DUF2358 dc | GO:00071 |
| | Homeodomain-like containing protein | |
| [Os] grain size (TO:0000397) | Class I formin protein, Regulation of grai | GO:00300 |
| | Conserved hypothetical protein | GO:00517 |
| | Transcriptional factor B3 family protein | |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | EF hand domain containing protein | GO:00068 |
| | Bromodomain containing protein | |
| | Protein of unknown function DUF296 domain contai | |
| | Conserved hypothetical protein | |
| | Serine/threonine protein kinase domain c | GO:00064 |
| [Ta] heat tolerance TO:0000259\| salt tolerance TO:0006001 | Bromodomain containing protein | |
| | Similar to MEE44 (maternal effect embryo | GO:00311 |
| | Conserved hypothetical protein | |
| | Zm00001e023273 | GO:00065 |
| | Pentatricopeptide repeat domain containing protein | |
| | Kelch-type beta propeller domain contai | GO:00094 |
| | Similar to Signal peptidase I family protei | GO:00064 |
| | Lipase, class 3 family protein | GO:00066 |
| | Similar to Maternal pumilio protein. Splic | GO:00064 |
| [Os] radiation response trait (TO:0000161) | Similar to RING-H2 finger protein RHB1a | GO:00165 |
| | Conserved hypothetical protein | |
| | Similar to Ribonucleases P/MRP protein s | GO:00016 |
| [Ta] salt tolerance TO:0006001\| heat tolerance TO:0000259 | Bromodomain domain containing protein | |
| | Nucleolar 27S pre-rRNA processing, Urb | GO:00422 |
| | Conserved hypothetical protein | |
| | Non-protein coding transcript | GO:00000 |

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|---|---|---|
| [Os] grain size (TO:0000397) \| floury endosperm (TO:0000104) \| heat tolerance (TO:0000259) \| endosperm storage protein-1 content (TO:0000107) \| grain weight (TO:0000590) \| seed development trait (TO:0000653) \| endosperm storage protein content (TO:0002653) \| protein content (TO:0000598) \| endosperm storage protein-2 content (TO:0000109) \| starch content (TO:0000696) \| endosperm color (TO:0000487) \| temperature response trait (TO:0000432) \| amylose content (TO:0000196); [Os] tiller angle TO:0000567\| cold tolerance TO:0000303\| drought tolerance TO:0000276\| plant height TO:0000207; | bZIP transcription factor, bZIP-1 domain | GO:00063 |
| | KIP1-like domain containing protein | |
| | Similar to predicted protein | |
| | BRO1 domain containing protein | GO:00433 |
| | Similar to Glutathione S-transferase I (EC | GO:00067 |
| [Os] phyllotaxy (TO:0006014) \| lignin biosynthesis trait (TO:0000733) \| primary branching of inflorescence (TO:0000052) \| grain shattering (TO:0000473) \| secondary branch number (TO:0000557) \| inflorescence development trait (TO:0000621) \| grain number (TO:0002759) \| spikelet number (TO:0000456) \| shoot apical meristem development (TO:0006020) \| inflorescence anatomy and morphology trait (TO:0000373) \| grain yield (TO:0000396) \| primary branch number (TO:0000547) \| secondary branching of inflorescence (TO:0000142); [Os] grain weight TO:0000919 | Similar to Homeodomain protein JUBEL2 | GO:00063 |
| | Similar to myosin-like protein | GO:00301 |
| | Katanin P80 ortholog, Katanin regulatory | GO:00070 |
| | Glycosyl transferase, family 31 protein | GO:00064 |
| | Similar to Phosphate starvation response | GO:00063 |
| | Similar to BZIP-like protein | GO:00063 |

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|---|---|---|
| | Zm00001e041065 | GO:00063 |
| | KIP1-like domain containing protein | GO:00163 |
| | Similar to SAP domain containing protein | GO:00068 |
| | Calcium-binding EF-hand domain containing protei | |
| | Rad21/Rec8 like protein, C-terminal dom | GO:00063 |
| | Similar to Alpha-2,8-sialyltransferase 8B | GO:00064 |
| | Similar to Polyubiquitin-like protein | GO:00002 |
| | Similar to Neuralized protein | |
| | Zm00001e027790 | |
| [Os] drought tolerance (TO:0000276) \| germination rate (TO:0000430) \| heat tolerance (TO:0000259) \| abscisic acid sensitivity (TO:0000615) \| cytokinin sensitivity (TO:0000167) \| salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| blast disease (TO:0000074) | Similar to NIN-like protein 2 (Fragment) | |
| | Similar to microtubule-associated protein TORTIFOL | |
| | Similar to Leucine Rich Repeat family protein, expres | |
| | Alpha/beta hydrolase family protein | |
| [Os] abscisic acid sensitivity (TO:0000615) \| cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) | Similar to Sad1-unc84-like protein | GO:00069 |
| | Conserved hypothetical protein | |
| | Forkhead-associated domain containing protein | |
| | Survival motor neuron interacting protein | GO:00003 |
| | Alpha/beta hydrolase fold-1 domain containing pro | |
| | Similar to MYC1 | GO:00063 |
| | | |
| | Longin domain containing protein | |
| | Mitochodrial transcription termination fa | GO:00063 |

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|---|---|---|
| [Os] hydrogen peroxide content (TO:0000605) \| osmotic response sensitivity (TO:0000095) \| abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| abscisic acid content (TO:0002667) \| oxidative stress (TO:0002657) \| heat tolerance (TO:0000259) | RING finger ubiquitin E3 ligase, Heat tolerance, Mod | |
| | RabGAP/TBC domain containing protein | GO:00068 |
| | Zm00001e030996 | |
| | Similar to ENTH1 protein (Fragment) | GO:00066 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| [Os] blast disease (TO:0000074) \| temperature response trait (TO:0000432) \| cold tolerance (TO:0000303) \| jasmonic acid | Zm00001e005777 | |
| | Transcription elongation factor, TFIIS/CRSP70, N-te | |
| [Os] starch content (TO:0000696) \| breakdown viscosity (TO:0000374) \| hot paste viscosity (TO:0000408) \| peak viscosity (TO:0000409) \| 1000-seed weight (TO:0000382) \| grain thickness (TO:0000399) \| grain length (TO:0000734) \| amylose content (TO:0000196) \| protein content (TO:0000598) \| starch grain size (TO:0002655) \| shrunken endosperm (TO:0000100) \| endosperm related trait (TO:0000575) \| seed development trait (TO:0000653) \| floury endosperm (TO:0000104) \| endosperm color (TO:0000487) | Similar to rf1 protein | |
| | NAD(P)-binding domain containing prote | GO:00066 |
| | IQ calmodulin-binding region domain containing pr | |
| | Transferase family protein | |
| [Os] bacterial blight disease resistance (TO:0000175) \| plant height (TO:0000207) \| blast disease (TO:0000074) | Similar to VOZ transcription factor | GO:00063 |

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|---|---|---|
| | Mitochodrial transcription termination fa | GO:00063 |
| | Auxin responsive SAUR protein family pr | GO:00097 |
| | Mitochondrial glycoprotein family protein | GO:00701 |
| | Zinc finger, C2H2-like domain containing protein | |
| | Annexin repeat, conserved site domain containing p | |
| | Similar to nodulin protein | |
| | Glycosyl transferase, family 14 protein | |
| [Os] osmotic response sensitivity (TO:0000095) \| cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| yield trait (TO:0000371) \| relative yield (TO:0000153) \| relative biomass (TO:0000143) \| osmotic adjustment capacity (TO:0000507) | | |
| | Snf7 family protein | GO:00069 |
| | Conserved hypothetical protein | |
| | Similar to BZIP-like protein | GO:00063 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Adenylate kinase family protein | GO:00061 |
| | Protein prenyltransferase domain contain | GO:00183 |
| | Similar to ATPase, AAA family protein | GO:00062 |
| [Os] root hair length (TO:0002665) \| abiotic stress trait (TO:0000168) | MYB-CC domain containing transcription | GO:00063 |
| | Uncharacterised protein family UPF0057 domain co | |
| [Os] abscisic acid sensitivity (TO:0000615) \| light sensitivity (TO:0000075) | | |
| | Defective in cullin neddylation domain co | GO:00097 |
| | Hypothetical conserved gene | GO:00712 |
| [Os] potassium uptake (TO:0000514) \| salt tolerance (TO:0006001) \| potassium sensitivity (TO:0000008) \| potassium content (TO:0000609) | Similar to Potassium transporter | GO:00068 |

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|---|---|---|
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF1751, ir | GO:00068 |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF1399 family protei | |
| | Similar to ATP binding protein | GO:00163 |
| | Similar to predicted protein | GO:00066 |
| [Ta] oxidative stress TO:0002657 | Similar to Glutathione S-transferase GSTF | GO:00067 |
| [Os] magnesium sensitivity (TO:0000010) | Similar to TATA-binding protein associated factor 2 | |
| [Os] callus induction TO:0000428\| amylose content TO:0000196 | Similar to ER66 protein (Fragment) | GO:00063 |
| | Plant disease resistance response protein | GO:00096 |
| [Os] plant growth hormone sensitivity (TO:0000401) \| nitrogen sensitivity (TO:0000011) \| salt tolerance (TO:0006001) \| root development trait (TO:0000656) \| cytokinin sensitivity (TO:0000167) \| auxin sensitivity (TO:0000163); [Os] tiller number TO:0000346 | Auxin efflux carrier domain containing p | GO:00097 |
| | Zm00001e014562 | GO:00102 |
| [Os] heat tolerance (TO:0000259) \| polysaccharide content (TO:0006007) \| male sterility (TO:0000437) | Endoplasmic reticulum (ER) membrane pr | GO:00064 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to Prep (Fragment) | GO:00063 |
| | Peptidase C12, ubiquitin carboxyl-termin | GO:00003 |
| [Os] viral disease resistance (TO:0000148) \| jasmonic acid sensitivity (TO:0000172); [Os] drought tolerance TO:0000276 | Similar to NF-YA subunit | GO:00063 |
| | Zinc finger, PHD-type domain containing | GO:00459 |
| | Conserved hypothetical protein | |
| | Zm00001e029838 | GO:00063 |
| | KIP1-like domain containing protein | GO:00163 |
| | Similar to structural constituent of riboso | GO:00064 |
| | bZIP transcription factor, bZIP-1 domain | GO:00063 |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| [Ta] seed coat color TO:0000190\| seed dormancy TO:0000253 | MYB transcription factor, Regulation of c | GO:00301 |
| | Hypothetical conserved gene | GO:00065 |

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|---|---|---|
| | Cupredoxin domain containing protein | |
| | Similar to PPR repeat domain containing protein | |
| [Os] relative chlorophyll content (TO:0001016) \| salt tolerance (TO:0006001) | | |
| | Similar to Senescence-associated protein 12 | |
| | Similar to XPG I-region family protein, ex | GO:00062 |
| | Similar to Non-specific lipid-transfer pro | GO:00068 |
| | Cupredoxin domain containing protein | |
| | Similar to F5D14.6 protein | GO:00466 |
| [Os] tiller number TO:0000346\| plant height TO:0000207 | | |
| | Protein of unknown function DUF1604 d | GO:00063 |
| [Os] brown planthopper resistance (TO:0000424) \| oxygen sensitivity (TO:0000015) \| ethylene sensitivity (TO:0000173) | Leucine-rich repeat, cysteine-containing | GO:00065 |
| [Os] cold tolerance (TO:0000303) \| temperature response trait (TO:0000432) | Circadian-associated rice pseudo respon | GO:00001 |
| [Os] drought tolerance (TO:0000276) \| panicle length (TO:0000040) \| filled grain number (TO:0000447) \| relative yield (TO:0000153) \| nitrogen sensitivity (TO:0000011) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| yield trait (TO:0000371) \| plant height (TO:0000207) | LATERAL ORGAN BOUNDARIES DOMAIN ( | GO:00104 |
| [Os] heat tolerance (TO:0000259) \| spikelet fertility (TO:0000180) \| starch content (TO:0000696) \| seed quality (TO:0000162); [Os] starch content TO:0000696\| floury endosperm TO:0000104 | CBM48 domain-containing protein, Com | GO:00105 |
| | Uncharacterised protein family UPF0136, | GO:00159 |
| | Hypothetical conserved gene | |
| | Cyclin D domain containing protein | GO:00000 |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Eukaryotic translation initiation factor 4B | GO:00064 |

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|---|---|---|
| | Serine/threonine protein kinase domain c | GO:00001 |
| [Os] abiotic stress trait (TO:0000168) \| drought tolerance (TO:0000276) \| internode length (TO:0000145) \| flowering time (TO:0002616) \| temperature response trait (TO:0000432) \| stress trait | Phytochrome-interacting factor-like bHL | GO:00063 |
| | Ribonuclease P/MRP, subunit p29 domai | GO:00016 |
| | Serine/threonine protein kinase domain c | GO:00064 |
| | Plant disease resistance response protein | GO:00096 |
| [Os] blast disease (TO:0000074) \| hydrogen peroxide content (TO:0000605) \| salt tolerance (TO:0006001); [Os] salt tolerance TO:0006001 | | |
| | Serine/threonine protein kinase-related c | GO:00064 |
| | Armadillo-like helical domain containing | GO:00165 |
| | Similar to predicted protein | GO:00064 |
| | Major facilitator superfamily, general substrate trans | |
| | Similar to Myosin-like protein | GO:00301 |
| [Os] abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| white-backed planthopper resistance (TO:0000205) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) \| bacterial blight disease resistance (TO:0000175) \| salt tolerance (TO:0006001) | PAMP (pathogen-associated molecular pa | GO:00063 |
| | Hypothetical conserved gene | |
| [Os] temperature response trait (TO:0000432) \| blast disease (TO:0000074) \| stress trait (TO:0000164) | Dof transcription facto | GO:00063 |
| | Single-stranded nucleic acid binding R3H domain c | |
| | WW/Rsp5/WWP domain containing protein | |
| | Similar to Homeobox-leucine zipper prot | GO:00063 |
| | Kinesin, motor region domain containing | GO:00070 |

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|---|---|---|
| | Glycosyl transferase, family 8 domain containing pr | |
| | Actin-binding FH2 domain containing pr | GO:00300 |
| | Hypothetical conserved gene | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| [Os] grain yield per plant (TO:0000449) | Spen (Split ends)-like protein, Vegetative | GO:00063 |
| | Similar to harpin-induced protein | |
| [Os] jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615) \| viral disease resistance (TO:0000148) | Similar to Nuclear transcription factor Y s | GO:00063 |
| [Os] submergence tolerance (TO:0000524) \| abiotic stress trait (TO:0000168); [Os] disease resistance TO:0000112 | Similar to Heat stress transcription factor | GO:00063 |
| | Similar to pherophorin like protein | GO:00096 |
| | Similar to Auxin-induced protein IAA4 | GO:00063 |
| [Os] mimic response (TO:0000063) \| plant height (TO:0000207) \| disease resistance (TO:0000112) \| stem strength (TO:0000051); [Os] adventitious root length TO:0020103\| stem diameter TO:0020083\| carbon isotope discrimination TO:0002643\| adventitious root number TO:0001006\| root length TO:0000227\| root number | MLG (mixed-linkage glucan) synthase, B | GO:00098 |
| | Prefoldin domain containing protein | GO:00001 |
| | DOMON related domain containing prote | GO:00551 |
| | Conserved hypothetical protein | GO:00104 |
| [Os] seed set percent (TO:0000455) \| male sterility (TO:0000437) \| tiller number (TO:0000346) \| pollen fertility (TO:0000421) \| pollen abortion type (TO:0000218) \| anther length (TO:0000531) \| anther color (TO:0000187) \| starch content (TO:0000696) \| sterility or fertility trait (TO:0000392) | Protein kinase, catalytic domain domain | GO:00022 |
| | Harpin-induced 1 domain containing protein | |
| [Ta] stem elongation TO:0006036\| drought tolerance TO:0000276 | Helix-loop-helix DNA-binding domain c | GO:00063 |

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|---|---|---|
| | Nucleotide-binding, alpha-beta plait don | GO:00164 |
| | Hypothetical conserved gene | GO:00512 |
| [Os] germination rate (TO:0000430) \| salt sensitivity (TO:0000429) \| fertility related trait (TO:0000420) \| drought tolerance (TO:0000276) \| germinability at low temperature (TO:0000483) \| pollen sterility (TO:0000053) \| plant growth hormone sensitivity (TO:0000401) \| cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| seed dormancy (TO:0000253) \| auxin sensitivity (TO:0000163) \| hydrogen peroxide content (TO:0000605) \| jasmonic acid sensitivity (TO:0000172); [Os] oxidative | bZIP transcription factor, Stress response | GO:00063 |
| | F-box protein, Mediation of bouquet forr | GO:00614 |
| | Conserved hypothetical protein | |
| | EF hand domain containing protein | |
| | Similar to outward rectifying potassium c | GO:00303 |
| | Iron(III)-deoxymugineic acid transporter, | GO:00356 |
| [Os] bacterial blight disease resistance (TO:0000175) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| cold tolerance (TO:0000303) | Cinnamoyl-CoA reductase-like gene fam | GO:00066 |
| [Os] ethylene sensitivity (TO:0000173) | Lipase, GDSL domain containing protein | |
| | Similar to Superoxide dismutase [Fe], chl | GO:00068 |
| | Similar to protein kinase | GO:00064 |
| | Hypothetical conserved gene | GO:00165 |
| | Phytosulfokine family protein | GO:00071 |
| | Transcriptional coactivator SAGA-type co | GO:00063 |
| | Similar to RING-H2 finger protein ATL1B | GO:00165 |
| | Zm00001e006454 | |
| | Armadillo-like helical domain containing | GO:00064 |
| | Similar to low temperature viability protei | GO:00000 |
| | PRC-barrel domain containing protein | GO:00063 |

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|---|---|---|
| | Protein of unknown function DUF231, pla | GO:19909 |
| | Similar to beta3-glucuronyltransferase | GO:00098 |
| | Coactivator CBP, KIX domain containing | GO:00063 |
| | GrpE protein homolog | GO:00064 |
| | GC-rich sequence DNA-binding factor-li | GO:00001 |
| [Os] bacterial blight disease resistance (TO:0000175) \| seed maturation (TO:0002661) \| leaf senescence (TO:0000249) \| endosperm related trait (TO:0000575) \| aborted uni-nucleate stage (TO:0000060) \| leaf area (TO:0000540) \| spikelet fertility (TO:0000180) \| salt tolerance (TO:0006001) \| yield trait (TO:0000371) \| starch content (TO:0000696); [Os] plant height TO:0000207\| disease resistance TO:0000112\| panicle length | Similar to MtN3-like protein | GO:00068 |
| | Tetratricopeptide-like helical domain containing pro | |
| | LsmAD domain domain containing protei | GO:00106 |
| [Os] drought tolerance (TO:0000276) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| submergence tolerance (TO:0000524) \| bacterial blight disease resistance (TO:0000175); [Os] plant height TO:0000207 | WRKY transcription factor 10 | GO:00063 |
| | Hypothetical conserved gene | GO:00156 |
| | Hypothetical conserved gene | |
| | Conserved hypothetical protein | |
| | Tetratricopeptide region domain containi | GO:00063 |
| | Cytochrome b561 family protein | |
| | DNA polymerase V family protein | GO:00063 |

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|---|---|---|
| [Os] gibberellic acid content (TO:0002675) \| panicle length (TO:0000040) \| grain length (TO:0000734) \| inflorescence exsertion (TO:0001002) \| grain size (TO:0000397) \| plant height (TO:0000207) \| stem length (TO:0000576) \| salt tolerance (TO:0006001) \| internode length (TO:0000145) \| 1000-seed weight (TO:0000382) \| inflorescence development trait (TO:0000621) \| iron sensitivity (TO:0000224) \| flag leaf angle (TO:0000124); [Os] plant height | Cytochrome P450 monooxygenase, Gibb | GO:00454 |
| [Os] disease resistance TO:0000112 | Similar to Scarecrow-like 9 (Fragment) | GO:00063 |
| | Zm00001e031127 | |
| | Protein of unknown function DUF1068 family protei | |
| [Os] grain size (TO:0000397) \| plant height (TO:0000207) \| leaf lamina joint bending (TO:0002688) \| cell elongation trait (TO:0002687) \| brassinosteroid sensitivity (TO:0002677) \| leaf angle (TO:0000206) | Basic helix-loop-helix (bHLH) transcripti | GO:00063 |
| | Hypothetical conserved gene | |
| [Os] viral disease resistance (TO:0000148) \| jasmonic acid sensitivity (TO:0000172) | Similar to Nf-Y-A subunit | GO:00063 |
| | Similar to 50S ribosomal protein L31 | GO:00064 |
| | Ubiquitin domain containing protein | GO:00304 |
| | Conserved hypothetical protein | GO:00435 |
| | Zm00001e000301 | GO:00094 |
| | Similar to secretory protein-like | |
| [Os] lignin biosynthesis trait (TO:0000733) | Transferase family protein | |
| | Similar to RNA binding protein | GO:00314 |

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|---|---|---|
| | Myb, DNA-binding domain containing pr | GO:0073 |
| | Similar to RING finger family protein | GO:0016 |
| | Conserved hypothetical protein | GO:0030 |
| | Similar to SNF1-related protein kinase re | GO:0016 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Hypothetical conserved gene | GO:0045 |
| | Pentatricopeptide repeat domain containing protein | |
| | Hypothetical conserved gene | GO:0006 |
| [Os] oxidative stress TO:0002657 | U-box/ARM repeat E3 ligase, Stress resp | GO:0016 |
| | Similar to Kinesin heavy chain (Fragment) | GO:0007 |
| [Os] salt tolerance (TO:0006001) \| growth hormone content (TO:0000476) \| tillering ability (TO:0000329) \| bacterial blight disease resistance (TO:0000175) \| abscisic acid sensitivity | GRAS-domain transcription factor, Strigo | GO:0006 |
| | Disease resistance/zinc finger/chromosome conden | |
| | Conserved hypothetical protein | |
| | Similar to EIL3 | GO:0006 |
| | Similar to T-cell activation protein phosphatase 2C- | |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) | | |
| | Cyclin-like F-box domain containing pro | GO:0000 |
| [Os] seed maturation (TO:0002661) \| grain width (TO:0000402) \| grain size (TO:0000397) \| grain shape (TO:0002730) \| grain length (TO:0000734) \| grain length to width ratio (TO:0002731) \| grain yield (TO:0000396) \| seed quality | Transcription factor, Positive regulator of cell prolife | |
| | Sporulation stage II, protein E C-terminal domain co | |
| | Immunoglobulin-like domain containing protein | |
| [Os] blast disease (TO:0000074) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| filled grain number (TO:0000447) \| ethylene sensitivity (TO:0000173) | Member of the CONSTANS-like (COL) fam | GO:0006 |
| | Hypothetical conserved gene | |

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|---|---|---|
| | Similar to Small heat stress protein class | GO:00003 |
| | C2H2 transcription factor, Leaf developm | GO:00063 |
| | Conserved hypothetical protein | |
| | Similar to STF-1 (Fragment) | GO:00519 |
| [Os] cold tolerance (TO:0000303) \| grain yield (TO:0000396) \| root anatomy and morphology trait (TO:0000043) \| nitrogen sensitivity (TO:0000011) \| heat tolerance (TO:0000259) \| iron sensitivity (TO:0000224) \| tiller number (TO:0000346) \| bacterial blight disease | WRKY transcription factor, Tolerance to p | GO:00063 |
| [Os] male sterility TO:0000437\| leaf angle TO:0000206\| flag leaf angle | FAS1 domain domain containing protein | |
| | Nucleotide-diphospho-sugar transferase domain co | |
| | Chaperonin Cpn60/TCP-1 family protein | GO:00163 |
| | Conserved hypothetical protein | |
| [Os] grain weight (TO:0000590) \| grain length (TO:0000734) | | |
| | Similar to VHS1 protein (Fragment) | GO:00068 |
| [Os] lignin biosynthesis trait (TO:0000733) | Transferase family protein | |
| | t-snare domain containing protein | |
| [Os] drought tolerance (TO:0000276) | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | Tetratricopeptide-like helical domain con | GO:00064 |
| | Similar to TIS11 protein (dTIS11) | GO:00611 |
| | Conserved hypothetical protein | |
| | Aminoglycoside phosphotransferase dom | GO:00064 |
| | S1, RNA binding domain containing prote | GO:00343 |
| | Pentatricopeptide repeat domain containing protein | |
| | Photosystem II oxygen evolving complex | GO:00097 |
| | Rop nucleotide exchanger, PRONE domai | GO:00507 |

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|---|---|---|
| [Os] root length (TO:0000227) \| plant height (TO:0000207) \| salt tolerance (TO:0006001) \| stomatal frequency (TO:0000566) \| root development trait (TO:0000656) \| gibberellic acid sensitivity (TO:0000166) \| root meristem development (TO:0002692) \| sheath blight disease resistance (TO:0000255) \| tillering ability (TO:0000329) \| abscisic acid sensitivity (TO:0000615); [Os] leaf area index | SHR transcription factor, Formation of ro | GO:00063 |
| | Hypothetical conserved gene | GO:00068 |
| | Hypothetical conserved gene | GO:00063 |
| | Protein of unknown function DUF632 do | GO:00712 |
| | Hypothetical conserved gene | GO:00064 |
| | Similar to MCB2 protein | |
| [Os] tiller number (TO:0000346) \| plant height (TO:0000207) | Putative protease inhibitor I family protei | GO:00096 |
| | Mitochondrial distribution and morpholo | GO:00453 |
| | Zinc finger, TRAF-type domain containing protein | |
| [Os] salt tolerance (TO:0006001) | Ankyrin domain containing protein | GO:00063 |
| | Conserved hypothetical protein | GO:00004 |
| | Similar to ADL064Wp | GO:00165 |
| | Peptidase S26A, signal peptidase I family | GO:00064 |
| | Similar to NDR1/HIN1-Like protein 2 | |
| | WD40 repeat-like domain containing pro | GO:00000 |
| | Zm00001e024679 | GO:00094 |
| | Zm00001e015771 | GO:00300 |
| | IQ calmodulin-binding region domain containing pr | |
| | Hypothetical conserved gene | |
| [Os] drought tolerance (TO:0000276) | Armadillo-like helical domain containing | GO:00165 |
| | EF-Hand type domain containing protein | GO:00197 |
| | Hypothetical conserved gene | GO:00002 |

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|---|---|---|
| [Os] relative chlorophyll content (TO:0001016) \| drought tolerance (TO:0000276) \| iron sensitivity (TO:0000224) \| leaf color (TO:0000326) \| nitrogen sensitivity (TO:0000011) \| grain yield (TO:0000396) \| chlorophyll content (TO:0000495) \| plant height (TO:0000207) \| salt tolerance (TO:0006001) \| leaf senescence (TO:0000249) \| days to heading (TO:0000137) \| cold tolerance (TO:0000303) \| heat tolerance (TO:0000259) \| auxin sensitivity (TO:0000163) \| abscisic acid sensitivity (TO:0000615) \| gibberellic acid sensitivity (TO:0000166) \| relative water content (TO:0000136) \| hydrogen peroxide content (TO:0000605) | NAC transcription factor, Positive regulat | GO:00063 |
| | Phosphorylated adapter RNA export prot | GO:00064 |
| | Homeodomain-like containing protein | GO:00022 |
| [Os] seed development trait (TO:0000653) \| tiller number (TO:0000346) \| grain number (TO:0002759) \| leaf length (TO:0000135) \| gibberellic acid sensitivity (TO:0000166) \| grain yield (TO:0000396) \| anatomy and morphology related trait (TO:0000017) \| gibberellic acid content (TO:0002675) \| total soluble sugar content (TO:0000340) \| biotic stress trait (TO:0000179) \| leaf sheath length (TO:0002689) \| inflorescence development trait (TO:0000621) \| cold tolerance (TO:0000303) \| growth and development trait (TO:0000357) \| blast disease (TO:0000074) \| primary branch number (TO:0000547) \| inflorescence branching (TO:0000050) \| panicle number (TO:0000152) \| seed set percent (TO:0000455) \| bacterial blight disease resistance (TO:0000175) \| filled grain number (TO:0000447) \| tillering ability (TO:0000329) \| nitrogen | Squamosa promter-binding-like transcri | GO:00458 |
| | Tyrosyl-DNA phosphodiesterase family p | GO:00000 |

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|---|---|---|
| | Transcriptional factor B3 family protein | GO:00063 |
| | Similar to Helix-loop-helix DNA-binding | GO:00063 |
| | Mitochondrial import inner membrane tr | GO:00450 |
| | Zinc finger, FYVE-type domain containing protein | |
| | Similar to Zinc finger, C3HC4 type family protein, ex | |
| | Similar to OSIGBa0142I02-OSIGBa0101B | GO:00069 |
| [Os] oxidative stress TO:0002657 | Serine/threonine protein kinase-related | GO:00064 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Protein kinase, core domain containing p | GO:00064 |
| | Protein of unknown function DUF594 domain contai | |
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| [Os] grain weight TO:0000919 | Armadillo-type fold domain containing p | GO:00067 |
| [Os] inflorescence branching (TO:0000050) \| growth and development trait (TO:0000357) \| tiller number (TO:0000346) \| inflorescence development trait (TO:0000621) \| tillering ability (TO:0000329) | Similar to Squamosa-promoter binding protein 2 | |
| [Os] gibberellic acid sensitivity (TO:0000166) \| drought tolerance (TO:0000276) \| tiller angle (TO:0000567) \| gravity response trait (TO:0002693) \| plant growth hormone sensitivity (TO:0000401) \| cold tolerance (TO:0000303) \| auxin sensitivity (TO:0000163) \| embryo development trait (TO:0000620) \| cytokinin sensitivity (TO:0000167); [Os] root meristem development | Similar to WUSCHEL-related homeobox 6 | GO:00063 |
| | WD40/YVTN repeat-like domain containi | GO:00515 |
| | | |
| [Os] inflorescence development trait (TO:0000621); [Os] leaf color TO:0000326 | Transcription factor, DNA-binding interm | GO:00072 |
| | Zm00001e019396 | GO:00004 |
| | | |
| [Bd] | Transferase family protein | |
| | Zm00001e024448 | GO:00310 |
| | Protein of unknown function DUF604 family protein | |
| | Shikimate kinase domain containing prot | GO:00096 |
| | Similar to peptide-N4-asparagine amidase A | |

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|---|---|---|
| | Alpha/beta hydrolase fold-1 domain containing pro | |
| | SAC3/GANP family protein | |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Similar to Pre-rRNA-processing protein T | GO:00004 |
| | Heat shock protein DnaJ, N-terminal domain contai | |
| | | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | SET domain containing protein | |
| | Pentatricopeptide repeat domain containing protein | |
| | Protein kinase, core domain containing p | GO:00064 |
| | WD40 repeat domain containing protein | GO:00171 |
| | Hypothetical conserved gene | GO:00003 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to protein ABIL1 | |
| | Myb, DNA-binding domain containing pr | GO:00063 |
| | K Homology, type 1, subgroup domain c | GO:00069 |
| | EPS15 homology (EH) domain containing | GO:00068 |
| | | |
| | Pentatricopeptide repeat domain containi | GO:00064 |
| | Serine-threonine/tyrosine-protein kinase | GO:00064 |
| | Similar to predicted protein | GO:00165 |
| | Hypothetical conserved gene | GO:00068 |
| | Heat shock protein DnaJ, N-terminal dom | GO:00064 |
| | Armadillo-like helical domain containing | GO:00064 |
| | Similar to protein binding protein | |
| [Os] flower number (TO:0002736) \| days to heading (TO:0000137) \| spikelet fertility (TO:0000180) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| chlorophyll content (TO:0000495) \| leaf senescence (TO:0000249) \| grain number (TO:0002759) \| blast disease (TO:0000074) \| flag leaf length (TO:0002757) \| bacterial disease resistance (TO:0000315) \| grain weight (TO:0000590) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| viral disease resistance (TO:0000148) \| flowering time (TO:0002616) \| root length | Jasmonate ZIM-domain protein, Jasmona | GO:00069 |
| | Zm00001e004563 | |
| | Zm00001e158406 | |
| | | |
| | Similar to Expansin-B7 | GO:00096 |

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|---|---|---|
| [Os] nitrogen sensitivity (TO:0000011) \| auxin sensitivity (TO:0000163) \| lateral root number (TO:0001013) \| lateral root length (TO:0001012) \| copper sensitivity (TO:0000021) \| shoot development trait (TO:0000654) \| jasmonic acid sensitivity (TO:0000172) | High-affinity nitrate transporter, Nitrate t | GO:0015 |
| | Transferase family protein | |
| | | |
| | Conserved hypothetical protein | |
| | Conserved hypothetical protein | GO:0010 |
| | Protein of unknown function DUF408 fam | GO:0030 |
| | Similar to Ythdf2-prov protein | GO:0061 |
| | Similar to VHS and GAT domain protein | GO:0006 |
| | Kinesin, motor region domain containing | GO:0007 |
| | Similar to Zinc finger, DHHC domain cont | GO:0006 |
| | DNA/RNA helicase, DEAD/DEAH box type, N-termin | |
| [Ta] grain number TO:0002759 | Hypothetical conserved gene | GO:0007 |
| | Similar to Zinc finger, C2H2-type | |
| | Similar to IQD1 | |
| | Harpin-induced 1 domain containing pro | GO:0098 |
| | Similar to AP2 domain containing protein | GO:0006 |
| | Similar to Histone H1 | GO:0006 |
| [Os] abscisic acid sensitivity (TO:0000615) \| osmotic response sensitivity (TO:0000095) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) \| brown planthopper resistance (TO:0000424) \| bacterial blight disease resistance (TO:0000175); [Os] drought tolerance TO:0000276\| drought sensitivity | | |

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|---|---|---|
| [Os] growth and development trait (TO:0000357) \| grain size (TO:0000397) \| tiller number (TO:0000346) \| brassinosteroid sensitivity (TO:0002677) \| plant height (TO:0000207) \| stem length (TO:0000576) \| leaf angle (TO:0000206) \| brassinosteroid content (TO:0002676) \| seedling height (TO:0000019) \| root length (TO:0000227) \| inflorescence development trait (TO:0000621) \| leaf color (TO:0000326) \| plant cell size (TO:0002684) \| stamen size (TO:0002601) \| pistil size (TO:0002602) \| leaf lamina joint bending (TO:0002688) \| nitrogen sensitivity (TO:0000011) \| internode length (TO:0000145) \| tillering ability (TO:0000329) \| seed size (TO:0000391) \| flowering time (TO:0002616) \| leaf size (TO:0002637) \| stem width (TO:0001035) \| panicle length | GAI-RGA-SCR (GRAS) family protein, Bras | GO:00073 |
| [Os] abscisic acid sensitivity (TO:0000615) \| root length (TO:0000227) \| plant height (TO:0000207) \| root development trait (TO:0000656) \| hydrogen peroxide content (TO:0000605); [Os] male | Similar to Annexin-like protein RJ4 | GO:00094 |
| [Os] plant height (TO:0000207) \| jasmonic acid sensitivity (TO:0000172) \| chlorophyll content (TO:0000495) \| viral disease resistance (TO:0000148) \| photosynthetic ability (TO:0000316) \| panicle number (TO:0000152) \| filled grain number (TO:0000447) \| spikelet fertility (TO:0000180) \| root length (TO:0000227) \| leaf senescence (TO:0000249) \| abscisic acid sensitivity (TO:0000615) \| abscisic acid content (TO:0002667) \| light intensity sensitivity (TO:0000460) \| ethylene sensitivity (TO:0000173) \| leaf color | NAC-domain protein, Resistance to rice c | GO:00063 |
| | KRR1 interacting protein 1 domain contai | GO:00004 |

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|---|---|---|
| [Os] fungal disease resistance (TO:0000439) \| temperature response trait (TO:0000432) \| disease resistance (TO:0000112) \| jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074) \| lateral root number (TO:0001013) | Peptidoglycan-binding Lysin subgroup d | GO:00069 |
| | Similar to TRAF-type zinc finger family protein | |
| | Tetratricopeptide-like helical domain containing pr | |
| | GPCR, family 3, metabotropic glutamate receptor-li | |
| [Os] viral disease resistance (TO:0000148) \| black streak dwarf virus resistance (TO:0000020) \| rice ragged stunt virus resistance (TO:0000386); [Os] salt tolerance TO:0006001\| drought tolerance TO:0000276\| days to heading TO:0000137 | Tetratricopeptide-like helical domain containing pr | |
| [Os] flag leaf angle (TO:0000124) \| yield trait (TO:0000371) \| leaf development trait (TO:0000655) \| inflorescence development trait (TO:0000621) \| meristem identity (TO:0006017) \| leaf angle (TO:0000206) \| awn length (TO:0000072) \| flower anatomy and morphology trait (TO:0000499) \| vascular bundle number (TO:0000472) \| awn anatomy and morphology trait (TO:0002718); [Ta] plant height TO:0000207 | Putative transcription factor, Carpel speci | GO:00072 |
| | Similar to p21Cip1-binding protein-relat | GO:00000 |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) | Chloroplast group IIA intron splicing fact | GO:00003 |
| [Os] spikelet fertility (TO:0000180) \| pollen fertility (TO:0000421) \| sterility related trait (TO:0000485) | Hypothetical conserved gene | GO:00065 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |

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|---|---|---|
| | Clathrin, heavy chain/VPS, 7-fold repeat | GO:00066 |
| | Conserved hypothetical protein | GO:00004 |
| [Os] inflorescence development trait (TO:0000621) \| panicle size (TO:0006032) | H3K4-specific demethylase, JmjC domai | GO:00063 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Ribosomal protein L18/L5 domain contai | GO:00064 |
| | Similar to GRAS family transcription facto | GO:00063 |
| | Conserved hypothetical protein | GO:00095 |
| | DOMON domain containing protein | GO:00551 |
| | Zm00001e033476 | |
| | DREPP plasma membrane polypeptide family protei | |
| [Os] cold tolerance (TO:0000303) | Hypothetical conserved gene | GO:00065 |
| | Di-trans-poly-cis-decaprenylcistransfera | GO:00160 |
| | Conserved hypothetical protein | GO:00064 |
| [Ta] root dry weight TO:0000078\| shoot dry weight TO:0000552\| water use efficiency TO:0001017\| root length TO:0000227 | Zm00001e019639 | GO:00062 |
| | Similar to Peptidase | GO:00164 |
| | Similar to DnAJ-like protein slr0093 | |
| [Os] radiation response trait (TO:0000161) \| jasmonic acid sensitivity (TO:0000172) | UDP-glucuronosyl/UDP-glucosyltransfera | GO:00096 |
| [Os] flower development trait (TO:0000622) \| sterile lemma length (TO:0000240) \| floral organ development trait (TO:0006022) | H3K9 demethylase, Floral organ develop | GO:00458 |
| | Similar to Sigma factor SIG2B | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Conserved hypothetical protein | GO:00096 |
| [Os] pesticide sensitivity (TO:0002649) | Glycosyltransferase AER61, uncharacterized domain | |

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|---|---|---|
| [Os] grain number (TO:0002759) \| cytokinin content (TO:0002660) \| awn length (TO:0000072) \| spikelet number (TO:0000456) \| grain length (TO:0000734) \| grain size (TO:0000397) \| seed size (TO:0000391) \| filled grain number (TO:0000447) \| primary branch number (TO:0000547) \| panicle size (TO:0006032) \| seed development trait (TO:0000653) \| secondary branch number (TO:0000557) \| grain weight (TO:0000590) \| seed weight | Mitogen-activated protein kinase (MAPK) | GO:00064 |
| | Similar to Expansin-B12 | GO:00096 |
| | Hypothetical conserved gene | |
| | Glycolipid transfer protein domain domai | GO:00356 |
| [Os] disease resistance TO:0000112 | | |
| | Hypothetical conserved gene | GO:00070 |
| | Pentatricopeptide repeat domain containi | GO:00003 |
| | Tetratricopeptide-like helical domain con | GO:00063 |
| | Rop nucleotide exchanger, PRONE domai | GO:00507 |
| | Zinc finger, B-box domain containing prc | GO:00063 |
| [Zm] | Beta-expansin precursor | GO:00096 |
| | Mediator complex, subunit Med17 domai | GO:00063 |
| | Similar to Cyclin-P3-1 | GO:00000 |
| | Conserved hypothetical protein | GO:00159 |
| | Plant lipid transfer protein/seed storage/ | GO:00096 |
| | Transcriptional factor B3 family protein | |
| | Ribosomal protein L1 family protein | GO:00004 |
| | SAM dependent carboxyl methyltransfera | GO:00322 |
| | Tyrosine protein kinase domain containir | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] bacterial blight disease resistance (TO:0000175) \| embryo development trait (TO:0000620) \| seed development trait (TO:0000653) | Similar to WERKY protein (Fragment) | GO:00063 |
| | Tetratricopeptide-like helical domain containing prc | |
| | Ankyrin repeat containing protein | |
| | Conserved hypothetical protein | GO:00311 |

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|---|---|---|
| [Os] leaf color (TO:0000326) \| chloroplast development trait (TO:0002715) | Pentatricopeptide repeat protein, Regulat | GO:00427 |
| | WD40 repeat-like domain containing protein | |
| | Protein of unknown function DUF668 fam | GO:00459 |
| | Protein of unknown function DUF1666 fa | GO:00064 |
| | Acyl-CoA N-acyltransferase domain containing prot | |
| | Similar to Avr9/Cf-9 rapidly elicited prote | GO:00066 |
| [Os] salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| flowering time (TO:0002616) \| bacterial disease resistance (TO:0000315) \| spikelet anatomy and morphology trait (TO:0000657) \| panicle length (TO:0000040) \| flower number (TO:0002736) \| glume number (TO:0006029) \| days to heading (TO:0000137) \| seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| spikelet fertility (TO:0000180) \| plant height (TO:0000207) \| carpel number (TO:0006013) \| seed width (TO:0000149) \| seed weight (TO:0000181) \| seed size (TO:0000391) \| floral organ number (TO:0006038) \| lodicule number (TO:0006010) \| stem length (TO:0000576) \| grain size (TO:0000397) \| grain weight (TO:0000590) \| jasmonic acid content (TO:0002668) \| stamen anatomy and morphology trait (TO:0000215) \| grain yield (TO:0000396) \| panicle size (TO:0006032) \| filled grain number (TO:0000447) \| grain yield per panicle (TO:0000450) \| grain yield per plant (TO:0000449) \| brown planthopper | Tify domain containing protein | GO:00096 |
| | Peptidase A1 domain containing protein | GO:00065 |

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|---|---|---|
| [Os] gravity response trait (TO:0002693) \| meristem identity (TO:0006017) \| cytokinin sensitivity (TO:0000167) \| root length (TO:0000227) \| drought tolerance (TO:0000276) \| herbicide sensitivity (TO:0000058) \| grain yield (TO:0000396) \| embryo development trait (TO:0000620) \| plant height (TO:0000207) \| osmotic response sensitivity (TO:0000095) \| seed size (TO:0000391) \| grain length (TO:0000734) \| root meristem development (TO:0002692) \| auxin sensitivity (TO:0000163) \| salt tolerance | WD40/YVTN repeat-like domain containi | GO:00304 |
| [Os] grain yield (TO:0000396) \| grain yield per plant (TO:0000449) \| plant height (TO:0000207) \| grain size (TO:0000397) \| gibberellic acid sensitivity (TO:0000166)<br>[Os] grain number (TO:0002759) \| inflorescence branching (TO:0000050) \| grain yield (TO:0000396); [Os] grain shape TO:0002730 | Patatin-related phospholipase A, Regulat | GO:00066 |
| | Ankyrin repeat containing protein | GO:20007 |
| | Conserved hypothetical protein | |
| [Os] cytokinin sensitivity (TO:0000167) \| blast disease (TO:0000074) | Kelch-type beta propeller domain contai | GO:00800 |
| | Similar to Pentatricopeptide repeat protei | GO:00094 |
| | Similar to Protein Brevis radix-like 4 | |
| | Replication protein A 30kDa | GO:00007 |
| | IQ calmodulin-binding region domain containing pr | |
| | Tetratricopeptide-like helical domain containing pr | |
| | Zm00001e039699 | |
| | Xyloglucan fucosyltransferase family prot | GO:00099 |
| | MAP65/ASE1 family protein | GO:00002 |
| | Similar to B0403H10-OSIGBa0105A11.22 | GO:00064 |
| | Tetratricopeptide-like helical domain containing pr | |

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|---|---|---|
| [Os] leaf color (TO:0000326) \| photosynthetic ability (TO:0000316) \| carotenoid content (TO:0000496) \| chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| days to heading (TO:0000137) \| filled grain number (TO:0000447) \| panicle length (TO:0000040) \| leaf senescence (TO:0000249) \| temperature response trait (TO:0000432) \| hydrogen peroxide content (TO:0000605) \| plant height (TO:0000207) \| tiller number (TO:0000346) \| chlorophyll content (TO:0000495) \| chloroplast development trait (TO:0002715); [Os] carbon content TO:0000466 | Chloroplast signal recognition particle 43 | GO:00096 |
| | Nucleic acid-binding, OB-fold-like doma | GO:00062 |
| | YY1 protein precursor | GO:00066 |
| | Similar to Protein ABIL1 | |
| | Similar to Protein ABIL1 | |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Protein of unknown function DUF966 far | GO:00512 |
| | Zm00001e006049 | GO:00097 |
| | Zinc finger, RING/FYVE/PHD-type domair | GO:00072 |
| | Leucine-rich repeat, cysteine-containing | GO:00065 |
| | Similar to Protein serine/threonine kinase | GO:00094 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| [Os] chlorophyll ratio (TO:0000298) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| cold tolerance (TO:0000303) \| carotenoid content (TO:0000496) \| chloroplast development trait (TO:0002715) \| leaf development trait (TO:0000655) \| photosynthetic ability (TO:0000316) \| lutein content (TO:0002701) \| chlorophyll content | Chaperone-like protein of protochlorophyllide oxido | |
| | Histone acetyltransferase type B, catalytic | GO:00063 |
| | Similar to Transcription factor AP2D8 | GO:00063 |
| | Similar to ETG1 (E2F TARGET GENE 1) | GO:00062 |

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|---|---|---|
| | Ubiquitin domain containing protein | GO:00508 |
| | Similar to cDNA clone:J013157P20, full ir | GO:00301 |
| | Cytochrome B561-related domain containing protei | |
| [Os] seed width (TO:0000149) \| leaf shape (TO:0000492) \| germination rate (TO:0000430) \| seed set percent (TO:0000455) \| leaf width (TO:0000370) \| acid detergent fiber (TO:0002641) \| seed size (TO:0000391) \| leaf rolling (TO:0000085) \| leaf development trait (TO:0000655) \| plant height (TO:0000207); [Os] rolled leaf TO:0006064\| cellulose content TO:0000993\| lignin content | Modulation of leaf rolling, Regulation of | GO:00095 |
| | Pentatricopeptide repeat domain containing protein | |
| | Nucleoporin, Common symbiosis signalir | GO:00009 |
| | Zinc finger, CCCH-type domain containing protein | |
| | Similar to N-acetyltransferase ESCO1 | GO:00000 |
| | Similar to CCT motif family protein, expre | GO:00063 |
| | Similar to PDE225/PTAC7 | GO:00427 |
| | Pectin lyase fold/virulence factor domain | GO:00059 |
| [Os] root length (TO:0000227) \| cold tolerance (TO:0000303) \| fructose content (TO:0006005) \| glucose content (TO:0000300) \| tiller number (TO:0000346) \| panicle size (TO:0006032) \| plant height (TO:0000207) \| sucrose content (TO:0000328) \| bacterial blight disease | Similar to Dof-like protein 34 | GO:00063 |
| [Os] cell elongation trait (TO:0002687) \| gibberellic acid sensitivity (TO:0000166) \| gibberellic acid content (TO:0002675) | Similar to TA1 protein (Fragment) | GO:00063 |

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|---|---|---|
| [Os] sterile lemma length (TO:0000240) \| embryo development trait (TO:0000620) \| seed development trait (TO:0000653) \| blast disease (TO:0000074) \| plant height (TO:0000207) \| floral organ development trait (TO:0006022) \| gibberellic acid content (TO:0002675) \| grain yield (TO:0000396) \| heat tolerance (TO:0000259) \| gibberellic | Transcription factor, Floral organ develo | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to microtubule-associated protein TORTIFO | |
| | Exonuclease domain containing protein | GO:00903 |
| | | |
| | Similar to Chromosome condensation regulator pro | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | | |
| | Similar to Small basic membrane integral | GO:00098 |
| [Os] jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615) \| seed dormancy (TO:0000253) \| cold tolerance (TO:0000303) \| pollen fertility (TO:0000421) \| gibberellic acid content (TO:0002675) \| seed set percent (TO:0000455) | Serine/threonine protein kinase domain | GO:00064 |
| | Histone acetylation protein 2 domain con | GO:00020 |
| | Similar to Potyviral helper component pr | GO:00072 |
| [Os] floral organ number TO:0006038\| phyllotaxy TO:0006014 | Similar to Aspartic proteinase Asp1 precu | GO:00065 |
| | Similar to Thioredoxin h | GO:00066 |
| | Myosin II heavy chain-like family protein | GO:00070 |
| | CHD5-like protein domain containing pr | GO:00487 |
| | | |
| [Os] plant height (TO:0000207) \| inflorescence development trait (TO:0000621) | Similar to Cytochrome P450 CYP714B3 | |
| | Uncharacterised protein family UPF0497, trans-me | |
| | E2F Family domain containing protein | GO:00001 |
| | Protein of unknown function DUF1005 family prote | |
| | Similar to membrane protein-like | GO:00349 |
| | Conserved hypothetical protein | GO:00062 |
| | VHS domain containing protein | GO:00068 |
| | Esterase, SGNH hydrolase-type domain containing | |
| | | |
| | Similar to Exostosin family protein, expre | GO:00064 |

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|---|---|---|
| | Vacuolar ATPase assembly integral memb | GO:00700 |
| | Tetratricopeptide-like helical domain con | GO:00063 |
| | Hypothetical conserved gene | |
| | Similar to SET domain-containing protein | GO:00165 |
| | Uncharacterised domain NUC173 domain | GO:00063 |
| | Photosystem II oxygen evolving complex | GO:00097 |
| [Os] plant height (TO:0000207) | | |
| [Os] growth and development trait (TO:0000357) \| anatomy and morphology related trait (TO:0000017) \| sterility or fertility trait (TO:0000392) | Similar to PAUSED | GO:00064 |
| | Similar to MCM10 minichromosome main | GO:00062 |
| | ATPase, AAA-type, core domain containing protein | |
| | Origin recognition complex subunit 3, La | GO:00062 |
| | Zinc finger, C2H2-like domain containing protein | |
| | Integrase, N-terminal zinc-binding doma | GO:00000 |
| | Similar to Outer membrane cytochrome b(5) (Fragm | |
| | Zm00001e005605 | GO:00001 |
| | Rickettsia 17 kDa surface antigen family | GO:00060 |
| | Protein kinase, core domain containing p | GO:00064 |
| | ENTH/VHS domain containing protein | GO:00068 |
| | Similar to H0311C03.4 protein | GO:00062 |
| | Similar to OSIGBa0113I13.6 protein | |
| | Zm00001e019062 | GO:00064 |
| [Os] salt tolerance TO:0006001\| oxidative stress TO:0002657 | Similar to ZPT2-13 | |
| | WD40 repeat-like domain containing pro | GO:00310 |
| | Tetratricopeptide-like helical domain containing pro | |
| | Hypothetical conserved gene | GO:00102 |

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|---|---|---|
| [Os] bacterial blight disease resistance (TO:0000175) \| jasmonic acid content (TO:0002668) \| mimic response (TO:0000063) \| blast disease (TO:0000074) \| abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276); [Os] disease resistance TO:0000112 | Mitogen-activated protein kinase kinase | GO:00064 |
| | F5O11.14 (ACR8) | |
| [Os] salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| abscisic acid sensitivity (TO:0000615) \| osmotic response sensitivity (TO:0000095) \| drought tolerance (TO:0000276) | RING Ub E3 ligase, Positive regulator of s | GO:00165 |
| | Protein of unknown function DUF679 fam | GO:00102 |
| [Os] salt tolerance TO:0006001\| oxidative stress TO:0002657\| drought tolerance TO:0000276\| root length TO:0000227\| relative yield TO:0000153 | Late embryogenesis abundant (LEA) grou | GO:00097 |
| | Similar to OSIGBa0127A14.6 protein | |
| [Os] tiller number (TO:0000346) \| harvest index (TO:0000128) \| chlorophyll content (TO:0000495) \| total biomass yield (TO:0000457) \| days to flower (TO:0000344) \| flowering time (TO:0002616) \| yield trait (TO:0000371) \| starch concentration (TO:0000702) \| total soluble sugar content (TO:0000340) \| root development trait (TO:0000656) \| root length (TO:0000227) \| root number (TO:0000084) \| plant height (TO:0000207) \| seed number (TO:0000445) \| grain yield per plant (TO:0000449) \| chloroplast development trait (TO:0002715) \| leaf color (TO:0000326) \| amino acid content (TO:0002673) \| leaf senescence (TO:0000249) \| leaf number | Zm00001e006272 | GO:00063 |
| | Similar to heavy-metal-associated domai | GO:00300 |
| | Similar to H0307D04.4 protein | |
| | Conserved hypothetical protein | GO:00458 |
| | Pectinesterase inhibitor domain containin | GO:00430 |

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|---|---|---|
| | Cyclin, A/B/D/E domain containing prote | GO:00000 |
| | Similar to calcium ion binding protein | |
| | Dof transcription factor, Promotion of nu | GO:00063 |
| [Os] tiller number TO:0000346\| plant height TO:0000207 | Zinc finger, RING/FYVE/PHD-type domai | GO:00069 |
| | Similar to AFL190Cp | |
| [Os] stomatal frequency (TO:0000566) \| leaf curling (TO:0002681) \| leaf lamina joint bending (TO:0002688) \| leaf angle (TO:0000206) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| grain shape (TO:0002730) \| tillering ability (TO:0000329) \| auxin sensitivity (TO:0000163) \| net photosynthetic rate (TO:0001027) \| tiller bud dormancy (TO:0000661) \| transpiration rate (TO:0001018) \| seed set percent (TO:0000455) \| drought tolerance (TO:0000276) \| tiller number (TO:0000346) \| filled grain number (TO:0000447) \| auxin content (TO:0002672) \| plant height | DUF630 and DUF632 domains containing | GO:00301 |
| | UBX domain containing protein | GO:00304 |
| | Hypothetical conserved gene | GO:00063 |
| | Protein of unknown function DUF599 family protein | |
| | Serine/threonine protein kinase domain c | GO:00064 |
| | Mis12 family protein | GO:00000 |
| | Uncharacterised protein family UPF0497, trans-mem | |
| | Hypothetical conserved gene | GO:00003 |
| | Protein of unknown function YGGT family | GO:00100 |
| [Os] salt tolerance TO:0006001\| grain number TO:0002759\| brown planthopper resistance TO:0000424 | Myb transcription factor domain containi | GO:00063 |
| | Armadillo-like helical domain containing protein | |
| | DNA polymerase III, clamp loader comple | GO:00062 |
| | Similar to indole-3-acetate beta-glucosyltransferas | |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00065 |
| | Similar to binding protein | GO:00482 |
| | Exodeoxyribonuclease III xth family prote | GO:00062 |
| [Os] zinc sensitivity (TO:0000351) | | |

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|---|---|---|
| | Similar to CUC1 | GO:00063 |
| | Zm00001e009972 | GO:00063 |
| | Hypothetical conserved gene | GO:19909 |
| | Armadillo-type fold domain containing p | GO:00070 |
| | Pentatricopeptide repeat domain containing protein | |
| | Photosystem I reaction centre subunit N f | GO:00159 |
| [Os] salt tolerance (TO:0006001) \| plant height (TO:0000207) \| heat tolerance (TO:0000259) \| panicle length (TO:0000040) \| grain weight (TO:0000590) \| grain yield per plant (TO:0000449) \| 1000-seed weight (TO:0000382) \| growth and development trait (TO:0000357) \| relative root length (TO:0000516) | Armadillo-like helical domain containing protein | |
| | Similar to Protein kinase domain containi | GO:00064 |
| | Domain of unknown function DUF2215 domain cont | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to H0306F12.6 protein | |
| | Similar to Too many mouths protein | |
| [Os] abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | Similar to EDR1 | GO:00064 |
| [Os] proline content TO:0006002\| drought tolerance TO:0000276 | Uncharacterised protein family UPF0120 | GO:00105 |
| | Zinc finger, DHHC-type domain containir | GO:00066 |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Autophagy protein 9 domain containing | GO:00000 |
| | Zinc finger, RanBP2-type domain containing protein | |
| | Myb transcription factor domain containing protein | |
| | GTP1/OBG domain containing protein | |
| | Lipase, GDSL domain containing protein | |
| | Conserved hypothetical protein | |
| | Zm00001e028469 | GO:00069 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Lumazine-binding protein family protein | GO:00092 |
| | Similar to LPA2 (low psii accumulation2) | |

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|---|---|---|
| [Os] blast disease (TO:0000074) | Target protein of bacterial effector, Xoo v | GO:00063 |
| | Hypothetical conserved gene | |
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| | Homeodomain-like containing protein | |
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| | | |
| | DNA repair protein (XPGC)/yeast Rad fam | GO:00062 |
| [Os] floral organ number TO:0006038\| phyllotaxy TO:0006014 | Peptidase A1 domain containing protein | GO:00065 |
| [Os] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| heat tolerance | Arsenic-induced RING E3 ligase, Abiotic stress resp | |
| | Mitochondrial glycoprotein family protein | GO:00701 |
| | Transferase family protein | |
| | WD40 repeat-like domain containing protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | | |
| | Zm00001e009510 | GO:00065 |
| | Protein of unknown function DUF679 fa | GO:00102 |
| | Hypothetical conserved gene | GO:00422 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00459 |
| | | |
| | WD40 repeat-like domain containing pro | GO:00096 |
| | Similar to H0303G06.9 protein | GO:00094 |
| | WD40 repeat-like domain containing pro | GO:00431 |
| | Protein kinase, catalytic domain domain c | GO:00064 |
| | 2OG-Fe(II) oxygenase domain containing protein | |
| | Similar to ATP binding protein | GO:00064 |
| [Os] blast disease (TO:0000074) \| leaf senescence (TO:0000249) \| salt tolerance (TO:0006001) | | |
| | Cytochrome P450 family protein | GO:00072 |
| | Plant lipid transfer protein/Par allergen f | GO:00068 |
| | Cystathionine beta-synthase, core domai | GO:00064 |
| | Zm00001e015227 | GO:00064 |
| | Zm00001e041933 | GO:00007 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Syntaxin 6, N-terminal domain containin | GO:00150 |
| | Serine/threonine protein kinase-related c | GO:00064 |

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|---|---|---|
| [Os] crown rootless TO:0000230 | | |
| | Protein of unknown function DUF1195 family protei | |
| | Uncharacterised protein family UPF0090 | GO:0042 |
| [Os] drought tolerance (TO:0000276) | SBP domain containing protein | GO:0063 |
| | Nucleotide-diphospho-sugar transferase | GO:0071 |
| | Similar to Pectin methylesterase (Fragme | GO:00425 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Thioredoxin-like fold domain containing | GO:0063 |
| [Os] cold tolerance (TO:0000303) | | |
| | Zinc finger, RanBP2-type domain containing protein | |
| | Similar to Ser-thr protein kinase (Fragme | GO:00064 |
| | Protein of unknown function DUF296 domain contai | |
| | E2F Family domain containing protein | GO:0001 |
| | Similar to predicted protein | GO:00096 |
| | Similar to chloroplast outer envelope pro | GO:00150 |
| | WD40 repeat-like domain containing pro | GO:00063 |
| | Conserved hypothetical protein | |
| [Os] auxin content (TO:0002672) \| seed development trait (TO:0000653) \| embryo development trait (TO:0000620) \| inflorescence development trait (TO:0000621) \| growth hormone content (TO:0000476) \| female sterility (TO:0000358) \| auxin sensitivity (TO:0000163) \| seed maturation (TO:0002661) | MADS box transcription factor, Regulator | GO:0063 |
| | Patatin family protein | GO:00066 |
| | Leucine-rich repeat, cysteine-containing | GO:00065 |
| | Similar to MRNA, complete cds, clone: RA | GO:00070 |
| | Zinc finger, C2H2-type domain containin | GO:00165 |
| | Protein prenyltransferase domain contain | GO:00001 |
| | Leucine-rich repeat, SDS22 containing protein | |
| | SGT1 family protein | |
| | WD40 repeat-like domain containing pro | GO:00069 |

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|---|---|---|
| | Hypothetical conserved gene | GO:00099 |
| | Similar to Nudix hydrolase 15, mitochon | GO:00159 |
| | Tetratricopeptide-like helical domain containing pr | |
| | Similar to BZIP transcription factor family | GO:00063 |
| | Similar to EIN2 | GO:00098 |
| | Similar to mtn21-like protein | GO:00091 |
| | Proteasome maturation factor UMP1 fami | GO:00432 |
| [Os] flowering time (TO:0002616) \| plant height (TO:0000207) \| grain length (TO:0000734) \| days to heading (TO:0000137) | GAGA binding-like family protein | GO:00063 |
| | Glucosidase II beta subunit-like domain | GO:00096 |
| | Protein prenyltransferase domain containing protein | |
| [Os] chloroplast development trait (TO:0002715) \| cold tolerance (TO:0000303) | Pentatricopeptide repeat (PPR) protein, E | GO:00003 |
| | Tyrosine protein kinase domain containi | GO:00064 |
| | Similar to GC4 (golgin candidate 4) | GO:00068 |
| | Protein of unknown function DUF1352 d | GO:00070 |
| [Os] days to heading (TO:0000137) \| total biomass yield (TO:0000457) \| grain yield (TO:0000396) \| seed fertility (TO:0000639) \| plant height (TO:0000207) \| flowering time (TO:0002616); [Os] grain number TO:0002759\| plant height TO:0000207 | Protein containing PHD domain, FNIII do | GO:00069 |
| | Similar to Phosphorylation regulatory pro | GO:00004 |
| [Os] stem length (TO:0000576) \| root length (TO:0000227) \| leaf length (TO:0000135) \| gibberellic acid sensitivity (TO:0000166) \| leaf development trait (TO:0000655) \| panicle length (TO:0000040) \| seed length (TO:0000146) \| plant height (TO:0000207) \| seed development trait | Patatin-related phospholipase A, Modula | GO:00066 |
| | Conserved hypothetical protein | |
| | Lipase, GDSL domain containing protein | |
| | Similar to Nonspecific lipid-transfer prot | GO:00068 |
| | MPPN family protein | GO:00066 |
| [Os] submergence tolerance (TO:0000524) | | |
| | EF hand domain containing protein | |
| | NLI interacting factor domain containing protein | |

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|---|---|---|
| | Conserved hypothetical protein | GO:00096 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Peptidase C12, ubiquitin carboxyl-terminal hydrolas | |
| | Zinc finger, C3HC-like domain containing protein | |
| | Similar to Transcription factor MYBS2 | GO:00096 |
| [Os] leaf width (TO:0000370) \| root number (TO:0000084) \| root thickness (TO:0000306) \| seed shape (TO:0000484) \| grain size (TO:0000397) \| sterility related trait (TO:0000485) \| stem length (TO:0000576) \| leaf size (TO:0002637) \| cell growth and development trait (TO:0002686) \| spikelet anatomy and morphology trait (TO:0000657) \| lemma shape (TO:0000614) \| inflorescence development trait (TO:0000621) \| internode length (TO:0000145) \| panicle length (TO:0000040) \| leaf development trait (TO:0000655); [Os] | SSXT family protein | GO:00082 |
| | Protein of unknown function DUF537 fa | GO:00104 |
| | K Homology, type 1, subgroup domain c | GO:00104 |
| | tRNA pseudouridine synthase family prot | GO:00015 |
| | Similar to Amine oxidase, flavin-containi | GO:00063 |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | PREG-like protein | GO:00000 |
| | Lipase, GDSL domain containing protein | |
| | Methyl-CpG DNA binding domain containing protei | |
| | Zm00001e001952 | GO:00063 |

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|---|---|---|
| [Os] chlorophyll-b content (TO:0000295) \| panicle length (TO:0000040) \| grain length (TO:0000734) \| leaf development trait (TO:0000655) \| plant height (TO:0000207) \| seed set percent (TO:0000455) \| 1000-seed weight (TO:0000382) \| panicle number (TO:0000152) \| chlorophyll content (TO:0000495) \| chlorophyll-a content (TO:0000293) \| net photosynthetic rate (TO:0001027) \| stomatal conductance (TO:0000522) \| transpiration rate (TO:0001018) \| UV-B light sensitivity (TO:0000601) \| drought tolerance (TO:0000276) \| bacterial blight disease resistance (TO:0000175) \| abscisic acid sensitivity (TO:0000615) \| growth and development trait (TO:0000357) \| heat tolerance (TO:0000259) \| grain yield per plant (TO:0000449) \| relative water content (TO:0000136) \| filled grain number (TO:0000447) \| grain yield (TO:0000396) \| secondary branch number (TO:0000557) \| photosynthetic rate (TO:0001015) \| hydrogen peroxide | Double-stranded RNA-binding-like dom | GO:00351 |
| | Zinc-finger protein R2931 | GO:00635 |
| | RNA polymerase II, Rpb4, core domain co | GO:00063 |
| | Cytochrome P450 family protein | |
| | Similar to Cold-induced protein | GO:00064 |
| | Pentatricopeptide repeat domain containing protein | |
| | Conserved hypothetical protein | GO:00100 |
| | Beta-expansin precursor (Beta-expansin | GO:00096 |
| | DNA repair metallo-beta-lactamase dom | GO:00063 |
| [Os] viral disease resistance (TO:0000148) \| submergence tolerance (TO:0000524) \| leaf senescence (TO:0000249) \| black streak dwarf virus resistance (TO:0000020) | Red chlorophyll catabolite reductase, Lea | GO:00159 |

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|---|---|---|
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) \| plant height (TO:0000207) \| grain size (TO:0000397) \| panicle length (TO:0000040) \| tiller number (TO:0000346) \| filled grain number (TO:0000447) \| growth and development trait (TO:0000357) | Histone chaperone domain CHZ domain containing | |
| | Similar to DNA-directed RNA polymerase | GO:00063 |
| | Di-trans-poly-cis-decaprenylcistransfera | GO:00015 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Protein of unknown function DUF604 family protein | |
| [Os] shoot development trait (TO:0000654) \| grain weight (TO:0000590) \| inflorescence development trait (TO:0000621) \| grain shape (TO:0002730); [Os] grain shape TO:0002730\| grain weight TO:0000919 | NHL domain-containing protein, Determination of p | |
| [Os] salt tolerance TO:0006001\| oxidative stress TO:0002657\| drought tolerance TO:0000276\| blast disease resistance TO:0000074; [Ta] male sterility TO:0000437 | Tyrosine protein kinase domain containin | GO:00064 |
| | Similar to Harpin-induced protein 1 containing prot | |
| [Ta] leaf water potential TO:0000131\| stomatal resistance TO:0000522\| stomatal resistance TO:0000523 | Protein of unknown function DUF1637 fa | GO:00181 |
| | Similar to Phosphate starvation regulator | GO:00063 |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | Protein of unknown function DUF1675 dc | GO:00071 |
| | Similar to predicted protein | |
| | Protein of unknown function DUF607 fam | GO:00068 |
| | Protein of unknown function DUF537 fam | GO:00104 |
| | Kelch-type beta propeller domain containing protei | |
| | Copper chaperone SCO1/SenC domain cc | GO:00336 |
| | Ribosomal L11 methyltransferase family | GO:00064 |
| | AIG1 domain containing protein | |
| | Protein of unknown function DUF827, pla | GO:00099 |
| [Os] flowering time (TO:0002616) \| days to heading (TO:0000137) | C2H2-type zinc finger transcription facto | GO:00063 |

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|---|---|---|
| [Os] leaf lamina joint bending (TO:0002688) \| brassinosteroid sensitivity (TO:0002677) \| leaf angle (TO:0000206) | Similar to Helix-loop-helix protein homo | GO:00063 |
| [Os] gravity response trait (TO:0002693) \| auxin sensitivity (TO:0000163) \| relative yield (TO:0000153) \| root anatomy and morphology trait (TO:0000043) \| salt | Similar to UPF0496 protein 4 | |
| [Os] abiotic stress trait (TO:0000168) \| cold tolerance (TO:0000303) \| mimic response (TO:0000063) \| heat tolerance (TO:0000259) \| disease resistance (TO:0000112) \| variegated leaf (TO:0000069) \| hydrogen peroxide content (TO:0000605) | Heat stress transcription factor Spl7 (Hea | GO:00063 |
| | Similar to SEU3A protein | GO:00001 |
| | Lipase, class 3 family protein | GO:00066 |
| | | |
| | Basic helix-loop-helix dimerisation regio | GO:00063 |
| | Timeless protein domain containing prot | GO:00000 |
| | Hypothetical conserved gene | |
| [Ta] stomatal opening TO:0020097 | | |
| | Reticulon family protein | GO:00096 |
| | Glycoside hydrolase, family 28 domain cc | GO:00059 |
| | Pentatricopeptide repeat domain containing protein | |
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| | Zinc finger, CCHC-type domain containin | GO:00000 |
| | Cyclin-related 2 domain containing prote | GO:00000 |
| | Serine/threonine protein kinase domain c | GO:00064 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | Similar to Polcalcin Jun o 2 (Calcium-binding pollen | |
| [Os] | Cellulose synthase family protein | GO:00098 |
| | Pentatricopeptide repeat domain containing protein | |
| | | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Conserved hypothetical protein | GO:00094 |

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|---|---|---|
| | Protein kinase, core domain containing p | GO:00064 |
| | C2 calcium-dependent membrane targeti | GO:00097 |
| | Conserved hypothetical protein | GO:00100 |
| | Similar to Cdc48 cell division control prot | GO:00066 |
| | Similar to metal ion binding protein | GO:00300 |
| | Similar to 10A19I.14 | GO:00063 |
| [Os] blast disease (TO:0000074) | Component of Exo70 exocyst complex, R | GO:00068 |
| | Nodulin-like domain containing protein | |
| [Os] oxidative stress TO:0002657 | Heat stress transcriptioon factor, High-te | GO:00063 |
| | COBRA-like protein 7 precursor | GO:00102 |
| | Similar to HEAT repeat family protein | GO:00000 |
| | Similar to Shaggy-related protein kinase | GO:00063 |
| | Auxin responsive SAUR protein family pro | GO:00097 |
| | Protein of unknown function DUF1644 family protei | |
| [Os] salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) | S-adenosylmethionine decarboxylase, Po | GO:00065 |
| | Similar to cytokinin-O-glucosyltransferase 2 | |
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| | Similar to Calmodulin-binding receptor-l | GO:00064 |

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|---|---|---|
| | Zm00001e034314 | GO:00098 |
| | Serine/threonine protein kinase domain c | GO:00064 |
| [Os] seed maturation (TO:0002661) \| starch grain size (TO:0002655) \| leaf size (TO:0002637) \| starch content (TO:0000696) \| grain size (TO:0000397) \| seed development trait (TO:0000653) \| gibberellic acid content (TO:0002675) \| cytokinin content (TO:0002660) \| male sterility type (TO:0000106) \| leaf senescence (TO:0000249) \| chalky endosperm | NAD(P)-binding domain containing prote | GO:00000 |
| | Similar to PAPA-1-like conserved region | GO:00063 |
| | Armadillo-type fold domain containing p | GO:00432 |
| | Peptidase C12, ubiquitin carboxyl-terminal hydrolas | |
| [Os] organ identity TO:0006018 | Lipase, class 3 family protein | GO:00066 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Cytochrome P450 family protein | |
| | Six-bladed beta-propeller, TolB-like domain contai | |
| | Similar to BABY BOOM | GO:00063 |
| | Glutathione S-transferase GSTF15 | GO:00067 |
| | Vacuolar protein sorting-associated prot | GO:00068 |
| [Os] plant height (TO:0000207) \| mimic response (TO:0000063) \| hydrogen peroxide content (TO:0000605) \| leaf senescence (TO:0000249) \| disease resistance (TO:0000112) \| chlorophyll content (TO:0000495) \| bacterial blight disease resistance (TO:0000175) \| grain size (TO:0000397) \| 100-seed weight (TO:0000269) \| blast disease (TO:0000074) | | |
| | Similar to predicted protein | |
| | EF hand domain containing protein | |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Glycoside hydrolase, family 14 protein | GO:00002 |
| | Similar to HMGc1 protein | |
| | Mg2+ transporter protein, CorA-like don | GO:00068 |
| [Os] drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) \| leaf senescence (TO:0000249); [Os] salt tolerance TO:0006001\| drought tolerance TO:0000276\| seed dormancy | Similar to BZIP transcription factor ABI5 | GO:00063 |
| | Hypothetical conserved gene | |
| | GCN5-related N-acetyltransferase (GNAT) domain d | |
| | Programmed cell death protein 2, C-terminal domai | |

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|---|---|---|
| | Pentatricopeptide repeat domain containi | GO:0009 |
| [Os] herbicide sensitivity (TO:0000058) | | |
| | Similar to (RAP Annotation release2) Prot | GO:00064 |
| | Hypothetical conserved gene | GO:00000 |
| [Os] cold tolerance (TO:0000303) \| polysaccharide content (TO:0006007) \| hydrogen peroxide content (TO:0000605) | tRNA-binding arm domain containing protein | |
| [Os] plastochron (TO:0000735) \| leaf senescence (TO:0000249) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| growth and development trait (TO:0000357) \| growth hormone content (TO:0000476) \| leaf number (TO:0000241) \| leaf width (TO:0000370) \| plant height (TO:0000207) \| tiller number (TO:0000346) \| leaf length | Homolog of Arabidopsis LHP | GO:00063 |
| | Similar to Zinc finger, C3HC4 type family | GO:00165 |
| [Os] bacterial blight disease resistance (TO:0000175) | Hypothetical conserved gene | GO:00068 |
| [Os] grain size (TO:0000397) \| grain yield (TO:0000396) \| seed width (TO:0000149) \| 1000-dehulled grain weight (TO:0000592) | Peptidase C19, ubiquitin carboxyl-termin | GO:00065 |
| | Phosphatidic acid phosphatase type 2/ha | GO:00064 |
| | EF-Hand type domain containing protein | GO:00000 |
| | Similar to BCS1 protein-like protein | GO:0006 |

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|---|---|---|
| | Zinc finger, NF-X1-type domain containi | GO:00063 |
| [Os] heat tolerance (TO:0000259) | Similar to CG-1 protein (Fragment) | GO:00063 |
| | Similar to S3 self-incompatibility locus-li | GO:00349 |
| | Similar to Oxidoreductase, short chain dehydrogena | |
| [Os] iron sensitivity (TO:0000224) | No apical meristem (NAM) protein domai | GO:00063 |
| | Lipase, GDSL domain containing protein | |
| [Os] flooding related trait (TO:0000114) \| blast disease (TO:0000074) \| submergence tolerance (TO:0000524); [Os] endospermless TO:0000231 | SNF2-related domain containing protein | GO:00801 |
| | Mu2 adaptin subunit (AP50) of AP2 doma | GO:00150 |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| oxygen sensitivity (TO:0000015) \| cold tolerance (TO:0000303) \| brown planthopper resistance (TO:0000424) \| abscisic acid sensitivity (TO:0000615) \| stem borer resistance (TO:0000454) \| sheath blight disease resistance (TO:0000255) \| temperature response trait (TO:0000432) \| heat tolerance (TO:0000259); [Os] salt tolerance TO:0006001\| grain size TO:0000397 | WRKY transcription factor 24 (WRKY24) | GO:00063 |
| | Similar to Leucine Rich Repeat family pro | GO:00065 |
| | Pentatricopeptide repeat domain containing protein | |
| | Conserved hypothetical protein | |
| [Os] iron sensitivity (TO:0000224) \| jasmonic acid sensitivity (TO:0000172) \| leaf color (TO:0000326) | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Protein of unknown function DUF605 fa | GO:00150 |
| [Os] tiller number (TO:0000346) \| plant height (TO:0000207) \| growth and development trait (TO:0000357) \| lateral root number (TO:0001013) | Similar to Squamosa promoter-binding-like protein | |

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|---|---|---|
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Metallophosphoesterase domain domain containing | |
| | Barley B recombinant like-protein B (Barl | GO:00063 |
| | Cytochrome P450 family protein | |
| [Os] drought tolerance (TO:0000276) \| bacterial blight disease resistance (TO:0000175) \| blast disease (TO:0000074) \| iron sensitivity (TO:0000224) | NAC transcription factor, Negative regula | GO:00063 |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to TA11 protein (Fragment) | GO:00063 |
| | Zm00001e025988 | |
| | Beta tubulin, autoregulation binding site | GO:00344 |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Transferase family protein | |
| | Glycoside hydrolase, family 1 protein | GO:00059 |
| | Pentatricopeptide repeat domain containing protein | |
| | Zm00001e000461 | GO:00063 |
| | Hypothetical conserved gene | |
| | Amino acid transporter, transmembrane | GO:00033 |
| | Zm00001e009956 | GO:00457 |
| | Similar to Ceramide kinase | |

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|---|---|---|
| [Os] sterility related trait (TO:0000485) \| pollen sterility (TO:0000053) | a member of the TopoVIB-like protein fa | GO:00071 |
| [Os] vivipary (TO:0000619) \| seed dormancy (TO:0000253) \| abscisic acid sensitivity (TO:0000615); [Os] seed maturation TO:0002661 |  |  |
|  | Similar to Zinc finger, C2H2 type family p | GO:00063 |
|  | Calmodulin binding protein-like domain | GO:00063 |
| [Os] oxygen sensitivity (TO:0000015) \| salt tolerance (TO:0006001) |  |  |
| [Os] salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) | Similar to Heat shock protein 26 | GO:00094 |
|  | Zm00001e016078 | GO:00065 |
|  | Alpha/beta hydrolase fold-3 domain containing pro |  |
|  | Heavy metal transport/detoxification pro | GO:00300 |
|  | Similar to OSIGBa0152K17.7 protein |  |
|  |  |  |
|  | Conserved hypothetical protein |  |
| [Os] hydrogen peroxide content (TO:0000605) \| grain length (TO:0000734) \| salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| black streak dwarf virus resistance (TO:0000020) \| cytokinin content (TO:0002660) \| abscisic acid sensitivity (TO:0000615) | Argonaute and Dicer protein, PAZ domai | GO:00310 |
|  | Similar to Kinesin heavy chain (Fragment) | GO:00070 |
|  | Similar to Methyl-binding domain protein MBD111 |  |
| [Os] days to heading (TO:0000137) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| filled grain number (TO:0000447) \| flowering time (TO:0002616) | Zinc finger, B-box domain containing pr | GO:00063 |
|  | Sterile alpha motif SAM domain containing protein |  |
|  | Zinc finger, RING/FYVE/PHD-type domai | GO:00007 |

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|---|---|---|
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Conserved hypothetical protein | |
| [Os] zinc sensitivity (TO:0000351) | Zinc transporter, Preferential distribution | GO:00000 |
| | Similar to Protein kinase domain containing protein, | |
| | Zm00001e013184 | GO:00097 |
| | Zm00001e026884 | GO:00096 |
| | Similar to Inhibitor I family protein | GO:00096 |
| | Acyl-CoA N-acyltransferase domain cont | GO:00060 |
| | Esterase, SGNH hydrolase-type domain containing p | |
| | Similar to Epstein-Barr nuclear antigen-1 (EBNA-1) | |
| | RNA-processing protein, HAT helix doma | GO:00063 |
| [Os] nematode damage resistance (TO:0000384) \| pollen sterility (TO:0000053) | Sucrose transporter | GO:00059 |
| | Cyclin-like F-box domain containing protein | |
| [Os] chalky endosperm (TO:0000266) \| protein composition related trait (TO:0000490) \| grain size (TO:0000397) \| floury endosperm (TO:0000104) \| dull endosperm (TO:0000105) \| abscisic acid sensitivity (TO:0000615) \| grain weight (TO:0000590) \| seed maturation (TO:0002661) \| amylose content (TO:0000196) \| seed quality (TO:0000162); [Os] grain size TO:0000397\| heat tolerance TO:0000259\| amylose content TO:0000196\| floury endosperm | Tetratricopeptide repeat (TPR) domain co | GO:00069 |
| | Exocyst complex subunit Sec15-like fami | GO:00068 |
| | Similar to F-box domain containing protein | |
| | Bifunctional inhibitor/plant lipid transfer | GO:00065 |
| | Similar to predicted protein | |
| [Os] abscisic acid sensitivity (TO:0000615) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| drought tolerance | bZIP transcription factor, Modulation of t | GO:00063 |
| | Glycosyltransferase AER61, uncharacterized domain | |
| | Similar to H0523F07.9 protein | GO:00063 |

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|---|---|---|
| | Tetratricopeptide-like helical domain con | GO:00068 |
| | Galactosyl transferase family protein | GO:00099 |
| [Os] chlorophyll content (TO:0000495) \| chloroplast development trait (TO:0002715) \| leaf color (TO:0000326) | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] male sterility (TO:0000437) \| female sterility (TO:0000358); [Os] female sterility TO:0000358 | Similar to OSIGBa0130K07.4 protein | GO:00421 |
| | PetM of cytochrome b6/f complex subunit 7 domain | |
| | Similar to Lysine and histidine specific tr | GO:00070 |
| | Zm00001e024616 | GO:00064 |
| [Os] seed weight (TO:0000181) \| relative plant height (TO:0001034) \| heat tolerance (TO:0000259) \| temperature response trait (TO:0000432) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| panicle weight (TO:0000014) \| grain length (TO:0000734) \| panicle length (TO:0000040) \| blast disease (TO:0000074) \| yield trait (TO:0000371) \| grain size (TO:0000397) \| filled grain number (TO:0000447) \| panicle number (TO:0000152) \| panicle size (TO:0006032) \| grain number (TO:0002759) \| seed development trait (TO:0000653) \| growth and development trait (TO:0000357) \| days to heading (TO:0000137) \| salt tolerance (TO:0006001) \| seed set percent (TO:0000455) \| cold tolerance | | |
| | Similar to Plastid division protein | GO:00100 |
| | Similar to Similarities with spP40209 Sac | GO:00063 |
| | Similar to predicted protein | GO:00066 |
| | Hypothetical conserved gene | GO:00094 |
| | Similar to Beta-fructofuranosidase (EC 3. | GO:00059 |
| | DNA double-strand break repair and VJ r | GO:00062 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Clathrin light chain family protein | GO:00068 |

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| [Os] inflorescence development trait (TO:0000621) \| grain size (TO:0000397) \| seed length (TO:0000146) \| grain length (TO:0000734) \| seed width (TO:0000149) \| 1000-dehulled grain weight (TO:0000592) \| grain shape (TO:0002730) \| auxin sensitivity | IQ calmodulin-binding region domain containing pr | |
| | Zm00001e021042 | |
| | Peptidase S10, serine carboxypeptidase f | GO:00065 |
| | Similar to predicted protein | GO:00550 |
| [Os] cold tolerance (TO:0000303) \| blast disease (TO:0000074) \| disease resistance (TO:0000112) \| submergence tolerance (TO:0000524) | Transcriptional activator Rb homolog (Fra | GO:00063 |
| | Similar to Amidophosphoribosyltransfera | GO:00061 |
| [Os] root hair length (TO:0002665) | ROOT HAIR DEFECTIVE-SIX LIKE (RSL) clas | GO:00063 |
| | Phosphatidic acid phosphatase type 2/ha | GO:00468 |
| [Os] UV light sensitivity (TO:0000160) | Prenylated rab acceptor PRA1 family prot | GO:00161 |
| [Os] viral disease resistance (TO:0000148) | Similar to Auxin response factor 1 | GO:00063 |
| | Protein of unknown function DUF1740 d | GO:00063 |
| | Similar to glucan endo-1,3-beta-glucosi | GO:00059 |

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|---|---|---|
| [Os] seed development trait (TO:0000653) \| days to heading (TO:0000137) \| inflorescence development trait (TO:0000621) \| grain number (TO:0002759) \| endosperm related trait (TO:0000575) \| endosperm color (TO:0000487) \| grain size (TO:0000397) \| carbohydrate content (TO:0000291) \| sucrose content (TO:0000328) \| grain yield (TO:0000396) \| fructose content (TO:0006005) \| starch grain size (TO:0002655) \| glucose content (TO:0000300) \| starch grain shape (TO:0002656) \| starch content (TO:0000696) \| filled grain number | Similar to MATE efflux family protein, ex | GO:00068 |
| | Zinc finger, DHHC-type, palmitoyltransfe | GO:00066 |
| [Os] brown planthopper resistance (TO:0000424) \| insect damage resistance (TO:0000261) \| salt tolerance (TO:0006001) \| jasmonic acid sensitivity (TO:0000172) | Similar to Isoform 2 of Homeobox-leucin | GO:00063 |
| | Plant-specific kinesin-14, Processive min | GO:00070 |
| | S1, RNA binding domain containing protein | |
| | Similar to predicted protein | GO:00066 |
| [Os] abiotic stress trait (TO:0000168) | Heat stress transcription facto | GO:00063 |
| | Zm00001e036384 | GO:00901 |
| | Mannose-binding lectin domain containing protein | |
| [Os] blast disease (TO:0000074) \| aluminum sensitivity (TO:0000354) \| polysaccharide content (TO:0006007) \| light intensity sensitivity (TO:0000460) | Similar to Polygalacturonase (Fragment) | GO:00059 |

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|---|---|---|
| [Os] plant height (TO:0000207) \| vascular bundle number (TO:0000472) \| seed thickness (TO:0000304) \| seed weight (TO:0000181) \| starch grain size (TO:0002655) \| leaf width (TO:0000370) \| internode length (TO:0000145) \| panicle size (TO:0006032) \| stem length (TO:0000576) \| seed shape (TO:0000484) \| stem elongation (TO:0006036) \| root length (TO:0000227) \| total root number | Homolog of xylanase inhibitor, Chitinase· | GO:00002 |
| [Os] blast disease (TO:0000074) | | |
| | UBX domain containing protein | GO:00304 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Similar to Transfactor-like protein | GO:00063 |
| | Similar to Plastocyanin-like domain conta | GO:00229 |
| | Conserved hypothetical protein | GO:00169 |
| | Similar to Homeodomain leucine zipper p | GO:00063 |
| | Similar to H0525C06.10 protein | GO:00001 |
| [Os] chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| leaf color (TO:0000326) \| chloroplast development trait (TO:0002715) \| carotenoid content (TO:0000496) \| cold tolerance | Pentatricopeptide repeat domain containing protein | |
| | Senescence-associated family protein | |
| | Similar to Cytochrome P450 86A1 (EC 1.14.-.-) (CYP | |
| | Heat shock protein Hsp20 domain contai | GO:00094 |
| | Similar to protein phosphatase 2C contai | GO:00064 |
| | Peptidase A1 domain containing protein | GO:00065 |
| | tRNA/rRNA methyltransferase, SpoU dom | GO:00015 |
| | Zinc finger, RING/FYVE/PHD-type domair | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domair | GO:00165 |
| | Protein of unknown function DUF639 family protein | |
| | Similar to MutS homolog 7 (Fragment) | GO:00007 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to 60S ribosomal protein L24-A (I | GO:00000 |
| | Conserved hypothetical protein | |

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|---|---|---|
| | Similar to Acyl carrier protein I, chloropla | GO:00066 |
| | Septum formation topological specificity | GO:00100 |
| | Steroid nuclear receptor, ligand-binding domain co | |
| [Os] plant height (TO:0000207) | Kinesin-related protein, Regulation of cel | GO:00070 |
| | Alpha-isopropylmalate/homocitrate synthase, cons | |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | Basic helix-loop-helix, Nulp1-type domain containi | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Zm00001e040394 | GO:00322 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Tetratricopeptide-like helical domain containing pr | |
| | Conserved hypothetical protein | |
| | WD40/YVTN repeat-like domain containing protein | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| [Os] spikelet fertility TO:0000180 | Nucleotide-binding, alpha-beta plait don | GO:00064 |
| | Helix-loop-helix DNA-binding domain c | GO:00063 |
| | D111/G-patch domain containing protei | GO:00003 |
| [Os] salt tolerance (TO:0006001) \| seed set percent (TO:0000455) | Cupredoxin domain containing protein | GO:00229 |
| | Zm00001e020208 | GO:00459 |
| | Mediator complex, subunit Med4 domain | GO:00063 |
| | Armadillo-type fold domain containing p | GO:00062 |
| | Hypothetical conserved gene | GO:00165 |
| | Similar to Arm repeat-containing protein | GO:00165 |
| | Regulatory protein RecX family protein | GO:00062 |
| | Pentatricopeptide repeat domain containing protein | |
| | Conserved hypothetical protein | |
| | Similar to Transcriptional adaptor (Fragm | GO:00063 |
| | UBX domain containing protein | GO:00329 |
| | Similar to SET domain protein SDG111 | GO:00165 |

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| | Cyclin, A/B/D/E domain containing prote | GO:00000 |
| | Serine/threonine protein kinase domain c | GO:00064 |
| | Uncharacterised protein family UPF0497, trans-mem | |
| | Similar to Cyclin-dependent protein kina | GO:00064 |
| | Poly(A) polymerase, central region domai | GO:00063 |
| | Protein of unknown function DUF1218 family protei | |
| | WD40 repeat domain containing protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Acyl-CoA N-acyltransferase domain cont | GO:00070 |
| | Similar to Low molecular weight heat sho | GO:00069 |
| [Os] grain weight (TO:0000590) \| grain thickness (TO:0000399) \| grain length (TO:0000734) \| hydrogen peroxide content (TO:0000605) | | |
| | RNA-directed DNA polymerase (reverse t | GO:00062 |
| | Zm00001e028446 | GO:00068 |
| | Similar to cDNA clone:J033042L23, full insert seque | |
| | Hypothetical conserved gene | GO:00064 |
| | Glycosyl transferase, family 19 protein | GO:00066 |
| | Photosystem II oxygen evolving complex | GO:00094 |
| | Alpha/beta hydrolase fold-1 domain containing pro | |
| | Similar to plant viral-response family protein | |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Pollen Ole e 1 allergen and extensin domain contain | |
| | Hypothetical conserved gene | GO:00094 |
| | Similar to Prep (Fragment) | GO:00063 |
| | FF domain containing protein | GO:00063 |
| | Similar to catalytic/ protein phosphatase | GO:00359 |
| | Transcription factor IIIC, subunit 5 domai | GO:00063 |
| [Os] days to heading (TO:0000137) \| heat tolerance (TO:0000259) \| ethylene sensitivity (TO:0000173) \| flowering time (TO:0002616); [Os] seed weight TO:0000181\| ethylene sensitivity TO:0000173 | Similar to Ethylene receptor-like protein | GO:00001 |
| | Exo70 exocyst complex subunit family p | GO:00068 |
| | Calmodulin binding protein-like family p | GO:00022 |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) \| bacterial blight disease resistance (TO:0000175) | Inward rectifying shaker-like potassium c | GO:00068 |
| [Os] seed development trait (TO:0000653) \| amylose content (TO:0000196) \| starch content (TO:0000696) \| total fat content (TO:0000602) \| floury endosperm (TO:0000104) | Pentatricopeptide repeat domain containing protein | |
| | tRNA-splicing endonuclease, subunit Sen | GO:00003 |
| | Aldo/keto reductase domain containing protein | |
| | Similar to Disease resistance protein ADR | GO:00069 |
| | Hypothetical conserved gene | GO:00430 |
| | Phosphatidylinositol 4-phosphate 5-kina | GO:00464 |
| | Zm00001e024681 | GO:00063 |
| | Similar to 60S ribosomal protein L15 | GO:00064 |
| | Similar to predicted protein | |
| | Similar to Auxin response factor 14 | GO:00063 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Serine/threonine protein kinase-related c | GO:00064 |
| | Nodulin-like domain containing protein | |
| | Zm00001e020723 | |
| | Zm00001e018948 | GO:00066 |
| | Similar to F-box protein | |
| | Bacterial methyltransferase family protei | GO:00322 |
| | RNA polymerase Rpb7, N-terminal domai | GO:00063 |
| | Similar to Galactoside 2-alpha-L-fucosyl | GO:00099 |

| | | |
|---|---|---|
| [Os] leaf chlorosis TO:0020113\| quantum yield TO:0012004\| leaf area index TO:0012001\| percent germination TO:0010001\| leaf chlorosis TO:0006060\| meristem identity TO:0006017\| proline content TO:0006002\| salt tolerance TO:0006001\| spikelet length TO:0002768\| seed maturation TO:0002661\| oxidative stress TO:0002657\| carbon isotope discrimination TO:0002643\| water use efficiency TO:0001017\| grain weight TO:0000919\| plastochron TO:0000735\| starch content TO:0000696\| 1000-grain weight TO:0000533\| sodium concentration TO:0000526\| chlorophyll content TO:0000495\| spikelet number TO:0000456\| grain yield per plant TO:0000449\| male sterility TO:0000437\| germination rate TO:0000430\| callus induction TO:0000428\| gall midge resistance TO:0000423\| pollen fertility TO:0000421\| grain size TO:0000397\| seed size TO:0000391\| 1000-grain weight TO:0000382\| heterosis TO:0000355\| tiller number TO:0000346\| self-incompatibility | Peptidase S59, nucleoporin family proteir | GO:00009 |
| | WW/Rsp5/WWP domain containing protein | |
| [Os] gibberellic acid sensitivity (TO:0000166) \| brassinosteroid sensitivity (TO:0002677) \| UV-B light sensitivity (TO:0000601) \| jasmonic acid sensitivity (TO:0000172) \| auxin sensitivity (TO:0000163) \| drought tolerance (TO:0000276) \| heat tolerance (TO:0000259) \| plant growth hormone sensitivity (TO:0000401) \| cold tolerance (TO:0000303) \| UV light sensitivity (TO:0000160) \| ethylene sensitivity (TO:0000173) \| salt tolerance (TO:0006001) \| biotic stress trait (TO:0000179) \| cytokinin sensitivity (TO:0000167) \| abscisic acid sensitivity (TO:0000615) | Aromatic L-amino acid decarboxylase (A | GO:00065 |
| | Cytochrome P450 family protein | |

|  |  |  |
|---|---|---|
|  | Protein of unknown function DUF151 dor | GO:00165 |
|  | Anti-sense to fibroblast growth factor protein GFG f |  |
| [Os] abscisic acid sensitivity (TO:0000615) \| drought tolerance (TO:0000276) \| salt tolerance (TO:0006001); [Os] salt tolerance |  |  |
| [Os] oxidative stress TO:0002657 | Protein kinase, core domain containing p | GO:00064 |
|  | Pentatricopeptide repeat domain containi | GO:00000 |
|  | Similar to H0404F02.16 protein | GO:00068 |
| [Os] cold tolerance TO:0000303 |  |  |
|  | Pentatricopeptide repeat domain containi | GO:00094 |
|  | tRNA intron endonuclease, catalytic dom | GO:00003 |
|  | Protein kinase, catalytic domain domain ( | GO:00064 |
|  | ATPase, AAA+ type, core domain contain | GO:00007 |
|  | Smg8/Smg9 domain containing protein | GO:00001 |
| [Os] iron sensitivity (TO:0000224); [Os] drought tolerance TO:0000276\| disease resistance TO:0000112 | Similar to Helix-loop-helix-like protein (I | GO:00063 |
|  | BRO1 domain domain containing protein |  |
|  | Cytochrome P450 family protein |  |
|  | Zm00001e019132 | GO:00007 |
| [Os] salt tolerance (TO:0006001) \| chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| leaf color (TO:0000326) \| chloroplast development trait (TO:0002715) \| chlorophyll content (TO:0000495) \| carotenoid content (TO:0000496) \| cold tolerance (TO:0000303) | RNA-binding, CRM domain domain conta | GO:00003 |
|  | Nucleotide-sensitive chloride conductanc | GO:00003 |
|  | Similar to Ankyrin repeat-rich membrane | GO:00063 |
|  | Hypothetical conserved gene | GO:00229 |
|  | Myeloid leukemia factor domain containing protein |  |
| [Os] salt tolerance (TO:0006001) \| grain size (TO:0000397) \| tiller angle (TO:0000567) \| leaf length (TO:0000135) \| grain number | Similar to Triose-phosphate Transporter | GO:00068 |
|  | Conserved hypothetical protein |  |

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|---|---|---|
| [Os] oxidative stress TO:0002657\| shoot branching TO:0002639\| plastochron TO:0000735\| acid sensitivity TO:0000479\| tiller number TO:0000346\| disease resistance TO:0000112\| blast disease resistance TO:0000074; [Ta] plant height TO:0000207\| grain weight TO:0000919\| panicle length TO:0000040\| spikelet number | Similar to Squamosa promoter-binding-like protein | |
| | Peptidase aspartic, catalytic domain cont | GO:00065 |
| | Mitochondrial import inner membrane tr | GO:00450 |
| | Similar to Benzoyl coenzyme A: benzyl alcohol benz | |
| | Toll-Interleukin receptor domain containi | GO:00007 |
| | Similar to H/ACA ribonucleoprotein comp | GO:00068 |
| | Transferase family protein | |
| | Similar to histone acetyltransferase | GO:00063 |
| | Dimethylaniline monooxygenase, N-oxide-forming | |
| | Conserved hypothetical protein | |
| | | |
| | Targeting for Xklp2 family protein | GO:00321 |
| [Os] bacterial blight disease resistance (TO:0000175) \| cold tolerance (TO:0000303) | WRKY transcription factor, Cold toleranc | GO:00063 |
| | Similar to Chloroplast protein import con | GO:00150 |
| [Os] sterility related trait (TO:0000485) | Ser/Thr kinase, Generation of proper ten | GO:00064 |
| | Armadillo-like helical domain containing protein | |
| [Os] male sterility (TO:0000437) | Similar to Male sterility MS5 | |
| [Os] pollen sterility (TO:0000053) | Similar to H0718E12.6 protein | GO:00063 |

| | | |
|---|---|---|
| [Os] carotenoid content (TO:0000496) \| chlorophyll-b content (TO:0000295) \| chlorophyll-a content (TO:0000293) \| chlorophyll content (TO:0000495) \| leaf color (TO:0000326) | Similar to EMB2279 (EMBRYO DEFECTIVE | GO:00096 |
| | Similar to (1,4)-beta-xylan endohydrolas | GO:00002 |
| [Os] cold tolerance (TO:0000303) | FAS1 domain domain containing protein | |
| | Serine/threonine protein kinase-related c | GO:00064 |
| | Similar to RING-H2 finger protein ATL1G | GO:00065 |
| [Os] hydrogen peroxide content (TO:0000605) \| leaf color (TO:0000326) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| carotenoid content (TO:0000496) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| seed set percent (TO:0000455) \| 1000-seed weight (TO:0000382) \| leaf width (TO:0000370) \| relative water content (TO:0000136) \| stomatal frequency (TO:0000566) \| internode length (TO:0000145) \| chloroplast development trait (TO:0002715) \| leaf senescence (TO:0000249) \| leaf development trait (TO:0000655); [Os] sporogenesis TO:0000727 | Protein kinase, catalytic domain domain c | GO:00064 |
| | Uncharacterized plant-specific domain 0 | GO:00098 |
| | Conserved hypothetical protein | |
| [Os] tiller number (TO:0000346) \| tillering ability (TO:0000329) | Circadian-associated rice pseudo respon | GO:00001 |
| | Zm00001e006057 | GO:00063 |
| | WD40 repeat-like domain containing pro | GO:00034 |
| | Plant organelle RNA recognition domain domain con | |
| | Pentatricopeptide repeat domain containi | GO:00063 |
| | Zm00001e020568 | |
| | Similar to SAC domain protein 3 | GO:00360 |
| [Os] brittle culm TO:0000200 | Protein of unknown function DUF266, plant family p | |

| | | |
|---|---|---|
| [Os] cold tolerance (TO:0000303) \| bacterial blight disease resistance (TO:0000175) | Zm00001e029958 | GO:00064 |
| [Os] mimic response (TO:0000063) | Double stranded RNA binding domain (ds | GO:00709 |
| [Os] abscisic acid sensitivity (TO:0000615) \| starch content (TO:0000696) \| drought tolerance (TO:0000276) \| flowering time | | |
| | Armadillo-type fold domain containing p | GO:00002 |
| | Conserved hypothetical protein | |
| | Similar to 60S ribosomal protein L7 | GO:00004 |
| | Sec1-like protein family protein | GO:00068 |
| | Hypothetical conserved gene | |
| | Similar to MPI | GO:00096 |
| | Similar to OSIGBa0155K17.8 protein | GO:00063 |
| [Os] days to heading (TO:0000137) \| primary branching of inflorescence (TO:0000052); [Os] protein content TO:0000598\| basic vegetative phase TO:0000461; [Ta] relative root length TO:0000516\| beta-glucan content TO:0020068\| seed maturation TO:0002661\| male sterility TO:0000437\| root length TO:0000227\| amino acid content TO:0002673\| flavonoid content TO:0000290\| oxidative stress TO:0002657\| aphid resistance TO:0006067\| disease resistance TO:0000112\| protein content TO:0000598\| carotenoid content TO:0000496\| grain weight TO:0000919\| photosynthetic rate TO:0001015\| heterosis TO:0000355\| net photosynthetic rate TO:0001027\| embryoless TO:0000189\| plant height TO:0000207\| respiration rate TO:0001026 | FCA-like protein, FCA gamma protein, Fl | GO:00083 |
| | Cyclin-like F-box domain containing protein | |

| | | |
|---|---|---|
| [Os] mimic response (TO:0000063) \| plant height (TO:0000207) \| bacterial blight disease resistance (TO:0000175) \| sheath blight disease resistance (TO:0000255) | Similar to NPR1-like protein | GO:0006 |
| [Os] bacterial blight disease resistance (TO:0000175) \| salt tolerance (TO:0006001) \| seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| drought tolerance (TO:0000276) \| submergence tolerance (TO:0000524) | Protein kinase, core domain containing p | GO:00064 |
| | Hypothetical protein | |
| | Region of unknown function DUF1767 domain conta | |
| | Similar to Protein binding protein Zm00001e005334 | GO:00717 |
| | Similar to H0307D04.13 protein | GO:00063 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] grain yield (TO:0000396) \| mimic response (TO:0000063) \| filled grain number (TO:0000447) \| hydrogen peroxide content (TO:0000605) \| disease resistance (TO:0000112) \| panicle length (TO:0000040) \| plant height (TO:0000207) \| tiller number (TO:0000346) \| bacterial blight disease resistance (TO:0000175) \| blast disease (TO:0000074) | Zinc finger, RING-type domain containin | GO:00165 |

[Os] carotenoid content (TO:0000496) | leaf color (TO:0000326) | grain number (TO:0002759) | leaf rolling (TO:0000085) | secondary branch number (TO:0000557) | filled grain number (TO:0000447) | spikelet fertility (TO:0000180) | chloroplast development trait (TO:0002715) | grain weight (TO:0000590) | primary branch number (TO:0000547) | panicle number (TO:0000152) | grain yield per plant (TO:0000449) | root development trait (TO:0000656) | chlorophyll content (TO:0000495) | panicle length (TO:0000040) | fertility related trait (TO:0000420) | plant height (TO:0000207) | yield trait (TO:0000371) | salt tolerance (TO:0006001) | drought tolerance (TO:0000276) | leaf shape (TO:0000492) | grain yield (TO:0000396) | hydrogen peroxide content (TO:0000605) | leaf width (TO:0000370) | flowering time (TO:0002616) | blast disease (TO:0000074) | variegated leaf

Apoptosis regulator Bcl-2 protein, BAG d GO:0050
Zinc finger, C2H2-type domain containing protein
Small-subunit processome, Utp14 domai GO:00063

[Os] total fat content (TO:0000602) | pollen free (TO:0000245) | male sterility (TO:0000437) | sterility or fertility trait (TO:0000392) | anther color (TO:0000187); [Os] male sterility TO:0000437

Glycerol-3-phosphate acyltransferase, Anther devel
Similar to Cytochrome P450 monooxygenase CYP72
NLI interacting factor domain containing protein
Zm00001e040682 GO:00094
Hypothetical conserved gene GO:00094

Similar to MAP3K gamma protein kinase ( GO:00001
IQ calmodulin-binding region domain co GO:00070
WD40/YVTN repeat-like domain containing protein

<table>
<tr><td></td><td>Resolvase, holliday junction-type, YqgF-l</td><td>GO:00009</td></tr>
<tr><td>[Os] blast disease (TO:0000074) | cold tolerance (TO:0000303) | drought tolerance (TO:0000276) | salt tolerance (TO:0006001) | heat tolerance (TO:0000259) | jasmonic acid sensitivity (TO:0000172) | abscisic acid sensitivity (TO:0000615) | bacterial blight disease resistance (TO:0000175) | sheath blight disease resistance</td><td>Peptidase C14, caspase catalytic domain</td><td>GO:00065</td></tr>
<tr><td></td><td>Similar to predicted protein</td><td>GO:00065</td></tr>
<tr><td></td><td></td><td></td></tr>
<tr><td></td><td>Trigger factor, ribosome-binding, bacteri</td><td>GO:00064</td></tr>
<tr><td>[Os] salt tolerance (TO:0006001) | flower development trait (TO:0000622) | gibberellic acid content (TO:0002675) | starch content (TO:0000696) | sugar content (TO:0000333) | plant height (TO:0000207)</td><td>B3 domain transcriptional repressor, Regulator of se</td><td></td></tr>
<tr><td></td><td>TGF-beta receptor, type I/II extracellular</td><td>GO:00429</td></tr>
<tr><td></td><td>WD40 repeat-like domain containing pro</td><td>GO:20000</td></tr>
<tr><td></td><td>Similar to ORW1943Ba0077G13.3 protein</td><td>GO:00059</td></tr>
<tr><td>[Os] drought tolerance (TO:0000276) | abscisic acid sensitivity (TO:0000615) | salt tolerance (TO:0006001) | cold tolerance (TO:0000303) | heat tolerance (TO:0000259) | bacterial blight disease resistance (TO:0000175) | blast disease (TO:0000074) | leaf senescence (TO:0000249)</td><td>WRKY transcription factor 26</td><td>GO:00063</td></tr>
<tr><td></td><td>Similar to ATMAP65-6; microtubule bindi</td><td>GO:00002</td></tr>
<tr><td></td><td>Similar to plectin-related</td><td>GO:00070</td></tr>
<tr><td></td><td>Zm00001e033486</td><td>GO:00311</td></tr>
<tr><td></td><td>Zm00001e005696</td><td>GO:00098</td></tr>
<tr><td></td><td>Kelch repeat type 1 domain containing pr</td><td>GO:00349</td></tr>
<tr><td></td><td>Heat shock protein DnaJ, N-terminal domain contai</td><td></td></tr>
<tr><td>[Os] cytoplasmic male sterility TO:0000580| male sterility TO:0000437| drought tolerance TO:0000276| brown rice protein TO:0000138| disease resistance TO:0000112; [Ta] respiration rate TO:0001026| chlorophyll content</td><td>K Homology, type 1, subgroup domain co</td><td>GO:00104</td></tr>
<tr><td></td><td>Nucleic acid-binding, OB-fold domain co</td><td>GO:00108</td></tr>
<tr><td></td><td>Similar to TAR RNA loop binding protein</td><td>GO:00063</td></tr>
</table>

| | | |
|---|---|---|
| [Os] cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| plant growth hormone sensitivity (TO:0000401) \| brassinosteroid sensitivity (TO:0002677) \| plant height | | |
| | Pentatricopeptide repeat domain containing protein | |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to GRAS family transcription facto | GO:00063 |
| | Protein kinase, catalytic domain domain c | GO:00064 |
| [Os] disease resistance (TO:0000112) \| oxidative stress (TO:0002657) | Similar to DEAD-box ATP-dependent RN | GO:00069 |
| | Similar to OSIGBa0131J24.2 protein | GO:00061 |
| | Glycosyl transferase, family 8 protein | GO:00454 |
| | Similar to OSIGBa0124N08.6 protein | GO:00159 |
| | Zm00001e039768 | GO:00064 |
| | Protein kinase, core domain containing p | GO:00064 |
| [Os] UV light sensitivity (TO:0000160) | | |
| [Os] grain number TO:0002759\| chlorophyll content TO:0000495\| seed shape TO:0000484\| grain size TO:0000397\| plant height TO:0000207 | RNA polymerase sigma factor, region 2 d | GO:00063 |
| | Similar to Resistance protein candidate (F | GO:00064 |
| | Lupus La protein family protein | GO:00063 |
| | Protein of unknown function DUF3537 domain conta | |
| | K Homology domain containing protein | GO:00104 |
| [Os] chromium sensitivity (TO:0000034) | Serine carboxypeptidase, Regulation of g | GO:00065 |
| | Zinc finger, FYVE/PHD-type domain containing prot | |
| [Os] spikelet fertility (TO:0000180) \| amino acid content (TO:0002673) \| protein content (TO:0000598) \| seed quality (TO:0000162) \| pollen fertility (TO:0000421) \| seed set percent (TO:0000455) \| grain yield | Dicer-like protein, Phased small RNA bio | GO:00063 |
| | Similar to Glutathione S-transferase GST | GO:00067 |

| | | |
|---|---|---|
| | PAP/25A core domain containing protein | GO:00311 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Protein of unknown function DUF579, pla | GO:00098 |
| | Similar to Fatty acyl coA reductase | GO:00066 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] male sterility (TO:0000437); [Os] organ identity TO:0006018\| male sterility TO:0000437 | bZIP transcription factor, Tapetum devel | GO:00063 |
| | Exonuclease domain containing protein | GO:00063 |
| | Tetratricopeptide-like helical domain containing pr | |
| | Cell cycle regulated microtubule associat | GO:00321 |
| | Similar to OSIGBa0158F13.10 protein | |
| [Os] jasmonic acid sensitivity (TO:0000172) \| plant height (TO:0000207) \| grain yield (TO:0000396) \| salt tolerance (TO:0006001) \| iron sensitivity (TO:0000224) \| cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) \| gibberellic acid | Zinc finger, B-box domain containing pr | GO:00063 |
| | Similar to Beta-1,3 glucanase precursor ( | GO:00059 |
| | Pectin lyase fold/virulence factor domain | GO:00059 |
| | Protein of unknown function DUF662 family protein | |
| | WD40 repeat domain containing protein | |
| [Os] disease resistance TO:0000112 | Exo70 exocyst complex subunit family p | GO:00068 |
| | Conserved hypothetical protein | GO:00439 |
| | Protein kinase, catalytic domain domain | GO:00064 |
| | Similar to Aldose 1-epimerase-like prote | GO:00059 |
| | Harpin-induced 1 domain containing pro | GO:00985 |
| | Similar to S-locus protein 5 (Fragment) | |
| [Os] growth and development trait (TO:0000357) \| oxidative stress (TO:0002657) | Matrix metalloproteinase, Plant develop | GO:00065 |
| [Os] heat tolerance (TO:0000259) | Rossmann-like alpha/beta/alpha sandwi | GO:00020 |
| | CCAAT-binding factor domain containin | GO:00062 |

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|---|---|---|
| | Protein of unknown function DUF668 fam | GO:00459 |
| | Protein-tyrosine phosphatase, dual speci | GO:00064 |
| [Os] tiller angle TO:0000567 | Zinc finger, RING/FYVE/PHD-type domair | GO:00165 |
| | Glycosyl transferase, family 8 protein | GO:00454 |
| | Similar to DnaJ domain containing protein, expresse | |
| | Similar to T24D18.25 protein | |
| | SET domain containing protein | GO:00180 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] oxidative stress (TO:0002657) \| drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) | | |
| [Os] anther length (TO:0000531) \| male sterility (TO:0000437) \| anther shape (TO:0000214) | | |
| | 50S ribosomal protein L34 | GO:00064 |
| | Zm00001e032219 | GO:00063 |
| | Thiolase-like, subgroup domain containi | GO:00066 |
| [Os] leaf color (TO:0000326) \| panicle color (TO:0000201) \| heat tolerance (TO:0000259) \| photosynthetic ability (TO:0000316) \| chlorophyll content (TO:0000495) | Carbohydrate/purine kinase domain cont | GO:00096 |
| | Similar to SKIP interacting protein 18 (Fra | GO:00070 |
| [Os] disease resistance TO:0000112 | Similar to Salicylic acid-binding protein 2 | GO:00096 |
| [Os] tillering ability (TO:0000329) \| tiller number (TO:0000346) | Bromo adjacent region domain containin | GO:00319 |

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|---|---|---|
| [Os] temperature response trait (TO:0000432) \| pollen free (TO:0000245) \| anther length (TO:0000531) \| pollen abortion type (TO:0000218) \| genic male sterility-thermo sensitive (TO:0000067) \| anther color (TO:0000187) \| pollen fertility (TO:0000421) \| male sterility (TO:0000437) \| stamen anatomy and morphology trait (TO:0000215) \| microsporocyte development trait | Putative glucose-methanol-choline oxidoreductase, | |
| | Similar to predicted protein | GO:00171 |
| [Os] stem length (TO:0000576) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| growth and development trait (TO:0000357) \| seed development trait (TO:0000653) \| panicle length (TO:0000040) \| spikelet number (TO:0000456) \| grain shattering (TO:0000473) | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | CARP motif domain containing protein | GO:00002 |
| | Similar to NodH (Fragment) | |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Similar to Nodulin-like protein | GO:00550 |
| | Similar to PRLI-interacting factor G (Frag | GO:00165 |
| | Zm00001e033010 | |
| | Zm00001e034440 | |
| [Os] bacterial blight disease resistance (TO:0000175) | ACC oxidase, Ethylene biosynthesi | |
| | Similar to KH domain containing protein, | GO:00099 |
| | Ribosomal protein S5, bacterial-type do | GO:00064 |
| | Protein of unknown function DUF679 fa | GO:00102 |
| | Lipase, class 3 family protein | GO:00066 |
| | Similar to GTP cyclohydrolase 1 isoform | GO:00067 |
| | Dynein light chain, type 1 family protein | GO:00070 |
| | Plant-specific protein with a short C-ter | GO:00363 |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) \| seed development trait (TO:0000653) | RmlC-like jelly roll fold domain containin | GO:00065 |
| | bZIP DNA-binding protein, Disease resist | GO:00063 |
| | Similar to DNA binding protein | GO:00063 |
| | Similar to E2F homolog (Fragment) | GO:00001 |
| | D111/G-patch domain containing protei | GO:00421 |
| [Os] root meristem development (TO:0002692) \| auxin sensitivity (TO:0000163) \| leaf size (TO:0002637) \| root length (TO:0000227) \| seed size (TO:0000391) \| stamen size (TO:0002601) \| pistil size (TO:0002602) \| stem width (TO:0001035) \| brassinosteroid sensitivity (TO:0002677) \| yield trait (TO:0000371) \| tillering ability (TO:0000329) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| leaf angle (TO:0000206) \| plant cell size (TO:0002684) \| grain length | Similar to AP2-1 protein (Fragment) | GO:00063 |
| | Protein of unknown function DUF155 dor | GO:00100 |
| | Conserved hypothetical protein | |
| | IQ calmodulin-binding region domain containing pr | |
| | Similar to H0525G02.7 protein | |
| | Domain of unknown function DUF250 do | GO:00068 |
| [Os] salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| 1000-seed weight (TO:0000382) | Similar to Very-long-chain fatty acid con | GO:00066 |
| | Similar to Basic leucine zipper protein (Li | GO:00063 |
| [Os] leaf senescence (TO:0000249) \| salt tolerance (TO:0006001) \| shoot development trait (TO:0000654) \| auxin sensitivity (TO:0000163) \| chlorophyll content (TO:0000495) \| cell membrane stability (TO:0000467) \| cytokinin sensitivity (TO:0000167) \| percent germination (TO:0010001) \| hydrogen peroxide content (TO:0000605) | 2OG-Fe(II) oxygenase domain containing | GO:00801 |

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|---|---|---|
| | Similar to X1 (Fragment) | GO:00310 |
| | Lecithin:cholesterol acyltransferase famil | GO:00066 |
| | ATP-binding region, ATPase-like domain | GO:00028 |
| [Os] radiation response trait (TO:0000161) | Ortholog of Arabidopsis NLA (AtNLA), RI | GO:00165 |
| [Os] gibberellic acid sensitivity (TO:0000166) \| jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615) | Similar to GGDP synthase | GO:00082 |
| | Similar to Type II membrane protein | |
| | Similar to Protein N-terminal asparagine | GO:00065 |
| | Conserved hypothetical protein | GO:00430 |
| | DEAD-like helicase, N-terminal domain c | GO:00094 |
| | Similar to OSIGBa0118P15.11 protein | GO:00059 |
| | Zm00001e007278 | |
| | Plant lipid transfer protein/Par allergen f | GO:00065 |
| | E2F-associated phosphoprotein domain | GO:00082 |
| [Ta] disease resistance TO:0000112\| fungal disease resistance TO:0000439 | Hypothetical conserved gene | GO:00064 |
| | Similar to LRR14 | GO:00069 |
| | Similar to OSIGBa0134P10.2 protein | GO:00067 |
| | Six-bladed beta-propeller, TolB-like dom | GO:00090 |
| | Methyladenine glycosylase domain conta | GO:00062 |
| | Zm00001e013363 | GO:00063 |
| | Helicase-like, DEXD box c2 type domain | GO:00061 |
| | Serine/threonine protein kinase domain | GO:00000 |
| [Os] meristem identity TO:0006017\| oxidative stress TO:0002657 | DDT domain containing protein | GO:00063 |
| | Cupredoxin domain containing protein | GO:00229 |
| [Os] salt tolerance (TO:0006001) | Similar to CRS1/YhbY domain containing | GO:00003 |
| | Protein of unknown function DUF6, transmembrane | |
| | Similar to Protein phosphatase type 2C | GO:00097 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to Steroid membrane binding protein-like | |
| | Conserved hypothetical protein | GO:00060 |
| | Similar to Protein translocase/ protein tr | GO:00450 |
| | Lipase, GDSL domain containing protein | |

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|---|---|---|
| [Os] leaf senescence (TO:0000249) \| starch content (TO:0000696) \| cytokinin sensitivity (TO:0000167) \| auxin sensitivity (TO:0000163) \| seed maturation (TO:0002661) \| endosperm related trait (TO:0000575) \| gibberellic acid sensitivity (TO:0000166); [Os] grain weight TO:0000919\| plant height TO:0000207\| disease resistance TO:0000112 | Similar to MtN3 protein precursor | GO:00086 |
| | BTB domain containing protein | GO:00165 |
| | Hypothetical conserved gene | GO:00485 |
| | RNA-binding, CRM domain domain conta | GO:00003 |
| | EF-Hand type domain containing protein | |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Similar to predicted protein | |
| | Glycosyl transferase, family 43 protein | GO:00059 |
| | Protein of unknown function, transmemb | GO:00071 |
| | 4'-phosphopantetheinyl transferase dom | GO:00066 |
| | Protein of unknown function DUF652 fa | GO:00063 |
| | Similar to Chaperone protein dnaJ | |
| | Similar to glycerophosphodiester phosph | GO:00060 |
| | Nucleic acid-binding, OB-fold domain co | GO:00063 |
| | Similar to Yarrowia lipolytica chromosom | GO:00064 |
| | Hypothetical conserved gene | GO:00163 |
| | Nucleotide-binding, alpha-beta plait do | GO:00104 |
| [Os] brassinosteroid sensitivity (TO:0002677) \| leaf lamina joint bending (TO:0002688) \| flag leaf length (TO:0002757) \| flag leaf lamina width (TO:0002758) \| 1000-seed weight (TO:0000382) \| seedling height (TO:0000019) \| seed set percent (TO:0000455) \| grain size (TO:0000397) \| leaf angle (TO:0000206) \| plant height | Similar to NLI interacting factor-like phos | GO:00096 |
| | Hypothetical conserved gene | GO:00064 |
| [Os] silicon sensitivity (TO:0000031) | Aquaporin NIP III subfamily protein, Aqua | GO:00157 |

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|---|---|---|
| [Os] osmotic response sensitivity (TO:0000095) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| hydrogen peroxide content (TO:0000605) \| abscisic acid sensitivity (TO:0000615) | Bet v I allergen family protein | GO:00069 |
| [Os] bacterial blight disease resistance (TO:0000175) \| stem borer resistance (TO:0000454) \| sheath blight disease resistance (TO:0000255) \| heat tolerance (TO:0000259) \| salt tolerance (TO:0006001); [Os] drought tolerance TO:0000276 | WRKY transcription factor 30 | GO:00063 |
| | Protein kinase, catalytic domain domain | GO:00064 |
| | Similar to RhoGAP domain containing pro | GO:00071 |
| [Os] spikelet fertility (TO:0000180) \| sterility related trait (TO:0000485) | A member of the synaptonemal complex | GO:00070 |
| | Similar to Gt-2 | |
| [Os] endosperm storage protein content (TO:0002653) | Splicing isoform of OsRMR | GO:00150 |
| | Similar to Sorbitol transporter | GO:00086 |
| [Os] days to heading (TO:0000137) \| seed maturation (TO:0002661) \| endosperm storage protein content (TO:0002653) \| plant height (TO:0000207) \| chlorophyll content (TO:0000495) \| tiller number (TO:0000346) \| grain size (TO:0000397) \| spikelet fertility (TO:0000180) \| flowering time (TO:0002616) \| sterility related trait | RNA-binding region RNP-1 (RNA recogn | GO:00510 |
| [Os] temperature response trait (TO:0000432) \| male sterility (TO:0000437) | Radc1 | GO:00065 |
| [Os] chlorophyll-a content (TO:0000293) \| leaf color (TO:0000326) \| chlorophyll content (TO:0000495) \| chlorophyll-b content (TO:0000295) \| chloroplast development trait | Similar to MAP3K beta 3 protein kinase (E | GO:00001 |
| | Conserved hypothetical protein | |

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|---|---|---|
| | Similar to MutS domain V family protein, | GO:00062 |
| | Nop14-like protein family protein | GO:00304 |
| | Protein of unknown function DUF579, pla | GO:00098 |
| [Os] relative chlorophyll content (TO:0001016) \| total soluble sugar content (TO:0000340) \| hydrogen peroxide content (TO:0000605) \| salt tolerance (TO:0006001) \| proline content (TO:0006002) | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] stress trait (TO:0000164) \| drought tolerance (TO:0000276) \| oxidative stress (TO:0002657) \| salt tolerance (TO:0006001) | Similar to ABI3-interacting protein 2-1 p | GO:00065 |
| | Protein kinase, core domain containing p | GO:00064 |
| [Os] plant height (TO:0000207) \| abscisic acid sensitivity (TO:0000615) \| auxin sensitivity (TO:0000163) \| lateral root number (TO:0001013) \| leaf senescence (TO:0000249) \| chlorophyll content (TO:0000495) \| grain yield (TO:0000396) \| sucrose content (TO:0000328) \| shoot potassium content (TO:0020003) \| shoot sodium content (TO:0020004) \| herbicide sensitivity (TO:0000058) \| osmotic response sensitivity (TO:0000095) \| cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) \| jasmonic acid content (TO:0002668) \| salt tolerance (TO:0006001) \| root development trait (TO:0000656) \| abscisic acid content | Putative methyltransferase, Pectin synthe | GO:00322 |
| | Similar to Protein kinase domain containi | GO:00064 |
| | Cytochrome p450 (CYP78A9) | |
| | Nucleotide-binding, alpha-beta plait don | GO:00003 |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | bZIP transcription factor, Modulation of t | GO:00063 |

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|---|---|---|
| [Os] tiller number (TO:0000346) \| plant height (TO:0000207); [Ta] ash content TO:0000607 | Similar to CONSTANS interacting protein | GO:00017 |
|  | Similar to aspartic proteinase nepenthesi | GO:00065 |
|  | Zm00001e027986 | GO:00063 |
|  | Similar to Lipoxygenase (Fragment) | GO:00066 |
|  | Thioredoxin domain 2 containing protein | GO:00454 |
|  | Hypothetical conserved gene |  |
|  | Ribosomal protein L7/L12 family protein | GO:00064 |
|  | Transmembrane receptor, eukaryota domain contai |  |
| [Os] submergence tolerance (TO:0000524) | Serine/threonine protein kinase-related | GO:00064 |
|  | Similar to Glycosyl hydrolase family 10 p | GO:00002 |
|  | Similar to 50S ribosomal protein L18, chl | GO:00064 |
|  | Protein of unknown function DUF716 family protein |  |
|  | TB2/DP1 and HVA22 related protein family protein |  |
|  | Pectinesterase inhibitor domain containi | GO:00430 |
|  | Cupredoxin domain containing protein | GO:00229 |
|  | Pentatricopeptide repeat domain containi | GO:00094 |
|  | Glycosyl transferase, family 31 domain c | GO:00064 |
|  | Ubiquitin-conjugating enzyme/RWD-like | GO:00165 |
|  | Similar to Cytochrome P450 |  |
|  | Similar to DNA replication complex GINS | GO:00062 |
|  | VRR-NUC domain containing protein | GO:00062 |
|  | Alpha/beta hydrolase fold-3 domain containing pro |  |
| [Os] plant height (TO:0000207) \| gibberellic acid content (TO:0002675); [Os] stem elongation TO:0006036 | Similar to GA 2-oxidase 5 | GO:00454 |
|  | Protein of unknown function DUF231, pla | GO:19909 |
|  | Serine/threonine protein kinase-related | GO:00064 |
|  | Similar to seed maturation protein | GO:00096 |
|  | Peptidase A22A, presenilin family protein | GO:00065 |

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|---|---|---|
| [Os] plant height (TO:0000207) | Thiolase-like, subgroup domain containi | GO:00066 |
| [Os] plant height (TO:0000207) \| mesocotyl length (TO:0000544) \| light intensity sensitivity (TO:0000460) \| stem elongation (TO:0006036); [Os] shoot branching TO:0002639 | | |
| | Similar to Haemolysin-III related family p | GO:00097 |
| | Zm00001e016450 | GO:00063 |
| | Similar to RNA helicase (Fragment) | |
| | Similar to Protein-O-fucosyltransferase 1 | GO:00060 |
| [Os] days to heading (TO:0000137) \| flowering time (TO:0002616) | Cys2/His2-type zinc finger transcription | GO:00063 |
| | Cyclin-like F-box domain containing protein | |
| [Os] salt tolerance (TO:0006001) | Similar to Fatty acyl coA reductase | GO:00066 |
| [Os] plant height (TO:0000207) | YT521-B-like protein family protein | GO:00611 |
| | Uncharacterised protein family UPF0497, | GO:00072 |
| | Similar to 61 kDa protein homolog | GO:00007 |
| | RabGAP/TBC domain containing protein | GO:00068 |
| | Similar to predicted protein | |
| [Os] plant height (TO:0000207) \| spikelet fertility (TO:0000180) \| days to heading (TO:0000137) | E3 ligases of H2Bub1, Transcriptional reg | GO:00063 |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Similar to Myb-like DNA-binding domain | GO:00101 |
| | Pentatricopeptide repeat domain containi | GO:00094 |

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|---|---|---|
| [Os] drought tolerance (TO:0000276) \| hydrogen peroxide content (TO:0000605) \| leaf rolling (TO:0000085) | Uncharacterised protein family UPF0089 ( | GO:00194 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to RNA-binding protein EWS | |
| | Zm00001e003516.m1 | GO:00064 |
| | Similar to predicted protein | |
| | Similar to predicted protein | |
| | UDP-glucuronosyl/UDP-glucosyltransferase family p | |
| [Os] cold tolerance (TO:0000303) \| jasmonic acid sensitivity (TO:0000172) \| auxin sensitivity (TO:0000163) \| gibberellic acid sensitivity (TO:0000166) \| cytokinin sensitivity (TO:0000167) \| ethylene sensitivity (TO:0000173) \| abscisic acid sensitivity (TO:0000615) \| biotic stress trait (TO:0000179) \| light sensitivity (TO:0000075) \| heat tolerance (TO:0000259) \| blast disease (TO:0000074) \| drought tolerance | Aromatic L-amino acid decarboxylase (A | GO:00065 |
| | Glutathione S-transferase, C-terminal-lik | GO:00066 |
| | Similar to small auxin up RNA1 | GO:00097 |
| | Plant disease resistance response protein | GO:00096 |
| | Protein of unknown function DUF3506 dc | GO:00003 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to microtubule motor | GO:00070 |
| [Os] cytokinin sensitivity (TO:0000167) \| abscisic acid sensitivity (TO:0000615) \| cold tolerance (TO:0000303) \| auxin sensitivity (TO:0000163) \| ethylene sensitivity (TO:0000173) \| blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) \| mimic response (TO:0000063) \| bacterial disease resistance (TO:0000315) | Similar to Cyclic nucleotide-gated channe | GO:00068 |
| | Similar to Spc97/Spc98 family protein, e | GO:00002 |
| | Similar to EF-hand calcium bining protein | |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |

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|---|---|---|
| [Os] gibberellic acid sensitivity (TO:0000166) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| flowering time (TO:0002616); [Os] seed weight TO:0000181 | Peptidase C48, SUMO/Sentrin/Ubl1 famil | GO:00065 |
| [Os] auxin sensitivity (TO:0000163) \| leaf development trait (TO:0000655) \| plant height (TO:0000207) \| basal tiller number (TO:0001004) \| glume opening (TO:0000474) \| water stress trait (TO:0000237) \| gravity response trait (TO:0002693) \| awn anatomy and morphology trait (TO:0002718) \| seed development trait (TO:0000653) | Similar to Auxin response factor 2 | GO:00063 |
| | PapD-like domain containing protein | GO:00618 |
| | Similar to Peptide-N4-(N-acetyl-beta-glucosaminyl) | |
| | Tyrosine protein kinase domain containin | GO:00064 |
| | Protein kinase, core domain containing p | GO:00064 |
| | | |
| [Os] drought tolerance (TO:0000276) | HMG1 protein (HMGB1) | |
| | Similar to nodulin protein | GO:00550 |
| | Zm00001e040138 | GO:00063 |
| [Os] hydrogen peroxide content (TO:0000605) \| grain yield (TO:0000396) \| panicle length (TO:0000040) \| panicle size (TO:0006032) \| plant height (TO:0000207) \| filled grain number (TO:0000447) \| grain size (TO:0000397) \| grain weight (TO:0000590) \| inflorescence development trait (TO:0000621) \| | Aluminum-activated malate transporter, | GO:00157 |
| | Uncharacterised conserved protein UCP022348 dom | |
| | Zm00001e015358 | GO:00094 |
| | Hypothetical conserved gene | GO:00324 |
| | Protein kinase, catalytic domain domain c | GO:00064 |
| | | |
| | Clathrin light chain family protein | GO:00068 |
| | Similar to STE20/SPS1-related proline-al | GO:00064 |
| | Similar to ABI3-interacting protein 2 | GO:00099 |
| | Similar to H0510A06.1 protein | GO:00059 |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Nuclear hormone receptor, ligand-binding domain c | |

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|---|---|---|
| [Os] pistil anatomy and morphology trait (TO:0000223) \| inflorescence development trait (TO:0000621) \| female sterility (TO:0000358) | Transcription factor | GO:00063 |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| embryo development trait (TO:0000620) \| heat tolerance (TO:0000259) | Core subunit of exon junction complex ( | GO:00018 |
| | Similar to Protein kinase | GO:00064 |
| | Similar to Xyloglucan endotransglucosyla | GO:00059 |
| | Serine/threonine protein kinase-related | GO:00064 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Katanin P80 ortholog, Katanin regulatory | GO:00510 |
| | Similar to AINTEGUMENTA-like protein | GO:00063 |
| | Similar to Nudix hydrolase 18, mitochondrial precur | |
| | Glycosyl transferase, family 8 protein | GO:00454 |
| | Similar to 50S ribosomal protein L21, chl | GO:00064 |
| [Os] growth and development trait (TO:0000357); [Ta] peduncle length TO:0002691\| drought tolerance TO:0000276 | Similar to 65kD microtubule associated p | GO:00002 |
| | Zinc finger, RING-type domain containin | GO:00065 |
| [Os] heat tolerance (TO:0000259) \| blast disease (TO:0000074) \| gibberellic acid sensitivity (TO:0000166) \| plant height (TO:0000207) \| flowering time (TO:0002616); [Os] leaf size TO:0002637 | Zm00001e007049 | GO:00063 |
| | Similar to Transcription factor MYB86 (M | GO:00101 |
| | Pentatricopeptide repeat domain containing protein | |
| | Esterase, SGNH hydrolase-type domain containing p | |
| [Os] seed maturation (TO:0002661) \| leaf shape (TO:0000492) \| seed dormancy (TO:0000253) \| leaf width (TO:0000370); [Os] grain weight TO:0000919\| tiller number TO:0000346 | Zm00001e115211 | |

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|---|---|---|
| [Os] mineral and ion content related trait (TO:0000465) \| potassium content (TO:0000609) \| sodium to potassium content ratio (TO:0000525) \| blast disease (TO:0000074) \| salt tolerance (TO:0006001) \| bacterial blight disease resistance (TO:0000175) \| relative shoot dry weight (TO:0000636) \| relative chlorophyll content (TO:0001016) \| relative root dry weight (TO:0000644) \| relative root length (TO:0000516) \| leaf rolling tolerance (TO:0002662) \| leaf yellowing tolerance (TO:0002664) \| hydrogen peroxide | Two-pore K+ channel family protein, K+ | GO:00068 |
| | Conserved hypothetical protein | |
| | | |
| | Hypothetical conserved gene | GO:00096 |
| | Similar to 30S ribosomal protein S6, chlo | GO:00064 |
| [Os] seed number (TO:0000445) \| grain width (TO:0000402) \| plant height (TO:0000207) \| temperature response trait (TO:0000432) \| chlorophyll content (TO:0000495) \| grain yield (TO:0000396) \| cytokinin content (TO:0002660) \| gibberellic acid content (TO:0002675) \| grain weight | CC-type glutaredoxin, Homeostatic regul | GO:00454 |
| | Major facilitator superfamily, general sub | GO:00068 |
| | Similar to Enoyl CoA hydratase-like prote | GO:00066 |
| [Os] root hair length (TO:0002665) \| stem length (TO:0000576) \| root length (TO:0000227) \| blast disease (TO:0000074) \| drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) \| plant height (TO:0000207) | | |
| [Os] cold tolerance (TO:0000303) \| plant height (TO:0000207) \| drought tolerance (TO:0000276) \| photoperiod sensitivity (TO:0000229) | Similar to Lipid transfer protein | GO:00068 |
| | Conserved hypothetical protein | GO:00070 |
| | Heat shock protein DnaJ family protein | GO:00304 |
| | Pentatricopeptide repeat containing protein | |
| | Vitamin K epoxide reductase domain containing pro | |

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|---|---|---|
| [Os] abiotic stress trait (TO:0000168) \| plant growth hormone sensitivity (TO:0000401) \| mimic response (TO:0000063) \| light intensity sensitivity (TO:0000460) \| root development trait (TO:0000656) \| blast disease (TO:0000074) \| ethylene sensitivity (TO:0000173) \| plant height (TO:0000207) \| biotic stress trait (TO:0000179) \| cytokinin sensitivity (TO:0000167) | Beta-glucanase precursor | GO:00059 |
| | Similar to Pollen allergen Phl p 11 | |
| [Os] seed development trait (TO:0000653) \| grain size (TO:0000397) \| grain weight (TO:0000590); [Os] grain size | Auxin response factor (ARF) family protei | GO:00063 |
| [Os] spikelet fertility (TO:0000180) | Pollen-specific phospholipase, Patatin lik | GO:00066 |
| | Similar to Protein kinase | GO:00064 |
| | WD40 repeat-like domain containing protein | |
| [Os] organ identity TO:0006018\| male sterility TO:0000437 | Similar to Transcription factor HBP-1b(C3 | GO:00063 |
| | Similar to phosphatidylinositolglycan-rel | GO:00065 |
| | Hypothetical conserved gene | GO:00109 |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | Protein of unknown function DUF668 fam | GO:00459 |
| | Similar to UDP-glucose flavonoid-3-O-glucosyltrans | |
| | Reticulon family protein | GO:00096 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | 2OG-Fe(II) oxygenase domain containing | GO:00064 |
| | Similar to RNA helicase-like protein DB1 | GO:00001 |
| [Ta] root length TO:0000227\| root to shoot ratio TO:0000278 | Similar to IAA6 (Fragment) | GO:00063 |
| | Protein kinase, ATP binding site domain containing | |
| | Aldo/keto reductase domain containing protein | |
| | Cupredoxin domain containing protein | GO:00229 |
| | C2 calcium-dependent membrane targeti | GO:00068 |
| | Protein of unknown function DUF544 fam | GO:00711 |
| | Similar to oxidoreductase | |
| | | |
| | Cyclin-D2-1 | GO:00000 |
| | Similar to ARF GAP-like zinc finger-conta | GO:00102 |
| | MtN3 and saliva related transmembrane | GO:00086 |
| | Armadillo-like helical domain containing protein | |
| | Zinc finger, CCCH-type domain containing protein | |

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|---|---|---|
| [Os] abscisic acid sensitivity (TO:0000615) \| seed phosphorus content (TO:0002666) | Myo-inositol kinase, Phytic acid (PA) bios | GO:00102 |
| | ATP-NAD kinase, PpnK-type, all-beta do | GO:00067 |
| [Os] salt tolerance (TO:0006001) | Similar to SET domain protein SDG111 | GO:00165 |
| | Transcription factor jumonji/aspartyl bet | GO:00092 |
| | Zm00001e004948 | GO:00066 |
| | Cytochrome P450 family protein | GO:00423 |
| | Similar to F20D23.3 protein | GO:00060 |
| | RNA recognition motif, RNP-1 domain co | GO:00004 |
| | Cupredoxin domain containing protein | GO:00229 |
| | FAD dependent oxidoreductase family protein | |
| | Kinesin, motor region domain containing | GO:00070 |
| | Similar to (1-4)-beta-mannan endohydr | GO:00463 |
| | Peptidyl-tRNA hydrolase, PTH2 domain containing | |
| | Nucleotide-binding, alpha-beta plait don | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] abscisic acid sensitivity (TO:0000615) | Inositol 1, 3, 4-trisphosphate 56-kinase | GO:00102 |
| | Similar to Leucine Rich Repeat family pro | GO:00065 |
| [Os] submergence tolerance (TO:0000524) \| viral disease resistance (TO:0000148) \| bacterial blight disease resistance (TO:0000175) \| drought tolerance (TO:0000276) | Serine/threonine protein kinase-related | GO:00064 |
| | Armadillo-like helical domain containing | GO:00066 |
| | Similar to adenosine 5'-phosphosulfate | GO:00454 |
| | Survival protein SurE family protein | |
| | Similar to Ferredoxin-thioredoxin reduct | GO:00159 |
| | Zinc finger, C2H2-type domain containin | GO:00063 |
| | Lipase, class 3 family protein | GO:00066 |

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|---|---|---|
| [Os] temperature response trait (TO:0000432) \| leaf color (TO:0000326) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| carotenoid content (TO:0000496) \| chlorophyll content (TO:0000495) \| cold tolerance (TO:0000303) \| chloroplast development trait (TO:0002715) | Plastid ribosomal small subunit protein S | GO:00063 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | NPH3 domain containing protein | GO:00165 |
| | Similar to Transfactor-like protein | GO:00063 |
| | Similar to predicted protein | |
| | Armadillo-like helical domain containing protein | |
| | GPCR, family 3, metabotropic glutamate | GO:00068 |
| [Os] brown planthopper resistance (TO:0000424) \| jasmonic acid sensitivity (TO:0000172) \| flavonoid content (TO:0000290) \| insect damage resistance (TO:0000261) | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| [Os] oxidative stress TO:0002657 | Similar to SRF8 (STRUBBELIG-RECEPTOR F | GO:00064 |
| | Putative protein phosphatase 2C 76 | GO:00359 |
| | Uncharacterised protein family UPF0497, trans-me | |
| | Similar to cDNA clone:J033051C12, full insert seque | |
| | Similar to SSE1 | GO:00066 |
| | Similar to Ubiquitin-protein ligase | |
| | Methyladenine glycosylase domain contai | GO:00062 |
| | YT521-B-like protein family protein | GO:00063 |
| [Os] grain weight TO:0000919 | S-adenosylmethionine decarboxylase | GO:00065 |
| | Long-chain base kinase, Regulation of di | GO:00066 |
| | Similar to Polygalacturonase B (Fragment | GO:00059 |
| [Os] brassinosteroid content (TO:0002676) \| gibberellic acid content (TO:0002675) \| plant height (TO:0000207) \| flowering time (TO:0002616) \| growth and development trait (TO:0000357); [Ta] quantum yield TO:0012004\| photosynthetic rate TO:0001015 | SPla/RYanodine receptor SPRY domain co | GO:00063 |
| | Similar to Acyl-ACP thioesterase (Fragme | GO:00066 |
| | Similar to DnaJ-like protein | GO:00064 |
| | Uncharacterised protein family UPF0497, trans-me | |

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|---|---|---|
| | Similar to PRMT3 (PROTEIN ARGININE ME | GO:00063 |
| [Os] salt tolerance TO:0006001\| salt sensitivity TO:0000429 | Concanavalin A-like lectin/glucanase dor | GO:00022 |
| | Similar to subtilisin-like protease | GO:00065 |
| | Similar to RKF3 (RECEPTOR-LIKE KINASE I | GO:00064 |
| | Similar to Chaperone protein dnaJ | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Pyridoxal phosphate-dependent transferase, major | |
| | Hypothetical conserved gene | GO:00712 |
| [Os] alkali sensitivity (TO:0000481) \| salt tolerance (TO:0006001) \| blast disease (TO:0000074) \| drought tolerance (TO:0000276) \| oxidative stress (TO:0002657) \| hydrogen peroxide content (TO:0000605) | Zinc finger, RING/FYVE/PHD-type domai | GO:00062 |
| | Glycoside hydrolase, family 17 protein | GO:00059 |
| [Os] salt tolerance (TO:0006001) \| gibberellic acid sensitivity (TO:0000166) \| auxin sensitivity (TO:0000163); [Os] grain weight TO:0000919\| disease resistance | Similar to Senescence-associated protein | GO:00086 |
| | Sad1/UNC-like, C-terminal domain conta | GO:00349 |
| [Os] seed shape (TO:0000484) \| seed development trait (TO:0000653) \| seed size (TO:0000391) \| seed fertility (TO:0000639) | | |
| | Similar to SLL2 | GO:00180 |
| | Similar to Glycosyl hydrolase family 10 pr | GO:00002 |
| | Multi antimicrobial extrusion protein Mat | GO:00068 |
| | UDP-3-O-acyl N-acetylglucosamine deac | GO:00066 |
| | Similar to OSIGBa0115K01-H0319F09.16 protein | |
| | Similar to triacylglycerol lipase | GO:00066 |
| | Similar to Bx2-like protein | |

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|---|---|---|
| | Hypothetical conserved gene | GO:00064 |
| | Protein of unknown function DUF1630 fa | GO:00507 |
| [Os] growth and development trait (TO:0000357) \| seed development trait (TO:0000653) \| pollen fertility (TO:0000421) \| grain length (TO:0000734) \| grain size (TO:0000397); [Os] auxin content TO:0002672\| tiller angle TO:0000567 | Lupus La protein family protein | GO:00063 |
| | DNA-binding protein | |
| | Diacylglycerol kinase, catalytic region do | GO:00066 |
| | Similar to JmjC domain containing protei | GO:00063 |
| | Zm00001e009775 | GO:00064 |
| [Os] grain yield (TO:0000396) \| inflorescence development trait (TO:0000621) \| brassinosteroid content (TO:0002676) \| grain weight (TO:0000590) \| leaf angle (TO:0000206) \| grain length (TO:0000734) \| grain size | BAHD acyltransferase-like protein, Contr | GO:00100 |
| | Thioredoxin domain 2 containing protein | GO:00066 |
| | AMP-dependent synthetase and ligase dc | GO:00096 |
| | Ankyrin domain containing protein | |
| | Armadillo-like helical domain containing protein | |
| | Glucose/ribitol dehydrogenase family protein | |
| | | |
| | Xyloglucan fucosyltransferase family prot | GO:00099 |
| | Asp/Glu racemase, active site domain co | GO:00094 |
| | Similar to Selenium-binding protein-like | GO:00094 |
| | Heavy metal transport/detoxification pro | GO:00300 |
| | Conserved hypothetical protein | |
| [Os] oxidative stress (TO:0002657) \| osmotic response sensitivity (TO:0000095) \| drought tolerance (TO:0000276) \| hydrogen peroxide content (TO:0000605) \| blast disease (TO:0000074) \| abscisic acid sensitivity (TO:0000615) \| total soluble sugar content (TO:0000340) \| salt tolerance (TO:0006001) \| proline content (TO:0006002) | Similar to NAC-domain containing protei | GO:00063 |
| | Similar to OSIGBa0130B08.10 protein | GO:00550 |
| | Heavy metal transport/detoxification pro | GO:00300 |

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|---|---|---|
| [Os] chloroplast development trait (TO:0002715) \| leaf color (TO:0000326) | Plastid adenine nucleotide uniporter, Chl | GO:0015 |
| [Os] zinc sensitivity (TO:0000351); [Os] zinc concentration TO:0006053 | | |
| [Os] shoot potassium content (TO:0020003) \| growth and development trait (TO:0000357) \| grain yield (TO:0000396) \| leaf angle (TO:0000206) \| days to heading (TO:0000137) \| flowering time (TO:0002616) \| salt tolerance (TO:0006001) \| hydrogen peroxide content (TO:0000605) \| plant height (TO:0000207) \| grain size (TO:0000397) \| grain weight (TO:0000590) \| shoot sodium content (TO:0020004) \| sodium to potassium content ratio (TO:0000525) \| alkali | Similar to Trithorax 5 (Fragment) | |
| | CCAAT-binding factor domain containing | GO:0009 |
| [Os] tiller angle (TO:0000567) \| oxygen sensitivity (TO:0000015) \| blast disease (TO:0000074) \| leaf angle (TO:0000206) \| viral disease resistance (TO:0000148) \| plant growth hormone sensitivity (TO:0000401) \| auxin sensitivity (TO:0000163) \| gravity response trait (TO:0002693); [Os] nitrogen content TO:0020093\| disease resistance TO:0000112\| blast disease resistance TO:0000074 | Transcription factor, Regulator for phosp | GO:0006 |
| | Hypothetical conserved gene | GO:0006 |
| | WD40 repeat-like domain containing protein | |
| | AMP-dependent synthetase/ligase domai | GO:0006 |
| | | |
| | Phox-like domain containing protein | |
| | Similar to PITSLRE serine/threonine-prot | GO:0006 |
| [Os] drought tolerance (TO:0000276) \| submergence tolerance (TO:0000524) \| cold tolerance (TO:0000303) | | |
| | Alpha/beta hydrolase fold-1 domain containing pro | |
| | Protein kinase, core domain containing p | GO:0006 |
| | Protein of unknown function DUF221 do | GO:0034 |
| | Ankyrin repeat containing protein | GO:0030 |

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|---|---|---|
|  | Similar to predicted protein |  |
|  | Histone deacetylase superfamily protein |  |
|  | Similar to Chitinase 2 (EC 3.2.1.14) (Tulip | GO:00059 |
|  | Similar to Arginyl-tRNA--protein transfe | GO:00165 |
|  | Thyroid hormone receptor-associated pr | GO:00063 |
|  | Similar to Sucrose-phosphate synthase 9 | GO:00059 |
|  | Transmembrane receptor, eukaryota domain contai |  |
|  | Similar to UDP-glucuronyltransferase-l |  |
|  | Eukaryotic initiation factor 3, gamma sub | GO:00080 |
|  | Survival protein SurE family protein |  |
|  | Similar to SNAP25 homologous protein S | GO:00150 |
|  | Esterase, SGNH hydrolase-type domain containing |  |
|  | Similar to H0105C05.10 protein | GO:00064 |
|  | Similar to atypical receptor-like kinase M | GO:00064 |
|  | Similar to AtPIP5K1 | GO:00163 |
|  | Similar to Receptor-like protein kinase 4 | GO:00064 |
|  | Synaptojanin, N-terminal domain contain | GO:00360 |
|  | Similar to predicted protein |  |
|  | Similar to exonuclease | GO:00903 |
|  | Similar to Cytochrome P450 CYP721B4 |  |
|  | Similar to Myosin XI-K headless derivativ | GO:00070 |
|  | Tetratricopeptide-like helical domain containing pr |  |
| [Os] iron sensitivity (TO:0000224) | bHLH transcription factor, Regulation of i | GO:00063 |
|  | Zinc finger, CCCH-type domain containin | GO:00003 |
|  | Similar to hydrolase, hydrolyzing O-glyc | GO:00002 |
|  | ABC transporter-like domain containing | GO:00068 |
|  | tRNA-binding arm domain containing pr | GO:00069 |
|  | Similar to H0207B04.10 protein | GO:00320 |
| [Os] inflorescence development trait (TO:0000621) \| leaf development trait (TO:0000655) \| flower development trait (TO:0000622) | Transcription factor with zinc finger dom | GO:00072 |

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|---|---|---|
| | Similar to SET domain-containing protein | GO:00102 |
| | Transmembrane receptor, eukaryota domain contai | |
| [Os] flavonoid content (TO:0000290) \| grain size (TO:0000397) \| salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| grain yield (TO:0000396) \| spikelet anatomy and morphology trait (TO:0000657) \| 1000-dehulled grain weight (TO:0000592) \| grain length (TO:0000734) \| auxin content (TO:0002672) \| drought tolerance (TO:0000276) | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Protein of unknown function DUF707 family protein | |
| [Os] pollen fertility (TO:0000421) \| chloroplast development trait (TO:0002715); [Os] pollen fertility TO:0000421 | Transfactor-like protein | GO:00106 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Hypothetical conserved gene | |
| | Protein of unknown function DUF639 family protein | |
| | Ribonuclease CAF1 family protein | GO:00905 |
| | Inner membrane protein OXA1-like, mito | GO:00329 |
| | Similar to ATP synthase protein I -related | GO:00336 |
| | Similar to Aluminum-activated malate tra | GO:00157 |
| | Ankyrin repeat containing protein | GO:00353 |
| | DEAD-like helicase, N-terminal domain c | GO:00004 |
| [Os] fungal disease resistance (TO:0000439) \| disease resistance (TO:0000112) | Similar to Anamorsin (Cytokine induced a | GO:00162 |
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| | Zinc finger, C2H2-type domain containin | GO:00063 |
| | Similar to AML1 | GO:00003 |
| | Pyridoxal phosphate-dependent enzyme, beta subu | |
| | Similar to Rac GTPase activating protein | GO:00071 |
| | Similar to Avr9/Cf-9 rapidly elicited protein 231 pre | |

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|---|---|---|
| [Os] leaf color (TO:0000326) \| light sensitivity (TO:0000075) \| chloroplast development trait (TO:0002715) \| temperature response trait (TO:0000432) \| photosynthetic ability (TO:0000316) | Mitochodrial transcription termination fa | GO:00063 |
| | Cellular retinaldehyde-binding/triple function, C-te | |
| | Conserved hypothetical protein | GO:00512 |
| | Tetratricopeptide-like helical domain containing pr | |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) | NAC transcription factor, Drought and sa | GO:00063 |
| | Cation/H+ exchanger domain containing | GO:00068 |
| | Annexin family protein | GO:00069 |
| [Os] seed maturation TO:0002661 | Similar to MYBY1 protein (Fragment) | GO:00063 |
| | Zm00001e017952 | GO:00065 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| [Ta] disease resistance TO:0000112 | | |
| | Similar to Chaperone protein dnaJ | |
| | Zm00001e040423 | GO:00067 |
| | Mitochodrial transcription termination fa | GO:00063 |
| | SEP domain containing protein | GO:00000 |
| | Thiolase-like, subgroup domain containi | GO:00066 |
| | Hypothetical conserved gene | |
| | Zm00001e009576 | |
| | Zm00001e008087 | GO:00162 |
| [Os] male sterility TO:0000437\| reversible male sterility TO:0000004 | Myb transcription factor domain containi | GO:00301 |
| | Conserved hypothetical protein | GO:00060 |
| | Similar to RING-H2 finger protein ATL2E | GO:00065 |
| | Pectin lyase fold domain containing prote | GO:00425 |
| [Os] seed weight (TO:0000181) \| gibberellic acid sensitivity (TO:0000166) \| plant height (TO:0000207) \| fertility related trait (TO:0000420); [Os] seed weight TO:0000181 | Similar to Ulp1 protease family, C-termin | GO:00065 |

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|---|---|---|
| | EF-HAND 2 domain containing protein | |
| | Cyclin-like F-box domain containing pro | GO:00065 |
| | Similar to H0622F05.1 protein | GO:19010 |
| [Os] proline content (TO:0006002) \| drought tolerance (TO:0000276); [Os] floral organ identity TO:0006019\| organ identity TO:0006018\| salt tolerance TO:0006001\| oxidative stress TO:0002657\| mannose content TO:0000932\| male sterility TO:0000437\| drought tolerance TO:0000276\| amylose content | C2H2 zinc finger protein, Transcriptional | GO:00063 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to Tonoplast intrinsic protein | GO:00550 |
| | Similar to Glutathione transferase III(B) (E | GO:00067 |
| | Transcription elongation factor, TFIIS/CR | GO:00064 |
| | Armadillo-like helical domain containing protein | |
| | Nucleoside phosphorylase, family 1 dom | GO:00091 |
| | Esterase, SGNH hydrolase-type domain containing p | |
| | Cytochrome P450 | |
| | Concanavalin A-like lectin/glucanase dor | GO:00059 |
| | Zm00001e025173 | GO:00229 |
| | Similar to Beta-1,3-glucanase (Fragment) | GO:00059 |
| [Os] blast disease (TO:0000074) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) | DEAD-like helicase, N-terminal domain c | GO:00062 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] disease resistance TO:0000112 | Similar to Nuclease PA3 | GO:00063 |
| | Protein kinase, catalytic domain domain c | GO:00064 |
| | Senescence-associated family protein | |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | E2F transcription facto | GO:00001 |
| | Similar to Glutathione S-transferase GST | GO:00067 |
| | Mov34/MPN/PAD-1 family protein | GO:00165 |
| | Similar to hydrolase, hydrolyzing O-glyc | GO:00059 |
| | Pentatricopeptide repeat domain containi | GO:00094 |

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|---|---|---|
| | Cyclin-like F-box domain containing pro | GO:00165 |
| | Similar to Riboflavin biosynthesis protein | GO:00092 |
| | Protein of unknown function DUF827, pla | GO:00099 |
| [Os] female sterility (TO:0000358) \| male sterility (TO:0000437) \| meiotic cell cycle trait (TO:0000729) | Conserved hypothetical protein | GO:00002 |
| | RNA-processing protein, HAT helix doma | GO:00003 |
| | Conserved hypothetical protein | |
| [Os] leaf color (TO:0000326) \| chlorophyll-a content (TO:0000293) \| carotenoid content (TO:0000496) \| chlorophyll-b content (TO:0000295) \| photosynthetic rate (TO:0001015) | Regulator of the Magnesium-chelatase s | GO:00100 |
| | NAD(P)-binding domain containing prote | GO:00066 |
| | Tetratricopeptide-like helical domain containing pr | |
| [Os] heat tolerance (TO:0000259) \| gibberellic acid sensitivity (TO:0000166) \| auxin sensitivity (TO:0000163) \| jasmonic acid sensitivity (TO:0000172) \| cold tolerance (TO:0000303) \| biotic stress trait (TO:0000179) \| abscisic acid sensitivity (TO:0000615) \| ethylene sensitivity (TO:0000173) \| cytokinin sensitivity (TO:0000167) \| light sensitivity (TO:0000075) \| drought tolerance (TO:0000276) \| salt tolerance | Similar to Acyl carrier protein III, chloropl | GO:00066 |
| [Os] salt tolerance (TO:0006001) \| light sensitivity (TO:0000075) \| drought tolerance (TO:0000276) \| cold tolerance (TO:0000303); [Os] proline content TO:0006002\| oxidative stress TO:0002657 | WNK (With No Lysine) kinase, Ser/thr pro | GO:00064 |
| | Similar to PIT1 | GO:00165 |
| | Similar to Transmembrane protein kinase | GO:00064 |
| | Uncharacterised domain XH domain cont | GO:00310 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Similar to Ervatamin C (EC 3.4.22.-) (ERV | GO:00065 |
| | MT-A70 family protein | GO:00160 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |

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|---|---|---|
| [Os] leaf shape (TO:0000492) \| leaf development trait (TO:0000655) \| viral disease resistance (TO:0000148) \| root length (TO:0000227) \| root development trait (TO:0000656) | Flavin-containing monooxygenase (FMO) | GO:00098 |
| [Os] blast disease (TO:0000074) \| shoot apical meristem development (TO:0006020) \| flower development trait (TO:0000622) \| alkali sensitivity (TO:0000481) \| disease resistance (TO:0000112) \| white-backed planthopper resistance (TO:0000205) \| herbicide sensitivity (TO:0000058) \| bacterial disease resistance (TO:0000315) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| temperature response | Similar to NAC domain protein | GO:00063 |
| | Similar to predicted protein | GO:00063 |
| | Ankyrin domain containing protein | GO:00165 |
| [Os] chloroplast development trait (TO:0002715) \| leaf color (TO:0000326) \| plant height (TO:0000207) \| photosynthetic ability (TO:0000316) \| chlorophyll content (TO:0000495) | Pentatricopeptide repeats protein, Splicin | GO:00003 |
| | Kelch-type beta propeller domain containing protei | |
| | Hypoxia induced protein conserved region family pr | |
| | Similar to ATSWI3B | |
| | Similar to H0801D08.12 protein | GO:00064 |
| | PLC-like phosphodiesterase, TIM beta/al | GO:00060 |
| | Zm00001e035100 | GO:00064 |
| | Cupredoxin domain containing protein | GO:00229 |
| | Zm00001e037244 | GO:00063 |
| [Os] salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| calcium sensitivity (TO:0000006) \| osmotic response sensitivity (TO:0000095); [Os] salt tolerance TO:0006001\| carotenoid content TO:0000496 | Small calcium-binding protein with one EF-hand mo | |
| | Chaperonin Cpn60/TCP-1 family protein | GO:00468 |

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|---|---|---|
| [Os] seed development trait (TO:0000653) \| ethylene sensitivity (TO:0000173) \| root length (TO:0000227) \| root anatomy and morphology trait (TO:0000043) \| embryo development trait (TO:0000620) \| leaf senescence (TO:0000249) \| relative biomass (TO:0000143) \| root development trait (TO:0000656) \| biomass yield (TO:0000327); [Os] salt tolerance TO:0006001\| grain weight | Transcription factor involved in the ethyl | GO:0009 |
| | Similar to strictosidine synthase 1 | GO:00090 |
| | Zm00001e035726 | |
| | | |
| | Zinc finger, PHD-type domain containing | GO:00459 |
| | SET domain containing protein | GO:00180 |
| | Similar to H0425E08.7 protein | |
| | Conserved hypothetical protein | |
| | Similar to DNA polymerase I | GO:00062 |
| | Biopterin transport-related protein BT1 family prote | |
| | Similar to TAF15b (TBP-ASSOCIATED FACTOR 15b); | |
| [Os] spikelet fertility TO:0000180 | Similar to H0103C06.10 protein | GO:00100 |
| | Similar to TTN10 | GO:00062 |
| | Cupin, RmlC-type domain containing protein | |
| | Glutamate receptor-related domain cont | GO:00068 |
| | Protein of unknown function DUF862, eu | GO:00165 |
| | Histone deacetylation protein Rxt3 doma | GO:00165 |
| [Os] phyllotaxy TO:0006014 | Similar to ADP ribosylation GTPase-like p | GO:00161 |
| | Similar to lipid binding protein | GO:00104 |
| | Domain of unknown function DUF231, pl | GO:19909 |
| [Os] grain yield (TO:0000396) \| seedling height (TO:0000019) \| seed development trait (TO:0000653) | Phosphate (Pi) transporter, Root-to-shoo | GO:00067 |
| | Conserved hypothetical protein | |
| | | |
| | Protein of unknown function DUF250 dor | GO:00068 |
| | Cytochrome b561/ferric reductase transr | GO:00551 |
| | Similar to Beta-1,3-glucanase precursor | GO:00059 |
| | Hypothetical conserved gene | GO:00065 |
| | Zinc finger, Zim17-type family protein | GO:00064 |
| | Similar to protein kinase family protein / | GO:00064 |
| | Similar to Phosphoenolpyruvate carboxyl | GO:00064 |
| | Similar to Eukaryotic initiation factor 4B ( | GO:00064 |
| | Similar to SC35-like splicing factor SCL2 | GO:00003 |
| | | |
| | Similar to zinc finger helicase family prot | GO:00001 |

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|---|---|---|
|  | Cellular retinaldehyde-binding/triple fun | GO:00159 |
| [Os] brassinosteroid sensitivity (TO:0002677) \| gibberellic acid sensitivity (TO:0000166) \| auxin sensitivity (TO:0000163) \| leaf senescence (TO:0000249) \| abiotic stress trait (TO:0000168) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| jasmonic acid sensitivity (TO:0000172) \| abscisic acid sensitivity (TO:0000615); [Os] grain length TO:0002760\| grain length TO:0000734\| submergence tolerance TO:0000524\| heterosis TO:0000355 | Similar to MYB transcription factor R2R3 | GO:00063 |
| [Ta] seed dormancy TO:0000253 | IQ calmodulin-binding region domain containing pr |  |
|  | WD-40 repeat containing protein | GO:00064 |
|  | Similar to Fasciclin-like protein FLA22 | GO:00097 |
|  | Zinc finger, DHHC-type domain containi | GO:00066 |
|  | Protein of unknown function DUF632 do | GO:00712 |
|  | WD40/YVTN repeat-like domain containi | GO:00069 |
|  | Similar to ABC transporter-like protein | GO:00550 |
|  | Serine/threonine protein kinase domain | GO:00064 |
|  | Similar to H0306F03.12 protein |  |
|  | Pentatricopeptide repeat domain containing protein |  |
|  | Polynucleotide adenylyltransferase regio | GO:00016 |
|  | Zinc finger, DHHC-type domain containi | GO:00066 |
|  | Similar to gibberellin receptor GID1L2 |  |
| [Ta] protein content TO:0000598 | Quinoprotein amine dehydrogenase, bet | GO:00100 |
|  | Similar to H0112G12.8 protein | GO:00300 |
|  | Similar to SNF1 kinase complex anchoring protein ( |  |
|  | Armadillo-type fold domain containing protein |  |
|  | Nucleotide-binding, alpha-beta plait domain contai |  |
|  | Glycoside hydrolase, family 20 protein | GO:00059 |
|  | Similar to PUX2 (PLANT UBX DOMAIN-CO | GO:00508 |
|  | Similar to predicted protein |  |
|  | Kinesin, motor region domain containing | GO:00070 |

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|---|---|---|
| [Os] leaf angle (TO:0000206) \| jasmonic acid sensitivity (TO:0000172) \| grain length (TO:0000734) \| leaf lamina joint bending (TO:0002688) \| grain size (TO:0000397) \| brassinosteroid sensitivity (TO:0002677) \| ethylene sensitivity (TO:0000173); [Os] grain size | Helix-loop-helix protein, Brassinosteroid | GO:00063 |
| | Similar to Auxin response factor 5 | GO:00063 |
| | BTB/POZ fold domain containing protein | GO:00165 |
| | Glycosyltransferase AER61, uncharacterized domain | |
| | Mitochodrial transcription termination fa | GO:00063 |
| | Similar to Colon cancer-associated protei | GO:00105 |
| | Kelch repeat type 2 domain containing protein | |
| | Protein of unknown function DUF1032 fa | GO:00100 |
| | Similar to H0211B05.13 protein | |
| | Hypothetical conserved gene | |
| | Cupredoxin domain containing protein | GO:00229 |
| | WD40/YVTN repeat-like domain containi | GO:00068 |
| [Os] grain size (TO:0000397) \| inflorescence development trait (TO:0000621) \| awn presence (TO:0002734) \| awn length (TO:0000072) \| seed development trait | Conserved hypothetical protein | GO:00100 |
| [Os] plant height (TO:0000207) | YT521-B-like protein family protein | GO:00611 |
| | Hypothetical conserved gene | GO:00064 |
| | Similar to male sterility protein 2 | GO:00066 |
| | Similar to strictosidine synthase 1 | GO:00090 |
| [Os] proline content (TO:0006002) \| anther color (TO:0000187) \| grain number (TO:0002759) \| pollen fertility (TO:0000421) \| osmotic response sensitivity (TO:0000095) \| abiotic stress trait (TO:0000168) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) | Protein phosphatase inhibitor 2 (IPP-2) fa | GO:00099 |
| | Protein of unknown function DUF221 do | GO:00342 |

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|---|---|---|
| | Cystathionine beta-synthase, core domain containin | |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to DANA2 | GO:00068 |
| | Hyccin domain containing protein | GO:00468 |
| | Similar to ribosomal RNA adenine dimeth | GO:00001 |
| | Tetratricopeptide-like helical domain containing pr | |
| [Os] seed size (TO:0000391) \| pollen fertility (TO:0000421) \| auxin content (TO:0002672) \| male sterility (TO:0000437) \| starch content (TO:0000696) \| sucrose content (TO:0000328) \| seed shape (TO:0000484) \| seed viability (TO:0000345); [Os] pollen fertility | 2OG-Fe(II) oxygenase domain containing | GO:00098 |
| | 2OG-Fe(II) oxygenase domain containing | GO:00066 |
| | Amino acid transporter, transmembrane | GO:00033 |
| | Zm00001e131464 | GO:00059 |
| | Thioredoxin fold domain containing prot | GO:00454 |
| | Ankyrin repeat containing protein | |
| | Alpha/beta hydrolase fold-1 domain containing pro | |
| | Similar to Hemolysin-III related family pr | GO:00097 |
| | | |
| | Auxin efflux carrier domain containing p | GO:00550 |
| | Zinc finger, C6HC-type domain containin | GO:00002 |
| | Similar to Frataxin | GO:00067 |
| | Cyclin-like F-box domain containing pro | GO:00065 |
| | Similar to SNF1 kinase complex anchoring protein ( | |
| | | |
| | Hypothetical conserved gene | |
| | Protein of unknown function DUF303, acetylesterase | |
| | Uncharacterised protein family UPF0005 domain co | |
| | BRCT domain containing protein | GO:00096 |
| | Peptidase S54, rhomboid domain containing protein | |
| | Similar to AML1 | GO:00003 |
| | | |
| | Protein of unknown function DUF246, pla | GO:00060 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] cytoplasmic male sterility TO:0000580\| male sterility TO:0000437 | Similar to LSTK-1-like kinase | GO:00064 |
| | Glutamine-Leucine-Glutamine, QLQ dom | GO:00063 |
| | Similar to Early nodulin | |
| | Dimethylaniline monooxygenase, N-oxide-forming | |
| | | |
| | Ubiquitin domain containing protein | GO:00063 |
| | GTP-binding protein, HSR1-related doma | GO:00064 |
| | | |
| [Ta] plant height TO:0000207 | Similar to Purple acid phosphatase | |

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|---|---|---|
| | G-protein, beta subunit family protein | GO:00007 |
| | Zm00001e026409 | |
| | Major facilitator superfamily, general sub | GO:00086 |
| | Similar to predicted protein | GO:00070 |
| | UV radiation resistance protein/autophag | GO:00354 |
| | Zinc finger, C6HC-type domain containin | GO:00002 |
| [Os] shoot apical meristem development (TO:0006020) \| secondary branch number (TO:0000557) \| leaf width (TO:0000370) \| stem thickness (TO:0000339) \| panicle size (TO:0006032) \| primary branch number (TO:0000547) \| grain number | Similar to E3 ubiquitin protein ligase UPL | GO:00002 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to Myosin heavy chain-like | GO:00099 |
| | Hypothetical conserved gene | GO:00094 |
| [Os] salt tolerance (TO:0006001) \| brassinosteroid sensitivity (TO:0002677) \| abscisic acid sensitivity | Similar to Glutamate receptor 3.3 precurs | GO:00068 |
| [Os] flowering time (TO:0002616) \| days to heading (TO:0000137) | Zinc finger, C2H2-like domain containin | GO:00063 |
| | Protein of unknown function DUF6, trans | GO:00550 |
| [Os] plant height (TO:0000207) \| tiller number (TO:0000346) \| chlorophyll content (TO:0000495) \| osmotic response sensitivity (TO:0000095) \| hydrogen peroxide content (TO:0000605) \| mimic response (TO:0000063) \| salt tolerance (TO:0006001) \| photosynthetic ability (TO:0000316) \| chloroplast development trait (TO:0002715) \| bacterial blight disease resistance (TO:0000175) \| carotenoid content (TO:0000496) \| abscisic acid sensitivity | Ubiquitin system component Cue domain containin | |
| | Nse1 non-SMC component of SMC5-6 co | GO:00007 |
| | Hypothetical conserved gene | |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Photosystem I PsaO domain containing protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Protein of unknown function DUF607 far | GO:00068 |
| | Similar to NOI protein | |
| | Protein of unknown function DUF26 dom | GO:00104 |
| | Similar to presenilin | GO:00065 |

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|---|---|---|
| | Similar to Kinesin heavy chain (Fragment) | GO:00070 |
| | Domain of unknown function DUF231, pl | GO:19909 |
| | Uncharacterised protein family UPF0565 domain co | |
| | Cupredoxin domain containing protein | GO:00229 |
| | Ubiquitin system component Cue domain containin | |
| | Similar to BRASSINOSTEROID INSENSITIVE | GO:00064 |
| [Os] days to heading TO:0000137 | Similar to Transcription initiation factor T | GO:00063 |
| | Zm00001e007782 | GO:00508 |
| | Similar to CF9 | |
| | Cyclin, A/B/D/E domain containing prote | GO:00000 |
| | Similar to Type I inositol-1,4,5-trisphosp | GO:00468 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Modifier of rudimentary, Modr family pro | GO:00066 |
| | Protein of unknown function DUF231 dor | GO:19909 |
| | Similar to Microsomal signal peptidase 2 | GO:00064 |
| [Os] bacterial blight disease resistance (TO:0000175) \| heat tolerance (TO:0000259) | Similar to WRKY transcription factor 34 | GO:00063 |
| [Os] transpiration rate (TO:0001018) \| carotenoid content (TO:0000496) \| net photosynthetic rate (TO:0001027) \| chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| stomatal conductance (TO:0000522) \| chloroplast development trait (TO:0002715) \| leaf color (TO:0000326) | Pentatricopeptide repeat domain containing protein | |
| | Similar to plasminogen activator inhibitor 1 RNA-bi | |
| | Lipase, class 3 family protein | GO:00066 |
| | Similar to zinc ion binding protein | GO:19000 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to predicted protein | GO:00007 |
| [Os] shoot apical meristem development (TO:0006020) \| leaf development trait (TO:0000655) \| leaf curling (TO:0002681) \| flowering time (TO:0002616) \| days to heading (TO:0000137) \| leaf width | IKI3 family protein | GO:00020 |
| [Os] seed maturation TO:0002661 | Similar to Protein phosphatase 2C | |
| | Protein kinase, core domain containing p | GO:00064 |
| | Cysteine proteinase inhibitor- | GO:00065 |
| | Trimeric LpxA-like domain containing pr | GO:00064 |
| | Similar to CLP protease regulatory subuni | GO:00064 |
| | Similar to predicted protein | GO:00432 |
| | K Homology domain containing protein | GO:00104 |

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|---|---|---|
| | Similar to CigA protein | GO:00060 |
| [Os] drought tolerance (TO:0000276) | Myb, DNA-binding domain containing pr | GO:00063 |
| | Defects-in-morphology protein 1-like, m | GO:00362 |
| [Os] chlorophyll-a content (TO:0000293) \| chlorophyll-b content (TO:0000295) \| leaf color (TO:0000326) \| chloroplast development trait | Peptidase S14, ClpP family protein | GO:00065 |
| | Hypothetical conserved gene | GO:00064 |
| | SET domain containing protein | |
| [Os] chromium sensitivity (TO:0000034) \| abscisic acid sensitivity (TO:0000615) | Ferric reductase-like transmembrane component fa | |
| | Similar to Autophagy 4a | GO:00065 |
| [Os] seed width (TO:0000149) \| grain size (TO:0000397) \| grain length (TO:0000734) \| 1000-dehulled grain weight (TO:0000592) \| grain weight (TO:0000590) \| grain yield (TO:0000396) \| grain number (TO:0002759) \| auxin content (TO:0002672) \| abscisic acid content (TO:0002667) \| seed thickness (TO:0000304) \| drought related trait | Thioesterase superfamily domain containing protein | |
| [Os] days to heading (TO:0000137) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| abscisic acid sensitivity (TO:0000615) | Histone-fold domain containing protein | GO:00063 |
| | Similar to Ser-thr protein kinase (Fragme | GO:00064 |
| | Ovarian tumour, otubain domain containi | GO:00165 |
| [Os] stem thickness (TO:0000339) \| chlorophyll content (TO:0000495) \| flowering time (TO:0002616) \| leaf color (TO:0000326) \| variegated leaf (TO:0000069) \| seed color (TO:0000486) | Divalent ion symporter domain containin | GO:00550 |
| | RhoGAP domain containing protein | GO:00071 |

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|---|---|---|
| [Os] bacterial blight disease resistance (TO:0000175) \| sheath blight disease resistance (TO:0000255) | Serine/threonine protein kinase-related | GO:00064 |
| | UV radiation resistance protein/autophag | GO:00354 |
| | Protein phosphatase 2C-like protein | GO:00359 |
| | Zm00001e022169 | GO:00062 |
| | WD-40 repeat containing protein | GO:00000 |
| | rRNA-processing protein EFG1 domain c | GO:00004 |
| | Similar to ischemia/reperfusion inducible | GO:00064 |
| | Methyltransferase type 11 domain containing protei | |
| | Protein kinase domain containing protein | GO:00064 |
| | Similar to Ubiquitin conjugating enzyme 2 | |
| | Similar to Catalytic/ oxidoreductase, acti | GO:00064 |
| | Similar to Transparent testa 12 protein | GO:00068 |
| | Pentatricopeptide repeat protein, Chloroplast devel | |
| | Plant lipid transfer protein/seed storage/ | GO:00096 |
| | Similar to DNA cross-link repair protein- | GO:00063 |
| [Os] leaf sheath length (TO:0002689) \| days to heading (TO:0000137) \| growth hormone content (TO:0000476) \| blast disease (TO:0000074) \| leaf length (TO:0000135) \| plant height (TO:0000207) | | |
| [Os] brown planthopper resistance (TO:0000424) \| grain yield (TO:0000396) \| jasmonic acid sensitivity (TO:0000172) \| spikelet anatomy and morphology trait (TO:0000657) \| chlorophyll ratio (TO:0000298) \| insect damage resistance (TO:0000261) \| black streak dwarf virus resistance (TO:0000020) \| blast disease (TO:0000074) \| silicon sensitivity (TO:0000031) \| leaf senescence (TO:0000249) \| grain weight (TO:0000590) \| spikelet fertility (TO:0000180) \| stay green trait (TO:0002712); [Os] grain weight TO:0000919\| spikelet fertility | Component of the SCF E3 ubiquitin ligas | GO:00069 |
| | Similar to H0505F09.5 protein | GO:00342 |

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|---|---|---|
| | Homeodomain-related containing protei | GO:00063 |
| [Os] cold tolerance (TO:0000303) | Leucine-rich repeat receptor-like kinas | GO:00064 |
| | Rossmann-like alpha/beta/alpha sandwi | GO:00067 |
| | Uncharacterised protein family UPF0005 | GO:00157 |
| | Thioredoxin domain 2 containing protein | GO:00454 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Long-chain base kinase, Regulation of di | GO:00066 |
| | Kelch related domain containing protein | GO:00096 |
| | Zm00001e035856 | GO:00063 |
| | Glycosyl transferase, family 8 protein | GO:00104 |
| | Hypothetical conserved gene | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Alpha/beta hydrolase family protein | |
| | Pentatricopeptide repeat domain containi | GO:00069 |
| | Zm00001e000290 | GO:00096 |
| | UDP-N-acetylmuramoylalanyl-D-glutam | GO:00083 |
| [Os] seed set percent (TO:0000455) \| 1000-dehulled grain weight (TO:0000592) \| filled grain number (TO:0000447) \| panicle length (TO:0000040) \| pollen fertility (TO:0000421) \| cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) \| plant height (TO:0000207) \| submergence tolerance (TO:0000524) \| bacterial blight disease resistance (TO:0000175) \| panicle number (TO:0000152) \| yield trait | | |
| | Similar to Amidophosphoribosyltransfera | GO:00061 |
| | SET domain containing protein | GO:00165 |
| | Similar to Ethylene signal transcription fa | GO:00063 |
| | Similar to phosphoglycerate mutase gpmB | |
| | Similar to prenylated rab acceptor family | GO:00161 |
| [Os] auxin content (TO:0002672) \| root development trait (TO:0000656); [Os] auxin content TO:0002672\| seed size TO:0000391 | Mannosyl-oligosaccharide glucosidase, N | GO:00059 |
| | Zm00001e033407 | GO:00096 |
| | Similar to N-acetyltransferase | |

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|---|---|---|
| [Os] root development trait (TO:0000656) \| plant height (TO:0000207) \| drought tolerance (TO:0000276) \| heat tolerance (TO:0000259) \| lemma and palea anatomy and morphology trait (TO:0000079) \| spikelet number (TO:0000456) \| root branching (TO:0000257) \| spikelet sterility (TO:0000436) \| adventitious root number (TO:0001006) \| stem length (TO:0000576) \| 1000-dehulled grain weight (TO:0000592) \| panicle size (TO:0006032) \| leaf angle (TO:0000206) \| leaf size (TO:0002637) \| root number (TO:0000084) \| auxin content (TO:0002672) \| tiller number (TO:0000346) \| leaf shape (TO:0000492) \| auxin sensitivity (TO:0000163) \| silicon sensitivity (TO:0000031) \| leaf curling (TO:0002681) \| grain size (TO:0000397) \| grain number | Tryptophan aminotransferase, Indole-3- | GO:00098 |
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| | Carbohydrate/purine kinase domain cont | GO:00163 |
| | Uncharacterised conserved protein UCP0 | GO:00551 |
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| [Os] grain yield (TO:0000396) \| growth and development trait (TO:0000357) \| tiller number (TO:0000346) \| grain number per plant (TO:0000440) \| filled grain number (TO:0000447) \| amino acid content (TO:0002673) \| shoot branching (TO:0002639) | TGF-beta receptor, type I/II extracellular | GO:00068 |
| | Similar to CFM6 | |
| [Os] temperature response trait (TO:0000432) \| chlorophyll-a content (TO:0000293) \| chloroplast development trait (TO:0002715) \| cold tolerance (TO:0000303) \| chlorophyll-b content (TO:0000295) \| variegated leaf (TO:0000069) \| leaf color (TO:0000326) \| light sensitivity (TO:0000075) | | |
| | Pentatricopeptide repeat domain containing protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Protein of unknown function DUF1191 family protei | |
| | Similar to H0402C08.12 protein | GO:00064 |
| | Heat shock protein Hsp20 domain contai | GO:00003 |

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|---|---|---|
| [Os] copper sensitivity (TO:0000021) \| bacterial blight disease resistance (TO:0000175) \| bacterial leaf streak disease resistance (TO:0000203) \| drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| UV light sensitivity (TO:0000160) \| disease resistance (TO:0000112) \| cold tolerance (TO:0000303) \| lignin content (TO:0000731) \| lignin biosynthesis trait (TO:0000733) | Similar to Cinnamoyl-CoA reductase (EC 1.2.1.44) | |
| [Os] drought tolerance (TO:0000276) | Zm00001e019190 | |
| | Protein prenyltransferase domain containing protein | |
| | Similar to amino acid transport protein | GO:00033 |
| | Nucleoporin, Common symbiosis signalir | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] drought tolerance (TO:0000276) \| cold tolerance (TO:0000303); [Ta] root dry weight TO:0000078 | | |
| | Armadillo-like helical domain containing | GO:00068 |
| | Heat shock cognate protein B, C-termina | GO:00162 |
| | Pentatricopeptide repeat containing protein | |
| | Uncharacterised protein family UPF0172 domain cor | |
| | Similar to Pollen-specific kinase partner | GO:00507 |
| | Similar to C4-dicarboxylate transporter/ | GO:00068 |
| [Os] sodium to potassium content ratio (TO:0000525) \| rice grassy stunt 1 and 2 virus resistance (TO:0000213) \| jasmonic acid sensitivity (TO:0000172) \| brassinosteroid sensitivity (TO:0002677) \| sodium content (TO:0000608) \| salt tolerance (TO:0006001) \| potassium content (TO:0000609); [Os] salt tolerance | Na<sup>+</sup> transporter, A memb | GO:00068 |
| [Os] male sterility TO:0000437 | Similar to DNA-directed DNA polymerase | GO:00062 |
| | Polynucleotide adenylyltransferase regior | GO:00016 |

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|---|---|---|
| | 2OG-Fe(II) oxygenase domain containing protein | |
| | Photosystem II oxygen evolving complex | GO:00097 |
| | Epsin-like, N-terminal domain containing | GO:00068 |
| [Os] abscisic acid sensitivity (TO:0000615) \| leaf water potential (TO:0000131)<br>[Ta] fungal disease resistance TO:0000439\| disease resistance TO:0000112 | Similar to Protein phosphatase 2C | |
| | BR receptor kinase, Brassinosteroid (BR) p | GO:00064 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to Glutathione-conjugate transpo | GO:00550 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] chloroplast development trait (TO:0002715) \| jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074) \| leaf color (TO:0000326) \| photosynthetic rate (TO:0001015) \| leaf development trait (TO:0000655);<br>[Os] leaf chlorosis TO:0020113\| leaf chlorosis TO:0006060 | Similar to Plastid (P)ppGpp synthase | GO:00159 |
| | Protein of unknown function DUF617, pla | GO:00102 |
| | Early nodulin | |
| | Pentatricopeptide repeat domain containi | GO:00094 |

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|---|---|---|
| [Os] yield trait (TO:0000371) \| filled grain percentage (TO:0000448) \| days to heading (TO:0000137) \| panicle size (TO:0006032) \| flowering time (TO:0002616) \| inflorescence branching (TO:0000050) \| photoperiod sensitivity (TO:0000229) \| grain number (TO:0002759) \| plant height (TO:0000207) \| light sensitivity (TO:0000075) \| temperature response trait (TO:0000432) \| days to maturity (TO:0000469); [Os] meristem identity TO:0006017\| grain number TO:0002759\| amino acid content TO:0002673\| oxidative stress TO:0002657\| grain weight TO:0000919\| basic vegetative phase TO:0000461\| grain yield per plant TO:0000449\| heterosis TO:0000355\| cold tolerance TO:0000303\| plant height TO:0000207\| amylose content TO:0000196\| days to heading | Zinc finger protein, Heading dat | GO:00099 |
| [Ta] seed dormancy TO:0000253\| male sterility TO:0000437 | Similar to Extracellular calcium sensing r | GO:00097 |
| [Os] secondary branch number (TO:0000557) \| grain yield (TO:0000396) \| spikelet number (TO:0000456) \| spikelet weight (TO:0000501) \| inflorescence branching (TO:0000050) \| inflorescence development trait (TO:0000621) | Ribbon-helix-helix domain containing pr | GO:00064 |
| | Similar to predicted protein Zm00001e041403 | |
| | Nucleic acid-binding, OB-fold domain co | GO:00063 |
| | Peptidase M14, carboxypeptidase A famil | GO:00065 |
| | WD40 repeat domain containing protein | GO:00070 |
| | Conserved hypothetical protein | |
| [Os] salt tolerance TO:0006001\| grain weight TO:0000919\| 1000-grain weight TO:0000533\| grain yield per plant TO:0000449\| 1000-grain weight TO:0000382 | Similar to Phototropin | GO:00096 |
| | Similar to Receptor-like protein kinase pr | GO:00064 |

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|---|---|---|
| | Similar to Basic blue protein (Cusacyanin) | GO:00229 |
| | ENTH/VHS domain containing protein | GO:00068 |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | Similar to Beta-D-xylosidase | GO:00059 |
| | Small nuclear RNA activating complex (S | GO:00427 |
| [Os] chloroplast development trait (TO:0002715) \| pollen fertility (TO:0000421) | Sugar transporter, conserved site domain | GO:00094 |
| [Os] salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| proline content (TO:0006002) \| drought tolerance (TO:0000276) | | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Multi antimicrobial extrusion protein Mat | GO:00068 |
| | Protein of unknown function DUF3769 d | GO:00341 |
| | Similar to Alcohol dehydrogenase (Fragment) | |
| | Harpin-induced 1 domain containing protein | |
| | UBX domain containing protein | GO:00304 |
| | Similar to tac7077 | GO:00092 |
| | U3 small nucleolar RNA-associated prote | GO:00004 |
| | Similar to Acetyltransferase, GNAT family protein, e | |
| | Pentatricopeptide repeat domain containi | GO:00009 |
| [Os] drought sensitivity (TO:0000188) \| bacterial blight disease resistance (TO:0000175) | Similar to WRKY DNA binding domain co | GO:00063 |
| [Os] iron sensitivity (TO:0000224); [Os] plant height TO:0000207 | Mitochondrial carrier protein domain con | GO:00157 |
| | Peptidase A1 domain containing protein | GO:00065 |
| | SET domain containing protein | GO:00180 |
| | Similar to Cdk-activating kinase 1At (Cdk | GO:00064 |
| [Os] bacterial blight disease resistance (TO:0000175) \| salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| sheath blight disease resistance (TO:0000255) | Similar to Chitin-inducible gibberellin-re | GO:00063 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| [Os] blast disease (TO:0000074) | Glycoside hydrolase, family 10 protein | GO:00002 |

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|---|---|---|
| | Glycosyl transferase, family 43 protein | GO:00059 |
| | Region of unknown function XS domain c | GO:00310 |
| | Armadillo-type fold domain containing p | GO:00101 |
| | Similar to PDE135 (PIGMENT DEFECTIVE E | GO:00342 |
| | Phosphotransferase system, HPr serine p | GO:00430 |
| | Similar to predicted protein | GO:00064 |
| [Os] starch content TO:0000696\| submergence tolerance TO:0000524\| phosphorus uptake TO:0000511\| gall midge resistance TO:0000423\| plant height TO:0000207 | Similar to SUB1; calcium ion binding | GO:00060 |
| | Multi antimicrobial extrusion protein Mat | GO:00068 |
| | Major facilitator superfamily MFS_1 prote | GO:00550 |
| [Os] abiotic stress trait (TO:0000168) \| cold tolerance (TO:0000303) \| jasmonic acid sensitivity (TO:0000172) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| biotic stress trait (TO:0000179); [Os] anthocyanin content TO:0000071 | Similar to Leucoanthocyanidin dioxygenase-like pro | |
| | Phospholipid/glycerol acyltransferase do | GO:00101 |
| | Protein prenyltransferase domain contain | GO:00094 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Leucine-rich repeat domain containing protein | |
| | Zm00001e022433 | |
| [Os] oxygen sensitivity (TO:0000015) \| tiller angle (TO:0000567) \| starch content (TO:0000696) | NRR alternative splicing variant, Regulation of root d | |
| | Similar to WAK80 - OsWAK receptor-like | GO:00064 |
| | Similar to Acyl-ACP thioesterase (Fragme | GO:00066 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | COG complex component, COG2 family p | GO:00068 |
| | Similar to VirE2-interacting protein VIP1 | GO:00063 |
| | Similar to Heat shock protein | GO:00104 |
| | Similar to protein binding protein | GO:00508 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |

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|---|---|---|
| [Os] fungal disease resistance (TO:0000439) \| bacterial disease resistance (TO:0000315) | Lysin motif-containing protein, Pattern re | GO:00023 |
| [Os] cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) | | |
| | PLC-like phosphodiesterase, TIM beta/al | GO:00060 |
| | Similar to GST6 protein (EC 2.5.1.18) | GO:00067 |
| [Os] grain yield (TO:0000396) \| grain number (TO:0002759) \| transpiration rate (TO:0001018) \| osmotic response sensitivity (TO:0000095) \| plant height (TO:0000207) \| carbohydrate content (TO:0000291) \| photosynthetic rate (TO:0001015) \| oligosaccharide content (TO:0006003) \| cold tolerance (TO:0000303) \| salt tolerance (TO:0006001) \| germination rate (TO:0000430) \| abscisic acid content (TO:0002667) \| abscisic acid sensitivity (TO:0000615) \| root length (TO:0000227) \| flooding related trait (TO:0000114) \| grain size | Similar to Trehalose-6-phosphate phosp | GO:00059 |
| [Os] coleoptile length (TO:0001007) \| cold tolerance (TO:0000303) | | |
| | ATPase, AAA-type, core domain containi | GO:00304 |
| | Tetratricopeptide-like helical domain containing pro | |
| | Protein of unknown function DUF760 family protein | |
| | Serine/threonine protein kinase domain | GO:00064 |
| | DNA polymerase eta domain containing | GO:00062 |
| | Similar to Extensin protein-like | |
| [Os] nutrient sensitivity (TO:0000480) \| jasmonic acid sensitivity (TO:0000172) | Defensin-like protein, Positive regulation | GO:00069 |
| | Hypothetical conserved gene | GO:00063 |
| | Haem oxygenase-like, multi-helical dom | GO:00067 |
| | Similar to RNA-binding protein Nova-1 | GO:00104 |
| | Similar to anthranilic acid methyltransfer | GO:00322 |
| | Similar to atypical receptor-like kinase M | GO:00064 |
| | Cyclic nucleotide-binding domain contai | GO:00068 |

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|---|---|---|
| [Os] heat tolerance (TO:0000259) \| leaf color (TO:0000326) | PfkB family fructokinase, WLP2 paralog, C | GO:00063 |
| [Os] salt tolerance (TO:0006001) \| rice grassy stunt 1 and 2 virus resistance (TO:0000213) \| plant height (TO:0000207) | Potassium transporter, Potassium mediat | GO:00718 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Esterase, SGNH hydrolase-type, subgroup domain c | |
| | BTB domain containing protein | GO:00165 |
| [Os] blast disease (TO:0000074) | Similar to Gda-1 protein | GO:00349 |
| | Amino acid/polyamine transporter I famil | GO:00550 |
| | Similar to ACL098Cp | GO:00096 |
| | Armadillo-type fold domain containing p | GO:00431 |
| | Ankyrin repeat containing protein | GO:00353 |
| | Gas vesicle protein GvpC repeat containing protein | |
| | Exoribonuclease domain containing prot | GO:00004 |
| | Ubiquitin-conjugating enzyme/RWD-like | GO:00165 |
| | Similar to NADPH-dependent codeinone reductase ( | |
| | Similar to Galactoside 2-alpha-L-fucosyl | GO:00099 |
| | Similar to Type II inositol-1,4,5-trisphos | GO:00075 |
| | Similar to Plastid-specific 30S ribosomal | GO:00094 |
| | Similar to DOT2 (DEFECTIVELY ORGANIZE | GO:00003 |
| | Similar to H0321H01.3 protein | |
| | Lipase, class 3 family protein | GO:00066 |
| | Similar to Nuclear RNA binding protein B (Fragment) | |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Resolvase, holliday junction-type, YqgF-l | GO:00009 |
| | Hypothetical conserved gene | |
| | Ankyrin repeat containing protein | |
| | Protein kinase, core domain containing p | GO:00064 |
| | Alkaline-phosphatase-like, core domain | GO:00065 |

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| | Homolog of Arabidopsis suppressor of g | GO:00310 |
| | Similar to Protein kinase-like protein | GO:00064 |
| [Os] salt tolerance (TO:0006001) \| blast disease (TO:0000074); [Os] drought sensitivity TO:0000188 | Cell wall invertase (EC 3.2.1.26) | GO:00059 |
| | Uncharacterised protein family UPF0406 | GO:00344 |
| | Nucleoside phosphatase GDA1/CD39 fa | GO:00091 |
| | Similar to Dopamine beta-monooxygena | GO:00551 |
| | Protein of unknown function DUF632 do | GO:00712 |
| | Cyclophilin-like domain containing prote | GO:00004 |
| | Calponin homology domain domain cont | GO:00070 |
| | Similar to Secondary cell wall-related gly | GO:00095 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] grain size (TO:0000397) \| brassinosteroid sensitivity (TO:0002677) \| leaf angle (TO:0000206) \| leaf lamina joint | Similar to H0423H10.4 protein | GO:00063 |
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| | Similar to Alpha-expansin OsEXPA16 (Fra | GO:00069 |
| [Os] meristem identity TO:0006017 | Zinc finger, C2H2-type domain containin | GO:00063 |

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|---|---|---|
| [Os] silicon sensitivity (TO:0000031) \| bacterial blight disease resistance (TO:0000175) \| insect damage resistance (TO:0000261) \| leaf senescence (TO:0000249) \| black streak dwarf virus resistance (TO:0000020) \| heat tolerance (TO:0000259) \| brown planthopper resistance (TO:0000424) \| jasmonic acid sensitivity (TO:0000172) \| blast disease (TO:0000074); [Ta] root length TO:0000227 | Component of the SCF E3 ubiquitin ligas | GO:00022 |
| | Initiator tRNA phosphoribosyl transferas | GO:00199 |
| | Similar to H0219H12.4 protein | GO:00009 |
| | Similar to Heat shock transcription factor | GO:00063 |
| | Zinc finger, U1-C type domain containin | GO:00003 |
| [Os] bacterial blight disease resistance (TO:0000175) | | |
| | Zinc finger, C2H2-like domain containing protein | |
| | Thioredoxin fold domain containing prot | GO:00355 |
| [Os] seed set percent (TO:0000455) | Similar to ECA1 protein | GO:00095 |
| | Zm00001e006359 | |
| [Os] growth and development trait (TO:0000357) \| photosynthetic ability (TO:0000316) \| chlorophyll content (TO:0000495) \| cold tolerance (TO:0000303) \| leaf width (TO:0000370) \| yield trait (TO:0000371) \| grain weight (TO:0000590) \| plant height (TO:0000207) \| leaf color (TO:0000326) \| plastid development trait (TO:0002714) \| leaf length (TO:0000135) \| panicle length (TO:0000040) \| pollen sterility | Plastid-localized pentatricopeptide repea | GO:00096 |
| | Ribosomal RNA methyltransferase RrmJ/F | GO:00322 |
| | Similar to CF9 | |
| | Similar to F-box-containing protein 2 | |
| | Similar to selT-like protein | GO:00454 |
| | Protein of unknown function DUF2359, TMEM214 d | |
| | Leucine-rich repeat, cysteine-containing | GO:00102 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to Toc34-2 protein | GO:00068 |

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|---|---|---|
| [Ta] allelopathic effect TO:0000624 | | |
| | Apolipophorin III-like domain containing | GO:00019 |
| | Similar to GAMYB-binding protein (Fragm | GO:00101 |
| | Ubiquitin domain containing protein | |
| [Os] inflorescence development trait (TO:0000621) \| grain length (TO:0000734) \| seed length (TO:0000146) \| seed size (TO:0000391) | Similar to cDNA clone:001-036-C03, full insert seq | |
| | Zm00001e018893 | GO:00161 |
| | Similar to Transcription factor IIA large s | GO:00063 |
| | Similar to Glycosyltransferase QUASIMOD | GO:00454 |
| [Os] grain size TO:0000397\| leaf angle TO:0000206 | Control of wax biosynthesi | |
| [Os] flower anatomy and morphology trait (TO:0000499) \| cytoplasmic male sterility (TO:0000580) \| flower development trait (TO:0000622) | Similar to PISTILLATA-like MADS box pro | GO:00063 |
| | GTP1/OBG domain containing protein | |
| | Similar to predicted protein | GO:00064 |
| | Similar to cell number regulator 5 | |
| | Amino acid-binding ACT domain containing protein | |
| | Protein phosphatase 2C-like domain con | GO:00064 |
| | Armadillo-type fold domain containing p | GO:00002 |
| | Similar to STE20/SPS1-related proline-al | GO:00064 |
| | Glutathione S-transferase, C-terminal-lik | GO:00422 |
| | Isopenicillin N synthase family protein | |

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|---|---|---|
| [Os] spikelet length (TO:0002768) \| panicle length (TO:0000040) \| hydrogen peroxide content (TO:0000605) \| grain yield per panicle (TO:0000450) \| auxin sensitivity (TO:0000163) \| osmotic response sensitivity (TO:0000095) \| germination rate (TO:0000430) \| tiller number (TO:0000346) \| abscisic acid sensitivity (TO:0000615) \| abscisic acid content (TO:0002667) \| gibberellic acid sensitivity (TO:0000166) \| grain number (TO:0002759) \| tiller angle (TO:0000567) \| shoot branching (TO:0002639) \| leaf senescence (TO:0000249) \| plant height (TO:0000207) \| grain yield (TO:0000396) \| flowering time (TO:0002616) \| cytokinin content (TO:0002660) \| crown root number (TO:0002685) \| root length (TO:0000227) \| root development trait (TO:0000656) \| drought tolerance (TO:0000276) \| cytokinin sensitivity (TO:0000167) \| anatomy and morphology related trait (TO:0000017) \| internode length (TO:0000145) \| ethylene sensitivity (TO:0000173) \| salt | Similar to H0219H12.10 protein | GO:00063 |
| | Machado-Joseph disease protein MJD fam | GO:00065 |
| | NAD(P)-binding domain containing protein | |
| | Pseudouridine synthase domain containi | GO:00015 |
| | Phox-associated domain domain containing protein | |
| | EGF-like, alliinase domain containing pro | GO:00065 |
| | Alpha-1, 2 glucosyltransferase Alg10 do | GO:00064 |
| [Os] seed size (TO:0000391) \| plant height (TO:0000207) \| chalky endosperm (TO:0000266) \| leaf curling (TO:0002681) \| auxin sensitivity (TO:0000163) \| seed development trait (TO:0000653); [Ta] root length TO:0000227\| shoot fresh weight TO:0000571\| plant height TO:0000207 | Tryptophan aminotransferase, Indole-3- | GO:00098 |
| | GRAS-domain transcription factor, Strigo | GO:00063 |
| | Protein kinase, core domain containing p | GO:00064 |
| | DEAD-like helicase, N-terminal domain containing p | |
| | Kelch-type beta propeller domain containing protei | |

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|---|---|---|
| [Os] shoot apical meristem development (TO:0006020) \| stamen number (TO:0000225) \| leaf development trait (TO:0000655) | Similar to Nam-like protein 16 | GO:00063 |
| [Os] temperature response trait (TO:0000432) \| lignin content (TO:0000731) \| lignin biosynthesis trait (TO:0000733) \| copper sensitivity (TO:0000021) \| light intensity sensitivity (TO:0000460) | Similar to Caffeoyl-CoA O-methyltransfe | GO:00322 |
| [Os] sporogenesis TO:0000727 | Protein kinase, core domain containing p | GO:00064 |
| | Major facilitator superfamily protein | GO:00550 |
| | Methyltransferase type 11 domain contai | GO:00322 |
| | Membrane attack complex component/p | GO:00069 |
| | PDZ/DHR/GLGF domain containing prote | GO:00706 |
| | RNA polymerase II accessory factor, Cdc7 | GO:00063 |
| | NAD-binding site containing protein | |
| [Os] root number (TO:0000084) \| tillering ability (TO:0000329) \| amino acid content (TO:0002673) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| proline content (TO:0006002) \| hydrogen peroxide content (TO:0000605) \| leaf senescence (TO:0000249) \| mimic response (TO:0000063) \| root length (TO:0000227) \| panicle number (TO:0000152) \| grain yield | Amino acid permease, Transport of amin | GO:00033 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Zm00001e022213 | |
| | Methyltransferase small domain containi | GO:00064 |
| | Similar to Transcription initiation factor II | GO:00011 |
| | Similar to 60S ribosomal protein L18A | |
| | Paralog of FACTOR OF DNA METHYLATIO | GO:00310 |
| | OST3/OST6 family protein | GO:00182 |
| | Similar to ESK1 (ESKIMO 1) | GO:19909 |
| | Protein of unknown function DUF231, pla | GO:00059 |
| | Similar to Oxysterol-binding protein | GO:00159 |
| | Ribosomal RNA methyltransferase J doma | GO:00015 |
| | Similar to OSIGBa0130K07.9 protein | GO:00165 |
| | Zm00001e000876 | GO:00064 |

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|---|---|---|
| [Os] drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| bacterial blight disease resistance (TO:0000175) \| inflorescence development trait (TO:0000621); [Os] drought tolerance TO:0000276 | MADS-box transcription factor, Regulato | GO:00063 |
| | Conserved hypothetical protein | |
| | Zinc finger, HIT-type domain containing protein | |
| | Protein phosphatase 2C family protein | GO:00064 |
| | Similar to peptide transporter PTR2 | GO:00550 |
| | Dynamin family protein | GO:00100 |
| | Protein of unknown function DUF247, plant family p | |
| [Os] cold tolerance (TO:0000303) \| drought tolerance (TO:0000276) | | |
| | Similar to 3-ketoacyl-CoA synthase | GO:00066 |
| | Similar to Patatin-like phospholipase fam | GO:00066 |
| | Vps51/Vps67 domain containing protein | GO:00019 |
| | Similar to H0525G02.2 protein | GO:00003 |
| | Zinc finger, CCCH-type domain containing protein | |
| | Cyclin-like F-box domain containing protein | |
| | Similar to aromatic and neutral amino aci | GO:00033 |
| | Peptidase aspartic, catalytic domain cont | GO:00065 |
| | Similar to Peroxidase 16 precursor (EC 1. | GO:00069 |
| | Similar to Auxin-binding protein 4 precu | GO:00009 |
| | Protein of unknown function DUF296 dor | GO:00063 |
| | Similar to H0114G12.10 protein | GO:00508 |
| | Zm00001e013693 | GO:00064 |
| | Zm00001e002100 | |
| | Protein of unknown function DUF821, CAP10-like fa | |
| [Os] plant height (TO:0000207) \| grain size (TO:0000397) \| grain length (TO:0000734) | YbaK/aminoacyl-tRNA synthetase associa | GO:00063 |
| | Allene oxide synthase | GO:00432 |
| [Os] cold tolerance (TO:0000303) | Pentatricopeptide repeat domain containing protein | |
| | Similar to Peptide transporter PTR2-B | GO:00550 |
| | Calmodulin binding protein-like family p | GO:00063 |
| [Os] bacterial blight disease resistance (TO:0000175) | Similar to SUSIBA2-like (WRKY transcripti | GO:00063 |
| | Similar to SAUR family protein | GO:00097 |

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|---|---|---|
| [Os] disease resistance TO:0000112 | Similar to Ankyrin repeat BTB/POZ domai | GO:00069 |
| [Ta] meristem identity TO:0006017\| callus induction TO:0000428\| tiller number TO:0000346 | Similar to MADS-box transcription factor | GO:00063 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to Glutathione S-transferase GST | GO:00067 |
| | Protein-tyrosine phosphatase, dual speci | GO:00059 |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | | |
| | Snf7 family protein | GO:00069 |
| | Similar to Subtilisin-type protease | GO:00065 |
| | Zinc finger, DHHC-type domain containi | GO:00066 |
| | Similar to Glutaredoxin-like protein | GO:00068 |
| | Ribosome biogenesis protein Nop16 dom | GO:00422 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | | |
| | Protein of unknown function DUF221 do | GO:00342 |
| | Similar to DNA topoisomerase | GO:00062 |
| [Os] bacterial blight disease resistance (TO:0000175) \| growth hormone content (TO:0000476) \| white-backed planthopper resistance (TO:0000205) \| biotic stress trait (TO:0000179) \| lignin content (TO:0000731) \| plant growth hormone sensitivity (TO:0000401) \| amino acid content (TO:0002673) \| jasmonic acid content (TO:0002668) | Similar to Chorismate mutase CM2 (EC 5. | GO:00086 |
| | Alba, DNA/RNA-binding protein family p | GO:00482 |
| [Os] plant height (TO:0000207) | YT521-B-like protein family protein | GO:00611 |
| [Os] abiotic stress trait (TO:0000168) \| oxidative stress (TO:0002657) \| salt tolerance (TO:0006001) \| panicle size (TO:0006032) \| tiller number (TO:0000346) \| herbicide sensitivity (TO:0000058) \| grain yield | Similar to predicted protein | GO:00063 |
| | Similar to Fortune-1 | |
| [Os] inflorescence anatomy and morphology trait (TO:0000373) \| chlorophyll content (TO:0000495) \| temperature response trait (TO:0000432) \| leaf lamina color | Plastid RNA-binding protein, Regulation | GO:00063 |

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|---|---|---|
| | Similar to GDA1/CD39 family protein, ex | GO:00091 |
| | A/G-specific adenine glycosylase MutY, | GO:00062 |
| | Protein of unknown function DUF303, acetylesterase | |
| [Os] submergence tolerance TO:0000524\| stomatal resistance TO:0000523\| stomatal resistance | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Zm00001e002259 | GO:00068 |
| | Alpha/beta hydrolase fold-1 domain con | GO:00065 |
| [Os] seed set percent (TO:0000455) \| drought tolerance (TO:0000276) \| panicle number (TO:0000152) \| leaf development trait (TO:0000655) \| relative water content (TO:0000136) \| blast disease (TO:0000074) \| salt tolerance (TO:0006001) \| bacterial blight disease resistance (TO:0000175) \| grain yield (TO:0000396); [Os] disease resistance TO:0000112 | Protein kinase, core domain containing p | GO:00064 |
| | Serine/threonine protein kinase-related | GO:00002 |
| [Os] salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| heat tolerance (TO:0000259) | Sad1/UNC-like, C-terminal domain cont | GO:00069 |
| | Thioredoxin fold domain containing prot | GO:00454 |
| | Pectinacetylesterase family protein | GO:00715 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to Homeobox-like resistance | |
| | Similar to histone-lysine N-methyltransf | GO:00165 |
| | Zm00001e008358 | GO:00300 |
| [Os] leaf senescence (TO:0000249) \| bacterial blight disease resistance (TO:0000175) \| brown spot disease resistance (TO:0000356) \| jasmonic acid content (TO:0002668) \| blast disease (TO:0000074) | | |
| [Os] cold tolerance (TO:0000303) | Actin depolymerizing factor, Actin-bindi | GO:00070 |
| | MD-2-related lipid-recognition domain | GO:00159 |
| | Tetratricopeptide-like helical domain containing pro | |
| | Zm00001e000068 | GO:00064 |
| | Zm00001e022133 | GO:00063 |
| | WD40 repeat-like domain containing pro | GO:00000 |

<table>
<tr><td></td><td>EXTL2, alpha-1,4-N-acetylhexosaminyltr</td><td>GO:00064</td></tr>
<tr><td></td><td>Similar to CBL-interacting protein kinase</td><td>GO:00064</td></tr>
<tr><td></td><td>Similar to thaumatin-like protein 1</td><td>GO:00069</td></tr>
<tr><td></td><td>BZR1, transcriptional repressor domain c</td><td>GO:00063</td></tr>
<tr><td></td><td>Conserved hypothetical protein</td><td></td></tr>
<tr><td></td><td>Similar to H0105C05.7 protein</td><td>GO:00059</td></tr>
<tr><td></td><td>GTP-binding protein, HSR1-related doma</td><td>GO:00097</td></tr>
<tr><td></td><td>Zm00001e010288</td><td>GO:00097</td></tr>
<tr><td></td><td>Similar to Translocon-associated protein alpha subu</td><td></td></tr>
<tr><td>[Os] starch content (TO:0000696) | leaf development trait (TO:0000655) | plant height (TO:0000207) | nitrogen sensitivity (TO:0000011) | stem strength (TO:0000051) | 1000-dehulled grain weight (TO:0000592) | chlorophyll content (TO:0000495) | monosaccharide content (TO:0006006) | glucose content (TO:0000300); [Os] nitrogen content TO:0020093| relative chlorophyll content TO:0001016| chlorophyll content TO:0000495</td><td>Glycosyl transferase, family 8 protein</td><td>GO:00454</td></tr>
<tr><td></td><td>Putative ripening-related protein 6</td><td></td></tr>
<tr><td>[Os] abscisic acid sensitivity (TO:0000615) | jasmonic acid sensitivity (TO:0000172) | alkali</td><td>ACC oxidase, Ethylene biosynthesi</td><td></td></tr>
<tr><td>[Os] days to heading (TO:0000137) | plant height (TO:0000207) | salt tolerance (TO:0006001) | cold tolerance (TO:0000303) | drought tolerance (TO:0000276) | jasmonic acid sensitivity (TO:0000172) | gibberellic acid sensitivity (TO:0000166) | iron sensitivity (TO:0000224) | flowering time (TO:0002616); [Os] meristem identity TO:0006017| grain weight TO:0000919| plant height TO:0000207| amylose content TO:0000196| days to heading TO:0000137</td><td>CONSTANS-like protein, Heading promotion under l</td><td></td></tr>
<tr><td></td><td>Similar to emb2411 (embryo defective 24</td><td>GO:00062</td></tr>
<tr><td></td><td>Peptidase A22B, signal peptide peptidase</td><td>GO:00065</td></tr>
<tr><td></td><td>Similar to Seven transmembrane protein</td><td>GO:00069</td></tr>
<tr><td></td><td>Similar to YTH domain protein 2 (High-gl</td><td>GO:00611</td></tr>
</table>

| | | |
|---|---|---|
| | Twin-arginine translocation protein TatB | GO:00068 |
| | BTB domain containing protein | |
| | Hypothetical conserved gene | GO:00094 |
| | Src homology-3 domain containing protein | |
| | Protein of unknown function DUF296 do | GO:00063 |
| | BTB domain containing protein | |
| | Leucine-rich repeat, typical subtype containing prot | |
| | Pectin lyase fold/virulence factor domain | GO:00059 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:00165 |
| | Heat shock factor (HSF)-type, DNA-bindi | GO:00063 |
| | Similar to DEM2 | |
| | Similar to Toc64 | |
| | Similar to predicted protein | GO:00068 |
| [Os] pollen fertility (TO:0000421) \| root development trait (TO:0000656) \| auxin sensitivity (TO:0000163) \| spikelet anatomy and morphology trait (TO:0000657) \| anther length (TO:0000531) \| spikelet density (TO:0000625) \| spikelet width (TO:0000564) \| carpel number (TO:0006013) \| stamen number (TO:0000225) \| glume number (TO:0006029) \| 100-seed weight (TO:0000269) \| grain length (TO:0000734) \| seed size (TO:0000391) \| filled grain number (TO:0000447) \| root length (TO:0000227) \| tiller number (TO:0000346) \| plant height (TO:0000207) \| grain weight (TO:0000590) \| grain size (TO:0000397) \| flower organ size (TO:0002600) \| floral organ number (TO:0006038) \| seed development trait (TO:0000653) \| inflorescence development trait (TO:0000621) \| yield trait (TO:0000371) \| flower development trait (TO:0000622) \| growth and development trait (TO:0000357) \| drought tolerance | Kelch-domain-containing F-box protein, | GO:00311 |
| [Os] bacterial disease resistance (TO:0000315) \| drought tolerance (TO:0000276) \| viral disease resistance (TO:0000148) | Similar to Receptor-like protein kinase 6 | GO:00064 |

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|---|---|---|
| | Zinc finger, RING/FYVE/PHD-type domain containin | |
| [Os] cytokinin sensitivity (TO:0000167) | FAD linked oxidase, N-terminal domain c | GO:00096 |
| | Similar to Transcription factor HBP-1b(C3 | GO:00063 |
| | Homeodomain-like containing protein | |
| | RNA binding protein PufA | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | HhH-GPD domain domain containing pro | GO:00062 |
| | Protein of unknown function DUF231, plant domain | |
| [Os] blast disease (TO:0000074) \| salt tolerance (TO:0006001) \| auxin sensitivity (TO:0000163) \| plant height (TO:0000207) \| tiller angle (TO:0000567) \| plant growth hormone sensitivity (TO:0000401) \| gravity response trait (TO:0002693) \| grain length (TO:0000734); [Os] grain length TO:0002760\| grain length TO:0000734 | Transcriptional factor B3 family protein | GO:00063 |
| | WD40 repeat domain containing protein | GO:00069 |
| | Lupus La protein family protein | GO:00063 |
| | Similar to Josephin-like protein | GO:00065 |
| | Molecular chaperone, heat shock protein, | GO:00064 |
| | Similar to Rac GTPase activating protein | GO:00071 |
| | 3'-5' exonuclease domain containing pro | GO:00061 |
| | Similar to Potassium transporter 22 | GO:00068 |
| | Haem peroxidase family protein | GO:00069 |
| | Similar to Auxin-responsive protein IAA1 | GO:00034 |
| | Ubiquitin ligase, Det1/DDB1-complexing | GO:00097 |
| | Endonuclease/exonuclease/phosphatase | GO:00468 |
| | Zm00001e036968 | GO:00102 |
| [Os] root length (TO:0000227) \| plant height (TO:0000207) \| stomatal frequency (TO:0000566); [Os] crown rootless TO:0000230 | Similar to Cyclin A-like protein (Fragmen | GO:00000 |
| | Reticulon family protein | GO:00096 |
| [Os] disease resistance TO:0000112 | GRAS transcription factor domain contain | GO:00063 |
| | Similar to Beta-phosphoglucomutase | |
| | Voltage-dependent anion channel | GO:00068 |

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|---|---|---|
| [Os] lodging incidence (TO:0000068) \| plant height (TO:0000207) \| stem strength (TO:0000051) | | |
| | Similar to Cys/Met metabolism PLP-depe | GO:00090 |
| | Similar to Phosphoinositide-specific pho | GO:00066 |
| | FYVE finger-containing phosphoinositide | GO:00362 |
| | Nodule-specific protein-like | |
| [Os] heat tolerance (TO:0000259) \| salt tolerance (TO:0006001) | Arginine decarboxylase, Chilling stress re | GO:00065 |
| | Ribosomal protein L25 family protein | GO:00064 |
| | Similar to Heat shock transcription factor | GO:00063 |
| [Os] leaf development trait (TO:0000655) \| lateral root number (TO:0001013) \| root development trait (TO:0000656) \| grain yield (TO:0000396) \| seminal root length (TO:0000586) \| lateral root length (TO:0001012) \| root length (TO:0000227) \| leaf curling | Similar to Hydroxyproline-rich glycoprot | GO:00063 |
| | Similar to Actin-depolymerizing factor 6 | GO:00070 |
| | Similar to DRP1 protein | GO:00063 |
| | Mitotic checkpoint serine/threonine prot | GO:00070 |
| | Transcriptional factor B3 family protein | GO:00063 |
| | Zm00001e007816 | GO:00064 |
| | Similar to carbohydrate transporter/ sug | GO:00550 |
| | Similar to Histone mRNA exonuclease 1 | GO:00004 |
| [Os] salt tolerance (TO:0006001) \| osmotic response sensitivity (TO:0000095); [Os] oxidative stress TO:0002657 | GTPase-activating protein, Regulation of | GO:00068 |
| | Armadillo-type fold domain containing p | GO:00062 |
| | Amine oxidase domain containing protei | GO:00717 |
| | Zm00001e024638 | GO:00063 |
| | NIF system FeS cluster assembly, NifU, C- | GO:00162 |
| | Similar to plectin-related | GO:00070 |
| | Protein of unknown function DUF773 fa | GO:00000 |
| | Spectrin repeat containing protein | GO:00069 |
| | Domain of unknown function DUF632 do | GO:00712 |
| | TATA-binding related factor domain con | GO:00063 |
| | Peptidase C78, ubiquitin fold modifier-s | GO:00104 |
| | Similar to Lipoate protein ligase-like prot | GO:00362 |

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|---|---|---|
| [Os] alpha-linolenic acid content (TO:0005005) \| lignin content (TO:0000731) \| days to heading (TO:0000137) \| stem length (TO:0000576) \| spikelets per panicle length (TO:0000565) \| spikelet fertility (TO:0000180) \| 1000-dehulled grain weight (TO:0000592) \| linoleic acid content (TO:0005001); [Os] oxidative stress TO:0002657 | Similar to Lipoxygenase | |
| | Cyclin-like F-box domain containing pro | GO:00508 |
| | Similar to tRNA adenylyltransferase-like | GO:00016 |
| | TRAM, LAG1 and CLN8 homology domain containin | |
| | Nucleotide-binding, alpha-beta plait don | GO:00004 |
| [Os] bacterial blight disease resistance (TO:0000175) \| bacterial leaf streak disease resistance (TO:0000203) | Zinc finger, RING/FYVE/PHD-type domai | GO:00705 |
| | WD40 repeat-like domain containing protein | |
| | Similar to F-box domain containing protein | |
| [Os] starch content (TO:0000696) \| seed maturation (TO:0002661) \| filled grain number (TO:0000447) \| gibberellic acid sensitivity (TO:0000166) \| cytokinin sensitivity (TO:0000167) \| auxin sensitivity (TO:0000163) \| leaf senescence (TO:0000249) \| sugar content (TO:0000333) \| shrunken endosperm (TO:0000100) | RAG1-activating protein 1 homologue do | GO:00086 |
| | Pentatricopeptide repeat domain containing protein | |
| | WD40 subfamily protein, Salt stres | |
| | Cytochrome b561 family protein | |
| [Os] oxidative stress TO:0002657\| protein content TO:0000598\| drought tolerance TO:0000276\| disease resistance TO:0000112 | | |
| | Similar to MCB1 protein | |
| | Conserved hypothetical protein | |
| | Similar to SH3 domain-containing protein 3 | |
| | Zm00001e036914 | |

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|---|---|---|
| | Similar to Calcium/calmodulin-regulated | GO:00064 |
| | Metallophosphoesterase domain containing protein | |
| | Peptidase A1 domain containing protein | GO:00065 |
| | Similar to Chloride channel protein CLC-f | GO:00068 |
| [Os] salt tolerance (TO:0006001) \| radiation response trait (TO:0000161) \| sodium to potassium content ratio (TO:0000525) | Protein kinase, core domain containing p | GO:00064 |
| | Similar to Plant acid phosphatase family protein, exp | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Ribosomal protein, PSRP-3/Ycf65 domai | GO:00064 |
| | Similar to Potassium transporter | GO:00068 |
| | Protein of unknown function DUF292, eu | GO:00081 |
| | Similar to Beta-1,3-glucanase-like protei | GO:00059 |
| [Os] chlorophyll content (TO:0000495) \| nitrogen sensitivity (TO:0000011) \| drought tolerance (TO:0000276) | Nitrate-inducible and autorepressible tra | GO:00063 |
| | Conserved hypothetical protein | GO:00065 |
| | Armadillo-type fold domain containing p | GO:00161 |
| [Os] pollen free (TO:0000245) \| flowering time (TO:0002616) \| inflorescence anatomy and morphology trait (TO:0000373) | MADS-box transcription factor, Control o | GO:00063 |
| | Protein of unknown function DUF231, plant domain | |
| [Os] drought tolerance (TO:0000276) \| blast disease (TO:0000074) \| inflorescence development trait (TO:0000621) \| seed development trait (TO:0000653) \| sheath blight disease resistance (TO:0000255) \| bacterial blight disease resistance (TO:0000175) | | |
| | Protein similar to CwfJ, C-terminal 2 dom | GO:00003 |
| | BRCT domain containing protein | GO:00000 |
| | Hypothetical conserved gene | GO:00020 |
| | Mitochondrial import inner membrane tra | GO:00068 |
| | Pentatricopeptide repeat domain containing protein | |

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|---|---|---|
| | Similar to FKBP-type peptidyl-prolyl cis-t | GO:00004 |
| | Similar to Transporter-like protein | GO:00550 |
| | Pentatricopeptide repeat domain containing protein | |
| | Similar to IBS1 (IMPAIRED IN BABA-INDUC | GO:00064 |
| | Serine/threonine protein kinase domain | GO:00064 |
| | Similar to RNase H domain-containing pr | GO:00905 |
| [Os] animal damage resistance (TO:0000054) | Similar to Cystatin (Fragment) | GO:00069 |
| | Adenylate cyclase domain containing protein | |
| | Phosphate-induced protein 1 conserved region fami | |
| | Cyclin-like F-box domain containing protein | |
| | Similar to protein kinase APK1B | GO:00064 |
| [Os] oxygen sensitivity (TO:0000015) \| leaf lamina joint bending (TO:0002688) \| leaf angle (TO:0000206) \| phosphorus sensitivity (TO:0000102) \| oxidative stress (TO:0002657) \| cold tolerance (TO:0000303); [Os] cold tolerance TO:0000303 | SPX domain-containing protein, Phospha | GO:00160 |
| | Similar to Cytochrome P450 | |
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] seed viability TO:0000345 | Similar to Fatty aldehyde dehydrogenase | GO:00060 |
| | Similar to cDNA clone:002-125-A07, full | GO:00104 |
| [Os] cytokinin sensitivity (TO:0000167) \| root development trait (TO:0000656); [Os] leaf width TO:0000370 | Similar to Histidine kinase | GO:00001 |
| | Similar to cDNA clone:J013000F18, full i | GO:00715 |
| | Zm00001e021168 | |
| | Similar to transducin family protein / WD | GO:00063 |
| | Similar to Condensin complex subunit 2 | GO:00070 |
| | Similar to predicted protein | |
| | Similar to endonuclease, polyU-specific | GO:00905 |
| | Similar to Calmodulin-binding protein MPCBP | |

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|---|---|---|
| [Os] plant height (TO:0000207) \| gibberellic acid content (TO:0002675) | Cytochrome P450 family protein | |
| | TB2/DP1 and HVA22 related protein family protein | |
| [Os] cellulose content TO:0000993 | Similar to Type B-like cyclin (Fragment) | GO:00704 |
| | Similar to binding / catalytic | |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF794, plant family p | |
| | Similar to transcription factor jumonji (jm | GO:00331 |
| | 4Fe-4S ferredoxin, iron-sulpur binding d | GO:00000 |
| [Os] seed size TO:0000391; [Ta] root length TO:0000227\| root volume TO:0000233 | Zinc finger, RING/FYVE/PHD-type domair | GO:00165 |
| | Tetratricopeptide-like helical domain con | GO:00159 |
| [Os] drought related trait (TO:0000394) | TGF-beta receptor, type I/II extracellular | GO:00101 |
| | Zm00001e107346 | GO:00064 |
| | Similar to Receptor-like protein kinase | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| [Os] viral disease resistance (TO:0000148) | Similar to XRN3 | GO:00009 |
| | Endonuclease/exonuclease/phosphatase | GO:00905 |
| | Similar to D-mannose binding lectin family protein, | |
| | Similar to NOT2/NOT3/NOT5 family prot | GO:00063 |
| | Plant lipid transfer protein and hydrophol | GO:00065 |
| | Lipase, GDSL domain containing protein | |
| | Similar to Nodulin-like protein | GO:00550 |
| [Os] male sterility (TO:0000437) | Similar to GDSL-motif lipase/hydrolase family prote | |
| | Major facilitator superfamily MFS_1 prote | GO:00550 |
| | Asp/Glu racemase, active site domain co | GO:00094 |
| | Protein kinase, core domain containing p | GO:00064 |
| | Similar to predicted protein | GO:00063 |
| | Zm00001e013646 | GO:00064 |
| | Lipase, GDSL domain containing protein | |

| | | |
|---|---|---|
| | Uncharacterised protein family UPF0005 | GO:00157 |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to Histidine-containing phosphot | GO:00070 |
| | Protein of unknown function DUF828, pla | GO:00097 |
| | Chalcone isomerase domain containing protein | |
| | Zm00001e016398 | GO:00165 |
| | Similar to PEPC kinase | GO:00064 |
| | Mitochondrial glycoprotein family protein | |
| | Similar to integral membrane family protein | |
| [Os] root hair length (TO:0002665) | Similar to Pollen-specific kinase partner | GO:00507 |
| | Transferase family protein | |
| | Similar to Transmembrane protein 18 | |
| [Os] salt tolerance (TO:0006001) \| cold tolerance (TO:0000303) \| alkali sensitivity (TO:0000481) | Similar to protein binding / zinc ion binding | |
| | Protein of unknown function DUF604 family protein | |
| | Similar to Protein phosphatase-2C | GO:00064 |
| | Methyltransferase type 12 domain contai | GO:00063 |
| [Os] bacterial blight disease resistance (TO:0000175) \| cold tolerance (TO:0000303) \| abscisic acid sensitivity (TO:0000615) \| oxidative stress (TO:0002657) \| osmotic response sensitivity (TO:0000095) \| auxin sensitivity (TO:0000163) \| gibberellic acid sensitivity (TO:0000166) \| salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| blast disease (TO:0000074) \| abscisic acid content (TO:0002667) \| drought tolerance (TO:0000276) \| hydrogen peroxide content (TO:0000605); [Os] heat tolerance TO:0000259 | Similar to NAC-type transcription factor | GO:00063 |

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|---|---|---|
| [Os] hydrogen peroxide content (TO:0000605) \| panicle blast disease resistance (TO:0000477) | Similar to Oxalate oxidase 1 (EC 1.2.3.4) (Germin) | |
| [Os] red light sensitivity (TO:0000158) \| blue light sensitivity (TO:0000159) \| far red light sensitivity (TO:0000130) \| light sensitivity (TO:0000075) \| light intensity sensitivity (TO:0000460) \| auxin sensitivity (TO:0000163) | Cytochrome P450 family protein | GO:00072 |
| | Mitochodrial transcription termination fa | GO:00063 |
| | Zm00001e014234 | GO:00080 |
| | DEAD-like helicase, N-terminal domain containing | |
| [Os] gibberellic acid sensitivity (TO:0000166) \| jasmonic acid sensitivity (TO:0000172); [Os] sucrose content TO:0000328\| carbohydrate content TO:0000291 | Similar to Geranyl diphosphate synthase | GO:00067 |
| | Similar to Hydroxyanthranilate hydroxycinnamoyltra | |
| | TIP41-like protein family protein | GO:00071 |
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| | Similar to Leucine Rich Repeat family pro | GO:00064 |
| | Exostosin-like family protein | GO:00064 |
| | Similar to Carbonate dehydratase-like pr | GO:00100 |
| | HSP20-like chaperone domain containin | GO:00069 |
| | Similar to Hexokinase-10 | GO:00016 |
| | Zm00001e148701 | GO:00065 |
| [Os] mimic response (TO:0000063) \| growth hormone content (TO:0000476) \| disease resistance (TO:0000112) \| variegated leaf (TO:0000069) \| tryptophan content (TO:0002674) | Cleavage and polyadenylation specificity | GO:00003 |
| | ABC transporter-like domain containing | GO:00550 |
| | Similar to fringe-related protein | |
| [Os] grain weight (TO:0000590) \| abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| filled grain number (TO:0000447) \| panicle length (TO:0000040) \| seed development trait (TO:0000653) \| drought tolerance (TO:0000276) \| grain length (TO:0000734) \| grain size (TO:0000397) \| auxin sensitivity | Ubiquitin-conjugating enzyme/RWD-like | GO:00002 |

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|---|---|---|
| | Similar to T3/T7-like RNA polymerase (Fr | GO:00063 |
| | Peptidase S54, rhomboid domain containing protein | |
| | Ribosome recycling factor family protein | GO:00064 |
| | Similar to ATCNGC15 | GO:00068 |
| | Armadillo-like helical domain containing protein | |
| | Mitochondrial substrate carrier family protein | |
| | Armadillo-like helical domain containing protein | |
| | Cyclin-like F-box domain containing protein | |
| | Similar to Dihydrofolate synthetase /folyl | GO:00067 |
| | Similar to DNA binding / nuclease | |
| | Zm00001e027490 | GO:00094 |
| | Zm00001e027923 | GO:00064 |
| | Class I peptide chain release factor doma | GO:00064 |
| | Cyclin-like F-box domain containing protein | |
| [Os] inflorescence development trait (TO:0000621) | | |
| | Serine/threonine-specific protein kinase | GO:00064 |
| | Similar to RNA binding protein (Fragment) | |
| | Protein of unknown function DUF339 fam | GO:00060 |
| | Similar to H0624F09.2 protein | GO:00165 |
| | Zm00001e021342 | GO:00068 |
| | Similar to predicted protein | |
| [Os] panicle length (TO:0000040) \| grain size (TO:0000397) \| grain shape (TO:0002730) \| grain yield (TO:0000396) \| inflorescence branching (TO:0000050) \| plant height (TO:0000207) \| grain length | mRNA splicing factor SYF2 family protein | GO:00003 |
| | Cytochrome P450 family protein | |
| | Similar to Thioredoxin H-type 5 (TRX-H- | GO:00066 |
| | Acyl-CoA N-acyltransferase domain containing prot | |
| | Peptidase T2, asparaginase 2 domain cor | GO:00516 |
| [Os] salt tolerance (TO:0006001) | ABC transporter-like domain containing | GO:00097 |
| | Glucose-methanol-choline (GMC) oxidoreductase fa | |

|  |  |  |
|---|---|---|
|  | FAS1 domain domain containing protein | GO:00098 |
|  | UDP-glucuronosyl/UDP-glucosyltransferase family |  |
|  | Similar to Peptide deformylase, chloropla | GO:00064 |
|  | Similar to Cytochrome P450 CYP71Y10 |  |
|  | Similar to Phosphoenolpyruvate carboxyl | GO:00064 |
|  | RINT-1/TIP-1 family protein | GO:00066 |
|  | Similar to Ferredoxin (Bacterial type ferre | GO:00229 |
|  | Protein of unknown function DUF1168 fa | GO:00064 |
| [Os] drought tolerance (TO:0000276) \| stomatal conductance (TO:0000522) \| abscisic acid sensitivity (TO:0000615) | Similar to Farnesyltransferase beta subun | GO:00183 |
|  | Ribose 5-phosphate isomerase family pr | GO:00060 |
|  | Nicastrin family protein | GO:00164 |
|  | Similar to predicted protein | GO:00550 |
|  | Domain of unknown function DUF1995 domain cont |  |
|  | Similar to Surfeit 1 homolog |  |
|  | Similar to FPF1 | GO:00099 |
| [Os] heat tolerance (TO:0000259) \| drought tolerance (TO:0000276) \| photosynthetic ability (TO:0000316) \| hydrogen peroxide content (TO:0000605) \| relative chlorophyll content (TO:0001016) \| relative root length (TO:0000516) \| alkali sensitivity (TO:0000481) \| herbicide sensitivity (TO:0000058) \| salt tolerance (TO:0006001) | Similar to predicted protein | GO:00094 |
|  | Tetratricopeptide-like helical domain con | GO:00094 |
| [Os] white-backed planthopper resistance (TO:0000205) \| bacterial blight disease resistance (TO:0000175) | Hypothetical conserved gene | GO:00063 |
|  | Zinc finger, C6HC-type domain containin | GO:00002 |
|  | Similar to predicted protein | GO:00002 |
|  | Similar to indole-3-acetate beta-glucosyltransferas |  |
|  | Similar to Gpi-anchored protein (Fragment) |  |

| | | |
|---|---|---|
| [Os] male sterility (TO:0000437) \| starch content (TO:0000696) \| bacterial blight disease resistance (TO:0000175); [Os] grain weight TO:0000919\| plant height TO:0000207\| disease resistance TO:0000112 | Similar to MTN3 | GO:00086 |
| | Uncharacterised protein family UPF0497, trans-mem | |
| [Ta] bacterial blight disease resistance TO:0000770\| disease resistance TO:0000112\| oxidative stress TO:0002657 | Similar to OSIGBa0142I02-OSIGBa0101B | GO:00069 |
| | Similar to Hydroxyisourate hydrolase | GO:00059 |
| | Similar to serine/threonine protein kinas | GO:00064 |
| | WD40 repeat domain containing protein | |
| | Protein of unknown function DUF778 fan | GO:00097 |
| | Similar to protein kinase family protein | GO:00064 |
| | Similar to Low temperature-responsive R | GO:00801 |
| | Similar to predicted protein | GO:00059 |
| | Nucleotide-binding, alpha-beta plait domain contai | |
| | Zm00001e000017 | |
| | Conserved hypothetical protein | GO:00099 |
| | Similar to Endoribonuclease E-like protein | |
| | Zm00001e011729 | GO:00066 |
| | Similar to Guanylate kinase (EC 2.7.4.8) | GO:00061 |
| | Similar to Myosin heavy chain class VIII A | GO:00070 |
| | Peptidase M20 domain containing protei | GO:00002 |
| | Cornichon family protein | GO:00161 |
| | Tetratricopeptide-like helical domain con | GO:00063 |
| [Os] shoot branching (TO:0002639) \| leaf size (TO:0002637) \| leaf shape (TO:0000492) | Cytochrome P450 family member, | Homolog of Arab |
| | Similar to Beta-galactosidase | GO:00059 |

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|---|---|---|
| [Os] salt tolerance (TO:0006001) \| oxidative stress (TO:0002657) \| abscisic acid sensitivity (TO:0000615) \| hydrogen peroxide content (TO:0000605) \| drought tolerance (TO:0000276); [Os] salt tolerance TO:0006001\| oxidative stress TO:0002657\| drought tolerance | CS domain containing protein | GO:00069 |
| | Phospholipase A2 family protein | GO:00066 |
| | Zm00001e026179 | GO:00322 |
| | Protein of unknown function DUF296 domain contai | |
| | Similar to mitochondrial protein | |
| | Non-protein coding transcript | GO:00064 |
| | Protein of unknown function DUF914, eu | GO:00550 |
| | Similar to chloroplast post-illumination c | GO:00101 |
| | Pentatricopeptide repeat domain containing protein | |
| [Os] disease resistance TO:0000112 | Similar to Glycosyl hydrolases family 17 | GO:00059 |
| | Protein of unknown function DUF231, pla | GO:19909 |
| | Transmembrane receptor, eukaryota domain contai | |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) | Conserved hypothetical protein | GO:00001 |
| | Hepatocellular carcinoma-associated anti | GO:00003 |
| | Similar to Pectin methylesterase-like prot | GO:00425 |
| | Zm00001e001296 | GO:00159 |
| [Os] iron sensitivity (TO:0000224) \| zinc sensitivity (TO:0000351) \| gibberellic acid sensitivity (TO:0000166) \| copper sensitivity (TO:0000021) \| drought tolerance (TO:0000276) | Similar to Nicotianamine aminotransferas | GO:00065 |
| | Haloacid dehalogenase-like hydrolase domain conta | |
| | Zm00001e030412 | GO:00062 |

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|---|---|---|
| [Os] hydrogen peroxide content (TO:0000605) \| submergence tolerance (TO:0000524) \| relative water content (TO:0000136) \| 1000-seed weight (TO:0000382) \| germination rate (TO:0000430) \| abscisic acid content (TO:0002667) \| blast disease (TO:0000074) \| stomatal closure rate (TO:0000520) \| drought tolerance (TO:0000276) \| osmotic response sensitivity (TO:0000095) \| salt tolerance (TO:0006001) \| auxin sensitivity (TO:0000163) \| fungal disease resistance (TO:0000439) \| disease resistance (TO:0000112) \| false smut disease resistance (TO:0000129) \| jasmonic acid sensitivity (TO:0000172) \| proline content (TO:0006002) \| abscisic acid sensitivity (TO:0000615);<br>[Os] drought tolerance TO:0000276\| | Similar to Respiratory burst oxidase hom | GO:00988 |
| | Cyclin-like F-box domain containing protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | AT-rich interaction region domain contai | GO:00063 |
| [Os] seed dormancy TO:0000253 | Similar to protein phosphatase 2C ABI1 | GO:00097 |
| | Similar to cDNA clone:J023074C15, full insert seque | |
| [Os] embryo development trait (TO:0000620) \| bacterial blight disease resistance (TO:0000175) \| seed development trait (TO:0000653); [Os] male sterility TO:0000437 | Similar to TA11 protein (Fragment) | GO:00064 |
| | Similar to zinc finger, C2H2 type family p | GO:00063 |
| | Similar to Hydroxyanthranilate hydroxycinnamoyltra | |
| | Cyclin-like F-box domain containing protein | |
| | Glucose/ribitol dehydrogenase family protein | |
| | Similar to Pattern formation protein EMB | GO:00320 |
| | Similar to Phosphoglycerate kinase | GO:00060 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Iojap-related protein family protein | GO:00171 |
| | DNA-directed RNA polymerase, RPB5 sub | GO:00063 |
| | Similar to Diacylglycerol kinase 1 (EC 2.7. | GO:00071 |
| | Tetraspanin domain containing protein | GO:00097 |
| | WD40 repeat-like domain containing pro | GO:00095 |

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|---|---|---|
| | Similar to Phosphoglycerate mutase family protein | |
| | Saposin family protein | GO:00065 |
| | Similar to Nonspecific lipid-transfer prot | GO:00068 |
| | Serine/threonine protein kinase domain c | GO:00064 |
| | Acyl-CoA N-acyltransferase domain cont | GO:00064 |
| | UvrB/UvrC protein domain containing protein | |
| | Similar to cDNA clone:J013112C08, full i | GO:00454 |
| | WD40 repeat-like domain containing protein | |
| | tRNA isopentenyltransferase family prote | GO:00064 |
| | Similar to RNA helicase (Fragment) | |
| | Similar to Topoisomerase-like protein | GO:00064 |
| | SufBD family protein | GO:00097 |
| | Protein of unknown function DUF1715, e | GO:00422 |
| | Similar to B-cell receptor-associated prot | GO:00068 |
| | Esterase, SGNH hydrolase-type domain containing p | |
| | Uncharacterised protein family UPF0310 domain co | |
| | Similar to NADPH-dependent codeinone | GO:00192 |
| | Similar to Protein binding protein | GO:00062 |
| | Multi antimicrobial extrusion protein Mat | GO:00068 |
| | ATPase, AAA-type, core domain containi | GO:00096 |
| | Zm00001e028355 | GO:00094 |
| | Protein of unknown function DUF6, transmembrane | |
| | Similar to predicted protein | GO:00096 |
| [Os] root length (TO:0000227) \| aluminum sensitivity (TO:0000354) | Ribosomal protein L32p domain containi | GO:00064 |
| [Os] biotic stress trait (TO:0000179) \| jasmonic acid sensitivity (TO:0000172) \| fungal disease resistance (TO:0000439) \| drought tolerance (TO:0000276) \| salt tolerance | Caleosin related family protein | |
| | Protein of unknown function DUF547 domain contai | |
| | Similar to Pherophorin-S precursor | |
| | 3-dehydroquinate synthase family protei | GO:00086 |
| | RNA-binding region RNP-1 (RNA recognition motif) | |
| | Similar to Conserved protein | |
| | Pentatricopeptide repeat domain containi | GO:00094 |

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|---|---|---|
| | Six-bladed beta-propeller, TolB-like dom | GO:00090 |
| | Similar to TRNA isopentenyl transferase- | GO:00064 |
| | Similar to Serine/threonine-protein kinas | GO:00064 |
| | Pentatricopeptide repeat domain containing protein | |
| | Conserved hypothetical protein | |
| | Protein of unknown function DUF221 dor | GO:00066 |
| | RabGAP/TBC domain containing protein | GO:00068 |
| [Os] abscisic acid sensitivity (TO:0000615) \| blast disease (TO:0000074) \| internode length (TO:0000145) \| grain length (TO:0000734) \| grain size (TO:0000397) \| root length (TO:0000227) \| bacterial blight disease resistance (TO:0000175) \| plant height (TO:0000207) \| aluminum sensitivity (TO:0000354) \| brown planthopper resistance (TO:0000424) \| root development trait (TO:0000656) \| root thickness (TO:0000306) \| 1000- | Expansin, Al-inducible expansin, Root ce | GO:00096 |
| | Tensin phosphatase, C2 domain domain | GO:00066 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Similar to bromodomain protein 103 | GO:00319 |
| [Os] 1000-seed weight (TO:0000382) \| seedling vigor (TO:0000280) \| embryo development trait (TO:0000620) \| seed development trait (TO:0000653) \| chalky endosperm (TO:0000266) \| spikelet fertility (TO:0000180) \| seed quality (TO:0000162) \| fat and essential oil content (TO:0000604) | | |
| | FeS cluster insertion domain containing | GO:00162 |
| | Similar to SIGE (RNA polymerase sigma s | GO:00063 |

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|---|---|---|
| [Os] seed development trait (TO:0000653) \| protein content (TO:0000598) \| light intensity sensitivity (TO:0000460) \| inflorescence development trait (TO:0000621) \| salt tolerance (TO:0006001) \| heat tolerance (TO:0000259) \| 1000-seed weight (TO:0000382) \| floury endosperm (TO:0000104) \| chalky endosperm (TO:0000266) \| cold tolerance (TO:0000303) \| sugar content (TO:0000333); [Ta] grain length TO:0002760\| grain length TO:0000734 | Protein disulfide isomerase-like enzyme, | GO:00064 |
| | Similar to 30S Ribosomal protein S18 | GO:00064 |
| [Os] salt tolerance (TO:0006001) \| brassinosteroid sensitivity (TO:0002677); [Os] salt tolerance TO:0006001; [Ta] salt tolerance | High-affinity K+ transporter (HKT) family | GO:00068 |
| | Similar to predicted protein | GO:00068 |
| [Os] brassinosteroid content (TO:0002676) \| black streak dwarf virus resistance (TO:0000020) \| blue light sensitivity (TO:0000159) \| jasmonic acid sensitivity (TO:0000172); [Os] leaf angle TO:0000206 | Similar to Cytochrome P450 90A1 (EC 1.1 | GO:00066 |
| [Os] seed development trait (TO:0000653) \| chalky endosperm (TO:0000266) \| auxin content (TO:0002672) | FAD-dependent pyridine nucleotide-disulphide oxi | |
| | RabGAP/TBC domain containing protein | GO:00068 |
| | Zm00001e000930 | |

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|---|---|---|
| [Os] chlorophyll content (TO:0000495) \| grain size (TO:0000397) \| tiller number (TO:0000346) \| hydrogen peroxide content (TO:0000605) \| monosaccharide content (TO:0006006) \| leaf senescence (TO:0000249) \| basal internode diameter (TO:0000132) \| panicle length (TO:0000040) \| leaf margin color (TO:0000695) \| leaf color (TO:0000326) \| plant height (TO:0000207) \| days to heading (TO:0000137) \| grain weight (TO:0000590) \| seed development trait (TO:0000653) \| lateral root number (TO:0001013) \| root length (TO:0000227) \| internode length | Pectate lyase (PEL) precursor, Maintenance of norma | |
| | Expansin-like protein A | GO:00096 |
| | | |
| | | |
| | | |
| | | |
| | | |
| | Cellular retinaldehyde-binding/triple fun | GO:00159 |
| | Similar to PTAC6 (PLASTID TRANSCRIPTIONALLY AC | |
| | Phosphatidylinositol 3- and 4-kinase, ca | GO:00468 |
| | Protein of unknown function DUF2485 domain cont | |
| | Molecular chaperone, heat shock protein, | GO:00610 |
| [Os] drought tolerance (TO:0000276) \| bacterial blight disease resistance (TO:0000175); [Os] grain weight TO:0000919\| plant height TO:0000207\| disease resistance TO:0000112 | Sucrose transporter, TAL effector PthXo2 | GO:00086 |
| | | |
| | Cyclin-like F-box domain containing pro | GO:00065 |
| | Similar to Hin19 (Fragment) | GO:00064 |
| | Cyclin-like F-box domain containing protein | |
| | Similar to Plastid 5,10-methylene-tetrah | GO:00067 |
| | Queuine/other tRNA-ribosyltransferase f | GO:00064 |
| [Os] grain length (TO:0000734) \| glume length (TO:0020033) \| internode length (TO:0000145) \| grain size (TO:0000397) \| plant height (TO:0000207); [Os] glume length TO:0020033\| grain number TO:0002759\| grain size TO:0000397 | Kinesin 13 protein, Regulation of grain le | GO:00070 |
| | Similar to snRK1-interacting protein 1 | GO:00007 |
| | K Homology, type 1, subgroup domain c | GO:00104 |
| | Similar to BRASSINOSTEROID INSENSITIVE | GO:00064 |
| | Ankyrin repeat containing protein | |

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|---|---|---|
| | HR-like lesion-inducer family protein | |
| | Cystathionine beta-synthase, core domain containi | |
| [Os] starch content TO:0000696 | Zm00001e033142 | GO:00063 |
| | Phenazine biosynthesis PhzC/PhzF protei | GO:00090 |
| | Exo70 exocyst complex subunit family pr | GO:00068 |
| | Phytochrome A, Photorecepto | GO:00001 |
| | Hypothetical conserved gene | |
| | Zm00001e015618 | |
| [Os] seed width (TO:0000149) \| starch grain size (TO:0002655) \| chalky endosperm (TO:0000266) \| chloroplast development trait (TO:0002715) \| chlorophyll content (TO:0000495) | Amyloplast-localized protein containing | GO:00093 |
| [Os] drought tolerance (TO:0000276) \| heat tolerance (TO:0000259) \| salt tolerance (TO:0006001); [Os] male sterility TO:0000437; [Ta] male sterility TO:0000437\| oxidative stress TO:0002657\| drought tolerance TO:0000276 | Calcium-binding protein, Annexin, Heat | GO:00094 |
| | Zm00001e025277 | |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | PDIL5-3 - Zea mays protein disulfide iso | GO:00064 |
| | Cyclin-like F-box domain containing protein | |
| | Similar to Non-phototropic hypocotyl 3 | GO:00165 |
| | Pseudouridine synthase domain containi | GO:00004 |
| | Similar to Leucine Rich Repeat family pro | GO:00064 |
| | Tetratricopeptide-like helical domain containing pr | |
| | Kinesin, motor region domain containing | GO:00070 |
| | Protein of unknown function DUF858, me | GO:00064 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | t-snare domain containing protein | GO:00096 |
| | Tyrosine protein kinase domain containi | GO:00064 |
| | Hypothetical conserved gene | GO:00063 |
| | Similar to (1,4)-beta-xylan endohydrolas | GO:00002 |
| | Similar to Dihydrofolate synthetase /folyl | GO:00067 |

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|---|---|---|
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | | |
| | Conserved hypothetical protein | |
| | Glycoside hydrolase, family 17 protein | GO:00059 |
| | | |
| | Ribophorin II family protein | GO:00064 |
| | UDP-glucuronosyl/UDP-glucosyltransferase family | |
| | Similar to Nucleotide sugar epimerase-like protein ( | |
| | Tetratricopeptide-like helical domain con | GO:00002 |
| [Os] heat tolerance (TO:0000259) \| drought tolerance (TO:0000276) \| sheath blight disease resistance (TO:0000255) \| blast disease (TO:0000074) \| abscisic acid sensitivity (TO:0000615) \| insect damage resistance (TO:0000261) \| salt tolerance | | |
| | Conserved hypothetical protein | |
| | Similar to VAP27 | GO:00618 |
| | Exoribonuclease domain containing prot | GO:00160 |
| | Zm00001e036528 | GO:00003 |
| | Rhodanese-like domain containing prote | GO:00097 |
| | Acyl-CoA N-acyltransferase domain cont | GO:00171 |
| | Homeodomain-like containing protein | |
| | | |
| | Similar to OSIGBa0138H21-OSIGBa0138E | GO:00096 |
| | Similar to AT.I.24-1 protein (Fragment) | GO:00454 |
| | Similar to NONA protein | |
| | Conserved hypothetical protein | |
| | Zm00001e008798 | |
| | Tubulin/FtsZ, GTPase domain containing protein | |
| | SNARE associated Golgi protein domain containing | |
| | Conserved hypothetical protein | GO:00902 |
| | TGF-beta receptor, type I/II extracellular | GO:00550 |
| | Thioredoxin fold domain containing protein | |
| | Similar to proline-rich family protein | GO:00616 |
| | | |
| | | |
| | Similar to ER66 protein (Fragment) | GO:00063 |
| | Protein of unknown function DUF250 dor | GO:00068 |
| | Similar to Glycine-rich protein | GO:00165 |
| | DNA/RNA helicase, C-terminal domain containing | |
| | Similar to SAC domain protein 1 (FIG4-lik | GO:00070 |
| [Os] spikelet fertility TO:0000180 | Similar to RNA-binding region containing | GO:00301 |
| | Methyltransferase type 11 domain containing protei | |

| | | |
|---|---|---|
| [Hv] abscisic acid sensitivity (TO:0000615) \| salt tolerance (TO:0006001) \| drought tolerance (TO:0000276) \| stomatal conductance (TO:0000522) \| leaf water potential | Guard cell anion channel protein, Nitrate- | GO:00068 |
| | Thioredoxin domain 2 containing protein | GO:00064 |
| | Alpha/beta hydrolase fold-3 domain containing pro | |
| | Similar to NPL4 family protein | GO:00065 |
| | Glycoside hydrolase, family 35 protein | GO:00059 |
| | Hypothetical conserved gene | |
| | Similar to H0211B05.12 protein | GO:00060 |
| [Os] chalky endosperm (TO:0000266) \| sucrose content (TO:0000328) \| grain yield (TO:0000396) \| seed size (TO:0000391) \| seed maturation (TO:0002661) \| amylopectin content (TO:0000097) \| grain weight (TO:0000590) \| fructose content (TO:0006005) \| seed quality (TO:0000162) \| starch content (TO:0000696) \| seed thickness (TO:0000304) \| seed width (TO:0000149) \| seed length (TO:0000146) \| starch grain shape (TO:0002656) \| glume color (TO:0000221) \| seed set percent (TO:0000455) \| amylose content (TO:0000196) \| filled grain number (TO:0000447) \| spikelet number (TO:0000456) \| invertase activity (TO:0000311) \| glucose content (TO:0000300) \| endosperm color (TO:0000487) \| endosperm related trait (TO:0000575) \| 1000-dehulled grain weight (TO:0000592); [Os] grain size | Cell-wall invertase, Carbon partitioning d | GO:00059 |
| | Protein of unknown function DUF6, trans | GO:00550 |
| | Pentatricopeptide repeat domain containi | GO:00094 |
| | Zinc finger, RING/FYVE/PHD-type domai | GO:19000 |
| | Conserved hypothetical protein | |
| | Metallophosphoesterase domain containi | GO:00065 |
| | ATP-NAD kinase, PpnK-type domain con | GO:00067 |

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|---|---|---|
| [Os] blast disease (TO:0000074) \| salt tolerance (TO:0006001) | | |
| | Mpv17/PMP22 family protein | |
| | HAD-superfamily subfamily IB hydrolase, hypothetic | |
| [Os] drought tolerance (TO:0000276) \| salt tolerance (TO:0006001) \| abscisic acid sensitivity (TO:0000615) \| brown planthopper resistance (TO:0000424) \| nematode damage resistance (TO:0000384) | Ricin B-related lectin domain containing protein | |
| | Ovarian tumour, otubain domain containi | GO:00165 |
| | UBX domain containing protein | GO:00431 |
| [Os] cold tolerance (TO:0000303) | Similar to Trehalose-6-phosphate phosp | GO:00059 |

Ensembl plants annotation from domains, h

| biological_ | biological_ | biological_process ( | molecular_function | molecular_function |
|---|---|---|---|---|
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA | | |
| defense re | Reactions, | IEA; IEA | GO:0005524; GO:0 | ATP binding; ADP b |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| translation | The cellula | IEA; IEA; IBA | GO:0003743; GO:0 | translation initiatio |
| plastid tra | The chemi | IBA | | |
| CDP-choli | The phosp | IEA | GO:0004142 | diacylglycerol choli |
| response t | Any proces | IEA; IEA | GO:0003676 | nucleic acid binding |
| domain containing protein | | | | |
| proteolysis | The hydrol | IEA | GO:0008234; GO:0 | cysteine-type pepti |
| response t | Any proces | IEA; IBA; IEA | GO:0005515 | protein binding |
| otein | | | GO:0005515 | protein binding |
| response t | Any proces | IEA; IBA; IBA; IBA; IB | GO:0005509; GO:0 | calcium ion binding |
| aining protein | | | | |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
|  |  |  |  |  |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008324 | cation transmembra |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |

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|---|---|---|---|---|
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
|  |  |  |  |  |
|  |  |  | GO:0016747; GO:0 | acyltransferase acti |

|  |  |  |  |  |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| negative re | Any proces | IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| signal pep | The protec | IEA; IEA; IEA; IBA | GO:0004175; GO:0 | endopeptidase acti |
|  |  |  | GO:0004497; GO:0 | monooxygenase ac |

|  |  |  |  |  |
|---|---|---|---|---|
| response t | Any proces | IBA; IMP; IBA; IMP; I | GO:0005515 | protein binding |
| cutin biosy | The chemi | IBA | GO:0016746; GO:0 | acyltransferase acti |
| mRNA exp | The direct | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| lipid trans | The direct | IEA | GO:0008289 | lipid binding |

|  |  |  |  |  |
|---|---|---|---|---|
| negative re | Any proces | IBA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; trans |
| photosynth | A process, | IBA; IEA |  | GO:0005509; GO:0 | calcium ion binding |
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| mRNA exp | The direct | IBA; IBA; IBA; IEA; IB | GO:0000822; GO:0 | inositol hexakispho |
| gravitropis | The orient | IEA; IEA; IEA |  |  |
| DNA replic | The proces | IBA; IBA; IBA |  |  |
| vesicle-me | A cellular t | IEA; IEA | GO:0005085; GO:0 | guanyl-nucleotide |
| regulation | Any proces | IEA |  |  |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| DNA replic | The cellula | IEA; IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| carbohydr | The proces | IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| intracellul | The direct | IEA; IBA; IBA; IBA; IE | GO:0005198; GO:0 | structural molecule |
| translation | The cellula | IEA; IEA; IEA; IEA; IE | GO:0000340; GO:0 | RNA 7-methylguan |
| DNA-temp | The synthe | IEA; IEA; IBA | GO:0003712; GO:0 | transcription coreg |
| chromatin | A dynamic | IBA | GO:0003677; GO:0 | DNA binding; chron |
|  |  |  | GO:0005515 | protein binding |
| oligosacch | The chemi | IEA | GO:0008455 | alpha-1,6-mannos |
| positive gr | The orient | IEA |  |  |
|  |  |  | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| glycolytic p | The chemi | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| mRNA 3'-e | Any proces | IEA | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| cell cycle; | The progre | IEA; IEA; IEA; IEA | GO:0004860; GO:0 | protein kinase inhib |
| porphyrin- | The chemi | IEA; IEA; IEA; IEA | GO:0004325; GO:0 | ferrochelatase activ |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| negative re | Any proces | IEA; IEA; IBA; IBA; IB | GO:0000976; GO:0 | transcription cis-re |
| cytokinin b | The chemi | IEA | GO:0016787; GO:0 | hydrolase activity; h |
| rotein | | | GO:0005515 | protein binding |
| response t | Any proces | IEA | | |
| DNA catab | The chemi | IBA; IEA | GO:0003676; GO:0 | nucleic acid binding |

|  |  |  |  |  |
|---|---|---|---|---|
| protein ub | The proces | IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein de | The proces | IEA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| phospholi | The direct | IBA | GO:0005548; GO:0 | phospholipid trans |
| regulation | Any proces | IEA | GO:0043565 | sequence-specific |
| photosynt | The synthe | IEA |  |  |
| protein ph | The proces | IEA; IBA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| xenobiotic | The direct | IEA; IEA | GO:0015297; GO:0 | antiporter activity; |
|  |  |  | GO:0005524; GO:0 | ATP binding; ATP h |
| carbohydr | The chemi | IEA; IEA; IBA; IEA | GO:0004367; GO:0 | glycerol-3-phosph |
| negative r | Any proces | IEA; IBA | GO:0004865; GO:0 | protein serine/thre |
|  |  |  | GO:0030246 | carbohydrate bindi |
| anatomical | The proces | IEA; IEA; IEA |  |  |
| ubiquitin- | The chemi | IBA; IEA; IBA | GO:0043130; GO:0 | ubiquitin binding; u |
| calcium-m | Any intrac | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| protein gly | A protein r | IEA | GO:0008194; GO:0 | UDP-glycosyltransf |
| flavonoid | The chemi | IEA | GO:0004497; GO:0 | monooxygenase ac |
| rotein |  |  | GO:0003723; GO:0 | RNA binding; doubl |
| nuclear-tr | The nonse | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; mRN |
| immune sy | Any proces | IEA; IEA; IEA |  |  |

| | | | | |
|---|---|---|---|---|
| phosphore | A conserv | IEA; IEA; IEA; IEA; IE | GO:0005515 | protein binding |
| protein ph | The proce | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| translation | The proce | IBA; IBA | | |
| | | | GO:0001228; GO:0 | DNA-binding trans |
| lipid meta | The chemi | IEA | GO:0016787 | hydrolase activity |
| xyloglucan | The chemi | IEA; IEA | GO:0016413; GO:0 | O-acetyltransferase |
| phosphati | The chemi | IBA; IEA | GO:0004142; GO:0 | diacylglycerol choli |
| transmem | The proce | IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proce | IEA; IEA; IEA; IEA; IE | GO:0003712; GO:0 | transcription coreg |
| regulation | Any proce | IEA; IEA; IEA | GO:0005515 | protein binding |
| protein ph | The proce | IEA; IBA; IBA | GO:0004672; GO:0 | protein kinase activ |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| signal tran | The cellula | IEA; IEA | GO:0005096 | GTPase activator ac |
| rotein | | | | |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| actin filam | A process | IBA; IBA | GO:0000146; GO:0 | microfilament moto |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| uence | | | | |
| tRNA proc | The proces | IEA | GO:0016432; GO:0 | tRNA-uridine amin |
| cytokinin r | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; ox |
| transmem | The proces | IEA | | |
| ein | | | GO:0005200; GO:0 | structural constitue |

| | | | | |
|---|---|---|---|---|
| | | | GO:0004497; GO:0 | monooxygenase ac |
| protein ins | The proces | IBA | GO:0008565; GO:0 | obsolete protein tra |
| gibberellic | The series | IBA; IEA; IBA | GO:0005515 | protein binding |
| DNA metal | Any cellula | IEA; IEA; IBA; IBA; IB | GO:0003677; GO:0 | DNA binding; doubl |
| peptidyl-s | The phosp | IBA; IBA | GO:0004674 | protein serine/thre |
| protein de | The proces | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| RNA stabili | Prevention | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| domain containing protein | | | GO:0008270 | zinc ion binding |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IBA | GO:0005515; GO:0 | protein binding; zin |
| mRNA pol | The enzym | IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| phosphore | A conserve | IEA; IEA; IBA; IEA; IM | GO:0009927; GO:0 | histidine phosphotr |
| n | | | GO:0003677 | DNA binding |
| asymmetri | The asymn | IEA | | |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| phosphate | The chemi | IEA | GO:0000287; GO:0 | magnesium ion bin |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| brassinost | The series | IEA | GO:0004672 | protein kinase activ |
| histone H3 | The modifi | IEA | GO:0000976; GO:0 | transcription cis-re |
| response t | Any proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| male meio | A cell cycl | IEA | | |
| carbohydr | The chemi | IEA; IMP; IEA | GO:0004553; GO:0 | hydrolase activity, |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0000287; GO:0 | magnesium ion bin |
| flower dev | The proces | IEA; IMP | GO:0004430; GO:0 | 1-phosphatidylinos |
| cation tran | The direct | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| HC4 RING fusion protein) | | | | |
| DNA repair | The proces | IBA; IBA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| small GTP | The series | IEA; IBA | GO:0005085 | guanyl-nucleotide |
| | | | GO:0016788 | hydrolase activity, |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ubiquitin- | The chemi | IBA; IBA; IBA; IEA | GO:0061630 | ubiquitin protein li |
| cytoplasmi | The chemi | IBA; IEA | GO:0003735; GO:0 | structural constitue |
| DNA-temp | The synthe | IEA; IBA; IEA | GO:0003690; GO:0 | double-stranded D |

| | | | | |
|---|---|---|---|---|
| protein de | The proces | IEA; IEA; IEA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| transmemb | The proces | IEA | GO:0140359 | ABC-type transport |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| protein | | | GO:0016787 | hydrolase activity |
| protein ph | The proces | IBA; IBA; IBA | GO:0016208; GO:0 | AMP binding; protei |
| DNA recon | The aggre | IBA; IEA; IEA; IBA; IM | GO:0000150; GO:0 | DNA strand exchan |
| transmemb | The proces | IEA | GO:0015267 | channel activity |
| fatty acid r | The chemi | IEA; IEA; IEA | GO:0010181; GO:0 | FMN binding; oxido |
| ubiquinon | The chemi | IEA; IEA; IEA; IEA | GO:0016301 | kinase activity |
| proteolysis | The hydrol | IEA; IBA | GO:0003677; GO:0 | DNA binding; aspar |
| chromatin | The assem | IBA; IBA; IEA; IEA; IB | GO:0003677; GO:0 | DNA binding; chron |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| to abiotic stress (salt, dehydration, ABA, k | | | GO:0003676; GO:0 | nucleic acid binding |
| protein ub | The proces | IEA | GO:0005515 | protein binding |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| dolichol-li | The chemi | IEA; IBA | | |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| monocarb | The direct | IEA; IEA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; |
| double-str | The repair | IBA; IEA | GO:0003697; GO:0 | single-stranded DN |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| histone H3 | The modifi | IBA | GO:0001135; GO:0 | obsolete RNA polym |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| proteolysis | The hydrol | IEA | GO:0008233 | peptidase activity |
| mitochond | The aggre | IBA | | |
| tricarboxyl | A nearly u | IEA; IEA | | |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| mily protein | | | | |
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding transc |
| mRNA spli | The joining | IEA; IEA; IEA | | |
| response t | Any proces | IEA | | |
| regulation | Any proces | IEA | | |
| photosynt | The synthe | IEA | | |
| endocytosi | A vesicle-r | IEA; IBA; IEA; IEA; IB | GO:0000149; GO:0 | SNARE binding; phc |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| multicellul | The biolog | IEA; IDA | GO:0001216; GO:0 | DNA-binding transc |
| rRNA proc | Any proces | IEA; IEA; IBA; IBA | GO:0004652; GO:0 | polynucleotide ader |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0005524 | ATP binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| egulatory protein of P- starvation acclimat | | | GO:0003700 | DNA-binding transc |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| endocytosi | A vesicle-r | IEA; IBA; IEA; IEA; IB | GO:0000149; GO:0 | SNARE binding; phc |
| regulation | Any proces | IEA; IEA; IEA; IEA; IE | GO:0000976; GO:0 | transcription cis-re |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| pre-mRNA | The target | IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |

| | | | | |
|---|---|---|---|---|
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| ion transp | The directe | IEA; IEA; IEA | GO:0005381 | iron ion transmemb |
| telomere n | Any proces | IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; single |
| tyrosine bi | The chemi | IEA | GO:0004665; GO:0 | prephenate dehydro |
| defense re | Reactions | IBA; IBA; IBA | GO:0004675; GO:0 | transmembrane rec |
| mRNA pro | Any proces | IEA; IEA; IEA; IEA | | |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| defense re | Reactions, | IEA; IEA; IEA | GO:0004869; GO:0 | cysteine-type endo |
| regulation | Any proces | IEA; IEA; IEA | GO:0019901 | protein kinase bind |
| hesi | | | GO:0004497; GO:0 | monooxygenase ac |
| cyclic nucl | The chemi | IBA | GO:0004112; GO:0 | cyclic-nucleotide p |
| | | | GO:0008375; GO:0 | acetylglucosaminylt |
| cell wall or | A process | IEA; IEA | GO:0016757; GO:0 | glycosyltransferase |
| maturation | Any proces | IBA; IEA; IEA; IEA | | |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| negative re | Any proces | IEA; IBA | GO:0005515 | protein binding |
| ribosome | A cellular | IEA; IEA | | |
| cellular me | Any proces | IBA | | |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| intra-Golg | The directe | IEA; IBA | | |

| | | | | |
|---|---|---|---|---|
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| | | | GO:0046872 | metal ion binding |
| | | | GO:0003700; GO:0 | DNA-binding trans |
| protein ins | The proces | IBA; IBA | GO:0032977 | membrane inserta |
| protein gly | A protein r | IEA; IBA; IBA; IEA | GO:0003980; GO:0 | UDP-glucose:glyco |
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| cellular res | Any proces | IEA; IEA; IBA; IBA; IE | GO:1901612 | cardiolipin binding |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| response t | Any proces | IEA | GO:0019904 | protein domain spe |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| regulation | Any proces | IEA | GO:0005096; GO:0 | GTPase activator ac |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515; GO:0 | protein binding; ub |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| cell wall m | The series | IEA; IEA | GO:0016787; GO:0 | hydrolase activity; |
| carbohydr | The chemi | IEA; IEA; IBA | GO:0016787; GO:0 | hydrolase activity; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| | | | GO:0005509; GO:0 | calcium ion binding |
| | | | GO:0003677; GO:0 | DNA binding; DNA- |
| methylatio | The proces | IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; meth |
| mitochond | The transf | IEA; IBA; IBA | | |
| containing protein | | | GO:0016740; GO:0 | transferase activity; |
| NLS-bearin | The direct | IBA; IEA; IBA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| anatomical | The proces | IEA; IEA; IEA | | |
| protein ub | The proces | IEA | | |
| protein loc | A process | IBA | | |

| | | | | |
|---|---|---|---|---|
| | | | GO:0003843 | 1,3-beta-D-glucan |
| response t | Any proces | IBA; IEA; IEA | GO:0008137; GO:0 | NADH dehydrogena |
| agment) | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| microtubul | The remov | IBA; IEA | GO:0005515; GO:0 | protein binding; mi |
| cytoskelet | A process | IBA; IBA | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IC | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016788 | hydrolase activity, a |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| carbohydra | The direct | IEA; IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| ntaining protein | | | | |
| in | | | GO:0005515 | protein binding |
| | | | GO:0016787 | hydrolase activity |
| | | | GO:0005515 | protein binding |
| peptidyl-ly | The methy | IBA; IEA | GO:0008168; GO:0 | methyltransferase a |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| translation | The cellula | IEA; IBA | GO:0003735 | structural constitue |
| | | | GO:0030246 | carbohydrate bindi |
| protein gly | A protein r | IEA | GO:0016757 | glycosyltransferase |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IC; IEA; IMP; IMP; IM | GO:0000978; GO:0 | RNA polymerase II c |
| double-str | The repair | IBA; IEA; IEA; IBA; IB | GO:0003682 | chromatin binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| proteolysis | The hydrol | IEA; IEA | GO:0004190; GO:0 | aspartic-type endo |
|  |  |  | GO:0005515 | protein binding |
| protein ub | The proces | IBA | GO:0031625 | ubiquitin protein lig |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| nsation-like region domain containing protein |  |  |  |  |
| inositol ph | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; ph |
| glycerol m | The chemi | IEA; IEA | GO:0004144; GO:0 | diacylglycerol O-ac |
|  |  |  | GO:0005509 | calcium ion binding |
| RNA catab | The chemi | IEA; IEA; IBA; IEA; IE | GO:0005515 | protein binding |
| water tran | The direct | IBA; IEA | GO:0015250; GO:0 | water channel activi |
| nucleotide | A DNA rep | IEA; IEA | GO:0003684; GO:0 | damaged DNA bind |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| negative re | Any proces | IEA | GO:0004867 | serine-type endope |

|  |  |  |  |  |
|---|---|---|---|---|
| protein gly | A protein r | IEA | GO:0016740; GO:0 | transferase activity; |
| gene silen | A process | IEA; IEA; IEA |  |  |
|  |  |  | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| mRNA exp | The direct | IBA | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| protein pr | Any protei | IEA; IEA; IEA | GO:0004175; GO:0 | endopeptidase activ |
| (Blt101) (Blt101.1) |  |  |  |  |
| ntaining protein |  |  | GO:0005515 | protein binding |
| response t | Any proces | IEA; IBA | GO:0005515; GO:0 | protein binding; pr |
| defense re | Reactions | IEA |  |  |
| ase component |  |  |  |  |
| protein ub | The proces | IEA | GO:0008270; GO:0 | zinc ion binding; ub |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |

| | | | | |
|---|---|---|---|---|
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0004867; GO:0 | serine-type endope |
| alternative | The proces | IBA; IEA | | |
| rotein | | | | |
| protein | | | | |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| tRNA modi | The covale | IBA; IEA; IEA; IEA; IE | GO:0000049; GO:0 | tRNA binding; nucle |
| | | | GO:0016787; GO:0 | hydrolase activity; |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| chloroplas | The divisio | IEA | | |
| embryo de | The proces | IEA; IEA | GO:0003958; GO:0 | NADPH-hemoprotei |
| photosynt | The synthe | IEA | | |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA; IEA; IEA; IE | GO:0003712; GO:0 | transcription coregu |
| | | | GO:0003676 | nucleic acid bindin |
| lipid meta | The chemi | IEA; IEA; IBA; IEA | | |
| activation | Any proces | IEA; IEA; IBA | GO:0008017; GO:0 | microtubule bindin |
| n | | | | |
| ning protein | | | GO:0005515 | protein binding |
| ABC transporter) | | | GO:0005524; GO:0 | ATP binding; ABC-t |
| ing protein | | | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA | GO:0008233; GO:0 | peptidase activity; |
| | | | GO:0016788 | hydrolase activity, |
| IMP biosyn | The chemi | IBA; IEA; IEA; IBA | GO:0003876; GO:0 | AMP deaminase act |
| ontaining protein | | | GO:0004721; GO:0 | phosphoprotein ph |
| defense re | Reactions, | IEA | GO:0043531 | ADP binding |
| | | | GO:0030247 | polysaccharide bin |
| siRNA proc | A process | IBA; IEA; IEA | GO:0003723; GO:0 | RNA binding; ribon |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IEA | GO:0005515; GO:0 | protein binding; pr |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| /-4 | | | GO:0005524 | ATP binding |
| protein de | The remov | IBA; IEA | GO:0008233; GO:0 | peptidase activity; |
| protein ph | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| DNA metal | Any cellula | IEA; IEA; IEA | GO:0003824; GO:0 | catalytic activity; 5'- |
| gene silen | A process | IEA; IBA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0016788 | hydrolase activity, a |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016740 | transferase activity |
| protein ub | The proces | IBA | GO:0061630 | ubiquitin protein lig |
| protein | | | GO:0005515 | protein binding |
| cell fate de | A process | IBA | | |
| multicellul | The biolog | IEA; IDA; IMP | GO:0003677; GO:0 | DNA binding; prote |
| | | | GO:0016787 | hydrolase activity |
| nbrane plant domain containing protein | | | | |

| | | | | |
|---|---|---|---|---|
| polysaccha | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| otein | | | GO:0005515 | protein binding |
| | | | GO:0003723 | RNA binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| DNA repai | The proces | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| response t | Any proces | IEA | | |
| chloroplas | A process | IEA; IEA | | |
| response t | Any proces | IC | | |
| mitochond | The mainte | IEA; IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| fatty acid | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| ain containing protein | | | | |
| auxin-acti | The series | IBA; IBA; IBA | | |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| negative re | Any proces | IEA | | |
| | | | GO:0005515; GO:0 | protein binding; m |
| pectin cata | The chemi | IEA | GO:0016829; GO:0 | lyase activity; pecta |
| nuclear-tr | The chemi | IEA; IBA; IBA; IBA; IE | GO:0000175; GO:0 | 3'-5'-exoribonucle |
| lipid biosy | The chemi | IEA | GO:0004497; GO:0 | monooxygenase ac |
| RNA polym | The aggre | IBA | GO:0001156 | TFIIIC-class transcr |
| protein m | A protein r | IBA | GO:0008233 | peptidase activity |
| | | | GO:0005509; GO:0 | calcium ion binding |
| nucleobase | Any cellula | IEA; IEA | GO:0003676; GO:0 | nucleic acid bindin |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| morphoge | The proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| DNA topol | The proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| RNA phosp | The chemi | IEA | GO:0003676; GO:0 | nucleic acid binding |
| rotein | | | GO:0003723; GO:0 | RNA binding; helica |
| regulation | Any proces | IEA; IEA; IEA; IBA; IB | GO:0003712; GO:0 | transcription coregu |
| microtubul | A process | IBA | GO:0008017 | microtubule binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| mRNA pro | Any proces | IEA | | |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| protein ph | The proces | IBA; IEA | GO:0004672; GO:0 | protein kinase activ |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| carbohydra | The directe | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| proteolysis | The hydrol | IEA | GO:0008233; GO:0 | peptidase activity; l |
| DNA repair | The proces | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; nucle |
| DNA repair | The proces | IEA; IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| cellular ox | Any proces | IEA | GO:0000293; GO:0 | ferric-chelate reduc |
| negative re | Any proces | IEA | GO:0019210 | kinase inhibitor acti |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| | | | GO:0005515 | protein binding |
| miRNA pro | A process | IBA | GO:0003729; GO:0 | mRNA binding; prot |
| regulation | Any proces | IEA; IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

|  |  |  |  |  |
|---|---|---|---|---|
| cation tran | The direct | IBA; IEA; IEA | GO:0008324 | cation transmembra |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| actin cytos | A process | IEA; IEA | GO:0003779; GO:0 | actin binding; actin |
| obsolete o | OBSOLETE. | IBA; IEA | GO:0016209 | antioxidant activity |
| regulation | Any proces | IEA | GO:0043565 | sequence-specific D |
| domain containing protein |  |  |  |  |
| maturation | Any proces | IBA |  |  |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0003677 | DNA binding |
|  |  |  | GO:0016407; GO:0 | acetyltransferase ac |
| regulation | Any proces | IBA; IBA; IEA; IBA | GO:0016740; GO:0 | transferase activity; |
| response t | Any proces | IEA | GO:0030246 | carbohydrate bindir |
| intracellula | The direct | IEA; IEA; IEA; IEA | GO:0008565 | obsolete protein tra |
| cell differe | The proces | IBA | GO:0043565 | sequence-specific D |
| ethylene-a | The series | IEA; IDA; IDA; IMP; I | GO:0003677; GO:0 | DNA binding; DNA- |
| transmemb | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| negative re | Any proces | IEA | GO:0019210 | kinase inhibitor acti |
| protein po | Addition o | IBA; IBA; IEA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| cutin biosy | The chemi | IBA | GO:0016791; GO:0 | phosphatase activit |
| regulation | Any proces | IMP; IBA; IMP; IMP; I | GO:0000978; GO:0 | RNA polymerase II c |
| microtubul | Any cellula | IEA; IBA | GO:0003774; GO:0 | cytoskeletal motor a |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0003676; GO:0 | nucleic acid binding |
| carbohydra | The directe | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| cell surface | The series | IEA | GO:0005515 | protein binding |
| otein | | | GO:0005515 | protein binding |
| chromatin | The assem | IEA; IBA; IEA; IEA; IE | GO:0001227; GO:0 | DNA-binding transc |
| phosphate | The directe | IEA; IEA | GO:0015293; GO:0 | symporter activity; |
| defense re | Reactions, | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| in | | | GO:0005515; GO:0 | protein binding; cal |
| lipid trans | The directe | IEA | GO:0008289 | lipid binding |

| | | | | |
|---|---|---|---|---|
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| sucrose m | The chemi | IEA; IEA | GO:0003824; GO:0 | catalytic activity; su |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| | | | GO:0003779 | actin binding |
| response t | Any proces | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| negative re | Any proces | IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| purine nuc | The chemi | IEA; IEA; IEA | GO:0004038; GO:0 | allantoinase activity |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| GPI anchor | The chemi | IEA | GO:0016788 | hydrolase activity, a |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0015297; GO:0 | antiporter activity; |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| male meio | A cell cycle | IEA; IEA | | |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |

| | | | | |
|---|---|---|---|---|
| carbohydra | The direct | IBA; IDA; IEA | GO:0008515; GO:0 | sucrose transmemb |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| amino acid | The proces | IEA; IBA; IEA; IBA; IE | GO:0005313; GO:0 | L-glutamate transm |
| | | | GO:0003779; GO:0 | actin binding; actin |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA; IBA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0010296; GO:0 | prenylcysteine meth |
| nbrane plant domain containing protein | | | | |
| pseudouri | The intram | IEA; IEA | GO:0004730; GO:0 | pseudouridylate syn |
| rRNA proc | Any proces | IEA; IEA | GO:0008168; GO:0 | methyltransferase a |
| regulation | Any proces | IEA | GO:0008270 | zinc ion binding |
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| g protein | | | GO:0008270 | zinc ion binding |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| protein fol | The proces | IEA; IBA; IEA | GO:0005524; GO:0 | ATP binding; metal |
| chloroplas | The divisio | IEA | | |
| proteolysis | The hydrol | IEA; IBA | GO:0004185; GO:0 | serine-type carbox |
| | | | GO:0016746 | acyltransferase acti |
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded D |
| chloroplas | A process | IBA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| DNA repai | The proces | IEA; IEA; IBA; IBA | GO:0008198; GO:0 | ferrous iron binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| response t | Any proces | IBA; IEA; IEA; IEA; IE | GO:0004601; GO:0 | peroxidase activity; |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| protein ph | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA; IBA | GO:0004197; GO:0 | cysteine-type endo |
|  |  |  | GO:0005516 | calmodulin binding |
| obsolete o | OBSOLETE. | IEA |  |  |
| protein pol | Addition o | IBA; IBA; IEA; IBA; IE | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| cation tran | The direct | IEA; IEA | GO:0005216 | ion channel activity |
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| cellular am | The chemi | IEA; IEA; IEA; IEA | GO:0008839; GO:0 | 4-hydroxy-tetrahy |
| single stra | The repair | IBA; IEA; IBA; IEA | GO:0003677; GO:0 | DNA binding; single |
| regulation | Any proces | IC | GO:0003677; GO:0 | DNA binding; DNA- |
| entrainme | The synch | IBA; IEA; IEA |  |  |
| intracellul | The direct | IBA; IBA | GO:0003924; GO:0 | GTPase activity; GT |
| protein tar | The proces | IBA; IBA |  |  |

| | | | | |
|---|---|---|---|---|
| DNA repai | The proces | IBA; IEA | | |
| rRNA proc | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| glutathion | The chemi | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| transmem | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| leucine cat | The chemi | IBA; IBA; IBA | GO:0003824; GO:0 | catalytic activity; hy |
| regulation | Any proces | IEA; IBA | GO:0003680; GO:0 | minor groove of ad |
| cell cycle; | The progre | IEA; IEA | | |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| GPI anchor | The chemi | IBA | | |
| | | | GO:0016740; GO:0 | transferase activity; |
| intra-Golg | The direct | IEA | GO:0042803 | protein homodimer |
| regulation | Any proces | IEA; IC; IEA | GO:0005515 | protein binding |
| response t | Any proces | IEA; IEA | GO:0005507; GO:0 | copper ion binding; |
| | | | GO:0000976; GO:0 | transcription cis-re |
| purine nuc | The direct | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| chromatin | The assem | IEA; IBA | GO:0003677; GO:0 | DNA binding; histo |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| cytokinesi | The proces | IEA | | |
| response t | Any proces | IEA | | |
| protein ub | The proces | IBA | GO:0004842 | ubiquitin-protein tr |
| double-str | The error- | IBA; IEA; IEA; IEA; IE | GO:0004842; GO:0 | ubiquitin-protein tr |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| protein ub | The proces | IBA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| defense re | Reactions, | IBA | | |
| | | | GO:0016747; GO:0 | acyltransferase acti |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| protein tra | The directe | IEA | GO:1901981 | phosphatidylinosito |
| transmem | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| protein ph | The proces | IEA; IEA; IMP; IEA; I | GO:0000166; GO:0 | nucleotide binding; |

ining protein

| | | | | |
|---|---|---|---|---|
| microtubul | A microtu | IEA; IEA | GO:0003777; GO:0 | microtubule motor |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| auxin-acti | The series | IEA; IEA; IBA | GO:0000822; GO:0 | inositol hexakispho |
| carbohydr | The chemi | IEA; IEA; IEA | GO:0004650; GO:0 | polygalacturonase |
| protein de | The proces | IEA; IEA; IEA; IEA; IE | GO:0004721; GO:0 | phosphoprotein ph |
| carbohydr | The chemi | IEA; IBA; IBA | GO:0004560; GO:0 | alpha-L-fucosidase |
| regulation | Any proces | IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
| protein de | The proces | IBA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| response t | Any proces | IEA; IEA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| chlorophyl | The chemi | IEA; IEA; IEA | GO:0008685 | 2-C-methyl-D-eryt |

| | | | | |
|---|---|---|---|---|
| secondary | The proces | IMP; IMP | GO:0005506; GO:0 | iron ion binding; is |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| ntaining protein | | | | |
| negative re | Any proces | IEA; IBA | GO:0000977; GO:0 | RNA polymerase II t |
| DNA meta | Any cellula | IEA; IEA; IEA | GO:0003824; GO:0 | catalytic activity; 5'- |
| al domain containing protein | | | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0003676 | nucleic acid binding |
| defense re | Reactions | IEA | | |
| multicellul | The biolog | IEA; IBA; IBA; IBA; IE | GO:0046872 | metal ion binding |
| mitotic cel | Progressio | IBA; IEA; IEA; IEA; IB | GO:0003688 | DNA replication ori |
| protein ph | The proces | IEA; IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0003677; GO:0 | DNA binding; mino |

|  |  |  |  |  |
|---|---|---|---|---|
| ive haloacid dehalogenase (HAD)-like hyd |  |  | GO:0016787 | hydrolase activity |
| proteolysis | The hydrol | IEA; IBA | GO:0004180; GO:0 | carboxypeptidase a |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| ling protein |  |  |  |  |
|  |  |  | GO:0005515 | protein binding |
| lipid trans | The direct | IEA; IEA | GO:0008289; GO:0 | lipid binding; sterol |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IEA; IBA; IBA; IBA; IB | GO:0000981; GO:0 | DNA-binding trans |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| negative re | Any proces | IEA |  |  |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0019863; GO:0 | IgE binding; nutrien |
| protein ph | The proces | IBA; IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IEA; IBA; IEA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| protein ub | The proces | IEA; IBA | GO:0005515 | protein binding |
| tRNA modi | The covale | IBA | GO:0016740; GO:0 | transferase activity; |
| protein ph | The proces | IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| trehalose | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; tre |
|  |  |  | GO:0005515; GO:0 | protein binding; tra |
| response t | Any proces | IEA; IEA; IBA | GO:0005515; GO:0 | protein binding; tra |
| arginine bi | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; ar |
| response t | Any proces | IEA |  |  |
| protein ph | The proces | IBA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |

| | | | | | |
|---|---|---|---|---|---|
| | carbohydra | The chemi | IBA; IBA; IBA; IEA | GO:0015018; GO:0 | galactosylgalactosy |
| | regulation | Any proces | IEA | GO:0043565 | sequence-specific |
| t) | | | | GO:0004032; GO:0 | alditol:NADP+ 1-ox |
| | cutin biosy | The chemi | IBA | GO:0016746; GO:0 | acyltransferase acti |
| | carbohydra | The chemi | IEA; IEA; IEA | GO:0004568; GO:0 | chitinase activity; h |
| | regulation | Any proces | IEA | | |
| | methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| | | | | GO:0003677 | DNA binding |
| | cellular lip | The chemi | IBA | GO:0016298 | lipase activity |
| | regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| | | | | GO:0004497; GO:0 | monooxygenase ac |
| | response t | Any proces | IBA; IBA; IBA; IBA; IB | GO:0003824; GO:0 | catalytic activity; ph |
| | protein tar | The proces | IEA; IEA; IEA; IBA; IE | GO:0005515 | protein binding |
| | cellular am | The chemi | IEA; IEA | GO:0004046; GO:0 | aminoacylase activi |
| | RNA modif | The covale | IBA | GO:0005515 | protein binding |
| tein | | | | GO:0016787 | hydrolase activity |
| | triglycerid | The chemi | IEA; IEA | GO:0004144; GO:0 | diacylglycerol O-ac |
| | regulation | Any proces | IEA | GO:0003677 | DNA binding |
| | regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| | protein ub | The proces | IBA | GO:0003677; GO:0 | DNA binding; ubiqu |
| | carbohydra | The directe | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| | protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| vesicle-me | A cellular t | IBA | | |
| proteolysis | The hydrol | IEA | GO:0008234; GO:0 | cysteine-type pepti |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| transmem | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| photosyste | Proteolysis | IEA; IEA | | |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| rotein | | | GO:0016491; GO:0 | oxidoreductase acti |
| lipid meta | The chemi | IEA; IEA; IEA; IEA; IB | GO:0010181; GO:0 | FMN binding; oxido |
| mRNA cata | The chemi | IEA; IEA; IBA; IEA; IB | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| plant-type | A cellular | IEA; IBA; IEA; IEA; IB | GO:0016740; GO:0 | transferase activity; |
| protein ub | The proces | IEA | | |
| eight, yield, and plant biomas | | | GO:0016407; GO:0 | acetyltransferase ac |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| response t | Any proces | IEA; IEA | | |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| | | | GO:0016740; GO:0 | transferase activity; |
| rotein | | | GO:0008375; GO:0 | acetylglucosaminylt |
| xyloglucan | The chemi | IBA; IEA; IEA | GO:0008107; GO:0 | galactoside 2-alpha |
| phospholi | The mover | IBA | GO:0000287; GO:0 | magnesium ion bin |
| ein | | | GO:0003723 | RNA binding |
| oligopepti | The proces | IEA; IEA | GO:0035673 | oligopeptide transm |

| | | | | |
|---|---|---|---|---|
| RNA proce | Any proces | IEA; IBA; IEA; IEA | GO:0004525 | ribonuclease III acti |
| regulation | Any proces | IBA; IBA; IEA | GO:0003700; GO:0 | DNA-binding transc |
| otein | | | GO:0005515 | protein binding |
| ressed | | | GO:0003676 | nucleic acid bindin |
| | | | GO:0016597 | amino acid binding |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |
| DNA repai | The proces | IBA; IBA; IBA | GO:0003677; GO:0 | DNA binding; doubl |
| photosynt | The synthe | IEA | | |
| protein pe | The modifi | IEA; IBA; IBA | GO:0003755; GO:0 | peptidyl-prolyl cis- |
| -like protein | | | GO:0004721; GO:0 | phosphoprotein ph |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| cytoplasmi | A process | IBA | GO:0005524; GO:0 | ATP binding; micro |
| ining protein | | | GO:0003677; GO:0 | DNA binding; mino |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0003677; GO:0 | DNA binding; zinc i |
| (Mercaptopyruvate sulfurtransferase Mst2 | | | GO:0004792; GO:0 | thiosulfate sulfurtra |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| mRNA exp | The direct | IBA | GO:0003676; GO:0 | nucleic acid binding |
| trehalose b | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; tre |
| transcripti | The synthe | IEA; IBA; IEA; IBA | GO:0003677; GO:0 | DNA binding; transl |
| | | | GO:0005515; GO:1 | protein binding; pro |
| MAPK casc | An intracel | IBA; IBA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| obsolete cl | OBSOLETE. | IEA | GO:0046872 | metal ion binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| | | | GO:0008017 | microtubule binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| gene silen | A small RN | IEA | GO:0000166; GO:0 | nucleotide binding; |
| defense re | Reactions, | IEA; IEA | GO:0005516 | calmodulin binding |
| pectin cata | The chemi | IEA | GO:0016829; GO:0 | lyase activity; pecta |
| cal 1 protein | | | GO:0016791; GO:0 | phosphatase activit |
| protein fol | The proces | IBA | | |
| DNA-temp | The initial | IEA; IEA; IEA; IBA | GO:0000995; GO:0 | RNA polymerase III |
| | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| root meris | The specifi | IBA; IBA; IBA; IBA | | |
| regulation | Any proces | IEA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| ion transp | The directe | IEA; IEA; IEA; IEA; IB | GO:0005385; GO:0 | zinc ion transmemb |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| chloroplas | A process | IBA; IBA | | |
| lipid meta | The chemi | IEA | GO:0016298; GO:0 | lipase activity; hydr |
| protein ref | The proces | IBA; IBA | GO:0051082 | unfolded protein bi |
| stem cell p | The proces | IEA; IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| phospholi | The direct | IEA; IEA | GO:0008526 | phosphatidylinosito |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| transmem | The proces | IEA; IEA | GO:0022857 | transmembrane tra |
| | | | GO:0004721 | phosphoprotein ph |
| regulation | Any proces | IEA; IBA; IEA; IBA | GO:0000993; GO:0 | RNA polymerase II |

| | | | | |
|---|---|---|---|---|
| transmemb | The proces | IEA | GO:0015267 | channel activity |
| | | | GO:0005516 | calmodulin binding |
| negative re | Any proces | IBA; IEA; IEA; IBA | GO:0004407; GO:0 | histone deacetylase |
| velopmen | | | GO:0003677; GO:0 | DNA binding; metal |
| rotein | | | GO:0003677 | DNA binding |
| | | | GO:0005515 | protein binding |
| amily protein | | | GO:0046527 | glucosyltransferase |
| peptidyl-th | The remov | IBA | GO:0004722; GO:0 | protein serine/threo |
| tRNA modi | The covale | IEA | GO:0003723 | RNA binding |
| histone H3 | The modifi | IBA | GO:0005515; GO:0 | protein binding; his |
| glycerol-3- | The chemi | IEA; IEA; IEA; IBA; IE | GO:0004367; GO:0 | glycerol-3-phospha |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding transc |
| chloroplas | A process | IBA | | |
| hormone-m | The series | IBA; IMP; IBA; IMP | GO:0042803 | protein homodimer |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IMP; IDA; IMP | GO:0003677; GO:0 | DNA binding; DNA- |
| cortical mi | A process | IEA | | |
| protein ph | The proces | IEA; IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| otein | | | GO:0005515 | protein binding |
| ontaining protein | | | GO:0061631 | ubiquitin conjugati |
| response t | Any proces | IBA; IEA; IBA | | |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| ubiquitin-( | The chemi | IEA; IEA | GO:0004197; GO:0 | cysteine-type endo |
| cell cycle; | The progre | IEA; IEA | | |
| protein loc | Any proces | IBA; IEA | | |
| regulation | Any proces | IEA | GO:0046983 | protein dimerizatio |
| se 1 domain containing protein | | | GO:0003723 | RNA binding |

| | | | | |
|---|---|---|---|---|
| proteolysis | The hydrol | IEA | GO:0004197; GO:0 | cysteine-type endo |
| oligopeptid | The directe | IEA; IBA | GO:0015333; GO:0 | peptide:proton sym |
| spliceosom | The aggreg | IEA; IEA; IEA; IEA | GO:0003723 | RNA binding |
| | | | GO:0004721; GO:0 | phosphoprotein ph |
| ein | | | GO:0003677 | DNA binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| nucleic aci | The nuclei | IEA | GO:0003676; GO:0 | nucleic acid binding |
| phosphatid | The chemi | IBA; IBA; IEA | GO:0004103; GO:0 | choline kinase activ |
| oligopeptid | The proces | IEA; IEA | GO:0035673 | oligopeptide transm |
| double-str | The repair | IBA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| recognition | A cell reco | IEA | | |
| regulation | Any proces | IBA; IBA | GO:0008270 | zinc ion binding |
| cytokinin r | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; ox |
| protein ub | The proces | IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| malate tra | The directe | IEA | | |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| plant-type | A process | IEA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| guard cell | The proces | IEA; IEA |  |  |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| triglyceride | The chemi | IEA; IEA | GO:0004144; GO:0 | diacylglycerol O-ac |
| lipid metab | The chemi | IEA; IEA; IBA; IEA; IE | GO:0004497; GO:0 | monooxygenase ac |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
|  |  |  | GO:0005509; GO:0 | calcium ion binding |
| chlorophyl | The chemi | IEA | GO:0008168; GO:0 | methyltransferase a |
|  |  |  | GO:0003677 | DNA binding |
| ning protein |  |  | GO:0003676; GO:0 | nucleic acid binding |
| RNA modif | The covale | IBA; IBA | GO:0005515; GO:0 | protein binding; zin |
|  |  |  | GO:0045735 | nutrient reservoir a |
| response t | Any proces | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding transc |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| N-glycan p | The conver | IBA |  |  |
| transmemb | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| t) |  |  | GO:0051015 | actin filament bindi |

|  |  |  |  |  |
|---|---|---|---|---|
| ubiquitin- | The chemi | IBA; IEA | GO:0061630 | ubiquitin protein li |
| lignin cata | The chemi | IEA | GO:0005507; GO:0 | copper ion binding; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| plant-type | A cellular | IEA; IDA | GO:0016413; GO:0 | O-acetyltransferase |
| proline bio | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004022; GO:0 | alcohol dehydrogen |
| double-str | The repair | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| aerobic ele | A process | IBA; IBA | GO:0003955; GO:0 | NAD(P)H dehydroge |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
|  |  |  | GO:0016788 | hydrolase activity, a |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| hydrotropi | Growth or | IEA |  |  |
| negative re | Any proces | IBA; IBA; IBA; IBA |  |  |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| cortical mi | A process | IBA |  |  |
| response t | Any proces | IBA; IEP; IBA; IDA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| double fer | Fertilizatio | IEA | | |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IEA; IEA; IEA | GO:0005515 | protein binding |
| guanosine | The chemi | IEA | | |
| glutathion | The chemi | IEA; IEA | GO:0004364; GO:0 | glutathione transfe |
| maturation | Any proces | IBA; IEA; IEA; IEA; IE | GO:0019843; GO:0 | rRNA binding; U3 s |
| | | | GO:0046872 | metal ion binding |
| regulation | Any proces | IEA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| organic an | The direct | IEA; IEA; IEA; IEA | GO:0022857 | transmembrane tra |
| ubiquitin- | The chemi | IBA; IBA | GO:0008270; GO:0 | zinc ion binding; m |
| defense re | Reactions, | IBA | | |
| glycerol m | The chemi | IEA; IEA | GO:0008081; GO:0 | phosphoric diester |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| | | | GO:0046983 | protein dimerizatio |
| RNA proce | Any proces | IEA | GO:0000976; GO:0 | transcription cis-re |
| chromatin | The assem | IBA; IEA; IBA; IEA; IE | GO:0003713; GO:0 | transcription coacti |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| steroid bio | The chemi | IEA | GO:0003854; GO:0 | 3-beta-hydroxy-de |
| transmeml | The proces | IEA | GO:0015297; GO:0 | antiporter activity; t |
| protein im | The direct | IBA; IBA; IBA | GO:0005515; GO:0 | protein binding; nu |
| DNA replic | The cellula | IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; single |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| metabolic | The chemi | IEA; IBA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| ning protein | | | | |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IEA; IEA; IEA | GO:0008506; GO:0 | sucrose:proton sym |
| l polygalacturonase, Defence respons | | | GO:0005515 | protein binding |
| carbohydra | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004553; GO:0 | hydrolase activity, h |
| carbohydra | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004553; GO:0 | hydrolase activity, h |
| DNA-temp | The compl | IEA; IEA; IEA; IMP; IE | GO:0000166; GO:0 | nucleotide binding; |
| cell differe | The proces | IBA | GO:0043565 | sequence-specific D |
| inositol ph | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; ph |
| | | | GO:0016787; GO:0 | hydrolase activity; a |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| lignin cata | The chemi | IEA | GO:0005507; GO:0 | copper ion binding; |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| regulation | Any proces | IEA; IBA | GO:0003677 | DNA binding |
| cellular zin | Any proces | IBA; IEA; IEA; IBA | GO:0005385; GO:0 | zinc ion transmemb |
| regulation | Any proces | IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| region domain containing protein | | | GO:0003824 | catalytic activity |
| protein fol | The proces | IBA | GO:0005515; GO:0 | protein binding; cha |
| clathrin co | The disagg | IBA; IBA | GO:0030276 | clathrin binding |
| )rotein | | | | |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IEA | | |
| negative re | Any proces | IMP; IMP; IMP; IEA; I | GO:0003676; GO:0 | nucleic acid bindin |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| cytokinesi | The proces | IEA; IEA; IEA; IBA; IE | GO:0005515 | protein binding |
| cellular res | Any proces | IEA | GO:0003697; GO:0 | single-stranded DN |
| defense re | Reactions, | IEA; IEA | GO:0005524; GO:0 | ATP binding; ADP b |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0016491 | oxidoreductase acti |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515; GO:0 | protein binding; zin |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| mitotic cel | Progressio | IEA; IEA | | |
| exonucleol | Exonucleol | IBA | GO:0000175; GO:0 | 3'-5'-exoribonucle |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| DNA-temp | The synthe | IEA; IBA; IEA | GO:0000976; GO:0 | transcription cis-re |

| | | | | |
|---|---|---|---|---|
| protein gly | A protein r | IEA | GO:0016757 | glycosyltransferase |
| | | | GO:0016788 | hydrolase activity, a |
| | | | GO:0005515 | protein binding |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| n | | | GO:0003676; GO:0 | nucleic acid binding |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| protein me | The additio | IEA | GO:0008276 | protein methyltrans |
| rRNA proc | Any proces | IEA | GO:0003723; GO:0 | RNA binding; protei |
| proteolysis | The hydrol | IEA; IEA; IEA; IEA | GO:0004175; GO:0 | endopeptidase activ |
| taining protein | | | | |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IEA; IEA; IEA; IBA; IE | GO:0003756; GO:0 | protein disulfide is |
| lipid meta | The chemi | IEA | GO:0008374 | O-acyltransferase a |
| xylan acet | The additio | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| G1/S trans | The mitoti | IEA; IEA; IEA; IEA; IE | GO:0000977 | RNA polymerase II t |
| carbohydra | The chemi | IEA; IEA; IEA; IEA; IB | GO:0004348; GO:0 | glucosylceramidase |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| | | | GO:0005200; GO:0 | structural constitue |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| nuclear-tr | The nonse | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; RNA |
| regulation | Any proces | IMP; IEA; IMP; IEA | GO:0000166; GO:0 | nucleotide binding; |
| plant-type | A cellular | IBA | | |
| valine cata | The chemi | IBA; IBA | GO:0003860; GO:0 | 3-hydroxyisobutyry |
| | | | GO:0030246 | carbohydrate bindi |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| blue light | The series | IEA | | |
| centrosom | The cell cy | IBA; IBA | GO:0008017 | microtubule bindin |
| tRNA proc | The proces | IEA; IMP; IEA; IEA | GO:0008168; GO:0 | methyltransferase a |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; RNA |
| fatty acid | The chemi | IBA | GO:0005504; GO:0 | fatty acid binding; i |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |

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|---|---|---|---|---|
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| aining protein | | | GO:0004180 | carboxypeptidase a |
| dephosph | The proces | IBA; IEA; IEA | GO:0008441; GO:0 | 3'(2'),5'-bisphosph |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| regulation | Any proces | IDA; IEA; IMP | GO:0000976; GO:0 | transcription cis-re |
| | | | GO:0080115 | myosin XI tail bindi |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| intracellul | The proces | IBA; IEA; IEA; IEA | GO:0005381; GO:0 | iron ion transmemb |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| nitrogen c | The chemi | IEA; IBA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| response t | Any proces | IEA; IEA; IEA; IEA; IE | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| gene silen | A process | IEA | GO:0003676; GO:0 | nucleic acid binding |
| defense re | Reactions, | IEA; IEA | GO:0005524; GO:0 | ATP binding; ADP b |
| | | | GO:0005515 | protein binding |
| DNA-temp | The synthe | IEA; IEA; IEA; IDA | GO:0003677; GO:0 | DNA binding; DNA- |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008308 | voltage-gated anion |
| defense re | Reactions, | IEA; IEA; IEA; IEA | GO:0005457; GO:0 | GDP-fucose transm |

| | | | | |
|---|---|---|---|---|
| telomere n | Any proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ning protein | | | | |
| cutin biosy | The chemi | IBA | GO:0016746; GO:0 | acyltransferase acti |
| protein im | The targeti | IBA | GO:0033328 | peroxisome membr |
| proteolysis | The hydrol | IEA | GO:0004177; GO:0 | aminopeptidase act |
| regulation | Any proces | IBA; IEA | GO:0000978; GO:0 | RNA polymerase II |
| | | | GO:0022857 | transmembrane tra |
| mRNA spli | The joining | IEA; IEA; IEA | | |
| translation | The cellula | IEA; IEA; IEA | GO:0003746 | translation elongati |
| cleavage ir | Endonucle | IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proces | IEA | | |
| sterol tran | The directe | IBA | GO:0032934 | sterol binding |
| chromatin | The assem | IBA | GO:0003677; GO:0 | DNA binding; struct |
| RNA methy | Posttransc | IEA; IBA; IBA | GO:0008171; GO:0 | O-methyltransferas |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| protein ph | The proce | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ub | The proce | IEA | GO:0004842 | ubiquitin-protein tr |
| DNA endo | Regulated | IEA | GO:0003677 | DNA binding |
| regulation | Any proce | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| chlorophyl | The chemi | IEA; IEA | GO:0003824; GO:0 | catalytic activity; ox |
| lipid meta | The chemi | IEA; IEA; IEA; IBA; I | GO:0009922; GO:0 | fatty acid elongase |
| sphingolip | The chemi | IEA; IEA | GO:0016787; GO:0 | hydrolase activity; |
| regulation | Any proce | IBA | GO:0000978; GO:0 | RNA polymerase II |
| regulation | Any proce | IBA; IBA; IBA; IBA; I | GO:0003700; GO:0 | DNA-binding trans |
| lipid trans | The direct | IBA | GO:0000062; GO:0 | fatty-acyl-CoA bin |
| response t | Any proce | IEA | | |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| fucose me | The chemi | IEA; IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proce | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| | | | GO:0005515 | protein binding |
| response t | Any proce | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| homologo | The meioti | IMP; IEA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA; IDA; IMP | GO:0003677; GO:0 | DNA binding; prote |
| multicellul | The biolog | IEA; IEA |  |  |
| negative re | Any proces | IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IEA; IBA; IBA |  |  |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| tRNA wob | The proces | IEA; IEA; IBA | GO:0050660 | flavin adenine dinu |
| glutathion | The chemi | IEA | GO:0003839 | gamma-glutamylcy |
| negative re | Any proces | IEA | GO:0003677 | DNA binding |
| defense re | Reactions, | IEA |  |  |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| n factor, Drought tolerance, Lignin biosyn |  |  | GO:0003677; GO:0 | DNA binding; lipid |
| regulation | Any proces | IEA |  |  |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| n |  |  |  |  |
| membrane | The memb | IEA | GO:0005484 | SNAP receptor activ |
|  |  |  | GO:0003677 | DNA binding |

| | | | | |
|---|---|---|---|---|
| protein tar | The proces | IEA; IEA | GO:0004040; GO:0 | amidase activity; pr |
| amily protein | | | GO:0046527 | glucosyltransferase |
| | | | GO:0005524; GO:0 | ATP binding; ATP h |
| response t | Any proces | IEA | | |
| autophago | The forma | IBA; IBA; IBA; IBA; IB | GO:0005515; GO:0 | protein binding; ph |
| regulation | Any proces | IBA; IEA | GO:0000978; GO:0 | RNA polymerase II c |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| biosynthet | The chemi | IEA | GO:0016787; GO:0 | hydrolase activity; s |
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| sphingolip | The chemi | IEA; IBA; IBA | GO:0016740; GO:0 | transferase activity; |
| proteasom | The chemi | IBA | GO:0005515 | protein binding |
| SRP-depen | The targeti | IEA | GO:0003723; GO:0 | RNA binding; signal |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| mitochond | A process | IBA | | |
| carbohydra | The chemi | IEA; IBA; IEA; IEA | GO:0004645; GO:0 | 1,4-alpha-oligoglu |
| galactolipi | The chemi | IBA | GO:0016757; GO:0 | glycosyltransferase |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| generation | Conformat | IEA; IBA | | |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IEA | | |
| galactolipi | The chemi | IBA | GO:0016757; GO:0 | glycosyltransferase |
| | | | GO:0016747; GO:0 | acyltransferase acti |
| ons | | | GO:0005507; GO:0 | copper ion binding; |
| endoplasm | A process | IEA | | |
| mRNA pro | Any proces | IEA | | |
| protein ub | The proces | IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| protein | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| ubiquitin- | The chemi | IBA; IBA; IBA; IEA | GO:0061630 | ubiquitin protein lig |
| hormone- | The series | IBA; IBA | | |
| alternative | The proces | IEA; IEA; IBA; IEA; IE | GO:0000339; GO:0 | RNA cap binding; n |
| translation | The cellula | IEA; IEA; IBA | GO:0003743; GO:0 | translation initiatio |
| mRNA tran | The direct | IDA | GO:0003676; GO:0 | nucleic acid bindin |
| double-str | The error- | IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IBA; IBA | GO:0003677; GO:0 | DNA binding; seque |

| | | | | |
|---|---|---|---|---|
| rotein | | | GO:0005515 | protein binding |
| aining protein | | | | |
| gene silen | A process | IEA; IEA | | |
| regulation | Any proces | IBA | | |
| gluconeog | The format | IBA; IEA; IBA; IBA | GO:0004807; GO:0 | triose-phosphate is |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| regulation | Any proces | IEA; IEP; IMP; IMP; I | GO:0003677; GO:0 | DNA binding; DNA- |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| cell cycle; | The progre | IEA; IEA | GO:0008289 | lipid binding |
| n | | | | |
| triterpenoi | The chemi | IEA | GO:0016853; GO:0 | isomerase activity; i |
| metal ion t | The direct | IEA; IEA; IBA | GO:0005507; GO:0 | copper ion binding; |
| male meio | A cell cycle | IEA | | |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| containing protein | | | | |
| carbohydra | The chemi | IEA; IEA; IEA; IEA; IE | GO:0008194; GO:0 | UDP-glycosyltransf |
| cation tran | The direct | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| multicellul | The biolog | IEA | | |
| pectin bios | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| positive re | Any proces | IBA | | |
| protein fol | The proces | IBA | | |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |

|  |  |  |  |  |
|---|---|---|---|---|
| aining protein |  |  |  |  |
| n |  |  | GO:0003677 | DNA binding |
| DNA repai | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| pectin cata | The chemi | IEA | GO:0016829; GO:0 | lyase activity; pecta |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| aining protein |  |  | GO:0003677 | DNA binding |
| sphingoid | The chemi | IBA |  |  |
| auxin bios | The chemi | IDA; IDA | GO:0004499; GO:0 | N,N-dimethylanilin |

| | | | | |
|---|---|---|---|---|
| ht resistanc | | | GO:0030145; GO:0 | manganese ion bin |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| double-str | The error- | IBA; IBA; IEA; IBA; IB | GO:0004672; GO:0 | protein kinase activ |
| mRNA pro | Any proces | IEA; IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; RNA |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| nucleosom | The aggre | IBA; IBA; IBA; IBA; IB | GO:0003677; GO:0 | DNA binding; histo |
| auxin-acti | The series | IEA | | |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| ubiquitin- | The chemi | IBA; IEA | GO:0061630 | ubiquitin protein li |
| regulation | Any proces | IEA; IMP; IMP; IEA; I | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0003677; GO:0 | DNA binding; mino |
| response t | Any proces | IBA; IC; IBA; IBA; IB | GO:0016491; GO:0 | oxidoreductase acti |
| rRNA modi | The covale | IBA; IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; RNA |
| male meio | A cell cycle | IEA | | |
| se 1 domain containing protein | | | GO:0003723 | RNA binding |
| mitochond | The divisio | IBA | GO:0003924; GO:0 | GTPase activity; GT |
| cellular res | Any proces | IEA | | |
| .1.-) | | | GO:0016491 | oxidoreductase acti |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA– |
| DNA repai | The proces | IBA; IEA; IEA; IEA; IEA; IEA | | |
| translation | The cellula | IBA | GO:0003729; GO:0 | mRNA binding; stru |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| intracellula | The directe | IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
| | | | GO:0008168 | methyltransferase a |
| protein gly | A protein r | IEA | GO:0016740; GO:0 | transferase activity; |
| DNA–temp | The synthe | IEA; IEA; IBA; IBA; IB | GO:0000978; GO:0 | RNA polymerase II c |
| tein | | | GO:0016787 | hydrolase activity |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| chloroplas | Any rRNA | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| domain containing protein | | | GO:0016787 | hydrolase activity |
| tein | | | | |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| tRNA wob | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; tR |
| intracellula | The directe | IBA; IBA | GO:0005096 | GTPase activator ac |
| | | | GO:0003677 | DNA binding |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| cell wall m | The series | IEA; IEA; IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| regulation | Any proces | IEA; IBA; IBA; IEA; IE | GO:0000977; GO:0 | RNA polymerase II t |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| Drought tolerance, Regulation of root dev | | | GO:0003677; GO:0 | DNA binding; minor |
| purine nuc | The directe | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |
| DNA-temp | The synthe | IEA; IEA | GO:0003712 | transcription coregu |
| intracellula | The directe | IBA; IBA; IEA; IBA | GO:0000149; GO:0 | SNARE binding; SNA |
| negative re | Any proces | IEA | GO:0003677; GO:0 | DNA binding; transc |

| | | | | |
|---|---|---|---|---|
| | | | GO:0046872 | metal ion binding |
| ining protein | | | GO:0003677; GO:0 | DNA binding; mino |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| resolution | The cleava | IBA; IEA; IEA; IEA; IE | GO:0003682; GO:0 | chromatin binding; |
| protein loc | A process | IEA | | |
| MAPK casc | An intracel | IBA; IBA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| cellular lip | The chemi | IBA | | |
| protein ub | The proces | IEA | GO:0061631 | ubiquitin conjugatin |
| rRNA proc | Any proces | IEA; IEA; IEA | GO:0000179; GO:0 | rRNA (adenine-N6,N |
| DNA-temp | The synthe | IEA; IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| exonucleo | Exonucleo | IBA; IEA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA | | |
| protein de | The remov | IBA | GO:0004843 | cysteine-type deubi |
| negative re | Any proces | IEA | GO:0004857 | enzyme inhibitor ac |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| maturation | Any proces | IBA | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proces | IEA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| protein ph | The proces | IEA; IMP; IEA; IEA; I | GO:0000166; GO:0 | nucleotide binding; |
| egulation of flowerin |  |  | GO:0005515; GO:0 | protein binding; zin |
| gibberellin | The chemi | IMP; IBA | GO:0045543; GO:0 | gibberellin 2-beta- |
| regulation | Any proces | IEA; IMP; IEA; IEA; I | GO:0003677; GO:0 | DNA binding; prote |
|  |  |  | GO:0005515 | protein binding |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |

| | | | | |
|---|---|---|---|---|
| mRNA pro | Any proces | IEA; IBA | GO:0000993 | RNA polymerase II |
| regulation | Any proces | IC; IBA | GO:0000978; GO:0 | RNA polymerase II |
| carbohydra | The direct | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| DNA repai | The proces | IEA; IEA; IEA; IBA; IEA; TAS; IMP; IMP; TAS | | |
| carbohydra | The direct | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| defense re | Reactions | IBA; IEA; IBA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA; IBA; IMP | GO:0003677; GO:0 | DNA binding; DNA- |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| protein fol | The proces | IBA | GO:0005515; GO:0 | protein binding; ch |
| xyloglucan | The chemi | IBA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IBA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| plastid tra | The chemi | IBA | | |
| DNA-temp | The synthe | IEA; IEA; IBA | GO:0000976; GO:0 | transcription cis-re |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| translation | The cellula | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| maltose m | The chemi | IEA; IEA | GO:0005363 | maltose transmem |
| root hair e | The proces | IEA; IEA; IEA | GO:0016491 | oxidoreductase acti |
| protein gly | A protein r | IEA | GO:0016757 | glycosyltransferase |

|  |  |  |  |  |
|---|---|---|---|---|
| actin filam | A process | IEA; IBA | GO:0003779; GO:0 | actin binding; actin |
| proteolysis | The hydrol | IEA | GO:0004222; GO:0 | metalloendopeptida |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| embryo de | The proces | IEA | GO:0003723; GO:0 | RNA binding; mRNA |
| photosynt | The synthe | IEA; IEA | GO:0016491; GO:0 | oxidoreductase acti |
| amino acid | The proces | IEA; IBA; IEA | GO:0015171; GO:0 | amino acid transme |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| pha amylase inhibitor domain containing protein |  |  |  |  |
| regulation | Any proces | IEA; IEA; IMP | GO:0003700; GO:0 | DNA-binding trans |
| tricarboxyl | A nearly ur | IEA; IEA; IEA | GO:0003735; GO:0 | structural constitue |

| | | | | |
|---|---|---|---|---|
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| circadian r | Any biolog | IEA | | |
| intracellula | The direct | IEA; IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| g protein | | | GO:0003729 | mRNA binding |
| cell wall m | The series | IEA; IEA; IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| | | | GO:0003755; GO:0 | peptidyl-prolyl cis- |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| endoplasm | The direct | IBA; IEA | | |
| | | | GO:0005515 | protein binding |
| cytochrom | Formation | IEA | | |
| rRNA proc | Any proces | IEA; IBA; IBA; IBA; IB | GO:0003676; GO:0 | nucleic acid binding |
| cell fate de | A process | IBA; IMP; IMP; IEA | GO:0005515 | protein binding |
| DNA-temp | The synthe | IEA | GO:0043565 | sequence-specific |
| ubiquitin- | The chemi | IEA; IEA; IBA | GO:0044390; GO:0 | ubiquitin-like prote |

| | | | | |
|---|---|---|---|---|
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| box C/D R | Any proces | IBA; IEA; IBA; IEA; IB | GO:0003723; GO:0 | RNA binding; methy |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0005524 | ATP binding |

| | | | | |
|---|---|---|---|---|
| porphyrin- | The chemi | IEA; IEA; IBA; IEA | GO:0004853; GO:0 | uroporphyrinogen c |
| vesicle-me | A cellular t | IBA | | |
| n | | | GO:0003723; GO:0 | RNA binding; mRNA |
| ethylene bi | The chemi | IEA; IEA; IEA; IEA | GO:0003824; GO:0 | catalytic activity; D- |
| | | | GO:0009055 | electron transfer ac |
| response t | Any proces | IEA | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IBA; IBA; IEA; IE | GO:0000977; GO:0 | RNA polymerase II t |
| mitotic cel | Progressio | IBA; IBA; IBA | GO:0005515; GO:0 | protein binding; cal |
| otein, Silicon-promoted formation of Cas | | | GO:0005524; GO:0 | ATP binding; ABC-t |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |

| | | | | |
|---|---|---|---|---|
| mitochond | The divisio | IBA | GO:0003924; GO:0 | GTPase activity; GT |
| positive re | Any proces | IEA | | |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| defense re | Reactions, | IEA; IEA | GO:0016413; GO:0 | O-acetyltransferase |
| defense re | Reactions, | IEA | GO:0043531 | ADP binding |
| nding Protein) DNA binding protein, Cont | | | GO:0003677; GO:0 | DNA binding; metal |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| | | | GO:0017022; GO:0 | myosin binding; my |
| double-str | The repair | IBA; IBA | GO:0003950; GO:0 | NAD+ ADP-ribosylt |

| | | | | |
|---|---|---|---|---|
| transcripti | The extens | IBA; IEA; IBA; IBA; IB | GO:0031491; GO:0 | nucleosome bindin |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| defense re | Reactions, | IBA | | |
| RNA-temp | The synthe | IEA; IBA; IEA | GO:0003723; GO:0 | RNA binding; RNA- |
| protein ph | The proces | IBA; IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| lipid meta | The chemi | IEA | GO:0008374; GO:0 | O-acyltransferase a |
| regulation | Any proces | IC; IBA | GO:0000978; GO:0 | RNA polymerase II |
| lipid meta | The chemi | IEA; IBA; IEA; IEA; IE | GO:0003841; GO:0 | 1-acylglycerol-3-p |
| | | | GO:0003743 | translation initiatio |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ily protein | | | | |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| water tran | The direct | IBA; IEA; IEA | GO:0015204; GO:0 | urea transmembran |

| | | | | |
|---|---|---|---|---|
| regulation | An epigen | IMP; IMP; ISS; ISS; IE | GO:0003677; GO:0 | DNA binding; chron |
| tricarboxyl | A nearly u | IBA; IBA; IEA | GO:0004449 | isocitrate dehydrog |
| DNA-temp | The synth | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0046983 | protein dimerizatio |
| maturation | Any proces | IBA | GO:0005515 | protein binding |
| microtubul | Any cellula | IEA; IBA | GO:0045505; GO:0 | dynein intermediate |
| DNA-temp | The synth | IEA; IEA; IBA; IEA | GO:0000976; GO:0 | transcription cis-re |
| negative r | Any proces | IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| acetyl-Co | The chemi | IEA; IEA | GO:0004742; GO:0 | dihydrolipoyllysine- |
| g protein | | | GO:0046872 | metal ion binding |
| | | | GO:0005515 | protein binding |
| phosphati | The chemi | IEA | GO:0004430 | 1-phosphatidylinos |

| | | | | |
|---|---|---|---|---|
| autophago | The forma | IBA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| regulation | Any proces | IEA; IEA | | |
| n | | | GO:0008289 | lipid binding |
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| ion transp | The direct | IEA; IEA; IEA | GO:0015095 | magnesium ion tran |
| | | | GO:0003677 | DNA binding |
| microtubul | A process | IEA | GO:0008017 | microtubule bindin |
| response t | Any proces | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| ed storage domain containing protein | | | | |
| protein pol | Addition o | IBA; IEA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| signal tran | The cellula | IEA | | |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| ubiquitin- | The chemi | IEA; IBA; IBA | GO:0031593 | polyubiquitin modif |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| response t | Any proce | IBA; IBA | GO:0003677 | DNA binding |
| transcripti | The nucle | IEA; IBA | GO:0005515; GO:0 | protein binding; his |
| protein ph | The proce | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| actin cytos | A process | IBA; IBA | GO:0003779; GO:0 | actin binding; prote |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| receptor-n | An endocy | IBA; IBA; IBA | GO:0030276 | clathrin binding |
| | | | GO:0003774 | cytoskeletal motor |
| regulation | Any proce | IEA | | |

| | | | | |
|---|---|---|---|---|
| rRNA proc | Any proces | IEA; IEA | | |
| anatomical | The biolog | IEA | | |
| | | | GO:0005515 | protein binding |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| regulation | Any proces | IBA | | |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| regulation | Any proces | IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
| | | | GO:0003729; GO:0 | mRNA binding; prot |
| regulation | Any proces | IBA; IBA | | |
| containing protein | | | GO:0016740; GO:0 | transferase activity; |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| positive re | Any proces | IEA; IEA | | |
| rotein | | | | |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| g protein | | | | |
| defense re | Reactions, | IEA; IEA; IEA | GO:0016787; GO:0 | hydrolase activity; r |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| pollen dev | The proces | IBA; IMP | | |
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| chromatin | The assem | IBA | GO:0003677; GO:0 | DNA binding; struc |
| regulation | Any proces | IEA | | |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| cell redox | Any proces | IBA; IEA | | |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| mRNA spli | The joinin | IBA; IEA | GO:0005515; GO:0 | protein binding; pr |
| | | | GO:0005515 | protein binding |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA; IMP; IEA; IMP; II | GO:0003677; GO:0 | DNA binding; DNA- |
| phototropi | The mover | IEA |  |  |
| negative re | Any proces | IBA; IBA | GO:0004407; GO:0 | histone deacetylase |
|  |  |  | GO:0000062; GO:0 | fatty-acyl-CoA binc |
| regulation | Any proces | IBA; IEA; IEA | GO:0005515; GO:0 | protein binding; me |
| xpressed |  |  | GO:0008270 | zinc ion binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; single |

| | | | | |
|---|---|---|---|---|
| dephosph | The proces | IBA | GO:0016791 | phosphatase activit |
| multicellul | The biolog | IEA; IBA; IBA; ISS | GO:0003677 | DNA binding |
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0004177; GO:0 | aminopeptidase act |
| xylem dev | The forma | IEA | | |
| regulation | Any proces | IEA | | |
| | | | GO:0004721; GO:0 | phosphoprotein ph |
| regulation | Any proces | IEA | GO:0043565 | sequence-specific |
| DNA replic | The cellula | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| in, expressed | | | GO:0005515 | protein binding |
| ribosomal | The aggre | IBA; IBA | | |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IBA; IBA; IEA; IE | GO:0000977; GO:0 | RNA polymerase II t |
| entrainme | The synch | IBA; IEA | | |
| g protein | | | GO:0046872 | metal ion binding |
| ion transp | The direct | IEA; IEA | GO:0004970; GO:0 | ionotropic glutama |
| transcripti | A transcri | IEA | GO:0003677 | DNA binding |

| | | | | |
|---|---|---|---|---|
| ribosomal | The directe | IBA; IBA | | |
| chaperone | The proces | IBA | | |
| plant-type | A cellular p | IBA; IBA; IEA; IEA | | |
| | | | GO:0005515 | protein binding |
| transmemb | The proces | IEA; IEA | GO:0022857 | transmembrane tra |
| rRNA proce | Any proces | IEA; IEA | | |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IEA | | |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; cataly |
| regulation | Any proces | IEA; IBA; IMP; IMP; II | GO:0000978; GO:0 | RNA polymerase II c |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0005515 | protein binding |
| enic toleranc | | | | |
| regulation | Any proces | IEA; IBA; IBA; IEA; IE | GO:0000977; GO:0 | RNA polymerase II t |
| response t | Any proces | IEA; IEA | GO:0005515 | protein binding |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| | | | GO:0016740 | transferase activity |

| | | | | |
|---|---|---|---|---|
| etolactate synthase-inhibiting herbicides ( | | | GO:0004497; GO:0 | monooxygenase act |
| main containing protein | | | GO:0008168 | methyltransferase a |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| transmemb | The proces | IEA | GO:0005524; GO:0 | ATP binding; ATPas |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0003677 | DNA binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| phenylpro | The chemi | IEA | | |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| 1 | | | GO:0005515 | protein binding |
| multicellul | The biolog | IBA; IBA; IBA; IBA; IB | GO:0004497; GO:0 | monooxygenase act |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| flavonoid b | The chemi | IEA; IDA; IDA | GO:0004497; GO:0 | monooxygenase act |
| phosphore | A conserve | IEA; IEA; IMP | | |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IMP; IEA; IMP; IMP; I | GO:0003677; GO:0 | DNA binding; DNA- |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |
| | | | GO:0017022; GO:0 | myosin binding; my |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| plant-type | A cellular | IBA; IEA; IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| g protein | | | | |
| ining protein | | | | |
| | | | GO:0005515 | protein binding |
| tricarboxyl | A nearly u | IEA; IBA; IBA | GO:0000104; GO:0 | succinate dehydrog |
| xylem dev | The forma | IEA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| in containing protein |  |  | GO:0003950; GO:0 | NAD+ ADP-ribosylt |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| cation tran | The direct | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| plasmodes | The mover | IEA | GO:0008017 | microtubule bindin |
| regulation | Any proces | IEA |  |  |
| defense re | Reactions, | IEA; IEA; IEA; IEA | GO:0005515; GO:0 | protein binding; AD |
| regulation | Any proces | IEA |  |  |
| centrosom | The cell cy | IBA; IBA | GO:0008017 | microtubule bindin |
| regulation | Any proces | IBA; IEA | GO:0003700; GO:0 | DNA-binding trans |
| defense re | Reactions | IEA |  |  |
| carbohydr | The proces | IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| regulation | Any proces | IEA; IEA |  |  |
| g protein |  |  | GO:0004857; GO:0 | enzyme inhibitor ac |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| regulation | Any proces | IEA |  |  |
| histone H4 | The modifi | IEA; IEA; IEA; IBA | GO:0002151; GO:0 | G-quadruplex RNA |
|  |  |  | GO:0005515 | protein binding |
| flower dev | The proces | IEA; IEA |  |  |

| | | | | |
|---|---|---|---|---|
| | | | GO:0080115 | myosin XI tail bindi |
| reciprocal | The cell cy | IBA | | |
| | | | GO:0005515 | protein binding |
| signal tran | The cellula | IEA; IBA; IBA; IEA | | |
| | | | GO:0005524 | ATP binding |
| nuclear me | A process | IBA | | |
| regulation | Any proces | IEA | | |
| regulation | Any proces | IEA; IEA | | |
| negative re | Any proces | IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| regulation | Any proces | IEA | | |
| ing protein | | | | |
| containing protein | | | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| positive re | Any proces | IEA | | |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| | | | GO:0008270; GO:0 | zinc ion binding; m |
| class family protein | | | GO:0003677 | DNA binding |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |
| ain containing protein | | | | |
| protein tra | The direct | IEA; IEA; IEA | | |
| regulation | Any proces | IBA | GO:0005515 | protein binding |
| nbrane plant subgroup domain containing protein | | | | |
| poly(A)+ m | The direct | IBA | GO:0003677; GO:0 | DNA binding; mRN |
| protein loc | Any proces | IBA; IEA | | |
| ubiquitin- | The chemi | IEA; IEA | GO:0004197; GO:0 | cysteine-type endo |
| DNA-temp | The initial | IEA; IEA; IEA; IBA | GO:0001006; GO:0 | RNA polymerase III |
| resolution | The cleava | IBA; IEA | | |
| asymmetri | The asymn | IEA | | |

| | | | | |
|---|---|---|---|---|
| defense re | Reactions, | IEA; IEA; IEA; IEA; IB | GO:0004864; GO:0 | protein phosphatas |
| nucleus or | A process | IEA | | |
| ning protein | | | | |
| regulation | Any proces | IEA; IBA; IBA; IBA; IB | GO:0000978; GO:0 | RNA polymerase II |
| DNA replic | A signal tr | IBA; IBA; IBA; IBA; IB | GO:0003677; GO:0 | DNA binding; DNA |
| coenzyme | The chemi | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA | | |
| regulation | Any proces | IBA | | |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| autophago | The forma | IEA; IBA; IBA; IEA; IB | GO:0019887; GO:0 | protein kinase regu |
| g protein | | | GO:0008233; GO:0 | peptidase activity; |
| ubiquitin- | The chemi | IEA; IEA; IBA | GO:0044390; GO:0 | ubiquitin-like prote |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| se) polymerase (PARP) domain protein, Al | | | GO:0003950 | NAD+ ADP-ribosylt |

|  |  |  |  |  |
|---|---|---|---|---|
| protein ub | The proces | IEA; IEA | GO:0005515; GO:0 | protein binding; tra |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
|  |  |  | GO:0008017 | microtubule binding |
| nuclear-tr | The nonse | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; mRNA |
| containing protein |  |  | GO:0016757 | glycosyltransferase |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
|  |  |  | GO:0005515 | protein binding |
| cation tran | The direct | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| protein loc | Any proces | IBA; IEA |  |  |
| maturation | Any proces | IBA |  |  |
|  |  |  | GO:0046872 | metal ion binding |
|  |  |  | GO:0003676 | nucleic acid binding |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| ning protein |  |  |  |  |
| regulation | Any proces | IC; IEA | GO:0003677; GO:0 | DNA binding; prote |
| transmem | The proces | IBA | GO:0022857 | transmembrane tra |
| defense re | Reactions, | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA | GO:0003700; GO:0 | DNA-binding trans |
| protein ub | The proces | IEA; IBA | GO:0005515 | protein binding |
|  |  |  | GO:0004857 | enzyme inhibitor ac |

|  |  |  |  |  |
|---|---|---|---|---|
| DNA-temp | The compl | IEA; IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
|  |  |  | GO:0016757 | glycosyltransferase |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| male meio | A cell cycle | IEA; IEA |  |  |
| response t | Any proces | IEA |  |  |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| autophago | The forma | IEA; IBA; IBA; IEA; IB | GO:0019887; GO:0 | protein kinase regu |
| mRNA pro | Any proces | IEA | GO:0003723 | RNA binding |
| peroxisom | The direct | IEA | GO:0016301 | kinase activity |
| regulation | Any proces | IEA; IEA; IEA; IEA; I | GO:0003677; GO:0 | DNA binding; DNA- |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ubiquitin- | The chemi | IBA; IBA; IBA; IEA | GO:0061630 | ubiquitin protein lig |
| ng protein | | | | |
| | | | GO:0005515 | protein binding |
| DNA replic | The cellula | IEA; IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005200; GO:0 | structural constitue |
| containing protein | | | GO:0016757 | glycosyltransferase |
| ubiquitin- | The chemi | IEA | GO:0031625 | ubiquitin protein lig |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| DNA-temp | The synthe | IEA; IEA | GO:0043565 | sequence-specific |
| regulation | Any proces | IEA | | |
| cation tran | The direct | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| regulation | Any proces | IBA | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| protein | | | GO:0005516 | calmodulin binding |

| | | | | |
|---|---|---|---|---|
| | | | GO:0003677 | DNA binding |
| mitotic cel | Progressio | IBA; IBA; IBA; IBA; IB | GO:0003676; GO:0 | nucleic acid binding |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| tRNA 5'-le | Generation | IBA; IEA; IEA | GO:0004526; GO:0 | ribonuclease P activ |
| activation | Any proces | IEA; IEA; IBA | GO:0008017; GO:0 | microtubule binding |
| metal ion t | The directe | IEA; IEA | GO:0046872 | metal ion binding |
| otein | | | | |
| | | | GO:0030247 | polysaccharide bin |
| regulation | Any proces | IBA; IBA | GO:0003677; GO:0 | DNA binding; seque |
| | | | GO:0005515 | protein binding |
| response t | Any proces | IEA; IEA | | |
| aining protein | | | | |

|  |  |  |  |  |
|---|---|---|---|---|
| ein |  |  |  |  |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA– |
| nuclear–tr | The nonse | IBA | GO:0003723; GO:0 | RNA binding; helica |
| male meio | A cell cycle | IEA |  |  |
|  |  |  | GO:0017022; GO:0 | myosin binding; my |
| RNA polym | The aggreg | IEA; IEA | GO:0001164 | RNA polymerase I c |
| regulation | Any proces | IEA | GO:0046983 | protein dimerizatio |
| otein |  |  | GO:0005515 | protein binding |
| tRNA modi | The covale | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin–dependent p |
| regulation | Any proces | IDA | GO:0000976; GO:0 | transcription cis–re |
| ain containing protein |  |  | GO:0003677; GO:0 | DNA binding; DNA– |
| regulation | Any proces | IEA; IBA; IBA | GO:0003690 | double–stranded D |

| | | | | |
|---|---|---|---|---|
| rotein | | | GO:0003676; GO:0 | nucleic acid binding |
| gene silen | A small RN | IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016787 | hydrolase activity |
| regulation | Any proces | IEA; IBA | GO:0008270; GO:0 | zinc ion binding; se |
| | | | GO:0080115 | myosin XI tail bindi |
| regulation | Any proces | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0005515 | protein binding |
| transcripti | The synthe | IEA | | |
| defense re | Reactions, | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| mRNA 5'-s | Recognitio | IBA; IEA | GO:0003723 | RNA binding |
| n containing protein | | | | |
| regulation | Any proces | IBA | GO:0005515 | protein binding |
| n | | | GO:0005515 | protein binding |
| actin filam | A process | IBA; IBA | GO:0000146; GO:0 | microfilament moto |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding trans |
| response t | Any proces | IEA; IEA | | |
| | | | GO:0016410; GO:0 | N-acyltransferase a |
| protein fol | The proces | IEA; IBA | GO:0051082; GO:0 | unfolded protein bi |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| | | | GO:0046872 | metal ion binding |
| defense re | Reactions | IEA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
|  |  |  | GO:0030246 | carbohydrate bindir |
|  |  |  | GO:0016747; GO:0 | acyltransferase acti |
| f the premeiotic G1/S-phase transition of |  |  | GO:0003676; GO:0 | nucleic acid binding |
| carbohydra | The chemi | IBA; IBA; IBA; IDA; II | GO:0015018; GO:0 | galactosylgalactosy |
| fluoride tra | The proces | IEA | GO:1903425 | fluoride transmemb |
| regulation | Any proces | IBA; IEA | GO:0003714; GO:0 | transcription corepr |
| mRNA spli | The joining | IEA | GO:0003676 | nucleic acid binding |
| defense re | Reactions, | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| lipid meta | The chemi | IEA | GO:0008374; GO:0 | O-acyltransferase a |
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| proteolysis | The hydrol | IBA | GO:0004197 | cysteine-type endo |
|  |  |  | GO:0005515 | protein binding |
| asymmetri | The asymn | IEA |  |  |

|  |  |  |  |  |
|---|---|---|---|---|
|  |  |  | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA– |
| RNA proce | Any proces | IEA |  |  |
| containing protein |  |  | GO:0016740; GO:0 | transferase activity; |
| chloroplas | A process | IBA; IMP; IMP |  |  |
| regulation | Any proces | IC | GO:0003677; GO:0 | DNA binding; prote |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
|  |  |  | GO:0008270; GO:0 | zinc ion binding; m |
|  |  |  | GO:0016747; GO:0 | acyltransferase acti |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin–protein tr |
| cytokinin r | The chemi | IEA; IEA; IEA |  |  |

|  |  |  |  |  |
|---|---|---|---|---|
| protein tra | The directe | IEA; IEA | GO:0005102; GO:0 | signaling receptor b |
| regulation | Any proces | IEA; IEA |  |  |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II c |
| regulation | Any proces | IEA; IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
|  |  |  | GO:0003677; GO:0 | DNA binding; metal |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| vesicle-me | A cellular t | IBA |  |  |
| cellular res | Any proces | IEA |  |  |
| regulation | Any proces | IEA |  |  |
|  |  |  | GO:0003677; GO:0 | DNA binding; prote |
| n containing protein |  |  |  |  |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| microtubul | A process | IEA | GO:0008017 | microtubule bindin |
| g protein |  |  | GO:0046872 | metal ion binding |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
|  |  |  | GO:0003729; GO:0 | mRNA binding; prot |
|  |  |  | GO:0003779; GO:0 | actin binding; kinas |
|  |  |  | GO:0005515 | protein binding |

|  |  |  |  |  |
|---|---|---|---|---|
|  |  |  | GO:0003676 | nucleic acid bindin |
| ning protein |  |  | GO:0003676; GO:0 | nucleic acid bindin |
| assium channel 1 (AtKCO1) |  |  |  |  |
| phosphore | A conserve | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| photosynt | A photosy | IEA |  |  |
| DNA-temp | The synthe | IEA; IEA; IBA; IBA; I | GO:0003677; GO:0 | DNA binding; trans |
| DNA-temp | The synthe | IEA | GO:0043565 | sequence-specific |
|  |  |  | GO:0008270 | zinc ion binding |
|  |  |  | GO:0051213 | dioxygenase activit |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| response t | Any proces | IEP; IEP; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IC; IMP | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IC | GO:0046983 | protein dimerizatio |
| DNA-temp | The initial | IEA; IEA; IEA; IEA; IE | GO:0003700 | DNA-binding trans |
| protein ub | The proces | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| n | | | GO:0005515 | protein binding |
| | | | GO:0016788 | hydrolase activity, a |
| | | | GO:0016410; GO:0 | N-acyltransferase a |
| positive re | Any proces | IBA | GO:0003729; GO:0 | mRNA binding; tran |

| | | | | |
|---|---|---|---|---|
| phosphore | A conserve | IEA; IEA; IEA | GO:0005515 | protein binding |
| lipid meta | The chemi | IEA | GO:0008374; GO:0 | O-acyltransferase |
| | | | GO:0008017 | microtubule bindin |
| n | | | GO:0005515; GO:0 | protein binding; ki |
| rotein | | | GO:0016788 | hydrolase activity, |
| phosphore | A conserve | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
| | | | GO:0004721; GO:0 | phosphoprotein ph |
| | | | GO:0005509 | calcium ion binding |
| chloroplas | A process | IBA | | |
| ning protein | | | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |
| of stomatal closure, Abiotic stress respo | | | GO:0003950 | NAD+ ADP-ribosylt |
| | | | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IBA; IEA | GO:0003700; GO:0 | DNA-binding trans |
| lipid meta | The chemi | IEA; IEA | GO:0016787 | hydrolase activity |
| defense re | Reactions | IEA | | |
| poly(A)+ m | The direct | IBA | GO:0003729 | mRNA binding |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| DNA-temp | The synth | IBA | | |
| | | | GO:0005515 | protein binding |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |

|  |  |  |  |  |
|---|---|---|---|---|
| ntaining protein |  |  |  |  |
|  |  |  | GO:0016788 | hydrolase activity, a |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding transc |
| protein ub | The proces | IBA | GO:0004842 | ubiquitin-protein tr |
| terminatio | A transcrip | IEA; IEA; IEA; IEA | GO:0000993; GO:0 | RNA polymerase II c |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0003779; GO:0 | actin binding; kinas |
| regulation | Any proces | IEA; IBA | GO:0000976; GO:0 | transcription cis-re |
| male meio | A cell cycle | IEA; IEA |  |  |
| containing protein |  |  | GO:0016757 | glycosyltransferase |
| g protein |  |  | GO:0046872 | metal ion binding |
| protein po | The proces | IEA; IEA; IEA; IEA |  |  |
| plasmodes | The mover | IEA | GO:0008017 | microtubule binding |
|  |  |  | GO:0005515 | protein binding |
| ning protein |  |  | GO:0003676; GO:0 | nucleic acid binding |
| mRNA pro | Any proces | IBA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| cell differe | The proces | IEA; IEA; IMP | GO:0004857; GO:0 | enzyme inhibitor ac |
| mRNA pro | Any proces | IEA |  |  |
|  |  |  | GO:0003677; GO:0 | DNA binding; metal |

|  |  |  |  |  |
|---|---|---|---|---|
| main containing protein |  |  | GO:0001228; GO:0 | DNA-binding transc |
| containing protein |  |  |  |  |
| regulation | Any proces | IEA; IEA; IEP; IEA; IM | GO:0000977; GO:0 | RNA polymerase II t |
| g protein |  |  | GO:0046872 | metal ion binding |
| uence |  |  |  |  |
| ing protein, expressed |  |  | GO:0003950 | NAD+ ADP-ribosylt |
|  |  |  | GO:0003723 | RNA binding |
| ubiquitin- | The chemi | IBA; IEA | GO:0016740; GO:0 | transferase activity; |
| actin cytos | A process | IEA; IEA | GO:0003779; GO:0 | actin binding; actin |
| ubiquitin- | The chemi | IBA; IBA | GO:0005515 | protein binding |
| regulation | Any proces | IC; IBA | GO:0000978; GO:0 | RNA polymerase II |
|  |  |  | GO:0046982 | protein heterodime |
| DNA-temp | The synthe | IEA | GO:0043565 | sequence-specific |
| regulation | Any proces | IEA | GO:0003700 | DNA-binding transc |
| protein tra | The directe | IEA; IEA | GO:0005102; GO:0 | signaling receptor |
| pectin bios | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| flower dev | The proces | IEA; IEA |  |  |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IC | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IEA; IEA | | |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| response t | Any proces | IEA; IEA; IEA | GO:0005515 | protein binding |
| carbohydra | The chemi | IEA | GO:0004568 | chitinase activity |
| | | | GO:0003676 | nucleic acid bindin |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| ipid homeostasis, Submergence toleranc | | | GO:0016491 | oxidoreductase acti |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| chloroplas | The reloca | IBA; IBA | | |

| | | | | |
|---|---|---|---|---|
| DNA-temp | The initial | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| response t | Any proces | IBA; IBA; IBA | GO:0005515 | protein binding |
| intercellula | The mover | IBA | | |
| ein | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| n | | | GO:0003676 | nucleic acid binding |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| positive re | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| ining protein | | | GO:0003677; GO:0 | DNA binding; mino |
| carbohydra | The chemi | IEA; IBA | GO:0004568; GO:0 | chitinase activity; c |
| plant-type | A cellular p | IBA; IEA; IEA; IEA; IE | GO:0016740; GO:0 | transferase activity; |
| male meio | A cell cycle | IEA | | |
| regulation | Any proces | IBA; IBA | GO:0003723 | RNA binding |
| negative re | Any proces | IBA; IBA | GO:0046982 | protein heterodime |
| defense re | Reactions, | IEA | | |
| cellular res | Any proces | IBA; IBA; IEA | | |

| | | | | |
|---|---|---|---|---|
| | | | GO:0005515 | protein binding |
| | | | GO:0016740; GO:0 | transferase activity; |
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded DI |
| n | | | GO:0047617 | acyl-CoA hydrolase |
| tein | | | GO:0008080; GO:0 | N-acetyltransferase |
| cation tran | The directe | IEA; IBA; IEA; IEA | GO:0015299 | solute:proton antip |
| RNA polym | The aggreg | IBA; IEA; IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0003677 | DNA binding |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0005524 | ATP binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0016788 | hydrolase activity, a |
| terminatio | A transcrip | IEA; IEA; IEA; IEA | GO:0000993; GO:0 | RNA polymerase II c |
| double-str | The repair | IBA; IEA; IBA | GO:0003682; GO:0 | chromatin binding; |
| | | | GO:0005515; GO:0 | protein binding; zin |
| | | | GO:0016788 | hydrolase activity, a |

|  |  |  |  |  |
|---|---|---|---|---|
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003676 | nucleic acid binding |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| of Arabidopsis CER2, Leaf cuticular wax s |  |  | GO:0016747 | acyltransferase acti |
| nucleocyto | The directe | IEA; IEA; IEA | GO:0003924; GO:0 | GTPase activity; GT |
|  |  |  | GO:0005515; GO:0 | protein binding; zin |
|  |  |  | GO:0003779; GO:0 | actin binding; kinas |
|  |  |  | GO:0016788 | hydrolase activity, a |
| reciprocal | The cell cy | IBA |  |  |
| DNA replic | The cellula | IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; single |
| ein |  |  | GO:0003677 | DNA binding |
|  |  |  | GO:0008017 | microtubule binding |
| response t | Any proces | IEA | GO:0005524; GO:0 | ATP binding; ATP h |

|  |  |  |  |  |
|---|---|---|---|---|
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| phosphore | A conserve | IEA; IEA; IDA | GO:0003677; GO:0 | DNA binding; DNA- |
| intracellula | The directe | IEA; IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
|  |  |  | GO:0005515 | protein binding |
| chromatin | The assem | IEA; IEA; IBA; IBA | GO:0003712; GO:0 | transcription coregu |
| regulation | Any proces | IBA | GO:0000977; GO:0 | RNA polymerase II t |
| regulation | Any proces | IEA; IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding transc |
| ining protein |  |  | GO:0017022; GO:0 | myosin binding; my |
| phosphory | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| protein ub | The proces | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
|  |  |  | GO:0003677 | DNA binding |
| protein po | The proces | IEA; IEA; IEA; IEA |  |  |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IBA; IBA; IBA | GO:0005515 | protein binding |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| 6 | | | GO:0003677; GO:0 | DNA binding; metal |
| ubiquitin- | The chemi | IBA; IEA | GO:0061630 | ubiquitin protein lig |
| protein tra | The direct | IEA | GO:0035091 | phosphatidylinosito |
| embryo de | The proces | IEA | | |
| rminal domain containing protein | | | | |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; singl |
| stomatal c | The region | IEA; IEA | GO:0019901; GO:0 | protein kinase bind |
| response t | Any proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| transmeml | The proces | IEA | GO:0022857 | transmembrane trai |
| n | | | | |
| regulation | Any proces | IEA; IBA | GO:0000976; GO:0 | transcription cis-re |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| transcripti | A transcrip | IEA; IBA | GO:0001002; GO:0 | RNA polymerase III |
| | | | GO:0005515 | protein binding |
| DNA-temp | The synthe | IEA; IBA; IBA | GO:0003712; GO:0 | transcription coregu |
| | | | GO:0016410; GO:0 | N-acyltransferase a |
| fication in grass cell wal | | | GO:0016410; GO:0 | N-acyltransferase a |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| DNA replic | A signal tr | IBA; IBA; IBA; IBA; IE | GO:0003677; GO:0 | DNA binding; DNA |
| iolesterase | | | | |
| regulation | Any proces | IEA; IEA; IEA; IEA; IE | GO:0000976; GO:0 | transcription cis-re |
| chloroplas | The divisio | IBA; IBA | | |
| ribosomal | The directe | IEA; IEA; IBA; IBA; IE | GO:0017056 | structural constitue |
| | | | GO:0016788 | hydrolase activity, a |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| carbohydra | The chemi | IBA; IBA; IBA; IDA; IE | GO:0015018; GO:0 | galactosylgalactosy |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| defense re | Reactions, | IEA | | |
| pollen tub | The proces | IEA | GO:0036033 | mediator complex |
| reproducti | The produ | IBA; IEA; IBA; IBA | GO:0003677 | DNA binding |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| otein | | | | |
| regulation | Any proces | IEA | GO:0043565 | sequence-specific |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA | | |
| gravitropis | The orient | IEA; IMP; IEA | | |
| DNA replic | The cellula | IEA; IBA; IBA; IBA | GO:0003887 | DNA-directed DNA |
| ning protein | | | GO:0003676; GO:0 | nucleic acid binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; |
| DNA replic | The cellula | IEA; IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| hydrotropi | Growth or | IEA | | |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; |
| rRNA proc | Any proces | IBA; IBA; IBA; IBA; IE | GO:0003697; GO:0 | single-stranded DN |
| ning protein | | | GO:0003676 | nucleic acid binding |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| defense re | Reactions, | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA– |
| protein de | The proces | IBA; IEA | GO:0019888 | protein phosphatas |
| response t | Any proces | IEA; IEA; IEA; IEA; IE | GO:0016787 | hydrolase activity |
| rotein | | | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| chloroplas | The reloca | IBA; IBA | | |
| rotein | | | GO:0005515 | protein binding |
| cellular res | Any proces | IEA | | |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0005515 | protein binding |
| | | | GO:0016410; GO:0 | N–acyltransferase a |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| protein tar | The proces | IBA; IBA | | |

|  |  |  |  |  |
|---|---|---|---|---|
| defense re | Reactions, | IEA | GO:0016740; GO:0 | transferase activity; |
| GPI anchor | The chemi | IEA |  |  |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| plant-type | A process | IBA | GO:0016740; GO:0 | transferase activity; |
| telomere | Any proces | IBA; IEA; IEA |  |  |
| ubiquitin- | The chemi | IEA; IEA | GO:0004197; GO:0 | cysteine-type endo |
| rRNA proc | Any proces | IEA | GO:0003723 | RNA binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| phosphore | A conserve | IEA; IEA; IEA; IEA; IE | GO:0000155; GO:0 | phosphorelay senso |
| maturatio | Any proces | IBA; IBA; IEA; IEA | GO:0004519 | endonuclease activi |
| regulation | Any proces | IBA | GO:0046872 | metal ion binding |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| defense re | Reactions, | IEA; IEA; IEA | GO:0004869; GO:0 | cysteine-type endo |
| protein su | The proces | IEA | GO:0008270; GO:0 | zinc ion binding; S |
| ein |  |  | GO:0016407; GO:0 | acetyltransferase ac |

| | | | | |
|---|---|---|---|---|
| signal tran | The cellula | IEA | GO:0005515 | protein binding |
| response t | Any proces | IEA | GO:0004867 | serine-type endope |
| | | | GO:0004722; GO:0 | protein serine/thre |
| g protein | | | GO:0046872 | metal ion binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0016740; GO:0 | transferase activity; |
| vegetative | The proces | IBA | GO:0003677 | DNA binding |
| DNA-temp | The initial | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| DNA-temp | The initial | IEA; IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; trans |
| | | | GO:0003729; GO:0 | mRNA binding; pro |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| aromatic c | The chemi | IBA; IBA | GO:0008168; GO:0 | methyltransferase a |
| negative re | Any proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| on of grain siz | | | GO:0046983 | protein dimerizatio |
| chromatin | A dynamic | IEA | | |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| defense re | Reactions | IEA | | |
| | | | GO:0005515 | protein binding |
| protein me | The chemi | IEA; IDA | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| protein ub | The proces | IEA; IBA | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| cellular res | Any proces | IEA | | |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| ein | | | GO:0003677 | DNA binding |
| proteolysis | The hydrol | IEA; IBA; IEA | GO:0004190; GO:0 | aspartic-type endo |
| | | | GO:0005515 | protein binding |
| positive re | Any proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| post-trans | The target | IBA; IBA; IBA | GO:0005515; GO:0 | protein binding; mc |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| ubiquitin- | The chemi | IBA; IBA; IBA; IEA | GO:0061630 | ubiquitin protein li |
| cellular co | A process | IEA; IEA; IEA; IEA | | |
| phenylpro | The chemi | IEA | | |
| response t | Any proces | IEA | | |
| negative re | Any proces | IEA | | |
| reciprocal | The cell cy | IBA | | |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| mediating stress and rhythm responsive | | | GO:0003677 | DNA binding |
| protein loc | Any proces | IBA; IEA | | |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| lipid meta | The chemi | IEA; IEA | GO:0016787 | hydrolase activity |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| double-str | The error- | IEA; IEA; IEA; IEA; IE | GO:0003684; GO:0 | damaged DNA bind |
| positive re | Any proces | IBA | GO:0003729; GO:0 | mRNA binding; tran |
| rRNA proc | Any proces | IBA | | |
| mRNA pro | Any proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016410; GO:0 | N-acyltransferase a |
| | | | GO:0016788 | hydrolase activity, a |
| cell wall m | The series | IEA; IEA; IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| regulation | Any proces | IC; IMP; IMP | GO:0003700; GO:0 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| plant-type | A cellular | IBA; IEA; IEA; IEA; IE | GO:0016740; GO:0 | transferase activity; |
| flower dev | The proces | IEA | GO:0003677; GO:0 | DNA binding; single |
| melatonin | The chemi | IEA; IEA | GO:0008168; GO:0 | methyltransferase a |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| g protein | | | | |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| positive re | Any proces | IBA | GO:0003729; GO:0 | mRNA binding; tran |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ub | The proces | IEA | | |
| cell cycle; | The progre | IEA; IBA; IBA; IEA; IB | GO:0044877 | protein-containing |
| | | | GO:0005515 | protein binding |
| | | | GO:0016747; GO:0 | acyltransferase acti |
| | | | GO:0005515 | protein binding |
| phenylpro | The chemi | IEA | | |
| ein | | | | |

| | | | | |
|---|---|---|---|---|
| | | | GO:0016740; GO:0 | transferase activity; |
| adenylate | A G protei | IBA; IBA | GO:0004930 | G protein-coupled |
| | | | GO:0000976; GO:0 | transcription cis-re |
| actin cytos | A process | IEA; IEA | GO:0003779; GO:0 | actin binding; actin |
| regulation | Any proces | IEA | | |
| | | | GO:0003677; GO:0 | DNA binding; zinc i |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| endocytosi | A vesicle- | IBA; IBA | GO:0005509; GO:0 | calcium ion binding |
| | | | GO:0005515 | protein binding |
| ining protein | | | GO:0003677; GO:0 | DNA binding; mino |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| RNA 3'-en | Any proces | IBA; IEA | GO:0004652 | polynucleotide ade |
| proteolysis | The hydrol | IEA; IEA; IBA | GO:0004197; GO:0 | cysteine-type endo |
| | | | GO:0005515 | protein binding |
| response t | Any proces | IEA | GO:0005515 | protein binding |
| signal pep | The protec | IEA; IEA; IBA; IEA | GO:0004252; GO:0 | serine-type endope |
| lipid meta | The chemi | IEA | GO:0016787 | hydrolase activity |
| regulation | Any proces | IEA; IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| tRNA 5'-le | Generation | IEA; IBA; IBA | GO:0000171; GO:0 | ribonuclease MRP a |
| | | | GO:0005515 | protein binding |
| ribosome | A cellular | IBA | | |
| ribosomal | The direct | IBA; IBA; IBA; IBA; IE | GO:0003723 | RNA binding |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA; IBA; IMP | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0003779 | actin binding |
| | | | GO:0008017 | microtubule bindin |
| protein tra | The proces | IBA; IEA | | |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| cell differe | The proces | IEA | | |
| microtubul | The remov | IBA; IEA | GO:0005515; GO:0 | protein binding; mi |
| protein gly | A protein r | IEA | GO:0008378; GO:0 | galactosyltransfera |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |

|  |  |  |  |  |
|---|---|---|---|---|
| mRNA pro | Any proces | IEA; IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| phosphory | The proces | IEA | GO:0003779; GO:0 | actin binding; kinas |
| nitrogen c | The chemi | IEA; IEA; IEA | GO:0003676 | nucleic acid binding |
| n |  |  | GO:0005509 | calcium ion binding |
| double-str | The repair | IBA; IEA; IEA | GO:0003682; GO:0 | chromatin binding; |
| protein gly | A protein r | IEA; IEA | GO:0008373; GO:0 | sialyltransferase act |
| protein pol | Addition o | IBA; IEA; IEA; IBA; IE | GO:0004842; GO:0 | ubiquitin-protein tr |
|  |  |  | GO:0016874 | ligase activity |
|  |  |  | GO:0005509 | calcium ion binding |
|  |  |  | GO:0003700; GO:0 | DNA-binding trans |
| IA1 |  |  | GO:0008017 | microtubule binding |
| ssed |  |  | GO:0005200; GO:0 | structural constitue |
|  |  |  | GO:0016787 | hydrolase activity |
| nuclear en | A process | IBA | GO:0043495; GO:0 | protein-membrane |
|  |  |  | GO:0003700; GO:0 | DNA-binding trans |
| spliceoso | The aggre | IEA |  |  |
| tein |  |  | GO:0016787 | hydrolase activity |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded D |

| | | | | |
|---|---|---|---|---|
| ulation of hydrogen peroxide-induced st | | | GO:0008270; GO:0 | zinc ion binding; lig |
| intracellula | The direct | IBA; IBA | GO:0005096 | GTPase activator ac |
| | | | GO:0016787 | hydrolase activity |
| protein tar | The proces | IEA; IBA | GO:0005543; GO:0 | phospholipid bindir |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| | | | GO:0003700 | DNA-binding transc |
| rminal domain containing protein | | | GO:0003682 | chromatin binding |
| | | | GO:0005515 | protein binding |
| steroid bio | The chemi | IEA | GO:0003854; GO:0 | 3-beta-hydroxy-de |
| otein | | | GO:0005515 | protein binding |
| | | | GO:0016747; GO:0 | acyltransferase acti |
| regulation | Any proces | IEA; IBA; IEA | GO:0043565 | sequence-specific D |

| | | | | |
|---|---|---|---|---|
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded D |
| response t | Any proce | IEA | | |
| positive re | Any proce | IBA | GO:0003729; GO:0 | mRNA binding; tran |
| | | | GO:0003676 | nucleic acid binding |
| rotein | | | GO:0003729; GO:0 | mRNA binding; pro |
| | | | GO:0022857 | transmembrane tra |
| | | | GO:0008375; GO:0 | acetylglucosaminylt |
| vesicle buc | The evagin | IBA; IEA; IBA | | |
| regulation | Any proce | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proce | IEA; IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| nucleobas | Any cellula | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein pr | The covale | IEA; IBA | GO:0005515; GO:0 | protein binding; pr |
| DNA replic | The cellula | IEA; IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proce | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ntaining protein | | | | |
| auxin-acti | The series | IEA; IBA; IBA | GO:0031624; GO:0 | ubiquitin conjugati |
| cellular res | Any proce | IEA | | |
| ion transp | The direct | IEA; IEA; IEA | GO:0015079 | potassium ion trans |

| | | | | |
|---|---|---|---|---|
| retrograde | The directe | IEA | | |
| n | | | | |
| phosphory | The proces | IEA | GO:0016301 | kinase activity |
| protein im | The directe | IBA; IBA; IEA | GO:0005049; GO:0 | nuclear export sign |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| N (RNA-binding protein 56) (TAFII68) (TA | | | GO:0003723; GO:0 | RNA binding; metal |
| DNA-temp | The synthe | IEA; IBA; IBA | GO:0001228; GO:0 | DNA-binding trans |
| phenylpro | The chemi | IEA | | |
| auxin-acti | The series | IEA; IBA; IBA; IBA; IE | GO:0010329 | auxin efflux transm |
| endomem | A process | IBA | | |
| signal pep | The protec | IEA; IMP; IEA | GO:0008233 | peptidase activity |
| | | | GO:0005515; GO:0 | protein binding; zin |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| Group II in | The splicin | IEA; IEA | GO:0003723 | RNA binding |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| positive re | Any proces | IBA | GO:0000977; GO:0 | RNA polymerase II t |
| | | | GO:0003723; GO:0 | RNA binding; mRN |
| DNA-temp | The synthe | IEA | | |
| phosphory | The proces | IEA | GO:0003779; GO:0 | actin binding; kinas |
| translation | The cellula | IBA; IEA | GO:0003735 | structural constitue |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003676 | nucleic acid bindin |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| ubiquitin- | The chemi | IBA; IEA; IEA; IEA | GO:0004866; GO:0 | endopeptidase inhi |

| | | | | |
|---|---|---|---|---|
| | | | GO:0009055 | electron transfer ac |
| | | | GO:0005515 | protein binding |
| DNA repai | The proces | IEA; IEA; IEA; IBA; IB | GO:0003677; GO:0 | DNA binding; singl |
| lipid trans | The direct | IEA | GO:0008233; GO:0 | peptidase activity; l |
| | | | GO:0009055 | electron transfer ac |
| negative re | Any proces | IEA | GO:0010997 | anaphase-promoti |
| RNA proce | Any proces | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid bindin |
| ubiquitin- | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| phosphore | A conserve | IEA; IEA; IEA | GO:0005515 | protein binding |
| regulation | Any proces | IBA | | |
| regulation | An proces | IEA; IMP; IMP | GO:0005515; GO:2 | protein binding; am |
| fatty acid t | The direct | IBA | GO:0015245 | fatty acid transmem |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0005515; GO:0 | protein binding; cy |
| proteolysis | The hydrol | IEA; IBA | GO:0003677; GO:0 | DNA binding; aspar |
| translation | The proces | IEA | GO:0003729; GO:0 | mRNA binding; tran |

| | | | | |
|---|---|---|---|---|
| MAPK casc | An intracel | IBA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IDA; IDA; IMP; IDA | GO:0003677; GO:0 | DNA binding; prote |
| tRNA 5'-le | Generation | IEA; IBA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; ribon |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| phenylpro | The chemi | IEA | | |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| sporter domain containing protein | | | | |
| cell differe | The proces | IEA | | |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ontaining protein | | | GO:0003676 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IEA; IBA | GO:0000981; GO:0 | DNA-binding trans |
| microtubul | A microtub | IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |

|  |  |  |  |  |
|---|---|---|---|---|
| otein |  |  | GO:0016740; GO:0 | transferase activity; |
| actin cytos | A process | IEA; IEA | GO:0003779; GO:0 | actin binding; actin |
| DNA-temp | The synthe | IEA; IEA; IBA; IBA | GO:0001228; GO:0 | DNA-binding transc |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| mRNA poly | The enzym | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| regulation | Any proces | IEA; IBA; IEA; IBA; IE | GO:0000978; GO:0 | RNA polymerase II c |
| chloroplas | A process | IBA |  |  |
| regulation | Any proces | IEA; IC; IEA | GO:0005515 | protein binding |
| plant-type | A cellular p | IBA; IEA; IEA; IEA; IE | GO:0016740; GO:0 | transferase activity; |
| negative re | Any proces | IBA; IEA; IEA; IBA | GO:0003682; GO:0 | chromatin binding; |
| obsolete o | OBSOLETE. | IEA | GO:0046872 | metal ion binding |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| defense re | Reactions | IBA; IEA; IBA; IEA; IM | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IC | GO:0003677; GO:0 | DNA binding; prote |

| | | | | |
|---|---|---|---|---|
| post-trans | The inactiv | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| protein po | The proces | IEA | | |
| regulation | Any proces | IEA; IMP; IMP; IMP; I | GO:0003677; GO:0 | DNA binding; DNA- |
| reproducti | The progre | IBA | GO:0005515 | protein binding |
| | | | GO:0005509 | calcium ion binding |
| stabilizatic | The accom | IBA; IEA | GO:0005267; GO:0 | potassium channel |
| oligopepti | The proces | IEA; IEA | GO:0035673 | oligopeptide transm |
| steroid bio | The chemi | IEA; IEA; IEA; IMP | GO:0003854; GO:0 | 3-beta-hydroxy-de |
| | | | GO:0016788 | hydrolase activity, a |
| superoxide | The chemi | IEA; IEA | GO:0004784; GO:0 | superoxide dismuta |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| protein ub | The proces | IEA; IEA; IEA; IEA; IE | GO:0008270; GO:0 | zinc ion binding; tra |
| signal tran | The cellula | IEA; IEA; IEA | GO:0008083 | growth factor activi |
| regulation | Any proces | IBA; IBA; IEA | GO:0003713 | transcription coacti |
| protein ub | The proces | IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| regulation | Any proces | IEA; IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| ribosomal | The directe | IBA; IEA | | |
| rRNA proc | Any proces | IEA | GO:0043022 | ribosome binding |

| | | | | |
|---|---|---|---|---|
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| plant-type | A cellular | IBA; IBA; IEA | GO:0015018; GO:0 | galactosylgalactosy |
| DNA-temp | The synth | IEA; IEA; IEA | GO:0003712; GO:0 | transcription coreg |
| protein fol | The proces | IEA; IEA; IBA | GO:0000774; GO:0 | adenyl-nucleotide e |
| negative re | Any proces | IBA; IEA; IEA; IEA; IE | GO:0000978; GO:0 | RNA polymerase II |
| copper ion | The direct | IMP; IEA; IBA; IDA; I | GO:0005515; GO:0 | protein binding; su |
| otein | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA; IBA | GO:0003723 | RNA binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| molybdate | The direct | IEA | GO:0015098 | molybdate ion trans |
| DNA replic | The forma | IBA; IBA | GO:0005515; GO:0 | protein binding; his |
| | | | GO:0016491 | oxidoreductase acti |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; trans |

|  |  |  |  |  |
|---|---|---|---|---|
| gibberellin | The chemi | IDA | GO:0004497; GO:0 | monooxygenase ac |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
|  |  |  | GO:0016788 | hydrolase activity, a |
| n |  |  |  |  |
| regulation | Any proces | IEA; IEP; IDA; IMP; I | GO:0003700; GO:0 | DNA-binding trans |
|  |  |  | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| ubiquitin- | The series | IBA | GO:0005515; GO:0 | protein binding; po |
| positive re | Any proces | IEA | GO:0005096 | GTPase activator ac |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
|  |  |  | GO:0016410; GO:0 | N-acyltransferase a |
| chloroplas | The conve | IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |

| | | | | |
|---|---|---|---|---|
| pattern sp | Any devel | IBA | GO:0003677; GO:0 | DNA binding; chron |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| cell differe | The proces | IEA | | |
| phosphory | The proces | IEA | GO:0005515; GO:0 | protein binding; kin |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| pectin bios | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0005515 | protein binding |
| DNA-temp | The initial | IEA; IEA | | |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| microtubul | A microtu | IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| sation-like region domain containing protein | | | | |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| -like protein | | | GO:0004721; GO:0 | phosphoprotein ph |
| protein po | Addition o | IBA; IBA | GO:0005515 | protein binding |
| eration, Control of grain size, shape and q | | | GO:0003677; GO:0 | DNA binding; metal |
| ntaining protein | | | GO:0003824; GO:0 | catalytic activity; ph |
| regulation | Any proces | IBA | GO:0005515; GO:0 | protein binding; zin |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IBA; IBA; IEA; IEA; IB | GO:0043621; GO:0 | protein self-associa |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| sulfation | The additi | IBA | GO:0008146; GO:0 | sulfotransferase act |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| ntaining protein | | | | |
| phosphory | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| intracellula | The direct | IEA; IEA | GO:0030276; GO:0 | clathrin binding; ph |
| | | | GO:0016410; GO:0 | N-acyltransferase a |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| mRNA cata | The chemi | IBA; IBA | GO:0005515 | protein binding |
| 3'-UTR-m | An mRNA | IBA | GO:0003677; GO:0 | DNA binding; mRN |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| RNA foldin | The proces | IEA; IEA | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |
| photosynth | A process, | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| regulation | Any proces | IEA | GO:0005085 | guanyl-nucleotide |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IBA; IBA; IBA; IB | GO:0003700; GO:0 | DNA-binding transc |
| intracellula | The directe | IBA; IBA | GO:0005096 | GTPase activator ac |
| DNA-temp | The synthe | IEA; IEA | GO:0003714 | transcription corepr |
| cellular res | Any proces | IEA | | |
| regulation | Any proces | IEA; IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| | | | GO:0003677 | DNA binding |
| response t | Any proces | IEA | GO:0004867 | serine-type endope |
| phospholip | The mover | IBA; IEA | GO:1990050 | phosphatidic acid t |
| | | | GO:0008270; GO:0 | zinc ion binding; tra |
| DNA-temp | The synthe | IEA; IEA; IBA; IBA | GO:0001228; GO:0 | DNA-binding transc |
| box C/D s | The aggreg | IBA | GO:0062064 | box C/D snoRNP co |
| protein ub | The proces | IBA | GO:0004842 | ubiquitin-protein tr |
| signal pep | The protec | IEA; IEA; IBA; IEA | GO:0004252; GO:0 | serine-type endope |
| ribosomal | The aggreg | IBA; IBA; IBA; IBA; IB | GO:0005515 | protein binding |
| RNA modif | The covale | IEA; IEA | GO:0003723; GO:0 | RNA binding; protei |
| actin cytos | A process | IEA; IEA | GO:0003779; GO:0 | actin binding; actin |
| otein | | | GO:0005515 | protein binding |
| | | | GO:0003682 | chromatin binding |
| protein ub | The proces | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| calcium-m | Any intrac | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| protein po | Addition o | IBA; IEA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| snRNA exp | The directe | IEA; IEA | GO:0003723 | RNA binding |
| defense re | Reactions | IEA; IBA; IEA; IEA; IE | GO:0000981; GO:0 | DNA-binding transc |
| positive re | Any proces | IDA; IMP; IDA | GO:0001216; GO:0 | DNA-binding transc |
| single stra | The repair | IBA; IEA; IBA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |

| | | | | | |
|---|---|---|---|---|---|
| | regulation | Any proces | IEA; IEA; IEA | GO:0003677 | DNA binding |
| | regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II c |
| | protein tar | The proces | IBA; IEA; IEA | GO:0008320 | protein transmembr |
| | | | | GO:0005515; GO:0 | protein binding; me |
| xpressed | | | | | |
| | defense re | Reactions, | IEA; IBA; IEA; IBA | GO:0004864; GO:0 | protein phosphatas |
| | protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| tein | | | | GO:0016787 | hydrolase activity |
| | protein ph | The proces | IEA; IBA; IBA | GO:0004672; GO:0 | protein kinase activ |
| ining protein | | | | | |
| | cuticle hyd | The chemi | IEA; IEA; IEA; IEA | | |
| | | | | GO:0003677; GO:0 | DNA binding; metal |
| | regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | histone H3 | The modifi | IBA | GO:0005515; GO:0 | protein binding; his |
| | multicellul | The biolog | IEA; IBA; IBA; IBA; IE | GO:0046872 | metal ion binding |
| | maturation | Any proces | IBA; IBA; IBA | GO:0046872 | metal ion binding |
| | | | | GO:0016747 | acyltransferase acti |
| | gene silen | A process | IEA | | |
| | | | | GO:0008375 | acetylglucosaminylt |
| | chloroplas | A process | IEA; IEA | GO:0004765 | shikimate kinase ac |

| | | | | | |
|---|---|---|---|---|---|
| tein | | | | GO:0003824; GO:0 | catalytic activity; hy |
| | | | | | |
| | proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| | maturation | Any proces | IBA; IEA | | |
| ning protein | | | | | |
| | | | | | |
| protein | | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| | | | | GO:0005515 | protein binding |
| | | | | GO:0005515 | protein binding |
| | protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | regulation | Any proces | IBA; IEA; IEA | GO:0005096; GO:0 | GTPase activator ac |
| | RNA splicir | Splicing of | IEA; IEA; IEA; IBA; IB | GO:0003690; GO:0 | double-stranded DI |
| | protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | | | |
| | chromatin | The assem | IEA | GO:0003677; GO:0 | DNA binding; prote |
| | response t | Any proces | IEA; IEA; IEA; IBA; IE | GO:0003676; GO:0 | nucleic acid binding |
| | endocytosi | A vesicle-r | IBA; IBA | GO:0005509; GO:0 | calcium ion binding |
| | | | | | |
| | protein fol | The proces | IBA; IBA | GO:0005509; GO:0 | calcium ion binding |
| | protein ph | The proces | IEA | GO:0004672 | protein kinase activ |
| | protein ub | The proces | IEA; IEA | GO:0008270; GO:0 | zinc ion binding; tr |
| | lipid trans | The direct | IEA | GO:0008289 | lipid binding |
| | protein fol | The proces | IEA; IBA | GO:0051082; GO:0 | unfolded protein bi |
| | regulation | Any proces | IEA; IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| | | | | GO:0005515 | protein binding |
| | | | | | |
| | defense re | Reactions, | IEA; IBA; IBA; IBA | GO:0005515 | protein binding |
| | | | | GO:0005515 | protein binding |
| | | | | | |
| | anatomical | The proces | IEA; IEA | | |

| | | | | |
|---|---|---|---|---|
| nitrate trar | The direct | IEA; IEA; IEA; IBA | GO:0015112; GO:0 | nitrate transmembr |
| | | | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0008821 | crossover junction |
| thylakoid r | A process | IEA | | |
| cell differe | The proces | IEA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| intracellula | The direct | IEA; IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
| microtubul | A microtub | IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransferas |
| al domain containing protein | | | GO:0003676; GO:0 | nucleic acid binding |
| resolution | The cleava | IEA; IEA; IEA; IEA | GO:0005515 | protein binding |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| defense re | Reactions | IEA | | |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| nucleosom | The aggre | IEA; IBA; IBA; IBA; IB | GO:0003677; GO:0 | DNA binding; doubl |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA; IMP | GO:0003700; GO:0 | DNA-binding trans |
| response t | Any proces | IBA; IBA; IBA; IBA | GO:0005509; GO:0 | calcium ion binding |
| regulation | Any proces | IEA; IEA | GO:0003677 | DNA binding |
| endonucle | Endonucle | IBA | | |

| | | | | |
|---|---|---|---|---|
| defense re | Reactions, | IEA | GO:0005515; GO:0 | protein binding; chi |
| | | | GO:0008270; GO:0 | zinc ion binding; m |
| otein | | | GO:0005515 | protein binding |
| ke protein | | | GO:0004970; GO:0 | ionotropic glutamat |
| otein | | | GO:0005515 | protein binding |
| multicellul | The biolog | IEA; IEA; IEA; IEA; IEA | | |
| ribosomal | The direct | IBA; IBA; IBA; IBA; IE | GO:0015631; GO:0 | tubulin binding; kin |
| RNA splicir | Splicing of | IEA | GO:0003723; GO:0 | RNA binding; mRNA |
| GPI anchor | The chemi | IEA | GO:0017176 | phosphatidylinosito |
| protein ub | The proces | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |

|  |  |  |  |  |
|---|---|---|---|---|
| protein tar | The proces | IEA; IEA; IEA; IBA |  |  |
| maturation | Any proces | IBA |  |  |
| chromatin | The assem | IEA; IBA; IEA; IEA; IM | GO:0001227; GO:0 | DNA-binding trans |
| protein ph | The proces | IEA; IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| translation | The cellula | IEA | GO:0003735; GO:0 | structural constitue |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| pollen dev | The proces | IEA; IEA; IEA |  |  |
| obsolete o | OBSOLETE. | IEA | GO:0046872 | metal ion binding |
|  |  |  | GO:0005515 | protein binding |
| ı |  |  |  |  |
| ubiquitin-( | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| polyprenol | The chemi | IBA | GO:0002094; GO:0 | polyprenyltransfera |
| mRNA cata | The chemi | IEA | GO:0003729; GO:0 | mRNA binding; dem |
| DNA replic | The cellula | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein pro | Any protei | IEA | GO:0004175; GO:0 | endopeptidase activ |
| response t | Any proces | IEA; IDA | GO:0000166; GO:0 | nucleotide binding; |
| epigenetic | An epigene | IMP; IMP | GO:0001227; GO:0 | DNA-binding trans |
| DNA-temp | The initial | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| chloroplas | A process | IBA |  |  |
| ı containing protein |  |  | GO:0016740; GO:0 | transferase activity; |

| | | | | |
|---|---|---|---|---|
| protein de | The proces | IEA; IEA | GO:0008138; GO:0 | protein tyrosine/se |
| anatomical | The proces | IEA; IEA | | |
| | | | GO:0016787 | hydrolase activity |
| ceramide t | The direct | IBA; IEA | GO:0008289; GO:0 | lipid binding; lipid t |
| cell cycle; | The progre | IEA; IEA; IEA | | |
| mRNA spli | The joining | IEA | GO:0005515 | protein binding |
| RNA proce | Any proces | IEA | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0005085 | guanyl-nucleotide e |
| regulation | Any proces | IBA; IBA | GO:0008270 | zinc ion binding |
| anatomical | The proces | IEA; IEA; IEA | | |
| DNA-temp | The synthe | IEA; IEA; IEA; IEA; IE | GO:0003712 | transcription coregu |
| regulation | Any proces | IEA | GO:0019901 | protein kinase bind |
| proton mo | The transp | IEA | GO:0046933 | proton-transporting |
| systemic a | The salicyl | IEA | GO:0005504 | fatty acid binding |
| | | | GO:0003677 | DNA binding |
| maturation | Any proces | IBA | GO:0003723 | RNA binding |
| methylatio | The proces | IBA | GO:0008168; GO:0 | methyltransferase a |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| regulation | Any proces | IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
| otein | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| mRNA 3'-e | Any proces | IBA | GO:0000993 | RNA polymerase II c |

| | | | | |
|---|---|---|---|---|
| plastid tra | The synthe | IMP; IMP | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| positive re | Any proces | IEA | GO:0016301 | kinase activity |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| ein | | | GO:0008080; GO:0 | N-acetyltransferase |
| lipid metal | The chemi | IEA | GO:0004620 | phospholipase activ |
| response t | Any proces | IBA; IBA; IBA | GO:0005515 | protein binding |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |

| | | | | |
|---|---|---|---|---|
| tRNA meth | The posttr | IBA | GO:0005515 | protein binding |
| lipid meta | The chemi | IEA | | |
| regulation | Any proces | IEA | | |
| | | | GO:0005515 | protein binding |
| negative re | Any proces | IEA; IEA | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| telomere n | Any recom | IBA; IBA; IEA; IBA; IB | GO:0003677; GO:0 | DNA binding; dama |
| otein | | | GO:0005515 | protein binding |
| otein | | | GO:0005515 | protein binding |
| xyloglucan | The chemi | IBA; IEA; IEA | GO:0008107; GO:0 | galactoside 2-alph |
| microtubul | A process | IBA | GO:0008017 | microtubule bindin |
| protein ph | The proces | IEA; IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| otein | | | GO:0004601; GO:0 | peroxidase activity; |

|  |  |  |  |  |
|---|---|---|---|---|
| response t | Any proces | IEA; IEA; IEA | GO:0005515; GO:0 | protein binding; pro |
| DNA replic | The cellula | IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; single |
| phospholi | The transf | ISS | GO:0005548 | phospholipid trans |
| ning protein |  |  | GO:0003676; GO:0 | nucleic acid binding |
| protein po | The proces | IEA; IEA; IEA; IEA |  |  |
| embryo de | The proces | IBA; IBA; IEA; IBA | GO:0016301 | kinase activity |
| Ras protei | The series | IBA; IEA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| ubiquitin- | The chemi | IBA; IEA; IBA |  |  |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| ning protein |  |  | GO:0003676; GO:0 | nucleic acid binding |
| reductase (POR), J-like protein, Chloroplast-localized protein containing DUF33 |  |  |  |  |
| chromatin | The assem | IEA; IEA; IEA; IBA | GO:0004402; GO:0 | histone acetyltransf |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| DNA replic | The cellula | IEA; IBA; IEA; IEA | GO:0003682 | chromatin binding |

| | | | | |
|---|---|---|---|---|
| protein sta | Any proces | IBA | GO:0000774; GO:0 | adenyl-nucleotide e |
| cell differe<br>n | The proces | IEA | | |
| pollen dev | The proces | IEA; IEA; IEA | | |
| | | | GO:0005515 | protein binding |
| transcripti | The chrom | IBA; IBA; IBA | GO:0005515; GO:0 | protein binding; str |
| | | | GO:0003677; GO:0 | DNA binding; mRN |
| mitotic sis | The cell cy | IEA; IBA; IEA; IEA; IB | GO:0016407; GO:0 | acetyltransferase ac |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |
| plastid tra | The synthe | IEA | | |
| carbohydr | The chemi | IEA; IEA | GO:0004650; GO:0 | polygalacturonase |
| regulation | Any proces | IEA; IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0005524 | ATP binding |
| | | | GO:0005515 | protein binding |
| IA1 | | | GO:0008017 | microtubule bindin |
| nucleic aci | The nuclei | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| tein (Fragment) | | | GO:0046872 | metal ion binding |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| pollen gern | The physic | IEA; IEA; IEA | GO:0015267 | channel activity |
| protein ph | The proces | IBA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| tRNA wobk | The proces | IEA; IBA; IEA | GO:0000049 | tRNA binding |
| multicellul | The biolog | IBA; IBA; IBA | GO:0008017; GO:0 | microtubule bindin |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| glycerol et | The chemi | IEA; IEA | GO:0003756; GO:0 | protein disulfide isc |
| cytoskelet | A process | IEA; IEA; IEA | GO:0008017 | microtubule bindin |
| root hair e | The proces | IEA; IEA | GO:0003735; GO:0 | structural constitue |
| | | | GO:0004497; GO:0 | monooxygenase act |
| nbrane plant subgroup domain containing | | | GO:0051539 | 4 iron, 4 sulfur clus |
| negative re | Any proces | IBA; IEA; IBA; IEA; IB | GO:0000978; GO:0 | RNA polymerase II c |
| n | | | | |
| protein fol | A protein f | IBA | GO:0043621 | protein self-associa |
| DNA repair | The proces | IEA | GO:0070182 | DNA polymerase bi |
| intracellula | The directe | IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
| protein | | | GO:0016788 | hydrolase activity, a |
| protein gly | A protein r | IEA | GO:0016757 | glycosyltransferase |

| | | | | |
|---|---|---|---|---|
| vacuolar p | The aggre | IEA | | |
| transcripti | The synthe | IEA | GO:0001004; GO:0 | obsolete RNA polym |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |
| rRNA proc | Any proces | IBA | | |
| photosynth | A process, | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| tRNA expo | The direct | IEA; IEA; IEA; IEA; IE | GO:0000049; GO:0 | tRNA binding; RNA |
| DNA replic | The cellula | IEA; IEA | GO:0003688; GO:0 | DNA replication ori |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| DNA replic | The cellula | IEA; IBA; IBA; IDA; I | GO:0003677; GO:0 | DNA binding; DNA |
| | | | GO:0003676 | nucleic acid binding |
| autophago | The forma | IEA; IEA; IBA; IEA; IE | GO:0004518; GO:0 | nuclease activity; en |
| ent) | | | GO:0020037; GO:0 | heme binding; meta |
| nuclear-tr | The nonse | IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| tricarboxyl | A nearly u | IEA | | |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| endocytosi | A vesicle-r | IBA | GO:0005543; GO:0 | phospholipid bindi |
| DNA repai | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; D |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0003676 | nucleic acid binding |
| deadenylat | Cleavage o | IEA | GO:0005515 | protein binding |
| otein | | | GO:0005515 | protein binding |
| floral orga | The contro | IEA | | |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016597 | amino acid binding |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| endomem | A process | IBA | | |
| embryo de | The proces | IEA | | |
| regulation | Any proces | IEA | GO:0008270; GO:0 | zinc ion binding; se |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| positive re | Any proces | IBA | GO:0003713 | transcription coacti |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
|  |  |  | GO:0005509 | calcium ion binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| organelle c | A process | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| cell differe | The proces | IEA; IEA |  |  |
| ubiquitin- | The series | IBA | GO:0005515; GO:0 | protein binding; ub |
| transcripti | The synthe | IEA |  |  |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| mitotic sis | The cell cy | IBA; IEA; IEA; IBA; IEA; IBA |  |  |
| brane plant subgroup domain containing |  |  | GO:0051539 | 4 iron, 4 sulfur clus |
| response t | Any proces | IBA; IEA |  |  |
| chloroplas | The divisio | IBA; IBA |  |  |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; DNA- |
|  |  |  | GO:0005515 | protein binding |
| DNA replic | The cellula | IEA; IBA; IBA | GO:0003677; GO:0 | DNA binding; DNA |
| e |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| ubiquitin- | The chemi | IEA; IEA; IBA | GO:0044390; GO:0 | ubiquitin-like prote |
| mRNA sta | Prevention | IEA | GO:0005515; GO:0 | protein binding; tra |
| DNA repai | The proces | IEA; IBA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; cataly |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IEA | GO:0003700; GO:0 | DNA-binding transc |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| regulation | Any proces | IEA; IBA; IBA; IBA | | |
| | | | GO:0005515 | protein binding |
| photosynt | The synthe | IEA | | |
| | | | GO:0000774 | adenyl-nucleotide e |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| taining protein | | | | |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| floral meri | The proces | IEA; IBA | | |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransferas |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| autophago | The forma | IBA; IBA; IEA; IEA; IEA; IBA; IBA | | |
| | | | GO:0003723; GO:0 | RNA binding; mRNA |
| | | | GO:0003677 | DNA binding |
| | | | GO:0003924; GO:0 | GTPase activity; GT |
| | | | GO:0016787; GO:0 | hydrolase activity; h |
| defense re | Reactions, | IEA; IEA; IEA | | |
| ning protein | | | GO:0003676; GO:0 | nucleic acid binding |
| riboflavin | The chemi | IEA | GO:0004746 | riboflavin synthase |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA; IEA | GO:0043565 | sequence-specific |
| | | | GO:0000976; GO:0 | transcription cis-re |
| DNA repai | The proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; cataly |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| ons | | | GO:0046872 | metal ion binding |
| positive re | Any proces | IBA | GO:0003729; GO:0 | mRNA binding; tran |
| | | | GO:0016747; GO:0 | acyltransferase acti |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IBA; IEA; IEA; IEA; IB | GO:0005515; GO:0 | protein binding; zin |
| proteolysis | The hydrol | IEA; IBA | GO:0004197; GO:0 | cysteine-type endo |
| endomem | A process | IBA | | |
| ribosomal | A cellular | IBA | GO:0042802; GO:0 | identical protein bi |
| positive re | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| photomor | The contro | IEA | GO:0005515 | protein binding |
| RNA modif | The covale | IEA; IEA | GO:0003723; GO:0 | RNA binding; perox |
| proteasom | The chemi | IBA | GO:0005515; GO:0 | protein binding; pro |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| multicellul | The biolog | IBA; IBA; IBA; IBA; IB | GO:0004497; GO:0 | monooxygenase ac |
| lipid trans | The direct | IEA | GO:0008233; GO:0 | peptidase activity; l |
| protein ph | The proces | IBA; IBA; IBA | GO:0016208; GO:0 | AMP binding; protei |
| protein ph | The proces | IBA; IBA; IBA | GO:0016208; GO:0 | AMP binding; protei |
| telomere n | Any proces | IEA; IBA; IBA; IBA | GO:0003677; GO:0 | DNA binding; telom |
| protein ub | The proces | IEA | GO:0005515; GO:0 | protein binding; tra |
| protein tra | The direct | IEA; IEA; IEA | | |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| n | | | | |
| ribosomal | A cellular p | IEA | | |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; seque |
| cell wall or | A process | IEA | GO:0016740; GO:0 | transferase activity; |
| cell wall m | The series | IEA; IEA; IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; u |
| regulation | Any proces | IEA; IEA | | |
| ı | | | GO:0003723; GO:0 | RNA binding; mRNA |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ining protein | | | GO:0003677; GO:0 | DNA binding; minor |
| negative re | Any proces | IBA; IEA; IBA; IEA; IB | GO:0000978; GO:0 | RNA polymerase II c |
| cold acclim | Any proces | IEA; IBA; IEA | | |
| protein tra | The directe | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| rRNA proce | Any proces | IBA; IEA; IEA; IBA | GO:0003729; GO:0 | mRNA binding; prot |
| regulation | Any proces | IEA; IBA; IMP; IMP; II | GO:0000977; GO:0 | RNA polymerase II t |
| lipid metal | The chemi | IEA; IEA; IEA | GO:0016298; GO:0 | lipase activity; hydr |
| ubiquitin-c | The chemi | IBA; IEA; IBA | | |
| cell cycle; a | The progre | IEA; IBA; IBA; IEA; IB | GO:0061630 | ubiquitin protein lig |
| protein ub | The proces | IEA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| nuclear-tra | The nonse | IBA; IBA; IBA; IEA | GO:0004540; GO:0 | ribonuclease activit |
| | | | GO:0005515 | protein binding |
| autophagy | The cellula | IEA; IEA | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| flower dev | The proces | IEA; IEA | | |
| coenzyme | The chemi | IBA | GO:0003986; GO:0 | acetyl-CoA hydrola |
| otein | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| ethylene-a | The series | IEA; IEA; IEA; IEA | GO:0005384; GO:0 | manganese ion tran |
| nucleoside | The chemi | IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| proteasom | The aggre | IEA | | |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| response t | Any proces | IEA; IEA; IEA; IBA; IE | GO:0030246 | carbohydrate bindi |
| n | | | GO:0005515 | protein binding |
| Group II in | The splicin | IEA; IEA | GO:0003723; GO:0 | RNA binding; protei |
| protein ph | The proces | IEA; IBA; IEA | GO:0004672; GO:0 | protein kinase activ |
| endoplasm | The direct | IBA; IBA | GO:0031267 | small GTPase bindi |
| endoplasm | A process | IBA; IBA | | |
| response t | Any proces | IEA; IEA; IEA | GO:0005515 | protein binding |
| cleavage i | Any phosp | IEA; IEA; IEA; IEA; IB | GO:0004518; GO:0 | nuclease activity; er |
| lipid meta | The chemi | IEA; IEA; IEA | GO:0016298; GO:0 | lipase activity; hydr |
| | | | GO:0016788 | hydrolase activity, a |
| lipid trans | The direct | IEA | | |
| NLS-beari | The direct | IBA; IEA; IBA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005509 | calcium ion binding |
| | | | GO:0004721; GO:0 | phosphoprotein ph |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IEA | | |
| protein ub | The proces | IEA | GO:0016740 | transferase activity |
| se 1 domain containing protein | | | GO:0003723 | RNA binding |
| | | | GO:0008270 | zinc ion binding |
| response t | Any proces | IBA; IBA; IBA; IBA; IB | GO:0003676; GO:0 | nucleic acid bindin |
| cell popula | The multip | IBA; IEA; IBA; IBA; IB | GO:0003713 | transcription coacti |
| regulation | Any proces | IEA; IEA; IEA | GO:0004540; GO:1 | ribonuclease activit |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| pseudouri | The intram | IEA; IEA; IEA; IEA; IB | GO:0003723; GO:0 | RNA binding; pseu |
| chromatin | The assem | IEA; IBA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA | GO:0019901 | protein kinase bind |
| | | | GO:0016788 | hydrolase activity, a |
| n | | | GO:0003677; GO:0 | DNA binding; zinc i |
| DNA-temp | The initial | IEA; IBA; IEA; IBA; IE | GO:0003713; GO:0 | transcription coacti |

| | | | | |
|---|---|---|---|---|
| miRNA pro | A process | IEA | GO:0003723; GO:0 | RNA binding; doubl |
| regulation | Any proces | IBA; IBA; IEA; IEA; IE | GO:0008270; GO:0 | zinc ion binding; se |
| transcripti | A transcrip | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| mRNA exp | The direct | IBA; IBA | GO:0003729 | mRNA binding |
| | | | GO:0005515 | protein binding |
| chloroplas | The divisio | IEA | | |
| anatomical | The proces | IEA; IEA; IEA | | |
| double-str | The repair | IBA; IBA; IBA | GO:0003684; GO:0 | damaged DNA bind |
| chlorophyl | The chemi | IEA | GO:0016491; GO:0 | oxidoreductase acti |

|  |  |  |  |  |
|---|---|---|---|---|
| protein |  |  |  |  |
| transcripti | The synthe | IEA | GO:0003899 | DNA-directed 5'-3' |
| angiogene | Blood vess | IEA; IBA; IBA | GO:0016765; GO:0 | transferase activity, |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
|  |  |  | GO:0008375 | acetylglucosaminylt |
| anicle architecture, grain shape and grain |  |  | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ein, expressed |  |  |  |  |
| peptidyl-c | The oxidat | IEA; IEA | GO:0016702; GO:0 | oxidoreductase acti |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| signal tran | The cellula | IEA; IBA |  |  |
| ion transp | The directe | IEA; IEA; IBA; IBA; IE | GO:0005262; GO:0 | calcium channel act |
| regulation | Any proces | IEA; IEA; IEA | GO:0004540; GO:1 | ribonuclease activit |
| n |  |  | GO:0005515 | protein binding |
| mitochond | The aggre | IBA; IEA |  |  |
| protein me | The additi | IEA; IBA | GO:0008276; GO:0 | protein methyltrans |
|  |  |  | GO:0000166; GO:0 | nucleotide binding; |
| chloroplas | The reloca | IBA; IBA |  |  |
| regulation | Any proces | IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IC; IBA | GO:0000978; GO:0 | RNA polymerase II |
|  |  |  |  |  |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| negative re | Any proces | IBA; IBA; IBA; IBA |  |  |
| lipid metal | The chemi | IEA | GO:0008970; GO:0 | phospholipase A1 a |
|  |  |  |  |  |
| regulation | Any proces | IC; IBA | GO:0000978; GO:0 | RNA polymerase II |
| DNA replic | A signal tr | IBA; IBA; IBA; IBA | GO:0003677 | DNA binding |
|  |  |  |  |  |
| response t | Any proces | IEA |  |  |
| carbohydra | The chemi | IEA; IEA | GO:0004650; GO:0 | polygalacturonase |
|  |  |  | GO:0005515 | protein binding |
|  |  |  |  |  |
| DNA replic | A signal tr | IEA; IEA; IEA; IBA; IE | GO:0003676; GO:0 | nucleic acid binding |
|  |  |  |  |  |
| regulation | Any proces | IEA | GO:0019901 | protein kinase bind |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| defense re | Reactions | IEA |  |  |
| allergen Jun o 2) |  |  | GO:0005509; GO:0 | calcium ion binding |
|  |  |  |  |  |
| plant-type | A cellular | IBA; IEA; IEA; IEA; IE | GO:0016740; GO:0 | transferase activity; |
|  |  |  | GO:0005515 | protein binding |
|  |  |  |  |  |
| protein |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| response t | Any proces | IEA |  |  |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| abscisic ac | The series | IEA | | |
| chloroplas | The divisio | IEA | | |
| protein tar | The proces | IBA; IEA; IBA; IBA | GO:0005524; GO:0 | ATP binding; ATP h |
| metal ion t | The directe | IEA | GO:0046872 | metal ion binding |
| double-str | The repair | IBA; IEA; IBA | GO:0003682; GO:0 | chromatin binding; |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| cellulose m | A process | IEA | | |
| mitotic sis | The cell cy | IBA | | |
| DNA meth | The covale | IBA; IEA | GO:0003677; GO:0 | DNA binding; meth |
| response t | Any proces | IEA | | |
| n | | | GO:0003676 | nucleic acid binding |
| obsolete S | OBSOLETE. | IEA; IEA; IEA; IEA | GO:0004014; GO:0 | adenosylmethionin |
| | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| transmemb | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| protein ph | The proces | IEA; IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| pollen ger | The physic | IEA; IEA; IEA; IEA; IE | GO:0046872 | metal ion binding |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| autophago | The forma | IBA; IBA; IBA; IBA; IB | GO:0008641; GO:0 | ubiquitin-like modi |
| chromatin | A dynamic | IEA | | |
| proteasom | The aggre | IEA | | |
| se 1 domain containing protein | | | GO:0003723 | RNA binding |
| lipid meta | The chemi | IEA | GO:0016787 | hydrolase activity |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| ning protein | | | | |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| intra-Golg | The direct | IEA; IEA | | |
| | | | GO:0005509 | calcium ion binding |
| tein | | | GO:0016787 | hydrolase activity |
| polysaccha | The chemi | IEA; IEA; IEA | GO:0016161; GO:0 | beta-amylase activi |
| | | | GO:0003677 | DNA binding |
| ion transp | The direct | IEA; IBA; IEA | GO:0015095 | magnesium ion tra |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0005515 | protein binding |
| lomain containing protein | | | GO:0016407; GO:0 | acetyltransferase ac |
| in containing protein | | | | |

| | | | | |
|---|---|---|---|---|
| RNA modif | The covale | IEA; IEA | GO:0003723; GO:0 | RNA binding; protei |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| DNA dama | A signal tr | IBA; IBA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| chromatin | The assem | IEA; IEA | | |
| protein ub | The proces | IEA | GO:0004842 | ubiquitin-protein tr |
| receptor-n | An endocy | IBA; IBA; IBA | GO:0030276 | clathrin binding |
| proteolysis | The hydrol | IEA; IEA; IEA; IEA; IE | GO:0004197; GO:0 | cysteine-type endo |
| protein N- | A protein g | IBA; IBA; IEA; IEA; IE | GO:0047874 | dolichyldiphosphat |
| very long- | The chemi | IEA; IEA | GO:0005509; GO:0 | calcium ion binding |
| response t | Any proces | IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IEA; IEA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| DNA-temp | The synthe | IEA; IEA; IBA; IBA | GO:0001228; GO:0 | DNA-binding trans |
| response t | Any proces | IBA; IBA | | |
| se/reductase family protein, expressed | | | GO:0016491 | oxidoreductase acti |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| | | | GO:0016788 | hydrolase activity, a |
| gene silen | A small RN | IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein tra | The direct | IEA | | |
| regulation | Any proces | IEA; IDA; IEA; IDA; I | GO:0003677; GO:0 | DNA binding; DNA- |
| ubiquitin- | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| regulation | Any proces | IC; IEA | GO:0003700; GO:0 | DNA-binding trans |
| protein ub | The proces | IEA; IBA; IEA; IEA | GO:0008270; GO:0 | zinc ion binding; tr |
| protein tra | The direct | IEA; IEA; IBA; IEA; IE | GO:0042803 | protein homodimer |
| 3 | | | GO:0003677; GO:0 | DNA binding; metal |

| | | | | |
|---|---|---|---|---|
| tein | | | GO:0016787 | hydrolase activity |
| protein | | | GO:0016787 | hydrolase activity |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA– |
| | | | GO:0004497; GO:0 | monooxygenase act |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IBA | | |
| regulation | Any proces | IEA; IBA; IEA; IEA; IE | GO:0004721; GO:0 | phosphoprotein ph |
| ncRNA pro | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA; IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0016740; GO:0 | transferase activity; |
| carbohydra | The chemi | IEA | GO:0004553; GO:0 | hydrolase activity, h |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IBA; IEA; IEA | GO:0000978; GO:0 | RNA polymerase II c |
| | | | GO:0005515 | protein binding |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| negative re | Any proces | IEA; IEA | GO:0004860; GO:0 | protein kinase inhib |
| | | | GO:0003951; GO:0 | NAD+ kinase activit |

|  |  |  |  |  |
|---|---|---|---|---|
| reciprocal | The cell cy | IBA; IEA | GO:0030674 | protein-macromole |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| regulation | Any proces | IEA; IBA | GO:0003700; GO:0 | DNA-binding transc |
| response t | Any proces | IEA |  |  |
| ubiquitin-c | The chemi | IBA; IBA; IBA | GO:0061630 | ubiquitin protein lig |
| tein |  |  | GO:0016787 | hydrolase activity |
| metal ion t | The directe | IEA | GO:0046872 | metal ion binding |
| gene silenc | A process | IEA; IBA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| microtubul | A microtub | IEA | GO:0003777; GO:0 | microtubule motor |
|  |  |  | GO:0003677; GO:0 | DNA binding; zinc i |
| regulation | Any proces | IBA; IBA | GO:0008270 | zinc ion binding |
|  |  |  | GO:0004620; GO:0 | phospholipase activ |
| double-str | The error- | IBA; IEA; IEA; IBA; IB | GO:0004842; GO:0 | ubiquitin-protein tr |

| | | | | |
|---|---|---|---|---|
| transmem | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| transition | The direct | IEA; IEA; IEA; IEA; IE | GO:0005385; GO:0 | zinc ion transmem |
| , expressed | | | | |
| response t | Any proces | IEA | | |
| response t | Any proces | IEA; IEA | | |
| response t | Any proces | IEA; IEA; IEA | GO:0004867; GO:0 | serine-type endope |
| N-acetylgl | The chemi | IBA; IEA | GO:0004343; GO:0 | glucosamine 6-pho |
| rotein | | | GO:0016788 | hydrolase activity, |
| | | | GO:0051539 | 4 iron, 4 sulfur clus |
| RNA proce | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| sucrose m | The chemi | IEA; IEA; IDA; IEA; IE | GO:0005364; GO:0 | maltose:proton sy |
| | | | GO:0005515 | protein binding |
| organelle | A process | IEA; IEA | GO:0005515 | protein binding |
| intracellul | The direct | IEA; IBA; IBA; IEA; IEA; IEA; IEA; IEA | | |
| | | | GO:0005515 | protein binding |
| proteolysis | The hydrol | IEA; IEA | GO:0008233; GO:0 | peptidase activity; |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| containing protein | | | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| Golgi to en | The directe | IEA | | |
| xyloglucan | The chemi | IBA | GO:0016740; GO:0 | transferase activity; |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| meiotic DN | The cell cy | IEA | | |
| containing protein | | | | |
| peroxisom | A process | IEA; IBA | GO:0030674 | protein-macromole |
| protein ph | The proces | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| chloroplas | The divisio | IBA | | |
| regulation | Any proces | IEA | GO:0000976; GO:0 | transcription cis-re |
| ceramide r | The chemi | IEA | GO:0016811 | hydrolase activity, a |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| DNA repair | The proces | IEA; IEA; IBA; IEA; IE | GO:0003677; GO:0 | DNA binding; prote |
| metal ion t | The directe | IEA; IEA | GO:0046872 | metal ion binding |
| intracellula | The directe | IEA; IEA; IBA; IBA | GO:0005198; GO:0 | structural molecule |

|  |  |  |  |  |
|---|---|---|---|---|
| otein |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| proteolysis | The hydrol | IEA; IBA | GO:0004180; GO:0 | carboxypeptidase a |
| transmeml | The proces | IBA | GO:0022857 | transmembrane tra |
| regulation | Any proces | IC; IEA; IMP | GO:0003677; GO:0 | DNA binding; DNA- |
| purine nuc | The chemi | IEA; IEA; IEA; IEA | GO:0004044; GO:0 | amidophosphoribos |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II |
| phospholi | The proces | IBA | GO:0042392 | sphingosine-1-pho |
| vesicle-me | A cellular t | IBA |  |  |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| RNA proce | Any proces | IEA; IBA; IBA | GO:0005515 | protein binding |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |

| | | | | |
|---|---|---|---|---|
| xenobiotic | The proces | IBA; IEA; IEA; IEA; IE | GO:0005381; GO:0 | iron ion transmemb |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransferas |
| regulation | Any proces | IEA | GO:0000981; GO:0 | DNA-binding trans |
| microtubul | A microtub | IEA | GO:0003777; GO:0 | microtubule motor |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| protein im | The direct | IBA | GO:0061608 | nuclear import sign |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| establishm | The direct | IEA | GO:0005515; GO:0 | protein binding; me |
| | | | GO:0030246 | carbohydrate bindi |
| carbohydr | The chemi | IEA; IEA | GO:0004650 | polygalacturonase |

|  |  |  |  |  |
|---|---|---|---|---|
| polysaccha | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004190; GO:0 | aspartic-type endo |
| ubiquitin- | The series | IBA | GO:0005515; GO:0 | protein binding; ub |
| tein |  |  | GO:0016787 | hydrolase activity |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| poly(A)+ m | The direct | IEA |  |  |
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| nuclear-tr | The nonse | IEA; IBA | GO:0003676; GO:0 | nucleic acid binding |
|  |  |  | GO:0005515 | protein binding |
| LXXXVI) (P450-dependent fatty acid ome |  |  | GO:0004497; GO:0 | monooxygenase ac |
| response t | Any proces | IEA |  |  |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| RNA meth | Posttransc | IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; meth |
| DNA-temp | The synthe | IEA; IBA; IBA | GO:0003712; GO:0 | transcription coreg |
| protein ub | The proces | IEA | GO:0046872; GO:0 | metal ion binding; |
| meiotic mi | A system f | IBA; IBA; IEA; IBA; IB | GO:0000400; GO:0 | four-way junction |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| ribosomal | The aggre | IBA; IBA; IBA; IBA | GO:0003723; GO:0 | RNA binding; mRN |

| | | | | | |
|---|---|---|---|---|---|
| | lipid meta | The chemi | IEA; IEA; IEA | GO:0000036 | acyl carrier activity |
| | chloroplas | The divisio | IBA; IEA; IEA | | |
| ntaining protein | | | | | |
| | microtubul | A microtu | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| erved site domain containing protein | | | | | |
| | protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ng protein | | | | | |
| | RNA modif | The covale | IBA | GO:0005515 | protein binding |
| | methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| tein | | | | GO:0016787 | hydrolase activity |
| otein | | | | GO:0005515 | protein binding |
| | | | | GO:0005515 | protein binding |
| rotein | | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| | regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| | regulation | Any proces | IC | GO:0003700; GO:0 | DNA-binding trans |
| | mRNA spli | The joinin | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| | electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| | positive re | Any proces | IBA | GO:0003682; GO:0 | chromatin binding; |
| | DNA-temp | The synthe | IEA; IEA | GO:0003712 | transcription coreg |
| | DNA repai | The proces | IEA; IEA; IEA; IBA | | |
| | protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| | protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| | regulation | Any proces | IEA | | |
| | | | | GO:0005515 | protein binding |
| | chromatin | A dynamic | IBA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; chro |
| | protein-co | The disag | IEA; IEA | GO:0005515; GO:0 | protein binding; AT |
| | histone m | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| protein ph | The proces | IEA; IBA; IBA; IEA | GO:0004672; GO:0 | protein kinase activ |
| nbrane plant domain containing protein | | | GO:0051539 | 4 iron, 4 sulfur clus |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| mRNA poly | The enzym | IBA; IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| n | | | | |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| mitotic sis | The cell cy | IBA; IBA | GO:0008080; GO:0 | N-acetyltransferase |
| response t | Any proces | IEP; IEA | | |
| RNA-temp | A DNA bio | IEA; IBA; IEA; IBA | GO:0003964 | RNA-directed DNA |
| exocytosis | A process | IEA; IEA | GO:0005546 | phosphatidylinosito |
| nce | | | | |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| lipid metab | The chemi | IEA; IEA; IEA | GO:0005543; GO:0 | phospholipid bindi |
| response t | Any proces | IEA; IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| tein | | | GO:0003824; GO:0 | catalytic activity; hy |
| proteolysis | The hydrol | IEA; IBA | GO:0003677; GO:0 | DNA binding; aspar |
| ing protein | | | | |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| regulation | Any proces | IEA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| DNA-temp | The synthe | IEA; IEA | GO:0003712; GO:0 | transcription coreg |
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| transcripti | A transcrip | IEA; IEA | | |
| phosphore | A conserve | IEA; IEA; IEA; IEA; IE | GO:0000155; GO:0 | phosphorelay sens |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| defense re | Reactions | IEA; IEA; IEA; IEA; IE | GO:0003700; GO:0 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0005216; GO:0 | ion channel activity |
| | | | GO:0005515 | protein binding |
| tRNA-type | RNA proce | IBA; IEA; IEA | | |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| defense re | Reactions, | IEA | GO:0043531 | ADP binding |
| negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |
| phosphati | The chemi | IEA | GO:0005524; GO:0 | ATP binding; phosp |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| translation | The cellula | IEA | GO:0003735; GO:0 | structural constitue |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677 | DNA binding |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0016887 | ATP hydrolysis activ |
| lipid meta | The chemi | IEA | | |
| | | | GO:0005515 | protein binding |
| methylatio | The proces | IEA; IBA | GO:0008168; GO:0 | methyltransferase a |
| DNA-temp | The synthe | IEA; IEA; IBA; IEA | GO:0003899 | DNA-directed 5'-3' |
| xyloglucan | The chemi | IBA; IEA; IEA | GO:0008107; GO:0 | galactoside 2-alpha |

| | | | | |
|---|---|---|---|---|
| post-trans | The chrom | IBA; IBA; IBA; IEA; IE | GO:0003723; GO:0<br>GO:0005515 | RNA binding; nucle<br>protein binding |
| cellular am | The chemi | IEA; IDA; IEA | GO:0003824; GO:0<br>GO:0004497; GO:0 | catalytic activity; ca<br>monooxygenase ac |

| | | | | |
|---|---|---|---|---|
| protein ub | The proces | IBA; IEA | GO:0004518; GO:0 | nuclease activity; hy |
| amily protein | | | GO:0016787; GO:0 | hydrolase activity; N |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA; IBA | GO:0005515 | protein binding |
| ion transp | The directe | IEA; IEA | | |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| tRNA-type | RNA proce | IBA; IEA; IEA; IEA; IE | GO:0000213; GO:0 | tRNA-intron endon |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| recombina | A DNA rep | IBA | | |
| nuclear-tr | The nonse | IBA | | |
| regulation | Any proces | IEA; IEA | GO:0003700; GO:0 | DNA-binding trans |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| double-str | The error- | IEA; IEA | GO:0003677; GO:0 | DNA binding; ATP b |
| Group II in | The splicin | IEA; IEA; IEA | GO:0003723 | RNA binding |
| spliceosom | The aggre | IEA; IEA; IEA; IBA | | |
| DNA-temp | The synthe | IEA; IEA; IBA; IDA; IE | GO:0001228; GO:0 | DNA-binding trans |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| purine nuc | The directe | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |

|  |  |  |  |  |
|---|---|---|---|---|
| 15 |  |  | GO:0003677 | DNA binding |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| protein ins | The proces | IEA; IEA | GO:0008320; GO:0 | protein transmemb |
| oyl transferase (Benzoyl- CoA:benzyl alco |  |  | GO:0016747; GO:0 | acyltransferase acti |
| recombina | A DNA rep | IBA; IEA | GO:0043531 | ADP binding |
| endoplasm | The direct | IEA; IBA |  |  |
|  |  |  | GO:0016747; GO:0 | acyltransferase acti |
| regulation | Any proces | IEA; IEA | GO:0003712; GO:0 | transcription coreg |
| domain containing protein |  |  | GO:0004497; GO:0 | monooxygenase ac |
| activation | Any proces | IEA; IEA; IBA | GO:0008017; GO:0 | microtubule binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein tra | The direct | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0005515 | protein binding |
| transcripti | The synthe | IEA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| chloroplas | A process | IEA; IEA; IEA | GO:0003729; GO:0 | mRNA binding; pro |
| polysaccha | The chemi | IEA; IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ubiquitin- | The chemi | IBA; IEA | GO:0008270; GO:0 | zinc ion binding; u |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| plant-type | A cellular | IBA; IBA; IEA; IEA | | |
| | | | GO:0008270 | zinc ion binding |
| phosphore | A conserve | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IBA; IBA; IEA | GO:0005085; GO:0 | guanyl-nucleotide |
| taining protein | | | GO:0003723 | RNA binding |
| regulation | Any proces | IEA; IEA; IEA | GO:0005515 | protein binding |
| phosphatic | The chemi | IEA; IBA | GO:0016791; GO:0 | phosphatase activit |
| rotein | | | GO:0008375; GO:0 | acetylglucosaminylt |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| dephospho | The proces | IEA | GO:0003723; GO:0 | RNA binding; protei |
| microtubul | A process | IBA | GO:0008017 | microtubule bindin |
| maturation | Any proces | IEA | GO:0003723; GO:0 | RNA binding; struct |
| intracellul | The direct | IBA; IEA; IEA; IBA; IEA; IEA | GO:0005524; GO:0 | ATP binding; ATP h |
| response t | Any proces | IEA; IEA; IEA | GO:0004867; GO:0 | serine-type endope |
| transcripti | The synthe | IEA | | |
| regulation | Any proces | IMP; IEA; IMP; IEA; I | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| defense re | Reactions, | IEA; IEA; IBA; IBA; IE | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| aining protein | | | | |
| organic su | The chemi | IEA | GO:0004497; GO:0 | monooxygenase act |
| regulation | Any proces | IEA | GO:0008270 | zinc ion binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| protein ub | The proces | IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |

| | | | | |
|---|---|---|---|---|
| protein sta | Any proces | IBA | GO:0000774; GO:0 | adenyl-nucleotide e |
| | | | GO:0003676 | nucleic acid binding |
| rRNA proc | Any proces | IEA | | |
| opment, Pollen formatio | | | GO:0016740; GO:0 | transferase activity; |
| A5 (Fragment) | | | GO:0004497; GO:0 | monooxygenase act |
| | | | GO:0004721; GO:0 | phosphoprotein ph |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| MAPK casc | An intracel | IBA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| microtubul | Any cellula | IEA; IEA; IEA; IEA; IE | GO:0005515; GO:0 | protein binding; cal |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| rRNA 5'-er | Any proces | IBA; IEA; IEA; IEA | | |
| proteolysis | The hydrol | IEA | GO:0004197; GO:0 | cysteine-type endo |
| cellular am | The chemi | IBA | GO:0004617 | phosphoglycerate d |
| protein fol | The proces | IEA; IEA; IBA; IBA; IB | GO:0003755; GO:0 | peptidyl-prolyl cis- |
| ed germination and seedling developmen | | | GO:0003677; GO:0 | DNA binding; zinc i |
| dipeptide t | The direct | IEA; IEA | GO:0015333; GO:0 | peptide:proton sym |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; prote |
| carbohydra | The chemi | IEA; IBA; IEA; IBA | GO:0003824; GO:0 | catalytic activity; al |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| microtubul | A process | IBA | GO:0008017 | microtubule bindin |
| actin filam | A process | IEA; IEA | GO:0003779 | actin binding |
| SCF-depen | The chemi | IBA | GO:0005515 | protein binding |
| multidime | The proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proces | IEA | GO:0005515 | protein binding |
| ning protein | | | | |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| telomere n | Any proces | IBA; IEA; IBA | GO:0003676; GO:0 | nucleic acid bindin |
| RNA proce | Any proces | IEA; IEA | GO:0003723; GO:0 | RNA binding; RNA r |

| | | | | |
|---|---|---|---|---|
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding transc |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| defense re | Reactions, | IEA; IDA; IDA; IEP; IE | GO:0000166; GO:0 | nucleotide binding; |
| nucleobase | Any cellula | IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| pectin bios | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| fatty acid t | The directe | IBA | GO:0015245 | fatty acid transmem |
| protein ph | The proces | IEA; IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| DNA-temp | The initial | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| RNA proce | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| aining protein | | | | |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| proteolysis | The hydrol | IEA; IBA | GO:0004180; GO:0 | carboxypeptidase a |
| ein | | | GO:0046872 | metal ion binding |
| RNA proce | Any proces | IEA; IBA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| glutathione | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |

|  |  |  |  |  |
|---|---|---|---|---|
| RNA 3'-en | Any proces | IBA | GO:0016740; GO:0 | transferase activity; |
| protein |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| plant-type | A cellular | IBA; IBA; IEA; IEA |  |  |
| lipid meta | The chemi | IEA; IBA; IBA | GO:0016491; GO:0 | oxidoreductase acti |
| g protein |  |  |  |  |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| rRNA proc | Any proces | IEA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| otein |  |  | GO:0005515 | protein binding |
| activation | Any proces | IEA; IEA; IBA | GO:0008017; GO:0 | microtubule binding |
|  |  |  | GO:0004497; GO:0 | monooxygenase act |
| regulation | Any proces | IBA | GO:0005515; GO:0 | protein binding; zin |
| carbohydr | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| carbohydr | The chemi | IEA; IEA; IEA | GO:0004650; GO:0 | polygalacturonase a |
|  |  |  | GO:0005515 | protein binding |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| histone H4 | The modifi | IBA; IBA; IBA |  |  |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| carbohydr | The chemi | IEA; IBA; IEA; IBA | GO:0003824; GO:0 | catalytic activity; alc |
| defense re | Reactions | IEA |  |  |
| proteolysis | The hydrol | IEA; IBA; IBA | GO:0004222; GO:0 | metalloendopeptida |
| tRNA wob | The proces | IEA; IEA; IEA | GO:0000049; GO:0 | tRNA binding; sulfu |
| DNA replic | The proces | IBA | GO:0003682 | chromatin binding |

| | | | | |
|---|---|---|---|---|
| positive re | Any proces | IEA | | |
| protein de | The proces | IEA; IEA; IEA; IEA | GO:0004439; GO:0 | phosphatidylinosito |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| pectin bios | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| ed | | | | |
| peptidyl-ly | The methy | IBA; IEA | GO:0005515; GO:0 | protein binding; me |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| regulation | Any proces | IEA; IBA | GO:0004497; GO:0 | monooxygenase act |
| fatty acid b | The chemi | IEA | GO:0016746; GO:0 | acyltransferase acti |
| chloroplas | A process | IEA; IEA | GO:0008865; GO:0 | fructokinase activity |
| microtubul | A microtub | IEA | GO:0003777; GO:0 | microtubule motor |
| jasmonic a | The chemi | IBA; IBA | GO:0080030; GO:0 | methyl indole-3-ac |
| obsolete n | OBSOLETE. | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |

| | | | | |
|---|---|---|---|---|
| Regulation of tapetum degeneration and | | | GO:0016614; GO:0 | oxidoreductase acti |
| peptidyl-d | The modifi | IEA | GO:0046872; GO:0 | metal ion binding; i |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| microtubul | A process | IEA; IEA; IBA; IBA; IE | GO:0015631 | tubulin binding |
| | | | GO:0008146; GO:0 | sulfotransferase act |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| protein ub | The proces | IEA | | |
| | | | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| positive re | Any proces | IEA; IBA | GO:0003676; GO:0 | nucleic acid bindin |
| translation | The cellula | IBA | GO:0003723; GO:0 | RNA binding; mRN |
| endomem | A process | IBA | | |
| lipid meta | The chemi | IEA; IEA | GO:0016787 | hydrolase activity |
| tetrahydro | The chemi | IBA; IEA; IEA | GO:0003934; GO:0 | GTP cyclohydrolase |
| microtubul | Any cellula | IEA; IBA | GO:0045505; GO:0 | dynein intermediate |
| arbuscular | A form of | IEA | GO:0043565 | sequence-specific |

| | | | | |
|---|---|---|---|---|
| proteolysis | The hydrol | IEA | GO:0008233; GO:0 | peptidase activity; r |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| DNA-temp | The synthe | IEA; IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| negative re | Any proces | IBA; IEA; IBA; IEA; IB | GO:0000978; GO:0 | RNA polymerase II |
| regulation | Any proces | IEA; IBA; IEA | GO:0003676 | nucleic acid bindin |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| regulation | Any proces | IEA; IEA; IEA | | |
| otein | | | GO:0005515 | protein binding |
| | | | GO:0022857 | transmembrane tra |
| purine nuc | The direct | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |
| fatty acid | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| DNA-temp | The synthe | IEA; IEA | GO:0003700; GO:0 | DNA-binding trans |
| response t | Any proces | IBA | GO:0016491; GO:0 | oxidoreductase acti |

| | | | | |
|---|---|---|---|---|
| gene silen | A process | IEA; IEA; IEA | | |
| lipid meta | The chemi | IBA | GO:0008374; GO:0 | O-acyltransferase a |
| positive re | Any proces | IEA; IEA; IEA; IEA; IE | GO:0004518; GO:0 | nuclease activity; en |
| protein ub | The proces | IEA | GO:0016740; GO:0 | transferase activity; |
| isoprenoid | The chemi | IEA | GO:0004311; GO:0 | farnesyltranstransfe |
| | | | GO:0003723; GO:0 | RNA binding; mRNA |
| ubiquitin- | The chemi | IBA | GO:0008418 | protein-N-terminal |
| negative re | Any proces | IBA | | |
| response t | Any proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| carbohydr | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004553; GO:0 | hydrolase activity, h |
| | | | GO:0005085 | guanyl-nucleotide e |
| proteolysis | The hydrol | IEA; IEA | GO:0008233; GO:0 | peptidase activity; l |
| positive re | Any proces | IBA | | |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| defense re | Reactions, | IEA | | |
| one-carbo | The chemi | IBA | GO:0004089; GO:0 | carbonate dehydrat |
| biosynthet | The chemi | IEA | GO:0016709; GO:0 | oxidoreductase acti |
| DNA repair | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; DN |
| chromatin | A dynamic | IBA; IEA; IEA | GO:0003677; GO:0 | DNA binding; meth |
| nucleobas | Any cellula | IEA; IBA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| autophago | The forma | IBA; IBA; IEA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| DNA-temp | The synthe | IEA; IEA; IEA | | |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| Group II in | The splicin | IEA; IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; mRNA |
| domain containing protein | | | GO:0022857 | transmembrane tra |
| abscisic ac | The series | IEA; IMP; IBA; IMP | GO:0004721; GO:0 | phosphoprotein ph |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| fucose me | The chemi | IEA | GO:0016757 | glycosyltransferase |
| protein tar | The proces | IBA; IEA; IEA | GO:0008320 | protein transmemb |
| | | | GO:0016787; GO:0 | hydrolase activity; h |

|  |  |  |  |  |
|---|---|---|---|---|
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| protein ub | The proces | IEA | GO:0005515 | protein binding |
| recognitio | A cell reco | IEA | GO:0016301 | kinase activity |
| Group II in | The splicin | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; mRNA |
|  |  |  | GO:0005509; GO:0 | calcium ion binding |
|  |  |  | GO:0005515 | protein binding |
| carbohydra | The chemi | IBA; IBA; IBA; IDA; IE | GO:0015018; GO:0 | galactosylgalactosy |
| G protein- | The series | IBA | GO:0004930 | G protein-coupled |
| fatty acid | The chemi | IEA; IEA; IBA | GO:0000287; GO:0 | magnesium ion bin |
| rRNA proc | Any proces | IEA; IEA | GO:0070181 | small ribosomal su |
| glycerol m | The chemi | IEA; IEA; IBA | GO:0008081; GO:0 | phosphoric diester |
| DNA-temp | The synthe | IEA; IEA | GO:0003697; GO:0 | single-stranded DN |
| protein ph | The proces | IEA; IEA; IBA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| phosphory | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| response t | Any proces | IEA; IEA; IEA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| protein ph | The proces | IEA; IBA; IBA; IEA | GO:0004672; GO:0 | protein kinase activ |
| silicic acid | The directe | IMP; IEA | GO:0005215; GO:0 | transporter activity; |

|  |  |  |  |  |
|---|---|---|---|---|
| defense re | Reactions, | IEA; IEA; IEA | GO:0004864; GO:0 | protein phosphatas |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein ph | The proces | IEA; IBA; IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| signal tran | The cellula | IEA | GO:0005096 | GTPase activator ac |
| regulation | Any proces | IEA; IEA |  |  |
|  |  |  | GO:0003700; GO:0 | DNA-binding trans |
| protein tra | The direct | IEA | GO:0046872 | metal ion binding |
| carbohydr | The direct | IEA; IEA; IEA | GO:0005351; GO:0 | carbohydrate:proto |
| mRNA tran | The direct | IDA | GO:0003676; GO:0 | nucleic acid bindin |
| proteolysis | The hydrol | IEA; IEA; IBA; IMP | GO:0004190; GO:0 | aspartic-type endo |
| MAPK casc | An intracel | IBA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| mismatch | A system f | IEA | GO:0000166; GO:0 | nucleotide binding; |
| maturatio | Any proces | IBA; IEA | | |
| plant-type | A cellular | IBA; IBA; IEA; IEA | GO:0016301 | kinase activity |
| g protein | | | GO:0008270 | zinc ion binding |
| ubiquitin- | The chemi | IBA; IEA; IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| mRNA spli | The joinin | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| regulation | Any proces | IEA; IEA | GO:0003700 | DNA-binding trans |

| | | | | | |
|---|---|---|---|---|---|
| | cell fate sp | The proces | IEA; IEA; IBA; IBA; IB | GO:0046872 | metal ion binding |
| | proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| | chromatin | A dynamic | IEA; IBA; IEA; IEA | GO:0005515; GO:0 | protein binding; me |
| | lipid meta | The chemi | IEA; IEA; IEA; IEA; IB | GO:0005515; GO:0 | protein binding; ox |
| | cell redox | Any proces | IEA | | |
| | | | | GO:0005515 | protein binding |
| | translation | The cellula | IBA | GO:0003729; GO:0 | mRNA binding; stru |
| ning protein | | | | | |
| | protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | polysaccha | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| | translation | The cellula | IEA | GO:0003723; GO:0 | RNA binding; struct |
| | negative re | Any proces | IBA | GO:0004857 | enzyme inhibitor ac |
| | electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| | RNA modif | The covale | IBA | GO:0005515 | protein binding |
| | protein gly | A protein r | IEA; IEA; IEA; IEA; IE | GO:0008378; GO:0 | galactosyltransferas |
| | protein ub | The proces | IEA | GO:0061631 | ubiquitin conjugatin |
| | | | | GO:0004497; GO:0 | monooxygenase act |
| | DNA replic | The cellula | IEA; IEA; IEA; IBA | GO:0043138 | 3'-5' DNA helicase |
| | DNA repai | The proces | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| tein | | | | GO:0016787 | hydrolase activity |
| | gibberellin | The chemi | IBA | GO:0046872; GO:0 | metal ion binding; |
| | xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| | protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | response t | Any proces | IEA | | |
| | proteolysis | The hydrol | IEA; IEA; IEA | GO:0004175; GO:0 | endopeptidase activ |

| | | | | |
|---|---|---|---|---|
| fatty acid | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| response t | Any proces | IBA; IEA | GO:0038023 | signaling receptor |
| regulation | Any proces | IBA; IEA | GO:0008168; GO:0 | methyltransferase a |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| fucose me | The chemi | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IMP; IMP; IMP; IMP; | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |
| lipid meta | The chemi | IEA; IBA; IBA | GO:0016491; GO:0 | oxidoreductase acti |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| multicellul | The biolog | IEA; IEP; IMP; IMP; I | GO:0003824; GO:0 | catalytic activity; 4 |
| telomere n | Any recom | IBA; IBA; IEA; IBA; IB | GO:0003676; GO:0 | nucleic acid bindin |
| intracellul | The direct | IBA; IBA | GO:0005096 | GTPase activator ac |
| | | | GO:0003676 | nucleic acid bindin |
| chromatin | The assem | IEA; IEA; IEA; IEA; IE | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| regulation | Any proces | IBA; IBA | GO:0003677; GO:0 | DNA binding; seque |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |

| | | | | |
|---|---|---|---|---|
| triglyceride | The chemi | IEA; IEA | GO:0004144; GO:0 | diacylglycerol O-ac |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| | | | GO:0005515 | protein binding |
| | | | GO:0003723; GO:0 | RNA binding; metal |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0030247 | polysaccharide binc |
| | | | GO:0016301; GO:0 | kinase activity; carb |
| rotein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| cellular am | The chemi | IEA; IEA; IDA | GO:0003824; GO:0 | catalytic activity; ty |
| protein tar | The proces | IBA; IEA | | |
| response t | Any proces | IEA | | |
| phenylprop | The chemi | IEA | | |
| response t | Any proces | IBA; IEA | | |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| microtubul | Any cellula | IEA; IBA | GO:0003774; GO:0 | cytoskeletal motor |
| ion transp | The direct | IEA; IEA | GO:0005216 | ion channel activity |
| microtubul | A process | IEA; IBA; IBA; IBA; IB | GO:0005200; GO:0 | structural constitue |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| g protein | | | GO:0008270 | zinc ion binding |

| | | | | |
|---|---|---|---|---|
| proteolysis | The hydrol | IEA; IBA | GO:0008233; GO:0 | peptidase activity; c |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677 | DNA binding |
| endoplasm | The attach | IBA; IBA | | |
| )asparagine amidase A (EC 3.5.1.52) (PNGase A) (Glycopeptide N-glycosidase) (N- | | | | |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0003677 | DNA binding |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| transcripti | The extens | IEA | | |
| malate tra | The direct | IEA; IEA | | |
| ain containing protein | | | | |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| endoplasm | Any proces | IEA | GO:0005509 | calcium ion binding |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| intracellula | The direct | IEA; IEA; IBA; IBA | GO:0005198; GO:0 | structural molecule |
| protein ph | The proces | IEA; IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| flower dev | The proces | IEA; IEA | | |
| carbohydra | The chemi | IEA; IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| containing protein | | | | |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA; IBA; TAS; II | GO:0000977; GO:0 | RNA polymerase II t |
| nuclear-tr | The nonse | IEA; IBA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| tein | | | GO:0016787 | hydrolase activity |
| microtubul | The proces | IEA | GO:0005515; GO:0 | protein binding; mi |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| sor (EC 3.6.1.-) (AtNUDT18) | | | GO:0016787 | hydrolase activity |
| pectin bios | The chemi | IEA; IEA | GO:0016757; GO:0 | glycosyltransferase |
| translation | The cellula | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; mRNA |
| microtubul | A process | IBA | GO:0008017 | microtubule binding |
| ubiquitin-( | The chemi | IBA; IEA | GO:0061630 | ubiquitin protein lig |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0005524 | ATP binding |
| regulation | Any proces | IBA; IBA | GO:0003677; GO:0 | DNA binding; seque |
| | | | GO:0005515 | protein binding |
| protein | | | GO:0016787; GO:0 | hydrolase activity; h |

| | | | | |
|---|---|---|---|---|
| ion transp | The direct | IEA; IEA; IEA; IBA; IE | GO:0005242; GO:0 | inward rectifier pot |
| chloroplas | A process | IMP; IMP | GO:0003727; GO:0 | single-stranded RN |
| translation | The cellula | IEA | GO:0003735; GO:0 | structural constitue |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
| ion transp | The direct | IEA; IBA; IEA; IEA; IE | GO:0005381 | iron ion transmemb |
| fatty acid | A fatty aci | IEA | GO:0003824; GO:0 | catalytic activity; de |
| lipid trans | The direct | IEA | GO:0008289 | lipid binding |
| cell cycle; | The progre | IEA; IBA; IEA; IEA | | |
| ubiquitin– | The series | IBA; IBA; IBA | GO:0030544 | Hsp70 protein bind |
| | | | GO:0005515 | protein binding |
| tein | | | GO:0016491; GO:0 | oxidoreductase acti |

| | | | | |
|---|---|---|---|---|
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| lipid metab | The chemi | IEA; IEA; IEA | GO:0004620; GO:0 | phospholipase activ |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| GPI anchor | The chemi | IEA | GO:0017176 | phosphatidylinosito |
| negative re | Any proces | IEA | GO:0004867 | serine-type endope |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| positive re | Any proces | IEA | | |
| sferase | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| response t | Any proces | IEA | | |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| mRNA cata | The chemi | IEA | GO:0003729; GO:0 | mRNA binding; oxic |
| nuclear-tra | The nonse | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IC; IEA | GO:0005515 | protein binding |
| protein | | | GO:0005515 | protein binding |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| lipid trans | The direct | IEA | GO:0008289 | lipid binding |
| protein K4 | A protein c | IBA | GO:0004843; GO:0 | cysteine-type deubi |
| | | | GO:0016491 | oxidoreductase acti |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| floral orga | The contro | IEA; IEA; IEA; IEA; IE | GO:0005096; GO:0 | GTPase activator ac |
| carbohydra | The direct | IBA; IEA | GO:0042802; GO:0 | identical protein bir |
| | | | GO:0005515 | protein binding |
| | | | GO:0003677; GO:0 | DNA binding; mRNA |

| | | | | |
|---|---|---|---|---|
| myo-inosi | The chemi | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| NADP bios | The chemi | IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |
| response t | Any proces | IEA; IEA; IEA; IEA; IE | GO:0016706; GO:0 | 2-oxoglutarate-de |
| fatty acid | The chemi | IEA; IEA; IEA; IEA | | |
| indole glu | The chemi | IBA; IBA | GO:0004497; GO:0 | monooxygenase ac |
| fucose me | The chemi | IEA; IEA | GO:0046922 | peptide-O-fucosylt |
| endonucle | Endonucle | IBA; IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid bindin |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| | | | GO:0008115; GO:0 | sarcosine oxidase a |
| microtubul | A microtu | IEA | GO:0003777; GO:0 | microtubule motor |
| mannan ca | The chemi | IBA | GO:0004553; GO:0 | hydrolase activity, |
| rotein | | | GO:0004045; GO:0 | aminoacyl-tRNA hy |
| mRNA pro | Any proces | IEA; IEA; IEA; IEA; IB | GO:0003676; GO:0 | nucleic acid bindin |
| | | | GO:0005515 | protein binding |
| myo-inosi | The chemi | IEA; IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| ubiquitin- | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ex | The direct | IBA; IEA | GO:0005049 | nuclear export sign |
| cell redox | Any proces | IEA | | |
| | | | GO:0008252; GO:0 | nucleotidase activit |
| photosynt | The synthe | IEA | GO:0016992; GO:0 | lipoate synthase ac |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| lipid meta | The chemi | IEA | GO:0016787 | hydrolase activity |

|  |  |  |  |  |
|---|---|---|---|---|
| rRNA proc | Any proces | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; struct |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| protein ub | The proces | IEA |  |  |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
|  |  |  | GO:0005509 | calcium ion binding |
|  |  |  | GO:0005515 | protein binding |
| ion transp | The direct | IEA; IEA | GO:0004970; GO:0 | ionotropic glutamat |
| protein |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| peptidyl-t | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| nbrane plant domain containing protein |  |  | GO:0051539 | 4 iron, 4 sulfur clus |
| ence |  |  |  |  |
| fatty acid | The chemi | IEA; IEA |  |  |
|  |  |  | GO:0005515 | protein binding |
| DNA repai | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; DN |
| mRNA pol | The enzym | IEA; IEA; IEA; IEA; IE | GO:0003677; GO:0 | DNA binding; RNA |
| obsolete S | OBSOLETE. | IEA; IEA; IEA; IEA | GO:0004014; GO:0 | adenosylmethionine |
| sphingolip | The chemi | IBA; IBA; IBA; IEA | GO:0001727; GO:0 | lipid kinase activity; |
| carbohydr | The chemi | IEA; IEA; IBA; IBA; IB | GO:0004650; GO:0 | polygalacturonase |
| DNA-temp | The synthe | IBA; IEA | GO:0000976; GO:0 | transcription cis-re |
| lipid meta | The chemi | IEA; IEA; IEA | GO:0000036; GO:0 | acyl carrier activity; |
| protein fol | The proces | IEA; IBA | GO:0051082; GO:0 | unfolded protein bi |
| nbrane plant domain containing protein |  |  | GO:0051539 | 4 iron, 4 sulfur clus |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IBA; IEA; IBA; IEA; IB | GO:0000976; GO:0 | transcription cis-re |
| defense re | Reactions | IBA; IEA; IBA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| region domain containing protein | | | GO:0003824 | catalytic activity |
| cellular res | Any proces | IEA | | |
| DNA repai | The proces | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| carbohydra | The directe | IBA; IEA; IEA | GO:0008515; GO:0 | sucrose transmemb |
| protein fol | A protein f | IBA | GO:0043621 | protein self-associa |
| peptidyl-ly | The methy | IEA; IBA; IBA; IEA | GO:0008168; GO:0 | methyltransferase a |
| polysaccha | The chemi | IEA; IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| lipid meta | The chemi | IEA; IEA; IEA | GO:0008759; GO:0 | UDP-3-O-[3-hydro |
| lipid meta | The chemi | IEA | GO:0008970; GO:0 | phospholipase A1 a |
| | | | GO:0004497; GO:0 | monooxygenase ac |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA | GO:0005085 | guanyl-nucleotide e |
| RNA proce | Any proces | IEA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| sphingolip | The chemi | IBA; IBA; IBA; IEA | GO:0001727; GO:0 | lipid kinase activity; |
| DNA-temp | The synthe | IEA; IBA; IEA; IEA; IE | GO:0000976; GO:0 | transcription cis-re |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| trichome n | The proces | IEA; IEA; IEA | GO:0016747; GO:0 | acyltransferase acti |
| glycerol et | The chemi | IEA; IEA | GO:0015035 | protein-disulfide re |
| phenylpro | The chemi | IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| xyloglucan | The chemi | IBA; IEA; IEA | GO:0008107; GO:0 | galactoside 2-alpha |
| RNA modif | The covale | IBA; IEA | GO:0003729; GO:0 | mRNA binding; prot |
| RNA modif | The covale | IBA | GO:0003729; GO:0 | mRNA binding; prot |
| metal ion t | The direct | IEA; IEA | GO:0046872 | metal ion binding |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| transmem | The proces | IEA | GO:0015333; GO:0 | peptide:proton sym |
| metal ion t | The direct | IEA; IEA | GO:0046872 | metal ion binding |

| | | | | |
|---|---|---|---|---|
| organic an | The direct | IEA; IEA; IEA; IEA | GO:0022857 | transmembrane tra |
| | | | GO:0005515; GO:0 | protein binding; his |
| embryo sa | The proces | IEA; IEA; IEA; IEA; IEA | | |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| fatty acid | The chemi | IEA; IEA | GO:0000036; GO:0 | acyl carrier activity; |
| | | | GO:0035091 | phosphatidylinosito |
| protein ph | The proces | IEA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| tein | | | GO:0016787 | hydrolase activity |
| protein ph | The proces | IEA; IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| ion transm | A process | IEA; IEA | GO:0005227 | calcium activated c |
| ubiquitin- | The series | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid bindin |

| | | | | |
|---|---|---|---|---|
| | | | GO:0008270 | zinc ion binding |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| protein arg | The conjug | IEA | GO:0004057; GO:0 | arginyltransferase a |
| DNA-temp | The synthe | IEA; IEA; IBA; IEA; IE | GO:0003712 | transcription coregu |
| sucrose m | The chemi | IEA; IEA | GO:0003824; GO:0 | catalytic activity; su |
| ning protein | | | | |
| | | | GO:0015018 | galactosylgalactosy |
| tRNA proce | The proces | IEA; IEA | | |
| | | | GO:0008252; GO:0 | nucleotidase activit |
| protein tra | The directe | IEA; IEA | GO:0005484 | SNAP receptor activ |
| protein | | | GO:0016788 | hydrolase activity, a |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| phosphory | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| phosphatid | The chemi | IEA; IEA | GO:0016791; GO:0 | phosphatase activit |
| | | | GO:0005515 | protein binding |
| nucleic aci | The nuclei | IEA | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0004497; GO:0 | monooxygenase act |
| actin filam | A process | IBA; IBA | GO:0000146; GO:0 | microfilament moto |
| tein | | | GO:0005515 | protein binding |
| regulation | Any proces | IC; IEA | GO:0003700; GO:0 | DNA-binding transc |
| mRNA spli | The joining | IEA | GO:0003723; GO:0 | RNA binding; pre-m |
| polysaccha | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| lipid trans | The directe | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| nuclear po | A process | IBA | GO:0017056 | structural constitue |
| regulation | Any proces | IEA; IEA | GO:0005085 | guanyl-nucleotide e |
| multicellul | The biolog | IEA; IBA; IBA; IBA; IE | GO:0046872 | metal ion binding |

| | | | | |
|---|---|---|---|---|
| maintenan | Any proces | IEA; IBA; IEA; IEA; IE | GO:0003690; GO:0 | double-stranded DI |
| ning protein | | | | |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| positive re | Any proces | IGI; IEA | GO:0000976; GO:0 | transcription cis-re |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| RNA phosp | The chemi | IEA | GO:0000175; GO:0 | 3'-5'-exoribonucle |
| protein ins | The proces | IBA; IBA | GO:0032977 | membrane insertas |
| chloroplas | The aggreg | IEA | | |
| malate trar | The directe | IEA; IEA | | |
| regulation | Any proces | IBA; IEA | GO:0005515; GO:0 | protein binding; prc |
| maturatior | Any proces | IBA | GO:0000166; GO:0 | nucleotide binding; |
| iron-sulfur | The incorp | IEA; IEA | GO:0009055; GO:0 | electron transfer ac |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II c |
| mRNA spli | The joining | IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| nit domain containing protein | | | GO:0019148 | D-cysteine desulfhy |
| signal tran | The cellula | IEA; IEA | GO:0005096 | GTPase activator ac |
| ecursor | | | GO:0016740; GO:0 | transferase activity; |

| | | | | |
|---|---|---|---|---|
| DNA-temp | The compl | IEA; IEA; IEA; IEA; IE | GO:0003690 | double-stranded D |
| rminal domain containing protein | | | | |
| spindle as | The aggre | IEA | | |
| otein | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IDA; IMP; IMP | GO:0003677; GO:0 | DNA binding; seque |
| cation tran | The direct | IEA; IBA; IEA | GO:0015299 | solute:proton antip |
| response t | Any proces | IEA; IBA; IBA; IBA; IB | GO:0005509; GO:0 | calcium ion binding |
| regulation | Any proces | IBA; IEA | GO:0000978; GO:0 | RNA polymerase II |
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0004843; GO:0 | cysteine-type deub |
| protein ub | The proces | IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| glutathione | The chemi | IBA; IDA; IDA; IEA | GO:0004364; GO:0 | glutathione transfe |
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded D |
| autophago | The forma | IBA; IBA; IBA; IBA; IB | GO:0005515; GO:0 | protein binding; ub |
| fatty acid | The chemi | IEA; IEA; IEA; IEA | GO:0009922; GO:0 | fatty acid elongase |
| | | | GO:0005515 | protein binding |
| | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| macroauto | The major | IBA | | |
| cell differe | The proces | IBA | GO:0003677; GO:0 | DNA binding; seque |
| tricarboxyl | A nearly u | IEA | | |
| ubiquitin- | The chemi | IBA; IBA; IBA; IEA | GO:0061630 | ubiquitin protein lig |
| cell wall m | The series | IEA; IEA | GO:0030599; GO:0 | pectinesterase activ |
| proteolysis | The hydrol | IEA; IBA | GO:0008233; GO:0 | peptidase activity; |

| | | | | |
|---|---|---|---|---|
| | | | GO:0005509; GO:0 | calcium ion binding |
| ubiquitin- | The chemi | IEA; IEA; IBA | GO:0005515 | protein binding |
| positive re | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| regulation | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| transmemb | The proces | IEA | GO:0015250; GO:0 | water channel activi |
| glutathion | The chemi | IBA; IEA | GO:0004364; GO:0 | glutathione transfe |
| translation | The succes | IEA | GO:0003746 | translation elongati |
| | | | GO:0005515 | protein binding |
| nucleoside | The chemi | IEA | GO:0003824 | catalytic activity |
| rotein | | | GO:0016788 | hydrolase activity, a |
| | | | GO:0004497; GO:0 | monooxygenase act |
| carbohydra | The chemi | IEA; IEA; IEA; IEA; IE | GO:0004553; GO:0 | hydrolase activity, h |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| DNA repair | The proces | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| RNA modif | The covale | IBA; IEA | GO:0005515 | protein binding |
| DNA catab | The cellula | IEA; IEA; IEA | GO:0000014; GO:0 | single-stranded DN |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| negative re | Any proces | IBA; IEA; IBA; IEA; IB | GO:0000978; GO:0 | RNA polymerase II c |
| glutathion | The chemi | IEA; IEA | GO:0004364; GO:0 | glutathione transfe |
| protein de | The remov | IEA; IEA; IBA | GO:0004843; GO:0 | cysteine-type deubi |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |

| | | | | |
|---|---|---|---|---|
| protein ub | The proces | IEA; IBA | | |
| riboflavin | The chemi | IEA; IEA; IEA | GO:0003824; GO:0 | catalytic activity; zi |
| chloroplas | The reloca | IBA; IBA | | |
| meiotic spi | A process | IEA; IBA; IBA; IEA | | |
| mRNA 5'-s | Recognitio | IBA; IEA; IEA | GO:0005515 | protein binding |
| chloroplas | The proces | IBA | GO:0046906 | tetrapyrrole bindin |
| steroid bio | The chemi | IEA | GO:0003854; GO:0 | 3-beta-hydroxy-de |
| otein | | | GO:0005515 | protein binding |
| lipid meta | The chemi | IEA; IEA; IEA | GO:0000036; GO:0 | acyl carrier activity; |
| protein ph | The proces | IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| protein ub | The proces | IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IBA | GO:0004672; GO:0 | protein kinase activ |
| gene silen | A process | IEA; IEA; IEA | | |
| ning protein | | | GO:0003676; GO:0 | nucleic acid bindin |
| proteolysis | The hydrol | IEA; IBA | GO:0004197; GO:0 | cysteine-type endo |
| RNA meta | The cellula | IEA; IEA; IEA; IBA | GO:0003676; GO:0 | nucleic acid bindin |
| g protein | | | | |

| | | | | |
|---|---|---|---|---|
| auxin bios | The chemi | IMP; IMP; IMP | GO:0004499; GO:0 | N,N-dimethylanilin |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| double-str | The repair | IBA; IEA; IBA; IBA; IE | GO:0003684; GO:0 | damaged DNA bind |
| protein ub | The proces | IEA | GO:0005515; GO:0 | protein binding; tra |
| Group II in | The splicin | IMP; IMP; IMP | GO:0004519; GO:0 | endonuclease activi |
| n | | | GO:0005515 | protein binding |
| otein | | | | |
| | | | GO:0003677 | DNA binding |
| protein ph | The proces | IEA; IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| glycerol m | The chemi | IEA; IEA | GO:0008081; GO:0 | phosphoric diester |
| tRNA modi | The covale | IEA; IEA; IBA; IBA; IE | GO:0005515; GO:0 | protein binding; me |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| regulation | Any proces | IEA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| otif, Positive regulation of osmotic and sal | | | GO:0005509 | calcium ion binding |
| phosphatic | The chemi | IBA | GO:0000285; GO:0 | 1-phosphatidylinos |

|  |  |  |  |  |
|---|---|---|---|---|
| ethylene-a | The series | IEA; IDA; IDA; IDA | GO:0003677; GO:0 | DNA binding; DNA- |
| biosynthet | The chemi | IEA | GO:0016844 | strictosidine syntha |
| positive re | Any proces | IBA | GO:0000977; GO:0 | RNA polymerase II t |
| peptidyl-ly | The methy | IBA; IEA | GO:0005515; GO:0 | protein binding; me |
|  |  |  | GO:0003723 | RNA binding |
| DNA-temp | A DNA rep | IEA; IBA; IEA; IEA | GO:0003677; GO:0 | DNA binding; cataly |
| in |  |  |  |  |
| binding / nucleic acid binding / nucleotid |  |  | GO:0003676; GO:0 | nucleic acid binding |
| chloroplas | The divisio | IBA | GO:0005515 | protein binding |
| DNA replic | The cellula | IEA; IBA |  |  |
| ion transp | The direct | IEA; IEA | GO:0004970; GO:0 | ionotropic glutamat |
| protein de | The remov | IBA; IBA | GO:0008233; GO:0 | peptidase activity; c |
| histone de | The modifi | IEA |  |  |
| vesicle-me | A cellular t | IEA; IEA | GO:0005096; GO:0 | GTPase activator ac |
| regulation | Any proces | IEA; IEA | GO:0001530; GO:0 | lipopolysaccharide |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| polyphosp | The chemi | IEA; IBA; IBA; IEA; IE | GO:0000822; GO:0 | inositol hexakispho |
| purine nuc | The direct | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |
| obsolete o | OBSOLETE. | IEA | GO:0016491; GO:0 | oxidoreductase acti |
| carbohydr | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| GPI anchor | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| protein fol | The proces | IBA; IBA; IBA | GO:0008270; GO:0 | zinc ion binding; m |
| protein ph | The proces | IBA; IBA; IEA; IBA; IE | GO:0004674; GO:0 | protein serine/thre |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| translation | The proces | IEA | GO:0003729; GO:0 | mRNA binding; tran |
| regulation | Any proces | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| nuclear-tr | The nonse | IBA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| phospholi | The direct | IEA; IEA | GO:0008526 | phosphatidylinosito |
| regulation | Any proces | IBA; IEA | GO:0000978; GO:0 | RNA polymerase II |
| otein | | | GO:0005515 | protein binding |
| tRNA modi | The covale | IEA; IEA; IEA; IEA; IE | GO:0005515 | protein binding |
| abscisic ac | The series | IBA; IBA; IBA; IBA | | |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransferas |
| cellular res | Any proces | IEA | | |
| autophagy | The cellula | IBA | GO:0005515 | protein binding |
| transmem | The proces | IBA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| tRNA 3'-te | Post-trans | IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; transf |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransferas |
| | | | GO:0016787 | hydrolase activity |
| meristem | Any proces | IEA; IEA | GO:0005515 | protein binding |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| ragment) | | | GO:0005515 | protein binding |
| ning protein | | | GO:0003676; GO:0 | nucleic acid bindin |
| carbohydr | The chemi | IEA; IEA; IBA | GO:0004553; GO:0 | hydrolase activity, |
| defense re | Reactions | IBA | GO:0005515 | protein binding |
| microtubul | A microtu | IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEP; IEA; IEP; IE | GO:0005515; GO:0 | protein binding; pro |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| protein ub | The proces | IEA | | |
| containing protein | | | GO:0016740; GO:0 | transferase activity; |
| DNA-temp | The compl | IEA; IEA; IEA; IEA; IE | GO:0003690; GO:1 | double-stranded D |
| regulation | Any proces | IEA | | |
| | | | GO:0005515 | protein binding |
| meiotic ch | Compactio | IBA; IEA; IEA; IBA; IB | GO:0003682 | chromatin binding |
| | | | GO:0005515 | protein binding |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| intracellul | The direct | IBA; IEA; IBA; IEA; IB | GO:0005198; GO:0 | structural molecule |
| guard cell | The proces | IEA; IEA | | |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRN |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| lipid meta | The chemi | IEA; IBA; IBA | GO:0016491; GO:0 | oxidoreductase acti |
| biosynthet | The chemi | IEA | GO:0016844 | strictosidine syntha |
| regulation | Any proces | IEA; IEA; IEA | GO:0004864 | protein phosphatas |
| ion transm | A process | IEA; IEA | GO:0005227 | calcium activated c |

| | | | | |
|---|---|---|---|---|
| g protein | | | GO:0003729; GO:0 | mRNA binding; prot |
| regulation | Any proces | IEA | | |
| ion transp | The direct | IEA; IEA; IEA; IEA | GO:0015288; GO:0 | porin activity; volta |
| phosphatic | The chemi | IBA; IBA | | |
| rRNA modi | The covale | IEA; IEA; IEA; IEA; IE | GO:0000179; GO:0 | rRNA (adenine-N6,N |
| otein | | | GO:0003729; GO:0 | mRNA binding; prot |
| auxin catal | The chemi | IBA; IBA | GO:0016491; GO:0 | oxidoreductase acti |
| fatty acid r | The chemi | IBA | GO:0016491 | oxidoreductase acti |
| amino acid | The proces | IBA; IEA; IEA; IEA | GO:0015171; GO:0 | amino acid transme |
| carbohydra | The chemi | IEA; IEA | GO:0003824; GO:0 | catalytic activity; po |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
| | | | GO:0005515 | protein binding |
| tein | | | GO:0016298; GO:0 | lipase activity; hydr |
| response t | Any proces | IBA; IEA | GO:0038023 | signaling receptor a |
| transmem | The proces | IEA; IEA | | |
| protein po | Addition o | IBA; IBA; IEA; IBA; IE | GO:0003676; GO:0 | nucleic acid bindin |
| heme bios | The chemi | IEA; IEA; IEA; IEA; IB | GO:0004322; GO:0 | ferroxidase activity; |
| ubiquitin- | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| ragment) | | | GO:0005515 | protein binding |
| e putative domain containing protein | | | GO:0016787 | hydrolase activity |
| ntaining protein | | | | |
| response t | Any proces | IEA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| | | | GO:0004175; GO:0 | endopeptidase acti |
| regulation | Any proces | IBA; IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid bindin |
| fucose me | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| chromatin | A dynamic | IEA; IEA; IEA; IBA | GO:0003677; GO:0 | DNA binding; ATP b |
| domain containing protein | | | GO:0004497; GO:0 | monooxygenase ac |
| RNA proce | Any proces | IEA; IEA | GO:0003723; GO:0 | RNA binding; protei |
| translation | The cellula | IBA; IBA | GO:0003924; GO:0 | GTPase activity; GT |
| | | | GO:0003993; GO:0 | acid phosphatase a |

| | | | | |
|---|---|---|---|---|
| double-str | The error- | IEA; IEA; IEA; IEA; IE | GO:0005515; GO:0 | protein binding; his |
| | | | GO:0030246 | carbohydrate bindi |
| carbohydra | The directe | IEA; IEA; IBA | GO:0005215; GO:0 | transporter activity; |
| microtubul | A microtub | IEA; IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| SNARE con | The aggreg | IBA | GO:0000149 | SNARE binding |
| protein po | Addition o | IBA; IBA; IEA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein po | Addition o | IBA; IEA; IBA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| chloroplas | The reloca | IBA; IBA | | |
| RNA modif | The covale | IEA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; protei |
| ion transp | The directe | IEA; IEA | GO:0004970; GO:0 | ionotropic glutamat |
| regulation | Any proces | IBA | GO:0003677; GO:0 | DNA binding; metal |
| transmeml | The proces | IEA | GO:0022857 | transmembrane trai |
| g protein | | | GO:0005515; GO:0 | protein binding; ub |
| double-str | The error- | IBA; IEA; IBA; IEA; IE | GO:0004842; GO:0 | ubiquitin-protein tr |
| | | | GO:0005515 | protein binding |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zir |
| ion transp | The directe | IEA; IEA; IBA; IBA; IE | GO:0005262; GO:0 | calcium channel act |
| plasmodes | The mover | IBA; IBA | | |
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0004175; GO:0 | endopeptidase activ |

| | | | | |
|---|---|---|---|---|
| microtubul | Any cellula | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| ntaining protein | | | | |
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| g protein | | | GO:0005515; GO:0 | protein binding; ub |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| transcripti | The synthe | IEA; IEA; IBA; IBA | GO:0001091; GO:0 | RNA polymerase II |
| protein sta | Any proces | IBA | GO:0000774; GO:0 | adenyl-nucleotide |
| regulation | Any proces | IBA; IBA; IEA; IEA; I | GO:0016538; GO:0 | cyclin-dependent p |
| inositol ph | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; ph |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| protein tar | The proces | IBA; IBA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| signal pep | The protec | IBA | GO:0005515; GO:0 | protein binding; pe |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0005515 | protein binding |
| nding protein | | | GO:0003723 | RNA binding |
| lipid meta | The chemi | IEA | GO:0016787 | hydrolase activity |
| regulation | Any proces | IBA | GO:0035091; GO:0 | phosphatidylinosito |
| | | | GO:0005515 | protein binding |
| double-str | The error- | IBA; IBA; IBA; IBA; I | GO:0000166; GO:0 | nucleotide binding; |
| tRNA wob | The proces | IEA; IBA; IEA; IEA; IE | GO:0000049; GO:0 | tRNA binding; prote |
| | | | GO:0043169 | cation binding |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA; IEA; IEA; IEA | GO:0004869; GO:0 | cysteine-type endo |
| translation | The proces | IEA; IEA; IEA | GO:0003743; GO:0 | translation initiatio |
| protein fol | The proces | IEA; IBA; IBA | GO:0004176; GO:0 | ATP-dependent pe |
| proteasom | The aggre | IEA | | |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid bindin |

| | | | | |
|---|---|---|---|---|
| fucose met | The chemi | IEA | GO:0016757 | glycosyltransferase |
| chromatin | The assem | IEA; IMP | GO:0003677; GO:0 | DNA binding; prote |
| interstranc | Removal o | IBA; IEA | GO:0045145 | single-stranded DN |
| proteolysis | The hydrol | IEA; IBA | GO:0004176; GO:0 | ATP-dependent pep |
| protein ph | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| mily protein | | | GO:0000293; GO:0 | ferric-chelate reduc |
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0008233; GO:0 | peptidase activity; c |
| n | | | GO:0047617 | acyl-CoA hydrolase |
| regulation | Any proces | IBA; IEA | GO:0001228; GO:0 | DNA-binding transc |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| histone de | The modifi | IEA; IEA | GO:0004843; GO:0 | cysteine-type deubi |
| transmemb | The proces | IEA | | |
| signal tran | The cellula | IEA | | |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| SNARE con | The aggre | IBA | GO:0000149 | SNARE binding |
| peptidyl-th | The remov | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| DNA repai | The proces | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| autophago | The forma | IBA; IBA; IBA; IBA; IB | GO:0005515; GO:0 | protein binding; ph |
| maturation | Any proces | IBA; IEA | | |
| regulation | Any proces | IBA | GO:0000049; GO:0 | tRNA binding; doub |
| n | | | GO:0008168 | methyltransferase a |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| protein fol | The proces | IEA; IBA; IBA | GO:0044183 | protein folding cha |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| pmen | | | GO:0004386; GO:0 | helicase activity; pr |
| systemic a | The salicyl | IEA | GO:0005504 | fatty acid binding |
| double-str | The repair | IBA; IBA; IBA; IEA | GO:0003684; GO:0 | damaged DNA bind |
| defense re | Reactions, | IEA; IEA; IBA; IMP | GO:0005515 | protein binding |
| carbohydra | The proces | IEA; IEA | GO:0015144; GO:0 | carbohydrate trans |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0000981; GO:0 | DNA-binding trans |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| FAD biosy | The chemi | IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| malate tra | The direct | IEA; IEA | | |
| cell redox | Any proces | IEA | GO:0016491; GO:0 | oxidoreductase acti |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| sphingolip | The chemi | IBA; IBA; IBA; IEA | GO:0001727; GO:0 | lipid kinase activity; |
| response t | Any proces | IEA | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| guard cell | Generation | IEA; IEA; IEA; IEA; IE | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| | | | GO:0016787 | hydrolase activity |
| response t | Any proces | IEA; IEA; IEA; IEA | GO:0005515 | protein binding |
| response t | Any proces | IEA | GO:0004364 | glutathione transfe |
| regulation | Any proces | IEA; IEA; IEA; IEA; IE | GO:0005524; GO:0 | ATP binding; acid-a |
| purine nuc | The chemi | IBA | GO:0004044 | amidophosphoribos |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded D |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| | | | GO:0003824; GO:0 | catalytic activity; ph |
| vesicle-me | A cellular t | IBA | | |
| carbohydr | The chemi | IEA; IEA; IEA; IEA | GO:0004573; GO:0 | Glc3Man9GlcNAc2 |
| anatomical | The proces | IEA; IEA; IEA | | |
| | | | GO:0008080 | N-acetyltransferase |

| | | | | |
|---|---|---|---|---|
| auxin bios | The chemi | IMP | GO:0003824; GO:0 | catalytic activity; ca |
| phosphory | The proces | IEA | GO:0016301 | kinase activity |
| obsolete o | OBSOLETE. | IEA | GO:0046872 | metal ion binding |
| oligopepti | The direct | IEA; IBA | GO:0015333; GO:0 | peptide:proton sym |
| | | | GO:0003723 | RNA binding |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| n | | | | |
| translation | The cellula | IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proces | IBA; IBA; IEA; IBA; IB | GO:0043621; GO:0 | protein self-associa |

| | | | | |
|---|---|---|---|---|
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| | | | GO:0003677 | DNA binding |
| n | | | GO:0005515 | protein binding |
| amino acid | The proces | IBA; IEA; IEA; IEA | GO:0015171; GO:0 | amino acid transme |
| mRNA exp | The direct | IBA; IBA; IEA; IBA | GO:0017056 | structural constitue |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| intracellula | The direct | IEA; IEA; IEA; IBA; IEA; IEA | | |
| iron-sulfu | The incorp | IEA; IEA; IEA; IEA; IB | GO:0001671; GO:0 | ATPase activator ac |
| | | | GO:0005515 | protein binding |
| ntaining protein | | | | |
| regulation | Any proces | IEA | GO:0005085 | guanyl-nucleotide e |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008308 | voltage-gated anio |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008324 | cation transmembra |
| DNA meta | Any cellula | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| tRNA 3'-te | Post-trans | IEA; IEA | GO:0003723; GO:0 | RNA binding; transf |

| | | | | |
|---|---|---|---|---|
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| photosynt | A process, | IBA; IEA | GO:0005509; GO:0 | calcium ion binding |
| endocytosi | A vesicle-r | IEA; IBA; IEA; IEA; IB | GO:0000149; GO:0 | SNARE binding; pho |
| | | | GO:0043169 | cation binding |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| transmem | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| g protein | | | GO:0008270 | zinc ion binding |
| guanosine | The chemi | IEA; IEA | GO:0005525; GO:0 | GTP binding; GTP d |
| hydrotropi | Growth or | IEA | | |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |

| | | | | |
|---|---|---|---|---|
| flower dev | The proces | IEA; IEA; IEA; IMP; IE | GO:0003677; GO:0 | DNA binding; DNA- |
| de-etiolati | The greeni | IEA; IEA; IEA | | |
| mRNA exp | The directe | IBA; IBA | GO:0017056 | structural constitue |
| | | | GO:0005515 | protein binding |
| | | | GO:0046983 | protein dimerizatio |
| rRNA proc | Any proces | IEA; IEA; IEA | GO:0003676; GO:0 | nucleic acid bindin |
| proteolysis | The hydrol | IEA | GO:0004181; GO:0 | metallocarboxypept |
| mitotic spi | A signal tr | IBA | GO:0005515; GO:0 | protein binding; ub |
| response t | Any proces | IEA; IEA | GO:0009881 | photoreceptor activ |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| electron tr | A process | IEA | GO:0009055 | electron transfer ac |
| intracellula | The direct | IEA; IEA | GO:0035091; GO:0 | phosphatidylinosito |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| carbohydra | The chemi | IEA; IEA; IBA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| snRNA tran | The synthe | IBA; IBA | GO:0043565 | sequence-specific D |
| response t | Any proces | IEA | GO:0003729; GO:0 | mRNA binding; prot |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| acylglycerc | The direct | IEA; IEA | GO:0042803; GO:0 | protein homodimer |
| | | | GO:0016616 | oxidoreductase acti |
| ubiquitin-( | The series | IBA | GO:0005515; GO:0 | protein binding; ub |
| deoxyribor | The chemi | IEA | GO:0008253 | 5'-nucleotidase acti |
| maturatior | Any proces | IEA; IEA | GO:0005515; GO:0 | protein binding; sn |
| xpressed | | | GO:0016407; GO:0 | acetyltransferase ac |
| mitochond | The conve | IEA; IEA | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| organic an | The direct | IEA; IEA; IBA; IEA; IE | GO:0005381; GO:0 | iron ion transmemb |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| peptidyl-ly | The methy | IBA | GO:0005515; GO:0 | protein binding; pro |
| protein ph | The proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
| ning protein | | | GO:0003676; GO:0 | nucleic acid binding |
| polysaccha | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |

|  |  |  |  |  |
|---|---|---|---|---|
| carbohydra | The chemi | IBA; IBA; IBA; IDA; IE | GO:0015018; GO:0 | galactosylgalactosy |
| gene silen | A process | IEA |  |  |
| leaf senesc | The last st | IEA; IBA |  |  |
| ion transm | A process | IEA; IEA; IEA; IEA; IE | GO:0015207; GO:0 | adenine transmemb |
| regulation | Any proces | IEA |  |  |
| protein ph | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |

|  |  |  |  |  |
|---|---|---|---|---|
| fucose me | The chemi | IEA | GO:0005509; GO:0 | calcium ion binding |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| phosphate | Any proces | IBA; IEA | GO:0022857 | transmembrane tra |

|  |  |  |  |  |
|---|---|---|---|---|
| tein |  |  | GO:0016491; GO:0 | oxidoreductase acti |
| cutin biosy | The chemi | IBA | GO:0016746; GO:0 | acyltransferase acti |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
|  |  |  | GO:0005515 | protein binding |
|  |  |  | GO:0004497; GO:0 | monooxygenase ac |

|  |  |  |  |  |
|---|---|---|---|---|
| development in response to macronutrien |  |  | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| lipid meta | The chemi | IEA; IEA; IEA | GO:0000036; GO:0 | acyl carrier activity; |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| intra-Golg | The direct | IBA; IEA; IEA; IEA | GO:0008565; GO:0 | obsolete protein tra |
| regulation | Any proces | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IBA | GO:0003682 | chromatin binding |

|  |  |  |  |  |
|---|---|---|---|---|
| protein sta | Any proces | IBA | GO:0000774; GO:0 | adenyl-nucleotide e |
| g protein |  |  | GO:0046872 | metal ion binding |

| | | | | |
|---|---|---|---|---|
| immune sy | Any proces | IEA; IEA; IEA | | |
| glycerol m | The chemi | IEA; IEA | GO:0008081; GO:0 | phosphoric diester |
| glutathion | The chemi | IEA; IEA | GO:0004364; GO:0 | glutathione transfe |
| trehalose b | The chemi | IBA; IGI; IGI | GO:0003824; GO:0 | catalytic activity; tre |
| ubiquitin- | The series | IBA; IBA; IBA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| otein | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| DNA repai | The proces | IEA; IBA; IEA; IEA; IB | GO:0003684; GO:0 | damaged DNA bind |
| | | | GO:0016301 | kinase activity |
| defense re | Reactions, | IEA; IMP | GO:0046870 | cadmium ion bindi |
| RNA proce | Any proces | IEA; IBA; IEA | | |
| thiamine m | The chemi | IEA; IEA | GO:0042131 | thiamine phosphate |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| methylatio | The proces | IBA | GO:0008168; GO:0 | methyltransferase a |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| ion transp | The direct | IEA; IEA; IEA | GO:0005216 | ion channel activity |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA; IEA; IEA | GO:0008865; GO:0 | fructokinase activity |
| potassium | A process | IEA | GO:0015079 | potassium ion trans |
| g protein |  |  | GO:0008270 | zinc ion binding |
| ontaining protein |  |  | GO:0016788 | hydrolase activity, a |
| protein ub | The proces | IEA | GO:0005515 | protein binding |
| response t | Any proces | IEA |  |  |
| transmemb | The proces | IEA | GO:0022857 | transmembrane tra |
| RNAi-medi | A post-tra | IEA; IEA | GO:0003723; GO:0 | RNA binding; helica |
| proteasom | The chemi | IBA |  |  |
| regulation | Any proces | IBA; IEA | GO:0005515; GO:0 | protein binding; pro |
| exonucleo | Exonucleo | IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA; IBA |  |  |
| protein ub | The proces | IEA | GO:0061631 | ubiquitin conjugati |
| EC 1.1.1.247) |  |  | GO:0004032; GO:0 | alditol:NADP+ 1-ox |
| xyloglucan | The chemi | IBA; IEA; IEA | GO:0008107; GO:0 | galactoside 2-alpha |
| response t | Any proces | IBA; IBA; IBA; IBA; IB | GO:0003824; GO:0 | catalytic activity; ph |
| response t | Any proces | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| mRNA spli | The joining | IEA; IBA; IBA |  |  |
|  |  |  | GO:0016491; GO:0 | oxidoreductase acti |
| lipid metab | The chemi | IEA | GO:0016787 | hydrolase activity |
| ) |  |  | GO:0003676; GO:0 | nucleic acid binding |
| g protein |  |  | GO:0005515; GO:0 | protein binding; me |
| rRNA 5'-en | Any proces | IBA; IEA; IEA; IEA |  |  |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| GPI anchor | The chemi | IEA | GO:0016772; GO:0 | transferase activity, |

| | | | | |
|---|---|---|---|---|
| gene silen | A process | IEA; IEA; IEA; IEA | | |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| U6 snRNA | Any proces | IEA; IEA; IEA | GO:0000175; GO:0 | 3'-5'-exoribonuclea |
| nucleoside | The chemi | IBA | GO:0000166; GO:0 | nucleotide binding; |
| obsolete o | OBSOLETE. | IEA | | |
| cellular res | Any proces | IEA | | |
| protein pe | The modifi | IEA | GO:0003755 | peptidyl-prolyl cis- |
| microtubul | A microtub | IEA | GO:0003777; GO:0 | microtubule motor |
| double fer | Fertilizatio | IEA; IEA | GO:0008375; GO:0 | acetylglucosaminylt |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| regulation | Any proces | IEA; IEP; IMP; IEA | GO:0005515; GO:0 | protein binding; pro |
| g protein | | | | |
| syncytium | The format | IEA; IEA; IEA; IEA; IEA | | |
| regulation | Any proces | IBA | GO:0000978; GO:0 | RNA polymerase II c |

| | | | | |
|---|---|---|---|---|
| defense re | A respons | IMP; IBA; IEA; IEA; IE | GO:0005515 | protein binding |
| charged-t | The covale | IEA | GO:0016763; GO:0 | pentosyltransferase |
| mitochond | Any proces | IBA; IBA; ISS; ISS; IS | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| mRNA spli | The joinin | IEA; IEA; IBA; IEA; IE | GO:0003676; GO:0 | nucleic acid bindin |
| intracellul | The proces | IEA; IEA | GO:0009055; GO:0 | electron transfer ac |
| double fer | Fertilizatio | IEA | | |
| | | | GO:0003824 | catalytic activity |
| chloroplas | A process | IEA; IEA; IEA | GO:0003729; GO:0 | mRNA binding; pro |
| methylatio | The proces | IEA | GO:0008168 | methyltransferase a |
| cell redox | Any proces | IBA; IEA | GO:0004791 | thioredoxin-disulfi |
| omain containing protein | | | | |
| auxin hom | A homeost | IEA; IEA | | |
| | | | GO:0005515 | protein binding |
| intracellul | The direct | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| exocyst as | The aggre | IBA; IEA; IBA; IEA | | |
| response t | Any proce | IBA | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| uence | | | GO:0004497; GO:0 | monooxygenase ac |
| snRNA pro | Any proce | IEA | | |
| transcripti | The synth | IBA; IEA | | |
| pectin bio | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proce | IEA; IBA; IEA; TAS; II | GO:0000977; GO:0 | RNA polymerase II t |
| | | | GO:0005525 | GTP binding |
| protein gly | A protein r | IEA; IBA; IEA; IBA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0016597 | amino acid binding |
| protein de | The proce | IEA | GO:0004722; GO:0 | protein serine/thre |
| microtubul | A process | IBA | GO:0008017 | microtubule bindin |
| protein ph | The proce | IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| response t | Any proce | IEA | GO:0004364 | glutathione transfe |
| | | | GO:0016491; GO:0 | oxidoreductase acti |

| | | | | |
|---|---|---|---|---|
| regulation | Any proce | IEA; IEA; IEA; IEA; IE | GO:0003677 | DNA binding |
| proteolysis | The hydrol | IEA; IEA | GO:0004843; GO:0 | cysteine-type deub |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| pseudouri | The intram | IEA; IEA | GO:0003723; GO:0 | RNA binding; pseu |
| | | | GO:0035091 | phosphatidylinosit |
| cellular am | The chemi | IBA | GO:0003824; GO:0 | catalytic activity; tr |
| protein N- | A protein | IEA; IEA; IEA; IEA | GO:0004583; GO:0 | dolichyl-phosphate |
| auxin bios | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; ca |
| regulation | Any proce | IBA; IMP; IMP | GO:0003700; GO:0 | DNA-binding trans |
| protein ph | The proce | IEA | GO:0004672; GO:0 | protein kinase activ |
| rotein | | | GO:0000166; GO:0 | nucleotide binding; |
| n | | | GO:0005515 | protein binding |

|  |  |  |  |  |
|---|---|---|---|---|
| regulation | Any proces | IEA; IEA | GO:0000976; GO:0 | transcription cis-re |
| methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| transmem | The proces | IEA | GO:0005215; GO:0 | transporter activity; |
| methylatio | The proces | IEA | GO:0008168; GO:0 | methyltransferase a |
| defense re | Reactions, | IEA; IBA; IBA; IEA; IEA |  |  |
| proteasom | The aggre | IEA | GO:0005515 | protein binding |
| transcripti | The extens | IEA; IEA; IEA; IEA; IB | GO:0000993 | RNA polymerase II |
|  |  |  | GO:0008115; GO:0 | sarcosine oxidase a |
| amino acid | The proces | IBA; IEA | GO:0015171 | amino acid transme |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
|  |  |  | GO:0005515; GO:0 | protein binding; un |
| translation | The proces | IEA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid bindin |
| transcripti | Any proces | IBA; IEA; IEA; IEA | GO:0000979; GO:0 | RNA polymerase II |
| gene silen | A process | IEA; IEA |  |  |
| protein N- | The glycos | IBA |  |  |
| xylan acet | The additi | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| carbohydr | The chemi | IBA; IBA; IBA; IBA; IE | GO:0016407; GO:0 | acetyltransferase ac |
| sterol tran | The direct | IEA | GO:0008289; GO:0 | lipid binding; sterol |
| RNA meth | Posttransc | IBA; IEA; IEA | GO:0008168; GO:0 | methyltransferase a |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein fol | The proces | IEA; IEA; IBA; IBA | GO:0005524; GO:0 | ATP binding; heat s |

| | | | | |
|---|---|---|---|---|
| regulation | Any proces | IEA; IBA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| | | | GO:0046872 | metal ion binding |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| transmeml | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| thylakoid r | A process | IEA; IEA; IEA; IEA | GO:0003824; GO:0 | catalytic activity; G |
| ›rotein | | | | |
| fatty acid t | The chemi | IEA | GO:0016746; GO:0 | acyltransferase acti |
| lipid metal | The chemi | IEA; IEA | GO:0016298 | lipase activity |
| exocyst as | The aggre | IBA; IEA; IBA | | |
| Group II in | The splicin | IEA; IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; zinc i |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| amino acid | The proces | IBA; IEA; IEA; IEA | GO:0015171; GO:0 | amino acid transme |
| proteolysis | The hydrol | IEA; IBA | GO:0004190 | aspartic-type endo |
| response t | Any proces | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| cytokinesis | The proces | IBA; IEA; IBA; IBA; IB | GO:0010011 | auxin binding |
| regulation | Any proces | IEA; IBA | GO:0003680; GO:0 | minor groove of ad |
| protein sta | Any proces | IBA | GO:0000774; GO:0 | adenyl-nucleotide e |
| RNA catab | The chemi | IEA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0008194 | UDP-glycosyltransf |
| amily protein | | | GO:0046527 | glucosyltransferase |
| tRNA meta | The chemi | IEA; IEA | GO:0002161; GO:0 | aminoacyl-tRNA ed |
| proteasom | The aggre | IBA | | |
| | | | GO:0003729; GO:0 | mRNA binding; pro |
| transmeml | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| regulation | Any proces | IEA; IBA | GO:0003700; GO:0 | DNA-binding trans |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| response t | Any proces | IEA | | |

| | | | | |
|---|---|---|---|---|
| defense re | Reactions, | IEA; IEA; IBA; IBA; IE | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IBA; IBA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| | | | GO:0005515 | protein binding |
| glutathion | The chemi | IEA; IEA | GO:0004364; GO:0 | glutathione transfe |
| starch cata | The chemi | IEA; IEA; IEA | GO:0008138; GO:0 | protein tyrosine/se |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| vesicle buc | The evagin | IBA; IEA; IBA | | |
| proteolysis | The hydrol | IEA | GO:0004252; GO:0 | serine-type endope |
| protein tar | The proces | IBA; IBA | GO:0016409; GO:0 | palmitoyltransfera |
| cation tran | The direct | IEA; IEA | GO:0009055; GO:0 | electron transfer ac |
| ribosomal | A cellular | IBA | | |
| ning protein | | | GO:0003676; GO:0 | nucleic acid binding |
| ion transm | A process | IEA; IEA | GO:0005227 | calcium activated c |
| DNA topol | The proces | IEA | GO:0003677; GO:0 | DNA binding; mRN |
| cellular am | The chemi | IEA; IEA; IEA | GO:0004106; GO:0 | chorismate mutase |
| pollen spe | The proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRN |
| mRNA pro | Any proces | IEA; IBA; IBA; IEA | GO:0003676; GO:0 | nucleic acid binding |
| DNA-temp | The compl | IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; mRN |

|  |  |  |  |  |
|---|---|---|---|---|
| nucleoside | The chemi | IBA | GO:0000166; GO:0 | nucleotide binding; |
| DNA metal | Any cellula | IEA; IEA; IEA; IBA; IE | GO:0000701; GO:0 | purine-specific mis |
| e putative domain containing protein |  |  | GO:0016787 | hydrolase activity |
| tein |  |  | GO:0016787 | hydrolase activity |
| ion transp | The direct | IEA; IBA; IEA; IEA; IE | GO:0015095; GO:0 | magnesium ion trar |
| proteolysis | The hydrol | IEA | GO:0008233 | peptidase activity |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| spliceoson | The aggre | IBA; IEA; IBA; IBA; IB | GO:0004672; GO:0 | protein kinase activ |
| nuclear en | A process | IBA | GO:0043495 | protein-membrane |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
| cell wall or | A process | IEA | GO:0016787; GO:0 | hydrolase activity; p |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
|  |  |  | GO:0003677; GO:0 | DNA binding; chron |
| histone me | The modifi | IBA; IEA | GO:0003690; GO:0 | double-stranded DI |
| metal ion t | The direct | IEA | GO:0046872 | metal ion binding |
| actin filam | A process | IEA; IBA | GO:0003779; GO:0 | actin binding; actin |
| sterol tran | The direct | IBA; IEA | GO:0032934 | sterol binding |
| otein |  |  | GO:0005515 | protein binding |
| protein gly | A protein r | IEA; IBA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IEA | GO:0001228; GO:0 | DNA-binding transc |
| autophago | The format | IEA | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| protein gly | A protein r | IEA; IMP | GO:0016757 | glycosyltransferase |
| protein ph | The proces | IBA; IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| defense re | Reactions, | IBA | | |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| carbohydr | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| response t | Any proces | IBA; IBA; IBA | GO:0005525 | GTP binding |
| response t | Any proces | IEA | | |

unit precursor (TRAP-alpha) (Signal sequence receptor alpha subunit) (SSR-alpha)

| | | | | |
|---|---|---|---|---|
| xylan bios | The chemi | IBA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0016491; GO:0 | oxidoreductase acti |
| long-day conditio | | | GO:0005515; GO:0 | protein binding; zin |
| DNA meta | Any cellula | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endo |
| defense re | Reactions, | IEA; IEA | GO:0005516 | calmodulin binding |
| mRNA des | Any proces | IBA | GO:0003723; GO:0 | RNA binding; mRN |

| | | | | |
|---|---|---|---|---|
| intracellula | The directe | IEA; IEA; IEA; IEA | GO:0008565 | obsolete protein tra |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; minor |
| | | | GO:0005515 | protein binding |
| ein | | | GO:0005515 | protein binding |
| carbohydra | The chemi | IEA; IEA; IEA | GO:0004650; GO:0 | polygalacturonase a |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II c |
| | | | GO:0005515 | protein binding |
| | | | GO:0004040; GO:0 | amidase activity; pr |
| intracellula | The directe | IBA; IBA | GO:0005096 | GTPase activator ac |
| SCF-depen | The chemi | IBA | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

|  |  |  |  |  |
|---|---|---|---|---|
| g protein |  |  | GO:0046872 | metal ion binding |
| cytokinin r | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; ox |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
|  |  |  | GO:0003677 | DNA binding |
| regulation | Any proces | IEA; IBA | GO:0003723; GO:0 | RNA binding; mRNA |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| DNA repai | The proces | IEA; IEA; IBA; IBA | GO:0003824; GO:0 | catalytic activity; DN |
| containing protein |  |  | GO:0016413; GO:0 | O-acetyltransferase |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| defense re | Reactions, | IEA; IEA; IEA |  |  |
| RNA proce | Any proces | IEA | GO:0003676; GO:0 | nucleic acid binding |
| proteolysis | The hydrol | IEA; IEA | GO:0004843; GO:0 | cysteine-type deubi |
| protein fol | The proces | IEA; IBA | GO:0051082; GO:0 | unfolded protein bi |
| signal tran | The cellula | IEA; IEA | GO:0005096 | GTPase activator ac |
| nucleobas | Any cellula | IEA | GO:0003676; GO:0 | nucleic acid binding |
| ion transp | The direct | IEA; IEA; IEA | GO:0015079 | potassium ion trans |
| response t | Any proces | IEA; IEA; IEA | GO:0004601; GO:0 | peroxidase activity; |
| regulation | Any proces | IBA; IEA; IEA; IBA; IB | GO:0005096; GO:0 | GTPase activator ac |
| negative re | Any proces | IEA; IEA; IBA |  |  |
| inositol ph | The proces | IEA; IEA | GO:0003824; GO:0 | catalytic activity; ph |
| hydrotropi | Growth or | IEA |  |  |
| regulation | Any proces | IBA; IBA; IEA; IEA; IB | GO:0016538; GO:0 | cyclin-dependent p |
| response t | Any proces | IEA |  |  |
| regulation | Any proces | IBA | GO:0003700; GO:0 | DNA-binding trans |
|  |  |  | GO:0016787 | hydrolase activity |
| ion transp | The direct | IEA; IEA; IEA; IEA | GO:0008308; GO:0 | voltage-gated anion |

|  |  |  |  |  |
|---|---|---|---|---|
| methionin | The chemi | IEA; IEA | GO:0003824; GO:0 | catalytic activity; cy |
| lipid meta | The chemi | IEA; IEA; IEA; IEA; IB | GO:0004435; GO:0 | phosphatidylinosito |
| multivesic | The aggre | IEA | GO:0043130; GO:0 | ubiquitin binding; n |
| arginine c | The chemi | IEA; IEA; IEP; IEA; IB | GO:0003824; GO:0 | catalytic activity; ar |
| translation | The cellula | IEA | GO:0003735; GO:0 | structural constitue |
| regulation | Any proces | IEA; IBA; IBA; IBA | GO:0000978; GO:0 | RNA polymerase II |
| regulation | Any proces | IBA | GO:0000976; GO:0 | transcription cis-re |
| actin filam | A process | IEA; IBA | GO:0003779; GO:0 | actin binding; actin |
| chromatin | A dynamic | IEA; IEA; IBA | GO:0140849 | ATP-dependent H2 |
| mitotic spi | A signal tr | IEA; IBA | GO:0004672 | protein kinase activ |
| regulation | Any proces | IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; prote |
| RNA catab | The chemi | IBA; IBA | GO:0004523 | RNA-DNA hybrid ri |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| exonucleo | Exonucleo | IBA | GO:0000175; GO:0 | 3'-5'-exoribonucle |
| intracellul | The direct | IBA; IBA | GO:0005096 | GTPase activator ac |
| DNA repai | The proces | IEA; IBA; IEA; IBA; IB | GO:0070182 | DNA polymerase bi |
| organic su | The chemi | IEA | GO:0016491; GO:0 | oxidoreductase acti |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| iron-sulfu | The incorp | IEA; IBA | GO:0005506; GO:0 | iron ion binding; irc |
| actin filam | A process | IEA; IEA | GO:0003779 | actin binding |
| regulation | Any proces | IBA; IBA |  |  |
| nucleocyto | The direct | IEA; IEA; IEA | GO:0008139; GO:0 | nuclear localization |
| cellular res | Any proces | IEA |  |  |
| DNA-temp | The synthe | IEA; IEA; IEA | GO:0003712; GO:0 | transcription coreg |
| regulation | Any proces | IBA |  |  |
| protein mc | The covale | IEA | GO:0016874 | ligase activity |

| | | | | |
|---|---|---|---|---|
| | | | GO:0005515; GO:0 | protein binding; ox |
| defense re | Reactions t | IEA | GO:0005515; GO:1 | protein binding; SC |
| tRNA 3'-te | Post-trans | IBA; IEA | GO:0003723; GO:0 | RNA binding; transf |
| g protein | | | | |
| maturatior | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| protein K6 | A protein u | IEA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| | | | GO:0005515 | protein binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0016491 | oxidoreductase acti |
| | | | GO:0003677 | DNA binding |
| | | | GO:0005515 | protein binding |
| | | | GO:0008289 | lipid binding |

| | | | | |
|---|---|---|---|---|
| protein ph | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0016787 | hydrolase activity |
| proteolysis | The hydrol | IEA; IBA | GO:0004190; GO:0 | aspartic-type endop |
| chloride tr | The directe | IEA; IEA; IEA | GO:0005247 | voltage-gated chlor |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| pressed | | | GO:0003993 | acid phosphatase a |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| ion transp | The directe | IEA; IEA; IEA | GO:0015079 | potassium ion trans |
| protein loc | Any proces | IBA; IEA | | |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| regulation | Any proces | IEA; IDA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| cellular am | The chemi | IBA | GO:0004617 | phosphoglycerate d |
| vesicle-me | A cellular t | IBA | | |
| regulation | Any proces | IEA; IBA; IBA; IEA; IE | GO:0000977; GO:0 | RNA polymerase II t |
| containing protein | | | GO:0016413; GO:0 | O-acetyltransferase |
| mRNA spli | The joining | IBA | | |
| single stra | The repair | IEA; IEA; IEA; IEA; IE | GO:0003684; GO:0 | damaged DNA bind |
| tRNA wobb | The proces | IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| intracellula | The directe | IEA; IBA | GO:0051087 | chaperone binding |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| protein pe | The modifi | IEA; IEA | GO:0003755; GO:0 | peptidyl-prolyl cis- |
| transmeml | The proces | IEA | GO:0015293; GO:0 | symporter activity; |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA; IEA; IBA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| RNA phosp | The chemi | IEA | GO:0003676; GO:0 | nucleic acid binding |
| defense re | Reactions, | IEA; IEA; IEA | GO:0004869; GO:0 | cysteine-type endo |
| | | | GO:0016462 | pyrophosphatase ac |
| ily protein | | | | |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| cellular res | Any proces | IEA; IMP; IEA; IMP; II | GO:0005515 | protein binding |
| | | | GO:0004497; GO:0 | monooxygenase act |
| transmeml | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| cellular ald | The chemi | IBA | GO:0004028; GO:0 | 3-chloroallyl aldeh |
| negative re | Any proces | IEA; IEA | GO:0004867; GO:0 | serine-type endope |
| phosphore | A conserve | IEA; IEA; IEA; IEA; IE | GO:0000155; GO:0 | phosphorelay senso |
| cell wall or | A process | IEA; IEA | GO:0016740; GO:0 | transferase activity; |
| regulation | Any proces | IBA; IBA; IBA | GO:0005515 | protein binding |
| cell cycle; | The progre | IEA; IEA; IEA | GO:0003682; GO:0 | chromatin binding; |
| | | | GO:0005515 | protein binding |
| RNA phosp | The chemi | IEA | GO:0004521; GO:0 | endoribonuclease a |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| | | | GO:0004497; GO:0 | monooxygenase ac |
| cell cycle; | The progre | IEA; IEA | | |
| rotein | | | GO:0003723 | RNA binding |
| histone H3 | The modifi | IEA | GO:0000976; GO:0 | transcription cis-re |
| ribosomal | The direct | IBA; IBA; IBA | GO:0005506; GO:0 | iron ion binding; A |
| protein ub | The proces | IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| chlorophyl | The chemi | IEA; IEA | GO:0005515 | protein binding |
| response t | Any proces | IBA; IEA | GO:0015112; GO:0 | nitrate transmembr |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| RNA modif | The covale | IEA; IEA; IEA | GO:0003723; GO:0 | RNA binding; protei |
| nuclear-tr | The chemi | IBA; IEA; IEA; IEA; IE | GO:0003676; GO:0 | nucleic acid binding |
| RNA phosp | The chemi | IEA | GO:0000175; GO:0 | 3'-5'-exoribonucle |
| expressed | | | GO:0003723 | RNA binding |
| regulation | Any proces | IEA; IBA | | |
| proteolysis | The hydrol | IEA | GO:0008233 | peptidase activity |
| | | | GO:0016788 | hydrolase activity, a |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| in | | | GO:0016788 | hydrolase activity, a |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| protein ph | The proces | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IBA; IEA | GO:0003713 | transcription coacti |
| protein gly | A protein r | IEA; IEA; IEA; IEA; IB | GO:0004168; GO:0 | dolichol kinase acti |
| | | | GO:0016788 | hydrolase activity, a |

| | | | | |
|---|---|---|---|---|
| malate tra | The direct | IEA; IEA | | |
| rRNA proc | Any proces | IBA; IEA; IEA; IEA; IE | GO:0003723; GO:0 | RNA binding; endo |
| microtubul | A microtub | IEA | GO:0003777; GO:0 | microtubule motor |
| auxin-acti | The series | IBA; IBA; IBA | | |
| | | | GO:0005504; GO:0 | fatty acid binding; i |
| protein ub | The proces | IEA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA | GO:0005085 | guanyl-nucleotide |
| | | | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0003677 | DNA binding |
| | | | GO:0008375 | acetylglucosaminylt |
| protein de | The proces | IBA | GO:0004721; GO:0 | phosphoprotein ph |
| regulation | Any proces | IBA; IEA; IBA; IEA; IB | GO:0008168; GO:0 | methyltransferase a |
| regulation | Any proces | IEA | GO:0003677; GO:0 | DNA binding; DNA- |

| | | | | |
|---|---|---|---|---|
| | | | GO:0030145; GO:0 | manganese ion bin |
| multicellul | The biolog | IBA; IBA; IBA; IBA; IB | GO:0004497; GO:0 | monooxygenase ac |
| DNA-temp | The compl | IEA; IEA; IBA; IBA | GO:0003690 | double-stranded D |
| tRNA proc | The proces | IEA; IMP; IMP; IMP | GO:0000166; GO:0 | nucleotide binding; |
| rotein | | | GO:0000166; GO:0 | nucleotide binding; |
| ubiquinon | The chemi | IBA; IBA; IEA; IDA | GO:0004311; GO:0 | farnesyltranstransfe |
| nsferase 3 | | | GO:0016740; GO:0 | transferase activity; |
| signal tran | The cellula | IBA; IEA; IBA | | |
| transmem | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| protein ph | The proces | IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| protein gly | A protein r | IEA; IBA | GO:0008378; GO:0 | galactosyltransfera |
| response t | Any proces | IBA; IBA; IEA | GO:0004089; GO:0 | carbonate dehydrat |
| response t | Any proces | IEA | | |
| cellular gl | A cellular | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| proteolysis | The hydrol | IEA; IBA | GO:0004197; GO:0 | cysteine-type endo |
| mRNA spli | The joinin | IBA | GO:0003676; GO:0 | nucleic acid bindin |
| transmem | The proces | IEA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0008375 | acetylglucosaminylt |
| protein po | Addition o | IBA; IEA; IEA; IEA | GO:0004842; GO:0 | ubiquitin-protein tr |

| | | | | |
|---|---|---|---|---|
| DNA-temp | The synthe | IEA; IBA | GO:0003677; GO:0 | DNA binding; DNA- |
| n | | | GO:0004252 | serine-type endope |
| translation | The cellula | IEA | GO:0043023 | ribosomal large sub |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0005216 | ion channel activity |
| | | | GO:0005515 | protein binding |
| | | | GO:0000774 | adenyl-nucleotide e |
| | | | GO:0005515; GO:0 | protein binding; my |
| one-carbo | The chemi | IEA; IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IEA | GO:0003723 | RNA binding |
| protein fol | The proces | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| translation | The proces | IEA | GO:0003747 | translation release f |
| | | | GO:0005515 | protein binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0003676; GO:0 | nucleic acid binding |
| tricarboxyl | A nearly ur | IBA; IBA; IBA; IBA; IE | GO:0008177 | succinate dehydrog |
| protein de | The remov | IBA | GO:0004843 | cysteine-type deubi |
| regulation | Any proces | IBA; IEA; IEA; IBA; IB | GO:0004430; GO:0 | 1-phosphatidylinos |
| mRNA spli | The joining | IEA; IEA; IEA | | |
| | | | GO:0004497; GO:0 | monooxygenase act |
| glycerol et | The chemi | IEA; IEA | GO:0015035 | protein-disulfide re |
| ein | | | GO:0016407; GO:0 | acetyltransferase ac |
| protein ma | Any proces | IBA | GO:0004298; GO:0 | threonine-type end |
| cytokinin- | The series | IEA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| amily protein, Hybrid breakdown (HB | | | GO:0016491; GO:0 | oxidoreductase acti |

| | | | | |
|---|---|---|---|---|
| plant-type | A cellular p | IBA | | |
| protein | | | GO:0008194; GO:0 | UDP-glycosyltransf |
| translation | The cellula | IEA; IBA; IBA; IBA | GO:0016787; GO:0 | hydrolase activity; p |
| | | | GO:0004497; GO:0 | monooxygenase act |
| protein ph | The proces | IEA; IBA; IEA; IBA; IB | GO:0000166; GO:0 | nucleotide binding; |
| protein tar | The proces | IEA; IEA; IEA; IBA; IBA | | |
| electron tr | A process | IEA | GO:0005506; GO:0 | iron ion binding; el |
| negative re | Any proces | IBA | GO:0003725; GO:0 | double-stranded RN |
| protein pre | The covale | IBA; IEA | GO:0003824; GO:0 | catalytic activity; pr |
| pentose-p | The metab | IEA; IEA | GO:0004751; GO:0 | ribose-5-phosphat |
| protein pro | Any protei | IEA | GO:0004175 | endopeptidase activ |
| transmemb | The proces | IEA; IEA | GO:0005458; GO:0 | GDP-mannose trans |
| taining protein | | | | |
| regulation | Any proces | IEA | | |
| response t | Any proces | IMP; IMP; IMP; IMP; IEA; IEA | | |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| regulation | Any proces | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| protein pol | Addition o | IBA; IBA; IEA; IBA | GO:0004842; GO:0 | ubiquitin-protein tr |
| protein pol | Addition o | IBA; IBA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| e | | | GO:0008194; GO:0 | UDP-glycosyltransf |

| | | | | |
|---|---|---|---|---|
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| brane plant subgroup domain containing | | | GO:0051539 | 4 iron, 4 sulfur clus |
| defense re | Reactions, | IEA; IBA; IEA; IBA | GO:0004864; GO:0 | protein phosphatas |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |
| response t | Any proces | IEA; IBA; IEA | | |
| protein ph | The proces | IEA; IEA; IEA; IBA; IE | GO:0000166; GO:0 | nucleotide binding; |
| mitochond | The covale | IBA | GO:0003676; GO:0 | nucleic acid binding |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| ning protein | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0003682 | chromatin binding |
| chloroplas | The proces | IEA | | |
| fatty acid | The chemi | IBA | GO:0019171 | 3-hydroxyacyl-[acy |
| purine nuc | The chemi | IEA; IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| actin filam | A process | IBA; IEA; IBA | GO:0000146; GO:0 | microfilament moto |
| allantoin c | The chemi | TAS; IEA; IEA; IEA | GO:0008237; GO:0 | metallopeptidase ac |
| vesicle-me | A cellular t | IEA | | |
| RNA proce | Any proces | IEA; IEA; IBA; IEA; IE | GO:0003727; GO:0 | single-stranded RN |
| idopsis MORE AXILLARY GROWTH 1 (MAX | | | GO:0004497; GO:0 | monooxygenase act |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |

| | | | | |
|---|---|---|---|---|
| response t | Any proces | IEA; IEA | | |
| lipid meta | The chemi | IEA; IBA; IEA; IEA | GO:0004623; GO:0 | phospholipase A2 a |
| methylatio | The proces | IEA; IEA | GO:0008168; GO:0 | methyltransferase a |
| ining protein | | | GO:0003677; GO:0 | DNA binding; mino |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| translation | The cellula | IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| nonphotoc | The proces | IEA; IEA; IEA | | |
| | | | GO:0005515 | protein binding |
| carbohydr | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| xylan acet | The additio | IEA | GO:0016413; GO:0 | O-acetyltransferase |
| ning protein | | | | |
| nuclear-tr | The nonse | IBA | GO:0003723; GO:0 | RNA binding; helica |
| mRNA spli | The joining | IBA; IEA; IBA; IEA; IEA; IEA | | |
| cell wall m | The series | IEA; IEA; IEA | GO:0004857; GO:0 | enzyme inhibitor ac |
| phospholi | The direct | IEA | GO:0005548 | phospholipid trans |
| cellular am | The chemi | IEA; IBA; IEA | GO:0003824; GO:0 | catalytic activity; L- |
| aining protein | | | GO:0050308 | sugar-phosphatase |
| RNA-temp | A DNA bio | IEA; IBA; IEA; IBA | GO:0003964 | RNA-directed DNA |

| | | | | |
|---|---|---|---|---|
| cellular ox | Any proces | IEA | GO:0000293; GO:0 | ferric-chelate reduc |
| | | | GO:0005515 | protein binding |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |
| regulation | Any proces | IBA; IEA | GO:0000977; GO:0 | RNA polymerase II t |
| abscisic ac | The series | IEA; IMP; IMP; IBA | GO:0004721; GO:0 | phosphoprotein ph |
| ence | | | GO:0016787; GO:0 | hydrolase activity; |
| protein de | The proces | IBA; IEA | GO:0004721; GO:0 | phosphoprotein ph |
| regulation | Any proces | IEA; IEA; IBA | GO:0003676; GO:0 | nucleic acid binding |
| nsferase 3 | | | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0005515 | protein binding |
| regulation | Any proces | IEA; IEA | GO:0005085 | guanyl-nucleotide |
| gluconeog | The forma | IBA; IEA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| RNA modif | The covale | IBA; IEA; IEA | GO:0005515 | protein binding |
| negative re | Any proces | IBA; IBA | GO:0043023 | ribosomal large sub |
| DNA-temp | The synthe | IEA; IEA; IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| signal tran | The cellula | IEA; IEA; IEA; IEA; IB | GO:0000166; GO:0 | nucleotide binding; |
| auxin-acti | The series | IEA | | |
| pollen dev | The proces | IEA; IEA; IBA; IEA | GO:0000149; GO:0 | SNARE binding; GT |

| | | | | |
|---|---|---|---|---|
| | | | GO:0016791 | phosphatase activit |
| proteolysis | The hydrol | IEA; IEA; IEA | GO:0004190; GO:0 | aspartic-type endo |
| lipid trans | The direct | IEA | GO:0008289 | lipid binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| N-terminal | The acetyl | IEA | GO:0008080; GO:0 | N-acetyltransferase |
| | | | GO:0003677; GO:0 | DNA binding; prote |
| xylan bios | The chemi | IBA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0005515 | protein binding |
| tRNA modi | The covale | IBA; IBA | GO:0016740; GO:0 | transferase activity; |
| | | | GO:0000166; GO:0 | nucleotide binding; |
| regulation | Any proces | IEA; IEA; IEA; IEA | GO:0043022 | ribosome binding |
| embryo de | The proces | IEA; IEA; IEA | | |
| ribosomal | A cellular | IBA | | |
| intracellul | The direct | IEA; IEA; IEA; IEA; IEA | | |
| rotein | | | GO:0016788 | hydrolase activity, a |
| ntaining protein | | | | |
| siderophor | The chemi | IDA; IEP; IEP | GO:0004032; GO:0 | alditol:NADP+ 1-ox |
| DNA replic | The cellula | IEA; IBA; IEA; IBA | | |
| xenobiotic | The proces | IBA; IEA; IEA | GO:0015297; GO:0 | antiporter activity; t |
| plastid org | A process | IEA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| domain containing protein | | | | |
| chloroplas | A process | IBA | | |
| translation | The cellula | IEA | GO:0003735 | structural constitue |
| | | | GO:0004497; GO:0 | monooxygenase ac |
| ining protein | | | | |
| cellular am | The chemi | IEA; IEA | GO:0003856; GO:0 | 3-dehydroquinate s |
| ) domain containing protein | | | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0016430 | tRNA (adenine-N6- |
| RNA modif | The covale | IBA | GO:0005515; GO:0 | protein binding; zin |

| | | | | |
|---|---|---|---|---|
| biosynthet | The chemi | IEA | GO:0016844 | strictosidine syntha |
| tRNA modi | The covale | IBA; IBA | GO:0016740; GO:0 | transferase activity; |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0003729; GO:0 | mRNA binding; prot |
| protein tar | The proces | IEA; IEA; IEA | GO:0005227 | calcium activated ca |
| intracellula | The direct | IBA; IBA | GO:0005096 | GTPase activator ac |
| anatomical | The proces | IEA; IEA; IEA | | |
| lipid metal | The chemi | IEA; IEA; IEA; IBA; IE | GO:0004721; GO:0 | phosphoprotein ph |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| obsolete n | OBSOLETE. | IBA; IBA; IEA | GO:0003682; GO:0 | chromatin binding; |
| iron-sulfu | The incorp | IEA; IEA | GO:0005198; GO:0 | structural molecule |
| DNA-temp | The initial | IEA; IEA; IEA; IEA; IE | GO:0003700 | DNA-binding trans |

| | | | | |
|---|---|---|---|---|
| protein fol | The proces | IBA; IMP; IMP; IBA; I | GO:0003756; GO:0 | protein disulfide is |
| translation | The cellula | IEA | GO:0003723; GO:0 | RNA binding; struct |
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008324 | cation transmembr |
| lipid trans | The direct | IEA | GO:0008289 | lipid binding |
| lipid meta | The chemi | IEA; IEA; IBA; IBA; IB | GO:0004497; GO:0 | monooxygenase ac |
| doreductase domain containing protein | | | GO:0004497; GO:0 | monooxygenase ac |
| intracellul | The direct | IBA; IBA | GO:0005096 | GTPase activator ac |
| | | | GO:0047429 | nucleoside triphosp |

| | | | | |
|---|---|---|---|---|
| l cell division, Induction of leaf senescenc | | | GO:0030570 | pectate lyase activit |
| anatomical | The proces | IEA | | |
| phospholip | The directe | IEA; IEA | GO:0008526 | phosphatidylinosito |
| TIVE6) | | | | |
| phosphatic | The chemi | IEA | GO:0004430; GO:0 | 1-phosphatidylinos |
| aining protein | | | GO:0016655; GO:0 | oxidoreductase acti |
| chaperone | The proces | IBA | GO:0044183; GO:0 | protein folding cha |
| carbohydra | The directe | IBA; IEA | GO:0051119 | sugar transmembra |
| ubiquitin-( | The chemi | IBA; IEA; IBA | GO:0005515 | protein binding |
| mRNA exp | The directe | IBA | GO:0003676; GO:0 | nucleic acid binding |
| | | | GO:0005515 | protein binding |
| one-carbo | The chemi | IEA; IBA; IBA | GO:0004477; GO:0 | methenyltetrahydro |
| tRNA modi | The covale | IEA; IEA; IBA | GO:0008479; GO:0 | queuine tRNA-ribos |
| microtubul | A microtuk | IEA; IBA; IEA; IEA; IE | GO:0000166; GO:0 | nucleotide binding; |
| double-str | The error- | IEA | GO:0003677 | DNA binding |
| regulation | Any proces | IBA | GO:0003676; GO:0 | nucleic acid binding |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| | | | GO:0005515 | protein binding |

| | | | | |
|---|---|---|---|---|
| ıg protein | | | | |
| regulation | Any proces | IEA | GO:0003677 | DNA binding |
| biosynthet | The chemi | IEA | GO:0003824; GO:0 | catalytic activity; isc |
| exocytosis | A process | IBA; IEA | GO:0005546 | phosphatidylinosito |
| phosphore | A conserve | IEA; IEA; IEA; IEA; IE | GO:0000155; GO:0 | phosphorelay senso |
| | | | GO:0005515 | protein binding |
| | | | GO:0016787 | hydrolase activity |
| protein sec | The contro | IEA; IMP; IEA | | |
| response t | Any proces | IBA; IBA; IBA; IBA | GO:0004601; GO:0 | peroxidase activity; |
| | | | GO:0003677; GO:0 | DNA binding; lipid l |
| RNA modif | The covale | IEA | GO:0003723; GO:0 | RNA binding; protei |
| protein fol | The proces | IBA; IBA; IEA | GO:0003756 | protein disulfide isc |
| | | | GO:0005515 | protein binding |
| protein ub | The proces | IEA | | |
| enzyme-di | The intram | IBA; IEA; IEA | GO:0003723; GO:0 | RNA binding; pseuc |
| protein ph | The proces | IEA | GO:0004672; GO:0 | protein kinase activ |
| otein | | | GO:0005515 | protein binding |
| microtubul | A microtub | IEA | GO:0000166; GO:0 | nucleotide binding; |
| N-termina | The methy | IEA | GO:0008168; GO:0 | methyltransferase a |
| RNA modif | The covale | IBA | GO:0005515 | protein binding |
| response t | Any proces | IEA; IEA | GO:0016301 | kinase activity |
| protein ph | The proces | IEA; IEA | GO:0004672; GO:0 | protein kinase activ |
| DNA-temp | The synthe | IEA; IEA | GO:0003677; GO:0 | DNA binding; DNA- |
| polysaccha | The chemi | IEA; IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| one-carbo | The chemi | IEA; IEA; IBA; IBA | GO:0000166; GO:0 | nucleotide binding; |

|  |  |  |  |  |
|---|---|---|---|---|
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
|  |  |  | GO:0062153; GO:1 | C5-methylcytidine- |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, h |
| protein gly | A protein r | IEA; IEA; IEA | GO:0016757 | glycosyltransferase |
| protein |  |  | GO:0008194; GO:0 | UDP-glycosyltransf |
| UDP-D-glucuronate 4- epimerase) (EC 5. |  |  | GO:0003824; GO:0 | catalytic activity; ob |
| mitochond | The divisio | IEA; IBA; IBA; IEA; IE | GO:0005515 | protein binding |
| endoplasm | The attach | IBA; IBA |  |  |
| rRNA catab | The chemi | IBA; IBA; IBA; IBA; IBA |  |  |
| mRNA spli | The joinin | IEA; IEA; IEA |  |  |
| response t | Any proces | IEA | GO:0003755; GO:0 | peptidyl-prolyl cis- |
| N-termina | The acetyl | IBA; IBA; IBA | GO:0004402; GO:0 | histone acetyltransf |
|  |  |  | GO:0003677 | DNA binding |
| response t | Any proces | IEA; IEA; IEA |  |  |
| cell redox | Any proces | IEA | GO:0009055; GO:0 | electron transfer ac |
|  |  |  | GO:0016787 | hydrolase activity |
|  |  |  | GO:0003682 | chromatin binding |
|  |  |  | GO:0046872 | metal ion binding |
| protein |  |  |  |  |
| regulation | Any proces | IEA |  |  |
| transmem | The proces | IBA | GO:0015333; GO:0 | peptide:proton sym |
| regulation | Any proces | IEA |  |  |
| DNA-temp | The synthe | IEA; IEA; IBA; IBA | GO:0001228; GO:0 | DNA-binding trans |
| purine nuc | The direct | IEA; IEA; IEA | GO:0005215; GO:0 | transporter activity; |
| protein im | The proces | IEA |  |  |
| protein |  |  | GO:0000166; GO:0 | nucleotide binding; |
| vacuole or | A process | IEA; IEA; IBA | GO:0016791; GO:0 | phosphatase activit |
| cell differe | The proces | IEA | GO:0003676; GO:0 | nucleic acid bindin |
| n |  |  | GO:0008168 | methyltransferase a |

| | | | | |
|---|---|---|---|---|
| ion transp | The direct | IEA; IEA; IEA; IEA; IE | GO:0008308; GO:0 | voltage-gated anio |
| protein fol | The proces | IBA; IBA; IEA | GO:0003756; GO:0 | protein disulfide is |
| tein | | | GO:0016787 | hydrolase activity |
| ubiquitin- | The chemi | IEA; IEA | GO:0005515; GO:0 | protein binding; ub |
| carbohydra | The chemi | IEA; IEA | GO:0004553; GO:0 | hydrolase activity, |
| | | | GO:0016614; GO:0 | oxidoreductase acti |
| fucose me | The chemi | IEA | GO:0016740; GO:0 | transferase activity; |

| | | | | |
|---|---|---|---|---|
| carbohydra | The chemi | IEA; IEA; IMP; IMP; I | GO:0004553; GO:0 | hydrolase activity, |
| transmem | The proces | IEA | GO:0022857 | transmembrane tra |
| RNA modif | The covale | IBA | GO:0003723; GO:0 | RNA binding; protei |
| regulation | Any proces | IBA | GO:0035091; GO:0 | phosphatidylinosito |
| | | | | |
| GPI anchor | The chemi | IEA; IBA; IEA | GO:0016787 | hydrolase activity |
| NADP bios | The chemi | IBA; IEA; IEA | GO:0000166; GO:0 | nucleotide binding; |

| | | | | |
|---|---|---|---|---|
| cal 1 protein | | | GO:0016791; GO:0 | phosphatase activit |
| | | | GO:0030246 | carbohydrate bindi |
| protein de | The remov | IBA | GO:0004843 | cysteine-type deubi |
| proteasom | The chemi | IBA | GO:0005515; GO:0 | protein binding; ub |
| trehalose | The chemi | IBA | GO:0003824; GO:0 | catalytic activity; tre |

omologs

| molecular_function | molecular_function | cellular_component | cellular_component |
|---|---|---|---|
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634; GO:0 | nucleus; membrane |
| Binding to ATP, ade | IEA; IEA | | |
| Catalysis of the tran | IDA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Functions in the init | IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0005739; GO:0 | mitochondrion; ribo |
| Catalysis of the reac | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; nucleolus |
| Binding to a protein | IEA | | |
| Binding to a calcium | IBA; IEA | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the tra | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binds to and stops, | IEA; IBA; IBA | | |
| Catalysis of the hyd | IBA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |
| Binding to a protein | IPI | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IBA; IBA | GO:0016020 | membrane |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a lipid. | IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IBA | GO:0000812; GO:0 | Swr1 complex; nucl |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a calciun | IEA; IBA | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to inositol | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; nuclear po |
| | | GO:0005634; GO:0 | nucleus; plasma me |
| Stimulates the exch | IBA; IBA | GO:0005829; GO:0 | cytosol; endocytic v |
| | | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; DNA replic |
| Enables the transfe | IBA; IEA; IEA | GO:0005887; GO:0 | integral component |
| The action of a mol | IEA; IEA | GO:0000139; GO:0 | Golgi membrane; m |
| Binding to a 7-met | IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0016592 | mediator complex |
| A transcription reg | IEA; IBA | GO:0005634; GO:0 | nucleus; mediator c |
| Any molecular func | IBA; IBA; IBA; IBA; IE | GO:0000785; GO:0 | chromatin; nucleus |
| Binding to a protein | IEA | | |
| Catalysis of the rea | IEA | GO:0005795; GO:0 | Golgi stack; integra |
| | | GO:0005783 | endoplasmic reticul |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binds to and stops, | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Catalysis of the ph | IEA; IEA | | |
| Binding to a specifi | IEA; IEA; IDA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IBA; IEA; IEA; IB | GO:0005737 | cytoplasm |
| Enables the directe | IBA; IEA | GO:0005634; GO:0 | nucleus; membrane |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| | | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Enables the active t | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to ATP, ade | IEA; IEA | GO:0005741 | mitochondrial outer |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Binds to and stops, | IEA; IBA | GO:0005634 | nucleus |
| Binding to a carboh | IEA | | |
| | | GO:0005576; GO:0 | extracellular region |
| | | GO:0005789; GO:0 | endoplasmic reticul |
| Binding to ubiquitin | IEA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a calcium | IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IBA; IBA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; er |
| Catalysis of the inc | IEA; IEA; IEA; IBA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IEA | | |
| Binding to an RNA r | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0005886; GO:0 | plasma membrane; |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0005634; GO:0 | nucleus; cytoplasm |
| A DNA-binding tran | IBA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the tran | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the rea | IBA; IBA; IEA; IEA | GO:0005789; GO:0 | endoplasmic reticul |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0000325; GO:0 | plant-type vacuole; |
| A transcription regu | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binds to and increa | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of an oxid | IEA; IEA; IBA | | |
| A motor activity tha | IBA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; actin cy |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0016021 | integral component |
| Catalysis of the rea | IEA; IEA | | |
| Catalysis of a bioch | IEA; IBA; IC; IEA; IE | GO:0005576; GO:0 | extracellular region |
| | | GO:0016020; GO:0 | membrane; integral |
| The action of a mol | IBA; IEA; IBA | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| Catalysis of the inc | IEA; IEA; IEA; IBA; IE | GO:0016020; GO:0 | membrane; integral |
| OBSOLETE. Enables | IBA; IEA | GO:0005743; GO:0 | mitochondrial inner |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA; IDA; IEA; IDA; I | GO:0000176; GO:0 | nuclear exosome (R |
| Catalysis of the rea | IBA | | |
| | | GO:0005829 | cytosol |
| Binding to a calcium | IEA; IBA | GO:0000159 | protein phosphatas |
| Binding to a nucleic | IEA; IBA | | |
| Binding to a zinc io | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Serves as a phosph | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |

|  |  |  |  |
|---|---|---|---|
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binding to a magne | IBA; IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; cytosol |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the phc | IEA |  |  |
| Binding to a specifi | IBA; IBA; IEA | GO:0000785; GO:0 | chromatin; nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IDA | | |
| Catalysis of the trar | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Binding to a magne | IEA; IEA; IEA; IEA; IE | GO:0005829 | cytosol |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; Fanconi an |
| | | GO:0005634; GO:0 | nucleus; MLL1 com |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Stimulates the exch | IBA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the trar | IBA | GO:0005768; GO:0 | endosome; trans-G |
| The action of a mol | IEA; IEA | GO:0005840; GO:0 | ribosome; cytosolic |
| Binding to double- | IBA; IBA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA |  |  |
| Primary active trans | IEA | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0009507 | chloroplast |
| Catalysis of the trar | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Catalysis of the hyd | IEA |  |  |
| Binding to AMP, ad | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the ide | IEA; IEA; IEA; IBA; IB | GO:0000794; GO:0 | condensed nuclear |
| Enables the energy- | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to flavin m | IEA; IEA |  |  |
| Catalysis of the trar | IBA | GO:0031314 | extrinsic componen |
| Any molecular func | IEA; IEA |  |  |
| Any molecular func | IBA; IBA; IBA; IBA; IE | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0005634; GO:0 | nucleus; chloroplas |
| Binding to a nucleic | IEA; IEA |  |  |
| Binding to a protein | IEA |  |  |
|  |  | GO:0009536; GO:0 | plastid; membrane; |
| Binding to a nucleo | IEA; IEA; IEA |  |  |
| Catalysis of the phc | IEA; IEA; IEA |  |  |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0005789; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IEA |  |  |
| Enables the active t | IBA; IEA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Binding to single-s | IBA; IEA; IEA; IEA; IE | GO:0005654; GO:0 | nucleoplasm; cytop |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA |  |  |
| OBSOLETE. The fun | IBA; IBA | GO:0000124; GO:0 | SAGA complex; nuc |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA |  |  |
|  |  | GO:0005743; GO:0 | mitochondrial inner |
|  |  | GO:0005743; GO:0 | mitochondrial inner |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0016020 | membrane |
| A DNA-binding trar | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005634; GO:0 | nucleus; U4/U6 x U |
| | | GO:0031213 | RSF complex |
| | | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a SNARE | IBA; IEA; IBA; IBA; IE | GO:0005794; GO:0 | Golgi apparatus; cla |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the trar | IEA; IEA | | |
| A DNA-binding trar | IDA; IEA; IEA; IPI; ID | GO:0005634 | nucleus |
| Catalysis of the tem | IEA; IEA | GO:0005730; GO:0 | nucleolus; TRAMP c |
| | | GO:0005634 | nucleus |
| Binding to ATP, ade | IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| A transcription regu | IEA | GO:0005634 | nucleus |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016021 | integral component |
| Binding to a SNARE | IBA; IEA; IBA; IBA; IE | GO:0005794; GO:0 | Golgi apparatus; cla |
| Binding to a specifi | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the phc | IEA; IBA; IEA; IEA; IB | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; mRNA clea |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA | GO:0005634 | nucleus |
|  |  |  |  |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IBA; IBA | GO:0000781; GO:0 | chromosome, telom |
|  |  |  |  |
| Catalysis of the rea | IEA; IEA; IEA | GO:0009507 | chloroplast |
|  |  |  |  |
|  |  |  |  |
| Combining with a s | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
|  |  |  |  |
|  |  | GO:0000974; GO:0 | Prp19 complex; nuc |
|  |  |  |  |
| Catalysis of an oxid | IEA; IEA; IBA |  |  |
| Binding to double-s | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromosom |
| Binding to a nucleo | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
|  |  | GO:0009507; GO:0 | chloroplast; chlorop |
| Binds to and stops, | IEA; IEA | GO:0005576 | extracellular region |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Binding to a protein | IEA |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Catalysis of the inc | IBA; IEA; IEA; IBA; IEA |  |  |
| Catalysis of the rea | IEA; IBA |  |  |
|  |  |  |  |
| Catalysis of the tran | IEA; IEA; IEA; IEA | GO:0016020 | membrane |
| Catalysis of the tran | IBA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
|  |  | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the tran | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
|  |  |  |  |
| Binding to a protein | IEA | GO:0005634 | nucleus |
|  |  |  |  |
|  |  | GO:0005743; GO:0 | mitochondrial inner |
|  |  |  |  |
|  |  |  |  |
| A DNA-binding tran | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA |  |  |
|  |  | GO:0000139; GO:0 | Golgi membrane; en |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009507; GO:0 | chloroplast; membr |
| Binding to a metal i | IEA | | |
| A transcription regu | IEA; IBA | GO:0005634 | nucleus |
| Binds transmembra | IBA | GO:0005743; GO:0 | mitochondrial inner |
| Catalysis of the add | IEA; IBA | GO:0005783 | endoplasmic reticul |
| A DNA-binding tran | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to cardiolip | IEA | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the rea | IEA; IBA | GO:0005737 | cytoplasm |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a specifi | IEA | | |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binds to and increa | IEA; IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | | |
| A transcription regu | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA; IBA | GO:0005618; GO:0 | cell wall; membrane |
| Catalysis of the hyd | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol; m |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a calciun | IBA; IBA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA; IEA; IEA; IE | GO:0005730; GO:0 | nucleolus; small-su |
| | | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the trar | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a nucleic | IEA; IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| | | GO:0005576; GO:0 | extracellular region |
| | | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005886; GO:0 | plasma membrane; |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IEA | GO:0016020 | membrane |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the trar | IBA; IBA; IBA | GO:0043231 | intracellular membr |
| Binding to a protein | IEA; IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a protein | IEA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the phc | IEA; IEA; IEA |  |  |
| Enables the transfe | IBA; IEA; IEA; IEA; IE | GO:0005887; GO:0 | integral component |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
| Catalysis of the hyd | IEA |  |  |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA |  |  |
| Catalysis of the trar | IEA; IBA; IEA | GO:0009570 | chloroplast stroma |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| The action of a mol | IEA | GO:0005762; GO:0 | mitochondrial large |
| Binding to a carboh | IEA |  |  |
| Catalysis of the trar | IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to a specifi | IEA; IMP; IEA; IBA; I | GO:0005634 | nucleus |
| Binding to chromati | IEA | GO:0000228; GO:0 | nuclear chromosom |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005615 | extracellular space |
| Binding to a protein | IEA | | |
| Binding to a ubiquit | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA; IBA; IEA; IB | GO:0005654; GO:0 | nucleoplasm; cytop |
| | | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA; IBA | | |
| Catalysis of the rea | IEA; IEA | GO:0005789; GO:0 | endoplasmic reticul |
| Binding to a calciu | IEA | | |
| Binding to a protein | IEA | GO:0005737; GO:0 | cytoplasm; intracell |
| Transport systems | IBA; IEA | GO:0005773; GO:0 | vacuole; vacuolar m |
| Binding to damage | IEA; IEA; IBA; IBA; IB | GO:0000502; GO:0 | proteasome comple |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binds to and stops, | IEA | GO:0005615 | extracellular space |
| | | GO:0016021 | integral component |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Binding to a protein | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the phc | IEA; IEA | GO:0016021 | integral component |
| Catalysis of the hyd | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016021 | integral component |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA; IEA | GO:0005829 | cytosol |
| | | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a zinc io | IEA; IEA | | |
| Catalysis of the phc | IBA; IEA | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| Binds to and stops, | IEA; IEA; IEA | GO:0005576 | extracellular region |
| | | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005737 | cytoplasm |
| | | GO:0071944 | cell periphery |
| Binding to a nucleic | IEA; IEA | | |
| Binding to a transfe | IEA; IEA; IBA; IEA; IE | GO:0005737; GO:0 | cytoplasm; mitocho |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005829 | cytosol |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| A transcription reg | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | | |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a microt | IBA; IBA | GO:0005737; GO:0 | cytoplasm; spindle; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005783 | endoplasmic reticul |
| Binding to ATP, ade | IEA; IEA | GO:0016020 | membrane |
| Binding to a nucleo | IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the rea | IBA; IEA | GO:0005829 | cytosol |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Binding to ADP, ade | IEA | | |
| Binding to a polysa | IEA | | |
| Binding to an RNA r | IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleic | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA | | |
| Binding to ATP, ade | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IBA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of a bioch | IEA; IBA; IBA | | |
| Binding to a nucleic | IEA; IBA; IBA; IEA | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA | | |
| Binding to a nucleo | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the tran | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tran | IBA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | | |
| Any molecular func | IEA; IPI; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0110165 | cellular anatomical |
| A transcription regu | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Binding to an RNA r | IEA |  |  |
| Catalysis of the pho | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0005576; GO:0 | extracellular region |
|  |  | GO:0009507; GO:0 | chloroplast; chlorop |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Catalysis of the tran | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA; IDA |  |  |
| Catalysis of the clea | IEA; IEA; IEA |  |  |
| Catalysis of the seq | IEA; IEA; IEA; IEA; IE | GO:0000178; GO:0 | exosome (RNase co |
| Catalysis of the inco | IEA; IEA; IEA; IEA; IE | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a genera | IBA | GO:0000126 | transcription factor |
| Catalysis of the hyd | IEA |  |  |
| Binding to a calcium | IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleic | IEA; IEA |  |  |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0016021 | integral component |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IEA; IEA; IEA |  |  |
| Binding to a nucleic | IEA; IEA |  |  |
|  |  | GO:0009507; GO:0 | chloroplast; chlorop |
|  |  | GO:0005774; GO:0 | vacuolar membrane |
| Binding to an RNA r | IEA; IEA; IEA |  |  |
| A transcription regu | IBA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a microtu | IBA | GO:0005737; GO:0 | cytoplasm; spindle; |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
|  |  | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular entit | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
| Enables the transfe | IBA; IEA; IEA; IEA | GO:0005887; GO:0 | integral component |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005773; GO:0 | vacuole; membrane |
| Any molecular func | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; Holliday ju |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Catalysis of the rea | IBA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binds to and stops, | IEA | GO:0005886 | plasma membrane |
| The action of a mol | IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Binding to messeng | IBA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005829 | cytosol |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to monome | IEA; IEA | GO:0016020 | membrane |
| Inhibition of the rea | IBA | GO:0009507 | chloroplast |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005730; GO:0 | nucleolus; small-su |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | | |
| Catalysis of the trar | IEA; IEA; IBA | GO:0005789 | endoplasmic reticul |
| Binding to a carboh | IEA | GO:0016020; GO:0 | membrane; integral |
| OBSOLETE. Enables | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| Any molecular func | IBA; IEA; IDA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Binds to and stops, | IEA | GO:0005886 | plasma membrane |
| Catalysis of the tra | IEA; IBA; IEA; IBA | GO:0000151; GO:0 | ubiquitin ligase con |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IBA; IEA; ISS; IP | GO:0005634; GO:0 | nucleus; cytoplasm |
| Generation of force | IEA; IBA; IBA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a nucleic | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear sp |
| Enables the transfe | IBA; IEA; IEA; IEA | GO:0005887; GO:0 | integral component |
| Binding to a protei | IEA | | |
| Binding to a protei | IEA | | |
| A DNA-binding tra | IBA; IEA; IBA; IEA; IB | GO:0005634; GO:0 | nucleus; histone me |
| Enables the active t | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| Binding to a protei | IEA; IEA | | |
| Binding to a lipid. | IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IEA | | |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; CCAAT-bi |
| Binding to monome | IEA | GO:0110165 | cellular anatomical |
| | | GO:0009535; GO:0 | chloroplast thylakoi |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| Binds to and stops, | IEA; IBA; IBA | | |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; endopla |
| Catalysis of an oxid | IBA; IEA | | |
| Catalysis of the hyd | IBA | GO:0000139; GO:0 | Golgi membrane; e |
| Enables the active t | IEA; IEA; IDA; IDA | GO:0005773; GO:0 | vacuole; vacuolar m |
| Catalysis of the trar | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Binds to and stops, | IEA | | |

| | | | |
|---|---|---|---|
| Enables the transfe | IDA; IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA | GO:0005576 | extracellular region |
| Enables the transfe | IBA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to monome | IEA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA | GO:0000139; GO:0 | Golgi membrane; e |
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005777; GO:0 | peroxisome; plasm |
| Catalysis of the tra | IEA; IEA | GO:0005634; GO:0 | nucleus; nucleolus |
| Binding to a zinc io | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Binding to a zinc io | IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to ATP, ade | IEA; IBA; IEA; IBA; IB | GO:0005759; GO:0 | mitochondrial matri |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009707 | chloroplast outer m |
| Catalysis of the hyd | IEA; IBA | | |
| Catalysis of the tra | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to double-s | IEA | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009707 | chloroplast outer m |

| | | | |
|---|---|---|---|
| Binding to a ferrou | IBA; IEA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IEA | | |
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005777; GO:0 | peroxisome; peroxi |
| Binding to a metal i | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0005615; GO:0 | extracellular space; |
| Binding to calmodu | IBA | GO:0005886 | plasma membrane |
| Binding to a nucleic | IEA; IEA; IEA; IBA; IE | GO:0000151; GO:0 | ubiquitin ligase con |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Enables the facilitat | IEA | GO:0009707; GO:0 | chloroplast outer m |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the ph | IEA; IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Any molecular func | IEA; IBA; IBA; IBA; IE | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IBA | GO:0005768; GO:0 | endosome; Golgi ap |
| | | GO:0005623; GO:0 | obsolete cell; extrin |

| | | | |
|---|---|---|---|
| | | GO:0000785; GO:0 | chromatin; nucleus |
| Binding to a nucleic | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of a bioch | IEA; IEA; IEA; IEA | GO:0005739 | mitochondrion |
| Binding to a DNA st | IEA; IBA | GO:0005634 | nucleus |
| | | GO:0000940; GO:0 | outer kinetochore; |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the tra | IEA; IEA; IBA; IEA | | |
| Binding to an identi | IEA | GO:0005794; GO:0 | Golgi apparatus; cy |
| Binding to a protei | IEA | GO:0005634 | nucleus |
| Binding to a copper | IEA; IBA; IBA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Binding to a specifi | IBA; IBA | GO:0005634 | nucleus |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA; IEA; IBA; IBA | GO:0043231 | intracellular membr |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Catalysis of the pho | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the tran | IBA | GO:0016020 | membrane |
| Catalysis of the tran | IBA; IEA | GO:0005694; GO:0 | chromosome; cytop |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; intracellula |
| Catalysis of the pho | IEA; IEA | | |
| Catalysis of the tran | IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IEA | | |
| Binding to a protein | IEA | | |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0016607 | nuclear speck |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to phospha | IBA | GO:0016020; GO:0 | membrane; early er |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |

| | | | |
|---|---|---|---|
| | | GO:0016020; GO:0 | membrane; integral |
| A motor activity tha | IEA; IEA; IEA; IEA; IE | GO:0005874 | microtubule |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binding to inositol | ISS; IEA; ISS | GO:0005634; GO:0 | nucleus; SCF ubiqui |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the ran | IEA; IEA; IEA | GO:0005576 | extracellular region |
| Catalysis of the rea | IBA; IEA; IBA; IEA; IB | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the rea | IEA; IEA | GO:0005764 | lysosome |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a protein | IEA | GO:0110165 | cellular anatomical |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA | GO:0009570 | chloroplast stroma |

| | | | |
|---|---|---|---|
| Binding to an iron ( | IEA; IEA; IDA; IEA; IE | GO:0009507; GO:0 | chloroplast; plastid |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0009535 | chloroplast thylakoi |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IBA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IBA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a nucleic | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a metal i | IEA | GO:0005634 | nucleus |
| Binding to a DNA re | IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005773 | vacuole |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Binding to a lipid.; | IEA; IBA; IBA | GO:0005829; GO:0 | cytosol; membrane; |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| A DNA-binding trar | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to an immu | IEA; IEA | GO:0005576 | extracellular region |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of the trar | IEA; IBA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of a bioch | IEA; IEA; IEA | | |
| Binding to a protein | IEA; IEA; IEA | | |
| Binding to a protein | IEA; IEA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Catalysis of a bioch | IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; cytosol |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a nucleo | IEA; IBA; IBA; IEA; IE | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| Catalysis of the rea | IBA; IBA; IEA | GO:0005829 | cytosol |
| Catalysis of the tran | IEA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IBA; IEA; IEA | GO:0005576 | extracellular region |
| | | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IEA; IBA; IEA | | |
| Any molecular func | IEA | | |
| Catalysis of the hyd | IBA | | |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Catalysis of a bioch | IEA; IBA | | |
| Binding to a protein | IEA | GO:0005770; GO:0 | late endosome; HO |
| Catalysis of the rea | IEA; IEA | GO:0005737; GO:0 | cytoplasm; vacuole; |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IB | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; intracellula |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA; IEA; IEA | | |
| Enables the transfe | IBA; IEA; IEA; IEA | GO:0005887; GO:0 | integral component |
| Catalysis of the tran | IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA | | |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0000325; GO:0 | plant-type vacuole; |
| | | GO:0009523; GO:0 | photosystem II; chl |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of an oxid | IEA; IEA | | |
| Binding to flavin m | IEA; IEA; IBA | GO:0005777 | peroxisome |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IBA; IBA | | |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IB | GO:0000307; GO:0 | cyclin-dependent p |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA; IBA; IEA; IE | GO:0005794; GO:0 | Golgi apparatus; tra |
| Catalysis of the trar | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA |  |  |
| A transcription regu | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA | GO:0005794 | Golgi apparatus |
| Catalysis of the trar | IEA; IEA; IEA | GO:0016020 | membrane |
| Catalysis of the rea | IEA; IBA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a magne | IEA; IEA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an RNA r | IEA | GO:0009507 | chloroplast |
| Enables the transfe | IEA | GO:0005774; GO:0 | vacuolar membrane |

| | | | |
|---|---|---|---|
| Catalysis of the end | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |

| | | | |
|---|---|---|---|
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binding to a protei | IEA | | |
| Binding to a nucleic | IEA | | |
| Binding to an amin | IEA | | |
| Binding to double- | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromoso |
| | | | |
| Any molecular func | IEA; IBA; IEA; IBA; IB | GO:0005634 | nucleus |
| | | GO:0009522; GO:0 | photosystem I; chlo |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IBA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; Golgi ap |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a metal i | IEA; IEA | | |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to ATP, ade | IEA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the ph | IEA; IEA | GO:0016020 | membrane |
| Any molecular func | IEA; IEA; IEA | | |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Catalysis of the phc | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to a protein | IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| Binding to a metal i | IEA | GO:0005758 | mitochondrial inter |
| Catalysis of the phc | IEA; IEA; IEA | | |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| Binding to a microt | IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a protein | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to calmodu | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the cle | IEA; IEA; IEA | | |
| Catalysis of the hyd | IBA; IEA | | |
| | | GO:0009506 | plasmodesma |
| A general transcript | IEA; IBA; IBA; IEA | GO:0000126; GO:0 | transcription factor |
| Catalysis of the tra | IEA; IEA; IBA; IBA | GO:0043231 | intracellular membr |
| | | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IBA; IEA; IEA; IB | GO:0090575 | RNA polymerase II t |
| Enables the transfe | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| | | GO:0005739; GO:0 | mitochondrion; chl |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| | | GO:0005741; GO:0 | mitochondrial oute |
| Binding to an unfol | IBA | GO:0005737; GO:0 | cytoplasm; endopla |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Removes phosphati | IBA | | |
| Binding to a nucleic | IEA; IEA | | |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA | | |
| Binding to an RNA | IBA; IEA | GO:0016593; GO:0 | Cdc73/Paf1 comple |

| | | | |
|---|---|---|---|
| Enables the energy- | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to calmodu | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA | GO:0000118; GO:0 | histone deacetylase |
| Any molecular func | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | | |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Catalysis of the tra | IBA | GO:0016021 | integral component |
| Catalysis of the rea | IEA; IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to an RNA | IEA | | |
| Binding to a protei | IEA; IBA | GO:0005634; GO:0 | nucleus; Set1C/CO |
| Catalysis of the rea | IBA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; gly |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0009707 | chloroplast outer m |
| Binding to an identi | IPI | GO:0005634 | nucleus |
| Binds to and stops, | IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005874; GO:0 | microtubule; cortica |
| Catalysis of the phc | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Isoenergetic transfe | IBA | | |
| | | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IBA; IEA | GO:0005634; GO:0 | nucleus; cytosol |
| | | GO:0005634 | nucleus |
| | | GO:0005739 | mitochondrion |
| The formation of a | IEA | | |
| Binding to an RNA r | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IBA; IEA | | |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IBA | GO:0005634; GO:0 | nucleus; spliceosom |
| Catalysis of the rea | IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA | | |
| Catalysis of the rea | IBA; IBA | GO:0005737 | cytoplasm |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; site of dou |
| | | GO:0016020 | membrane |
| Binding to a zinc io | IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Binding to a protein | IEA | | |
| Catalysis of the ph | IEA; IBA; IEA; IEA; IB | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0009705; GO:0 | plant-type vacuole |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| | | GO:0005576 | extracellular region |

| | | | |
|---|---|---|---|
| | | GO:0005576 | extracellular region |
| Catalysis of the tra | IEA; IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IB | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the inc | IBA; IEA; IEA; IBA; IE | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a calciu | IEA; IEA | | |
| Catalysis of the tra | IBA; IEA | | |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA | | |
| Binding to a protei | IEA; IEA | GO:0009507 | chloroplast |
| Functions in the sto | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0000325; GO:0 | plant-type vacuole; |
| Binding to an actin | IBA | GO:0005886 | plasma membrane |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IBA | | |
| Binding to a copper | IEA; IBA; IBA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the pho | IEA; IEA | GO:0016020 | membrane |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IDA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the rea | IEA; IEA; IEA; IEA | GO:0005829 | cytosol |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| A transcription regu | IEA | | |
| Catalysis of the rea | IBA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Catalysis of the trar | IEA | GO:0016020 | membrane |
| Catalysis of the hyd | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA | GO:0005737; GO:0 | cytoplasm; nuclear |
| | | GO:0005634; GO:0 | nucleus; transcripti |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0016020 | membrane |
| | | GO:0055028 | cortical microtubule |
| Any molecular func | IEA; IDA; IPI; IDA | GO:0005634; GO:0 | nucleus; cytoplasm |

| | | | |
|---|---|---|---|
| | | GO:0110165 | cellular anatomical |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the ph | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| | | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a riboso | IBA; IEA | GO:0005730; GO:0 | nucleolus; small-su |
| Binding to a metal i | IEA | | |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a zinc io | IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| The formation of a | IEA | | |
| Binding to a specifi | IEA; IEA; IEA; IEA; IEA | | |
| A transcription cor | IBA; IBA; IEA | GO:0000124; GO:0 | SAGA complex; nuc |
| Catalysis of the tra | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Catalysis of the rea | IEA; IBA; IEA | | |
| Enables the active t | IBA; IBA | GO:0005768; GO:0 | endosome; Golgi ap |
| Binding to a protein | IEA; IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; nuc |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005576 | extracellular region |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| | | GO:0005783 | endoplasmic reticul |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005886 | plasma membrane |
| Catalysis of the hyd | IEA; IEA | GO:0005618; GO:0 | cell wall; apoplast |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA; IBA | | |
| Catalysis of the hyd | IEA; IBA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a copper | IEA; IBA; IBA; IEA | GO:0005576; GO:0 | extracellular region |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0005886 | plasma membrane |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA | | |
| Binding to a protein | IEA; IEA | GO:0009506 | plasmodesma |
| Binding to a clathrin | IBA | GO:0005737; GO:0 | cytoplasm; vesicle; |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to single-st | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to ATP, ade | IEA; IEA | | |
| Catalysis of the phc | IEA; IEA | | |
| Catalysis of an oxid | IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| | | GO:0005634 | nucleus |
| Catalysis of the seq | IBA; IEA; IBA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0000118; GO:0 | histone deacetylase |
| | | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the tran | IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Catalysis of the hyd | IEA |  |  |
| Binding to a protein | IEA |  |  |
| Binding to a nucleic | IEA; IEA |  |  |
| Catalysis of the pho | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
| A transcription regu | IBA; IBA; IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA; IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| Catalysis of the tran | IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the hyd | IEA; IBA; IEA; IEA; IE | GO:0005783; GO:0 | endoplasmic reticul |
|  |  | GO:0005783 | endoplasmic reticul |
| Any molecular func | IEA; IEA |  |  |
| Catalysis of the rea | IBA; IEA | GO:0000427; GO:0 | plastid-encoded pla |
| Catalysis of the tran | IEA | GO:0016021 | integral component |
| Catalysis of the tran | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA | GO:0000785; GO:0 | chromatin; nucleus; |
| Catalysis of the rea | IEA; IEA; IBA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| The action of a mol | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA; IBA; IEA; IE | GO:0000932; GO:0 | P-body; cytoplasm; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a carboh | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a microt | IBA | GO:0005737; GO:0 | cytoplasm; centroso |
| Catalysis of the trar | IEA; IBA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Binding to a fatty ac | IBA; IEA | GO:0009570 | chloroplast stroma |
| Catalysis of the trar | IBA; IEA | | |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA |  |  |
| Catalysis of the rea | IBA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the trar | IEA; IEA; IBA; IBA | GO:0043231 | intracellular membr |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IDA; IEA; IEA | GO:0005634 | nucleus |
| Binding to the tail r | IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IBA; IEA | GO:0005623; GO:0 | obsolete cell; memb |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IBA; IBA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005576 | extracellular region |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA | | |
| Binding to ATP, ade | IEA; IEA | | |
| Binding to a protei | IEA | | |
| Any molecular func | IEA; IEA; IPI; IEA | GO:0005634 | nucleus |
| Enables the transm | IEA | GO:0005886; GO:0 | plasma membrane; |
| Enables the transfe | IEA; IEA; IBA; IBA | GO:0005794; GO:0 | Golgi apparatus; m |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005634; GO:0 | nucleus; Ku70:Ku8 |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IBA; IBA | GO:0016020 | membrane |
| Binding to a peroxis | IBA | GO:0005777; GO:0 | peroxisome; peroxi |
| Catalysis of the hyd | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; chloropl |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0005634; GO:0 | nucleus; spliceoson |
| Functions in chain | IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a sterol, | IBA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA | GO:0000786; GO:0 | nucleosome; nucleu |
| Catalysis of the trar | IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005654; GO:1 | nucleoplasm; ribon |
| Binding to a protein | IEA |  |  |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA |  |  |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IB | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the rea | IEA; IEA | GO:0005789; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IBA |  |  |
| A transcription reg | IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a fatty-a | IBA; IEA | GO:0005829 | cytosol |
| Binding to a metal i | IEA |  |  |
| Catalysis of the tra | IEA; IEA | GO:0005737; GO:0 | cytoplasm; Golgi ap |
| A DNA-binding tra | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
|  |  | GO:0005634; GO:0 | nucleus; chromoso |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IPI; IDA | GO:0005634; GO:0 | nucleus; endoplasm |
| Binds to and stops, | IEA; IBA; IBA | | |
| Catalysis of the ph | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| | | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to FAD, flav | IEA | GO:0005829 | cytosol |
| Catalysis of the rea | IEA | GO:0005737; GO:0 | cytoplasm; cytosol |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a metal i | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0031213 | RSF complex |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0009536; GO:0 | plastid; membrane; |
| Acting as a marker | IEA | GO:0016020; GO:0 | membrane; SNARE |
| Any molecular func | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA | GO:0005739; GO:0 | mitochondrion; me |
| Catalysis of the trar | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to ATP, ade | IEA; IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a proteir | IEA; IBA; IBA | GO:0005829; GO:0 | cytosol; extrinsic cc |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | | |
| Catalysis of the hyd | IBA; IEA | GO:0005773 | vacuole |
| Binding to a specifi | IBA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a proteir | IEA | | |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of the trar | IEA; IEA; IBA; IBA; IB | GO:0000139; GO:0 | Golgi membrane; er |
| Binding to a proteir | IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to an RNA r | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nucleolus; |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the phc | IEA; IEA; IEA | | |
| | | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; chloropl |
| Catalysis of the trar | IEA; IBA; IEA | GO:0009527; GO:0 | plastid outer memb |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IBA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| | | GO:0000974; GO:0 | Prp19 complex; nuc |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the tran | IEA; IBA; IEA | GO:0009707 | chloroplast outer m |
| Catalysis of the tran | IBA; IEA |  |  |
| Binding to a copper | IEA; IEA; IBA; IBA; IE | GO:0005576; GO:0 | extracellular region |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tran | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of an oxid | IBA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the tran | IBA | GO:0005768; GO:0 | endosome; trans-G |
|  |  | GO:0005634 | nucleus |
| Binding to a 7-meth | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Functions in the init | IEA; IBA |  |  |
| Binding to a nucleic | IEA; IEA; IDA; IPI | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA | GO:0009507 | chloroplast |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | GO:0005634 | nucleus |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA; IEA | GO:0005829 | cytosol |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; transcripti |
| Catalysis of the rea | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to a lipid. | IEA | GO:0005737 | cytoplasm |
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the geo | IEA; IEA | GO:0005811 | lipid droplet |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a copper | IBA; IBA; IEA | GO:0016020 | membrane |
| | | GO:0016021 | integral component |
| A transcription regu | IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IEA | GO:0005774; GO:0 | vacuolar membrane |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0016514 | SWI/SNF complex |
| | | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016021 | integral component |
| Catalysis of the hyd | IEA | | |

|  |  |  |  |
|---|---|---|---|
|  |  | GO:0005637; GO:0 | nuclear inner memb |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear rep |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol; rib |
| Catalysis of the clea | IEA; IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA |  |  |
| Any molecular func | IEA |  |  |
|  |  | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the rea | IEA; IEA; IEA; IDA |  |  |

| | | | |
|---|---|---|---|
| Binding to a manga | IEA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Catalysis of the hyd | IEA; IEA | | |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a proteir | IEA; IEA | | |
| Any molecular func | IBA; IBA | GO:0005730 | nucleolus |
| | | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IBA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of an oxid | IEA; IBA; IEA; IBA | | |
| Binding to an RNA r | IEA; IEA; IBA | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA | GO:0005634; GO:0 | nucleus; spliceoson |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; microtul |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of an oxid | IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0000785; GO:0 | chromatin; nucleus; |
| | | GO:0005774; GO:0 | vacuolar membrane |
| Binding to messeng | IBA; IBA; IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Binding to an inosit | IEA; IEA | GO:0005623 | obsolete cell |
| Catalysis of the trar | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Binding to a specifi | IBA; IBA; IEA; IBA; IB | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IBA | GO:0009507; GO:0 | chloroplast; chlorop |
| Catalysis of the hyd | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of a bioch | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binds to and increa | IBA | GO:0005623; GO:0 | obsolete cell; memb |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| The action of a mol | IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0009505; GO:0 | plant-type cell wall |
| Any molecular func | IEA; IEA | | |
| Binds to and stops, | IEA; IEA; IEA; IEA; IB | GO:0005618 | cell wall |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a protein | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IEA | GO:0005634; GO:0 | nucleus; mediator c |
| Binding to a SNARE | IBA; IBA | GO:0012505; GO:0 | endomembrane sys |
| Any molecular func | IBA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a metal i | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to chromati | IBA; IBA; IEA | GO:0043240; GO:0 | Fanconi anaemia nu |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| Isoenergetic transfe | IBA | | |
| Catalysis of the dim | IEA; IEA; IEA; IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; intracellula |
| | | GO:0000176; GO:0 | nuclear exosome (R |
| An thiol-dependent | IBA | | |
| Binds to and stops, | IEA | | |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005730 | nucleolus |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IDA; IEA; IBA; IBA; IDA; IDA; IDA | | |
| Any molecular func | IEA; IPI; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Binds to and stops, | IBA | | |
| A DNA-binding trar | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the phc | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to an RNA p | IBA | GO:0016591 | RNA polymerase II, |
| Binding to a specifi | IBA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Enables the transfe | IBA; IEA; IEA; IEA; IE | GO:0005887; GO:0 | integral component |
| | | GO:0005634; GO:0 | nucleus; CAF-1 con |
| Enables the transfe | IBA; IEA; IEA; IEA; IE | GO:0005887; GO:0 | integral component |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA; IEA | GO:0009506 | plasmodesma |
| Catalysis of the tra | IEA; IEA; IBA; IBA; IB | GO:0000139; GO:0 | Golgi membrane; e |
| Catalysis of the tra | IBA; IEA | GO:0000151 | ubiquitin ligase con |
| | | GO:0005840; GO:0 | ribosome; chloropla |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Enables the transfe | IBA | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of an oxid | IEA | GO:0005777 | peroxisome |
| Catalysis of the tra | IEA | GO:0005794; GO:0 | Golgi apparatus; m |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to monome | IEA; IBA | GO:0005737; GO:0 | cytoplasm; actin cy |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a protei | IEA | | |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of an oxid | IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IB | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IEA; IPI; IEA | GO:0005634 | nucleus |
| The action of a mol | IEA; IEA; IEA; IEA; IE | GO:0005739; GO:0 | mitochondrion; mit |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the phc | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0009508; GO:0 | plastid chromosom |
| Binding to an inosit | IEA; IEA | GO:0005623; GO:0 | obsolete cell; memb |
| A DNA-binding trar | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to messeng | IEA | | |
| Binds to and stops, | IEA; IEA; IEA; IEA; IB | GO:0005618 | cell wall |
| Catalysis of the rea | IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005634 | nucleus |
| | | GO:0000139; GO:0 | Golgi membrane; e |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009507; GO:0 | chloroplast; membr |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IPI | | |
| Binding to DNA of a | IEA | | |
| Binding to a ubiquit | IBA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA | | |
| | | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA; IBA; IEA; IB | GO:0005730; GO:0 | nucleolus; Cajal boc |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to ATP, ade | IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA | GO:0005829; GO:0 | cytosol; chloroplast |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an RNA r | IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Catalysis of a bioch | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; cyt |
| Any molecular entit | IEA | GO:0016021; GO:0 | integral component |
| Binding to a protein | IEA | | |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA; IEA | GO:0000922 | spindle pole |
| Binding to ATP, ade | IEA; IEA | | |
| Binding to a protein | IEA | | |
| Any molecular func | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; microtul |
| | | GO:0005794; GO:0 | Golgi apparatus; m |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to ADP, ad | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a myosir | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005840; GO:0 | ribosome; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; nucleolus |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IBA; IBA | GO:0008023 | transcription elong |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of an oxid | IEA; IEA; IEA | | |
| Binding to an RNA r | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear RN |
| Catalysis of the ph | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Functions in the ini | IEA | GO:0005671 | obsolete Ada2/Gcn |
| Catalysis of the tra | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Enables the transfe | IEA; IBA; IEA | GO:0005739; GO:0 | mitochondrion; vac |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the rea | IBA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| The formation of a | IEA | | |
| Binding to a protein | IEA | GO:0005730; GO:0 | nucleolus; small-su |
| Binding to an intern | IBA; IBA | GO:0005868; GO:0 | cytoplasmic dynein |
| Binding to a specifi | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| | | GO:0043231 | intracellular membr |
| Binds to and stops, | IEA; IBA; IBA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005739; GO:0 | mitochondrion; mit |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a metal i | IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0000407; GO:0 | phagophore assem |
| Catalysis of the tra | IEA; IEA; IEA; IEA | GO:0043231 | intracellular memb |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| | | GO:0005634 | nucleus |
| Binding to a lipid. | IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| A DNA-binding tra | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Enables the transfe | IEA | GO:0005768; GO:0 | endosome; early en |
| Any molecular func | IEA | | |
| Binding to a microt | IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IBA | GO:0034098 | VCP-NPL4-UFD1 A |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA; IBA | GO:0005634; GO:0 | nucleus; Set1C/CO |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020; GO:0 | membrane; integral |
| Binding to monome | IEA; IBA; IBA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Catalysis of an oxid | IEA; IEA; IBA |  |  |
| Binding to a clathrin | IBA | GO:0005737; GO:0 | cytoplasm; vesicle; |
| Generation of force | IEA | GO:0016459 | myosin complex |

| | | | |
|---|---|---|---|
| | | GO:0005576 | extracellular region |
| Binding to a protein | IEA | | |
| Catalysis of the tran | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| | | GO:0005886 | plasma membrane |
| Binding to a nucleic | IEA; IEA; IBA | | |
| Binding to a specifi | IEA; IEA | GO:0005634 | nucleus |
| Binding to messeng | IBA; IEA | GO:0016020 | membrane |
| | | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005634; GO:0 | nucleus; nuclear po |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016021 | integral component |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IBA; IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IPI; IEA; IEA; IEA; IEA | | |
| | | GO:0043668 | exine |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| Any molecular func | IEA; IEA; IEA | GO:0000786; GO:0 | nucleosome; nucleu |
| | | GO:0031213 | RSF complex |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | | |
| | | GO:0005623; GO:0 | obsolete cell; chlor |
| Catalysis of the hyd | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a protein | IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| A DNA-binding trar | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IPI | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the rea | IEA; IEA; IEA | GO:0000118; GO:0 | histone deacetylase |
| Binding to a fatty-a | IBA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA; IEA; IEA; IEA; IB | GO:0000785; GO:0 | chromatin; nucleus |
| Binding to a zinc io | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IBA | | |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; intracellula |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; vacuola |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005971 | ribonucleoside-dipl |
| Binding to a protei | IEA | | |
| | | GO:0032545; GO:0 | CURI complex; UTP- |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a metal i | IEA | | |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; G prote |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; transcripti |

| | | | |
|---|---|---|---|
| | | GO:0005634; GO:0 | nucleus; cytosol; pr |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a protei | IEA | | |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the ph | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0110165 | cellular anatomical |
| Catalysis of the tra | IEA | | |
| Catalysis of the tra | IEA | GO:0016020 | membrane |

| | | | |
|---|---|---|---|
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Catalysis of the trar | IBA | | |
| Binding to a nucleic | IEA; IEA | GO:0005634 | nucleus |
| Binding to ATP, ade | IEA; IBA; IEA | GO:0000325; GO:0 | plant-type vacuole; |
| Binding to a nucleic | IEA; IBA | GO:1990904 | ribonucleoprotein c |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA; IEA | | |
| | | GO:0005576; GO:0 | extracellular region |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the inc | IEA; IEA; IBA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA | | |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IDA; IPI; IDA | GO:0005634 | nucleus |
| Binds to and stops, | IEA | | |
| Binding to a myosi | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |
| Catalysis of the tra | IEA; IEA; IBA; IEA; IE | GO:0005794; GO:0 | Golgi apparatus; tra |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016021 | integral component |
| Binding to a protei | IEA | | |
| Catalysis of the rea | IEA; IBA; IEA; IBA; IE | GO:0005739; GO:0 | mitochondrion; mit |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| | | GO:0016020 | membrane |
| Catalysis of the rea | IEA; IEA; IEA | | |
| Binding to a metal i | IEA | | |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| Binding to a microtu | IEA | | |
| Binding to a protein | IEA; IEA | | |
| Binding to a microtu | IBA | GO:0005737; GO:0 | cytoplasm; centroso |
| A transcription regu | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005886; GO:0 | plasma membrane; |
| Enables the transfe | IBA; IEA; IEA | GO:0005887; GO:0 | integral component |
| Binds to and stops, | IEA; IBA; IBA | | |
| A transcription regu | IEA | GO:0005634 | nucleus |
| Binding to a G-qua | IEA; IEA | GO:0031011; GO:0 | Ino80 complex; NSL |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Binding to the tail r | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| | | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to ATP, ade | IEA | | |
| | | GO:0005635 | nuclear envelope |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634 | nucleus |
| Binds to and stops, | IEA; IDA | GO:0005576; GO:0 | extracellular region |
| | | GO:0071944 | cell periphery |
| Catalysis of the tran | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634 | nucleus |
| Binding to a zinc io | IEA; IEA | | |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0000178; GO:0 | exosome (RNase co |
| Binds to and stops, | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| | | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IBA; IEA | GO:0005623 | obsolete cell |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a sequen | IBA; IBA; IBA | GO:0000126; GO:0 | transcription factor |

| | | | |
|---|---|---|---|
| Binds to and stops, | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005634; GO:0 | nucleus; nuclear lar |
| | | GO:0005783 | endoplasmic reticul |
| Binding to a specifi | IBA; IBA; IEA; IEA; IB | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| | | GO:0012505 | endomembrane sys |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Modulates the activ | IBA; IBA | GO:0000407; GO:0 | phagophore assem |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a ubiquit | IBA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protei | IEA | | |
| Catalysis of the rea | IEA | | |
| | | GO:0009507 | chloroplast |

| | | | |
|---|---|---|---|
| Binding to a protein | IPI; IEA; IEA; IEA | | |
| A transcription regu | IEA; IEA | | |
| Binding to a microtu | IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to an RNA r | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the tran | IEA | GO:0016021 | integral component |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| | | GO:0005730 | nucleolus |
| Binding to a metal i | IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | | |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| | | GO:0071944 | cell periphery |
| Any molecular func | IEA; IPI; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA | | |
| A transcription regu | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binds to and stops, | IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA | | |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of the trar | IEA | GO:0016021 | integral component |
| Any molecular func | IEA | | |
| | | GO:0009535; GO:0 | chloroplast thylakoi |
| | | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IEA | | |
| Modulates the activ | IBA; IBA | GO:0000407; GO:0 | phagophore assembl |
| Binding to an RNA r | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the trar | IEA | GO:0005623; GO:0 | obsolete cell; memb |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005886 | plasma membrane |
| | | GO:0071944 | cell periphery |
| Catalysis of the tra | IBA | GO:0005768; GO:0 | endosome; trans-G |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; DNA replic |
| The action of a mol | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA | GO:0016021 | integral component |
| Binding to a ubiquit | IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to DNA of a | IEA | | |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| Binding to a protei | IEA | GO:0005829 | cytosol |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription reg | IEA | GO:0005634 | nucleus |
| Binding to calmodu | IEA | | |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; spliceosom |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the end | IBA; IEA |  |  |
| Binding to a microt | IBA; IBA | GO:0005819; GO:0 | spindle; microtubul |
| Binding to a metal i | IEA |  |  |
|  |  | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a polysa | IEA |  |  |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
|  |  | GO:0005739 | mitochondrion |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA | IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a myosin | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a regulat | IBA | GO:0001650 | fibrillar center |
| The formation of a | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binding to a specifi | IDA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to double- | IEA | GO:0009507 | chloroplast |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA | GO:0005634; GO:0 | nucleus; nucleolus |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Binding to a zinc io | IEA; IEA | GO:0005634 | nucleus |
| Binding to the tail | IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| | | GO:0000120 | RNA polymerase I t |
| Binding to a nucleo | IEA; IEA; IEA | | |
| Binding to an RNA | IEA | | |
| | | GO:0000118; GO:0 | histone deacetylase |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| A motor activity tha | IBA; IBA | GO:0005737; GO:0 | cytoplasm; actin cy |
| A transcription reg | IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IBA; IEA; IEA | | |
| Binding to an unfol | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the tra | IEA | | |
| Binding to a metal | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Binding to a carboh | IEA |  |  |
| Catalysis of the tra | IEA; IEA |  |  |
| Binding to a nucleic | IEA; IEA; IEA; IEA |  |  |
| Catalysis of the rea | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| A transcription core | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | GO:0005634; GO:0 | nucleus; spliceosom |
| Binding to a nucleo | IEA; IEA; IEA |  |  |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA | GO:0005615; GO:0 | extracellular space; |
| Binding to a protein | IEA |  |  |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
|  |  | GO:0005886 | plasma membrane |
| Catalysis of the trar | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
|  |  | GO:0009507 | chloroplast |
|  |  | GO:0005634 | nucleus |
|  |  | GO:0000124 | SAGA complex |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the phc | IEA; IEA |  |  |
| Binding to a zinc io | IEA; IEA |  |  |
|  |  | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA |  |  |
| Catalysis of the trar | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |

| | | | |
|---|---|---|---|
| | | GO:0009536 | plastid |
| Binding to one or m | IBA; IEA | GO:0005777; GO:0 | peroxisome; peroxi |
| | | GO:0005634; GO:0 | nucleus; Piccolo Nu |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IEA; IEA | | |
| | | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a microt | IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a metal i | IEA | | |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to messeng | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to monome | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA | | |
| Binding to a nucleic | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016021 | integral component |
| | | GO:0005634 | nucleus |
| | | GO:0009507 | chloroplast |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0009535; GO:0 | chloroplast thylakoi |
| Any molecular func | IEA; IBA; IBA; IPI; IB | GO:0000123; GO:0 | histone acetyltransf |
| Binding to DNA of a | IEA | | |
| Binding to a zinc io | IEA | GO:0005634 | nucleus |
| Catalysis of an oxid | IBA | | |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |

|  |  |  |  |
|---|---|---|---|
| A DNA-binding trar | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IPI; IEA; ID | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IPI; IEA | GO:0005634 | nucleus |
| The formation of a | IEA | GO:0005634 | nucleus |
| A transcription reg | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IBA |  |  |
| Binding to a protein | IEA |  |  |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the trar | IBA; IEA; IEA |  |  |
| Binding to messeng | IBA; IBA; IBA | GO:0005739; GO:0 | mitochondrion; mit |

|  |  |  |  |
|---|---|---|---|
| Binding to a protei | IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a microt | IEA | GO:0005874 | microtubule |
| Binding to a protei | IEA; IEA |  |  |
|  |  | GO:0009507 | chloroplast |
| Catalysis of the hyd | IEA |  |  |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular entit | IEA; IEA | GO:0005623; GO:0 | obsolete cell; plasm |
| Catalysis of the rea | IBA; IEA |  |  |
| Binding to a calciu | IBA | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0009707; GO:0 | chloroplast outer m |
| Binding to a nucleic | IEA; IEA |  |  |
| Binding to a protei | IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA |  |  |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| A transcription reg | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | GO:0005634 | nucleus |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Binding to messeng | IBA | GO:0005623 | obsolete cell |
| A transcription reg | IEA; IEA |  |  |
|  |  | GO:0005634 | nucleus |
| Binding to a protei | IEA |  |  |
| Catalysis of the tra | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |

| | | | |
|---|---|---|---|
| | | GO:0005764; GO:0 | lysosome; lysosoma |
| Catalysis of the hyd | IEA | | |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA | IEA; IEA | GO:0005737; GO:0 | cytoplasm; mRNA c |
| | | GO:0005634 | nucleus |
| Binding to a proteir | IEA | GO:0005739 | mitochondrion |
| Binding to monome | IEA; IEA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| | | GO:0005634 | nucleus |
| Catalysis of the trar | IEA | GO:0016021 | integral component |
| Binding to a metal i | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a microtu | IEA | | |
| Binding to a proteir | IEA | GO:0005739 | mitochondrion |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA | GO:1990904 | ribonucleoprotein c |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005730; GO:1 | nucleolus; ribonucle |
| Binds to and stops, | IDA; IEA | GO:0005576; GO:0 | extracellular region |
| Any molecular func | IEA; IEA | | |
| | | GO:0005737 | cytoplasm |

|  |  |  |  |
|---|---|---|---|
| A DNA-binding tra | IBA; IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IBA; IEA; IEA; IB | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a metal i | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA |  |  |
| Binding to an RNA r | IEA |  |  |
| Catalysis of the tra | IEA; IEA; IEA | GO:0005737 | cytoplasm |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to monome | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nonide | IEA | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to DNA of a | IEA |  |  |
| A transcription reg | IEA |  |  |
| Binding to one or | IBA; IEA | GO:0005777; GO:0 | peroxisome; peroxi |
| Catalysis of the tra | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0009508; GO:0 | plastid chromosom |
| Any molecular func | IEA; IEA | GO:0005739 | mitochondrion |
| Binding to a protei | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA | GO:0005576 | extracellular region |
| Binding to a nucleic | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of an oxid | IBA | GO:0005829; GO:0 | cytosol; membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| | | GO:0005829 | cytosol |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a protein | IPI | GO:0005634 | nucleus |
| | | GO:0005768 | endosome |
| Binding to a protein | IEA | GO:0005886 | plasma membrane |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleic | IEA | | |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleic | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA; IEA | GO:0005576 | extracellular region |
| Catalysis of the tran | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to an RNA r | IBA | GO:0010494 | cytoplasmic stress |
| Binding to a nonide | IEA | GO:0005634 | nucleus |
| | | GO:0043240 | Fanconi anaemia nu |

| | | | |
|---|---|---|---|
| Binding to a protei | IEA | | |
| | | | |
| | | | |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to double- | IEA | GO:0009507 | chloroplast |
| | | | |
| Catalysis of the rea | IEA | | |
| Catalysis of the tra | IEA; IEA; IEA | | |
| Enables the transfe | IEA | GO:0009536; GO:0 | plastid; chloroplast |
| Any molecular func | IEA; IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to ATP, ade | IEA | GO:0005634 | nucleus |
| | | | |
| Catalysis of the pho | IEA; IEA; IEA; IEA | | |
| | | | |
| | | | |
| | | | |
| | | | |
| Catalysis of the hyd | IEA | | |
| Binding to an RNA | IEA; IEA | GO:0005737; GO:0 | cytoplasm; mRNA c |
| | | | |
| Binding to chromat | IBA; IEA | GO:0000228; GO:0 | nuclear chromosom |
| | | | |
| | | | |
| | | | |
| Binding to a protei | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | | |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA | GO:0005829 | cytosol |
| Binding to a protein | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; autophago |
| Binding to monome | IEA; IEA | GO:0110165 | cellular anatomical |
| Catalysis of the hyd | IEA | | |
| Any molecular func | IEA; IEA | GO:0005739; GO:0 | mitochondrion; nuc |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a microtu | IEA | GO:0005874; GO:0 | microtubule; memb |
| Binding to ATP, ade | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the ph | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IDA | GO:0005634 | nucleus |
| Binding to an inosit | IEA; IEA | GO:0005623; GO:0 | obsolete cell; mem |
| Binding to a protei | IEA | | |
| A transcription reg | IEA; IBA; IBA; IEA; IE | GO:0000123; GO:0 | histone acetyltransf |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0090575 | RNA polymerase II t |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; plasma me |
| A DNA-binding tra | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a myosi | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0010008 | endosome membra |
| Catalysis of the tra | IEA; IBA | | |
| Any molecular func | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a protein | IPI | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IBA | | |
| Binding to an inosit | IEA | | |
| | | GO:0005829 | cytosol |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634 | nucleus |
| Binding to a metal i | IEA; IEA | GO:0005737 | cytoplasm |
| Any molecular func | IEA; IEA; IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Binding to a protein | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Binding to a sequen | IBA; IBA; IEA | GO:0000127; GO:0 | transcription factor |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| A transcription regu | IBA; IBA; IEA; IBA; IE | GO:0000123; GO:0 | histone acetyltransf |
| Catalysis of the tran | IBA; IEA; IEA; IEA; IEA | | |
| Catalysis of the tran | IBA; IEA; IEA; IEA; IEA | | |
| | | GO:0005739; GO:0 | mitochondrion; pla |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0009507; GO:0 | chloroplast; membr |
| The action of a mol | IEA | GO:0005634; GO:0 | nucleus; nuclear en |
| Catalysis of the hyd | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| A DNA-binding tran | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| A transcription regu | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a mediat | IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; nucleoplas |
| A DNA-binding tran | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| | | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IBA | GO:0005634; GO:0 | nucleus; nuclear lu |
| Binding to a nucleic | IEA; IEA | GO:0005783 | endoplasmic reticul |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a metal i | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; DNA replic |
| Binding to a metal i | IEA; IEA | | |
| Binding to single-s | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; nucleolus |
| Binding to a nucleic | IEA | | |
| | | GO:0009507; GO:0 | chloroplast; membr |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binds to and modul | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| | | GO:0016021 | integral component |
| Catalysis of the hyd | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleic | IEA; IEA; IBA | GO:0043229 | intracellular organe |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005829 | cytosol |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| Binding to a protein | IPI | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the trar | IBA; IEA; IEA; IEA; IEA | | |
| | | GO:0009507; GO:0 | chloroplast; membr |
| Binding to a specifi | IBA; IBA; IEA | | |
| | | GO:0019898 | extrinsic componen |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA; IBA; IEA |  |  |
|  |  | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; CCAAT-bi |
| Catalysis of the trar | IEA; IBA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
|  |  | GO:0000781; GO:0 | chromosome, telom |
| Catalysis of the hyd | IBA; IEA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to an RNA r | IBA | GO:0005634; GO:0 | nucleus; nucleolus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the phc | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA | GO:0030687; GO:0 | preribosome, large |
| Binding to a metal i | IEA |  |  |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binds to and stops, | IBA; IEA | GO:0005576 | extracellular region |
| Binding to a zinc io | IEA; IEA; IEA |  |  |
| Catalysis of the trar | IEA; IEA |  |  |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binds to and stops, | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a metal i | IEA | | |
| Binding to a protein | IEA | | |
| Catalysis of the tran | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA | GO:0000428; GO:0 | DNA-directed RNA |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IBA; IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to messeng | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to a protein | IEA | | |
| Catalysis of the tran | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IEA; IBA; IEA; IE | GO:0005829 | cytosol |
| | | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| The formation of a | IEA | | |
| | | GO:0031011 | Ino80 complex |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Binding to a protein | IPI | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | | |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0005634; GO:1 | nucleus; ribonucleo |
| Any molecular func | IEA | | |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a protei | IEA; IBA | GO:0005829; GO:0 | cytosol; membrane; |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IBA | GO:0005768; GO:0 | endosome; trans-G |
| | | GO:0000775; GO:0 | chromosome, centr |
| | | GO:0005576; GO:0 | extracellular region |
| | | GO:0005634 | nucleus |
| Binding to a metal i | IEA | | |
| A transcription reg | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nuclei | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Catalysis of the hyd | IEA | | |
| Catalysis of the tra | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to damage | IBA; IEA | GO:0016605; GO:0 | PML body; Mre11 c |
| Binding to messeng | IBA; IBA; IBA | GO:0005739; GO:0 | mitochondrion; mit |
| | | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the tra | IBA; IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| Binds to and stops, | IEA; IEA; IEA; IEA; IB | GO:0005618; GO:0 | cell wall; membran |
| Catalysis of the tra | IEA; IEA | | |
| A transcription reg | IBA; IPI; IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the trar | IBA; IEA | | |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to messeng | IBA; IBA; IBA | GO:0005739; GO:0 | mitochondrion; mit |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a macror | IBA | GO:0000775; GO:0 | chromosome, centr |
| Binding to a protein | IEA | | |
| Catalysis of the trar | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| | | GO:0005576; GO:0 | extracellular region |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Combining with an | IBA | GO:0005737; GO:0 | cytoplasm; plasma |
| Binding to a specifi | IBA; IBA | GO:0005634 | nucleus |
| | | | |
| | | | |
| | | | |
| Binding to monome | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | | |
| | | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | | |
| | | | |
| Binding to a calciun | IEA; IEA | | |
| Binding to a proteir | IEA | | |
| Any molecular func | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | | |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | | |
| Binding to a proteir | IEA | | |
| | | | |
| Catalysis of the tem | IBA | GO:0005730; GO:0 | nucleolus; TRAMP c |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IBA; IBA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol; m |
| Binding to a proteir | IEA | | |
| Binding to a proteir | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA | | |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| | | | |
| | | | |
| Catalysis of the trar | IBA | | |
| | | GO:0016021 | integral component |
| Catalysis of the site | IBA; IBA | GO:0000172; GO:0 | ribonuclease MRP c |
| | | | |
| Binding to a proteir | IEA | | |
| | | GO:0005730 | nucleolus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IBA | GO:0005730; GO:0 | nucleolus; 90S prer |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| Binding to monome | IEA | GO:0110165 | cellular anatomical |
| Binding to a microt | IBA | | |
| | | GO:0005768 | endosome |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; e |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to monome | IEA; IEA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| Binding to a nucleic | IEA |  |  |
| Binding to a calciu | IEA |  |  |
| Binding to chromati | IBA; IEA | GO:0000228; GO:0 | nuclear chromosom |
| Catalysis of the tra | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the tra | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| Catalysis of the joi | IEA |  |  |
| Binding to a calciu | IEA | GO:0005783 | endoplasmic reticul |
| A transcription reg | IEA; IEA |  |  |
| Binding to a microt | IEA | GO:0005874 | microtubule |
| The action of a mol | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| Catalysis of the hyd | IEA |  |  |
| The binding activity | IBA; IEA | GO:0005635; GO:0 | nuclear envelope; i |
|  |  | GO:0016020; GO:0 | membrane; integral |
| A transcription reg | IEA; IEA |  |  |
|  |  | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the hyd | IEA |  |  |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |
|  |  | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to double- | IEA | GO:0009507 | chloroplast |

|  |  |  |  |
|---|---|---|---|
| Binding to a zinc io | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| Catalysis of the hyd | IEA |  |  |
| Binding to a phosph | IBA; IEA | GO:0005768; GO:0 | endosome; Golgi ap |
| Binding to a protein | IEA |  |  |
| Catalysis of the tran | IEA; IEA |  |  |
| A transcription regu | IEA |  |  |
| Binding to chromati | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA |  |  |
| Catalysis of the tran | IBA; IEA |  |  |
| Binding to DNA of a | IBA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Binding to double- | IEA | GO:0009507 | chloroplast |
| Binding to messeng | IBA; IBA; IBA | GO:0005739; GO:0 | mitochondrion; mit |
| Binding to a nucleic | IEA |  |  |
| Binding to messeng | IEA; IEA | GO:0005739 | mitochondrion |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA; IEA | GO:0016020 | membrane |
|  |  | GO:0000815; GO:0 | ESCRT III complex; |
|  |  | GO:0005874 | microtubule |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the ph | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA |  |  |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; mitocho |
| Binding to a protein | IEA; IEA | GO:0005737; GO:0 | cytoplasm; Rab-pro |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; DNA replic |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a ubiquit | IBA; IBA; IBA | GO:0000151 | ubiquitin ligase con |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| | | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005794; GO:0 | Golgi apparatus; m |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005886 | plasma membrane |
| Catalysis of the tra | IEA | GO:0016020; GO:0 | membrane; integral |
| Combining with a | IBA; IEA; IEA | GO:0005635; GO:0 | nuclear envelope; c |
| Catalysis of the rea | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| Binding to an RNA | IBA; IEA | GO:0005737 | cytoplasm |
| A DNA-binding tra | IBA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| | | GO:0005576; GO:0 | extracellular region |
| Enables the transfe | IBA | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protei | IEA; IEA | GO:0005739 | mitochondrion |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to an RNA | IEA | GO:0005739 | mitochondrion |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; CCAAT-bi |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to an RNA | IBA; IBA | GO:0005737 | cytoplasm |
| | | GO:0005634 | nucleus |
| Binding to monome | IEA; IEA; IBA | GO:0110165 | cellular anatomical |
| The action of a mol | IBA | GO:0015934 | large ribosomal su |
| Any molecular func | IEA; IEA | | |
| Binding to a nucleic | IEA | | |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binds to and stops, | IEA; IEA | | |

|  |  |  |  |
|---|---|---|---|
| Any molecular entit | IEA | GO:0016021; GO:0 | integral component |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
|  |  | GO:0005886 | plasma membrane |
| Any molecular func | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA |  |  |
| Any molecular entit | IEA | GO:0046658 | anchored compone |
| Binding to an anapl | IEA |  |  |
| Binding to a nucleic | IEA; IBA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a protein | IPI; IDA; IDA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Enables the transfe | IBA | GO:0009706; GO:0 | chloroplast inner m |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a protein | IPI; IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Any molecular func | IEA; IEA; IEA; IEA |  |  |
| Binding to messeng | IBA; IBA |  |  |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA; IEA | GO:0000172; GO:0 | ribonuclease MRP c |
| Catalysis of the phc | IEA; IEA | GO:0016021 | integral component |
| | | GO:0005576; GO:0 | extracellular region |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the phc | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IEA; IEA | | |
| | | GO:0016021 | integral component |
| Any molecular func | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | | |
| Binding to a protein | IEA | | |
| A DNA-binding trar | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005871; GO:0 | kinesin complex; m |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA | GO:0005794 | Golgi apparatus |
| Binding to monome | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| A DNA-binding trar | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| Catalysis of the trar | IBA | | |
| Binding to a nucleic | IEA; IEA | GO:0000785; GO:0 | chromatin; nucleus; |
| | | GO:0005886 | plasma membrane |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; CCAAT-bi |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0009707 | chloroplast outer m |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to chromati | IBA; IBA; IBA | | |
| Binding to a metal i | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0009507; GO:0 | chloroplast; plastid; |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IP | GO:0005737; GO:0 | cytoplasm; cytosol; |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; mRNA clea |
| | | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA; IPI; IDA; ID | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a calciun | IEA | GO:0005739 | mitochondrion |
| Enables the facilitat | IEA; IBA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the phc | IEA; IEA | | |
| Binding to a zinc io | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; cytosol; |
| The function that st | IEA | GO:0005576 | extracellular region |
| A transcription core | IBA | GO:0000124; GO:0 | SAGA complex; nuc |
| Catalysis of the trar | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0005634; GO:0 | nucleus; cytosol; pr |
| Binding to a riboso | IEA | GO:0005737; GO:0 | cytoplasm; ribosom |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the rea | IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| A transcription regu | IEA; IEA; IEA | GO:0005634 | nucleus |
|  |  |  |  |
| Binds to and stimul | IEA; IEA; IEA; IEA; IE | GO:0001405; GO:0 | PAM complex, Tim2 |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
|  |  |  |  |
| Binding to a protein | IPI; IDA; IBA | GO:0005886; GO:0 | plasma membrane; |
|  |  |  |  |
| Binding to a protein | IEA |  |  |
| Binding to an RNA r | IBA | GO:0010494 | cytoplasmic stress |
|  |  |  |  |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
|  |  |  |  |
| Enables the transfe | IEA | GO:0016021 | integral component |
|  |  | GO:0005783 | endoplasmic reticul |
|  |  | GO:0016021 | integral component |
| Binding to a protein | IEA; IBA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Catalysis of an oxid | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; nucleolus; |

| | | | |
|---|---|---|---|
| Catalysis of the inc | RCA; IEA; IEA; IEA; I | GO:0005783; GO:0 | endoplasmic reticul |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IDA; IPI; IBA; IDA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a specifi | IBA; IBA; IEA; IEA | GO:0005634 | nucleus |
| The action of a mol | IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| Binding to a protein | IEA; IBA; IBA | GO:0071818 | BAT3 complex |
| Binds to and increa | IEA | GO:0005737 | cytoplasm |
| Binding to an RNA r | IEA; IEA; IEA | | |
| | | GO:0009506; GO:0 | plasmodesma; mem |
| Catalysis of the trar | IBA; IEA; IEA | | |
| Binding to a nucleic | IEA; IEA; IBA | GO:0009507; GO:0 | chloroplast; chlorop |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139 | Golgi membrane |
| Binding to a protein | IEA | | |
| | | GO:0005736 | RNA polymerase I c |
| Catalysis of the trar | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; ID | GO:0005871; GO:0 | kinesin complex; m |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |
| | | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |

| | | | |
|---|---|---|---|
| Binding to a domai | IBA; IBA | GO:0005737 | cytoplasm |
| Binding to a nucleic | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IBA; IEA | GO:0005737 | cytoplasm |
| A transcription reg | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0010008 | endosome membra |
| | | GO:0005634 | nucleus |
| Binding to a clathri | IEA; IEA; IEA | GO:0005768; GO:0 | endosome; Golgi ap |
| Catalysis of the tra | IBA; IEA; IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0030014 | CCR4-NOT comple |
| Any molecular func | IEA; IEA; IBA; IEA | GO:0005829 | cytosol |
| | | GO:0005634; GO:0 | nucleus; Ino80 com |
| Catalysis of the ph | IEA; IEA | | |
| Binding to a nucleic | IEA; IEA; IEA | GO:0009507 | chloroplast |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to a calciu | IEA; IBA | GO:0009507; GO:0 | chloroplast; photos |
| Stimulates the exch | IEA | | |

| | | | |
|---|---|---|---|
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| A transcription cor | IEA | GO:0005634; GO:0 | nucleus; cytosol |
| | | | |
| Binding to an RNA | IEA; IBA | GO:0005737 | cytoplasm |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | | |
| Binds to and stops, | IEA | | |
| Removes a phosph | IBA | GO:0005634; GO:0 | nucleus; mitochond |
| Binding to a zinc io | IEA; IEA | | |
| | | | |
| A DNA-binding tra | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| Binding to a box C/ | IBA | | |
| Catalysis of the tra | IEA | GO:0030014 | CCR4-NOT comple |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005886; GO:0 | plasma membrane; |
| | | | |
| Binding to a protei | IEA | GO:0005656; GO:0 | nuclear pre-replica |
| Binding to an RNA | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; intr |
| Binding to monome | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | | |
| | | | |
| Binding to chromat | IEA | | |
| | | | |
| Catalysis of the tra | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a calciu | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IEA | | |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA | GO:0005623; GO:0 | obsolete cell; nucle |
| A DNA-binding trar | IBA; IEA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| A DNA-binding trar | IDA; IEA; IPI; IDA; IE | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA | GO:0009941; GO:0 | chloroplast envelop |
| Binding to a protein | IEA; IEA | GO:0009506; GO:0 | plasmodesma; intra |
| | | GO:0016020; GO:0 | membrane; integral |
| Binds to and stops, | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886 | plasma membrane |
| Catalysis of the hyd | IEA | | |
| Catalysis of the pho | IEA; IBA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA; IBA | GO:0048188 | Set1C/COMPASS co |

| | | | |
|---|---|---|---|
| Binding to a metal i | IEA | GO:0005634 | nucleus |
| Binding to a metal i | IEA | GO:0005634; GO:0 | nucleus; pre-snoRN |

| | | | |
|---|---|---|---|
| Catalysis of the tran | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the tran | IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IBA | GO:0009507; GO:0 | chloroplast; chlorop |
| | | GO:0005773 | vacuole |

| | | | |
|---|---|---|---|
| Catalysis of a bioch | IEA; IEA | | |
| | | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005576 | extracellular region |
| | | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Binding to a proteir | IEA | GO:0043229 | intracellular organe |
| Binding to a proteir | IEA | GO:0005739; GO:0 | mitochondrion; cyto |
| Catalysis of the pho | IEA; IEA; IEA | GO:0005829; GO:0 | cytosol; plasma me |
| Binds to and increa | IBA; IEA; IBA; IBA | GO:0005737; GO:0 | cytoplasm; plasma |
| Binding to double-s | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chlo |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| | | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a calciun | IEA; IEA | | |
| Binding to a calciun | IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; endoplasm |
| Catalysis of the pho | IEA | | |
| Binding to a zinc io | IEA; IEA; IEA; IEA | GO:0000151; GO:0 | ubiquitin ligase con |
| Binding to a lipid. | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an unfol | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to a protein | IPI | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005576 | extracellular region |

| | | | |
|---|---|---|---|
| Enables the transfe | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA; IBA; IEA | | |
| Catalysis of the end | IEA | | |
| | | GO:0009535 | chloroplast thylakoi |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to an inosit | IEA; IEA | GO:0005623; GO:0 | obsolete cell; memb |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005871; GO:0 | kinesin complex; m |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a nucleic | IEA; IEA; IEA | | |
| Binding to a protein | IEA | GO:0009507 | chloroplast |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA; IEA; IBA | GO:0000786; GO:0 | nucleosome; nucleu |

| | | | |
|---|---|---|---|
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binding to a calciu | IBA; IEA | GO:0005737 | cytoplasm |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0005730; GO:0 | nucleolus; cytosol; |

| | | | |
|---|---|---|---|
| Binding to a protei | IPI; IEA; IDA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a zinc io | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a protei | IEA | GO:0005783 | endoplasmic reticul |
| Catalysis of the tra | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to monome | IBA; IBA | GO:0005634; GO:0 | nucleus; centrosom |
| Binding to an RNA | IEA; IEA | | |
| Catalysis of the rea | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IEA; IBA | | |

| | | | |
|---|---|---|---|
| | | GO:0005623; GO:0 | obsolete cell; late e |
| | | GO:0000176 | nuclear exosome (R |
| A DNA-binding tra | IBA; IBA; IDA; IEA; I | GO:0005634; GO:0 | nucleus; histone m |
| Catalysis of the ph | IEA; IBA; IEA; IEA; I | GO:0005886; GO:0 | plasma membrane; |
| The action of a mol | IEA; IBA | GO:0005737; GO:0 | cytoplasm; mitocho |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| | | GO:0005783 | endoplasmic reticul |
| Binding to a metal | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0009536; GO:0 | plastid; thylakoid |
| | | GO:0046658 | anchored compone |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of the tra | IBA; IEA; IEA | GO:0005783 | endoplasmic reticul |
| Binding to messeng | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0009360 | DNA polymerase III |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005777 | peroxisome |
| | | GO:0005783 | endoplasmic reticul |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0043231 | intracellular membr |
| A DNA-binding tra | IBA; IBA; IBA; IDA; I | GO:0000792; GO:0 | heterochromatin; n |
| Any molecular func | IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the tra | IBA | | |
| | | GO:0009707 | chloroplast outer m |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA | | |
| | | GO:0005576; GO:0 | extracellular region |
| Catalysis of the hyd | IEA | | |
| Binding to a lipid.; | IBA; IEA; IBA; IBA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| | | GO:0000775; GO:0 | chromosome, centr |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a protein | IEA | | |
| Stimulates the exch | IEA | | |
| Binding to a zinc io | IEA | GO:0005634 | nucleus |
| | | GO:0005576; GO:0 | extracellular region |
| A transcription regu | IEA | GO:0005634; GO:0 | nucleus; mediator c |
| Binding to a protein | IEA | | |
| Enables the synthes | IEA | GO:0045261 | proton-transportin |
| Binding to a fatty a | IEA | | |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to an RNA | IBA | GO:0030686 | 90S preribosome |
| Catalysis of the tra | IEA; IBA; IEA | | |
| Catalysis of the ph | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Binding to a protein | IEA | | |
| Binding to an RNA | IBA | GO:0016591 | RNA polymerase II, |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA | GO:0009507 | chloroplast |
| Binding to a protein | IEA |  |  |
| Catalysis of the tran | IEA |  |  |
| The action of a mol | IEA | GO:0005840; GO:0 | ribosome; membran |
| Catalysis of the tran | IBA; IEA; IEA |  |  |
| Catalysis of the hyd | IBA |  |  |
| Binding to a protein | IPI | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | GO:0005576 | extracellular region |

| | | | |
|---|---|---|---|
| Binding to a protei | IEA | GO:0005737 | cytoplasm |
| | | GO:0016592 | mediator complex |
| Binding to a protei | IEA | | |
| Binding to a protei | IEA | | |
| Binding to a protei | IEA | | |
| | | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA; IBA; IBA; IP | GO:0000781; GO:0 | chromosome, telom |
| Binding to a protei | IEA | | |
| Binding to a protei | IEA | GO:0043229 | intracellular organe |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IBA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; m |
| Binding to a microtu | IBA | GO:0005737; GO:0 | cytoplasm; spindle |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA; IEA | | |
| Catalysis of the rea | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to a protei | IEA; IEA; IEA; IEA; IE | GO:0005786; GO:0 | signal recognition |
| Any molecular func | IEA; IEA | GO:0005739; GO:0 | mitochondrion; nuc |
| Enables the directe | IEP | GO:0005576 | extracellular region |
| | | GO:0005737; GO:0 | cytoplasm; cytoskel |
| | | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a nucleic | IEA; IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IEA; IEA; IB | GO:0000151; GO:0 | ubiquitin ligase con |
| | | GO:0019005 | SCF ubiquitin ligase |
| Binding to a protei | IEA | | |
| Binding to a nucleic | IEA; IEA; IBA; IBA; IB | GO:0005634; GO:0 | nucleus; cytoplasm; |
| 53, Regulation of chlorophyll biosynthe | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IB | GO:0000781; GO:0 | chromosome, telom |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to chromat | IBA | GO:0005634; GO:0 | nucleus; chloroplas |

| | | | |
|---|---|---|---|
| Binds to and stimul | IBA; IEA; IBA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a protein | IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| Any molecular func | IEA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IEA; IEA; IEA; IB | GO:0000785; GO:0 | chromatin; nucleus |
| A transcription reg | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0000427 | plastid-encoded pl |
| Catalysis of the ran | IEA; IEA; IEA | GO:0009505 | plant-type cell wall |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| A transcription reg | IBA; IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to ATP, ade | IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to a microt | IEA | GO:0005874 | microtubule |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Binding to a metal i | IEA | | |
| Binding to a protei | IEA; IEA | | |
| Enables the energy- | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Binding to a transfe | IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a microt | IEA; IEA | GO:0005874; GO:0 | microtubule; cortica |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Catalysis of the rea | IEA; IEA | GO:0005829 | cytosol |
| Binding to a microt | IEA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| The action of a mol | IBA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IEA; IBA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; transcripti |
| | | GO:0009505 | plant-type cell wall |
| Binding to a domai | IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to a DNA p | IBA | | |
| Binding to an inosit | IEA; IEA | GO:0005623 | obsolete cell |
| Catalysis of the hyd | IEA | | |
| Catalysis of the tra | IEA | GO:0005794; GO:0 | Golgi apparatus; m |

|  |  |  |  |
|---|---|---|---|
|  |  | GO:0005773; GO:0 | vacuole; endoplasm |
| OBSOLETE. Initiatin | IEA; IEA | GO:0000127; GO:0 | transcription factor |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to double- | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromoso |
|  |  | GO:0005634; GO:0 | nucleus; nucleolus |
| Binding to a calciu | IEA; IBA | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a transfe | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| Binding to a DNA re | IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; replication |
| Binding to a nucleo | IEA; IEA; IEA |  |  |
| Any molecular func | IEA; IBA | GO:0005634; GO:0 | nucleus; nuclear pr |
| Binding to a nucleic | IEA |  |  |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005776; GO:0 | autophagosome; pl |
| Binding to a heme, | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005634 | nucleus |
|  |  | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the ph | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| Binding to a phosp | IBA; IBA | GO:0005768; GO:0 | endosome; Golgi a |
| Catalysis of a bioch | IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA |  |  |
| Binding to a nucleic | IEA |  |  |
| Binding to a protein | IEA | GO:0000932; GO:0 | P-body; cytoplasm |
| Binding to a protein | IEA |  |  |
|  |  | GO:0005615 | extracellular space |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Binding to an amin | IEA | | |
| Catalysis of the tra | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a zinc io | IEA; IEA | | |
| Binding to a metal i | IEA | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription cor | IBA | GO:0005634 | nucleus |
| Binds to and stops, | IEA | | |

| | | | |
|---|---|---|---|
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binding to a calciun | IBA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | GO:0009941; GO:0 | chloroplast envelop |
| | | GO:0005783 | endoplasmic reticul |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA; IBA | GO:0005783 | endoplasmic reticul |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the phc | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0000444; GO:0 | MIS12/MIND type c |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0009507; GO:0 | chloroplast; thylakc |
| | | GO:0009507; GO:0 | chloroplast; membr |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IBA | GO:0005634; GO:0 | nucleus; DNA replic |
| Catalysis of the trar | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Binding to a ubiquit | IBA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chlc |
| Any molecular func | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634 | nucleus |
| A transcription regu | IEA; IEA |  |  |
| Catalysis of the tran | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
|  |  | GO:0009507; GO:0 | chloroplast; photos |
| Binds to and stimul | IBA | GO:0005737; GO:0 | cytoplasm; endopla |
| Catalysis of the pho | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0005637; GO:0 | nuclear inner memb |
| Binding to a protein | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA; IEA |  |  |
|  |  | GO:0005634; GO:0 | nucleus; nucleoplas |
| Catalysis of the tran | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the pho | IEA; IEA |  |  |
|  |  | GO:0000407; GO:0 | phagophore assem |
| Binding to an RNA r | IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Any molecular func | IEA |  |  |
| Catalysis of the rea | IEA; IEA |  |  |
| Catalysis of the hyd | IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA; IEA; IEA |  |  |
| Catalysis of the rea | IEA | GO:0009507 | chloroplast |
|  |  | GO:0009507; GO:0 | chloroplast; chlorop |

| | | | |
|---|---|---|---|
| Binding to DNA of a | IBA | GO:0005634 | nucleus |
| | | GO:0005737 | cytoplasm |
| Binding to a specifi | IBA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to a metal i | IEA | | |
| Binding to messeng | IBA; IBA; IBA | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the trar | IEA; IEA | | |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0005615 | extracellular space |
| | | GO:0016021 | integral component |
| Binding to an identi | IEA; IEA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Binding to a specifi | IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | | |
| Binding to an RNA r | IEA; IBA; IEA | GO:0009505; GO:0 | plant-type cell wall; |
| Binding to a protein | IEA; IBA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of an oxid | IEA; IEA; IBA | | |
| Catalysis of the phc | IEA; IEA | | |
| Catalysis of the inc | IEA; IEA; IBA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to AMP, ade | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to AMP, ade | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA; IBA; IEA; IBA | GO:0000781; GO:0 | chromosome, telom |
| Binding to a protein | IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| | | GO:0016021 | integral component |
| | | GO:0005737 | cytoplasm |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binds to and stops, | IEA; IEA; IEA; IEA; IB | GO:0005618; GO:0 | cell wall; membrane |
| Binding to a metal i | IEA; IEA | GO:0005737 | cytoplasm |
| | | GO:0009507; GO:0 | chloroplast; plastid; |
| Binding to an RNA r | IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IBA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; transcripti |
| | | GO:0005829 | cytosol |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0009527; GO:0 | plastid outer memb |
| Binding to messeng | IEA; IEA | GO:0005634; GO:0 | nucleus; nucleolus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA | | |
| | | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of the trar | IBA | GO:0005680 | anaphase-promotir |
| Binding to a nucleic | IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IBA; IEA; IBA; IBA; IB | GO:0000932; GO:0 | P-body; telomerase |
| Binding to a protein | IEA | | |
| | | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005737 | cytoplasm |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IBA; IEA; IEA |  |  |
| Binding to a protein | IEA |  |  |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IBA | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0000502; GO:0 | proteasome comple |
| Any molecular func | IEA; IBA; IEA; IBA | GO:0005634; GO:0 | nucleus; nucleolus; |
| Binding to a carboh | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA r | IEA; IEA |  |  |
| Catalysis of the pho | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a small r | IBA | GO:0005794 | Golgi apparatus |
|  |  | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Catalysis of the hyd | IEA; IEA |  |  |
|  |  | GO:0005739 | mitochondrion |
| Catalysis of the hyd | IEA |  |  |
| Binding to a nucleic | IEA; IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| Binding to a calcium | IEA |  |  |
| Catalysis of the rea | IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the tran | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA | GO:0005634 | nucleus |
| Binding to a zinc io | IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| A transcription core | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA; IEA | GO:0005777 | peroxisome |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to an RNA r | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; intracellula |
| Any molecular func | IEA; IEA; IEA; IBA; IE | GO:0110165 | cellular anatomical |
| A transcription regu | IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| A transcription core | IBA; IEA; IBA; IEA | GO:0000124; GO:0 | SAGA complex; nuc |

| | | | |
|---|---|---|---|
| Binding to an RNA | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a zinc io | IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear sp |
| Binding to a nucleo | IEA; IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |
| Binding to messeng | IBA | GO:0000228; GO:0 | nuclear chromosom |
| Binding to a protein | IEA | | |
| | | GO:0009507; GO:0 | chloroplast; chlorop |
| | | GO:0005576; GO:0 | extracellular region |
| Binding to damage | IBA; IEA; IBA | | |
| Catalysis of an oxid | IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |

| | | | |
|---|---|---|---|
| | | GO:0005634 | nucleus |
| Catalysis of the rea | IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Catalysis of the trar | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the phc | IEA; IBA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016021 | integral component |
| Catalysis of an oxid | IEA; IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| | | GO:0005634 | nucleus |
| | | GO:0009507; GO:0 | chloroplast; integra |
| Enables the facilitat | IBA; IEA | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the hyd | IEA; IEA | GO:0005777 | peroxisome |
| Binding to a protein | IEA | | |
| | | GO:0005739 | mitochondrion |
| Catalysis of the trar | IBA; IBA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to a nucleo | IEA; IEA | | |
| | | GO:0005829 | cytosol |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005634; GO:0 | nucleus; transcripti |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Any molecular func | IBA | GO:0000228; GO:0 | nuclear chromosom |
| | | GO:0005886 | plasma membrane |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the ran | IEA; IEA; IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; replication |
| Binding to a protein | IEA | GO:0016021 | integral component |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a calciu | IEA; IEA | | |
| Catalysis of the tra | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the tra | IEA; IEA | GO:0043231 | intracellular membr |

| | | | |
|---|---|---|---|
| Catalysis of the phc | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634; GO:0 | nucleus; plasma me |
| Binding to ATP, ade | IEA; IEA | GO:0005778; GO:0 | peroxisomal memb |
| Binding to a metal i | IEA | | |
| Binding to chromati | IBA; IEA | GO:0005634; GO:0 | nucleus; cohesin co |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0000796; GO:0 | condensin complex |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005829 | cytosol |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a metal i | IEA | GO:0005634 | nucleus |
| Catalysis of the ph | IEA; IBA; IEA; IEA | | |
| Catalysis of the acti | IEA; IBA; IBA | GO:0000407; GO:0 | phagophore assem |
| | | GO:0031011 | Ino80 complex |
| | | GO:0005774; GO:0 | vacuolar membrane |
| Binding to an RNA | IEA | | |
| Catalysis of the hyd | IEA | | |
| Binding to a metal i | IEA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| | | GO:0005783 | endoplasmic reticul |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0005794; GO:0 | Golgi apparatus; cy |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a calciu | IEA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA | | |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Catalysis of the tra | IEA; IEA; IBA | | |
| | | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| Binding to an RNA | IBA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| Binding to a nucleo | IEA; IBA; IEA | GO:0005634 | nucleus |
| | | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0000792; GO:0 | heterochromatin; n |
| Catalysis of the tra | IEA | | |
| Binding to a clathri | IBA | GO:0005737; GO:0 | cytoplasm; vesicle; |
| Catalysis of the hyd | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the rea | IBA | GO:0005789; GO:0 | endoplasmic reticul |
| Binding to a calciu | IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to a specifi | IBA; IBA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; membrane |
| A DNA-binding tra | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of an oxid | IBA | GO:0005829; GO:0 | cytosol; membrane; |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020 | membrane |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0019005 | SCF ubiquitin ligase |
| Any molecular func | IEA; IEA | GO:0005739 | mitochondrion |
| | | GO:0016020; GO:0 | membrane; integral |
| A transcription reg | IEA; IEA | GO:0005634 | nucleus |
| Binding to a zinc io | IEA; IEA; IEA; IEA; IEA | | |
| Binding to an identi | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the hyd | IEA |  |  |
|  |  |  |  |
| Catalysis of the hyd | IEA |  |  |
|  |  |  |  |
| Any molecular func | IEA; IBA; IBA | GO:0005634; GO:0 | nucleus; intracellula |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Any molecular func | IEA | GO:0005634 | nucleus |
|  |  | GO:0005634; GO:0 | nucleus; intracellula |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005654; GO:0 | nucleoplasm; cataly |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Catalysis of the pho | IEA; IBA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
|  |  |  |  |
| Catalysis of the tra | IEA; IEA; IBA; IEA |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IEA |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; mitochond |
| Binding to a protein | IEA |  |  |
|  |  |  |  |
| Enables the transfe | IBA | GO:0005774; GO:0 | vacuolar membrane |
| Binds to and stops, | IEA; IEA | GO:0005634 | nucleus |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Catalysis of the rea | IEA; IEA |  |  |

| | | | |
|---|---|---|---|
| The binding activity | IBA | GO:0000793; GO:0 | condensed chromos |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| A transcription regu | IBA; IEA; IBA | GO:0005634 | nucleus |
| | | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the tran | IBA | GO:0005768; GO:0 | endosome; trans-G |
| Catalysis of the hyd | IEA | | |
| Binding to a metal i | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IBA; IBA; IEA | GO:0005737 | cytoplasm |
| A motor activity tha | IEA; IEA; IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a zinc io | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA; IEA | | |
| Catalysis of the tran | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| Binds to and stops, | IEA; IEA | | |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IB | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA | | |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IDA; IBA; IEA; IEA; I | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| | | GO:0000145; GO:0 | exocyst; cytosol; pl |
| Binding to a protein | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| | | GO:0005794; GO:0 | Golgi apparatus; cy |
| Catalysis of the tra | IEA; IEA; IBA; IBA; IB | GO:0000139; GO:0 | Golgi membrane; e |
| Binding to a protei | IEA; IEA | | |
| | | GO:0009512; GO:0 | cytochrome b6f co |
| The binding activity | IBA | GO:0005778; GO:0 | peroxisomal memb |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0009706; GO:0 | chloroplast inner m |
| Binding to a specifi | IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; DNA-depe |
| Binding to a metal i | IEA | | |
| The action of a mol | IEA; IBA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | | |
| Catalysis of the tra | IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005773 | vacuole |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IDA; IPI; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the rea | IBA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IBA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Enables the transfe | IEA; IEA; IBA; IEA | GO:0005770; GO:0 | late endosome; me |
| Catalysis of the tra | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| A DNA-binding tra | IEA; IEA; IEA | | |
| A motor activity tha | IEA; IEA; IEA; IEA | | |
| Binding to a nucleic | IEA; IEA | GO:0000427; GO:0 | plastid-encoded pl |
| Combining with a n | IBA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a specifi | IBA; IEA; IEA; IPI; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA; IEA | GO:0009536; GO:0 | plastid; thylakoid; |
| Binding to a carboh | IEA | | |
| Catalysis of the ran | IEA | GO:0005576; GO:0 | extracellular region |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IDA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Binding to a protein | IEA; IBA | GO:0005783 | endoplasmic reticul |
| Catalysis of the hyd | IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005634 | nucleus |
| A DNA-binding trar | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IBA | GO:0005730; GO:0 | nucleolus; cytoplas |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| | | GO:0005886 | plasma membrane |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005737 | cytoplasm |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to an RNA r | IEA; IEA; IEA; IEA | GO:0005739 | mitochondrion |
| A transcription regu | IBA; IBA; IBA; IEA | GO:0000123; GO:0 | histone acetyltransf |
| Binding to a metal i | IEA; IEA | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a DNA se | IBA; IBA; IEA; IBA; IE | GO:0032300; GO:0 | mismatch repair co |
| Binding to a protein | IEA | | |
| Binding to an RNA r | IBA; IBA; IBA | GO:0022625 | cytosolic large ribo |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding an acyl gro | IEA | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0009706 | chloroplast inner m |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005737; GO:0 | cytoplasm; kinesin |
| | | GO:0005829 | cytosol |
| Catalysis of the ph | IEA; IEA | | |
| | | GO:0005829; GO:1 | cytosol; RQC compl |
| Binding to a protei | IEA | | |
| Catalysis of the tra | IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| Binding to a protei | IEA | GO:0005737; GO:0 | cytoplasm; intracell |
| | | GO:0005739 | mitochondrion |
| Binding to a protei | IEA | GO:0005635; GO:0 | nuclear envelope; c |
| Catalysis of the tra | IEA; IEA; IBA; IBA | GO:0005829; GO:0 | cytosol; intracellula |
| Binding to a nucleic | IEA; IEA; IBA | GO:1990904 | ribonucleoprotein c |
| A transcription reg | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to chromati | IBA; IEA; IEA; IBA; IB | GO:0005634 | nucleus |
| A transcription reg | IEA | GO:0005634; GO:0 | nucleus; mediator c |
| | | GO:0005634; GO:0 | nucleus; CIA compl |
| Catalysis of the tra | IBA; IEA | | |
| Catalysis of the tra | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005737 | cytoplasm |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| | | GO:0016021 | integral component |
| Any molecular func | IEA; IBA; IDA; IPI; IE | GO:0005634; GO:0 | nucleus; intracellula |
| Binding to a protei | IEA; IEA | | |
| Binding to double- | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromoso |

| | | | |
|---|---|---|---|
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of the phc | IEA; IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; membrane |
| | | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the trar | IBA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; NatA co |
| | | GO:0005739 | mitochondrion |
| Catalysis of the rea | IBA | GO:0005737; GO:0 | cytoplasm; mitocho |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| | | GO:0005682 | U5 snRNP |
| Catalysis of the phc | IEA; IBA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a phospl | IBA; IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; cyto |
| Binding to a calciun | IEA; IBA | GO:0009507; GO:0 | chloroplast; photos |
| Catalysis of a bioch | IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA | | |
| | | GO:0071944 | cell periphery |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| A transcription regu | IBA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0000127 | transcription factor |
| Catalysis of the phc | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; endopla |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| A transcription regu | IBA; IEA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Enables the facilitat | IEA; IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| | | GO:0000214 | tRNA-intron endon |
| Binding to a nucleic | IEA; IEA | | |
| Binding to ADP, ade | IEA | | |
| Binds to and stops, | IEA | | |
| Binding to ATP, ade | IEA; IEA; IEA | | |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |
| The action of a mol | IEA; IEA | GO:0005739; GO:0 | mitochondrion; ribo |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Catalysis of the pho | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA | | |
| | | GO:0016020 | membrane |
| Binding to a protein | IEA | | |
| Catalysis of the tran | IEA; IEA; IBA | GO:0009507 | chloroplast |
| Catalysis of the rea | IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Catalysis of the rea | IEA; IBA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |

| | | | |
|---|---|---|---|
| Binding to an RNA r | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| Binding to a protei | IEA | | |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IDA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA | GO:0005634; GO:0 | nucleus; VCB compl |
| Catalysis of the hyd | IEA; IBA; IBA; IBA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886 | plasma membrane |
| Binding to a protein | IEA | GO:0005675 | transcription factor |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IEA | | |
| Catalysis of the end | IEA; IEA; IEA | GO:0000214; GO:0 | tRNA-intron endon |
| Catalysis of the ph | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IEA; IEA | | |
| | | GO:0005773 | vacuole |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Any molecular func | IEA; IEA; IEA | GO:0005657; GO:0 | replication fork; Ra |
| Binding to an RNA r | IEA | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0005634; GO:0 | nucleus; spliceosom |
| A DNA-binding tran | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005886 | plasma membrane |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
| Catalysis of the hyd | IEA; IEA; IEA |  |  |
| Enables the transfe | IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IBA; IEA |  |  |
| Binding to ADP, ade | IEA | GO:0005886 | plasma membrane |
|  |  | GO:0005802; GO:0 | trans-Golgi networ |
| Catalysis of the trar | IBA; IEA |  |  |
| A transcription regu | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a microt | IBA; IBA | GO:0005737; GO:0 | cytoplasm; spindle; |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0009527; GO:0 | plastid outer memb |
| Catalysis of the ph | IEA; IEA | GO:0000776 | kinetochore |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; intracellula |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; RNA polym |

| | | | |
|---|---|---|---|
| Binding to messeng | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0110165 | cellular anatomical |
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the pho | IEA; IEA | | |
| Binding to a zinc io | IEA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| | | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a zinc io | IEA | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; intracellula |
| Stimulates the exch | IEA; IBA; IEA; IBA | GO:0005789; GO:0 | endoplasmic reticul |
| Binding to an RNA r | IEA | | |
| Binding to a protein | IEA | GO:0005739; GO:0 | mitochondrion; chlo |
| | | GO:0009535 | chloroplast thylakoi |
| Catalysis of the hyd | IEA; IEA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| Catalysis of the tran | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Catalysis of the pho | IEA; IEA; IEA | GO:0016020 | membrane |
| Binding to an RNA r | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a microtu | IBA | GO:0005881 | cytoplasmic microtu |
| | | GO:0005762 | mitochondrial large |
| Binding to an RNA r | IBA; IEA | GO:0005730; GO:0 | nucleolus; cytosolic |
| | | GO:0005737; GO:0 | cytoplasm; vacuole; |
| Binding to ATP, ade | IEA; IEA | GO:0005741 | mitochondrial outer |
| Binds to and stops, | IEA; IEA | | |
| | | GO:0000127 | transcription factor |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; spliceosom |
| Binding to a protein | IEA | | |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0005739 | mitochondrion |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IEA; IEA |  |  |
| Binding to a zinc io | IEA |  |  |
| Binding to an RNA r | IBA; IEA | GO:0009507; GO:0 | chloroplast; intrace |
| Binding to a nucleic | IEA; IEA; IBA; IEA; IEA |  |  |

| | | | |
|---|---|---|---|
| Binds to and stimul | IBA; IEA; IBA | | |
| Binding to a nucleic | IEA | | |
| | | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the trar | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA | GO:0016021 | integral component |
| Catalysis of the rea | IBA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IEA | | |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| Binding to a protein | IEA; IEA | GO:0005635; GO:0 | nuclear envelope; |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IBA; IEA | | |
| Catalysis of the rea | IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IBA; IBA; IBA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IEA; IBA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a microt | IBA | GO:0005737; GO:0 | cytoplasm; spindle |
| Binding to monome | IEA | | |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a nucleo | IEA; IEA | | |
| Binding to a protein | IEA | | |
| | | GO:0005783; GO:0 | endoplasmic reticul |

| | | | |
|---|---|---|---|
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a nucleic | IEA; IBA; IBA; IBA | GO:0000781; GO:0 | chromosome, telom |
| Binding to an RNA | IEA; IEA; IEA | | |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a nucleic | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the tran | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Enables the transfer | IBA | GO:0009706; GO:0 | chloroplast inner m |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IB | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of the pho | IEA; IEA | | |
| Any molecular func | IEA; IEA; IEA | | |
| Catalysis of the pho | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IBA; IBA | GO:0005634; GO:0 | nucleus; polysome; |
| | | GO:0005634; GO:0 | nucleus; membrane |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA; IEA; IBA | | |
| Binding to a metal i | IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the rea | IBA; IEA; IBA | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| Catalysis of the tran | IEA; IBA | | |
| Catalysis of the tran | IEA; IEA; IEA; IEA; IB | GO:0043231 | intracellular membr |
| | | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of an oxid | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA | | |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Binding to a microtu | IBA; IBA | GO:0005819; GO:0 | spindle; microtubul |
| Catalysis of the inc | IEA; IEA; IEA; IEA | | |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the ran | IEA; IEA; IEA | GO:0005576 | extracellular region |
| | | GO:0005737; GO:0 | cytoplasm; Golgi ap |
| Binding to a protein | IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| | | GO:0000123; GO:0 | histone acetyltransf |
| Catalysis of the pho | IEA; IEA | | |
| Catalysis of a bioch | IEA; IEA; IEA; IEA | | |
| | | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0031012 | extracellular matrix |
| Binding to a transfe | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to chromati | IBA | GO:0005634; GO:0 | nucleus; nucleolus |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IBA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the trar | IEA; IEA | | |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0016021 | integral component |
| Binding to a proteir | IEA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a proteir | IEA | | |
| The action of a mol | IEA | GO:0005762; GO:0 | mitochondrial large |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA | GO:0016020 | membrane |
| Catalysis of the rea | IBA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| A motor activity tha | IEA; IEA; IEA | | |
| Catalysis of the rea | IBA; IBA; IBA | | |
| Binding to a nucleic | IEA; IEA; IBA | | |

|  |  |  |  |
|---|---|---|---|
| Catalysis of an oxid | IEA; IEA; IEA |  |  |
| Binding to a metal i | IEA; IEA; IEA |  |  |
| Catalysis of the trar | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to monome | IEA | GO:0005737 | cytoplasm |
| Catalysis of the trar | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the phc | IEA; IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Catalysis of an oxid | IEA; IEA |  |  |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to an RNA r | IEA; IEA; IEA; IEA | GO:0005763; GO:0 | mitochondrial small |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the rea | IEA; IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Binding to an intern | IBA; IBA | GO:0005868; GO:0 | cytoplasmic dynein |
| Binding to DNA of a | IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IEA; IDA; IE | GO:0005576 | extracellular region |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IBA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to a nucleic | IEA | GO:0005730 | nucleolus |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005739; GO:0 | mitochondrion; inte |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protei | IEA | | |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| A transcription reg | IEA; IEA | | |
| Catalysis of an oxid | IEA; IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | | |
| Catalysis of the rea | IBA; IBA; IEA | | |
| Binding to an RNA r | IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the rea | IBA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; nuclear en |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Stimulates the exch | IBA | GO:0005886 | plasma membrane |
| Catalysis of the hyd | IEA; IEA | | |
| | | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; plasma |
| Catalysis of the rea | IBA; IEA; IEA; IBA; IEA | | |
| Catalysis of an oxid | IBA; IEA | GO:0005773; GO:0 | vacuole; membrane |
| Catalysis of a bioch | IEA; IEA | | |
| Any molecular func | IEA; IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; Set1C/CO |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0000407; GO:0 | phagophore assem |
| | | GO:0005634; GO:0 | nucleus; intracellul |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an RNA r | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IPI; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the trar | IEA | GO:0005794; GO:0 | Golgi apparatus; m |
| Enables the transfe | IBA | GO:0009941; GO:0 | chloroplast envelop |
| Catalysis of the hyd | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Catalysis of the trar | IEA | GO:0016021 | integral component |
| Binding to an RNA r | IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a calciun | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| Combining with an | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a magne | IEA; IEA; IEA | GO:0005829 | cytosol |
| Binding to small rib | IBA | GO:0005730; GO:0 | nucleolus; small-su |
| | | GO:0005783 | endoplasmic reticul |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to single-st | IBA; IBA; IEA | GO:0000428 | DNA-directed RNA |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0010008 | endosome membra |
| Binding to a nucleic | IEA; IEA; IBA; IEA; IB | GO:0005654; GO:0 | nucleoplasm; cytop |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IBA; IEA | GO:0005737 | cytoplasm |
| Enables the directe | ISS; IDA; IEA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binds to and stops, | IEA; IEA; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the ph | IEA; IBA; IEA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binds to and increa | IEA | | |
| | | GO:0005634; GO:0 | nucleus; cytoplasm |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binding to a metal i | IEA | GO:0000139; GO:0 | Golgi membrane; v |
| Enables the transfe | IBA; IEA; IEA; IEA | GO:0005887; GO:0 | integral component |
| Binding to a nucleic | IEA; IEA; IDA; IPI | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0009505; GO:0 | plant-type cell wall |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005737 | cytoplasm |
| | | GO:0005761; GO:0 | mitochondrial ribos |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0032300 | mismatch repair co |
| | | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the tra | IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a zinc io | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IBA | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA; IEA | GO:0005737; GO:0 | cytoplasm; endoso |
| Catalysis of the ph | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA; IBA; IBA | | |
| A transcription reg | IEA | | |

| | | | |
|---|---|---|---|
| Binding to a metal i | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Binding to a protein | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA; IEA; IBA; IEA; IEA | | |
| | | GO:0005623; GO:0 | obsolete cell; memb |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to messeng | IBA; IBA; IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| | | GO:0016021 | integral component |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to an RNA r | IEA; IEA; IBA; IEA | GO:0005737; GO:0 | cytoplasm; ribosom |
| | | GO:0016021 | integral component |
| | | GO:0016020 | membrane |
| Binds to and stops, | IEA | | |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Catalysis of the tra | IEA; IEA; IBA; IEA; IE | GO:0000139; GO:0 | Golgi membrane; e |
| Isoenergetic transfe | IBA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Unwinding a DNA h | IBA | GO:0000811; GO:0 | GINS complex; nucl |
| Binding to a nucleic | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Binding to a metal i | IEA; IBA; IBA | | |
| Catalysis of the tra | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the ph | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; n |

| | | | |
|---|---|---|---|
| Catalysis of the tra | IEA; IEA; IEA | GO:0016020 | membrane |
| Receiving a signal a | IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tra | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IBA; IDA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0005737; GO:0 | cytoplasm; cytosol |
| Catalysis of an oxid | IEA; IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| Catalysis of a bioch | ISS; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IBA; IBA; IB | GO:0000781; GO:0 | chromosome, telom |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| Binding to a nucleic | IEA | | |
| Catalysis of the tra | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; mitochond |
| Catalysis of the ph | IEA; IEA; IEA | | |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IEA; IB | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| Binding to a protein | IEA | GO:0005739; GO:0 | mitochondrion; vac |
| Binding to an RNA r | IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a polysa | IEA | | |
| Catalysis of the trar | IEA; IBA; IBA | GO:0005777 | peroxisome |
| Catalysis of the trar | IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of a bioch | IEA; IDA; IEA; IEA; IEA | | |
| | | GO:0001401; GO:0 | SAM complex; cyto |
| | | GO:0005576; GO:0 | extracellular region |
| | | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of the phc | IEA; IBA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Generation of force | IEA; IBA; IBA | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Enables the facilitat | IEA | GO:0016020; GO:0 | membrane; integral |
| The action of a mol | IBA; IEA; IBA | GO:0000922; GO:0 | spindle pole; equat |
| Catalysis of the inc | IBA; IEA | | |
| Binding to a zinc io | IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0005789; GO:0 | endoplasmic reticul |
| -glycanase) [Contains: Peptide-N4-(N-a | | GO:0005773 | vacuole |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the pho | IEA; IEA | | |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005634; GO:0 | nucleus; elongin co |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009941; GO:0 | chloroplast envelop |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a calciun | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005737 | cytoplasm |
| The action of a mol | IEA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| | | GO:0005634; GO:0 | nucleus; membrane |

|  |  |  |  |
|---|---|---|---|
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the pho | IEA; IEA |  |  |
| Catalysis of the hyd | IEA |  |  |
| Binding to a protein | IEA; IEA | GO:0008352 | katanin complex |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the tran | IEA; IEA | GO:0000139 | Golgi membrane |
| Binding to an RNA r | IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a microtu | IBA | GO:0005737; GO:0 | cytoplasm; spindle |
| Catalysis of the tran | IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to ATP, ade | IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the hyd | IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Enables the transm | IDA; IEA; IEA; IBA; IE | GO:0005773; GO:0 | vacuole; vacuolar m |
| | | GO:0009507 | chloroplast |
| Binding to single-s | IDA; IDA; IEA | GO:0009507; GO:0 | chloroplast; chlorop |
| The action of a mol | IEA; IEA; IBA | GO:0005840; GO:1 | ribosome; ribonucle |
| Any molecular entit | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Enables the transfe | IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Catalysis of a bioch | IEA; IEA | GO:0005777 | peroxisome |
| Binding to a lipid. | IEA | | |
| | | GO:0005737; GO:0 | cytoplasm; centros |
| Binding to a Hsp70 | IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of an oxid | IEA; IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005615 | extracellular space |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA; IEA; IEA; IBA | | |
| Catalysis of the pho | IEA; IEA | | |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; nucleolus; |
| Any molecular func | IEA; IEA; IPI; IEA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA | GO:0000506; GO:0 | glycosylphosphatid |
| Binds to and stops, | IEA | GO:0005615 | extracellular space |
| Catalysis of the pho | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the tran | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA | | |
| Binding to messeng | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0005634; GO:1 | nucleus; ribonucleo |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleic | IEA; IEA | | |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a lipid. | IEA | GO:0016020; GO:0 | membrane; integral |
| An thiol-dependent | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytosol; pl |
| Catalysis of an oxid | IEA | GO:0005737 | cytoplasm |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Binds to and increa | IEA; IEA; IEA | GO:0005768; GO:0 | endosome; trans-G |
| Binding to an identi | IPI; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Any molecular func | IEA; IBA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA; IEA; IEA; IBA | | |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to double-s | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromoso |
| Catalysis of the rea | IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |
| Catalysis of the tra | IEA | GO:0016021 | integral component |
| Binding to a nucleic | IEA; IEA | GO:0005730 | nucleolus |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IBA; IEA; IEA | | |
| A motor activity tha | IEA; IEA; IEA; IBA | GO:0005871; GO:0 | kinesin complex; m |
| Catalysis of the hyd | IEA; IBA | | |
| Catalysis of the rea | IEA; IEA | GO:0005739; GO:0 | mitochondrion; cyt |
| Binding to a nucleic | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; cytosol |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Combining with a n | IEA | GO:0005634; GO:0 | nucleus; nuclear po |
| | | GO:0005623; GO:0 | obsolete cell; memb |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005829 | cytosol |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |

| | | | |
|---|---|---|---|
| Binding to an RNA r | IEA; IEA; IEA | GO:0005840; GO:0 | ribosome; chloropla |
| Binding to a protein | IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a calciun | IEA | GO:0005783 | endoplasmic reticul |
| Binding to a protein | IEA | | |
| Catalysis of the trar | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the phc | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016021 | integral component |
| | | GO:0005777; GO:0 | peroxisome; peroxi |
| Binding to a protein | IEA | | |
| Catalysis of a bioch | IEA; IEA | | |
| Any molecular func | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005829 | cytosol |
| Catalysis of the phc | IBA; IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Catalysis of the ran | IEA; IEA; IEA | GO:0005576 | extracellular region |
| Binding to a specifi | IBA; IEA | GO:0005634; GO:0 | nucleus; Set1C/CON |
| Binding an acyl grou | IBA; IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to an unfol | IBA; IBA | GO:0005829 | cytosol |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a specifi | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an RNA | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of a bioch | IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Enables the transfe | IEA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a domai | IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Catalysis of the tra | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rem | IEA; IEA; IEA; IEA | GO:0005739 | mitochondrion |
| | | GO:0010287 | plastoglobule |
| Catalysis of the rea | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020 | membrane |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Stimulates the exch | IEA | GO:0055037 | recycling endosom |
| Binding to a nucleic | IEA; IBA; IBA | GO:0005634; GO:1 | nucleus; ribonucleo |
| Any molecular func | IEA; IEA | GO:0005739 | mitochondrion |
| Catalysis of the pho | IBA; IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0000118; GO:0 | histone deacetylase |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the tra | IEA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the rea | IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IEA; IEA | | |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Catalysis of an oxid | IBA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| | | | |
| Catalysis of the rea | IEA; IBA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Binding to messeng | IEA; IEA; IEA | | |
| Binding to messeng | IEA; IEA; IEA | | |
| Binding to a metal i | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IEA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a metal i | IEA | | |

| | | | |
|---|---|---|---|
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0005634; GO:0 | nucleus; nucleolus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding an acyl gro | IBA; IEA; IEA; IEA; IB | GO:0005737 | cytoplasm |
| Binding to an inosit | IEA | GO:0005768; GO:0 | endosome; membra |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the pho | IEA; IEA | GO:0010006; GO:0 | Toc complex; meml |
| Enables the calcium | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; Cdc48p- |

| | | | |
|---|---|---|---|
| | | GO:0005886 | plasma membrane |
| Binding to a zinc io | IEA | | |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005737 | cytoplasm |
| A transcription regu | IEA | GO:0005634; GO:0 | nucleus; mediator c |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0005794; GO:0 | Golgi apparatus; me |
| Catalysis of the rea | IEA | GO:0016020 | membrane |
| | | GO:0005634; GO:0 | nucleus; tRNA (m1A |
| Catalysis of the rea | IEA; IEA; IEA | | |
| Acting as a marker | IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005886 | plasma membrane |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005774; GO:0 | vacuolar membrane |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Binding to a nucleic | IEA; IEA; IBA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| A motor activity tha | IBA; IBA | GO:0005737; GO:0 | cytoplasm; actin cy |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| A transcription regu | IEA; IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IBA; IEA | GO:0005681; GO:0 | spliceosomal compl |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IBA; IEA; IBA; IE | GO:0016020; GO:0 | membrane; integral |
| The action of a mol | IBA | GO:0005643; GO:0 | nuclear pore; nucle |
| Stimulates the exch | IEA | GO:0005829; GO:0 | cytosol; membrane |
| Binding to a metal i | IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to double-s | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromosor |
| | | GO:0016021 | integral component |
| Catalysis of the trar | IEA; IEA; IBA; IBA | GO:0043231 | intracellular membr |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IBA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the seq | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| Binds transmembra | IBA | GO:0005743; GO:0 | mitochondrial inner |
| | | GO:0009534; GO:0 | chloroplast thylakoi |
| | | GO:0009705; GO:0 | plant-type vacuole |
| Binding to a protein | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; nucleolus |
| Any molecular entit | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; mitocho |
| Binding to a specifi | IBA; IBA; IBA; IBA; IB | GO:0005634; GO:0 | nucleus; transcripti |
| Binding to a nucleic | IEA; IEA | GO:0016607 | nuclear speck |
| Catalysis of the rea | IBA | | |
| Binds to and increa | IEA | | |
| Catalysis of the trar | IEA; IEA | GO:0005794 | Golgi apparatus |

| | | | |
|---|---|---|---|
| Binding to double- | IEA | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005876; GO:0 | spindle microtubul |
| Binding to a protei | IEA | GO:0005634; GO:0 | nucleus; intracellul |
| Any molecular func | IEA; IDA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0012505; GO:0 | endomembrane sys |
| Binding to a calciu | IBA; IEA | GO:0005737 | cytoplasm |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| An thiol-dependent | IEA; IEA; IEA; IEA | | |
| Catalysis of the tra | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005783 | endoplasmic reticul |
| Catalysis of the rea | IBA; IEA; IDA; IBA | GO:0005737; GO:0 | cytoplasm; protein- |
| Binding to double- | IEA | GO:0009506; GO:0 | plasmodesma; chlo |
| Binding to a protei | IEA; IBA | GO:0005634; GO:0 | nucleus; cytosol |
| Catalysis of the rea | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Catalysis of the tra | IEA; IEA; IBA; IBA; IB | GO:0005737 | cytoplasm |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA; IBA | GO:0005634 | nucleus |
| | | GO:0005739; GO:0 | mitochondrion; mit |
| Catalysis of the tra | IBA | GO:0005768; GO:0 | endosome; trans-G |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005618 | cell wall |
| Catalysis of the hyd | IEA; IEA; IEA; IBA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a calciun | IBA; IBA | | |
| Binding to a protein | IEA | | |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; chloropl |
| Binding to a nucleic | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Transport systems | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| Functions in chain | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Catalysis of a bioch | IEA | | |
| Catalysis of the hyd | IEA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Any molecular entit | IEA | GO:0046658 | anchored compone |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the ph | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005886 | plasma membrane |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IEA; IBA; IBA; IBA; IE | GO:0005634; GO:0 | nucleus; transcripti |
| Catalysis of the rea | IEA; IEA | GO:0005737 | cytoplasm |
| An thiol-dependent | IBA; IEA; IEA; IEA; IE | GO:0005768; GO:0 | endosome; membra |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an RNA | IBA; IEA; IEA | GO:0043231 | intracellular membr |

| | | | |
|---|---|---|---|
| | | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of a bioch | IEA; IEA; IBA; IEA; IEA | | |
| | | GO:0005829 | cytosol |
| Binding to a protein | IEA | GO:0000243; GO:0 | commitment compl |
| | | GO:0005886 | plasma membrane |
| Binding to a tetrapy | IBA | GO:0009507 | chloroplast |
| Catalysis of the rea | IEA; IBA; IEA | | |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Binding an acyl gro | IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Catalysis of the tran | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the pho | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IBA; IBA; IBA; IB | GO:0005634; GO:0 | nucleus; cytosol; ri |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0005615; GO:0 | extracellular space; |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; RNA N6-m |
| | | GO:0016020; GO:0 | membrane; integral |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IDA | GO:0005783 | endoplasmic reticul |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to damage | IBA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a protei | IEA; IEA; IEA |  |  |
| Catalysis of the hyd | IEA; IEA | GO:0009507 | chloroplast |
| Binding to a protei | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886 | plasma membrane |
| Catalysis of the hyd | IEA; IEA |  |  |
| Binding to a protei | IEA; IEA; IBA; IEA; IE | GO:0005737 | cytoplasm |
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a specifi | IBA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a calciu | IEA |  |  |
| Catalysis of the rea | IBA; IEA | GO:0010008 | endosome membra |

| | | | |
|---|---|---|---|
| Any molecular func | IBA; IEA; IDA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA | GO:0005773; GO:0 | vacuole; endoplasm |
| | | GO:0005739 | mitochondrion |
| | | | |
| Binding to a specifi | IBA; IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA; IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; chloroplas |
| Binding to an RNA r | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA; IBA; IE | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA | GO:0009507 | chloroplast |
| Binding to a protein | IEA | GO:0031357 | integral component |
| | | GO:0000811; GO:0 | GINS complex; nucl |
| | | GO:0005768; GO:0 | endosome; trans-G |
| Catalysis of the trar | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IBA | | |
| | | | |
| Binds to and increa | IEA; IEA | | |
| Binding to a lipopol | IEA; IEA | GO:0005615; GO:0 | extracellular space; |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | | |
| | | | |
| Binding to inositol | IBA; IBA | GO:0005737; GO:0 | cytoplasm; Golgi ap |
| | | GO:0016020; GO:0 | membrane; integral |
| | | | |
| | | | |
| | | | |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of an oxid | IBA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IBA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a zinc io | IEA; IEA; IBA | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA; IEA | GO:0005770; GO:0 | late endosome; phc |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IB | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to messeng | IBA; IBA | | |
| Binding to a nucleic | IEA; IEA | GO:0005737; GO:0 | cytoplasm; nuclear |
| | | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0009507 | chloroplast |

|  |  |  |  |
|---|---|---|---|
| Removes phosphati | IBA |  |  |
| Binding to a specifi | IBA; IBA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytosol; tR |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protein | IEA | GO:0043231 | intracellular membr |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA r | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; chlo |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA |  |  |
| Binding to a protein | IEA | GO:0032040; GO:0 | small-subunit proc |
| Binding to a metal i | IEA |  |  |
| Binding to a protein | IEA | GO:0009507 | chloroplast |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IBA; IEA; IEA; IE | GO:0016020 | membrane |
| Binding to a protein | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005871; GO:0 | kinesin complex; m |

| | | | |
|---|---|---|---|
| Binding to a protein | IPI; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IBA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to double- | IEA; IEA | GO:0009507 | chloroplast |
| | | GO:0031902; GO:0 | late endosome mem |
| Binding to a protein | IEA | | |
| Binding to chromati | IBA | GO:0000793; GO:0 | condensed chromo |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005886 | plasma membrane |
| Any molecular entit | IEA | GO:0005773; GO:0 | vacuole; plasma me |
| The action of a mol | IBA; IEA | GO:0000139; GO:0 | Golgi membrane; e |
| | | GO:0005576 | extracellular region |
| Binding to an RNA | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA; IEA | | |
| Catalysis of an oxid | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the rea | IEA | GO:0005773; GO:0 | vacuole; endoplasm |
| Binds to and stops, | IEA | | |
| Enables the calcium | IEA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to messeng | IEA; IEA | GO:0005829 | cytosol |
| Enables the transfe | IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Catalysis of the dim | IEA; IEA; IEA; IEA; IE | GO:0005739 | mitochondrion |
| Binding to messeng | IEA; IEA | GO:0005739 | mitochondrion |
| Catalysis of an oxid | IEA; IEA; IBA; IEA | | |
| Catalysis of an oxid | IEA | GO:0005759 | mitochondrial matri |
| Enables the transfe | IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of a bioch | IEA; IEA; IEA; IEA; IEA | | |
| Any molecular entit | IEA; IEA | GO:0005623 | obsolete cell |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IBA; IEA | GO:0016020 | membrane |
| Receiving a signal a | IBA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016021 | integral component |
| Binding to a nucleic | IEA; IEA; IEA; IEA; IB | GO:0000151; GO:0 | ubiquitin ligase con |
| Catalysis of the rea | IEA; IBA; IEA; IEA; IB | GO:0005739; GO:0 | mitochondrion; chlo |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a protein | IEA | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the hyd | IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IEA | GO:0016607 | nuclear speck |
| Catalysis of the tra | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Any molecular func | IBA; IEA; IBA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IEA | | |
| Binding to an RNA r | IEA; IEA | GO:0005686; GO:0 | U2 snRNP; U2-type |
| Catalysis of the rea | IBA; IEA | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA; IBA | GO:0005634; GO:0 | nucleus; CAF-1 con |
| Binding to a carboh | IEA | | |
| Enables the directe | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; cytoskel |
| Binding to a SNARE | IBA | | |
| Catalysis of the trar | IEA; IEA; IBA; IEA; IB | GO:0000151; GO:0 | ubiquitin ligase con |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a protein | IEA | | |
| | | GO:0005829 | cytosol |
| Binding to an RNA r | IBA; IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; intr |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA; IBA | | |
| Catalysis of the trar | IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; Smc5-Smc |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the hyd | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | | |
| Binding to a protein | IEA; IEA | | |
| Enables the facilitat | IBA; IEA | GO:0005739; GO:0 | mitochondrion; mit |
| | | GO:0005886 | plasma membrane |
| | | GO:0009506; GO:0 | plasmodesma; mem |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; n |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005871; GO:0 | kinesin complex; m |
| Catalysis of the tra | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005739 | mitochondrion |
| Any molecular entit | IEA | | |
| Binding to a protei | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a basal R | IEA; IEA; IBA; IEA; IB | GO:0005634; GO:0 | nucleus; transcripti |
| Binds to and stimul | IBA; IEA; IBA; IBA | GO:0005737 | cytoplasm |
| | | GO:0016020; GO:0 | membrane; integral |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA; IBA | | |
| Binding to a protei | IEA | | |
| Catalysis of the tra | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| | | GO:0000813; GO:0 | ESCRT I complex; e |
| Catalysis of the tra | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a protei | IEA; IBA; IEA | GO:0005787 | signal peptidase co |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA | IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA | | |
| Binding to an inosit | IBA; IEA | GO:0032587 | ruffle membrane |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IBA; IEA; IBA; IB | GO:0000781; GO:0 | chromosome, telo |
| Binding to a transfe | IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a cation, | IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binds to and stops, | IEA; IEA; IEA | GO:0005576 | extracellular region |
| Functions in the ini | IBA; IEA; IEA; IEA; IE | GO:0005851 | eukaryotic translati |
| Catalysis of the hyd | IBA; IEA; IBA; IEA; IE | GO:0005759 | mitochondrial matri |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |

| | | | |
|---|---|---|---|
| Catalysis of the tra | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Catalysis of the seq | IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IBA | GO:0009368; GO:0 | endopeptidase Clp |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IB | GO:0000307; GO:0 | cyclin-dependent p |
| Binding to a protei | IEA | GO:0043229 | intracellular organe |
| Catalysis of the rea | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the rea | IEA | GO:0005777 | peroxisome |
| A DNA-binding tra | IBA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the ph | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| An thiol-dependent | IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a SNARE | IBA | GO:0000323; GO:0 | lytic vacuole; endos |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA; IBA; IBA | GO:0005829; GO:0 | cytosol; extrinsic c |
| | | GO:0005730; GO:0 | nucleolus; preribos |
| Binding to a transfe | IBA; IEA; IBA | GO:0005737 | cytoplasm |
| Catalysis of the tra | IEA | | |
| Catalysis of the ph | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IBA | GO:0005759 | mitochondrial matri |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA | GO:0005739 | mitochondrion |
| Binding to a fatty a | IEA | | |
| Binding to damage | IBA; IBA | | |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Enables the transfe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| A DNA-binding trar | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0009705; GO:0 | plant-type vacuole |
| Catalysis of an oxid | IEA; IEA | GO:0005623 | obsolete cell |
| Binding to a protein | IEA; IEA | | |
| Catalysis of the pho | IBA; IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; membra |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000137; GO:0 | Golgi cis cisterna; C |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the hyd | IEA | | |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the rea | IEA | | |
| Binding to ATP, ade | IEA; IEA | GO:0005737; GO:0 | cytoplasm; nucleoic |
| Catalysis of the rea | IBA | GO:0005737 | cytoplasm |
| Binding to double-s | IBA; IEA; IEA; IEA; IB | GO:0005634; GO:0 | nucleus; chromosor |
| Any molecular func | IBA; IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA | GO:0005737 | cytoplasm |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the exo | IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0005576 | extracellular region |
| Catalysis of the trar | IEA | GO:0009507 | chloroplast |

| | | | |
|---|---|---|---|
| Catalysis of a bioch | IEA; IEA; IEA | | |
| Catalysis of the tra | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a metal i | IEA | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA | IEA | | |
| Binding to a protei | IEA | GO:0005739 | mitochondrion |
| Binding to an RNA | IBA; IEA | GO:0043231 | intracellular memb |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IEA | | |
| Binding to a domai | IBA; IBA | GO:0005777; GO:0 | peroxisome; peroxi |

|  |  |  |  |
|---|---|---|---|
| Catalysis of an oxid | IBA; IBA; IEA |  |  |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA |  |  |
| Enables the transfe | IBA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| The action of a mol | IBA | GO:0031080; GO:0 | nuclear pore outer |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
|  |  | GO:0016020; GO:0 | membrane; membr |
| Binds to and increa | IEA; IEA | GO:0005737; GO:0 | cytoplasm; mitocho |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
|  |  | GO:0072546 | EMC complex |
| Stimulates the exch | IEA |  |  |
| Enables the transm | IEA | GO:0005886; GO:0 | plasma membrane; |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Binding to an RNA r | IEA; IEA; IEA |  |  |

|  |  |  |  |
|---|---|---|---|
| Catalysis of an oxid | IEA; IEA; IBA |  |  |
| Binding to a calciun | IEA; IBA | GO:0009507; GO:0 | chloroplast; photos |
| Binding to a SNARE | IBA; IEA; IBA; IBA; IE | GO:0005794; GO:0 | Golgi apparatus; cla |
| Binding to a cation, | IEA |  |  |
| Catalysis of the phc | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0000325; GO:0 | plant-type vacuole; |
| Binding to a zinc io | IEA | GO:0016021 | integral component |
| Binding to GTP, gua | IEA; IEA; IEA | GO:0009507 | chloroplast |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IEA |  |  |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA; ISS; IEA; IEA; IE | GO:0005634 | nucleus |
|  |  | GO:0005739; GO:0 | mitochondrion; chl |
| The action of a mol | IBA | GO:0005643 | nuclear pore |
| Binding to a protein | IEA |  |  |
| The formation of a | IEA |  |  |
| Binding to a nucleic | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; nucleolus; |
| Catalysis of the hyd | IEA; IEA | GO:0005615; GO:0 | extracellular space; |
| Binding to a protein | IEA; IBA | GO:0000776; GO:0 | kinetochore; phrag |
|  |  | GO:0005794 | Golgi apparatus |
| The function of abs | IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

|  |  |  |  |
|---|---|---|---|
| Any molecular entit | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an inosit | IEA; IEA | GO:0005886 | plasma membrane |
| Enables the transfe | IEA | GO:0016021 | integral component |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IB | GO:0005576; GO:0 | extracellular region |
| Binding to DNA of a | IBA | GO:0019185 | snRNA-activating p |
| Binding to messeng | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an identi | IEA; IEA | GO:0005739; GO:0 | mitochondrion; vac |
| Catalysis of an oxid | IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IBA | GO:0005783 | endoplasmic reticul |
| Catalysis of the rea | IEA |  |  |
| Binding to a protein | IEA; IEA | GO:0005634; GO:0 | nucleus; small-sub |
| Catalysis of the tra | IEA; IEA; IBA |  |  |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Enables the transfe | IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA | GO:0046658 | anchored compone |
| Binding to a protein | IEA; IBA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol; m |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Binding to a nucleic | IEA; IEA |  |  |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0110165 | cellular anatomical |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0009507 | chloroplast |
| Enables the transfe | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA | | |
| Binding to a calciun | IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; int |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Enables the transfe | IEA | GO:0005774; GO:0 | vacuolar membrane |
| Catalysis of an oxid | IEA; IEA; IBA; IBA | | |
| Catalysis of the trar | IEA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a protein | IEA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA | | |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding an acyl grou | IBA; IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; plastid |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| OBSOLETE. Enables | IBA; IEA | GO:0005773; GO:0 | vacuole; Golgi appa |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to chromati | IEA | GO:0005634 | nucleus |
| Binds to and stimul | IBA; IEA; IBA | | |
| Binding to a metal i | IEA | | |

| | | | |
|---|---|---|---|
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA; IEA | | |
| Catalysis of the rea | IEA; IEA | GO:0005737 | cytoplasm |
| Catalysis of a bioch | IEA; IBA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA | GO:0008540; GO:0 | proteasome regulat |
| Binding to a protein | IEA | GO:0009535; GO:0 | chloroplast thylakoi |
| | | GO:0009570 | chloroplast stroma |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0055028 | cortical microtubule |
| Binding to damagec | IEA; IBA | GO:0005634; GO:0 | nucleus; replication |
| Catalysis of the trar | IEA | | |
| Binding to a cadmiu | IDA | GO:0005615 | extracellular space |
| | | GO:0005634; GO:0 | nucleus; spliceosom |
| Catalysis of the rea | IEA | GO:0005739; GO:0 | mitochondrion; cyto |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005737 | cytoplasm |
| Catalysis of the trar | IEA; IBA | | |
| Catalysis of the phc | IEA; IEA | | |
| Enables the facilitat | IEA | GO:0016020; GO:0 | membrane; integral |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IBA; IBA | GO:0000427; GO:0 | plastid-encoded pla |
| Enables the transfe | IEA | GO:0016020 | membrane |
| Binding to a zinc io | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IBA |  |  |
| Binding to a protein | IEA |  |  |
| Enables the transfe | IEA | GO:0005774; GO:0 | vacuolar membrane |
| Binding to an RNA r | IBA; IEA | GO:0005829; GO:0 | cytosol; P granule |
|  |  | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to a protein | IEA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0005634 | nucleus |
|  |  | GO:0000176; GO:0 | nuclear exosome (R |
| Isoenergetic transfe | IBA |  |  |
| Catalysis of the rea | IBA; IBA; IEA; IEA | GO:0005829 | cytosol |
| Catalysis of the rea | IEA; IBA; IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA |  |  |
| Binding to a nucleic | IEA; IEA; IEA; IEA | GO:0005840; GO:0 | ribosome; chloropla |
|  |  | GO:0005634; GO:0 | nucleus; U4/U6 x U |
| Catalysis of an oxid | IEA; IEA; IBA |  |  |
| Catalysis of the hyd | IEA |  |  |
| Binding to a nucleic | IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA; IEA |  |  |
|  |  | GO:0005886; GO:0 | plasma membrane; |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the pho | IEA; IEA; IEA; IEA | GO:0016021 | integral component |
| Catalysis of the tra | IEA; IEA | GO:0005789; GO:0 | endoplasmic reticul |

| | | | |
|---|---|---|---|
| | | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Catalysis of the seq | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA; IBA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA | GO:0009507 | chloroplast |
| A motor activity tha | IEA; IEA; IEA; IEA | | |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0016020 | membrane |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a protein | IPI; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005576; GO:0 | extracellular region |
| Binding to a specifi | IBA; IBA; IBA; IBA; IB | GO:0005634; GO:0 | nucleus; transcripti |

| | | | |
|---|---|---|---|
| Binding to a protei | IEA | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of the tra | IBA; IEA | | |
| Binding to a nucleo | IEA; ISS; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; mitochond |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | | |
| Binding to a nucleic | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; spliceoso |
| | | | |
| | | GO:0016021 | integral component |
| Any molecular entit | IEA; IEA | GO:0005623 | obsolete cell |
| | | | |
| | | GO:0110165 | cellular anatomical |
| | | | |
| Catalysis of a bioch | IEA | | |
| | | | |
| Binding to messeng | IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Catalysis of the tra | IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0019005 | SCF ubiquitin ligase |
| Catalysis of the rea | IBA | GO:0005789 | endoplasmic reticul |
| | | GO:0005634; GO:0 | nucleus; vacuolar |
| | | | |
| Binding to a protei | IEA | | |
| | | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0009507; GO:0 | chloroplast; plastid |

| | | | |
|---|---|---|---|
| | | GO:0000145 | exocyst |
| Binding to a protei | IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | | |
| Catalysis of the inc | IEA; IEA; IEA; IEA | GO:0016020 | membrane |
| | | GO:0005634; GO:0 | nucleus; integrator |
| | | GO:0005634; GO:0 | nucleus; transcripti |
| Catalysis of the tra | IEA; IEA; IEA | | |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to GTP, gua | IEA | | |
| Catalysis of the tra | IEA; IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an amin | IEA | | |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a microt | IBA | GO:0005881 | cytoplasmic microt |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the rea | IEA | GO:0005886 | plasma membrane |
| Catalysis of an oxid | IEA; IEA; IBA | | |

| | | | |
|---|---|---|---|
| Any molecular func | IEA | GO:0005634 | nucleus |
| An thiol-dependent | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of an oxid | IEA; IEA; IBA; IBA; IE | GO:0005829 | cytosol |
| Binding to an RNA r | IEA; IEA; IEA | | |
| Binding to an inosit | IEA | GO:0005768; GO:0 | endosome; membra |
| Catalysis of a bioch | IEA; IBA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IEA; IEA; IEA; IEA; IB | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of a bioch | IEA; IEA; IEA | | |
| A transcription regu | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the pho | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IEA; IEA; IEA; IEA | | |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |

| | | | |
|---|---|---|---|
| Binding to a specifi | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Enables the directe | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the trar | IBA; IEA | | |
| | | GO:0005886 | plasma membrane |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Binding to an RNA | IBA | GO:0005634; GO:0 | nucleus; Cdc73/Paf |
| Catalysis of the rea | IBA; IEA; IEA | | |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA; IBA | | |
| Binding to a nucleic | IEA; IEA; IBA; IEA | GO:0005829; GO:0 | cytosol; eRF1 methy |
| Binding to a DNA se | IBA; IBA; IEA; IBA; IE | GO:0005634; GO:0 | nucleus; transcripti |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Catalysis of the trar | IBA; IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| Binding to a lipid.; | IEA; IBA; IBA | GO:0005829; GO:0 | cytosol; membrane; |
| Catalysis of the trar | IEA; IBA; IBA; IEA | | |
| Catalysis of the trar | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to ATP, ade | IEA; IEA; IEA; IEA | GO:0005737; GO:0 | cytoplasm; endopla |

|  |  |  |  |
|---|---|---|---|
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
|  |  | GO:0009507 | chloroplast |
| Binding to a metal i | IEA |  |  |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA; IEA |  |  |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of a bioch | IEA; IEA | GO:0009707; GO:0 | chloroplast outer m |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tran | IEA; IEA; IEA | GO:0016020 | membrane |
| Catalysis of the hyd | IEA |  |  |
|  |  | GO:0000145 | exocyst |
| Binding to an RNA r | IEA; IEA | GO:0009507 | chloroplast |
| Binding to a nucleic | IEA; IEA; IEA |  |  |
| Binding to a protein | IEA |  |  |
| Enables the transfe | IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576 | extracellular region |
| Binding to auxin, a | IEA | GO:0005788 | endoplasmic reticul |
| Binding to a DNA st | IEA; IBA | GO:0005634 | nucleus |
| Binds to and stimul | IBA; IEA; IBA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0055087 | Ski complex |
| Catalysis of the tran | IEA |  |  |
| Catalysis of the tran | IBA |  |  |
| The hydrolysis of an | IEA; IEA |  |  |
|  |  | GO:0005634; GO:0 | nucleus; cytosol |
| Binding to messeng | IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| A transcription regu | IBA; IEA; IBA | GO:0005634 | nucleus |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |

| | | | |
|---|---|---|---|
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; mitochond |
| Catalysis of the rea | IEA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the rea | IEA; IEA; IEA | GO:0009507; GO:0 | chloroplast; chlorop |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0000815; GO:0 | ESCRT III complex; |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Catalysis of the tra | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular entit | IEA; IEA; IBA; IEA; IE | GO:0005759; GO:0 | mitochondrial matri |
| | | GO:0005730 | nucleolus |
| Binding to a nucleic | IEA; IBA; IBA | GO:0005634; GO:0 | nucleus; polysome |
| Enables the calcium | IEA | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the rea | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleic | IEA; IBA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to a nucleic | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IEA | GO:0009507 | chloroplast |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IBA | GO:0016020 | membrane |
| Catalysis of the rem | IEA; IEA; IEA; IEA; IB | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the hyd | IEA |  |  |
| Enables the transfe | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA |  |  |
| Catalysis of the pho | IEA; IBA; IEA; IEA | GO:0005886 | plasma membrane |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| The binding activity | IBA | GO:0005635; GO:0 | nuclear envelope; ir |
| Any molecular entit | IEA; IEA; IEA; IEA; IE | GO:0005737 | cytoplasm |
| Catalysis of the hyd | IEA; IBA | GO:0005576; GO:0 | extracellular region |
| Binding to a protein | IEA |  |  |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to double-s | IBA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; chromosom |
| Binding to a metal i | IEA |  |  |
| Binding to monome | IEA; IBA | GO:0005737; GO:0 | cytoplasm; actin cy |
| Binding to a sterol, | IBA | GO:0005623 | obsolete cell |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |
| Catalysis of the tran | IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| A DNA-binding tran | IBA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | GO:0000421 | autophagosome me |

| | | | |
|---|---|---|---|
| Catalysis of the trar | IEA | GO:0016021 | integral component |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA; IEA; IEA | | |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA | | |
| Binding to GTP, gua | IEA | GO:0005739; GO:0 | mitochondrion; chl |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the trar | IEA; IBA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005576 | extracellular region |
| Catalysis of an oxid | IEA; IEA; IBA | | |
| Binding to a protein | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IE | GO:0005634; GO:0 | nucleus; chromosor |
| Catalysis of the hyd | IEA; IEA; IEA; IBA | GO:0005765; GO:0 | lysosomal membrar |
| Binding to calmodu | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| OBSOLETE. Enables | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | | |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to a protein | IEA | GO:0005886 | plasma membrane |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Binding to a protein | IEA | | |
| Catalysis of the ran | IEA; IEA; IEA | GO:0005576 | extracellular region |
| Catalysis of the trar | IEA; IEA; IEA; IEA | | |
| Binding to a specifi | IBA; IEA; IEA; IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Binding to a protein | IEA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the rea | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |

| | | | |
|---|---|---|---|
| Binding to a metal i | IEA | | |
| Catalysis of a bioch | IEA; IBA; IC; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Any molecular func | IEA; IEA; IPI; IEA | GO:0005634 | nucleus |
| Any molecular func | IEA | GO:0005634 | nucleus |
| Binding to an RNA r | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of a bioch | IEA; IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; protein-D |
| Catalysis of the tra | IEA; IEA | GO:0005794; GO:0 | Golgi apparatus; int |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IBA; IBA | GO:0005634; GO:0 | nucleus; polysome; |
| An thiol-dependent | IEA; IEA; IEA | | |
| Binding to an unfol | IEA; IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binds to and increa | IEA | | |
| Binding to a nucleic | IEA; IEA | GO:0005737 | cytoplasm |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IE | GO:0005576 | extracellular region |
| Binds to and increa | IBA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; c |
| | | GO:0005634; GO:0 | nucleus; Cul4-RING |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA; IBA | | |
| Modulates the activ | IBA; IBA | GO:0000307; GO:0 | cyclin-dependent p |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| A transcription reg | IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA | | |
| Enables the transm | IEA; IEA | GO:0005739; GO:0 | mitochondrion; mit |

|  |  |  |  |
|---|---|---|---|
| Catalysis of a bioch | IEA; IEA; IEA; IEA |  |  |
| Catalysis of the rea | IBA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to ubiquiti | IEA; IEA |  |  |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Catalysis of a bioch | IEA; IEA; IEA; IEA |  |  |
| The action of a mol | IEA; IEA | GO:0005840; GO:0 | ribosome; cytosolic |
| Binding to a specifi | IBA; IEA; IBA; IBA | GO:0005634 | nucleus |
| Binding to a specifi | IBA; IEA; IBA; IEA | GO:0005634 | nucleus |
| Binding to monome | IEA; IBA | GO:0005737; GO:0 | cytoplasm; actin cy |
| A histone chaperon | IEA | GO:0000812; GO:0 | Swr1 complex; nucl |
| Catalysis of the pho | IBA | GO:0043229 | intracellular organe |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the end | IBA | GO:0005634; GO:0 | nucleus; nucleoplas |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the seq | IBA; IEA; IBA |  |  |
| Binds to and increa | IBA | GO:0005737; GO:0 | cytoplasm; cytosol; |
| Binding to a DNA p | IBA | GO:0000793; GO:0 | condensed chromo |
| Catalysis of an oxid | IEA; IEA | GO:0009941; GO:0 | chloroplast envelop |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to an iron ( | IEA; IEA; IBA | GO:0005739; GO:0 | mitochondrion; chl |
| Binding to monome | IEA |  |  |
| Binding to a nuclea | IEA; IEA | GO:0005634; GO:0 | nucleus; nuclear en |
| A transcription regu | IEA; IBA | GO:0005634; GO:0 | nucleus; mediator c |
|  |  | GO:0005634 | nucleus |
| Catalysis of the join | IEA | GO:0005739 | mitochondrion |

|  |  |  |  |
|---|---|---|---|
| Binding to a protein | IEA; IEA; IEA; IEA |  |  |
| Binding to a protein | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA; IEA; IBA; IBA; IB | GO:0005759 | mitochondrial matri |
|  |  | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleic | IEA; IBA | GO:0005730 | nucleolus |
| Catalysis of the tran | IEA; IEA |  |  |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA |  |  |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a protein | IEA |  |  |
| Catalysis of an oxid | IEA | GO:0016020; GO:0 | membrane; integral |
| Any molecular func | IEA | GO:0005634 | nucleus |
|  |  | GO:0009507 | chloroplast |
| Binding to a protein | IEA |  |  |
| Binding to a lipid. | IEA | GO:0005615 | extracellular space |

|  |  |  |  |
|---|---|---|---|
| Binding to a nucleo | IEA; IEA; IEA; IEA; IEA; IEA |  |  |
| Catalysis of the hyd | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA |  |  |
|  |  |  |  |
| Enables the transm | IEA | GO:0009535; GO:0 | chloroplast thylakoi |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA | GO:0016020; GO:0 | membrane; integral |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Binding to a protein | IEA; IEA |  |  |
| The action of a mol | IEA | GO:0005840; GO:1 | ribosome; ribonucle |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
|  |  |  |  |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
|  |  |  |  |
|  |  |  |  |
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|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Any molecular func | IEA; IEA; IDA | GO:0005634 | nucleus |
| Catalysis of the rea | IBA | GO:0016020; GO:0 | membrane; integral |
|  |  |  |  |
|  |  | GO:0005802 | trans-Golgi networ |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| Binding to a specifi | IEA; IBA; IBA; IEA; IE | GO:0005634 | nucleus |
| Catalysis of the trar | IEA; IEA | GO:0005794 | Golgi apparatus |
|  |  |  |  |
|  |  |  |  |
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|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  | GO:0071014 | post-mRNA release |
|  |  |  |  |
|  |  |  |  |
| Binding to damage | IEA; IEA | GO:0005634 | nucleus |
|  |  | GO:0033588 | elongator holoenzy |
| Binding to a chaper | IBA | GO:0005739; GO:0 | mitochondrion; mit |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IBA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Enables the active t | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | | |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IB | GO:0000307; GO:0 | cyclin-dependent p |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IE | GO:0000776; GO:0 | kinetochore; nucleu |
| Binding to a nucleic | IEA; IEA | | |
| Binds to and stops, | IEA; IEA | | |
| Catalysis of the hyd | IEA | | |
| | | GO:0005615 | extracellular space |
| Binding to a protein | IEA | | |
| Catalysis of the ph | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding to a protein | IPI | GO:0005634 | nucleus |
| Catalysis of the inc | IEA; IEA; IEA; IEA | | |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the rea | IBA; IBA; IEA; IEA | GO:0005737 | cytoplasm |
| Binds to and stops, | IEA; IEA | GO:0005615 | extracellular space |
| Catalysis of the ph | IEA; IEA; IEA; IEA; IE | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the tra | IEA; IBA; IEA; IBA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005634; GO:0 | nucleus; nuclear ou |
| Binding to a protein | IEA | GO:0005634 | nucleus |
| Binding to chromati | IBA; IBA; IBA | GO:0000796; GO:0 | condensin complex |
| Binding to a protein | IEA | | |
| Catalysis of the hyd | IEA; IEA | | |
| Binding to a protein | IEA | GO:0043229 | intracellular organe |

| | | | |
|---|---|---|---|
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005634 | nucleus |
| | | GO:0009507 | chloroplast |
| | | GO:0016020; GO:0 | membrane; integral |
| Binding to an RNA r | IEA | | |
| Binding to a specifi | IBA; IBA; IEA | GO:0000785; GO:0 | chromatin; nucleus |
| Binding to an iron ( | IBA; IBA; IBA; IEA; IE | GO:0005623; GO:0 | obsolete cell; cellula |
| Catalysis of the trar | IEA; IBA | | |
| Binding to a protein | IEA | | |
| Enables the transfe | IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleo | IEA; IEA; IBA; IEA; IEA | | |
| Catalysis of the phc | IEA; IEA; IEA | GO:0016021 | integral component |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| Binding to a nucleic | IEA; IBA; IEA; IEA; IB | GO:0005634 | nucleus |
| Catalysis of the seq | IBA; IEA; IBA | | |
| Binding to an RNA r | IEA | | |
| | | GO:0000932; GO:0 | P-body; nucleus; C |
| Catalysis of the hyd | IEA | | |
| Catalysis of the hyd | IEA | | |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA | | |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IE | GO:0005886 | plasma membrane |
| A transcription core | IBA | GO:0005634; GO:0 | nucleus; mediator c |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA | | |

|  |  |  |  |
|---|---|---|---|
|  |  | GO:0009705; GO:0 | plant-type vacuole |
| Binding to an RNA r | IEA; IEA; IEA; IEA; IE | GO:0009507 | chloroplast |
| A motor activity tha | IEA; IEA; IEA; IEA |  |  |
| Binding to a fatty ac | IBA; IEA | GO:0009570 | chloroplast stroma |
| Catalysis of the trar | IEA; IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IB | GO:0005634; GO:0 | nucleus; cytoplasm |
|  |  | GO:0005759 | mitochondrial matri |
|  |  | GO:0016021 | integral component |
| Stimulates the exch | IEA |  |  |
| Catalysis of the trar | IEA; IEA; IBA; IEA |  |  |
| Any molecular func | IEA | GO:0005634; GO:0 | nucleus; membrane |
|  |  | GO:0016020 | membrane |
| Catalysis of the trar | IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA; IEA; IEA; IEA; IEA; IEA |  |  |
| Catalysis of the trar | IEA; IBA; IEA; IEA; IB | GO:0005829 | cytosol |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |

|  |  |  |  |
|---|---|---|---|
| Binding to a manga | IEA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Catalysis of the inc | IEA; IEA; IBA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Binding to double-s | IEA | GO:0009507 | chloroplast |
| Binding to a nucleo | IEA; IEA; IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the rea | IDA; IEA; IEA; IEA; IE | GO:0005739; GO:0 | mitochondrion; chlo |
| Catalysis of the tran | IEA; IEA; IBA; IEA |  |  |
|  |  | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tran | IBA; IEA | GO:0005794; GO:0 | Golgi apparatus; me |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005739; GO:0 | mitochondrion; cyto |
| Catalysis of the hyd | IBA; IEA; IEA; IEA | GO:0005615 | extracellular space |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; U2 snRNP |
| Binding to a nucleo | IEA; IEA; IBA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tran | IBA | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the tran | IEA; IBA | GO:0005634; GO:0 | nucleus; endoplasm |

|  |  |  |  |
|---|---|---|---|
| Any molecular func | IEA; IEA; IEA; IEA | GO:0000428; GO:0 | DNA-directed RNA |
| Catalysis of the hyd | IEA | GO:0016021; GO:0 | integral component |
| Binding to a large ri | IBA | GO:0005739 | mitochondrion |
| Enables the facilitat | IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA |  |  |
|  |  | GO:0009535; GO:0 | chloroplast thylakoi |
| Binds to and stimul | IBA | GO:0005737; GO:0 | cytoplasm; endopla |
| Binding to a protein | IEA; IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; mitocho |
| Binding to a protein | IEA |  |  |
| Binding to an RNA r | IEA |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0110165 | cellular anatomical |
| Involved in catalyzi | IEA |  |  |
| Binding to a protein | IEA |  |  |
| Catalysis of the pho | IEA; IEA | GO:0016021 | integral component |
| Binding to a nucleic | IEA; IEA |  |  |
| Catalysis of the rea | IEA | GO:0005739 | mitochondrion |
| An thiol-dependent | IBA |  |  |
| Catalysis of the rea | IBA; IEA | GO:0005737; GO:0 | cytoplasm; endome |
|  |  | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0000974; GO:0 | Prp19 complex; nuc |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IB | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the rea | IEA | GO:0005737 | cytoplasm |
| Catalysis of the tra | IEA; IEA; IEA |  |  |
| Catalysis of the hyd | IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of an oxid | IEA; IEA; IEA; IEA | GO:0016020 | membrane |

| | | | |
|---|---|---|---|
| | | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the tra | IEA; IEA | GO:0043231 | intracellular membr |
| | | | |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005739; GO:0 | mitochondrion; chl |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020 | membrane |
| Binding to a nucleo | IEA; IEA; IEA; IBA; IB | GO:0005634; GO:0 | nucleus; cytoplasm |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an iron ( | IEA; IEA; IEA; IEA | GO:0005783 | endoplasmic reticul |
| Binding to double- | IEA; IBA; IBA | GO:0005730 | nucleolus |
| | | | |
| Catalysis of a bioch | IEA; IEA; IBA; IEA; IE | GO:0005965 | protein farnesyltran |
| Catalysis of the rea | IEA; IEA | | |
| Catalysis of the hyd | IBA | GO:0005774; GO:0 | vacuolar membrane |
| Enables the transfe | IBA; IBA; IBA | GO:0005794; GO:0 | Golgi apparatus; me |
| | | GO:0009507 | chloroplast |
| | | GO:0005739; GO:0 | mitochondrion; mit |
| | | | |
| | | GO:0009507; GO:0 | chloroplast; chloro |
| Binding to an RNA | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| | | | |
| Any molecular func | IEA; IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the tra | IEA; IEA; IBA; IEA; IB | GO:0000151; GO:0 | ubiquitin ligase con |
| Binding to a nucleic | IEA; IEA; IEA; IEA; IB | GO:0000151; GO:0 | ubiquitin ligase con |
| Catalysis of the tra | IEA; IEA; IEA; IBA; IB | GO:0043231 | intracellular membr |
| | | GO:0016020; GO:0 | membrane; integral |

| | | | |
|---|---|---|---|
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a 4 iron, | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binds to and stops, | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the pho | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding to a protein | IEA | | |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005737; GO:0 | cytoplasm; mitocho |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a nucleic | IEA; IEA | GO:1990904 | ribonucleoprotein c |
| Binding to chromati | IEA | GO:0005634; GO:0 | nucleus; nuclear inr |
| | | GO:0005623 | obsolete cell |
| | | GO:0009535; GO:0 | chloroplast thylakoi |
| Catalysis of the rea | IBA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005634; GO:0 | nucleus; cytoplasm; |
| A motor activity tha | IBA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; actin cyt |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005783 | endoplasmic reticul |
| | | GO:0000139; GO:0 | Golgi membrane; er |
| Binding to single-st | IBA; IEA; IEA; IEA | GO:0005774; GO:0 | vacuolar membrane |
| Catalysis of the inc | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005618; GO:0 | cell wall; vacuole; a |

| | | | |
|---|---|---|---|
| | | GO:0009507 | chloroplast |
| Catalysis of the rea | IEA; IEA; IBA; IBA; IE | GO:0005576 | extracellular region |
| Catalysis of the trar | IEA; IEA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Binding to a nucleo | IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IEA | | |
| Enables the transfe | IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009570; GO:0 | chloroplast stroma; |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA; IEA; IEA | GO:0000139; GO:0 | Golgi membrane; G |
| | | GO:0005794; GO:0 | Golgi apparatus; m |
| Binding to an RNA r | IBA; IEA | GO:0005737 | cytoplasm |
| | | GO:0005634; GO:0 | nucleus; spliceoson |
| Binds to and stops, | IEA; IEA; IEA; IEA; IB | GO:0005618 | cell wall |
| Enables the directe | IEA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IEA; IEA; IEA; IEA | | |
| Catalysis of the rea | IEA | GO:0005829; GO:0 | cytosol; plasma me |
| Catalysis of the rea | IEA | GO:0005737; GO:0 | cytoplasm; mitocho |

|  |  |  |  |
|---|---|---|---|
| Catalysis of the rea | IBA; IEA; IEA; IPI; IB | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA |  |  |
| Binding to a protein | IEA; IEA |  |  |
| Binding to a specifi | IBA; IBA; IBA | GO:0005634 | nucleus |
| Catalysis of the rea | IEA; IBA; IPI; IEA; IE | GO:0005634; GO:0 | nucleus; cytosol |
|  |  |  |  |
| Catalysis of the hyd | IEA; IBA; IBA; IBA |  |  |
|  |  |  |  |
| Catalysis of the rea | IEA; IEA; IPI; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
|  |  |  |  |
| Binding to a nucleic | IEA; IEA | GO:0005634; GO:0 | nucleus; cellular an |
| Catalysis of the trar | IEA; IEA; IBA; IEA |  |  |
|  |  |  |  |
| Binding to a protein | IEA |  |  |
|  |  | GO:0005777 | peroxisome |
| Stimulates the exch | IEA | GO:0005829; GO:0 | cytosol; membrane |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005829 | cytosol |
| Binding to a protein | IEA | GO:0005739 | mitochondrion |
| Binding to a large ri | IBA | GO:0005739 | mitochondrion |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
|  |  |  |  |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0016020; GO:0 | membrane; integral |
|  |  | GO:0005886; GO:0 | plasma membrane; |
| Binding to a SNARE | IEA; IBA; IEA; IBA; IB | GO:0005737; GO:0 | cytoplasm; late end |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IBA | | |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005615; GO:0 | extracellular space; |
| Binding to a lipid. | IEA | | |
| Catalysis of the pho | IEA; IEA | | |
| Catalysis of the tran | IEA; IEA | GO:0009507 | chloroplast |
| Any molecular func | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the tran | IEA; IBA | | |
| Binding to a protein | IEA | GO:0005737 | cytoplasm |
| Catalysis of the tran | IEA; IBA | GO:0005739 | mitochondrion |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005730 | nucleolus |
| Binding to a riboso | IEA | GO:0005829 | cytosol |
| | | GO:0009507; GO:0 | chloroplast; plastid |
| | | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA | | |
| | | GO:0005634 | nucleus |
| Catalysis of the rea | IBA; IBA; IEA; IEA; IE | GO:0005829 | cytosol |
| | | GO:0000775; GO:0 | chromosome, centr |
| Enables the active t | IEA; IBA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a nucleo | IEA; IEA | GO:0009507; GO:0 | chloroplast; chlorop |
| Binding to an RNA r | IEA; IEA | GO:0005739; GO:0 | mitochondrion; intr |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009707 | chloroplast outer m |
| The action of a mol | IEA | GO:0005743; GO:0 | mitochondrial inner |
| Catalysis of the inc | IBA; IBA | | |
| | | GO:0009507 | chloroplast |
| | | GO:0005739; GO:0 | mitochondrion; chlo |
| Catalysis of the rea | IEA; IEA | | |
| Binding to a nucleic | IEA; IEA; IEA | | |
| Catalysis of the rea | IBA | | |
| Binding to a protein | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA | GO:0005773; GO:0 | vacuole; endoplasm |
| Catalysis of the trar | IEA; IBA | GO:0005739 | mitochondrion |
| Catalysis of the phc | IEA; IBA; IEA | GO:0005886 | plasma membrane |
| Binding to messeng | IEA; IEA | GO:0005739 | mitochondrion |
| | | GO:0016020; GO:0 | membrane; integral |
| Enables the calcium | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| | | GO:0005576; GO:0 | extracellular region |
| Catalysis of the rea | IEA; IEA; IBA; IEA; IE | GO:0005829 | cytosol |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| Binding to chromati | IBA; IEA; IEA; IEA; IE | GO:0005634 | nucleus |
| The action of a mol | IEA; IEA; IEA | GO:0009570 | chloroplast stroma |
| A transcription regu | IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to an RNA r | IEA; IEA; IBA | GO:0005763; GO:0 | mitochondrial small |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a lipid. | IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the inc | IEA; IEA; IBA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the inc | IBA; IEA; IBA; IEA | | |
| Binds to and increa | IBA | GO:0005623 | obsolete cell |
| Catalysis of the rea | IBA | | |

| | | | |
|---|---|---|---|
| Catalysis of the rea | IEA | | |
| | | GO:0005576 | extracellular region |
| Removes phosphati | IBA | | |
| | | GO:0000427 | plastid-encoded pl |
| Catalysis of the rea | IEA; IEA | | |
| Catalysis of an oxid | IEA; IEA | GO:0009507; GO:0 | chloroplast; chloro |
| Binding to a protein | IBA; IBA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm; |
| Enables the transfe | IBA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protein | IEA | GO:0019005 | SCF ubiquitin ligase |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634 | nucleus |
| Binding to a protein | IEA | | |
| Catalysis of the rea | IBA; IEA | GO:0005829 | cytosol |
| Catalysis of the rea | IEA; IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005783; GO:0 | endoplasmic reticul |
| Any molecular func | IEA | | |
| Binding to a nucleic | IEA; IEA; IBA | GO:0005634; GO:0 | nucleus; cytoplasm |
| Catalysis of the ph | IEA; IEA; IEA | GO:0016021 | integral component |
| Binding to a protein | IEA | | |

| | | | |
|---|---|---|---|
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005773 | vacuole |
| Any molecular func | IEA | | |
| Catalysis of a bioch | IEA; IBA | GO:0005737 | cytoplasm |
| Binding to phospha | IEA | GO:0000145 | exocyst |
| Catalysis of the ph | IEA; IEA; IEA; IEA | GO:0005634 | nucleus |
| Binding to a protei | IEA | | |
| Catalysis of the hyd | IEA | | |
| | | GO:0005887; GO:0 | integral component |
| Catalysis of the rea | IBA; IBA; IEA; IBA; IE | GO:0009579; GO:0 | thylakoid; apoplast |
| Any molecular func | IEA; IEA | GO:0005634; GO:0 | nucleus; membrane |
| Binding to an RNA | IBA; IEA | GO:0043231 | intracellular membr |
| Catalysis of the rea | IBA | GO:0005783; GO:0 | endoplasmic reticul |
| Binding to a protei | IEA | | |
| Binding to an RNA | IEA; IBA; IEA | GO:0005739 | mitochondrion |
| Catalysis of the ph | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to a protei | IEA | GO:0043229 | intracellular organe |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IB | GO:0005871; GO:0 | kinesin complex; m |
| Catalysis of the tra | IEA; IEA; IEA | GO:0005737 | cytoplasm |
| Binding to a protei | IEA | | |
| Catalysis of the tra | IEA | | |
| Catalysis of the ph | IEA; IBA; IEA; IEA; IE | GO:0005886; GO:0 | plasma membrane; |
| Any molecular func | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA; IEA | | |
| Binding to a nucleo | IEA; IEA; IEA; IEA; IE | GO:0005737; GO:0 | cytoplasm; mitocho |

| | | | |
|---|---|---|---|
| Binding to an RNA r | IBA; IEA | GO:0043231 | intracellular membr |
| Binding to an RNA r | IEA; IEA | GO:0005634 | nucleus |
| Catalysis of the hyd | IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the trar | IEA | GO:0005739; GO:0 | mitochondrion; vac |
| Catalysis of the trar | IEA; IEA; IEA; IEA | GO:0043231 | intracellular membr |
| Catalysis of a bioch | IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| Binding to a protein | IEA | GO:0005739; GO:0 | mitochondrion; mit |
| | | GO:0005737 | cytoplasm |
| | | GO:0005789; GO:0 | endoplasmic reticul |
| | | GO:0000176; GO:0 | nuclear exosome (R |
| | | GO:0005634; GO:0 | nucleus; spliceosom |
| Catalysis of the rea | IEA; IEA | GO:0009507 | chloroplast |
| Catalysis of the rea | IBA; IEA; IEA; IEA | GO:0000139 | Golgi membrane |
| Any molecular func | IEA | GO:0005634 | nucleus |
| | | GO:0009535; GO:0 | chloroplast thylakoi |
| Any molecular entit | IEA; IEA | GO:0005737 | cytoplasm |
| Catalysis of the hyd | IEA | GO:0009570 | chloroplast stroma |
| Binding to chromati | IEA | | |
| Binding to a metal i | IEA | | |
| | | GO:0005737; GO:0 | cytoplasm; mitocho |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005680 | anaphase-promotir |
| Enables the transfe | IBA; IBA; IBA; IBA | GO:0005886; GO:0 | plasma membrane; |
| | | GO:0016020; GO:0 | membrane; integral |
| | | GO:0009535 | chloroplast thylakoi |
| A DNA-binding trar | IBA; IEA; IBA; IBA; IE | GO:0005634 | nucleus |
| Enables the directe | IEA; IEA; IEA | GO:0016020; GO:0 | membrane; integral |
| | | GO:0005777; GO:0 | peroxisome; peroxi |
| Binding to a nucleo | IEA; IEA; IBA; IBA; IEA; IEA; IEA; IEA; IEA | | |
| Catalysis of the hyd | IEA; IEA; IBA | GO:0005774; GO:0 | vacuolar membrane |
| Binding to a nucleic | IEA; IEA; IEA | | |
| Catalysis of the trar | IEA | | |

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|---|---|---|---|
| Enables the transm | IEA; IEA; IEA; IEA | GO:0005886; GO:0 | plasma membrane; |
| Catalysis of the rea | IEA; IEA | GO:0005783; GO:0 | endoplasmic reticul |
| Catalysis of the hyd | IEA | | |
| Binding to a protei | IEA; IBA; IBA | GO:0005634; GO:0 | nucleus; endoplas |
| Catalysis of the hyd | IEA; IEA; IEA; IEA; IE | GO:0005576; GO:0 | extracellular region |
| Catalysis of an oxid | IEA; IEA | | |
| Catalysis of the tra | IEA; IEA | | |

| | | | |
|---|---|---|---|
| Catalysis of the hyd | IEA; IEA; IEA; IEA | GO:0005576; GO:0 | extracellular region |
| Enables the transfe | IEA | GO:0005886; GO:0 | plasma membrane; |
| Binding to an RNA r | IBA; IEA; IEA | GO:0043231 | intracellular membr |
| Binding to an inosit | IBA; IEA | GO:0032587 | ruffle membrane |
| | | GO:0016021 | integral component |
| Catalysis of the hyd | IEA | GO:0005768; GO:0 | endosome; endopla |
| Binding to a nucleo | IEA; IBA; IEA; IEA; IE | GO:0005737 | cytoplasm |

| | | | |
|---|---|---|---|
| | | GO:0005737; GO:0 | cytoplasm; chloropl |
| Catalysis of the hyd | IBA; IEA | | |
| Binding to a carboh | IEA | | |
| An thiol-dependent | IBA | | |
| Binding to a protei | IEA; IBA | GO:0005634 | nucleus |
| Catalysis of a bioch | IEA; IBA; IEA | | |

| cellular_component | cellular_component | maxposs_score | mingrp_relscore |
|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 475 | 0.908 |
| | | 569.6 | 0.870962079 |
| | | 880.7 | 0.904848416 |
| | | 1925.8 | 0.888461938 |
| | | 463.5 | 0.83214671 |
| A lipid bilayer alon | IEA; IEA | 309.1 | 0.829828534 |
| | | 860.3 | 0.879576892 |
| | | 171.4 | 0.823803967 |
| | | 188.4 | 0.799363057 |
| | | 136.4 | 0.797653959 |
| | | 1033.6 | 0.898897059 |
| | | 1650.1 | 0.842736804 |
| | | 858.1 | 0.859690013 |
| | | 847.2 | 0.846435316 |
| A lipid bilayer alon | IEA; IEA | 173.9 | 0.760782059 |
| | | 1843.8 | 0.891745309 |
| A membrane-boun | IEA; IEA; IEA | 292.2 | 0.884325804 |
| | | 2344.4 | 0.933287835 |
| A lipid bilayer alon | IEA; IEA | 513.8 | 0.883806929 |
| | | 1154.5 | 0.894759636 |
| | | 192.7 | 0.745718734 |
| The contents of a c | IEA | 647.6 | 0.739499691 |
| | | 313.2 | 0.739463602 |
| A semiautonomous | IEA; IEA; IBA; IEA | 182.3 | 0.739440483 |
| A lipid bilayer alon | IEA; IEA | 606 | 0.739438944 |
| | | 733.4 | 0.739432779 |
| A lipid bilayer alon | IEA; IEA | 587.9 | 0.739411465 |
| | | 542.6 | 0.739402875 |
| A membrane-boun | IEA; IBA | 1074 | 0.739385475 |
| | | 1136 | 0.739348592 |
| The contents of a c | IBA | 674.8 | 0.739330172 |
| A lipid bilayer alon | IEA; IEA | 989.6 | 0.739288601 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun( | IEA | 1220.5 | 0.739287177 |
|  |  | 606.2 | 0.739194985 |
| The membrane surr | IBA; IEA; IEA | 1018 | 0.739194499 |
| A membrane-boun( | IBA | 943.8 | 0.739139648 |
|  |  | 605.3 | 0.739137618 |
| The membrane surr | IBA; IEA | 1899.2 | 0.73904802 |
|  |  | 1293.5 | 0.739002706 |
|  |  | 1025.1 | 0.738952297 |
|  |  | 914.2 | 0.738897397 |
| A lipid bilayer alonç | IEA; IEA | 476.4 | 0.738874895 |
| A membrane-boun( | IBA; IBA; IEA; IBA | 1932.3 | 0.738808674 |
|  |  | 434.9 | 0.738790527 |
| A semiautonomous | IEA; IEA; IEA; IEA; IE | 338.7 | 0.73870682 |
| A lipid bilayer alonç | IEA | 1017.9 | 0.73867767 |
| A membrane-boun( | IEA | 419.4 | 0.738674297 |
| A lipid bilayer alonç | IBA | 1009.8 | 0.738661121 |
| A membrane-boun( | IBA | 611.8 | 0.738640078 |
|  |  | 232.6 | 0.738607051 |

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|---|---|---|---|
| A multisubunit prot | IBA; IEA; IEA; IEA | 987.7 | 0.73858459 |
| A lipid bilayer alon | IEA; IEA | 345.4 | 0.738563984 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA; IE | 451.3 | 0.738533127 |
| A membrane-boun | IBA | 927.8 | 0.738521233 |
| A membrane-boun | IEA; IEA; IBA; IBA | 1343.8 | 0.738502753 |
|  |  | 343.4 | 0.738497379 |
| A membrane-boun | IEA; IEA; IEA; IEA | 815.6 | 0.738474743 |
|  |  | 2089.9 | 0.738456385 |
| The part of the cyto | IBA; IBA | 769.2 | 0.738429537 |
|  |  | 1086.1 | 0.738421876 |
| A membrane-boun | IEA; IEA | 840.2 | 0.73839562 |
|  |  | 1475 | 0.738372881 |
| A membrane-boun | IBA | 838.1 | 0.738336714 |
| A membrane-boun | IBA; IBA; IEA | 2364.4 | 0.738326848 |
| The component of t | IBA; IEA; IEA | 932.7 | 0.738286695 |
| The lipid bilayer su | IEA; IEA; IEA; IBA | 2177.1 | 0.738275688 |
|  |  | 860.7 | 0.738120135 |
| A membrane-boun | IEA; IEA; IEA; IBA | 478.7 | 0.738040526 |
| A protein complex t | IEA | 357.2 | 0.737961926 |
| A membrane-boun | IEA; IEA | 439.2 | 0.737932605 |
| The ordered and or | IBA; IBA | 1799.9 | 0.737929885 |
|  |  | 980.9 | 0.737893771 |
| The set of thin, flat | IEA; IEA | 1002.1 | 0.737850514 |
|  |  | 445.9 | 0.737833595 |
| The irregular netwo | IEA | 891.6 | 0.737774787 |
|  |  | 748.9 | 0.737748698 |

| | | | |
|---|---|---|---|
| The contents of a c | IBA | 1201.1 | 0.737657148 |
| A membrane-boun | IEA | 1647.5 | 0.737602428 |
| A semiautonomous | IBA | 1549.4 | 0.737575836 |
| A lipid bilayer alon | IBA; IEA | 1062.7 | 0.737555284 |
| A membrane-boun | IEA | 470.5 | 0.737513284 |
| A semiautonomous | IEA; IEA; IEA; IEA; IE | 1060.1 | 0.737477596 |
| | | 833.8 | 0.737467018 |
| A membrane-boun | IDA | 704.9 | 0.737409562 |
| A membrane-boun | IBA; IBA | 483.2 | 0.737375828 |
| | | 377.7 | 0.737357691 |
| A membrane-boun | IEA | 740.9 | 0.737346471 |
| | | 1450.4 | 0.737313844 |
| | | 275.1 | 0.737186478 |
| The contents of a c | IBA | 555.1 | 0.737164475 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 357.9 | 0.737077396 |
| A lipid bilayer alon | IBA; IEA | 629.8 | 0.736900603 |
| The contents of a c | IBA | 452.3 | 0.736900287 |
| | | 605.8 | 0.736876857 |
| | | 281.6 | 0.736860795 |
| A membrane-boun | IEA; IEA; IEA | 885.3 | 0.73681238 |
| A membrane-boun | IBA | 588.9 | 0.736797419 |
| | | 257.2 | 0.736780715 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 311.5 | 0.736757624 |
| A membrane-boun | IBA; IBA | 1064 | 0.73674812 |
| | | 220.7 | 0.736746715 |
| The membrane surr | IBA | 798.3 | 0.736690467 |
| The membrane surr | IEA; IEA; IEA | 1086.5 | 0.736677405 |
| | | 944.8 | 0.736663844 |
| The outer, i.e. cyto | IBA | 2409.1 | 0.736582126 |
| The contents of a c | IEA; IEA; IEA | 1073.9 | 0.736567651 |
| | | 519.6 | 0.736528099 |
| A membrane-boun | IBA | 253.9 | 0.736510437 |
| | | 515 | 0.736504854 |
| The space external | IEA; IEA; IEA | 529 | 0.736483932 |
| The lipid bilayer su | IEA; IEA | 928.2 | 0.736479207 |
| The membrane surr | IBA; IEA; IEA | 1274.5 | 0.736445665 |
| A membrane-boun | IBA | 283.8 | 0.736434109 |
| The lipid bilayer su | IBA; IBA; IEA; IEA; IE | 886.6 | 0.736408753 |
| | | 551.9 | 0.736365284 |
| A lipid bilayer alon | IBA; IEA | 1055.5 | 0.736333491 |
| | | 1201.4 | 0.736307641 |
| A membrane-boun | IEA; IEA; IEA | 1456.9 | 0.736289382 |
| The membrane surr | IEA; IEA; IEA | 827.8 | 0.736168157 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun | IEA | 1532.8 | 0.736103862 |
|  |  | 1479.3 | 0.736091395 |
| The membrane surr | IBA; IEA; IEA | 1340.2 | 0.736084167 |
| A membrane-boun | IEA; IEA | 420.2 | 0.736078058 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun | IBA | 2043.7 | 0.736066937 |
|  |  | 763.7 | 0.736021998 |
|  |  | 178 | 0.735955056 |
| The lipid bilayer sur | IEA; IEA; IEA; IEA | 979 | 0.735955056 |
|  |  | 266.9 | 0.735856126 |
| The lipid bilayer sur | IBA; IBA; IEA; IEA | 864.3 | 0.735855606 |
| A lipid bilayer along | IEA; IEA | 328.6 | 0.735849057 |
| The membrane surr | IBA; IEA | 1196.9 | 0.735817529 |
| A closed structure t | IBA; IBA; IEA; IEA | 3366.1 | 0.735807017 |
| A membrane-boun | IBA | 700.8 | 0.735730594 |
| A membrane-boun | IEA | 472.6 | 0.735717309 |

|  |  |  |  |
|---|---|---|---|
| The membrane surr | IEA; IBA | 2472.6 | 0.735703308 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun | IBA | 640.1 | 0.735666302 |
| A membrane-boun | IEA | 1078.9 | 0.735656687 |
|  |  | 1032.7 | 0.735644427 |
|  |  | 522.4 | 0.735643185 |
| A lipid bilayer alon | IEA; IEA | 671.8 | 0.735635606 |

|  |  |  |  |
|---|---|---|---|
|  |  | 720.9 | 0.735608267 |
|  |  | 1062.4 | 0.735598645 |
|  |  | 450.7 | 0.735522521 |
| The contents of a c | IBA; IBA; IEA; IBA | 4657.6 | 0.735464617 |
| A membrane-boun | IBA; IBA; IEA | 1184.7 | 0.735460454 |
|  |  | 590.3 | 0.735388785 |
| The component of | IEA | 251.3 | 0.735376045 |
|  |  | 623.9 | 0.735374259 |
|  |  | 980.9 | 0.735345091 |

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|---|---|---|---|
| The space external | IEA; IEA | 1111.6 | 0.735336452 |
| A lipid bilayer alon | IEA; IEA | 1012.6 | 0.735334782 |
| The contents of a c | IBA | 1221.5 | 0.73532542 |

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|---|---|---|---|
| A lipid bilayer along | IBA; IEA | 1040.9 | 0.735325199 |
| The inner, i.e. lume | IBA; IEA; IEA | 190.8 | 0.735324948 |
| A membrane-boun | IEA; IBA; IBA | 433.6 | 0.735239852 |
| A ribonuclease com | IBA; IBA; IEA; IEA; IE | 533.3 | 0.735233452 |
| | | 1051.1 | 0.735229759 |
| The part of the cyto | IBA | 309.7 | 0.73522764 |
| A protein complex t | IBA | 1250 | 0.7352 |
| | | 1059.2 | 0.735177492 |
| A lipid bilayer along | IEA; IEA | 762.7 | 0.735151436 |
| A membrane-boun | IEA | 243.9 | 0.735137351 |
| A membrane-boun | IEA | 909.8 | 0.735106617 |
| A membrane-boun | IEA | 1621.6 | 0.735076468 |
| A membrane-boun | IBA; IEA; IEA | 304.2 | 0.735042735 |
| A membrane-boun | IEA | 634.8 | 0.735034657 |
| A lipid bilayer along | IEA; IEA | 263.8 | 0.735026535 |
| | | 792.5 | 0.735015773 |
| A lipid bilayer along | IEA; IEA | 1251.6 | 0.734979227 |

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| Cyclin-dependent p | IBA; IBA; IBA | 611.5 | 0.734914146 |
|  |  | 338.7 | 0.734868615 |
| The contents of a c | IEA; IBA | 656.2 | 0.73483694 |
|  |  | 1024.6 | 0.734823346 |
| A membrane-boun | IEA | 1462 | 0.734746922 |
|  |  | 1046.9 | 0.734740663 |
|  |  | 1080.7 | 0.734616452 |
| The ordered and or | IBA; IBA | 1314.3 | 0.73461158 |
|  |  | 1527.4 | 0.734581642 |
|  |  | 898.2 | 0.851480739 |
|  |  | 183.1 | 0.734571273 |

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|---|---|---|---|
| | | 1053.2 | 0.734523357 |
| | | 1735.6 | 0.734501037 |
| Organized structure | IBA | 912.9 | 0.73447256 |
| The membrane surr | IBA | 1398 | 0.734406295 |
| The membrane surr | IBA | 1325.2 | 0.734228796 |
| The part of the cyto | IBA | 1420 | 0.734225352 |
| A membrane-boun | IDA; IDA | 1145.7 | 0.734136336 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1680.7 | 0.734098887 |
| A lipid bilayer alon | IEA; IEA | 749.3 | 0.734018417 |
| A membrane-boun | IBA; IEA | 689.5 | 0.734010152 |
| A membrane-boun | IBA; IBA; IBA | 1956.4 | 0.734001227 |
| The membrane surr | IBA | 833.8 | 0.733988966 |
| | | 4358.1 | 0.733943691 |
| | | 821.6 | 0.733933788 |
| A membrane-boun | IBA; IBA; IBA | 1079.8 | 0.73393221 |
| A vacuole to which | IBA; IBA; IBA; IEA; IB | 430.3 | 0.733906577 |
| An intracellular org | IEA; IBA; IEA | 422.3 | 0.733838503 |
| A membrane-boun | IBA | 2993.4 | 0.733814392 |

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|  |  | 1995.9 | 0.733804299 |
| A lipid bilayer alon | IEA; IEA | 3133 | 0.733801468 |
| A chlorophyll-conta | IBA | 711 | 0.733755274 |
| Organized structur | IBA | 1049.7 | 0.733733448 |
|  |  | 571.5 | 0.73368329 |
| A membrane-boun | IBA; IBA; IEA; IBA | 996.5 | 0.733667837 |
| A highly compacted | IBA; IEA | 789.2 | 0.733654334 |
| A lipid bilayer alon | IEA; IEA | 582.7 | 0.733482066 |
|  |  | 166.1 | 0.733293197 |
|  |  | 794.8 | 0.73326623 |
|  |  | 492.2 | 0.733238521 |
| The component of | IBA | 1349.4 | 0.733214762 |
|  |  | 905.8 | 0.733164054 |
| A membrane-boun | IBA | 1442.6 | 0.733120754 |
| The membrane sur | IBA; IEA; IEA | 2111.4 | 0.733115468 |
| A membrane-boun | IEA; IEA | 532.4 | 0.733095417 |
|  |  | 771 | 0.73307393 |
|  |  | 1970.5 | 0.733011926 |
|  |  | 1146.3 | 0.732966937 |
|  |  | 876.8 | 0.732892336 |
| Any member of a fa | IEA; IEA; IEA | 364.9 | 0.732803508 |
|  |  | 599.1 | 0.732765815 |
|  |  | 2733 | 0.732747896 |
|  |  | 885.3 | 0.732745962 |
| The membrane sur | IEA; IBA; IEA | 927.2 | 0.732743745 |
|  |  | 1130 | 0.732743363 |
| The lipid bilayer su | IBA; IEA; IEA | 1142.3 | 0.732732207 |
|  |  | 1004.6 | 0.732729445 |
| A membrane-boun | IBA; IEA; IEA | 870.2 | 0.732705125 |
| That part of the nu | IBA; IBA; IBA | 803.2 | 0.732694223 |
|  |  | 775.9 | 0.73256863 |
|  |  | 1918.2 | 0.732561777 |
| A SAGA-type histor | IEA; IEA; IBA | 614.7 | 0.732552465 |
| The membrane sur | IBA; IBA | 332.4 | 0.732551143 |
|  |  | 572.8 | 0.732541899 |
| The inner, i.e. lume | IBA; IBA; IBA | 548.4 | 0.73249453 |
| The inner, i.e. lume | IEA; IEA; IEA; IEA | 450.6 | 0.732356858 |

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| A membrane-boun | IEA; IEA | 848.7 | 0.732296453 |
| A lipid bilayer alon | IEA | 804.2 | 0.732280527 |
| A membrane-boun | IEA | 527.4 | 0.732271521 |
| A membrane-boun | IEA; IEA | 1815.9 | 0.732253979 |
| | | 277.1 | 0.732226633 |
| An ISWI complex th | IEA | 1033.3 | 0.732217168 |
| A chlorophyll-conta | IEA; IEA; IBA; IEA; IE | 504.1 | 0.732195993 |
| A membrane-boun | IEA; IEA; IBA; IEA | 1196 | 0.732190635 |
| | | 960.7 | 0.732174456 |
| | | 565.6 | 0.732142857 |
| A membrane-boun | IEA | 734.2 | 0.732089349 |
| | | 869 | 0.731990794 |
| | | 277.2 | 0.731962482 |
| A small, dense bod | IBA; IEA | 1327.7 | 0.731942457 |
| | | 334.6 | 0.731918709 |
| A membrane-boun | IEA | 1171.6 | 0.731905087 |
| A membrane-boun | IEA | 895.2 | 0.731903485 |
| Organized structur | IBA | 1676.6 | 0.731897889 |
| A membrane-boun | IEA | 705.3 | 0.73188714 |
| The component of | IEA | 1474.6 | 0.731859487 |
| A membrane-boun | IEA; IEA; IBA; IEA | 1206.8 | 0.731852834 |
| A membrane-boun | IEA | 1929.3 | 0.731664334 |
| The membrane surr | IBA; IEA | 2295.4 | 0.731550057 |
| A membrane-boun | IEA; IBA | 1260.5 | 0.731535105 |
| | | 723.3 | 0.731508364 |
| | | 426.8 | 0.731490159 |

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|---|---|---|---|
| | | 1022.1 | 0.73143528 |
| A membrane-boun | IEA | 839.9 | 0.731277533 |
| | | 462.1 | 0.731227007 |
| A lipid bilayer along | IEA; IEA | 1136 | 0.731161972 |
| The end of a linear | IEA; IEA; IEA; IBA | 2635.9 | 0.731097538 |
| | | 538.1 | 0.731090875 |
| A chlorophyll-conta | IEA | 799.5 | 0.731081926 |
| The membrane sur | IBA; IEA; IEA | 574.4 | 0.731023677 |
| | | 858.6 | 0.730957372 |
| A protein complex | IBA; IEA; IEA; IBA | 557.1 | 0.73092802 |
| | | 356.4 | 0.730920314 |
| | | 758.1 | 0.730906213 |
| A membrane-boun | IEA; IEA | 1424.3 | 0.730885347 |
| A lipid bilayer along | IEA; IEA | 304.7 | 0.730882836 |
| | | 570 | 0.730877193 |
| A chlorophyll-conta | IBA; IEA | 325.5 | 0.730875576 |
| The space external | IEA | 207.7 | 0.73086182 |
| | | 446.9 | 0.730812262 |
| | | 871.8 | 0.730786878 |
| | | 403 | 0.730769231 |
| | | 323.1 | 0.730733519 |
| A lipid bilayer along | IEA | 939.5 | 0.730707823 |
| The lipid bilayer su | IEA; IBA; IEA; IEA | 1160.8 | 0.730616816 |
| A membrane-boun | IEA; IEA; IBA; IEA | 571.4 | 0.730486524 |
| Organized structure | IBA | 943.5 | 0.730471648 |
| | | 1072.7 | 0.730399925 |
| A membrane-boun | IBA | 2313.2 | 0.730287048 |
| | | 797.4 | 0.730248307 |
| The inner, i.e. lume | IEA; IEA; IEA | 2026.9 | 0.730228428 |
| A membrane-boun | IBA | 492.4 | 0.730097482 |
| | | 756.9 | 0.729951116 |
| The lipid bilayer su | IEA; IEA; IEA; IEA; IE | 1570.3 | 0.729924218 |

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|---|---|---|---|
| | | 792.7 | 0.729910433 |
| | | 1042.9 | 0.729887813 |
| A lipid bilayer alon | IEA; IEA | 603.4 | 0.729864103 |
| A chlorophyll-cont | IBA; IEA; IEA | 353.5 | 0.729844413 |
| | | 635.3 | 0.729733984 |
| | | 166.5 | 0.72972973 |
| | | 629.7 | 0.729712562 |
| A membrane-boun | IBA | 631.9 | 0.729704067 |
| | | 199 | 0.729648241 |
| The inner, i.e. lume | IBA; IEA; IEA | 911.4 | 0.729646697 |
| The irregular netwo | IBA | 3710.6 | 0.729639411 |
| | | 584.4 | 0.729637235 |
| A membrane-boun | IEA | 709.4 | 0.729630674 |
| A semiautonomous | IEA; IEA; IBA; IEA; IE | 1290.4 | 0.729618723 |
| The contents of a c | IBA | 468.5 | 0.729562433 |
| A membrane-boun | IEA | 566 | 0.7295053 |
| | | 719 | 0.729485396 |
| Cyclin-dependent | IBA; IBA; IBA | 722.4 | 0.729374308 |
| The contents of a c | IEA | 1731.6 | 0.729325479 |
| A lipid bilayer alon | IEA; IEA | 2007.7 | 0.729292225 |
| | | 326.9 | 0.729275008 |
| A membrane-boun | IEA | 1646 | 0.729222357 |
| | | 802.3 | 0.729153683 |
| The rigid or semi-r | IEA; IEA; IEA | 783 | 0.729118774 |
| The contents of a c | IBA | 582 | 0.729037801 |
| A membrane-boun | IBA; IBA; IBA | 987.9 | 0.729021156 |
| A membrane-boun | IEA | 572.3 | 0.728988293 |

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|---|---|---|---|
| A membrane-boun | IBA; IBA; IEA; IEA | 847.9 | 0.728977474 |
| | | 616.9 | 0.728967418 |
| | | 370.8 | 0.728964401 |
| The membrane surr | IBA; IBA | 258.6 | 0.728924981 |
| | | 197.7 | 0.728882145 |
| A membrane-boun | IEA | 590.7 | 0.728796343 |
| A small, dense bod | IBA; IBA | 621.8 | 0.728690897 |
| A semiautonomous | IEA; IEA; IEA; IEA | 260.2 | 0.728670254 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1102.5 | 0.72861678 |
| A membrane-boun | IEA; IEA; IEA; IBA; IB | 693.4 | 0.72858379 |
| | | 410.4 | 0.728557505 |
| | | 341.5 | 0.728550512 |
| The space external | IEA; IEA; IEA | 534.5 | 0.728531338 |
| | | 1178.3 | 0.728507171 |
| The lipid bilayer su | IEA; IEA; IEA; IBA; IE | 1332.2 | 0.72849422 |
| The membrane surr | IBA; IBA | 499.7 | 0.728437062 |

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| A lipid bilayer along | IEA | 4617.9 | 0.728404686 |
| A semiautonomous | IEA; IEA; IBA; IEA; IE | 359.7 | 0.728384765 |
| Organized structure | IBA | 1162.4 | 0.728320716 |
| | | 865.5 | 0.728249567 |
| The contents of a c | IEA; IEA; IEA; IEA | 1817 | 0.728233352 |
| | | 1399.7 | 0.728227477 |
| The contents of a c | IBA | 1041.3 | 0.728224335 |
| A semiautonomous | IBA | 2008 | 0.728187251 |
| A membrane-boun | IC | 1073.8 | 0.728161669 |
| A lipid bilayer along | IEA; IEA | 2218.4 | 0.728092319 |
| | | 785.5 | 0.728071292 |
| | | 1777.2 | 0.728055368 |
| | | 712.6 | 0.727897839 |
| The component of t | IBA; IEA; IEA; IEA; IE | 1126.2 | 0.727845853 |
| A lipid bilayer along | IEA; IEA | 425.8 | 0.727806482 |
| | | 1408.9 | 0.727801831 |
| | | 1721.7 | 0.727769065 |
| | | 357.7 | 0.727704781 |
| The membrane surr | IBA; IBA; IEA; IEA | 1089 | 0.727640037 |
| | | 1761.5 | 0.727561737 |
| The space enclosed | IBA | 1139.1 | 0.72750417 |
| A membrane-boun | IEA | 751.4 | 0.727442108 |
| | | 457.1 | 0.727411945 |
| The larger of the tw | IBA; IEA; IEA | 482 | 0.727385892 |
| | | 350.3 | 0.727376534 |
| | | 262.6 | 0.727341965 |
| A lipid bilayer along | IEA; IEA | 713.6 | 0.727298206 |

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| A membrane-boun | IC | 1085.3 | 0.727264351 |
| A chromosome tha | IBA; IBA; IEA; IBA | 3977.7 | 0.727254444 |
| A membrane-boun | IEA | 912.4 | 0.727202981 |
| | | 246.3 | 0.727161998 |
| That part of a multi | IBA | 469.1 | 0.727137071 |
| | | 2061.2 | 0.727003687 |
| A lipid bilayer alon | IEA; IEA | 883.1 | 0.726984486 |
| That part of the nu | IBA; IBA; IBA | 799.2 | 0.726976977 |
| | | 1229.9 | 0.726969672 |
| | | 1231.7 | 0.726881546 |
| A membrane-boun | IEA | 831.4 | 0.726846283 |
| | | 1090.4 | 0.726797506 |
| The lipid bilayer su | ISS; IBA; IEA | 1180.2 | 0.72674123 |
| | | 1377.8 | 0.726665699 |
| | | 536.7 | 0.72666294 |
| The contents of a c | IEA; IEA; IBA | 2664.1 | 0.726624376 |
| A closed structure, | IEA; IEA; IBA; IEA | 477.3 | 0.726587052 |
| A large multisubuni | IBA; IBA; IBA | 817.2 | 0.72650514 |
| A membrane-boun | IEA | 477.5 | 0.726492147 |
| A lipid bilayer alon | IEA; IEA | 216.8 | 0.726476015 |
| | | 361.2 | 0.726467331 |
| A membrane-boun | IBA | 915 | 0.726448087 |
| | | 303 | 0.72640264 |
| That part of a multi | IEA | 942.9 | 0.726270018 |
| The component of | IEA | 1236.2 | 0.726257887 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA | 1065.6 | 0.726257508 |
|  |  | 1257 | 0.726252983 |
|  |  | 945.6 | 0.726205584 |
|  |  | 1733.6 | 0.726176742 |
| A membrane-boun | IBA; IBA; IBA | 1057.5 | 0.726146572 |
|  |  | 1430.2 | 0.726122221 |
| The component of | IEA | 1365.9 | 0.726041438 |
| A lipid bilayer alon | IEA; IEA | 617.6 | 0.726036269 |
| The component of | IEA | 164.6 | 0.72600243 |
|  |  | 967.5 | 0.725994832 |
| The part of the cyt | IEA | 887.9 | 0.725982656 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 431.7 | 0.725967107 |
| A lipid bilayer alon | IEA; IEA | 424.4 | 0.72596607 |
|  |  | 530.1 | 0.725900773 |
| The contents of a c | IBA | 1439 | 0.725851286 |

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| | | 187.1 | 0.725815072 |
| The space external | IEA | 235.6 | 0.725806452 |
| A membrane-boun | IBA; IBA | 686.6 | 0.725750073 |
| | | 781 | 0.725736236 |
| The contents of a c | IBA | 1057.4 | 0.725647815 |
| The part of a cell e | IBA | 376.5 | 0.72563081 |
| | | 610.1 | 0.725618751 |
| | | 875.7 | 0.725590956 |
| The contents of a c | IEA; IEA; IBA; IBA | 2275 | 0.725494505 |
| The part of the cyt | IEA | 931.1 | 0.725485984 |
| A semiautonomous | IBA | 876.8 | 0.725479015 |
| | | 242.9 | 0.7254014 |
| Organized structur | IBA | 1061.7 | 0.725251954 |
| | | 535.7 | 0.725219339 |
| A membrane-boun | IEA; IEA; IBA; IEA; IE | 1422.9 | 0.72520908 |
| A chlorophyll-cont | IEA; IEA; IEA; IEA; IB | 309.3 | 0.725185904 |
| A membrane-boun | IBA | 1454.7 | 0.725166701 |
| A membrane-boun | IBA | 722.7 | 0.725058807 |
| | | 865.9 | 0.725025985 |
| The irregular netwo | IEA; IBA; IEA; IBA | 935.6 | 0.724989312 |
| The contents of a c | IEA; IEA; IEA; IEA; IB | 429.7 | 0.724924366 |
| A lipid bilayer alon | IEA; IEA | 345.7 | 0.724905988 |
| The irregular netwo | IEA | 2169.4 | 0.724900894 |
| | | 319.5 | 0.724882629 |
| A lipid bilayer alon | IEA | 3307.6 | 0.724876043 |
| | | 703.3 | 0.724868477 |
| | | 668.6 | 0.724798086 |
| | | 892.4 | 0.724787091 |
| The part of the cyt | IBA | 1972.5 | 0.724765526 |
| | | 1186.9 | 0.724745134 |
| | | 843.5 | 0.724718435 |
| | | 415.2 | 0.724710983 |
| A membrane-boun | IBA; IBA | 347.9 | 0.724633515 |
| | | 247.3 | 0.72462596 |

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| The membrane surr | IBA; IEA; IEA | 1211.7 | 0.724601799 |
| | | 965.1 | 0.724588126 |
| A lipid bilayer along | IEA; IEA | 592.9 | 0.724574127 |
| | | 1496.5 | 0.7245573 |
| | | 172.8 | 0.724537037 |
| | | 495.1 | 0.724500101 |
| A membrane-bound | IBA; IBA | 986.1 | 0.724470135 |
| | | 877.2 | 0.724464204 |
| The contents of a c | IBA | 2386.3 | 0.724343125 |
| A lipid bilayer along | IEA; IEA | 211.8 | 0.724268178 |
| | | 987.9 | 0.724162365 |
| | | 714.8 | 0.724118635 |
| A chlorophyll-conta | IBA | 1386.9 | 0.724060855 |
| | | 596.8 | 0.72402815 |
| A lipid bilayer along | IEA; IEA | 1082.6 | 0.723997783 |
| The contents of a c | IBA | 360.4 | 0.723917869 |
| | | 867.1 | 0.723907277 |
| | | 1313.3 | 0.723825478 |
| | | 290.7 | 0.72377021 |
| | | 536.1 | 0.72374557 |
| A membrane-bound | IEA | 435.8 | 0.72372648 |
| | | 650.8 | 0.723724647 |
| The membrane surr | IEA; IEA; IEA | 748.8 | 0.723691239 |

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|---|---|---|---|
| A part of a cellular | IEA | 1212.8 | 0.723614776 |
| | | 1057.8 | 0.723577236 |
| A membrane-boun | IC | 412.7 | 0.723527986 |
| | | 1005.8 | 0.723503679 |
| | | 831.9 | 0.723404255 |
| A lipid bilayer alon | IEA; IEA | 1344 | 0.723363095 |
| A membrane-boun | IBA | 1988.8 | 0.723350764 |
| | | 403.3 | 0.723282916 |
| | | 782 | 0.723273657 |
| A lipid bilayer alon | IEA; IEA | 442.3 | 0.723264752 |
| The space external | IEA; IBA | 339.3 | 0.723253758 |
| A chlorophyll-conta | IEA; IBA; IEA | 941.2 | 0.723225669 |
| | | 738.1 | 0.723208237 |
| | | 171.6 | 0.723193473 |
| | | 287.8 | 0.723071577 |
| A membrane-boun | IEA | 866.9 | 0.723036106 |
| | | 735 | 0.861360544 |
| A lipid bilayer alon | IEA; IEA | 1125.7 | 0.722927956 |
| | | 669.8 | 0.722902359 |
| | | 1309.5 | 0.722871325 |
| A lipid bilayer alon | IEA; IEA | 577.2 | 0.722799723 |
| | | 990.9 | 0.722777273 |
| | | 1318.9 | 0.722723482 |
| | | 486.8 | 0.722678718 |
| | | 735.2 | 0.722524483 |
| | | 632.4 | 0.722485769 |
| | | 729.2 | 0.722435546 |
| A ribonuclease com | IBA; IEA; IEA | 2360.1 | 0.722342274 |
| The irregular netwo | IEA; IEA; IBA; IEA | 554.5 | 0.722272317 |
| A transcription fact | IBA | 1528.8 | 0.722265829 |
| | | 635.1 | 0.722248465 |
| | | 416.9 | 0.722235548 |
| The contents of a c | IBA | 671.4 | 0.722222222 |
| | | 1098.9 | 0.722176722 |
| A lipid bilayer alon | IEA; IEA | 853.4 | 0.722170143 |
| The component of | IEA | 545.5 | 0.830797434 |
| | | 1514.6 | 0.721972798 |

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|---|---|---|---|
| | | 1450.3 | 0.721919603 |
| | | 765.6 | 0.72191745 |
| | | 631.1 | 0.721914118 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA | 367.8 | 0.721859706 |
| | | 350.4 | 0.721746575 |
| The lipid bilayer su | IBA; IEA; IEA | 769.4 | 0.721731219 |
| | | 1622 | 0.721701603 |
| A membrane-boun | IEA | 780.4 | 0.721681189 |
| | | 591 | 0.721658206 |
| The contents of a c | IBA; IBA; IEA; IEA | 1269.8 | 0.721609702 |
| Organized structur | IBA | 895.4 | 0.721576949 |
| A membrane-boun | IEA | 700.9 | 0.721500927 |
| A membrane-boun | IEA | 792.1 | 0.721499811 |
| A membrane-boun | IBA | 924.1 | 0.721458717 |
| A membrane-boun | IEA; IEA | 265.9 | 0.721323806 |
| A lipid bilayer alon | IEA; IEA | 1077.2 | 0.721314519 |
| | | 1273.8 | 0.721306328 |
| The component of t | IBA; IEA; IEA | 1153.3 | 0.72114801 |
| A closed structure, | IEA; IEA; IEA; IEA | 289.4 | 0.721147201 |
| A membrane-boun | IEA; IEA | 1083.4 | 0.721063319 |
| | | 583.5 | 0.720994002 |
| The contents of a c | IBA | 2966.6 | 0.72099373 |
| The membrane surr | IBA; IEA; IEA | 1778.3 | 0.720856998 |
| The membrane surr | IEA | 742.5 | 0.720808081 |
| An intracellular org | IEA; IEA | 318.4 | 0.720791457 |
| A membrane-boun | IBA | 646.7 | 0.720736045 |
| | | 443.9 | 0.720657806 |
| | | 439.2 | 0.720628415 |
| | | 290.6 | 0.720578114 |
| A membrane-boun | IBA | 966.5 | 0.720538024 |
| A membrane-boun | IEA | 750.2 | 0.72047454 |
| The part of the cyto | IEA | 1104.3 | 0.720365843 |

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|---|---|---|---|
| A lipid bilayer along | IBA; IEA | 1130.4 | 0.720364473 |
| A membrane-boun | IEA | 812.4 | 0.72033481 |
|  |  | 507 | 0.720118343 |
| A lipid bilayer along | IEA | 1744.9 | 0.720098573 |
|  |  | 327.8 | 0.71995119 |
| A chlorophyll-conta | IEA | 538.1 | 0.719940531 |
| A membrane-boun | IBA | 773.4 | 0.719937936 |
| A lipid bilayer along | IEA; IEA | 488 | 0.719877049 |
|  |  | 1175.7 | 0.719741431 |
|  |  | 243.7 | 0.719737382 |
| A small, dense bod | IBA; IBA | 677 | 0.719645495 |
| A lipid bilayer along | IEA; IEA | 741.1 | 0.719471057 |
|  |  | 2386.5 | 0.719421747 |
|  |  | 1371.8 | 0.71941974 |
| A semiautonomous | IBA | 1601.3 | 0.719415475 |
| A membrane-boun | IEA | 614.4 | 0.719401042 |
|  |  | 354.2 | 0.719367589 |
| The lipid bilayer su | IBA | 1826 | 0.719331873 |
| A lipid bilayer along | IEA; IEA | 952.1 | 0.719147148 |
| The membrane surr | IEA; IEA; IEA; IEA; IE | 317.9 | 0.719094055 |
| A membrane-boun | IBA | 813.4 | 0.719080403 |
| A membrane-boun | IEA | 1237.7 | 0.719075705 |
| A lipid bilayer along | IBA; IBA | 1308.8 | 0.719055623 |
|  |  | 1618.8 | 0.719051149 |
|  |  | 1474.6 | 0.719042452 |

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|---|---|---|---|
| A membrane-boun | IBA | 889.8 | 0.719037986 |
|  |  | 329.2 | 0.719015796 |
| The membrane sur | IEA | 582.5 | 0.718969957 |
| A protein complex | IBA; IBA | 1340.4 | 0.718964488 |
| The membrane sur | IBA; IBA | 962.1 | 0.718948134 |
| A lipid bilayer alon | IBA; IEA | 1136.9 | 0.718884686 |
| A membrane-boun | IMP; IEA | 792.9 | 0.718880061 |
| The contents of a c | IEA; IEA; IBA; IEA; IE | 265.7 | 0.718855852 |
| A membrane-boun | IEA; IBA | 488 | 0.718852459 |
| The component of | IBA; IEA; IEA | 1119.5 | 0.718803037 |
|  |  | 733.1 | 0.718728686 |
|  |  | 976 | 0.718647541 |
|  |  | 887.8 | 0.718630322 |
|  |  | 707.2 | 0.874434389 |
|  |  | 1441.7 | 0.718388014 |
|  |  | 341.5 | 0.718301611 |
|  |  | 263.4 | 0.718299165 |
| A membrane-boun | IBA; IBA | 2703.8 | 0.718174421 |
| A lipid bilayer alon | IEA; IEA | 1183 | 0.718174134 |
|  |  | 1885.8 | 0.71815675 |
|  |  | 1950.8 | 0.718115645 |
|  |  | 3352 | 0.855250597 |
| The membrane sur | IBA | 949.6 | 0.718091828 |
|  |  | 711.9 | 0.718078382 |
| A lipid bilayer alon | IEA; IEA | 297.6 | 0.718077957 |
| A lipid bilayer alon | IEA; IEA | 1663.1 | 0.787926162 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 324.5 | 0.718027735 |
| The membrane sur | IBA; IBA | 310.9 | 0.717915729 |
|  |  | 2461.2 | 0.717861206 |
| A membrane-boun | IEA; IEA | 619.5 | 0.717836965 |
|  |  | 464.5 | 0.717761033 |
|  |  | 634.2 | 0.717596973 |
| A part of a cellular | IEA | 3277.4 | 0.88155245 |
| The pigmented me | IBA; IEA; IEA | 279.3 | 0.717508056 |
| The space external | IEA; IBA; IBA | 699.8 | 0.717490712 |
| The contents of a c | IBA | 460.7 | 0.717386586 |
|  |  | 360.9 | 0.717373234 |
|  |  | 184.3 | 0.717308736 |
|  |  | 432.2 | 0.717260528 |
|  |  | 382.3 | 0.717237771 |
| The contents of a c | IBA; IEA | 1154.4 | 0.717169092 |
|  |  | 500.2 | 0.717113155 |
|  |  | 323.8 | 0.717109327 |
|  |  | 417 | 0.717026379 |
|  |  | 523.6 | 0.716959511 |
| The lipid bilayer su | IEA; IBA; IEA; IEA; IE | 763 | 0.716906946 |
| A closed structure, | IEA; IDA; IBA; IEA; IE | 1213.8 | 0.716839677 |
| Organized structur | IBA | 982.2 | 0.716758298 |
|  |  | 656.6 | 0.71672251 |
|  |  | 353.7 | 0.716709075 |

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|---|---|---|---|
| The membrane surr | ISS; ISS; IBA; IEA | 606.4 | 0.716688654 |
| | | 556.9 | 0.716645717 |
| | | 345.5 | 0.716642547 |
| A lipid bilayer along | IEA; IEA | 500.6 | 0.716540152 |
| | | 2119.8 | 0.716435513 |
| The space external | IBA | 929.4 | 0.716376157 |
| The membrane surr | IBA; IEA; IEA | 1265.7 | 0.716362487 |
| | | 1361.2 | 0.716353218 |
| The lipid bilayer su | IBA; IEA | 1252.2 | 0.716339243 |
| A membrane-boun | IEA | 699.7 | 0.716306989 |
| | | 339.8 | 0.716303708 |
| A membrane-boun | IEA | 838.2 | 0.716177523 |
| The lipid bilayer su | IEA; IEA; IEA; IEA; IE | 911.1 | 0.71616727 |
| The membrane surr | IEA; IBA; IEA | 359 | 0.716155989 |
| A small organelle e | IEA; IEA | 693.6 | 0.7161188 |
| A membrane-boun | IEA; IEA | 638.1 | 0.71603197 |
| | | 198.6 | 0.716012085 |
| | | 929.2 | 0.715992251 |
| | | 287.3 | 0.715976331 |
| A membrane-boun | IEA | 422.1 | 0.715944089 |
| A membrane-boun | IEA | 671.8 | 0.715838047 |
| | | 505.6 | 0.715783228 |
| The gel-like materi | IBA; IBA; IBA | 508.7 | 0.715746019 |
| A lipid bilayer along | IEA; IEA | 237.4 | 0.715669756 |
| | | 403 | 0.715632754 |
| The outer, i.e. cyto | IEA | 545.4 | 0.715621562 |
| | | 1088.3 | 0.715611504 |
| | | 1850.8 | 0.71552842 |
| A lipid bilayer along | IEA; IEA | 954 | 0.715513627 |
| A chlorophyll-conta | IBA | 1198.1 | 0.715466155 |
| A lipid bilayer along | IEA; IEA | 260.7 | 0.715381665 |
| The outer, i.e. cyto | IBA | 2073.3 | 0.715381276 |

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|---|---|---|---|
| A membrane-boun | IBA; IBA | 697.4 | 0.715371379 |
| | | 541.3 | 0.715314982 |
| A membrane-boun | IBA | 824.8 | 0.715203686 |
| | | 149.9 | 0.715143429 |
| A small organelle e | IEA; IEA; IBA; IEA; IE | 630.7 | 0.715078484 |
| | | 1043.4 | 0.71506613 |
| | | 693.1 | 0.715048334 |
| | | 417.6 | 0.715038314 |
| Cyclin-dependent | IBA; IBA | 678.3 | 0.714875424 |
| That part of a multi | IBA; IBA; IEA | 1004.8 | 0.714868631 |
| The membrane sur | IBA | 829.6 | 0.714802314 |
| | | 1739.8 | 0.857799747 |
| | | 903.8 | 0.714759903 |
| | | 269.9 | 0.714709152 |
| | | 259 | 0.714671815 |
| A protein complex | IBA; IBA | 1200.6 | 0.714642679 |
| The membrane sur | IBA; IEA; IEA | 1136.7 | 0.714524501 |
| | | 333.8 | 0.7144997 |
| | | 430 | 0.714418605 |
| | | 856.4 | 0.714385801 |
| The outer, i.e. cyto | IBA; IBA | 807.7 | 0.714374149 |
| | | 798.2 | 0.714357304 |
| The membrane sur | IBA; IEA; IEA | 1410.1 | 0.7143465 |
| A chlorophyll-conta | IEA; IEA; IBA | 739.7 | 0.714343653 |
| A membrane-boun | IBA | 1718.1 | 0.714335603 |
| A membrane-boun | IC | 664.3 | 0.714285714 |
| A membrane-boun | IEA | 257.2 | 0.714230171 |
| A vacuole to which | IBA; IBA | 522.7 | 0.714176392 |
| OBSOLETE. The bas | IEA; IBA | 7541.5 | 0.714168269 |
| | | 228.1 | 0.714160456 |

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|---|---|---|---|
| | | 1319.8 | 0.714123352 |
| The ordered and or | IBA; IBA | 1551.8 | 0.714073979 |
| | | 1002.9 | 0.714029315 |
| | | 700.4 | 0.71402056 |
| A chlorophyll-conta | IEA; IEA | 1127.5 | 0.713968958 |
| The membrane surr | IBA; IEA; IEA | 1681 | 0.713920286 |
| A semiautonomous | IEA | 900.4 | 0.713904931 |
| | | 626.6 | 0.713852538 |
| A membrane-boun | IBA | 616.7 | 0.713799254 |
| | | 964.3 | 0.713782018 |
| The region of a kin | IEA; IEA; IEA; IEA | 618.4 | 0.71377749 |
| The membrane surr | IBA | 1115.1 | 0.713657968 |
| The irregular netwo | IBA; IEA; IEA | 329.9 | 0.71354956 |
| | | 924.4 | 0.71354392 |
| A membrane-boun | IEA; IEA; IEA; IEA | 1885.1 | 0.713490001 |
| A membrane-boun | IEA | 671.5 | 0.71347729 |
| | | 1037.6 | 0.7134734 |
| The space external | IEA; IEA | 1265.9 | 0.713405482 |
| A membrane-boun | IBA | 721.2 | 0.713394343 |
| | | 1050.1 | 0.713360632 |
| A lipid bilayer alon | IEA; IEA | 748.3 | 0.713350261 |
| The membrane surr | IBA; IEA | 2467.2 | 0.713318742 |
| | | 500.1 | 0.713257349 |
| Organized structure | IBA | 956.2 | 0.713239908 |
| A membrane-boun | IEA | 1330.1 | 0.71317946 |
| The membrane surr | IEA; IEA; IEA | 1166.9 | 0.713085954 |

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| A lipid bilayer along | IEA; IEA | 1328.1 | 0.713048716 |
| A membrane-boun | IBA | 709.7 | 0.712977314 |
|  |  | 1468.5 | 0.712972421 |
|  |  | 309 | 0.712944984 |
| A lipid bilayer along | IBA | 526.7 | 0.712929561 |
| A structure compos | IEA; IEA; IBA; IBA; IB | 1327.1 | 0.712907844 |
| A membrane-boun | IEA; IEA | 1428.1 | 0.712905259 |
|  |  | 962 | 0.712889813 |
|  |  | 920.8 | 0.712858384 |
| A membrane-boun | IEA | 1195.5 | 0.712839816 |
|  |  | 430.4 | 0.712825279 |
|  |  | 933.7 | 0.712755703 |
|  |  | 435.5 | 0.712743972 |
|  |  | 1385.2 | 0.712604678 |
| A discrete extra-nu | IBA | 653.4 | 0.712580349 |
| The membrane surr | ISS; ISS; IBA; IEA | 552.3 | 0.712475104 |
| A lipid bilayer along | IEA; IBA | 2528.4 | 0.712466382 |
| A lipid bilayer along | IBA; IBA | 1216.9 | 0.712466102 |
| A membrane-boun | IBA; IBA; IBA | 974.1 | 0.71245252 |

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|---|---|---|---|
| | | 574 | 0.712369338 |
| A lipid bilayer alon | IEA; IEA | 1570.3 | 0.896898682 |
| | | 356.9 | 0.712244326 |
| Any of the long, ge | IEA | 480.1 | 0.712143303 |
| | | 762.5 | 0.712131148 |
| | | 521 | 0.712092131 |
| | | 331.7 | 0.712089237 |
| The membrane sur | IBA; IBA | 376.5 | 0.712084993 |
| | | 547.9 | 0.711991239 |
| A membrane-boun | IBA | 1005.5 | 0.711984088 |
| A membrane-boun | IEA; IBA; IBA | 1358.1 | 0.711950519 |
| A lipid bilayer alon | IEA; IEA | 1846.1 | 0.711933265 |
| The space external | IEA | 1035.1 | 0.711911893 |
| | | 170.4 | 0.71185446 |
| A membrane-boun | IEA; IEA; IEA | 418.5 | 0.711827957 |
| A small lytic vacuol | IBA | 1098.9 | 0.711802712 |
| A membrane-boun | IEA | 709.5 | 0.711768851 |
| A membrane-boun | IEA; IEA | 775.4 | 0.711632706 |
| A part of a cellular | IEA | 634.7 | 0.711517252 |
| The membrane sur | IBA; IEA; IEA | 1468.7 | 0.711513583 |
| The space enclosed | IEA | 499.5 | 0.711511512 |

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|---|---|---|---|
| | | 528.5 | 0.711447493 |
| | | 286.6 | 0.711444522 |
| | | 330.6 | 0.711433757 |
| A chlorophyll-conta | IEA; IEA | 590.8 | 0.71140826 |
| | | 478.8 | 0.811403509 |
| The membrane surr | IBA; IEA; IEA; IBA | 362.6 | 0.711252068 |
| | | 2002.2 | 0.711167716 |
| The pigmented mer | IBA | 313.3 | 0.711139483 |
| | | 326.6 | 0.710961421 |
| A lipid bilayer alonc | IEA; IEA | 354.8 | 0.710822999 |
| A membrane-bounc | IBA | 2801.2 | 0.710802513 |
| | | 941.4 | 0.710749947 |
| | | 1445.3 | 0.710717498 |
| | | 1110.4 | 0.710644813 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 481.3 | 0.710575525 |
| A membrane-bounc | IEA | 647.8 | 0.710558814 |
| A membrane-bounc | IEA | 1096.5 | 0.710533516 |
| A lipid bilayer alonc | IEA; IEA | 2286.5 | 0.710518259 |
| A membrane-bounc | IEA | 860.4 | 0.710483496 |

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|---|---|---|---|
| | | 616.4 | 0.710415315 |
| A closed structure, | IBA | 942.9 | 0.71036165 |
| A membrane-boun | IBA; IBA | 1441 | 0.710340042 |
| A membrane-boun | IBA | 583.4 | 0.710318821 |
| A lipid bilayer along | IEA; IEA | 266.7 | 0.71016123 |
| | | 995.7 | 0.710153661 |
| The part of the cyto | IBA; IBA; IBA | 1628.6 | 0.710119121 |
| The membrane surr | IBA | 1368.1 | 0.710035816 |
| A membrane-boun | IEA | 335.9 | 0.710032748 |
| | | 309 | 0.710032362 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1544.9 | 0.710013593 |
| | | 265.4 | 0.709871891 |
| A membrane-boun | IEA | 566.6 | 0.709848217 |
| A semiautonomous | IBA | 1515.9 | 0.709809354 |
| | | 191.2 | 0.709728033 |
| The space external | IEA | 332.4 | 0.709687124 |
| A membrane-boun | IBA | 880.3 | 0.709644439 |
| A membrane-boun | IEA; IEA | 745.5 | 0.709590879 |
| | | 1814.2 | 0.709568956 |
| A ubiquitin ligase c | IBA | 522.6 | 0.709529277 |
| A semiautonomous | IBA | 726.6 | 0.709468759 |
| The membrane surr | IBA; IEA; IEA | 2636.5 | 0.709463304 |
| | | 742.4 | 0.709455819 |
| | | 1136.4 | 0.709433298 |
| The contents of a c | IBA; IEA; IEA; IEA; IE | 2110.8 | 0.709351904 |
| The contents of a c | IBA; IBA | 690.7 | 0.70928044 |
| The irregular netwo | IEA; IEA; IEA; IEA | 462.3 | 0.709279689 |
| The contents of a c | IBA | 1456.9 | 0.70917702 |

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|---|---|---|---|
| | | 648.3 | 0.7090853 |
| | | 1997.1 | 0.913825046 |
| | | 2853.3 | 0.70900361 |
| The lipid bilayer su | IDA; IEA; IEA; IEA | 829.9 | 0.709001084 |
| A membrane-boun | IBA | 570 | 0.708947368 |
| The part of the cyto | IBA | 646.6 | 0.708939066 |
| A lipid bilayer alon | IEA; IEA | 1080.8 | 0.708919319 |
| The space external | IBA | 623.1 | 0.70887498 |
| A membrane-boun | IBA | 3274.3 | 0.708792719 |
| | | 564 | 0.708687943 |
| | | 1586.8 | 0.708658936 |
| | | 1330.2 | 0.708615246 |
| A membrane-boun | IEA | 1239 | 0.708555287 |
| A lipid bilayer alon | IEA | 1116.4 | 0.70852741 |
| | | 2372 | 0.708305228 |
| A prelysosomal end | IEA; IEA | 2190.9 | 0.708065179 |
| The contents of a c | IEA; IEA; IEA; IEA | 1015.1 | 0.708009063 |
| | | 1112.2 | 0.707966193 |
| | | 683.2 | 0.707845433 |
| The membrane surr | IEA; IEA | 1064.6 | 0.707777569 |
| A membrane-boun | IEA; IEA | 1114.6 | 0.707697829 |
| | | 710.3 | 0.707588343 |
| A lipid bilayer alon | IEA; IEA | 929.5 | 0.707584723 |
| | | 394.6 | 0.707551951 |
| A membrane-boun | IEA | 536.1 | 0.707517254 |
| | | 301.5 | 0.707462687 |
| The component of t | IBA; IEA; IEA | 1078.8 | 0.707452725 |
| | | 919.5 | 0.707340946 |

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|---|---|---|---|
|  |  | 505.3 | 0.706906788 |
| The membrane surr | IBA; IEA; IEA | 1483.1 | 0.706897714 |
|  |  | 187.5 | 0.706666667 |
|  |  | 1023 | 0.706549365 |
| The irregular netwo | IBA; IBA; IEA; IEA | 426.3 | 0.706544687 |
|  |  | 2082.6 | 0.706424661 |
| A membrane-bound | IEA | 506 | 0.706324111 |
| A lipid bilayer along | IEA; IEA | 1352.5 | 0.706321627 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 424.5 | 0.706242638 |
| A closed structure t | IBA; IBA; IEA; IEA | 3343.9 | 0.706121595 |
|  |  | 528.1 | 0.706116266 |
| A photosystem that | IEA; IBA | 386.8 | 0.706049638 |
| A membrane-bound | IBA | 350.7 | 0.706016538 |
|  |  | 914.6 | 0.70599169 |
| A small organelle e | IEA | 840.3 | 0.705938355 |
| A lipid bilayer along | IEA; IEA | 971.9 | 0.705936825 |
|  |  | 1145.8 | 0.705795078 |
|  |  | 840.2 | 0.705784337 |
|  |  | 757.6 | 0.705781415 |
| A membrane-bound | IEA | 676 | 0.705769231 |
|  |  | 1734.4 | 0.705719557 |
| Cyclin-dependent p | IBA; IBA | 1289 | 0.705663305 |
|  |  | 543.9 | 0.70564442 |
|  |  | 811.1 | 0.705585008 |

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|---|---|---|---|
| A membrane-boun | IBA; IBA; IEA; IEA; IE | 2498.6 | 0.705555111 |
| | | 1150.7 | 0.705396715 |
| A membrane-boun | IEA | 877 | 0.705359179 |
| | | 1065.7 | 0.705357981 |
| A membrane-boun | IEA | 276.2 | 0.705286025 |
| | | 1012.4 | 0.705156065 |
| | | 286.9 | 0.705123736 |
| A membrane-boun | IEA | 727.3 | 0.70507356 |
| A membrane-boun | IBA | 724.2 | 0.705053853 |
| A lipid bilayer alon | IEA | 727.9 | 0.705041901 |
| A membrane-boun | IEA; IEA; IEA; IEA | 1225.9 | 0.705033037 |
| A lipid bilayer alon | IBA; IEA | 749.2 | 0.705018687 |
| The membrane sur | IBA; IEA; IEA | 2418.5 | 0.704941079 |
| A chlorophyll-cont | IBA | 520.8 | 0.704877112 |
| The lipid bilayer su | IBA; IEA; IEA | 1421 | 0.704855735 |

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|---|---|---|---|
| | | 348.6 | 0.704819277 |
| | | 802.2 | 0.704811768 |
| | | 2316.8 | 0.704808356 |
| | | 682.6 | 0.704805157 |
| A membrane-boun | IBA; IBA; IBA | 1641.8 | 0.704775247 |
| A membrane-boun | IBA | 892.1 | 0.704629526 |
| | | 943.5 | 0.704610493 |
| | | 858.5 | 0.704601048 |
| | | 890.6 | 0.704581181 |
| A membrane-boun | IEA; IEA | 2334.9 | 0.704484132 |
| | | 1010.7 | 0.704462254 |
| A membrane-boun | IEA | 1040.8 | 0.704458109 |
| A photosystem that | IEA; IEA; IEA; IEA | 281.1 | 0.704375667 |
| The contents of a c | IBA; IBA; IBA; IBA; IB | 376.6 | 0.704195433 |
| | | 590.9 | 0.704180064 |
| | | 989.4 | 0.70416414 |

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|---|---|---|---|
| A membrane-boun | IEA | 555.5 | 0.704050405 |
| | | 1169.4 | 0.870531897 |
| Organized structur | IBA | 1047 | 0.704011461 |
| | | 241.5 | 0.703933747 |
| | | 2237.6 | 0.703879156 |
| The membrane sur | ISS; ISS; IBA; IEA | 560.4 | 0.703783012 |
| A membrane-boun | IBA | 911.1 | 0.70376468 |
| A membrane-boun | IEA | 788.3 | 0.703666117 |
| A lipid bilayer alon | IEA | 1234 | 0.703646677 |
| | | 283.7 | 0.703560099 |
| | | 896.8 | 0.703501338 |
| The membrane sur | IBA; IEA; IEA | 1735.1 | 0.703475304 |

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|---|---|---|---|
| | | 182.1 | 0.703459638 |
| The membrane surr | IBA | 884.5 | 0.703448276 |
| A membrane-boun | IBA | 522 | 0.703448276 |
| | | 813.1 | 0.703234534 |
| A membrane-boun | IEA; IEA | 556.9 | 0.703178308 |
| A membrane-boun | IBA | 1041.9 | 0.703042518 |
| | | 699.3 | 0.702988703 |
| The contents of a c | IBA | 1465.9 | 0.702981104 |
| The region between | IEA | 166.3 | 0.702946482 |
| | | 473.9 | 0.702890905 |
| | | 845.4 | 0.70286255 |
| | | 2158.8 | 0.702844173 |
| The membrane surr | IBA; IEA; IEA | 779.7 | 0.702834423 |
| | | 258.4 | 0.702786378 |
| A protein complex | IBA | 1382.3 | 0.702597121 |
| The contents of a c | IEA; IEA; IEA | 858.4 | 0.702586207 |
| | | 1220.4 | 0.702556539 |
| A membrane-boun | IEA | 1977.5 | 0.702503161 |
| | | 1877.3 | 0.835082299 |
| | | 1239.8 | 0.702452008 |
| | | 884.7 | 0.702384989 |
| | | 1005.9 | 0.702256686 |
| A lipid bilayer alon | IEA; IEA | 1144.6 | 0.702166696 |
| | | 923.3 | 0.702155312 |
| | | 578.1 | 0.70212766 |
| A fine cytoplasmic | IBA | 841.1 | 0.70205683 |
| A transcription fact | IBA; IBA | 1250.6 | 0.701983048 |
| Organized structur | IBA | 958.6 | 0.701961193 |
| A membrane-boun | IEA | 2792.6 | 0.701854902 |
| | | 462.1 | 0.701796148 |
| A transcription fact | IBA | 424.7 | 0.701671768 |
| The membrane surr | IEA; IBA; IEA | 691.6 | 0.701561596 |
| | | 1068.8 | 0.701440868 |
| The membrane surr | IBA; IEA; IEA | 1951.1 | 0.701399211 |

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|---|---|---|---|
| A semiautonomous | IEA; IBA | 298.7 | 0.701372615 |
| | | 713 | 0.701262272 |
| The outer, i.e. cyto | IBA; IEA; IBA | 843.8 | 0.70123252 |
| The contents of a c | IBA; IEA | 277.1 | 0.701190906 |
| A membrane-boun | IEA | 563.9 | 0.701188154 |
| | | 658.2 | 0.701154664 |
| | | 266.3 | 0.701088997 |
| | | 338.2 | 0.701064459 |
| | | 446.1 | 0.700963909 |
| A lipid bilayer alon | IEA; IEA | 1120.2 | 0.70085699 |
| | | 1168.2 | 0.700821777 |
| | | 803.1 | 0.70078446 |
| A multiprotein com | IBA; IEA | 2440.3 | 0.700774495 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA | 674.7 | 0.700755892 |
| | | 744.6 | 0.700644641 |
| A protein complex | IBA; IEA; IEA; IBA | 1367.2 | 0.700629023 |
| | | 1598 | 0.700625782 |
| A lipid bilayer alon | IEA; IEA | 1512.9 | 0.700575055 |
| | | 281.1 | 0.700462469 |
| A semiautonomous | IBA | 1546.6 | 0.700375016 |
| The component of | IEA | 1125.8 | 0.700302007 |
| | | 1066.9 | 0.70025307 |
| | | 1199.9 | 0.700225019 |
| A membrane-boun | IBA; IBA | 994.5 | 0.70015083 |
| | | 760.7 | 0.700144604 |
| A membrane-boun | IBA; IBA | 737.3 | 0.700122067 |
| A semiautonomous | IBA; IEA | 1455.4 | 0.700013742 |
| | | 309.8 | 0.699806327 |
| A membrane-boun | IBA | 700.3 | 0.699700129 |
| | | 1195.4 | 0.699682115 |
| | | 1100.1 | 0.699663667 |
| The outer, i.e. cyto | IBA | 876.1 | 0.770688278 |
| A membrane-boun | IBA | 510.6 | 0.699569134 |
| | | 340.8 | 0.699530516 |

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|---|---|---|---|
| A membrane-bound | IEA | 615.7 | 0.699528991 |
| Any of the long, ge | IEA; IBA | 245.6 | 0.699511401 |
| The membrane surr | IBA; IBA | 1798.6 | 0.699377293 |
| | | 421.4 | 0.699335548 |
| | | 1129.6 | 0.699274079 |
| A membrane-bound | IBA; IBA | 521.4 | 0.770042194 |
| A lipid bilayer along | IEA; IEA | 2238.5 | 0.699262899 |
| | | | |
| | | 1285.8 | 0.699175611 |
| A membrane-bound | IBA; IBA | 2177 | 0.699127239 |
| A membrane-bound | IEA | 705.1 | 0.69904978 |
| | | 638.6 | 0.699029126 |
| | | 771.5 | 0.699027868 |
| A semiautonomous | IEA | 1011.7 | 0.699021449 |
| | | 323.6 | 0.699011125 |
| | | 830.9 | 0.699001083 |

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|---|---|---|---|
|  |  | 744.7 | 0.69893917 |
| A lipid bilayer alon | IBA; IBA | 1149.1 | 0.698894787 |
| A lipid bilayer alon | IEA; IEA | 2330.2 | 0.69886705 |
| A membrane-boun | IEA; IEA; IBA; IBA; IB | 186.9 | 0.698769395 |
| A membrane-boun | IEA | 621.4 | 0.69874477 |
| A membrane-boun | IEA | 383.7 | 0.698722961 |
| A membrane-boun | IEA | 655.2 | 0.698717949 |

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|---|---|---|---|
|  |  | 411.9 | 0.69871328 |
|  |  | 530.7 | 0.69869983 |
| The contents of a c | IBA | 811 | 0.69864365 |
| A lipid bilayer alon | IEA; IEA | 1600 | 0.698625 |
| A membrane-boun | IBA; IBA | 765.1 | 0.69860149 |
| A lipid bilayer alon | IEA | 1679.9 | 0.698553485 |
|  |  | 348.3 | 0.698535745 |
|  |  | 877.7 | 0.69853025 |
|  |  | 769.1 | 0.698478741 |
| A membrane-boun | IBA | 706.9 | 0.698401471 |

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|---|---|---|---|
| The space external | IEA; IEA | 1124.2 | 0.698363281 |
|  |  | 805.9 | 0.698349671 |
| The membrane surr | IBA; IEA; IEA | 2282.4 | 0.698300035 |
| The lipid bilayer su | IBA; IEA | 1015.1 | 0.698256329 |
| Organized structur | IBA | 1351.3 | 0.698216532 |
| The space external | IEA | 571.2 | 0.698179272 |

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|---|---|---|---|
| The space external | IEA | 224.9 | 0.698088039 |
| | | 795.9 | 0.698077648 |
| The membrane surr | IEA; IEA | 1076.2 | 0.697918602 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1152.3 | 0.697908531 |
| | | 197.6 | 0.697874494 |
| A membrane-boun | IEA | 1139.2 | 0.697858146 |
| | | 328.3 | 0.697837344 |
| | | 676.4 | 0.697811946 |
| A membrane-boun | IEA | 917.3 | 0.697590755 |
| | | 742.6 | 0.697549152 |
| A chlorophyll-conta | IBA | 1324.1 | 0.697530398 |
| A lipid bilayer alon | IEA; IEA | 1224.2 | 0.697516746 |
| The space external | IEA; IBA; IBA | 702.5 | 0.697508897 |
| A membrane-boun | IC | 1070.9 | 0.697450742 |
| | | 1379.5 | 0.697426604 |
| | | 3642.7 | 0.697422242 |
| The membrane surr | IBA; IEA; IEA | 2077.9 | 0.697194283 |
| | | 462.6 | 0.697146563 |
| A membrane-boun | IEA | 523.3 | 0.697114466 |
| A lipid bilayer alon | IEA; IEA; IBA | 441 | 0.697052154 |
| A closed structure t | IBA; IBA; IEA; IEA | 3367.5 | 0.697045286 |
| The membrane surr | IBA | 3135 | 0.697033493 |

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|---|---|---|---|
| | | 322.4 | 0.696960298 |
| The space external | IEA; IEA | 1286.3 | 0.696960274 |
| The membrane surr | IBA; IEA; IEA | 1466.8 | 0.696891192 |
| A lipid bilayer alon | IEA | 1282.7 | 0.696811413 |
| | | 322.8 | 0.696716233 |
| A lipid bilayer alon | IEA; IEA | 844.4 | 0.785883468 |
| The lipid bilayer su | ISS; IEA; IEA | 953.8 | 0.696686936 |
| The part of the cyto | IEA | 600.3 | 0.696651674 |
| | | 598.6 | 0.696625459 |
| | | 667.1 | 0.696597212 |
| A semiautonomous | IBA; IBA | 1914.5 | 0.696578741 |
| A lipid bilayer alon | IEA | 718.7 | 0.696535411 |
| | | 802.4 | 0.696535394 |
| The membrane surr | IBA; IEA; IEA | 2425.9 | 0.696483779 |
| The contents of a c | IBA; IBA | 480 | 0.696458333 |
| | | 574.5 | 0.69643168 |
| A membrane-boun | IBA; IBA | 1696.1 | 0.696362243 |
| | | 1419.7 | 0.696344298 |
| | | 191.3 | 0.696288552 |
| | | 1817.4 | 0.696214372 |
| A lipid bilayer alon | IEA | 1639.7 | 0.695980972 |
| Arrays of microtubu | IBA | 2464.4 | 0.695950333 |
| A membrane-boun | IEA; IEA | 603.5 | 0.695940348 |
| | | 238.4 | 0.695889262 |
| | | 293.5 | 0.695741056 |
| | | 240.9 | 0.695724367 |

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|---|---|---|---|
| A part of a cellular | IEA | 258.6 | 0.695668987 |
| A lipid bilayer along | IEA; IEA | 1515.7 | 0.759121198 |
| | | 1487.1 | 0.695582005 |
| | | 678 | 0.695575221 |
| A membrane-boun | IEA | 672.4 | 0.695568114 |
| A chlorophyll-conta | IBA | 1974.6 | 0.695431986 |
| A lipid bilayer along | IEA; IEA | 714.1 | 0.695420809 |
| The contents of a c | IBA | 495.1 | 0.695415068 |
| A small, dense bod | IEA; IBA | 1414.5 | 0.695369388 |
| | | 1494.4 | 0.695329229 |
| A membrane-boun | IEA | 765.7 | 0.69531148 |
| | | 303.2 | 0.69525066 |
| | | 417 | 0.695203837 |
| A membrane-boun | IEA; IEA; IEA | 1474.4 | 0.695198047 |
| A lipid bilayer along | IEA; IEA | 792 | 0.695075758 |
| A membrane-boun | IBA | 647.1 | 0.694946685 |
| | | 781.8 | 0.694934766 |
| | | 1587.2 | 0.694934476 |
| The membrane surr | IBA; IEA; IEA | 2171.5 | 0.694819249 |
| Organized structure | IBA | 1061.5 | 0.69477155 |
| | | 694.2 | 0.694756554 |
| | | 1875 | 0.69472 |
| A SAGA-type histor | IEA; IEA; IEA; IEA | 1249.9 | 0.694695576 |
| Organized structure | IBA | 966.4 | 0.694639901 |
| | | 191.9 | 0.694632621 |
| | | 739 | 0.69458728 |
| A vacuole to which | IBA; IBA; IBA; IEA; IE | 802.8 | 0.694569008 |
| A membrane-boun | IBA; IEA; IBA; IBA | 2504 | 0.694528754 |
| A semiautonomous | IBA; IBA; IBA | 461.9 | 0.694522624 |
| The membrane surr | IBA; IEA; IEA | 1484.4 | 0.694421989 |
| The space external | IEA | 983.9 | 0.69437951 |
| | | 1059.8 | 0.69428194 |
| | | 146.2 | 0.694254446 |
| | | 280.6 | 0.694226657 |
| | | 1709.1 | 0.69416652 |
| The membrane surr | IBA; IBA | 418.5 | 0.694145759 |
| Organized structure | IBA | 1172.3 | 0.694105604 |
| The irregular netwo | IEA | 1044 | 0.694061303 |

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| A lipid bilayer along | IEA; IEA; IEA | 1352.9 | 0.693990687 |
| The membrane surr | IEA | 677.7 | 0.693964881 |
| The rigid or semi-ri | IEA; IEA | 634.7 | 0.69387112 |
| | | 896.9 | 0.693834318 |
| The space external | IEA; IEA; IEA | 731.2 | 0.693654267 |
| A membrane-boun | IEA; IBA; IBA | 3562.5 | 0.693642105 |
| A membrane-boun | IBA | 701.4 | 0.693612774 |
| | | 1277.9 | 0.693559746 |
| | | 259.4 | 0.693523516 |
| | | 451.9 | 0.693516265 |
| | | 314.5 | 0.693481717 |
| | | 3171.9 | 0.693338378 |
| A membrane-boun | IEA | 1147.5 | 0.693246187 |
| The space external | IEA; IEA | 1343.6 | 0.693212266 |
| A lipid bilayer along | IEA; IEA | 1049.4 | 0.693157995 |
| A membrane-boun | IEA | 429.2 | 0.693150047 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1021.3 | 0.693038285 |
| The membrane surr | IBA | 521.8 | 0.692985818 |
| A membrane-boun | IBA | 1130.3 | 0.692736442 |
| | | 2117.6 | 0.692718172 |
| A fine cytoplasmic | IBA | 403.2 | 0.692708333 |
| | | 1369.7 | 0.692706432 |
| The contents of a c | IBA; IBA; IBA | 693.9 | 0.692607004 |
| A lipid bilayer along | IEA; IEA | 1080.8 | 0.804496669 |
| | | 1305 | 0.832260536 |
| | | 388.9 | 0.69246593 |
| A membrane-boun | IBA | 1562.1 | 0.692465271 |

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| The membrane sur | IBA; IEA; IEA | 590.8 | 0.692450914 |
| | | 1525.6 | 0.692448873 |
| A membrane-boun | IEA | 546.2 | 0.692420359 |
| The lipid bilayer su | ISS; IEA; IEA | 856.3 | 0.692397524 |
| A lipid bilayer alon | IEA; IEA | 516 | 0.692248062 |
| | | 461.4 | 0.692241006 |
| The membrane sur | IEA; IEA; IBA | 2859.8 | 0.692181271 |
| A membrane-boun | IBA | 911.9 | 0.692071499 |
| | | 990 | 0.691919192 |
| | | 804 | 0.691915423 |
| | | 2616.5 | 0.691840245 |
| | | 355.6 | 0.691788526 |
| | | 554 | 0.691696751 |
| A semiautonomous | IBA | 1441.5 | 0.69157128 |
| A membrane-boun | IEA | 848.4 | 0.691537011 |
| A lipid bilayer alon | IEA; IEA | 2086.4 | 0.691526074 |
| The membrane sur | IBA | 744.6 | 0.691377921 |
| A membrane-boun | IEA | 281.5 | 0.691296625 |
| | | 512.5 | 0.691121951 |
| | | 560 | 0.691071429 |
| The membrane sur | IEA; IEA; IEA; IEA | 2190.5 | 0.69089249 |
| A protein complex | IBA; IBA; IEA | 1961.9 | 0.6908609 |
| A membrane-boun | IBA | 866.6 | 0.690860835 |

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|---|---|---|---|
| | | 300.4 | 0.798601864 |
| | | 613.7 | 0.690728369 |
| | | 335.9 | 0.690681751 |
| | | 407.3 | 0.690645716 |
| A membrane-boun | IEA; IEA | 957.9 | 0.690573129 |
| | | 766.9 | 0.690572434 |
| | | 823.6 | 0.690383681 |
| | | 1025 | 0.690341463 |
| | | 723.6 | 0.690298507 |
| A lipid bilayer alon | IEA; IEA | 868.7 | 0.690226776 |
| | | 223.3 | 0.690103 |
| | | 605.6 | 0.690059445 |
| | | 400.7 | 0.690042426 |
| A membrane-boun | IC | 850.4 | 0.690028222 |
| A lipid bilayer alon | IEA; IEA | 638.1 | 0.690017239 |
| | | 1639.6 | 0.689924372 |
| | | 265.4 | 0.689902035 |
| A lipid bilayer alon | IEA; IEA | 240.5 | 0.68981289 |
| A protein complex | IBA | 1404.1 | 0.689694466 |
| | | 779.8 | 0.689664016 |
| | | 484.3 | 0.689655172 |
| A membrane-boun | IBA | 518 | 0.68957529 |
| | | 179.1 | 0.689558906 |
| A membrane-boun | IEA; IEA; IBA; IEA | 1101.7 | 0.689298357 |
| The irregular netwo | IEA; IBA; IEA; IEA | 664.6 | 0.689286789 |
| The irregular netwo | IEA | 489.1 | 0.689225107 |
| | | 1777 | 0.689026449 |
| | | 792.4 | 0.688919738 |
| | | 1203.2 | 0.688912899 |
| An RNA polymerase | IEA; IBA; IEA; IEA; IE | 756.1 | 0.688797778 |
| The component of | IEA | 656.3 | 0.688709432 |
| The lipid bilayer su | IEA; IEA; IEA | 1737.5 | 0.688690647 |
| A lipid bilayer alon | IEA; IEA | 279.1 | 0.688642064 |
| The ordered and or | IBA; IEA; IBA; IEA | 2155.7 | 0.688639421 |
| A lipid bilayer alon | IEA; IBA | 2039.2 | 0.688603374 |
| | | 974.3 | 0.688596941 |
| | | 1220.2 | 0.688575643 |
| The membrane sur | IBA; IEA; IEA | 1653.9 | 0.688554326 |

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|---|---|---|---|
| The contents of a c | IBA | 1215.8 | 0.688435598 |
| The membrane surr | IBA; IEA; IEA | 691 | 0.688422576 |
| | | 658.8 | 0.688372799 |
| A focus in the cytop | IEA; IEA; IEA; IEA; IE | 3001.7 | 0.688343272 |
| The membrane surr | IEA; IEA; IEA | 2229.3 | 0.68833266 |
| A lipid bilayer along | IEA; IEA | 351.6 | 0.688282139 |
| The membrane surr | IEA; IEA | 464.5 | 0.688266954 |
| | | 951.4 | 0.688143788 |
| | | 270.8 | 0.687961595 |
| | | 794 | 0.68790932 |
| | | 1447.9 | 0.687823745 |
| | | 312.6 | 0.68777991 |
| | | 231.2 | 0.687716263 |
| | | 745.3 | 0.68764256 |
| The contents of a c | IBA; IBA; IBA | 1208.5 | 0.687629293 |
| A membrane-boun | IEA; IEA | 1002.3 | 0.687618478 |
| A membrane-boun | IBA; IBA; IBA | 694.3 | 0.687599021 |
| | | 363.3 | 0.687586017 |
| | | 293.2 | 0.833560709 |
| The space enclosed | IBA | 551.9 | 0.687443377 |
| | | 501 | 0.68742515 |
| | | 239.3 | 0.687421646 |

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|---|---|---|---|
| A membrane-boun‹ | IEA | 580.8 | 0.687327824 |
| | | 472.3 | 0.779589244 |
| | | 1587.3 | 0.687204687 |
| The contents of a c‹ | IBA | 875.1 | 0.687121472 |
| | | 3510.3 | 0.687063784 |
| Organized structur‹ | IBA | 980 | 0.687040816 |
| A membrane-boun‹ | IEA | 624.4 | 0.68673927 |
| | | 290.1 | 0.686659772 |
| The membrane surr | IEA; IBA; IEA | 1038.7 | 0.686627515 |
| A membrane-boun‹ | IEA | 630.5 | 0.686597938 |
| | | 1016.8 | 0.686565696 |
| A lipid bilayer along | IEA; IEA | 2096.5 | 0.686525161 |
| The lipid bilayer sur | IEA; IEA; IEA | 823.9 | 0.686491079 |
| A lipid bilayer along | IEA; IEA | 356.9 | 0.686466797 |
| OBSOLETE. The bas | IEA; IEA; IEA | 433.1 | 0.686446548 |
| A membrane-boun‹ | IEA | 732.4 | 0.686373566 |
| | | 717.4 | 0.686367438 |
| A membrane-boun‹ | IBA | 756.9 | 0.686352226 |

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|---|---|---|---|
| | | 463 | 0.686177106 |
| A lipid bilayer along | IEA; IEA | 345.4 | 0.686160973 |
| A membrane-boun | IBA; IEA; IEA | 1242.5 | 0.6861167 |
| The space external | IEA | 430.4 | 0.686105948 |
| | | 755.1 | 0.686001854 |
| | | 1589.4 | 0.685982132 |
| The membrane surr | IBA; IEA; IEA | 1394.3 | 0.685935595 |
| | | 479.2 | 0.685934891 |
| | | 2016.1 | 0.685928277 |
| | | 1890.8 | 0.685900148 |
| | | 265.5 | 0.685875706 |
| | | 1826.2 | 0.6858504 |
| | | 486.3 | 0.814312153 |
| A membrane-boun | IEA | 1163.3 | 0.685635692 |
| The membrane surr | IEA; IEA; IEA | 1305.4 | 0.685613605 |
| A membrane-boun | IEA; IEA; IEA | 837.4 | 0.685574397 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA | 1429.6 | 0.685506435 |
| A membrane-boun | IEA | 767.1 | 0.685438665 |
| A lipid bilayer alon | IEA; IEA | 1139.6 | 0.685415935 |
| | | 717.8 | 0.685288381 |
| A lipid bilayer alon | IBA | 1120.6 | 0.68516866 |
| A small organelle e | IEA; IBA | 553.9 | 0.685141722 |
| The contents of a c | IBA; IEA | 1142.3 | 0.685108991 |
| A membrane-boun | IBA | 1226.8 | 0.685034235 |
| The membrane sur | IBA; IEA | 700.7 | 0.684886542 |
| A membrane-boun | IEA; IEA; IEA | 912.4 | 0.684787374 |
| The contents of a c | IEA | 536.7 | 0.684740078 |
| | | 949 | 0.684720759 |
| A membrane-boun | IBA | 830.6 | 0.684685769 |
| A lipid bilayer alon | IEA; IEA | 455.4 | 0.684672815 |
| | | 194.4 | 0.684670782 |
| A lipid bilayer alon | IBA; IEA | 2938.2 | 0.684568784 |
| A complex compris | IEA; IEA; IEA | 294.2 | 0.684568321 |
| A membrane-boun | IBA; IBA | 2051.5 | 0.684523519 |
| A membrane-boun | IBA | 819 | 0.684493284 |
| That part of the nu | IBA; IBA | 737.4 | 0.684431787 |
| | | 946.7 | 0.684271681 |

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|---|---|---|---|
| The membrane surr | IBA; IEA; IEA | 1454.3 | 0.684246717 |
| A lipid bilayer along | IEA; IEA | 302.1 | 0.684210526 |
| | | 578.2 | 0.684192321 |
| | | 808.6 | 0.684145437 |
| | | 1535.2 | 0.764916623 |
| A membrane-boun | IBA | 1027.3 | 0.684026088 |
| A chlorophyll-conta | IEA; IEA | 1044.8 | 0.683958652 |
| The lipid bilayer su | IBA; IEA; IEA; IBA | 588.2 | 0.683951037 |
| | | 1018.8 | 0.683941892 |
| A lipid bilayer along | IEA; IEA | 613.7 | 0.683884634 |
| | | 1222.9 | 0.68386622 |
| A membrane-boun | IBA; IEA | 1394.1 | 0.683810344 |
| The part of the cyto | IBA | 1123.2 | 0.683582621 |
| | | 363.4 | 0.683544304 |
| | | 371.2 | 0.683459052 |
| | | 663.1 | 0.683305685 |
| | | 1595.2 | 0.6832999 |
| The contents of a c | IBA; IBA; IEA | 1490.5 | 0.683260651 |
| A membrane-boun | IEA | 445 | 0.683146067 |
| | | 1222.3 | 0.683138346 |
| A lipid bilayer along | IEA; IEA | 462.1 | 0.682969054 |
| | | 412.5 | 0.682909091 |
| The space external | IEA; IBA; IBA; IEA; IE | 717 | 0.682845188 |
| A membrane-boun | IEA; IEA | 1745.4 | 0.682823422 |

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|---|---|---|---|
| A membrane-bounc | IDA; IEA | 606.9 | 0.682814302 |
|  |  | 219.4 | 0.682771194 |
|  |  | 383 | 0.875456919 |
| The membrane surr | IBA | 1624.1 | 0.682716581 |
| A membrane-bounc | IBA | 172.4 | 0.682714617 |
| A membrane-bounc | IEA | 802.1 | 0.682707892 |
| The part of the cytc | IBA | 1640.7 | 0.68269641 |
| The contents of a c | IBA; IEA | 412.8 | 0.682655039 |
| A membrane-bounc | IEA | 486.4 | 0.682565789 |
|  |  | 696.1 | 0.68251688 |
|  |  | 624.6 | 0.682516811 |
| A membrane-bounc | IEA | 1327.8 | 0.682406989 |
| An ISWI complex th | IEA | 1651.1 | 0.682393556 |
| The membrane surr | IBA; IEA | 1632.8 | 0.682386085 |
|  |  | 770.7 | 0.68236668 |
|  |  | 248.7 | 0.682348211 |
| A membrane-bounc | IC | 318.9 | 0.682345563 |
| A membrane-bounc | IBA; IBA | 1066.1 | 0.682299972 |
| Any member of a fa | IEA; IEA; IEA | 552.4 | 0.682295438 |
| A lipid bilayer alonç | IEA; IEA | 595.8 | 0.682275932 |
|  |  | 698.6 | 0.682078443 |
|  |  | 1199.8 | 0.682030338 |

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|---|---|---|---|
| A semiautonomous | IEA; IEA; IEA; IEA | 1355.3 | 0.681989227 |
| A lipid bilayer alon | IEA; IEA | 1051.6 | 0.681818182 |
| | | 1060 | 0.681792453 |
| The membrane surr | IBA; IEA; IEA | 461.9 | 0.681749296 |
| The part of the cyto | IBA; IBA; IBA | 933.4 | 0.681701307 |
| | | 1861.6 | 0.897400086 |
| A membrane-boun | IBA | 529.2 | 0.68159486 |
| | | 790.9 | 0.681502086 |
| A closed structure, | IEA | 691.1 | 0.681377514 |
| | | 737.8 | 0.681349959 |
| A membrane-boun | IBA | 609.7 | 0.681318681 |
| | | 947.1 | 0.681237462 |
| | | 787.1 | 0.681107864 |
| Cyclin-dependent p | IBA; IBA; IBA | 623 | 0.68105939 |
| The lipid bilayer su | IBA; IBA; IBA; IBA; IB | 688.4 | 0.680999419 |
| A membrane-boun | IBA; IBA | 834.1 | 0.680973504 |
| | | 206.5 | 0.680871671 |
| | | 441.8 | 0.680851064 |
| A membrane-boun | IEA; IEA; IEA; IEA; IE | 1357.3 | 0.680836956 |
| A lipid bilayer alon | IEA; IEA | 282.6 | 0.680820948 |
| | | 964.5 | 0.680663556 |
| | | 810.1 | 0.680656709 |
| A semiautonomous | IEA; IEA; IEA | 630.9 | 0.680614994 |
| The contents of a c | IBA; IEA | 2260.5 | 0.680424685 |
| The outer, i.e. cyto | IEA; IEA; IEA | 1734.8 | 0.680366613 |
| A lipid bilayer alon | IEA; IEA | 1568.9 | 0.747848811 |
| The space external | IBA; IEA; IEA | 629.2 | 0.680228862 |
| | | 1416 | 0.739548023 |
| A protein complex | IBA; IEA; IBA; IBA; IB | 677 | 0.680206795 |

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|---|---|---|---|
| | | 712.9 | 0.771636976 |
| | | 163.5 | 0.680122324 |
| The outer, i.e. cytop | IBA | 1732.8 | 0.680113112 |
| | | 964 | 0.680082988 |
| The space external | IEA; IBA; IBA | 1314.6 | 0.679902632 |
| A lipid bilayer along | IEA; IEA; IBA | 868 | 0.67983871 |
| | | 1445.6 | 0.679717764 |
| | | 2131.1 | 0.762470086 |
| | | 467.3 | 0.679649048 |
| A lipid bilayer along | IBA; IEA | 545.6 | 0.679618768 |
| The irregular netwo | IBA; IEA; IEA | 657.2 | 0.679549604 |
| | | 819.1 | 0.679404224 |
| A semiautonomous | IBA | 1476.9 | 0.679396032 |
| A vacuole to which | IBA; IBA; IBA; IBA | 589.3 | 0.679280502 |
| A membrane-bound | IBA | 438.7 | 0.67927969 |
| A membrane-bound | IEA; IEA; IEA; IEA | 512.9 | 0.679274712 |
| | | 1038 | 0.679190751 |
| | | 462.5 | 0.679135135 |
| A membrane-bound | IEA; IEA; IBA | 947.5 | 0.679050132 |
| | | 150.8 | 0.679045093 |
| A chlorophyll-conta | IEA | 399.4 | 0.679018528 |
| A membrane-bound | IBA | 945 | 0.678941799 |

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|---|---|---|---|
| A membrane-boun | IEA | 739.4 | 0.678928861 |
| The irregular netwo | IBA; IEA; IEA; IEA | 332.3 | 0.678904604 |
|  |  | 1475 | 0.678847458 |
| A semiautonomous | IBA | 347.8 | 0.678838413 |
| The part of the cyt | IBA | 564.8 | 0.678824363 |
| A protein complex | IBA | 1214.7 | 0.67876842 |
|  |  | 374.4 | 0.678685897 |
|  |  | 510.4 | 0.678683386 |
| A membrane-boun | IDA; IDA | 1001.7 | 0.678646301 |
| The contents of a c | IBA | 443.4 | 0.678619756 |
| The contents of a c | IEA | 1242.5 | 0.678551308 |
|  |  | 343.7 | 0.678498691 |
|  |  | 143.7 | 0.678496868 |
|  |  | 1494.1 | 0.678468643 |
|  |  | 466.8 | 0.67823479 |
| The membrane surr | IEA; IEA; IEA | 398.1 | 0.678221552 |
| An intracellular non | IEA | 1762.6 | 0.678202655 |
| A lipid bilayer alon | IEA; IEA | 562.4 | 0.678165007 |
| A lipid bilayer alon | IBA | 299.3 | 0.677915135 |
|  |  | 925.9 | 0.677826979 |
| The component of | IEA | 278.1 | 0.677813736 |
|  |  | 529.4 | 0.677748394 |
| A membrane-boun | IEA | 263.1 | 0.677689092 |

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|---|---|---|---|
| | | 585.2 | 0.677546138 |
| | | 200.9 | 0.677451468 |
| | | 691.5 | 0.67736804 |
| A lipid bilayer along | IEA; IEA | 3569 | 0.677276548 |
| A lipid bilayer along | IEA; IEA | 1083.4 | 0.677219863 |
| The lipid bilayer su | IEA; IBA | 1412.1 | 0.677218327 |
| | | 678.6 | 0.677129384 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1675.9 | 0.677128707 |
| A lipid bilayer along | IEA; IEA | 482.5 | 0.677098446 |
| The lipid bilayer su | IEA; IEA | 1549 | 0.677081988 |
| | | 561.7 | 0.833719067 |
| | | 1916.7 | 0.852246048 |
| The contents of a c | IBA | 1492.9 | 0.677004488 |
| A SWI/SNF-type co | IBA | 746 | 0.6769437 |
| | | 1502.4 | 0.832800852 |
| | | 1205 | 0.676846473 |
| The contents of a c | IBA | 562.1 | 0.67674791 |
| A lipid bilayer along | IEA; IEA | 267.5 | 0.676635514 |
| The component of | IEA | 594.8 | 0.676529926 |
| | | 936.7 | 0.676523967 |

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|---|---|---|---|
| The inner, i.e. lume | IEA; IEA; IEA | 1045.1 | 0.676394603 |
| A membrane-boun | IEA | 832.7 | 0.676354029 |
| A membrane-boun | IEA; IBA | 1559.2 | 0.676308363 |
| A membrane-boun | IEA; IEA; IBA | 408.1 | 0.676304827 |
| | | 933.2 | 0.676168024 |
| A lipid bilayer alon | IEA; IEA | 394 | 0.676142132 |
| | | 1288.1 | 0.676112103 |
| | | 562.4 | 0.676031294 |
| The irregular netwo | IBA; IEA; IEA | 404 | 0.675990099 |
| | | 872.7 | 0.675948207 |

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| The space external | IEA; IBA; IEA | 462.2 | 0.67589788 |
|  |  | 838.6 | 0.675888385 |
|  |  | 1560.5 | 0.675873118 |
| A membrane-bound | IBA; IBA | 2043.1 | 0.675786795 |
|  |  | 892.3 | 0.788187829 |
| A membrane-bound | IEA; IEA | 921.9 | 0.675561341 |
|  |  | 470.3 | 0.67552626 |
|  |  | 1497.2 | 0.67546086 |
| A small, dense body | IBA | 846.4 | 0.67544896 |
| The membrane surr | IBA; IBA; IEA; IEA | 578.6 | 0.675423436 |
| A membrane-bound | IEA | 575.2 | 0.675243394 |
|  |  | 624.1 | 0.675052075 |
| A membrane-bound | IBA | 744.4 | 0.675040301 |
| A membrane-bound | IEA | 733.5 | 0.674982958 |
|  |  | 836.8 | 0.674952199 |
| A chlorophyll-conta | IBA | 1110.7 | 0.674799676 |
| A lipid bilayer along | IEA; IEA | 859 | 0.674388824 |
| A membrane-bound | IEA; IEA; IEA | 988.9 | 0.674385681 |
| The contents of a c | IEA; IBA; IBA | 1455.8 | 0.674337134 |
|  |  | 2023.2 | 0.674278371 |
| A lipid bilayer along | IEA; IEA | 548 | 0.674270073 |
|  |  | 259.7 | 0.674239507 |
|  |  | 629.2 | 0.674189447 |

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|---|---|---|---|
| A membrane-boun | IEA | 475.4 | 0.674169121 |
| The ordered and or | IBA; IEA; IEA; IEA; IE | 3384 | 0.674143026 |
| The lipid bilayer su | IBA; IEA; IEA | 422.5 | 0.67408284 |
|  |  | 222.1 | 0.674020711 |
| An intracellular org | IEA; IEA | 281.9 | 0.673997872 |
| A membrane-boun | IBA | 1474.1 | 0.67390272 |
|  |  | 600.7 | 0.673880473 |
| OBSOLETE. The bas | IEA | 1319.6 | 0.673840558 |
|  |  | 564.1 | 0.673816699 |
| A lipid bilayer alon | IEA; IEA | 485.6 | 0.673805601 |
| A membrane-boun | IEA; IEA | 1186.4 | 0.673803102 |
| A membrane-boun | IEA | 822.5 | 0.673799392 |
|  |  | 747.6 | 0.673756019 |
| The membrane surr | IBA; IEA; IEA; IBA | 1035.4 | 0.673749276 |
| A chlorophyll-conta | IEA; IBA; IBA | 617.6 | 0.673737047 |
|  |  | 614.2 | 0.673721915 |
|  |  | 854.7 | 0.673569674 |
| A lipid bilayer alon | IEA; IEA | 1179.4 | 0.673562829 |
|  |  | 1226.5 | 0.673542601 |
|  |  | 858.2 | 0.67350268 |
| The membrane surr | IBA; IBA; IBA | 3380.8 | 0.813061997 |
|  |  | 359.9 | 0.673242567 |
| OBSOLETE. The bas | IEA; IEA; IEA | 1230.6 | 0.673167561 |
| A membrane-boun | IEA | 989.1 | 0.673137195 |
|  |  | 960 | 0.758229167 |

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|---|---|---|---|
| An intracellular org | IEA; IEA | 200 | 0.673 |
|  |  | 459.5 | 0.672905332 |
| A more or less rigid | IBA; IEA | 914 | 0.672866521 |
|  |  | 1023 | 0.672825024 |
| The rigid or semi-ri | IEA | 1247.9 | 0.672810321 |
| A membrane-boun | IEA | 517.3 | 0.672723758 |
|  |  | 1093.3 | 0.672642459 |
|  |  | 569.6 | 0.672577247 |
| A membrane-boun | IEA | 748.5 | 0.67254509 |
| A lipid bilayer along | IEA; IEA | 776.8 | 0.672502575 |
| A membrane-boun | IEA; IEA | 4938.2 | 0.67243125 |
|  |  | 719.2 | 0.672413793 |
| A collection of mem | IBA; IBA; IBA; IBA | 548.5 | 0.672379216 |
| A membrane-boun | IBA | 1816.6 | 0.672299901 |

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|---|---|---|---|
|  |  | 233.7 | 0.672229354 |
|  |  | 1126.7 | 0.672228632 |
| A membrane-boun | IEA | 719.7 | 0.672224538 |
| A membrane-boun | IEA | 456.7 | 0.672213707 |
| A protein complex | IBA; IEA | 289.4 | 0.672080166 |
|  |  | 192.4 | 0.672037422 |
|  |  | 2366.5 | 0.672005071 |
| The contents of a c | IBA | 1510 | 0.671655629 |
|  |  | 962.6 | 0.671410763 |
|  |  | 262 | 0.671374046 |
|  |  | 661.5 | 0.671352986 |
|  |  | 1214 | 0.671334432 |
|  |  | 781.6 | 0.671187308 |
|  |  | 726.5 | 0.671163111 |
| A membrane-boun | IEA; IBA | 298.3 | 0.67113644 |
| A ribonuclease com | IBA; IBA; IEA; IEA; IE | 867.1 | 0.671087533 |
|  |  | 514.7 | 0.671070527 |
|  |  | 325.8 | 0.670963781 |
|  |  | 697.1 | 0.670922393 |
| A membrane-boun | IEA | 997 | 0.670912738 |
|  |  | 1187.3 | 0.670765603 |
| A membrane-boun | IEA | 742.9 | 0.670749764 |
|  |  | 748.3 | 0.670720299 |
| A small, dense bod | IBA | 1282.9 | 0.670668018 |
|  |  | 3184 | 0.670634422 |
|  |  | 867.1 | 0.670626225 |
|  |  | 213.1 | 0.670577194 |

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|---|---|---|---|
| The membrane surr | IBA; IEA; IEA | 2148.3 | 0.670530187 |
| A membrane-boun | IEA | 731.8 | 0.670401749 |
|  |  | 786.4 | 0.670396745 |
| A membrane-boun | IEA | 1249.3 | 0.670295365 |
|  |  | 839.2 | 0.67028122 |
|  |  | 1631 | 0.67020233 |
|  |  | 405.7 | 0.75523786 |
| A membrane-boun | IBA | 634.2 | 0.670135604 |
|  |  | 645.1 | 0.670128662 |
|  |  | 1231.4 | 0.670050349 |

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|---|---|---|---|
| A nuclear DNA-dire | IBA | 1008.9 | 0.670036674 |
| | | 1143.5 | 0.669960647 |
| | | 5333.7 | 0.669872696 |
| | | 821.7 | 0.669830839 |
| A membrane-bound | IC | 633.2 | 0.669772584 |
| | | 2426.5 | 0.669730064 |
| The component of t | IBA; IEA; IEA | 1129.8 | 0.669676049 |
| A membrane-bound | IEA; IBA | 1985.5 | 0.669654999 |
| | | 1501.7 | 0.669507891 |
| The component of t | IBA; IEA; IEA | 1133.8 | 0.669430235 |
| The membrane surr | IBA; IEA; IEA | 1509 | 0.669383698 |
| | | 632.1 | 0.669356115 |
| A membrane-bound | IBA; IEA; IBA; IEA; IE | 1411.3 | 0.669311982 |
| | | 2207.2 | 0.669309532 |
| A membrane-bound | IEA | 292.7 | 0.669285958 |
| A membrane-bound | IEA | 837.2 | 0.669254658 |
| A fine cytoplasmic c | IBA | 660.9 | 0.669238917 |
| The lipid bilayer su | IEA; IBA; IEA; IBA; IE | 933.6 | 0.669237361 |
| | | 1076.8 | 0.669205052 |
| A protein complex t | IBA | 700.6 | 0.669140737 |
| An intracellular org | IEA; IBA; IBA; IEA; IE | 262.3 | 0.669081205 |
| The membrane surr | IBA; IEA; IEA | 429.6 | 0.823091248 |
| A membrane-bound | IEA | 301.8 | 0.668986083 |
| | | 1617.2 | 0.66893396 |
| The contents of a c | IEA; IEA; IBA | 1362 | 0.668649046 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IB | 844.3 | 0.668601208 |
| A lipid bilayer along | IEA; IEA | 431.5 | 0.668597914 |
| A small organelle e | IEA | 551 | 0.668421053 |
| | | 649.3 | 0.668412136 |
| A membrane-bound | IEA; IEA; IEA | 1052.3 | 0.668345529 |
| A lipid bilayer along | IEA; IEA | 324 | 0.668209877 |

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|---|---|---|---|
| The contents of a c | IBA; IBA | 374.3 | 0.668180604 |
|  |  | 1083.6 | 0.667958656 |
|  |  | 812.2 | 0.667938931 |
|  |  | 1678.9 | 0.66793734 |
| A membrane-boun | IEA | 548.3 | 0.667882546 |
|  |  | 639.1 | 0.667814114 |
| A membrane-boun | IEA; IBA; IEA; IEA | 1635.5 | 0.66780801 |
| A chlorophyll-cont | IEA; IEA | 902.7 | 0.667774454 |
| A lipid bilayer alon | IEA; IEA | 885.3 | 0.667683271 |
| A lipid bilayer alon | IEA; IEA | 1393.4 | 0.667647481 |
| A membrane-boun | IBA; IBA | 1360.3 | 0.667646843 |
| The membrane sur | IBA; IBA | 484.4 | 0.667630058 |
| A lipid bilayer alon | IEA; IEA | 384 | 0.667447917 |
| A membrane-boun | IEA | 942.1 | 0.667338924 |
| A semiautonomous | IEA; IEA; IEA; IEA; IE | 792.6 | 0.667171335 |

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|---|---|---|---|
| The membrane surr | IEA; IBA; IEA | 1051.2 | 0.667142314 |
| The membrane surr | IBA; IEA | 1666.1 | 0.667126823 |
| A circular DNA mol | IEA; IEA; IEA; IEA; IE | 1025 | 0.667121951 |
| OBSOLETE. The bas | IEA; IEA | 1440.8 | 0.667059967 |
| A membrane-bound | IEA | 450.8 | 0.66703638 |
| | | 917.4 | 0.666993678 |
| The rigid or semi-ri | IEA | 1228.3 | 0.666938044 |
| | | 837.8 | 0.66674624 |
| A membrane-bound | IEA | 479.5 | 0.666736184 |
| A membrane-bound | IEA | 315.6 | 0.666666667 |
| The lipid bilayer su | IBA; IBA; IEA; IBA; IB | 176.7 | 0.666666667 |
| A lipid bilayer along | IEA; IEA | 576.5 | 0.666608846 |
| A semiautonomous | IBA | 1326.9 | 0.666515939 |
| | | 1427.6 | 0.793849818 |
| | | 2960.6 | 0.666418969 |
| A lipid bilayer along | IEA; IEA | 960.1 | 0.666388918 |
| | | 1289.9 | 0.820141096 |
| A chlorophyll-conta | IEA; IEA; IEA | 554.6 | 0.666245943 |
| | | 548.6 | 0.666241342 |
| A membrane-bound | IBA | 547.7 | 0.666240643 |
| | | 376.9 | 0.666224463 |
| | | 590.1 | 0.803592611 |
| | | 981.3 | 0.666157138 |
| The irregular netwo | IEA; IEA; IEA; IBA | 492.3 | 0.666057282 |

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|---|---|---|---|
| | | 429.4 | 0.666045645 |
| | | 917.4 | 0.666012644 |
| A membrane-boun | IEA | 820.3 | 0.665853956 |
| A small, dense bod | IBA; IBA; IBA; IBA | 689.2 | 0.665844457 |
| A lipid bilayer alon | IEA; IEA | 340.8 | 0.665786385 |
| A membrane-boun | IEA | 613.3 | 0.665742703 |
| | | 1281.9 | 0.665730556 |
| | | 556.4 | 0.665708124 |

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|---|---|---|---|
| The part of the cyto | IBA; IEA; IEA | 932 | 0.665665236 |
| The irregular netwo | IBA; IBA; IEA; IEA | 457 | 0.665645514 |
| | | 823.6 | 0.665492958 |
| The contents of a c | IBA | 759.3 | 0.665481364 |
| A semiautonomous | IEA; IEA; IEA | 939.8 | 0.665460736 |
| | | 766.7 | 0.665449328 |
| The component of a | IEA; IBA | 405.4 | 0.66526887 |
| | | 1618.2 | 0.665245334 |
| A membrane-boun | IEA | 532.7 | 0.665102309 |
| | | 978.3 | 0.664928958 |
| Either of the ends o | IBA | 2640.7 | 0.66486159 |
| | | 1712.9 | 0.66483741 |
| | | 2217.4 | 0.664832687 |
| | | 701.7 | 0.664814023 |
| | | 571.6 | 0.66480056 |

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|---|---|---|---|
| | | 1011.2 | 0.664754747 |
| The contents of a c | IEA; IBA; IBA | 1697.8 | 0.664565909 |
| | | 1865.2 | 0.664539996 |
| A membrane-boun | IEA; IEA; IEA | 594 | 0.664478114 |
| A membrane-boun | IEA; IEA; IEA | 1460.6 | 0.6643845 |
| The lipid bilayer su | ISS; IEA; IEA; IEA | 1006.4 | 0.664248808 |
| | | 2269.8 | 0.664155432 |
| | | 2404.6 | 0.664143725 |
| | | 1965.4 | 0.664037855 |
| A membrane-boun | IEA | 873.9 | 0.664034787 |
| The membrane surr | IEA; IBA; IEA | 895.3 | 0.664023232 |
| A lipid bilayer along | IEA; IEA | 1779.7 | 0.663988313 |
| | | 254.7 | 0.663918335 |
| | | 493.5 | 0.663829787 |
| An intracellular org | IEA; IEA | 390.8 | 0.663766633 |
| A membrane-boun | IEA; IBA | 1851.3 | 0.663749797 |

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|---|---|---|---|
| Any protein comple | IBA | 3657.5 | 0.663732057 |
|  |  | 776.1 | 0.663703131 |
| The membrane surr | IBA; IEA; IEA | 747.5 | 0.66367893 |
|  |  | 1074.9 | 0.663596614 |
|  |  | 528.8 | 0.663577912 |
| A membrane-bound | IBA; IBA | 2469.5 | 0.663575623 |
| The membrane surr | IBA | 892.3 | 0.663566065 |
|  |  | 813.8 | 0.663553699 |
|  |  | 464.8 | 0.663511188 |
| A lipid bilayer along | IEA; IEA | 669.7 | 0.663431387 |
|  |  | 283.7 | 0.663376806 |
|  |  | 1117.8 | 0.663356593 |
| A membrane-bound | IC | 610.9 | 0.66328368 |
| The irregular netwo | IBA; IEA; IEA; IEA; IE | 689 | 0.663280116 |
| OBSOLETE. A multip | IEA | 2617.2 | 0.798792603 |
| Organized structure | IBA | 951.2 | 0.663057191 |
|  |  | 1998.5 | 0.912034026 |
| A lipid bilayer along | IEA | 543.6 | 0.662987491 |
|  |  | 2087.9 | 0.662962786 |
| A membrane-bound | IEA | 629.9 | 0.66280362 |
|  |  | 808.7 | 0.662792136 |
|  |  | 1891.3 | 0.662771639 |
|  |  | 546.2 | 0.852801172 |
| A lipid bilayer along | IEA; IEA | 321.1 | 0.662410464 |
| A membrane-bound | IEA | 738.7 | 0.662379857 |
| A membrane-bound | IBA; IBA | 1431.4 | 0.66235853 |
| A semiautonomous | IEA; IEA; IEA; IBA; IE | 508.5 | 0.662340216 |

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|---|---|---|---|
| A membrane-boun | IEA | 3445.1 | 0.662302981 |
| A semiautonomous | IBA | 860.1 | 0.662248576 |
| A membrane-boun | IEA | 519.3 | 0.662237628 |
| | | 470 | 0.66212766 |
| A small, dense bod | IBA; IBA; IEA | 1065.8 | 0.662037906 |
| Any dynein comple | IBA; IEA; IEA | 386.9 | 0.661928147 |
| | | 786.8 | 0.661921708 |
| | | 181.3 | 0.661886376 |
| A membrane-boun | IEA | 411.4 | 0.661886242 |
| Organized structur | IBA | 625.2 | 0.661868202 |
| | | 740 | 0.661756757 |
| | | 373 | 0.866487936 |
| | | 737.7 | 0.661515521 |
| | | 623.5 | 0.661427426 |
| | | 1588.8 | 0.661190836 |
| A semiautonomous | IEA; IEA; IEA; IBA | 1046.6 | 0.661188611 |
| A lipid bilayer alon | IEA; IEA | 388.2 | 0.837970118 |
| | | 1116.5 | 0.660994178 |
| | | 572.2 | 0.660957707 |
| A semiautonomous | IBA | 1406.9 | 0.660956713 |
| | | 866.5 | 0.660934795 |

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|---|---|---|---|
| Punctate structures | IBA; IBA; IBA; IBA; IB | 1570.4 | 0.660659705 |
| Organized structure | IBA | 999.1 | 0.660594535 |
| | | 847.5 | 0.660530973 |
| A membrane-bound | IBA | 708.5 | 0.660409315 |
| A membrane-bound | IEA | 454 | 0.824229075 |
| A membrane-bound | IEA; IEA | 1711.1 | 0.660335457 |
| | | 1260.3 | 0.660239625 |
| | | 514.4 | 0.660186625 |
| A membrane-bound | IEA | 385.8 | 0.660186625 |
| A lipid bilayer along | IEA; IEA | 865.5 | 0.660080878 |
| The membrane surr | IBA; IBA | 954.2 | 0.660029344 |
| | | 1023.5 | 0.65999023 |
| A vacuole to which | IEA; IEA; IEA; IEA; IE | 947.1 | 0.659909196 |
| | | 626 | 0.659904153 |
| The contents of a c | IEA; IEA; IEA | 762.1 | 0.659887154 |
| The space external | IEA; IBA; IBA | 695.1 | 0.659761185 |
| A lipid bilayer along | IEA; IEA | 779.7 | 0.659740926 |
| A lipid bilayer along | IEA; IEA | 375.3 | 0.659738876 |
| | | 3397.4 | 0.659680932 |
| | | 432.5 | 0.659653179 |
| | | 2377.1 | 0.659627277 |
| | | 813.7 | 0.659456802 |
| A semiautonomous | IBA | 1499 | 0.659372915 |
| A membrane-bound | IEA | 603.7 | 0.659267848 |
| A membrane-bound | IEA | 469.7 | 0.867149244 |

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|---|---|---|---|
| | | 512.2 | 0.659117532 |
| | | 521.5 | 0.659060403 |
| | | 564.8 | 0.65881728 |
| | | 864.6 | 0.658801758 |
| A multiprotein ATPa | IBA | 534 | 0.658801498 |
| A protein complex | IBA | 1513.2 | 0.658604282 |
| A membrane-boun | IEA | 665.1 | 0.658397233 |
| A membrane-boun | IBA; IBA | 1018.3 | 0.658352156 |
| The membrane surr | IBA; IEA; IEA | 2075.6 | 0.658267489 |
| A lipid bilayer alon | IEA; IEA | 1089.9 | 0.658225525 |
| The contents of a c | IEA; IEA | 2711.6 | 0.819442396 |
| | | 712.1 | 0.658053644 |
| The contents of a c | IBA; IBA; IBA | 1829.3 | 0.658011261 |
| A protein complex, | IEA | 473.9 | 0.657944714 |
| | | 1282.7 | 0.657753177 |

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|---|---|---|---|
|  |  | 358.8 | 0.657748049 |
|  |  | 964.2 | 0.657747355 |
| The space external | IEA | 563 | 0.657726465 |
|  |  | 854.2 | 0.778623273 |
| Organized structur | IBA | 978.4 | 0.657604252 |
|  |  | 356 | 0.65758427 |
| The membrane surr | IBA | 960.1 | 0.657535673 |
|  |  | 473.6 | 0.657516892 |
|  |  | 505.7 | 0.657504449 |
|  |  | 718.2 | 0.657477026 |
| A membrane-boun | IBA | 984.6 | 0.657424335 |
| A lipid bilayer alon | IEA | 1640.2 | 0.657297891 |
| A membrane-boun | IBA | 536.9 | 0.657291861 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1144.3 | 0.657257712 |
| The membrane surr | IEA; IBA; IEA | 1008.9 | 0.657052235 |
|  |  | 914.7 | 0.657046026 |
| A membrane-boun | IBA; IEA; IBA; IBA | 958.1 | 0.657029538 |
|  |  | 1329.4 | 0.656988115 |
| A lipid bilayer alon | IEA; IEA | 1052.1 | 0.656971771 |

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|---|---|---|---|
| | | 643.6 | 0.752486016 |
| A membrane-boun | IBA | 986 | 0.656896552 |
| The component of | IEA | 542.2 | 0.65676872 |
| | | 593.8 | 0.65661839 |
| | | 487.4 | 0.656544932 |
| | | 410.5 | 0.656516443 |
| | | 3222.5 | 0.656508922 |
| A semiautonomous | IBA | 1159.5 | 0.836912462 |
| | | 1305.6 | 0.656479779 |
| | | 231.7 | 0.656452309 |
| | | 1168.1 | 0.656279428 |
| | | 509.1 | 0.656256138 |
| The outer layer of t | ISS | 732 | 0.656010929 |
| A membrane-boun | IBA; IBA | 746.2 | 0.655990351 |
| A complex compris | IEA; IEA; IEA | 291.7 | 0.655810764 |
| An ISWI complex th | IEA | 1401 | 0.655745896 |
| | | 949 | 0.655742887 |
| | | 1316.9 | 0.655630648 |
| | | 1771.3 | 0.655620166 |
| A membrane-boun | IEA | 744.5 | 0.65560779 |
| | | 297.6 | 0.655577957 |
| OBSOLETE. The bas | IEA; IBA | 589.1 | 0.655576303 |
| The membrane surr | IBA; IBA | 800.3 | 0.655504186 |
| A membrane-boun | IBA; IBA; IBA | 936.7 | 0.655492687 |
| | | 193.9 | 0.655492522 |
| A membrane-boun | IBA; IBA | 175.9 | 0.655486072 |
| | | 735.1 | 0.778397497 |
| | | 195.6 | 0.655419223 |

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|---|---|---|---|
| A membrane-boun | IEA | 1646.5 | 0.655329487 |
| A membrane-boun | IEA; IEA | 918 | 0.655119826 |
| | | 704 | 0.655113636 |
| | | 2605.6 | 0.792101627 |
| A protein complex | IBA; IEA; IBA | 1569.6 | 0.654943935 |
| | | 426.3 | 0.654937837 |
| | | 229.5 | 0.654901961 |
| The irregular netwo | IEA; IEA; IEA; IEA | 702.5 | 0.65480427 |
| The ordered and or | IBA; IEA | 721.3 | 0.654789963 |
| | | 408.9 | 0.654683297 |
| A lipid bilayer alon | IEA; IEA | 590.4 | 0.654640921 |
| | | 1194 | 0.654606365 |
| | | 577.8 | 0.654551748 |
| | | 1424 | 0.654494382 |
| | | 734.2 | 0.654453827 |

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|---|---|---|---|
|  |  | 534.8 | 0.654450262 |
| A membrane-boun | IBA; IEA | 511 | 0.654403131 |
| A lipid bilayer alon | IEA; IEA | 488.4 | 0.654381654 |
|  |  | 1165.4 | 0.654195984 |
| The contents of a c | IBA; IEA; IEA | 1106.2 | 0.65413126 |
|  |  | 344.3 | 0.808597154 |
|  |  | 1712.7 | 0.877328195 |
|  |  | 840 | 0.654047619 |
| The membrane sur | IEA | 907.2 | 0.6539903 |
| A membrane-boun | IBA | 443 | 0.653950339 |
| An enzyme comple | IBA | 1906 | 0.653777545 |
|  |  | 807.8 | 0.653750928 |
| A protein complex | IBA; IBA | 724.3 | 0.65373464 |
| A membrane-boun | IEA | 845.7 | 0.65365969 |
|  |  | 440 | 0.653636364 |
|  |  | 226.3 | 0.653557225 |
| A membrane-boun | IEA | 540.2 | 0.653461681 |
|  |  | 228.8 | 0.653409091 |
|  |  | 921.2 | 0.653278333 |
|  |  | 1464.3 | 0.653144847 |
| A lipid bilayer alon | IEA; IBA | 2082.4 | 0.653092585 |
| A membrane-boun | IEA; IEA | 549.5 | 0.652957234 |

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|---|---|---|---|
| A membrane-boun | IBA; IBA; IBA | 518.3 | 0.652903724 |
| The irregular netwo | IEA; IBA | 286.9 | 0.652840711 |
|  |  | 1016.2 | 0.652725841 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 669 | 0.652615845 |
|  |  | 660.3 | 0.652430713 |
|  |  | 979.4 | 0.652338166 |
| A lipid bilayer alon | IEA; IEA | 1161.8 | 0.652263729 |
|  |  | 191.8 | 0.652241919 |
| A membrane-boun | IEA; IEA; IEA; IBA; IE | 1092.9 | 0.652209717 |
| A lipid bilayer alon | IEA; IEA | 1338.5 | 0.652073216 |
|  |  | 395.4 | 0.651997977 |
|  |  | 1539.9 | 0.651990389 |
|  |  | 522.6 | 0.651932644 |
| A membrane-boun | IBA | 853.1 | 0.65185793 |
| A membrane-boun | IBA | 510.9 | 0.651790957 |
|  |  | 1391.1 | 0.863273668 |
| A membrane-boun | IEA | 650.4 | 0.651752768 |
|  |  | 3274.1 | 0.651751626 |
| A lipid bilayer alon | IEA; IEA | 907.1 | 0.651747327 |
| A membrane-boun | IEA | 444.5 | 0.651743532 |
| A part of a cellular | IEA | 687.1 | 0.65172464 |
|  |  | 889.2 | 0.651596941 |
| A lipid bilayer alon | IEA | 2133.4 | 0.82736477 |

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|---|---|---|---|
| A lipid bilayer along | IEA | 1134.1 | 0.651529847 |
|  |  | 184.5 | 0.651490515 |
|  |  | 875.8 | 0.65140443 |
|  |  | 1824.9 | 0.65132336 |
| A membrane-boun | IBA | 902.4 | 0.651263298 |
| A closed structure t | IBA; IBA; IEA; IEA | 3223.2 | 0.651216183 |
| A macromolecular c | IBA | 553.9 | 0.651200578 |
|  |  | 372.7 | 0.65119399 |
|  |  | 1583.1 | 0.651190702 |
| A membrane-boun | IEA | 586.5 | 0.651150895 |
|  |  | 1332.9 | 0.651136619 |
| The space external | IEA; IEA | 348.5 | 0.65107604 |
| The membrane surr | IBA; IEA; IEA | 2039.4 | 0.650975777 |
|  |  | 624.3 | 0.650969085 |
| A membrane-boun | IEA; IBA; IEA | 1013.4 | 0.650878232 |
|  |  | 564.2 | 0.650833038 |
| A lipid bilayer along | IEA; IEA | 990.6 | 0.650817686 |
|  |  | 532.1 | 0.650817516 |
|  |  | 1211.1 | 0.650730741 |
| A lipid bilayer along | IEA; IEA | 939.9 | 0.650707522 |
| A lipid bilayer along | IEA; IEA | 1053.8 | 0.650692731 |
|  |  | 2019.4 | 0.764088343 |
|  |  | 472.5 | 0.650582011 |

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|---|---|---|---|
| A membrane-bound | IDA | 864.8 | 0.650555042 |
| | | 533.9 | 0.650496348 |
| | | 147.3 | 0.650373388 |
| A lipid bilayer along | IEA; IEA | 1615.6 | 0.650099034 |
| A lipid bilayer along | IEA | 1155.5 | 0.650021636 |
| A membrane-bound | IBA; IBA; IEA; IEA; IE | 2571 | 0.650019448 |
| A lipid bilayer along | IEA; IEA | 314.3 | 0.650015908 |
| | | 668.2 | 0.847949716 |
| The component of a | IEA | 1535.7 | 0.870222049 |
| | | 1849.7 | 0.743742228 |
| | | 488.8 | 0.816489362 |
| | | 912.2 | 0.782942337 |
| | | 967.4 | 0.790882779 |
| A semiautonomous | IEA; IEA; IBA; IEA; IE | 264.1 | 0.828095418 |
| A lipid bilayer along | IEA; IEA | 503.3 | 0.742300815 |
| A lipid bilayer along | IEA; IEA | 1346.5 | 0.78967694 |
| | | 1707.1 | 0.840431141 |
| | | 419 | 0.845823389 |
| | | 152.7 | 0.863130321 |
| | | 1850.9 | 0.743043925 |
| | | 1375.6 | 0.785475429 |
| | | 990.9 | 0.774144717 |
| | | 840.6 | 0.877349512 |
| | | 1149.3 | 0.744888193 |

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|---|---|---|---|
| | | 224.2 | 0.814451383 |
| | | 1084.5 | 0.826002766 |
| A lipid bilayer along | IEA | 523.9 | 0.838709677 |
| | | 1825.5 | 0.847767735 |
| | | 397.6 | 0.767857143 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1713.7 | 0.881776274 |
| | | 929.1 | 0.778818211 |
| | | 1586.7 | 0.767378837 |
| | | 546.6 | 0.922612514 |
| | | 1011.8 | 0.880213481 |
| | | 1592 | 0.769723618 |
| | | 2015.9 | 0.857135771 |
| | | 1991 | 0.912807634 |
| | | 1304.5 | 0.879647374 |
| | | 1631.5 | 0.850260496 |
| | | 1130.3 | 0.937892595 |
| | | 471.3 | 0.862295778 |
| | | 2827.4 | 0.767100516 |
| The contents of a c | IBA; IBA; IBA | 1335.7 | 0.921389534 |
| A membrane-boun | IEA | 1975.1 | 0.934990633 |
| | | 663 | 0.745701357 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 462.1 | 0.81540792 |
| The component of t | IBA; IEA; IEA | 781.9 | 0.810845377 |
| | | 1205.8 | 0.761403218 |
| | | 332.5 | 0.851428571 |
| A membrane-boun | IEA | 846.1 | 0.815388252 |
| | | 1762.6 | 0.903097697 |
| A multisubunit prot | IEA; IBA; IEA | 1841.2 | 0.860254182 |
| | | 304.7 | 0.863800459 |
| | | 3301.1 | 0.878192118 |
| | | 201.3 | 0.777446597 |
| | | 1041.5 | 0.780028805 |
| | | 554.1 | 0.908500271 |

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| A lipid bilayer alon | IEA; IEA | 571.2 | 0.796218487 |
|  |  | 3653.4 | 0.843132425 |
|  |  | 847.3 | 0.740233683 |
| A membrane-boun | IEA | 1041.4 | 0.877472633 |
|  |  | 704.3 | 0.77594775 |
| A lipid bilayer alon | IEA; IEA | 765.3 | 0.79837972 |
|  |  | 872.8 | 0.752291476 |
| The double lipid bil | IBA | 1168 | 0.745719178 |
| A lipid bilayer alon | IEA; IEA | 1119.6 | 0.783404787 |
| A lipid bilayer alon | IEA; IEA | 589.4 | 0.817441466 |
|  |  | 737.9 | 0.803496409 |
|  |  | 1565.1 | 0.913871318 |
|  |  | 1875.8 | 0.915022924 |
|  |  | 1127.9 | 0.907172622 |
| A membrane-boun | IEA | 434.8 | 0.776448942 |
| The space external | IEA; IEA | 340.5 | 0.779148311 |
|  |  | 2270.3 | 0.892393076 |
|  |  | 1457 | 0.777419355 |
| The part of a cell e | IBA | 414.2 | 0.826170932 |
|  |  | 314.6 | 0.835346472 |
|  |  | 2752.7 | 0.926108911 |
|  |  | 930.1 | 0.763251263 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1175.1 | 0.929623011 |
| A membrane-boun | IEA | 538.1 | 0.799851329 |
|  |  | 2108.3 | 0.863634208 |
|  |  | 1049.5 | 0.911767508 |
|  |  | 838.3 | 0.760109746 |
|  |  | 953.5 | 0.916098584 |
|  |  | 1123.1 | 0.78158668 |
|  |  | 1899.9 | 0.892678562 |
| A lipid bilayer alon | IEA; IEA | 745.9 | 0.818742459 |
|  |  | 1037.8 | 0.889477741 |

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|---|---|---|---|
| A membrane-boun | IBA | 996.7 | 0.886525534 |
| | | 313.5 | 0.88261563 |
| A lipid bilayer alon | IEA; IEA | 417.8 | 0.758496888 |
| A membrane-boun | IBA | 401 | 0.771072319 |
| | | 3374.7 | 0.825940084 |
| | | 1175.1 | 0.851927496 |
| | | 480.8 | 0.77953411 |
| A membrane-boun | IEA | 731.5 | 0.85290499 |
| A ribonuclease com | IBA; IBA | 3618.3 | 0.849984799 |
| | | 373.9 | 0.848355175 |
| A lipid bilayer alon | IEA; IEA | 691.5 | 0.832682574 |
| A lipid bilayer alon | IEA; IEA; IEA | 716.6 | 0.855149316 |
| | | 721.2 | 0.880061009 |
| A membrane-boun | IEA | 902.9 | 0.806512349 |
| | | 1792.7 | 0.875216154 |
| | | 867.5 | 0.87815562 |
| | | 755 | 0.741986755 |
| The membrane surr | IEA; IEA; IEA | 369.2 | 0.764897075 |
| | | 474.5 | 0.87776607 |
| | | 284.5 | 0.87943761 |
| OBSOLETE. The bas | IEA | 1504.3 | 0.841720402 |
| | | 2187.7 | 0.842802944 |
| | | 367.7 | 0.765569758 |
| | | 952.1 | 0.936456255 |
| | | 1077.8 | 0.798663945 |
| A membrane-boun | IBA; IBA | 2255.8 | 0.834027839 |
| A transcription fact | IBA; IBA; IBA | 1185.3 | 0.875980764 |
| | | 3658.2 | 0.804439342 |
| | | 289.9 | 0.80200069 |
| | | 1360.3 | 0.841652577 |

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|---|---|---|---|
| A membrane-boun | IEA; IBA | 351.5 | 0.957894737 |
| | | 1098.2 | 0.795756693 |
| A membrane-boun | IEA; IEA; IEA | 2351.2 | 0.862665873 |
| | | 3167.4 | 0.768516765 |
| The irregular netwo | IEA | 848.6 | 0.798255951 |
| | | 649.3 | 0.796704143 |

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|---|---|---|---|
| A membrane-boun | IEA | 431.4 | 0.955493741 |
| | | 614.5 | 0.760618389 |
| A membrane-boun | IBA | 1153.3 | 0.844533079 |
| A membrane-boun | IBA; IBA | 1479.4 | 0.879005002 |
| | | 165.1 | 0.855239249 |
| A collection of mem | IBA | 1763.1 | 0.905280472 |
| | | 1890.6 | 0.771025071 |

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| A membrane-boun | IBA | 1554.6 | 0.882349157 |
| | | 887.8 | 0.789704888 |
| Punctate structures | IBA; IBA; IBA; IEA | 1162.7 | 0.912617184 |
| | | 1230 | 0.872520325 |
| The irregular netwo | IEA; IBA | 1178 | 0.780305603 |
| | | 1653.6 | 0.876572327 |

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|---|---|---|---|
| | | 1280.2 | 0.920559288 |

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|---|---|---|---|
| | | 579.3 | 0.862074918 |
| A chlorophyll-conta | IBA | 537.2 | 0.909717051 |

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|---|---|---|---|
| | | 1445.1 | 0.840564667 |
| | | 1686.9 | 0.875511293 |
| | | 539.7 | 0.790994997 |
| | | 985.9 | 0.886195354 |
| The contents of a c | IEA; IEA; IEA | 779.5 | 0.8944195 |
| A membrane-boun | IEA; IEA; IEA | 685.4 | 0.789174205 |
| | | 509.3 | 0.739642647 |
| | | 1887.3 | 0.882265671 |
| The component of a | IEA | 1301.4 | 0.908790533 |
| | | 1234.1 | 0.827080463 |
| | | 885.8 | 0.813389027 |
| A membrane-boun | IEA | 548.5 | 0.801276208 |
| A semiautonomous | IBA | 1510.1 | 0.952321038 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1762.6 | 0.890843073 |
| | | 1802.7 | 0.848837854 |
| | | 2301 | 0.760365059 |
| A small, dense bod | IBA | 431.1 | 0.888656924 |
| A membrane-boun | IBA | 2025.1 | 0.77764061 |
| | | 727.1 | 0.824370788 |
| | | 604.8 | 0.816468254 |
| A membrane-boun | IEA | 665.7 | 0.772420009 |
| The part of a cell er | IBA | 336.2 | 0.852171327 |
| A membrane-boun | IC | 765.3 | 0.82464393 |
| The membrane surr | IEA; IBA; IEA | 1031 | 0.887196896 |
| A lipid bilayer along | IBA; IEA | 2734.1 | 0.881021177 |
| | | 1606.5 | 0.867973856 |
| A membrane-boun | IEA | 715.1 | 0.87498252 |
| A ubiquitin ligase c | IBA | 577 | 0.859792028 |
| | | 333.4 | 0.807438512 |

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|---|---|---|---|
|  |  | 806.2 | 0.8721161 |
| Cyclin-dependent p | IBA; IBA; IBA | 663 | 0.906184012 |
|  |  | 2962.8 | 0.883724855 |
| The component of a | IEA | 1236.7 | 0.875555915 |
|  |  | 1871.4 | 0.897082398 |
|  |  | 1159.9 | 0.833864988 |
| The pigmented mer | IBA; IEA; IEA | 320.7 | 0.747115684 |
|  |  | 162.7 | 0.82052858 |
| A membrane-bound | IBA | 654.7 | 0.832595082 |
|  |  | 1563.1 | 0.869234214 |
| A lipid bilayer along | IEA; IEA | 364 | 0.79010989 |
|  |  | 704.3 | 0.87349141 |
| Punctate structures | IBA; IBA; IBA; IEA | 1295.9 | 0.886642488 |
| A membrane-bound | IEA; IEA | 707.9 | 0.80887131 |
|  |  | 468.1 | 0.750267037 |
| OBSOLETE. The bas | IEA; IEA; IEA | 750.9 | 0.917698761 |
| A membrane-bound | IEA; IEA; IEA; IEA; IE | 626.2 | 0.850846375 |
|  |  | 368.4 | 0.774701412 |
| A membrane-bound | IEA | 612.5 | 0.848979592 |
| A lipid bilayer along | IEA; IEA | 1007.9 | 0.908919536 |

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| A membrane-boun | IEA | 540.7 | 0.750878491 |
| The membrane surr | IBA | 462.8 | 0.805963699 |
| The part of a cell er | IBA | 342.8 | 0.796674446 |
| A vacuole to which | IBA; IBA; IBA; IEA; IB | 691.6 | 0.786292655 |
| A lipid bilayer alon | IEA; IEA | 1168.6 | 0.817987335 |
| | | 1241.5 | 0.926701571 |
| A membrane-boun | IBA; IBA; IEA | 2241.7 | 0.919391533 |
| The contents of a c | IBA | 1562.6 | 0.849609625 |
| A lipid bilayer alon | IEA; IEA | 525.8 | 0.881894256 |
| The component of | IEA | 1305.2 | 0.89488201 |
| | | 630.8 | 0.863665187 |
| A membrane-boun | IEA | 548.9 | 0.764620149 |
| A membrane-boun | IBA | 545.9 | 0.773951273 |
| A lipid bilayer alon | IEA; IEA | 183.8 | 0.774755169 |
| | | 472.1 | 0.936454141 |
| | | 922.8 | 0.809817945 |
| | | 169.3 | 0.815121087 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1665 | 0.87957958 |
| | | 326.3 | 0.831749923 |
| | | 502.9 | 0.818452973 |
| The part of the cyto | IBA | 814.2 | 0.861581921 |
| A lipid bilayer alon | IEA; IEA | 307.5 | 0.769105691 |
| A lipid bilayer alon | IEA; IEA | 450.4 | 0.767761989 |
| | | 308.6 | 0.865521711 |
| A membrane-boun | IEA | 797.6 | 0.76391675 |
| | | 1413.3 | 0.758862237 |

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|---|---|---|---|
| A membrane-boun | IEA | 1571 | 0.887205602 |
| | | 758.5 | 0.878444298 |
| A membrane-boun | IEA; IEA | 772.6 | 0.901113125 |
| A membrane-boun | IBA; IBA | 1235.1 | 0.825601166 |

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|---|---|---|---|
| | | 2658.8 | 0.917218294 |
| The array of microt | IEA; IEA; IBA; IBA | 942.3 | 0.813222965 |
| | | 441 | 0.741723356 |
| A chlorophyll-cont | IEA; IEA; IEA; IEA; IE | 578.9 | 0.90171014 |
| | | 524.5 | 0.799809342 |

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|---|---|---|---|
| A membrane-boun | IBA | 1003 | 0.961814556 |
| | | 879.4 | 0.762565385 |
| | | 1113.3 | 0.902901284 |
| | | 1130 | 0.822566372 |
| A semiautonomous | IBA | 171.9 | 0.909831297 |
| A lipid bilayer alon | IEA; IEA | 887.4 | 0.890917286 |
| A lipid bilayer alon | IEA; IEA | 1940 | 0.884896907 |

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|---|---|---|---|
| The irregular netwo | IEA; IEA | 792.1 | 0.848125237 |
| A membrane-boun | IEA | 1101.8 | 0.818569613 |
| The contents of a c | IBA | 3049.3 | 0.785885285 |
| | | 506.9 | 0.786348392 |
| | | 806 | 0.779652605 |
| A lipid bilayer alon | IEA; IEA | 1234.8 | 0.799643667 |
| | | 949.4 | 0.922372024 |
| | | 1008.5 | 0.865245414 |
| The membrane sur | IBA; IBA | 402.4 | 0.830765408 |
| A structure found | IBA | 1803.4 | 0.791338583 |
| | | 875.5 | 0.775671045 |
| | | 285.9 | 0.783140958 |
| A membrane-boun | IBA | 420.8 | 0.876188213 |
| | | 1232 | 0.913798701 |
| | | 1164.1 | 0.90971566 |
| Cyclin-dependent | IBA; IBA; IBA | 761.6 | 0.855173319 |
| A membrane-boun | IEA | 739.9 | 0.76659008 |
| | | 1051.9 | 0.933738949 |
| A membrane-boun | IEA | 982.8 | 0.757529508 |
| A lipid bilayer alon | IEA; IEA | 470.5 | 0.931987248 |
| | | 520.2 | 0.772202999 |
| | | 1297.8 | 0.855139467 |
| | | 1185.6 | 0.896676788 |
| A chlorophyll-cont | IBA | 827.4 | 0.805172831 |

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| A membrane-boun | IEA; IEA | 1143.2 | 0.841060182 |
| | | 3995.6 | 0.90059065 |
| | | 278.3 | 0.896514553 |
| A membrane-boun | IEA | 3008.7 | 0.801774853 |
| | | 787.5 | 0.89231746 |
| | | 742.9 | 0.946156952 |
| A membrane-boun | IBA | 861 | 0.775842044 |
| | | 720.5 | 0.758917418 |
| | | 350.2 | 0.828669332 |
| A membrane-boun | IEA | 1375.1 | 0.935568322 |
| | | 1795.6 | 0.874693696 |
| A transcription fact | IEA | 1412.3 | 0.787863768 |
| | | 1321 | 0.743679031 |
| | | 2182.8 | 0.749633498 |
| | | 906.2 | 0.763738689 |
| | | 1845.7 | 0.811236929 |
| | | 510.7 | 0.753084002 |
| A protein complex t | IEA; IEA | 1448.3 | 0.864185597 |
| A membrane-boun | IEA | 1025.9 | 0.789063262 |
| | | 726.8 | 0.804485416 |
| | | 1816.2 | 0.884814448 |
| The contents of a c | IBA; IBA; IBA | 628.2 | 0.753263292 |
| A membrane-boun | IEA | 1686.9 | 0.861046891 |
| | | 399.6 | 0.817317317 |
| | | 955.3 | 0.902334345 |
| The irregular netwo | IEA; IBA | 726.9 | 0.935066722 |
| | | 989.8 | 0.85572843 |
| | | 884.3 | 0.802555694 |
| | | 754.9 | 0.753344814 |
| | | 883.7 | 0.745728188 |
| | | 958.3 | 0.902640092 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 389.9 | 0.819184406 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA; IEA | 1376 | 0.822238372 |
| | | 1134 | 0.917283951 |
| | | 1382.7 | 0.881536125 |
| The membrane surr | IBA | 1183.9 | 0.851169862 |
| | | 633.2 | 0.900821226 |
| | | 807.6 | 0.942545815 |
| | | 333.9 | 0.780173705 |
| | | 974.5 | 0.830682401 |
| | | 2360 | 0.772923729 |
| | | 1425.5 | 0.844124868 |
| The lipid bilayer sur | IBA; IEA; IEA; IEA | 1008.3 | 0.942576614 |
| The membrane surr | IEA; IBA; IEA; IEA | 1066.7 | 0.943095528 |
| A membrane-boun | IBA | 2854 | 0.779957954 |
| A membrane-boun | IEA; IBA | 902.8 | 0.896322552 |
| | | 2454 | 0.901018745 |
| A lipid bilayer alon | IEA; IEA | 741.8 | 0.808978161 |
| A membrane-boun | IBA | 1395.8 | 0.943473277 |
| | | 2042.9 | 0.785501003 |
| | | 2260.5 | 0.785312984 |
| That part of a multi | IBA; IBA; IEA; IEA | 876.1 | 0.903435681 |
| | | 183.2 | 0.829694323 |
| | | 1840.7 | 0.815341989 |
| | | 615.7 | 0.75978561 |

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|---|---|---|---|
| A lipid bilayer alon | IBA; IEA | 1149.1 | 0.835175355 |
| A membrane-boun | IEA | 459.8 | 0.873423227 |
|  |  | 756.3 | 0.780642602 |
|  |  | 499 | 0.764128257 |
|  |  | 805.5 | 0.816139044 |
| The membrane sur | IBA | 1188.9 | 0.905963496 |
| The lipid bilayer su | IEA; IEA | 1257.5 | 0.911093439 |
|  |  | 4924.8 | 0.8576795 |
| A chlorophyll-cont | IDA | 323.6 | 0.788936959 |
|  |  | 644.6 | 0.927086565 |
| A membrane-boun | IEA | 816.9 | 0.764965112 |
| A SAGA-type histo | IEA | 708.4 | 0.759881423 |
| A membrane-boun | IC | 547.8 | 0.792807594 |
|  |  | 1312.8 | 0.821297989 |
|  |  | 740.7 | 0.900094505 |
|  |  | 2996.5 | 0.750208577 |
| The membrane sur | IBA; IEA; IEA | 617.8 | 0.850922629 |
| A lipid bilayer alon | IEA; IEA | 921.3 | 0.750569847 |
|  |  | 1855.5 | 0.795149555 |
|  |  | 892.6 | 0.822764956 |
| A membrane-boun | IBA; IBA | 1673.4 | 0.883291502 |
|  |  | 1259.2 | 0.764850699 |
|  |  | 155.2 | 0.742912371 |
|  |  | 411.3 | 0.74641381 |

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|---|---|---|---|
| | | 1146.2 | 0.900628163 |
| Any member of a fa | IBA | 638.4 | 0.807174185 |
| | | 2545.8 | 0.781011863 |
| A small organelle e | IEA; IEA; IEA; IBA | 942.3 | 0.807916799 |
| A membrane-boun | IEA; IEA; IEA | 1686 | 0.767615658 |
| A membrane-boun | IBA | 969.9 | 0.756160429 |
| A membrane-boun | IEA | 758.4 | 0.781777426 |
| | | 306.3 | 0.83610839 |
| A membrane-boun | IEA | 859.7 | 0.758171455 |
| A membrane-boun | IEA | 861.4 | 0.915022057 |
| The irregular netwo | IBA; IBA; IEA; IEA | 567 | 0.838977072 |
| | | 1186.6 | 0.890359009 |
| | | 350.7 | 0.863986313 |
| | | 1554.2 | 0.891005019 |
| A membrane-boun | IBA | 865.4 | 0.824243125 |
| A membrane-boun | IBA | 807.7 | 0.861087037 |
| | | 318.8 | 0.76944793 |
| The contents of a c | IEA; IEA; IEA | 751.4 | 0.850412563 |
| | | 488.8 | 0.796644845 |
| The membrane surr | IBA; IEA; IEA; IBA | 365.7 | 0.841673503 |
| | | 869.7 | 0.771760377 |
| A membrane-boun | IEA; IEA | 1934.1 | 0.784447547 |
| | | 2401 | 0.801082882 |
| A semiautonomous | IBA | 1159.5 | 0.843467012 |

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|---|---|---|---|
| | | 771.8 | 0.923037056 |
| | | 1103.1 | 0.805094733 |
| A membrane-boun | IBA | 2178.5 | 0.8145972 |
| | | 1150.9 | 0.762012338 |
| | | 300.8 | 0.814494681 |
| The component of | IEA | 1203.3 | 0.927948143 |
| | | 1203 | 0.856109726 |
| A membrane-boun | IEA | 1112.8 | 0.887041697 |
| A chlorophyll-cont | IBA | 617 | 0.790599676 |
| | | 1399.2 | 0.918524871 |
| | | 694.8 | 0.818221071 |
| A membrane-boun | IEA | 1550.9 | 0.925978464 |
| The pigmented me | IEA; IEA; IEA; IEA | 330.8 | 0.801390568 |
| | | 706.6 | 0.832437022 |
| | | 966.2 | 0.83409232 |
| A protein complex | IBA; IEA | 1118.3 | 0.79862291 |
| | | 474 | 0.808860759 |
| A membrane-boun | IEA | 1537 | 0.847560182 |
| | | 798.6 | 0.7774856 |
| A membrane-boun | IEA; IEA; IEA | 1462.7 | 0.742462569 |
| | | 2892 | 0.797925311 |
| | | 916.2 | 0.927199301 |
| | | 1417.3 | 0.884992592 |
| | | 988.9 | 0.784710284 |
| A lipid bilayer alon | IEA; IEA | 898.7 | 0.890508512 |

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|---|---|---|---|
| A membrane-boun | IBA | 536.5 | 0.79832246 |
|  |  | 363.3 | 0.815579411 |
| A membrane-boun | IEA | 707.5 | 0.869399293 |
|  |  | 1333.4 | 0.889905505 |
|  |  | 1542.1 | 0.88872317 |
| A lipid bilayer along | IEA; IEA | 1272.2 | 0.766781953 |
|  |  | 1860.4 | 0.848903462 |
| A membrane-boun | IC | 593.7 | 0.752905508 |
| A membrane-boun | IC | 798.9 | 0.755664038 |
|  |  | 1158.3 | 0.846326513 |
| A lipid bilayer along | IEA; IEA | 527.1 | 0.833807627 |
|  |  | 828.8 | 0.934483591 |
|  |  | 391.2 | 0.93890593 |
|  |  | 985.1 | 0.949345244 |
|  |  | 1762.5 | 0.808453901 |
|  |  | 942.2 | 0.912226703 |
|  |  | 958 | 0.872755741 |
| A semiautonomous | IBA; IEA | 563.1 | 0.845853312 |

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| A membrane-boun | IEA | 1520.6 | 0.779429173 |
| A lipid bilayer alon | IEA; IEA | 215.7 | 0.83310153 |
| A lipid bilayer alon | IEA; IEA | 736 | 0.907201087 |
| Any of the long, ge | IEA | 1849 | 0.9203894 |
| | | 804.5 | 0.902423866 |
| A chlorophyll-cont | IBA | 526.6 | 0.803076339 |
| | | 814.9 | 0.955331943 |
| | | 240.9 | 0.798671648 |
| A membrane-boun | IEA | 1306.7 | 0.908089079 |
| OBSOLETE. The bas | IEA; IEA | 951.9 | 0.860804706 |
| | | 926.3 | 0.8858901 |
| A lipid bilayer alon | IEA; IEA | 373.5 | 0.831593039 |
| The outer, i.e. cyto | IBA; IEA; IEA | 1298.3 | 0.842486328 |
| | | 385.4 | 0.840425532 |
| | | 528.5 | 0.916367077 |
| | | 791.8 | 0.748168729 |
| A membrane-boun | IEA | 1387.7 | 0.855732507 |
| | | 911.8 | 0.861153762 |
| The lipid bilayer su | IEA; IEA | 1084.7 | 0.919332534 |
| A membrane-boun | IEA | 1925.9 | 0.820655278 |
| | | 332.5 | 0.767518797 |
| A membrane-boun | IEA | 1399.2 | 0.93567753 |
| | | 1074.1 | 0.80234615 |
| The membrane sur | IBA; IBA; IEA; IEA; IB | 483.1 | 0.939557028 |
| OBSOLETE. The bas | IEA | 1334.8 | 0.770976925 |
| | | 1285.6 | 0.77520224 |
| | | 846.8 | 0.7485829 |
| A membrane-boun | IBA | 2344.2 | 0.78163126 |
| | | 2223.4 | 0.900557704 |
| Organized structur | IBA | 984.5 | 0.853224987 |

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|---|---|---|---|
| A small lytic vacuol | IEA; IEA; IEA | 568.3 | 0.895477741 |
| | | 817.6 | 0.965019569 |
| | | 1050.1 | 0.758403962 |
| | | 334.6 | 0.77286312 |
| | | 1421.5 | 0.844952515 |
| A membrane-boun | IBA | 1305.7 | 0.83441832 |
| A lipid bilayer alon | IEA; IEA | 369.1 | 0.781630994 |
| The contents of a c | IBA; IBA | 2125.8 | 0.830463825 |
| A membrane-boun | IBA | 337.9 | 0.746374667 |
| A semiautonomous | IBA | 1990 | 0.894422111 |
| The lipid bilayer su | IBA; IEA | 901.3 | 0.773771219 |
| A membrane-boun | IBA | 364.8 | 0.809758772 |
| A membrane-boun | IBA | 608.9 | 0.861389391 |
| The component of | IEA | 1054 | 0.873908918 |
| | | 255.9 | 0.796795623 |
| | | 404.4 | 0.827151335 |
| | | 1101.4 | 0.875885237 |
| The membrane sur | IEA; IEA; IEA | 1258.2 | 0.876251788 |
| | | 553.7 | 0.827885136 |
| | | 652 | 0.903220859 |
| A semiautonomous | IBA | 1352.6 | 0.901892651 |
| | | 1507.3 | 0.889139521 |
| A lipid bilayer alon | IEA; IEA | 432.4 | 0.848519889 |
| A macromolecular | IBA | 789.8 | 0.803874399 |
| A small, dense bod | IEA; IBA | 956.2 | 0.928571429 |
| | | 342.3 | 0.805725971 |
| The space external | IEA; IEA | 710 | 0.920985915 |
| | | 2725.2 | 0.820490239 |
| | | 2077.5 | 0.757545126 |
| | | 961.2 | 0.799521432 |
| The contents of a c | IBA | 888.9 | 0.871751603 |

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|---|---|---|---|
| A membrane-boun | IBA | 907.9 | 0.770569446 |
| A lipid bilayer along | IEA; IEA | 1398.7 | 0.890469722 |
| A membrane-boun | IEA; IEA; IBA | 509.9 | 0.815061777 |
|  |  | 4067.1 | 0.8043815 |
| A lipid bilayer along | IEA; IEA | 742.2 | 0.895311237 |
| A lipid bilayer along | IEA; IEA | 420.8 | 0.88141635 |
|  |  | 1165.3 | 0.853943191 |
|  |  | 1225.9 | 0.843054083 |
|  |  | 1327.3 | 0.914337377 |
| The contents of a c | IEA | 711 | 0.91209564 |
|  |  | 393.9 | 0.871541 |
| A lipid bilayer along | IEA; IEA | 735.5 | 0.886879674 |
|  |  | 330 | 0.806363636 |
| A lipid bilayer along | IEA; IEA | 1659.4 | 0.869772207 |
| A ubiquitin ligase c | IBA | 1262.2 | 0.900966566 |
| A membrane-boun | IC | 351.2 | 0.920842825 |
| A membrane-boun | IEA; IEA | 765 | 0.910065359 |
|  |  | 476.4 | 0.801217464 |
|  |  | 422.6 | 0.743729295 |
| A small organelle e | IEA; IEA; IEA; IEA; IB | 1013.3 | 0.779038784 |
| The lipid bilayer su | IEA; IEA | 1179.2 | 0.901797829 |
|  |  | 582 | 0.863745704 |
|  |  | 1303.6 | 0.884780608 |

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|---|---|---|---|
| | | 466.4 | 0.869425386 |
| | | 4175.1 | 0.882493832 |
| A membrane-boun | IC | 548.1 | 0.812260536 |
| A circular DNA mol | IEA; IEA | 733.1 | 0.909971355 |
| A semiautonomous | IBA | 1136.4 | 0.914466737 |
| A membrane-boun | IEA | 1664.4 | 0.904349916 |
| | | 2136.5 | 0.773742102 |
| The space external | IBA | 643.8 | 0.826809568 |
| | | 380.4 | 0.773659306 |
| A lipid bilayer along | IEA; IEA | 937.9 | 0.822475744 |
| | | 1675.8 | 0.827366034 |
| | | 182 | 0.748901099 |
| A membrane-boun | IEA; IBA | 2503 | 0.843827407 |
| The part of the cyto | IBA; IEA; IEA | 800.4 | 0.943278361 |
| A lipid bilayer along | IEA; IEA | 686.5 | 0.770866715 |
| A lipid bilayer along | IEA; IEA | 384.5 | 0.891547464 |
| | | 224 | 0.865178571 |
| | | 1653.7 | 0.784362339 |
| A membrane-boun | IBA | 841.3 | 0.875193153 |
| The part of the cyto | IBA | 544.9 | 0.7502294 |

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|---|---|---|---|
| A chlorophyll-conta | IEA; RCA | 1209.4 | 0.875640814 |
| | | 869.7 | 0.917327814 |
| A membrane-boun | IEA | 289.3 | 0.774628413 |
| A vacuole to which | IBA | 1689.5 | 0.837585084 |
| The membrane sur | IEA | 922.2 | 0.868575146 |
| A semiautonomous | IBA | 1287.3 | 0.899712577 |
| | | 740.5 | 0.95800135 |
| A membrane-boun | IEA; IBA | 2448.8 | 0.888884352 |
| A membrane-boun | IBA | 2020.1 | 0.85386862 |
| A membrane-boun | IEA | 819.1 | 0.762178 |
| The space external | IBA | 922.7 | 0.853256747 |
| The lipid bilayer su | IEA; IEA; IBA; IBA; IE | 1936 | 0.952737603 |
| | | 839.1 | 0.751877011 |
| A dense aggregatio | IBA | 923.5 | 0.773253925 |
| A membrane-boun | IBA | 571.5 | 0.920734908 |
| | | 491.4 | 0.811965812 |
| | | 528.5 | 0.770293283 |
| | | 1553.4 | 0.854577057 |
| A protein complex | IEA | 949.5 | 0.890258031 |

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|---|---|---|---|
| | | 344.5 | 0.848476052 |
| | | 997.9 | 0.899488927 |
| | | 963.6 | 0.905562474 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1130.1 | 0.860100876 |
| A chlorophyll-cont | IBA | 704.9 | 0.797134345 |
| | | 948.6 | 0.911132195 |
| | | 340.9 | 0.914344383 |
| | | 675.4 | 0.885105123 |
| Any member of a fa | IEA; IEA; IBA; IEA; IE | 1664.7 | 0.755151078 |
| A protein complex | IEA; IEA; IEA; IBA | 975.6 | 0.835280853 |
| A membrane-boun | IEA | 623.7 | 0.74987975 |
| A membrane-boun | IEA | 567.9 | 0.754182074 |
| | | 536.8 | 0.774962742 |
| | | 1732.6 | 0.858882604 |
| | | 862.2 | 0.930410578 |
| The contents of a c | IBA; IBA | 2226.3 | 0.762071599 |
| A chromosome that | IEA; IEA; IBA | 1338.9 | 0.7738442 |
| A membrane-boun | IEA | 1048 | 0.779389313 |
| | | 879.1 | 0.944033671 |

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|---|---|---|---|
| A membrane-bound | IEA | 1885.9 | 0.917811125 |
|  |  | 370.9 | 0.804259908 |
|  |  | 668.7 | 0.811873785 |
| A membrane-bound | IEA | 1437.4 | 0.900793099 |
|  |  | 1582.1 | 0.789520258 |
|  |  | 959.5 | 0.924231371 |
|  |  | 926.2 | 0.888145109 |
| The part of the cyto | IEA | 1541.6 | 0.813894655 |
|  |  | 601.2 | 0.830339321 |
| A membrane-bound | IEA; IEA | 1775.5 | 0.809180513 |
| A part of a cellular | IEA | 1837.4 | 0.848808098 |
|  |  | 838.9 | 0.951960901 |
|  |  | 1484.1 | 0.7928711 |
| A semiautonomous | IBA; IBA; IBA | 825.7 | 0.790601914 |
| A membrane-bound | IEA | 1104.9 | 0.793555978 |
| Any of the long, ge | IEA; IEA; IEA | 1223.5 | 0.749080507 |
|  |  | 1100.1 | 0.873284247 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1410.9 | 0.900276419 |
| A membrane-boun | IEA | 1454.5 | 0.861739429 |
| OBSOLETE. The bas | IEA; IEA | 1583.9 | 0.899236063 |
| | | 1112 | 0.867176259 |
| A protein complex | IBA; IEA; IBA | 2693.7 | 0.816943238 |
| | | 269.8 | 0.800222387 |
| | | 308.8 | 0.75615285 |
| A transcription fact | IBA | 384.8 | 0.784823285 |
| A membrane-boun | IEA; IEA; IEA | 1014.7 | 0.744062284 |
| A membrane-boun | IBA | 483.5 | 0.856256463 |
| | | 1947 | 0.740832049 |
| | | 218.6 | 0.752058554 |
| | | 1100.1 | 0.746477593 |
| The lipid bilayer su | IBA | 3544.2 | 0.849020936 |
| | | 536.4 | 0.915175242 |
| | | 1328.1 | 0.817182441 |
| | | 817.5 | 0.889785933 |
| The membrane sur | IEA; IEA; IEA | 841.3 | 0.836919054 |
| | | 422.1 | 0.831319593 |

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|---|---|---|---|
| A membrane-boun | IEA | 486.9 | 0.828301499 |
| | | 1866.6 | 0.794064074 |
| | | 2238.6 | 0.938488341 |
| A membrane-boun | IEA | 2173.5 | 0.923993559 |
| | | 593 | 0.762563238 |
| | | 586.4 | 0.747100955 |
| | | 1569.2 | 0.91887586 |
| | | 161.8 | 0.783065513 |
| | | 191.9 | 0.781136008 |
| The part of the cyto | IBA | 976.3 | 0.938953191 |
| A lipid bilayer along | IEA; IEA | 654.8 | 0.802687844 |
| A membrane-boun | IEA | 949 | 0.763540569 |
| | | 358.4 | 0.748046875 |
| | | 896 | 0.742522321 |
| The contents of a c | IBA | 641.6 | 0.967736908 |
| A protein complex t | IEA; IEA; IEA | 1098.5 | 0.867273555 |
| | | 275.1 | 0.897491821 |
| | | 1897 | 0.754770691 |
| | | 271.1 | 0.854297307 |
| | | 3616.1 | 0.79696358 |
| | | 1246 | 0.769582665 |
| | | 953.2 | 0.770981956 |

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|---|---|---|---|
| | | 307.6 | 0.796163849 |
| The membrane surr | IBA; IEA; IEA | 789.1 | 0.92206311 |
| A lipid bilayer along | IEA; IEA | 403.1 | 0.851649715 |
| A membrane-boun | IBA | 308.4 | 0.890077821 |
| | | 1219.2 | 0.951935696 |
| The contents of a c | IEA; IBA; IEA; IBA | 947.4 | 0.805467596 |
| A heterotrimeric tra | IEA; IEA | 3949 | 0.820764751 |
| A semiautonomous | IBA | 1358 | 0.877908689 |
| A protein complex | IBA; IEA | 935 | 0.819572193 |
| | | 958.6 | 0.85332777 |
| | | 951.9 | 0.825506881 |
| | | 644.3 | 0.80645662 |
| A semiautonomous | IEA; IEA | 814.7 | 0.841291273 |
| A membrane-boun | IBA; IBA; IBA | 1796.6 | 0.950350662 |
| A membrane-boun | IBA | 1184.9 | 0.837623428 |
| A lipid bilayer along | IEA; IEA | 681.8 | 0.875183338 |
| A membrane-boun | IEA | 2147.5 | 0.890710128 |
| A chlorophyll-conta | IBA; IEA | 340.6 | 0.795361127 |
| A membrane-boun | IEA; IEA; IEA | 1931.6 | 0.909763926 |
| | | 1370.4 | 0.875875657 |
| | | 862.7 | 0.935551177 |
| A membrane-boun | IEA | 923.8 | 0.911669192 |
| The lipid bilayer su | IBA; IEA; IEA; IEA | 994.8 | 0.884398874 |
| | | 1364.8 | 0.751978312 |
| | | 1802.8 | 0.76292434 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA | 962.8 | 0.914312422 |
| A membrane-boun | IBA | 577 | 0.83830156 |
| A membrane-boun | IC | 934.9 | 0.835383463 |
| | | 668.9 | 0.922858424 |
| | | 347.4 | 0.751007484 |
| A membrane-boun | IBA; IBA | 453.7 | 0.855411065 |
| | | 1131.1 | 0.757404297 |
| A membrane-boun | IEA; IBA; IEA | 1784.3 | 0.746735414 |
| A membrane-boun | IBA | 457.4 | 0.800612156 |
| | | 598.8 | 0.7750501 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 558.3 | 0.831452624 |
| | | 430.2 | 0.859600186 |
| | | 1490.6 | 0.858647524 |
| | | 245.3 | 0.792906645 |
| A membrane-boun | IBA | 716.3 | 0.779561636 |

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|---|---|---|---|
|  |  | 571.7 | 0.786426447 |
|  |  | 512.2 | 0.766497462 |
| A membrane-boun | IEA; IEA; IEA | 1083.7 | 0.91058411 |
| The irregular netwo | IEA | 629.2 | 0.879688493 |
| A membrane-boun | IEA | 946.3 | 0.808094685 |
|  |  | 1185 | 0.766244726 |
| A membrane-boun | IBA; IBA; IEA | 1784 | 0.79573991 |
|  |  | 551.6 | 0.802030457 |
|  |  | 1213.5 | 0.764565307 |
| A membrane-boun | IEA; IEA | 439.5 | 0.800682594 |
|  |  | 1244.3 | 0.804709475 |
|  |  | 2416.8 | 0.755544522 |
|  |  | 527.3 | 0.827233074 |
| A chlorophyll-conta | IBA; IEA; IEA | 553.4 | 0.949765089 |
| A membrane-boun | IBA | 620.9 | 0.814140763 |
|  |  | 1933.5 | 0.751383501 |

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|---|---|---|---|
| A membrane-bound | IEA | 622.7 | 0.784005139 |
| A membrane-bound | IBA; IBA; IEA; IEA | 610.9 | 0.824521198 |
| The component of a | IEA | 281.4 | 0.823738451 |
| A membrane-bound | IEA; IEA | 1410.5 | 0.873945409 |
| Organized structure | IEA | 2451.9 | 0.811207635 |
|  |  | 1257 | 0.780111376 |
| A lipid bilayer along | IEA | 1092.2 | 0.892327413 |
| A lipid bilayer along | IEA; IEA | 968.9 | 0.839818351 |
| The part of the cyto | IBA | 1184.5 | 0.835120304 |
|  |  | 505.9 | 0.74382289 |
|  |  | 1591.2 | 0.80260181 |
|  |  | 198.5 | 0.808060453 |
|  |  | 1588.9 | 0.827553653 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1274.4 | 0.914312618 |
|  |  | 966.7 | 0.817730423 |
|  |  | 809.8 | 0.896147197 |
| A chlorophyll-conta | IBA; IEA; IEA | 216.7 | 0.772958006 |
|  |  | 1395.7 | 0.889876048 |
|  |  | 635.6 | 0.807268722 |
| The component of a | IBA | 6915.3 | 0.827874423 |

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|---|---|---|---|
| | | 975.1 | 0.90185622 |
| | | 1581.9 | 0.925785448 |
| The irregular netwo | IEA; IEA; IEA; IEA | 599.4 | 0.847681014 |
| A membrane-bound | IEA; IEA | 520.7 | 0.883042059 |
| The lipid bilayer su | IBA; IEA; IEA; IEA | 1244.5 | 0.779268783 |
| | | 534.8 | 0.773560209 |
| The end of a linear | IEA; IEA; IEA | 2235.6 | 0.755233494 |
| | | 1449 | 0.795652174 |
| A membrane-bound | IBA; IBA | 1381.7 | 0.898747919 |
| | | 784.4 | 0.826746558 |
| A membrane-bound | IEA; IEA | 1554.7 | 0.832958127 |
| A membrane-bound | IEA | 481.9 | 0.814276821 |
| A membrane-bound | IEA | 946 | 0.861099366 |
| The membrane surr | IEA; IBA; IEA | 2051.9 | 0.797456016 |
| A preribosomal con | IBA; IEA | 1233.1 | 0.815343443 |
| | | 3191.3 | 0.812646884 |
| | | 566 | 0.88869258 |
| | | 710.8 | 0.877743388 |
| A membrane-bound | IEA | 679.9 | 0.811001618 |
| The space external | IEA | 340.3 | 0.83161916 |
| | | 1780.2 | 0.788787777 |
| | | 651.4 | 0.855848941 |
| | | 335.7 | 0.789395293 |
| | | 414.2 | 0.850072429 |
| | | 920.6 | 0.855311753 |

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|---|---|---|---|
| | | 308.6 | 0.781918341 |
| | | 2860.2 | 0.90969163 |
| A lipid bilayer along | IEA; IEA | 477.1 | 0.807797108 |
| | | 424.4 | 0.908105561 |
| | | 431.2 | 0.877087199 |
| | | 769.5 | 0.877582846 |
| | | 660.4 | 0.816020594 |
| A lipid bilayer along | IEA; IEA | 511.1 | 0.787321464 |
| | | 154.3 | 0.813998704 |
| A lipid bilayer along | IEA; IEA | 288.3 | 0.766562608 |
| | | 1469.8 | 0.755681045 |
| | | 1647 | 0.951973285 |
| | | 1061.1 | 0.850815192 |
| The lipid bilayer sur | IEA; IEA | 1385.5 | 0.79054493 |
| A membrane-bound | IEA | 2485 | 0.787645875 |
| A protein complex t | IEA; IEA; IEA | 462.4 | 0.836721453 |
| A lipid bilayer along | IEA; IEA | 402.5 | 0.868571429 |
| | | 378.7 | 0.770794824 |
| A membrane-bound | IEA; IEA; IEA | 1623.4 | 0.805901195 |
| A semiautonomous | IBA; IEA; IEA | 1149.1 | 0.942824819 |
| | | 1016.6 | 0.880483966 |
| A membrane-bound | IBA; IBA | 1563.7 | 0.833471894 |
| A membrane-bound | IEA | 2137.4 | 0.947646674 |
| A lipid bilayer along | IEA; IEA | 792.1 | 0.836384295 |
| A semiautonomous | IBA | 221.3 | 0.85539991 |
| A membrane-bound | IEA | 705 | 0.831205674 |
| The part of the cyto | IBA | 739.2 | 0.901515152 |
| A membrane-bound | IEA | 488.9 | 0.78686848 |

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|---|---|---|---|
| | | 578.1 | 0.811105345 |
| A multisubunit prot | IBA | 1095.4 | 0.798521088 |
| | | 1513.2 | 0.845096484 |
| A semiautonomous | IBA | 917.2 | 0.925861317 |
| A membrane-boun | IBA | 838.1 | 0.824961222 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 498.5 | 0.83671013 |
| | | 648.5 | 0.920123362 |
| | | 951.3 | 0.839482813 |
| | | 529.3 | 0.751558662 |
| | | 1927.3 | 0.807139522 |
| | | 190.7 | 0.912427897 |
| A membrane-boun | IDA | 2401.9 | 0.778925018 |
| A membrane-boun | IEA | 697.7 | 0.818689981 |
| A ubiquitin ligase c | IBA | 677.6 | 0.83677686 |
| A lipid bilayer along | IEA; IEA | 440.3 | 0.859641154 |
| | | 857.3 | 0.813134259 |
| | | 1869.3 | 0.913336543 |
| | | 1629 | 0.783425414 |
| A membrane-boun | IBA; IBA | 641.7 | 0.917095216 |
| | | 1200.9 | 0.852693813 |
| | | 818.1 | 0.82019313 |
| | | 1346.1 | 0.750612882 |
| | | 962.5 | 0.768415584 |

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|---|---|---|---|
| The part of the cyto | IBA; IBA; IEA; IBA | 1053.1 | 0.793656823 |
| The membrane surr | IBA; IBA | 376.5 | 0.833466135 |
| A vacuole to which | IBA; IBA; IBA; IBA | 232.8 | 0.851804124 |
| The region of a chr | IEA; IEA | 586.3 | 0.76343169 |
| | | 595.2 | 0.771337366 |
| The space external | IEA; IEA | 358 | 0.812290503 |
| | | 199.5 | 0.842105263 |
| A membrane-boun | IEA | 404 | 0.767821782 |
| | | 1498.7 | 0.779809168 |
| | | 272 | 0.753676471 |
| A membrane-boun | IC | 512.6 | 0.835544284 |
| | | 457.9 | 0.944529373 |
| | | 955.4 | 0.82771614 |
| A membrane-boun | IEA | 935.3 | 0.772051748 |
| | | 379.6 | 0.887249737 |
| The contents of a c | IEA; IBA; IEA; IBA | 999.7 | 0.868260478 |
| | | 1321.3 | 0.904336638 |
| A lipid bilayer along | IEA; IEA | 266.5 | 0.742213884 |
| A class of nuclear b | IEA; IEA | 1203.3 | 0.837696335 |
| A semiautonomous | IBA; IEA | 418.1 | 0.864864865 |
| A membrane-boun | IBA | 1868.3 | 0.818123428 |
| The irregular netwo | IEA; IEA; IEA; IEA; IB | 1903.5 | 0.828001051 |
| | | 960.7 | 0.825543874 |
| | | 918.8 | 0.922398781 |
| The rigid or semi-ri | IEA; IEA; IEA | 1242.5 | 0.915814889 |
| | | 2086.9 | 0.923714601 |
| | | 1711.4 | 0.858303144 |
| A membrane-boun | IC | 731.6 | 0.775970476 |

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|---|---|---|---|
| The lipid bilayer su | IEA; IEA; IBA; IBA; IE | 2002.8 | 0.906281206 |
| A membrane-boun | IEA | 2027.3 | 0.865387461 |
| A chlorophyll-conta | IEA; IEA | 723.8 | 0.899557889 |
| | | 784.7 | 0.908245189 |
| A lipid bilayer alon | IEA; IEA | 1381.6 | 0.87992183 |
| A lipid bilayer alon | IEA; IEA | 544.1 | 0.917110825 |
| A membrane-boun | IEA | 878.2 | 0.854361193 |
| A semiautonomous | IBA; IEA | 551.5 | 0.83463282 |
| A membrane-boun | IEA | 2012.8 | 0.881955485 |
| | | 1032.8 | 0.930189775 |
| The region of a chr | IEA; IEA; IEA; IEA | 847.9 | 0.862247907 |
| | | 1456.5 | 0.847579815 |
| | | 490.1 | 0.843909406 |
| | | 519.1 | 0.919476016 |
| | | 633.4 | 0.868171771 |
| | | 482.2 | 0.751970137 |
| | | 958.7 | 0.80671743 |
| A semiautonomous | IBA | 1714.8 | 0.943958479 |
| The space external | IEA; IEA | 310.7 | 0.878982942 |
| A lipid bilayer alon | IEA; IEA | 656.3 | 0.905226268 |
| | | 293.1 | 0.840327533 |
| | | 570 | 0.869649123 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1343 | 0.927699181 |
| The contents of a c | IBA; IBA | 629.1 | 0.907010014 |
| A membrane-boun | IBA | 655.7 | 0.742870215 |
| A lipid bilayer alon | IEA; IEA | 1653.6 | 0.874939526 |
| | | 1204.9 | 0.919910366 |
| A membrane-boun | IBA | 798.1 | 0.912542288 |
| A membrane-boun | IEA | 2180.3 | 0.924322341 |
| The membrane surr | IBA; IEA; IEA | 789.2 | 0.912696401 |
| | | 2696 | 0.855341246 |
| | | 955.6 | 0.841879447 |
| | | 2355.3 | 0.803506984 |
| | | 959.2 | 0.80264804 |
| | | 860.5 | 0.80615921 |
| A lipid bilayer alon | IEA; IEA | 1024.5 | 0.801268912 |
| | | 344.3 | 0.790299158 |
| A lipid bilayer alon | IEA; IEA | 1435.7 | 0.918506652 |
| | | 1213.7 | 0.788250803 |
| | | 2448.9 | 0.793948303 |
| A small, dense bod | IBA; IEA | 3474.8 | 0.875302176 |
| A lipid bilayer alon | IEA; IEA | 269.8 | 0.835804299 |
| A membrane-boun | IBA; IBA; IEA | 1505.8 | 0.750564484 |
| | | 1478.2 | 0.858679475 |
| | | 774.9 | 0.955865273 |
| The membrane surr | IBA; IBA; IEA; IEA | 980.1 | 0.85144373 |
| | | 1253.8 | 0.837932685 |
| The contents of a c | IBA | 2231.2 | 0.901129437 |
| | | 498 | 0.926506024 |
| The component of | IEA | 199.5 | 0.981954887 |
| A ribonucleoprotei | IEA; IEA | 1823.7 | 0.860503372 |
| | | 1012.8 | 0.791962875 |
| A small, dense bod | IBA | 4189.9 | 0.774600826 |
| A lipid bilayer alon | IBA; IEA | 709 | 0.93596615 |
| A small, dense bod | IBA; IBA; IBA | 1780.3 | 0.882323204 |

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|---|---|---|---|
| A membrane-boun( | IEA; IEA; IEA; IEA; IE | 1218.7 | 0.799212275 |
| A part of a cellular ( | IEA | 1911.1 | 0.799277903 |
|  |  | 1369.8 | 0.899474376 |
| A vacuole to which | IBA | 742.7 | 0.905345362 |
|  |  | 559.9 | 0.798178246 |
| The contents of a c( | IBA | 466.2 | 0.962676963 |

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|---|---|---|---|
| A membrane-boun( | IEA | 1270.6 | 0.770974343 |
| A lipid bilayer along | IEA; IEA | 650.2 | 0.808212858 |
|  |  | 1371.5 | 0.863507109 |
| The contents of a c( | IEA; IEA; IEA; IEA | 1857.7 | 0.88674167 |
|  |  | 527.1 | 0.760576741 |
|  |  | 638.3 | 0.880307066 |
| The lipid bilayer su | IBA; IBA; IEA; IEA; IE | 754.3 | 0.847408193 |
| A membrane-boun( | IEA | 626.9 | 0.926623066 |
| A membrane-boun( | IBA | 728.9 | 0.894772946 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun | IEA; IBA | 1444.1 | 0.861089952 |
| The lipid bilayer su | IBA; IEA | 1251.1 | 0.795619855 |
|  |  | 1485.6 | 0.846930533 |
|  |  | 372.7 | 0.804668634 |
|  |  | 1012 | 0.829051383 |
| A chromosome that | IEA; IEA | 2244.6 | 0.763877751 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 830.1 | 0.867485845 |
| The contents of a c | IBA | 1877.8 | 0.879060603 |
|  |  | 1677.8 | 0.861485278 |
| The irregular netwo | IBA | 856 | 0.899415888 |
|  |  | 736.1 | 0.746909387 |
|  |  | 437.9 | 0.91093857 |
|  |  | 2052.1 | 0.899078992 |
| Any of the long, ge | IEA | 1318.2 | 0.823774844 |
| The contents of a c | IBA | 2379.2 | 0.886852724 |
|  |  | 717.6 | 0.826086957 |
| The double lipid bil | IBA; IEA; IEA | 970.9 | 0.890101967 |
| A lipid bilayer alon | IEA; IEA | 1305.5 | 0.812179242 |
|  |  | 1839.5 | 0.888339223 |
| A membrane-boun | IBA; IBA; IBA | 773.3 | 0.853355748 |
|  |  | 682.3 | 0.849040012 |
| A membrane-boun | IEA | 740.1 | 0.787461154 |
|  |  | 1134.3 | 0.828969408 |
| The contents of a c | IEA; IEA; IEA | 590.4 | 0.754403794 |
| A chlorophyll-cont | IBA | 770.2 | 0.765645287 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 964.2 | 0.920763327 |
| OBSOLETE. The bas | IEA | 1815.4 | 0.93164041 |
| | | 572.8 | 0.848463687 |
| A vacuole to which | IBA; IEA; IBA; IBA; IE | 1298.3 | 0.887853347 |
| | | 1354.4 | 0.951860602 |
| | | 926.4 | 0.879209845 |
| | | 278.3 | 0.79338843 |
| | | 556.4 | 0.790438533 |
| A membrane-boun | IEA | 3478.2 | 0.866597665 |
| A semiautonomous | IBA | 973.2 | 0.913892314 |
| The irregular netwo | IEA; IEA; IEA; IEA; IE | 1223.4 | 0.855321236 |
| | | 700.7 | 0.884544027 |
| | | 861.1 | 0.861572407 |
| | | 2803.7 | 0.750008917 |
| A membrane-boun | IBA | 1257.5 | 0.903856859 |

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|---|---|---|---|
| A chlorophyll-conta | IBA | 755.5 | 0.783719391 |
| | | 233 | 0.787124464 |
| | | 1205.6 | 0.860318514 |
| A semiautonomous | IBA; IEA | 481.2 | 0.861180382 |
| | | 1154.5 | 0.865829363 |
| A semiautonomous | IBA | 1822.7 | 0.875514347 |
| | | 1203.7 | 0.766802359 |
| | | 923.7 | 0.950092021 |
| The membrane surr | IBA; IEA; IEA | 733.1 | 0.924566908 |
| A lipid bilayer along | IEA | 856.9 | 0.876881783 |
| | | 250.6 | 0.790103751 |
| | | 682.9 | 0.883731147 |
| A complex with me | IBA; IEA; IBA; IBA | 900.7 | 0.86210725 |
| Any of the long, ge | IBA | 421.4 | 0.84717608 |
| A membrane-boun | IBA | 826.8 | 0.824020319 |
| The membrane surr | IBA; IBA | 1627.9 | 0.8766509 |
| | | 1278.5 | 0.928040673 |
| The contents of a c | IBA; IBA | 651.3 | 0.919545524 |
| | | 1026.7 | 0.918281874 |
| | | 728 | 0.930906593 |
| The contents of a c | IBA; IBA | 1551.6 | 0.922209332 |
| A membrane-boun | IBA; IBA; IEA | 2518.1 | 0.865811525 |
| A membrane-boun | IEA | 990 | 0.87010101 |
| A lipid bilayer along | IEA; IEA | 167 | 0.926946108 |
| | | 368.2 | 0.902227051 |
| A protein complex | IBA | 641.8 | 0.844655656 |
| | | 1460.3 | 0.861055947 |
| | | 1918.4 | 0.776219766 |
| A lipid bilayer along | IEA; IEA | 1789.9 | 0.955975194 |
| | | 597.6 | 0.773594378 |

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|---|---|---|---|
| The membrane surr | IEA; IBA | 782.8 | 0.763285641 |
| A membrane-boun | IBA; IEA; IEA | 724.9 | 0.912815561 |
| A lipid bilayer alon | IEA; IEA | 759.3 | 0.860661135 |
| The membrane surr | IEA | 1601.4 | 0.921069065 |
| A lipid bilayer alon | IEA; IEA | 1005.7 | 0.776772397 |
| | | 2539.1 | 0.768343114 |
| The double lipid bil | IBA; IBA; IEA; IEA | 2243.3 | 0.95043017 |
| The contents of a c | IBA | 621.1 | 0.8586379 |
| The contents of a c | IBA | 288.6 | 0.93035343 |
| A membrane-boun | IBA | 2344.7 | 0.925918028 |
| The space external | IEA; IEA | 443.6 | 0.782912534 |
| The irregular netwo | IBA; IBA; IEA; IEA | 884.6 | 0.876554375 |
| A lipid bilayer alon | IEA; IEA | 427 | 0.894613583 |
| The irregular netwo | IEA; IEA; IEA; IEA; IE | 244.4 | 0.976268412 |
| A semiautonomous | IBA | 1469.6 | 0.843222646 |
| A membrane-boun | IEA | 1480.9 | 0.822742927 |
| A semiautonomous | IEA | 855.6 | 0.883239832 |
| A membrane-boun | IEA; IEA | 459 | 0.89869281 |
| A membrane-boun | IBA | 2095.4 | 0.80590818 |
| The contents of a c | IBA | 446.1 | 0.797579018 |
| A membrane-boun | IEA | 1389.7 | 0.780096424 |
| A part of a cellular | IEA | 693.4 | 0.804297664 |
| The larger of the tw | IBA | 418 | 0.923205742 |
| | | 789.1 | 0.878595869 |
| | | 902.3 | 0.756067827 |
| | | 639.4 | 0.75742884 |
| A membrane-boun | IBA | 739.5 | 0.809060176 |
| | | 639.5 | 0.882408131 |

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| The component of | IEA; IBA | 343.3 | 0.823478008 |
| A semiautonomous | IBA | 1533.6 | 0.840832029 |
| | | 1154 | 0.891854419 |
| The membrane surr | IBA | 1049.2 | 0.917270301 |
| A membrane-boun | IEA | 3126.2 | 0.868018681 |
| | | 382.5 | 0.905882353 |
| The component of t | IBA | 412.6 | 0.861609307 |
| | | 208.6 | 0.841323106 |
| | | 690.8 | 0.800376375 |
| A membrane-boun | IEA | 2137.4 | 0.926967344 |
| A ubiquitin ligase c | IBA | 1381.2 | 0.924268752 |
| | | 1847.5 | 0.774560217 |
| | | 399.5 | 0.806007509 |
| A membrane-boun | IEA | 1359.7 | 0.74641465 |
| | | 485.1 | 0.871572872 |
| A chlorophyll-cont | IEA; IEA | 1053.7 | 0.78656164 |
| The inner, i.e. lume | IBA; IBA; IEA | 461.5 | 0.826218852 |
| A semiautonomous | IBA | 2308.7 | 0.887772339 |
| Cyclin-dependent p | IBA; IBA; IBA | 680.8 | 0.767479436 |
| | | 989.3 | 0.916405539 |
| | | 1121.5 | 0.847079804 |

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|---|---|---|---|
| The contents of a c | IBA | 1643.2 | 0.827044791 |
| A membrane-boun | IDA | 882.4 | 0.765979148 |
| A ribonucleoprotei | IEA; IEA; IEA | 692.6 | 0.865578978 |
| The component of | IEA | 1446.9 | 0.936415785 |
|  |  | 785.7 | 0.876925035 |
| The space external | IEA; IEA | 328.6 | 0.805538649 |
|  |  | 1792.6 | 0.759511324 |
| The membrane sur | IBA; IEA; IEA | 1839.5 | 0.901277521 |
| A membrane-boun | IBA; IBA | 1389.8 | 0.94653907 |
|  |  | 1255.2 | 0.919694073 |
| A lipid bilayer alon | IEA; IEA | 1327.5 | 0.817627119 |
|  |  | 561.2 | 0.824839629 |
|  |  | 657.3 | 0.808610984 |
| The component of | IEA | 414.3 | 0.832488535 |
| A membrane-boun | IEA | 1028.1 | 0.845248517 |
|  |  | 650.2 | 0.841125807 |
|  |  | 437.5 | 0.7856 |
| A membrane-boun | IBA | 499.3 | 0.80612858 |
|  |  | 791.3 | 0.908378617 |
| Any complex that i | IBA; IEA | 1800.3 | 0.866188969 |

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|---|---|---|---|
| A membrane-boun | IBA | 780.6 | 0.868946964 |
| A lipid bilayer along | IEA; IEA | 1957.8 | 0.856522627 |
| A membrane-boun | IBA | 1812.5 | 0.863613793 |
|  |  | 376.8 | 0.917197452 |
|  |  | 804.3 | 0.841974388 |
| The ordered and or | IEA; IBA; IEA | 1905.5 | 0.769246917 |
| The membrane surr | IBA | 342.9 | 0.846602508 |
| A membrane-boun | IEA; IEA | 555 | 0.868468468 |
| A membrane-boun | IEA; IEA | 630.3 | 0.856893543 |
| The outer, i.e. cytop | IBA | 949.2 | 0.928887484 |
|  |  | 203.4 | 0.828908555 |
|  |  | 426.4 | 0.919090056 |
| A membrane-boun | IEA | 300.2 | 0.897401732 |
| The lipid bilayer su | IEA; IEA; IBA; IBA; IE | 2193.3 | 0.91319017 |
|  |  | 810 | 0.797901235 |
| A lipid bilayer along | IEA; IEA | 825.1 | 0.960610835 |
| A chlorophyll-conta | IEA; IEA; IEA | 373.6 | 0.887044968 |
| The contents of a c | IEA; IEA; IEA; IEA; IE | 1454.9 | 0.806103512 |
|  |  | 1038.6 | 0.813884075 |
| A lipid bilayer along | IEA; IEA | 456.6 | 0.830267192 |
| A membrane-boun | IC | 771.9 | 0.840523384 |

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|---|---|---|---|
| A membrane-boun | IEA; IBA | 1084 | 0.864114391 |
| The membrane surr | IEA; IEA | 787.6 | 0.764347384 |
| | | 836 | 0.770454545 |
| A membrane-boun | IMP | 808.4 | 0.789213261 |
| A membrane-boun | IBA | 775.7 | 0.857934769 |
| A lipid bilayer alon | IEA; IEA | 286.5 | 0.820244328 |
| | | 1814.9 | 0.751281062 |
| A semiautonomous | IEA | 378.3 | 0.93232884 |
| The lipid bilayer su | IEA; IBA; IBA; IBA; IE | 847.2 | 0.929532578 |
| The membrane surr | IBA; IBA; IEA | 1484.4 | 0.954661816 |
| | | 827.9 | 0.907114386 |
| | | 844.1 | 0.864352565 |
| A chlorophyll-cont | IEA; IEA; IBA | 813.7 | 0.833476711 |
| | | 1286.4 | 0.876088308 |
| The contents of a c | IEA; IEA; IEA | 4148.1 | 0.894843422 |
| The space external | IEA | 193.1 | 0.759192128 |
| A SAGA-type histo | IBA; IEA; IEA | 660 | 0.823787879 |
| A lipid bilayer alon | IEA; IEA | 811.4 | 0.830663052 |
| A lipid bilayer alon | IEA; IEA | 606.6 | 0.770524233 |
| The contents of a c | IBA | 1380 | 0.781014493 |
| A membrane-boun | IBA; IBA; IBA; IBA | 1055.9 | 0.81930107 |
| The contents of a c | IEA; IEA | 1387.6 | 0.867613145 |

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|---|---|---|---|
| The lipid bilayer su | IEA; IEA; IEA; IEA | 958.4 | 0.949290484 |
| The lipid bilayer su | IEA; IEA; IEA | 764.1 | 0.868734459 |
| A membrane-bound | IEA | 2822.5 | 0.855589017 |
|  |  | 342.8 | 0.901400233 |
| Protein complex loc | IBA; IEA; IEA; IEA; IE | 602 | 0.87923588 |
| A membrane-bound | IEA | 2065.8 | 0.885419692 |
| The membrane surr | IEA; IDA; IBA; IEA | 613.8 | 0.874226132 |
|  |  | 1814.7 | 0.954648151 |
|  |  | 685.7 | 0.797579116 |
| A dense aggregatio | IBA | 1289.8 | 0.86323461 |
| A membrane-bound | IEA | 440.3 | 0.831251419 |
|  |  | 496.5 | 0.837865055 |
| The component of a | IEA | 988.5 | 0.912493677 |
| The irregular netwo | IEA | 486.7 | 0.80480789 |
| The component of a | IEA | 137 | 0.864963504 |
| A membrane-bound | IBA; IBA; IEA | 940.2 | 0.888853435 |
| A lipid bilayer along | IEA; IEA | 457.7 | 0.93838759 |
| A membrane-bound | IEA; IEA; IEA | 2809.5 | 0.912795871 |

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|---|---|---|---|
| The irregular netwo | IEA; IEA; IEA; IEA | 1159.7 | 0.911701302 |
| A membrane-boun | IBA | 1815.1 | 0.867720787 |
| A lipid bilayer alon | IEA; IEA | 921.2 | 0.875705601 |
| A lipid bilayer alon | IEA; IEA | 386.7 | 0.942332558 |
| | | 1053.7 | 0.797001044 |

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|---|---|---|---|
| A membrane-boun | IEA | 582 | 0.837457045 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1014.9 | 0.840673958 |

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|---|---|---|---|
| A membrane-boun | IEA | 683.9 | 0.765024126 |
| An intracellular org | IEA; IEA | 302.7 | 0.830855633 |
| | | 456.1 | 0.877658408 |
| | | 232.4 | 0.869621343 |
| A protein complex | IBA | 1436.1 | 0.760671262 |
| The contents of a c | IEA | 1454.1 | 0.862870504 |

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|---|---|---|---|
| | | 1839.2 | 0.886309265 |
| | | 1770 | 0.928983051 |
| | | 2653.6 | 0.762963521 |
| A fine cytoplasmic | IBA; IEA; IEA | 644.6 | 0.789016444 |

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|---|---|---|---|
| | | 937.7 | 0.858163592 |
| | | 171.6 | 0.804778555 |
| A chlorophyll-conta | IEA; IBA; IEA; IBA | 687 | 0.871615721 |

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|---|---|---|---|
| A membrane-boun | IBA | 1641.5 | 0.864331404 |
| A lipid bilayer along | IEA; IEA | 836.4 | 0.820301291 |
| | | 1015.8 | 0.77367592 |
| A chlorophyll-conta | IEA | 691.9 | 0.909813557 |
| Organized structure | IBA | 1102.9 | 0.885302385 |
| The lipid bilayer su | IEA | 1143.4 | 0.956708064 |
| | | 1415.2 | 0.904819107 |
| RNA polymerase I, | IBA | 517.6 | 0.857032457 |
| A membrane-boun | IBA; IBA | 1859.2 | 0.947611876 |
| Any complex that i | IBA; IEA | 2171 | 0.932842008 |
| A membrane-boun | IEA | 1253.2 | 0.890360677 |
| A membrane-boun | IEA | 870.2 | 0.787290278 |
| | | 314.4 | 0.755089059 |
| A lipid bilayer along | IEA; IEA; IBA | 490.3 | 0.740567 |
| A membrane-boun | IEA | 1280.5 | 0.8695041 |
| | | 2173.4 | 0.777537499 |
| | | 609.4 | 0.793403348 |
| | | 506.7 | 0.904282613 |
| A ubiquitin ligase c | IBA | 508.2 | 0.918339237 |
| A membrane-boun | IEA | 885.1 | 0.778556095 |
| | | 1043.8 | 0.919524813 |
| | | 2270.1 | 0.907184706 |
| A lipid bilayer along | IEA; IEA | 1175.5 | 0.904040834 |
| A membrane-boun | IEA | 871.7 | 0.783985316 |
| | | 767.1 | 0.845000652 |
| A semiautonomous | IBA | 1319.1 | 0.827609734 |
| | | 1247.6 | 0.852997756 |

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|---|---|---|---|
| The contents of a c | IEA | 367.1 | 0.857259602 |
|  |  | 373.3 | 0.797481918 |
|  |  | 584.9 | 0.805778766 |
| A lipid bilayer along | IEA; IEA | 273.3 | 0.949506037 |
| The contents of a c | IBA | 716.1 | 0.885490853 |
| A membrane-boun | IBA | 635.8 | 0.752280591 |
| The membrane surr | IBA; IBA | 841.7 | 0.914102412 |
| A lipid bilayer along | IEA; IEA | 780.1 | 0.865401872 |
| The lipid bilayer su | IBA | 3591.2 | 0.913677879 |
| A membrane-boun | IBA | 1605.5 | 0.795702273 |
|  |  | 809.7 | 0.750277881 |
|  |  | 467.6 | 0.848802395 |
| A vacuole to which | IEA; IEA; IEA; IEA; IE | 1550.4 | 0.937951496 |
|  |  | 634.7 | 0.745706633 |
|  |  | 936.9 | 0.846088163 |
| A lipid bilayer along | IEA; IEA | 1345.3 | 0.931167769 |
| A membrane-boun | IBA | 838.5 | 0.768157424 |
|  |  | 766.7 | 0.757010565 |
| The Ccr4-Not comp | IEA | 1815.9 | 0.917891954 |
| The part of the cyto | IBA | 723.3 | 0.804092354 |
|  |  | 900.9 | 0.844377844 |
| A membrane-boun | IEA; IEA | 2787.8 | 0.758698615 |
|  |  | 2049.4 | 0.893432224 |
| A chlorophyll-conta | IEA | 1675.7 | 0.803962523 |
| A semiautonomous | IBA | 949.2 | 0.807416772 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA; IE | 452.3 | 0.857395534 |
|  |  | 1243.5 | 0.943948532 |

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|---|---|---|---|
| A membrane-boun | IEA | 1344.2 | 0.856122601 |
| OBSOLETE. The bas | IEA | 1603.5 | 0.836357967 |
| A membrane-boun | IBA; IEA | 1406 | 0.910170697 |
| | | 1522.7 | 0.810008537 |
| The contents of a c | IBA | 1640.9 | 0.775854714 |
| A membrane-boun | IEA | 619.8 | 0.826718296 |
| | | 831.7 | 0.788144764 |
| | | 151.2 | 0.90542328 |
| A membrane-boun | IBA; IBA | 216.8 | 0.911900369 |
| | | 747.5 | 0.916655518 |
| | | 1415.4 | 0.838985446 |
| | | 166.6 | 0.825930372 |
| | | 416.7 | 0.817134629 |
| A membrane-boun | IBA | 2237.9 | 0.877206309 |
| | | 379 | 0.816094987 |
| The Ccr4-Not comp | IBA | 726.9 | 0.740129316 |
| The membrane surr | IBA; IBA; IEA; IEA | 857.7 | 0.900198205 |
| The membrane surr | IBA; IEA; IEA | 605.7 | 0.776787188 |
| | | 255.6 | 0.89514867 |
| A protein-DNA com | IBA; IBA | 933.6 | 0.890102828 |
| A semiautonomous | IEA; IBA | 1836.8 | 0.888937282 |
| A lipid bilayer alon | IEA; IEA | 1882.1 | 0.774400935 |
| | | 938 | 0.876012793 |
| | | 440.4 | 0.975930972 |
| | | 1555.1 | 0.792810752 |
| A membrane-boun | IBA; IBA | 1602.5 | 0.869516381 |
| A membrane-boun | IBA | 373.2 | 0.803858521 |
| | | 2805.6 | 0.806387226 |

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|---|---|---|
| A membrane-bound IEA | 682.4 | 0.915445487 |
| OBSOLETE. The bas IEA; IEA; IEA | 545.7 | 0.858347077 |
| A membrane-bound IBA | 677.3 | 0.901225454 |

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|---|---|---|
| A membrane-bound IDA | 825 | 0.812242424 |
|  | 998.5 | 0.842563846 |
| A membrane-bound IBA | 2171.2 | 0.885455048 |

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|---|---|---|---|
| | | 401.5 | 0.876214197 |
| A membrane-boun | IEA | 1474.3 | 0.845079021 |
| A membrane-boun | IBA | 666.4 | 0.762755102 |
| The double lipid bil | IBA; IEA; IEA | 488.1 | 0.913747183 |
| A fine cytoplasmic | IEA; IEA | 2292.5 | 0.838037077 |
| A lipid bilayer along | IEA; IEA | 496.2 | 0.780330512 |
| A membrane-boun | IEA; IBA | 335.8 | 0.913341275 |
| The membrane surr | IBA | 1441.3 | 0.869423437 |
| | | 727.1 | 0.901251547 |
| | | 2500 | 0.89372 |
| A lipid bilayer along | IEA; IEA | 1574.4 | 0.791793699 |
| | | 564.8 | 0.777974504 |
| | | 3937.7 | 0.842446098 |
| A membrane-boun | IEA | 801.5 | 0.787772926 |
| A membrane-boun | IEA | 666.3 | 0.830856971 |
| A conserved proteir | IBA | 975.8 | 0.927034228 |
| | | 466.6 | 0.812687527 |
| A membrane-boun | IEA | 563.9 | 0.928888101 |
| A membrane-boun | IBA; IBA | 360.5 | 0.750069348 |
| | | 953.9 | 0.748610966 |
| | | 992.9 | 0.74468728 |
| A lipid bilayer along | IEA; IEA | 1155.6 | 0.894080997 |
| A chlorophyll-conta | IBA; IEA | 589.8 | 0.78467277 |
| A closed structure, | IBA | 1304 | 0.85851227 |

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|---|---|---|---|
| | | 716 | 0.950418994 |
| A membrane-boun | IBA | 2165.7 | 0.867248465 |
| The space external | IBA | 980.4 | 0.845573235 |
| A membrane-boun | IBA | 405.8 | 0.896747166 |
| A lipid bilayer alon | IEA; IEA | 655.9 | 0.927123037 |
| Organized structur | IBA | 1012.2 | 0.877198182 |
| Organized structur | IEA | 1694.3 | 0.917251962 |
| A semiautonomous | IBA; IEA | 1169.9 | 0.92922472 |
| The part of the cyto | IEA; IEA; IEA; IEA | 2400.3 | 0.969420489 |
| The contents of a c | IBA; IBA; IEA | 2269.8 | 0.855890387 |
| A semiautonomous | IEA; IBA | 633.1 | 0.813615543 |
| The contents of a c | IBA | 2749.4 | 0.75751073 |
| The contents of a c | IEA; IEA; IEA | 683.2 | 0.798741218 |
| A membrane-boun | IDA | 1231 | 0.798781478 |
| A membrane-boun | IBA; IBA; IEA | 1499.7 | 0.857571514 |
| | | 2668 | 0.770014993 |
| | | 867.7 | 0.884407053 |
| A membrane-boun | IEA; IBA; IEA | 1907.9 | 0.874888621 |
| | | 2530.3 | 0.837371063 |
| A protein complex | IBA; IBA | 4652.4 | 0.875096724 |
| The irregular netwo | IBA; IEA | 1759.8 | 0.861802478 |
| The irregular netwo | IEA; IBA | 765.7 | 0.938487658 |
| The contents of a c | IBA | 1070.2 | 0.866193235 |
| The contents of a c | IBA; IEA | 1386 | 0.812409812 |
| A membrane-boun | IEA; IEA; IEA | 447.3 | 0.749161636 |
| | | 1716.2 | 0.866449132 |
| A lipid bilayer alon | IEA; IEA | 169.4 | 0.755608028 |
| The space external | IEA | 656.8 | 0.869518879 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA; IEA | 1029.8 | 0.907360653 |
| | | 936.1 | 0.775664993 |
| | | 894.8 | 0.926464014 |
| | | 596.7 | 0.852522205 |
| The pigmented me | IBA | 320.7 | 0.84565014 |
| A membrane-boun | IEA; IBA; IEA | 1517.7 | 0.758450287 |
| The contents of a c | IBA | 1357 | 0.872733972 |
| OBSOLETE. The bas | IEA; IEA | 1309.5 | 0.878732341 |
| Any complex that i | IBA; IEA | 2437.3 | 0.875517991 |
| The irregular netwo | IBA; IBA; IEA; IEA | 1180.4 | 0.937987123 |
| | | 1080 | 0.871481481 |
| A chlorophyll-cont | IEA | 1991.6 | 0.868899377 |
| A membrane-boun | IBA | 1120.2 | 0.801642564 |
| | | 396.6 | 0.748361069 |
| | | 328.8 | 0.867396594 |
| | | 1036.6 | 0.929095119 |
| | | 2256.8 | 0.750221553 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 419.9 | 0.885687068 |
| A membrane-boun | IEA | 604.3 | 0.801754096 |
| | | 484.9 | 0.863270777 |
| A complex compris | IEA; IEA; IEA | 341.8 | 0.809245173 |
| | | 808.7 | 0.812291332 |

|  |  |  |  |
|---|---|---|---|
| A membrane-bound | IDA | 1334 | 0.82916042 |
| The contents of a c | IBA | 687.3 | 0.930161502 |
|  |  | 563.3 | 0.908041896 |
| A membrane-bound | IEA | 1503.1 | 0.816712128 |
| A small, dense body | IBA; IEA; IBA | 1240.6 | 0.840238594 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA | 720.1 | 0.89182058 |
| | | 640.8 | 0.79619226 |
| | | 835.8 | 0.836085188 |
| The contents of a c | IEA | 743.8 | 0.935869857 |
| The irregular netwo | IEA | 1344.2 | 0.905966374 |
| The membrane surr | IBA; IEA; IEA | 2045.8 | 0.884739466 |
| | | 369.8 | 0.879394267 |
| | | 878.2 | 0.841721703 |
| A semiautonomous | IBA | 904.1 | 0.819378387 |
| | | 454.8 | 0.912708883 |
| | | 243.7 | 0.874025441 |
| A membrane-boun | IBA; IBA; IBA; IBA; IB | 766.6 | 0.847378033 |
| | | 2014.9 | 0.872003573 |
| | | 2163.9 | 0.818383474 |
| A lipid bilayer alon | IEA; IEA | 1532.8 | 0.854188413 |
| | | 521.7 | 0.769407706 |

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|---|---|---|---|
| OBSOLETE. The bas | IEA; IBA; IBA | 4290.4 | 0.90014917 |
| A ribonuclease com | IBA | 401 | 0.782294264 |
| A membrane-boun | IBA; IBA | 2766.8 | 0.891860633 |
| The membrane sur | IBA; IEA; IEA | 1626.2 | 0.803345222 |
| The contents of a c | IEA; IEA; IEA; IEA; IE | 654.3 | 0.872841204 |
| A membrane-boun | IBA | 965.4 | 0.763103377 |
| The irregular netwo | IEA | 924.6 | 0.941596366 |
| A lipid bilayer alon | IEA; IEA | 788.1 | 0.902550438 |
| Any member of a fa | IEA; IEA | 1785.6 | 0.858422939 |
| The component of t | IEA | 377.5 | 0.822251656 |
| A ubiquitin ligase c | IBA | 1415.2 | 0.925028265 |
| The irregular netwo | IBA | 673.3 | 0.941185207 |
| | | 2519.7 | 0.840814383 |
| | | 1413.4 | 0.785481817 |
| | | 1324.4 | 0.78858351 |
| | | 657.9 | 0.873081015 |
| The DNA polymeras | IEA | 2619.6 | 0.819896167 |
| | | 1147.2 | 0.834553696 |
| | | 843.7 | 0.834419817 |
| A small organelle e | IEA | 1548.8 | 0.824509298 |
| The irregular netwo | IEA | 2129.7 | 0.744236277 |
| Organized structur | IBA | 1001.7 | 0.901966657 |
| A compact and hig | IDA; IBA; IBA | 1915.8 | 0.906618645 |
| A chlorophyll-conta | IEA; IEA | 1145.3 | 0.845891906 |
| | | 411.3 | 0.775346462 |
| The outer, i.e. cyto | IBA | 1827.5 | 0.941504788 |
| | | 545.1 | 0.82131719 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1038.9 | 0.808740013 |

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|---|---|---|---|
| | | 1712.5 | 0.898978102 |
| | | 200.7 | 0.751370204 |
| The space external | IEA; IEA; IEA | 656.1 | 0.933546715 |
| | | 661.6 | 0.821644498 |
| The contents of a c | IEA; IBA; IBA | 456.8 | 0.890980736 |
| | | 1449.9 | 0.880888337 |
| The region of a chr | IEA; IEA; IEA; IEA; IE | 620.4 | 0.792392005 |
| A semiautonomous | IEA | 1068.9 | 0.791654972 |
| | | 1069.9 | 0.82353491 |
| | | 1058.8 | 0.94125425 |
| | | 817.2 | 0.836514929 |
| A membrane-boun | IBA | 573.9 | 0.798396933 |
| The space external | IEA; IEA; IEA | 572.2 | 0.870499825 |
| A membrane-boun | IEA; IEA; IBA | 1457.2 | 0.926914631 |
| | | 494.3 | 0.937082743 |
| The sector of a hyd | IEA | 2570.2 | 0.750525251 |
| | | 195.8 | 0.846271706 |
| A membrane-boun | IEA | 351.2 | 0.80381549 |
| A large ribonucleop | IBA | 836.1 | 0.747757445 |
| | | 174.2 | 0.815729047 |
| | | 864.8 | 0.886447734 |
| A lipid bilayer alon | IEA; IEA | 1375.4 | 0.777591973 |
| | | 1130.8 | 0.867350548 |
| Organized structur | IBA | 1401 | 0.888365453 |
| A membrane-boun | IEA | 1052.8 | 0.748005319 |
| Organized structur | IEA | 1046.4 | 0.790902141 |
| | | 1583.4 | 0.897499053 |
| A nuclear DNA-dire | IBA | 1247.4 | 0.823232323 |

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|---|---|---|---|
| A chlorophyll-conta | IDA | 1988 | 0.927917505 |
|  |  | 1770 | 0.887514124 |
|  |  | 1336.4 | 0.894118527 |
| An intracellular org | IEA; IEA; IEA | 1340.3 | 0.755353279 |
|  |  | 507.6 | 0.914499606 |
|  |  | 1204.5 | 0.815276048 |
|  |  | 313.8 | 0.833970682 |
|  |  | 508.6 | 0.803775069 |
|  |  | 641.5 | 0.753858145 |
| A membrane-bound | IEA | 377.6 | 0.749735169 |
| The space external | IBA | 957.8 | 0.872415953 |

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|---|---|---|---|
| | | 473.7 | 0.802195482 |
| The contents of a c | IBA | 2913.9 | 0.9053159 |
| | | 184.8 | 0.852272727 |
| | | 855.6 | 0.819191211 |
| A protein complex | IEA | 2953.9 | 0.938454247 |
| | | 1814.7 | 0.882074172 |
| | | 1466.5 | 0.828162291 |
| | | 1106.6 | 0.789445147 |
| | | 806.6 | 0.840193404 |
| | | 1019.5 | 0.942815105 |
| | | 1409.4 | 0.765715907 |
| A membrane-boun | IEA | 810.7 | 0.780313309 |
| The end of a linear | IBA; IBA; IBA; IBA; IB | 600.8 | 0.843375499 |
| | | 971.4 | 0.930718551 |
| Organized structur | IEA | 1116.1 | 0.875817579 |
| | | 3167.2 | 0.768723162 |
| A lipid bilayer alon | IEA; IEA | 624.1 | 0.789456818 |
| A membrane-boun | IEA; IEA; IEA; IEA | 1198.1 | 0.855437776 |
| The contents of a c | IBA; IBA | 1329.7 | 0.86402948 |
| | | 2119.4 | 0.872133623 |
| | | 1107.6 | 0.837396172 |

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|---|---|---|---|
| A ribonucleoproteir | IEA; IEA; IEA; IEA; IE | 824.5 | 0.869981807 |
| | | 1826 | 0.823658269 |
| A semiautonomous | IBA; IBA; IBA | 662.6 | 0.875339571 |
| The space external | IEA | 185.3 | 0.759848894 |
| The contents of a c | IEA; IEA; IEA | 643.9 | 0.908681472 |
| The contents of a c | IEA; IEA; IEA | 669.7 | 0.919516201 |
| | | 911.5 | 0.904882063 |
| | | 451.2 | 0.750886525 |
| The membrane surr | IEA; IEA; IEA | 1140 | 0.808508772 |
| A membrane-bound | IBA | 5998.1 | 0.85582101 |
| A protein complex t | IEA; IBA | 1204.4 | 0.888990369 |
| A ubiquitin ligase c | IBA | 1168.3 | 0.856971668 |
| | | 1085 | 0.961751152 |
| A membrane-bound | IBA; IEA; IBA; IBA | 1424.1 | 0.925426585 |
| A lipid bilayer along | IEA; IEA | 593.5 | 0.941364785 |
| The end of a linear | IEA; IEA; IEA; IEA | 1028.1 | 0.910806342 |
| | | 907.9 | 0.747439145 |
| A membrane-bound | IEA | 778.2 | 0.790670779 |
| A membrane-bound | IEA; IEA; IBA | 1362.6 | 0.957434317 |
| | | 221.4 | 0.807136405 |

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|---|---|---|---|
| | | 696.1 | 0.83953455 |
| | | 692.2 | 0.849898873 |
| A lipid bilayer alon | IBA; IEA | 1491.8 | 0.941748224 |
| A membrane-boun | IEA; IEA; IEA | 2257.4 | 0.933861965 |
| A semiautonomous | IBA | 1924.3 | 0.888738762 |
| | | 285 | 0.867017544 |
| A membrane-boun | IEA; IEA; IEA; IBA | 2938.1 | 0.951669446 |
| A membrane-boun | IEA | 1060.5 | 0.874587459 |
| The ordered and or | IBA; IBA | 680.8 | 0.90893067 |
| A membrane-boun | IEA | 587.8 | 0.808268118 |
| An RNA polymerase | IEA | 391.9 | 0.883643787 |
| A more or less rigid | IBA | 905.9 | 0.935644111 |
| A membrane-boun | IEA | 628 | 0.766878981 |
| A membrane-boun | IEA | 629 | 0.783783784 |

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|---|---|---|---|
| A membrane-boun | IEA | 1268.1 | 0.787319612 |
| A semiautonomous | IBA | 1074.2 | 0.888195867 |
| Any of the long, ge | IEA | 1335.8 | 0.761116934 |
| A membrane-boun | IBA | 996.2 | 0.897410159 |
|  |  | 672.4 | 0.765466984 |
|  |  | 2292.6 | 0.829451278 |
|  |  | 1790.5 | 0.946607093 |
|  |  | 5405.7 | 0.854616423 |
|  |  | 256.2 | 0.816549571 |
| The irregular netwo | IEA; IEA; IEA | 537 | 0.903351955 |

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|---|---|---|---|
| The contents of a c | IBA | 859.2 | 0.796904097 |
| A membrane-boun | IBA; IEA; IBA; IBA | 841.8 | 0.923140889 |
| Any of the long, ge | IEA; IBA | 2049.8 | 0.904283345 |
|  |  |  |  |
|  |  | 924.1 | 0.909641814 |
| The part of the cyto | IEA | 280.3 | 0.922939707 |
| The contents of a c | IEA; IEA; IEA | 1083.5 | 0.871435164 |
| The irregular netwo | IBA; IEA; IEA; IEA; IB | 358.1 | 0.93214186 |
|  |  | 1865.2 | 0.745550075 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1177.3 | 0.90580141 |
| The membrane surr | IBA; IEA; IEA | 351.5 | 0.829018492 |
| A membrane-boun | IEA; IEA; IBA | 922 | 0.860086768 |
| A more or less rigid | IEA | 979.3 | 0.912080057 |
| The contents of a c | IBA; IEA | 1213.2 | 0.809676888 |
|  |  | 2860.8 | 0.793134787 |
| OBSOLETE. The bas | IEA | 1485.2 | 0.879612173 |
|  |  | 829.7 | 0.883572376 |
|  |  | 389.1 | 0.814700591 |
| A membrane-boun | IEA; IEA; IEA | 1100.5 | 0.782189914 |

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|---|---|---|---|
| | | 2103 | 0.913266762 |
| A closed structure, | IBA; IEA; IEA; IEA; IE | 233.8 | 0.968776732 |
| A heterotrimeric tra | IBA; IEA | 1926.1 | 0.906443071 |
| | | 898.1 | 0.845674201 |
| A lipid bilayer along | IEA; IEA | 1619.1 | 0.910567599 |
| A membrane-boun | IEA; IEA | 1807 | 0.748754842 |
| A membrane-boun | IEA; IBA | 2812 | 0.895768137 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA; IE | 261.1 | 0.862504787 |
| | | 620.9 | 0.928651957 |
| A membrane-boun | IEA; IBA; IEA; IEA; IB | 2197 | 0.943969049 |
| A membrane-boun | IEA; IBA; IBA | 893.1 | 0.87470608 |
| | | 1079.4 | 0.834074486 |
| A membrane-boun | IEA; IBA; IEA; IBA | 1590 | 0.883459119 |
| | | 408 | 0.784803922 |
| A double-membran | IEA; IEA; IBA; IBA; IB | 2488.5 | 0.920594736 |
| A lipid bilayer along | IBA; IEA; IBA | 312.3 | 0.857508806 |
| A membrane-boun | IBA | 8214.6 | 0.923063813 |
| A semiautonomous | IEA; IEA; IEA; IEA; IE | 316.1 | 0.922492882 |
| The membrane surr | IBA | 754.3 | 0.873790269 |
| A vacuole to which | IBA; IEA; IBA; IBA; IE | 2084.3 | 0.759775464 |
| | | 877.9 | 0.929946463 |
| A lipid bilayer along | IEA; IEA | 533.3 | 0.819613726 |
| | | 1493.6 | 0.904325121 |
| | | 263.8 | 0.792266869 |
| | | 771.5 | 0.863642255 |
| A focus in the cytop | IEA; IEA | 3002.9 | 0.908288654 |
| | | 550.2 | 0.758996728 |
| That part of a multi | IEA | 161.9 | 0.785052502 |

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|---|---|---|---|
| The contents of a c | IBA | 2255.9 | 0.901325413 |
| | | 993 | 0.930312185 |
| | | 794 | 0.809949622 |
| | | 843.5 | 0.802489627 |
| A lipid bilayer along | IEA; IEA | 463.1 | 0.872381775 |
| | | 1400.1 | 0.838797229 |
| | | 882.7 | 0.910728447 |
| | | 147.8 | 0.802435724 |
| A lipid bilayer along | IEA; IEA | 475.1 | 0.836455483 |
| | | 302.6 | 0.826503635 |
| A chlorophyll-conta | IBA | 322.1 | 0.806581807 |
| A lipid bilayer along | IEA; IEA | 523.1 | 0.851080099 |
| A membrane-bound | IBA | 912.8 | 0.948071867 |
| | | 392.4 | 0.754587156 |
| | | 802 | 0.890274314 |

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|---|---|---|---|
| Cyclin-dependent p | IBA; IBA; IBA | 733.7 | 0.868747444 |
|  |  | 492.4 | 0.880381803 |
|  |  | 357.2 | 0.86506159 |
| A membrane-boun | IEA | 1184.9 | 0.79551017 |
| The double lipid bil | IEA; IEA; IEA | 784.1 | 0.923479148 |
| The irregular netwo | IEA | 2156.1 | 0.753211818 |
| The membrane surr | IEA; IEA | 1742.7 | 0.900843519 |
| The irregular netwo | IBA | 1195.8 | 0.894296705 |
|  |  | 3344.8 | 0.827553217 |
| A lipid bilayer alon | IEA; IEA | 566.9 | 0.943552655 |
| The membrane surr | IBA; IEA; IEA | 1615.4 | 0.803887582 |
| A multiprotein kine | IBA; IEA; IEA; IBA; IE | 471.3 | 0.761298536 |
| The membrane surr | IEA; IEA; IEA | 388.1 | 0.837670703 |
| A chlorophyll-conta | IEA; IBA | 1519.5 | 0.749917736 |
|  |  | 1124.1 | 0.846721822 |
| A chlorophyll-conta | IBA; IEA | 490.8 | 0.874898126 |
| A membrane-boun | IEA | 541.8 | 0.946659284 |
| A membrane-boun | IBA; IBA | 990.2 | 0.913451828 |
| A membrane-boun | IBA; IBA | 1170.8 | 0.767338572 |
| Organized structur | IBA | 1022.3 | 0.887508559 |
| The irregular netwo | IEA; IEA; IEA; IBA | 530.6 | 0.926875236 |
| A semiautonomous | IBA; IBA | 2335.8 | 0.844721295 |
|  |  | 700.8 | 0.754708904 |
| A membrane-boun | IBA | 1381.3 | 0.903279519 |
|  |  | 1106.9 | 0.915168489 |

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|---|---|---|---|
| A membrane-boun | IEA | 756 | 0.857671958 |
| | | 403.7 | 0.765172158 |
| The lipid bilayer su | ISS; IEA; IEA | 1029.1 | 0.936838014 |
| | | 1913.1 | 0.803094454 |
| A semiautonomous | IBA | 1110.7 | 0.88610786 |
| A chlorophyll-cont | IEA; IEA; IEA; IEA | 267.7 | 0.829660067 |
| The contents of a c | IBA; IBA | 852.3 | 0.935703391 |
| A lipid bilayer alon | IEA; IEA | 1442.8 | 0.831646798 |
| The inner, i.e. lume | IEA; IEA; IEA | 1141 | 0.863365469 |
| | | 1702.5 | 0.819265786 |
| | | 252.3 | 0.804201348 |
| A lipid bilayer alon | IEA; IEA | 1511.7 | 0.947807105 |
| | | 958.4 | 0.918823038 |
| | | 2479.9 | 0.876124037 |
| | | 1541.4 | 0.82807837 |
| A membrane-boun | IEA; IEA; IEA; IBA; IB | 1451.7 | 0.835296549 |
| | | 1400.9 | 0.902205725 |
| The irregular netwo | IBA; IBA; IEA; IEA | 700.4 | 0.838663621 |
| | | 2438.3 | 0.905548948 |
| | | 1654.2 | 0.953935437 |
| Punctate structures | IBA; IBA; IEA; IEA; IE | 2011.9 | 0.944530046 |
| The contents of a c | IBA | 1140.2 | 0.871776881 |
| | | 1870.4 | 0.75855432 |
| | | 909.9 | 0.927354654 |
| | | 808.3 | 0.917481133 |
| A lipid bilayer alon | IEA; IEA | 152.9 | 0.966644866 |
| A lipid bilayer alon | IEA; IEA | 1098.8 | 0.859392064 |
| | | 1524.2 | 0.82836898 |
| | | 1550.5 | 0.893389229 |
| A chlorophyll-cont | IEA | 625.8 | 0.854426334 |
| A chlorophyll-cont | IBA; IEA; IEA; IEA | 324.8 | 0.806342365 |

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|---|---|---|---|
| A membrane-boun | IBA | 1295.7 | 0.822258239 |
| The contents of a c | IBA | 6949.1 | 0.89024478 |
|  |  | 536.9 | 0.851555224 |
| A membrane-boun | IBA | 684.1 | 0.752960094 |
| A membrane-boun | IEA | 1798.4 | 0.841414591 |
|  |  | 1259.7 | 0.906326903 |
|  |  | 1030.6 | 0.866776635 |
| A semiautonomous | IBA; IEA | 461.3 | 0.77194884 |
|  |  | 967.3 | 0.863847824 |
|  |  | 1658.2 | 0.87239175 |
| A chlorophyll-conta | IEA | 2425.5 | 0.821562564 |
|  |  | 940.8 | 0.782738095 |
| That part of a multi | IBA | 768.2 | 0.854985681 |
| The component of a | IEA | 448.2 | 0.887103971 |
| A membrane-boun | IEA; IEA; IEA; IEA; IB | 1684.2 | 0.913727586 |
| The contents of a c | IEA | 1618.7 | 0.877185396 |
|  |  | 2521 | 0.785640619 |
| A more or less rigid | IBA; IBA | 1234.9 | 0.918292979 |
| A membrane-boun | IBA | 1166.4 | 0.901748971 |
| The membrane surr | IBA; IEA | 1652.1 | 0.741117366 |
|  |  | 798.7 | 0.911856767 |
|  |  | 1616.2 | 0.837581982 |
|  |  | 325.8 | 0.760589319 |
| A lipid bilayer alon | IEA; IEA | 1218.9 | 0.884403971 |
|  |  | 357.6 | 0.771812081 |
| A membrane-boun | IBA; IBA; IBA | 792.6 | 0.817310119 |
| A membrane-boun | IBA; IBA; IBA | 798.7 | 0.772880932 |
| The end of a linear | IEA; IBA | 1042.2 | 0.823738246 |
|  |  | 1132.9 | 0.904669432 |
| A lipid bilayer alon | IEA; IEA; IEA | 753.2 | 0.785183218 |
|  |  | 1686.4 | 0.917753795 |

| | | | |
|---|---|---|---|
| | | 539.9 | 0.858121874 |
| | | 280.7 | 0.83683648 |
| The component of a | IEA | 348.1 | 0.911232404 |
| | | 869.6 | 0.927897884 |
| | | 703.4 | 0.772106909 |
| | | 592.2 | 0.854609929 |
| The contents of a c | IEA | 690.4 | 0.910052144 |
| A membrane-bound | IEA | 1862.6 | 0.750026844 |
| The lipid bilayer sur | IEA; IEA; IEA; IEA | 820.2 | 0.820043892 |
| The rigid or semi-ri | IEA; IEA; IEA | 1336.3 | 0.898151613 |
| The contents of a c | IBA | 799.1 | 0.759854837 |
| A chlorophyll-conta | IEA; IEA; IEA | 705.5 | 0.893692417 |
| | | 1018.5 | 0.886499755 |
| The contents of a c | IBA | 1018.9 | 0.785258612 |
| A lipid bilayer along | IEA; IEA | 1276.8 | 0.881030702 |
| A membrane-bound | IEA | 824.6 | 0.807785593 |
| A membrane-bound | IEA; IEA; IBA | 930.5 | 0.843202579 |
| The part of the cyto | IBA | 4839.7 | 0.937723413 |
| The outer, i.e. cytop | IEA; IEA; IEA | 1750.5 | 0.909625821 |
| A membrane-bound | IEA; IBA | 1163.8 | 0.90101392 |
| A lipid bilayer along | IEA; IEA | 1073.7 | 0.778336593 |
| A membrane-bound | IEA | 554.6 | 0.860259647 |
| | | 924.2 | 0.841376325 |
| | | 1320 | 0.89469697 |
| | | 391.7 | 0.759765126 |
| | | 1665.3 | 0.761064073 |
| A ubiquitin ligase c | IBA | 2061.3 | 0.766846165 |
| | | 370.8 | 0.929881338 |
| A ubiquitin ligase c | IEA | 2057.5 | 0.935698663 |
| | | 1082.4 | 0.755173688 |
| | | 621.1 | 0.789405893 |
| A focus in the cytop | IEA; IBA; IBA | 2179.4 | 0.866981738 |
| | | 925.2 | 0.826956334 |
| A membrane-bound | IBA | 1467.1 | 0.93994956 |
| The contents of a c | IBA | 1935.5 | 0.901885818 |
| | | 257.2 | 0.800155521 |

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|---|---|---|---|
|  |  | 1206.4 | 0.821700928 |
|  |  | 438 | 0.905251142 |
|  |  | 1656.1 | 0.801280116 |
|  |  | 550.4 | 0.894622093 |
|  |  | 755.9 | 0.809366318 |
| A membrane-boun | IEA | 629.8 | 0.766116227 |
| A lipid bilayer alon | IEA; IEA | 2598.8 | 0.825804217 |
| A lipid bilayer alon | IBA; IEA | 1633.2 | 0.963874602 |
| A large multisubuni | IEA; IBA; IBA | 307.8 | 0.963937622 |
| A membrane-boun | IEA; IEA; IEA | 750.3 | 0.919765427 |
| The irregular netwo | IEA; IBA | 663.4 | 0.906843533 |
| A semiautonomous | IBA | 1121.5 | 0.928845296 |
|  |  | 499.9 | 0.898179636 |
| The membrane surr | IBA; IEA; IEA | 1361 | 0.753416605 |
| A membrane-boun | IBA | 1534.2 | 0.825446487 |
|  |  | 443.9 | 0.921153413 |
| The irregular netwo | IEA; IBA; IEA; IEA | 355.2 | 0.873873874 |
| A membrane-boun | IEA | 1538.8 | 0.930400312 |
| A membrane-boun | IEA; IEA; IEA; IBA | 1283.9 | 0.91619285 |
|  |  | 1043.4 | 0.929748898 |
| A semiautonomous | IBA | 387.4 | 0.841249355 |
|  |  | 808.1 | 0.860537062 |
|  |  | 183.8 | 0.89445049 |
| A membrane-boun | IEA; IEA; IEA; IBA; IB | 701.9 | 0.743838154 |
|  |  | 275.3 | 0.7871413 |
|  |  | 403.2 | 0.845238095 |
|  |  | 547.9 | 0.804526373 |
| A membrane-boun | IEA | 999.2 | 0.795636509 |

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|---|---|---|---|
| | | 434.4 | 0.866482505 |
| | | 904.4 | 0.818664308 |
| A lipid bilayer along | IEA; IEA | 413.4 | 0.918722787 |
| A membrane-boun | IEA | 903.2 | 0.740699734 |
| A membrane-boun | IBA | 2123.3 | 0.916309518 |
| | | 428.4 | 0.83076564 |
| A membrane-boun | IEA | 799.2 | 0.885135135 |

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|---|---|---|---|
| A membrane-boun | IBA; IEA | 475.4 | 0.833193101 |
| A small organelle e | IEA | 1211.3 | 0.878395113 |
| A membrane-boun | IBA; IBA | 1354.7 | 0.770650328 |
| A membrane-boun | IBA; IEA | 1141.7 | 0.928615223 |
| A part of a cellular | IEA | 3799.7 | 0.856909756 |
| A membrane-boun | IC | 675.3 | 0.766177995 |
| | | 739 | 0.941136671 |

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|---|---|---|---|
| | | 444 | 0.880405405 |
| A lipid bilayer along | IEA; IEA | 768.1 | 0.919020961 |
| A membrane-boun | IEA | 387.2 | 0.915805785 |
| A SAGA-type histor | IBA; IEA; IBA | 491.5 | 0.879552391 |

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|---|---|---|---|
| The contents of a c | IEA | 1107.3 | 0.844938138 |
| A membrane-boun | IBA; IEA | 805.4 | 0.740004966 |
| A protein complex | IEA; IEA; IEA; IEA | 308.6 | 0.837005833 |
| A lipid bilayer alon | IEA | 1126.9 | 0.870263555 |
|  |  | 754.5 | 0.816699801 |
| A chromosome that | IBA; IBA; IEA | 1806.3 | 0.945579361 |
|  |  | 1194.7 | 0.822633297 |
| A chlorophyll-cont | IEA; IBA; IBA; IEA; IE | 661.9 | 0.855718386 |
| The space external | IEA; IEA; IEA | 546.8 | 0.870336503 |
|  |  | 1357.3 | 0.839387018 |
| A chlorophyll-cont | IEA; IEA | 654.2 | 0.826658514 |

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|---|---|---|---|
| A membrane-boun | IBA | 921.1 | 0.823037672 |
| A protein complex | IEA; IEA; IEA | 517.7 | 0.811280664 |
| The irregular netwo | IEA; IBA; IEA; IEA; IB | 575.4 | 0.878866875 |
| The membrane surr | IBA; IEA | 2267.4 | 0.888242039 |
| A lipid bilayer alon | IEA; IEA | 1227.5 | 0.925458248 |
| | | 1084.2 | 0.926858513 |
| A lipid bilayer alon | IEA; IEA | 1817.9 | 0.838659992 |
| The component of | IEA | 422.3 | 0.836372247 |
| | | 592.4 | 0.850945307 |
| A membrane-boun | IEA | 789.1 | 0.941325561 |
| | | 459.1 | 0.762361141 |
| | | 1099.4 | 0.835091868 |
| The membrane surr | IBA | 2321.1 | 0.791435095 |
| | | 455 | 0.907912088 |
| A membrane-boun | IEA | 632.8 | 0.755372946 |
| A chlorophyll-conta | IBA; IEA | 816 | 0.870343137 |
| | | 670.5 | 0.906935123 |
| A semiautonomous | IEA; IEA; IEA; IBA | 698.3 | 0.812115137 |
| | | 1894.6 | 0.832576797 |
| A small organelle e | IEA | 945.8 | 0.783252273 |
| | | 840.3 | 0.867785315 |
| A semiautonomous | IEA | 620.6 | 0.87802127 |
| A semiautonomous | IEA; IEA | 846.2 | 0.865516426 |
| | | 719.4 | 0.909368919 |
| | | 711.2 | 0.769685039 |
| The part of the cyto | IBA | 1610.8 | 0.86460144 |
| A membrane-boun | IBA | 1267.4 | 0.813949819 |

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|---|---|---|---|
| A membrane-boun | IC | 637.5 | 0.925803922 |
| | | 556 | 0.768165468 |
| A lipid bilayer alon | IEA; IEA | 926.7 | 0.79691378 |
| | | 1447.1 | 0.851426992 |
| A membrane-boun | IEA | 928.2 | 0.797134238 |
| A membrane-boun | IBA; IBA | 2021.2 | 0.847961607 |
| | | 1448 | 0.864917127 |
| A membrane-boun | IC | 875.7 | 0.763617677 |
| A chromosome that | IBA; IEA; IBA | 2664.9 | 0.808923412 |
| The membrane sur | IBA | 1682.3 | 0.899482851 |
| | | 1106.5 | 0.819430637 |
| The irregular netwo | IEA; IEA; IEA; IEA | 543.7 | 0.944454662 |
| | | 806.2 | 0.874844952 |
| A semiautonomous | IBA | 1184 | 0.860388514 |
| | | 301.6 | 0.806034483 |
| A membrane-boun | IEA; IBA | 643.9 | 0.832116788 |
| | | 493.9 | 0.844097996 |
| | | 1215.5 | 0.788646647 |
| The component of | IEA | 441.5 | 0.885164213 |
| The membrane sur | IBA | 766.5 | 0.859360731 |
| The membrane sur | IBA; IBA; IEA; IEA; IB | 473.7 | 0.887903737 |
| | | 373.7 | 0.881723307 |
| The lipid bilayer su | IEA; IEA; IBA; IBA; IE | 1949.6 | 0.865869922 |
| A semiautonomous | IBA | 846.2 | 0.859725833 |
| | | 805.2 | 0.755961252 |
| Organized structur | IBA | 1018 | 0.793516699 |
| | | 1514.1 | 0.825242718 |

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|---|---|---|---|
| | | 325.5 | 0.779416283 |
| A lipid bilayer alon | IEA; IEA | 1278.1 | 0.799859166 |
| | | 529.2 | 0.907218443 |
| A membrane-boun | IEA; IEA; IEA | 357.2 | 0.943729003 |
| | | 618.2 | 0.818990618 |
| The lipid bilayer su | IBA; IBA | 2091.7 | 0.914471483 |
| | | 242.3 | 0.848534874 |
| A membrane-boun | IEA; IBA | 1321.5 | 0.773060916 |
| | | 1329.1 | 0.897223685 |
| A protein complex | IBA | 1512.8 | 0.860523533 |
| A lipid bilayer alon | IBA; IEA | 1135 | 0.93092511 |
| | | 364.9 | 0.907371883 |
| A membrane-boun | IEA; IEA | 766 | 0.910313316 |
| A lipid bilayer alon | IEA; IEA; IEA | 1530.2 | 0.919749052 |
| A multisubunit prot | IBA; IBA | 2517.1 | 0.778673871 |
| A membrane-boun | IBA | 1373.2 | 0.822240023 |
| | | 247.3 | 0.792559644 |
| | | 722.6 | 0.875311376 |
| The part of the cyt | IBA | 888.1 | 0.930413242 |
| Organized structur | IBA | 975.4 | 0.879126512 |
| A lipid bilayer alon | IBA; IBA | 1222.2 | 0.826296842 |
| The membrane surr | IBA; IBA | 1177.1 | 0.936963724 |

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|---|---|---|---|
| A membrane-boun | IEA | 1498.9 | 0.857628928 |
| | | 1372.5 | 0.970418944 |
| Punctate structures | IBA; IEA | 2245 | 0.748953229 |
| A multisubunit prot | IEA | 1019.8 | 0.74808786 |
| The lipid bilayer su | IEA; IBA; IEA | 1138.4 | 0.908204498 |
| | | 812.8 | 0.836245079 |
| | | 680.5 | 0.858927259 |
| | | 796.9 | 0.954573974 |
| | | 411.3 | 0.789691223 |
| A lipid bilayer alon | IEA | 1019.3 | 0.846953792 |
| The irregular netwo | IBA | 701.9 | 0.868784727 |
| A membrane-boun | IEA | 1357.6 | 0.840601061 |
| The contents of a c | IBA | 504.6 | 0.9078478 |
| A membrane-boun | IEA; IEA; IEA; IEA | 2411.4 | 0.88264079 |
| | | 1974.3 | 0.755508281 |
| A lipid bilayer alon | IEA; IEA | 556.3 | 0.891785008 |
| | | 199.8 | 0.924424424 |
| | | 701 | 0.87617689 |
| | | 1129.9 | 0.852907337 |
| A membrane-boun | IEA | 280.9 | 0.861160555 |
| A lipid bilayer alon | IEA; IEA | 993.9 | 0.936009659 |
| A membrane-boun | IEA | 787.4 | 0.828930658 |
| A semiautonomous | IBA | 1331.2 | 0.759990986 |
| | | 910.6 | 0.78201186 |
| The contents of a c | IEA | 793.8 | 0.874527589 |

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|---|---|---|---|
| | | 821.3 | 0.768902959 |
| A semiautonomous | IEA; IEA; IBA | 1768 | 0.854751131 |
| | | 706.5 | 0.893701345 |
| The membrane surr | IBA | 1169.4 | 0.893706174 |
| A membrane-boun | IEA | 1355.1 | 0.828499742 |
| A membrane-boun | IEA; IEA; IEA | 2167.1 | 0.894190393 |
| A compact and hig | IEA; IEA | 767.4 | 0.743419338 |
| | | 984 | 0.848678862 |
| | | 496.2 | 0.879685611 |
| | | 1336.2 | 0.762460709 |
| The contents of a c | IBA; IBA; IBA | 1928.6 | 0.838483874 |
| | | 1278.1 | 0.830451451 |
| A membrane-boun | IEA; IEA; IBA; IEA | 2224.8 | 0.8014653 |
| The lipid bilayer su | IBA; IEA; IBA; IBA | 543.9 | 0.870196727 |
| | | 1250.8 | 0.933882315 |
| | | 840.1 | 0.836090942 |
| | | 501.4 | 0.915237335 |
| | | 1111.8 | 0.886940097 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA; IEA | 2001.7 | 0.938052655 |
| | | 887.5 | 0.73971831 |
| A membrane-boun | IBA | 2327.4 | 0.895935379 |
| | | 929.2 | 0.83329746 |
| The irregular netwo | IBA; IEA; IEA | 1496 | 0.95381016 |
| The part of the cyto | IBA; IEA; IEA | 788.6 | 0.916180573 |
| A membrane-boun | IEA | 887.8 | 0.755688218 |
| | | 753.6 | 0.800424628 |
| A membrane-boun | IEA | 2623.4 | 0.752611115 |
| A lipid bilayer alon | IEA | 1442.4 | 0.950291181 |
| A membrane-boun | IEA | 1204.4 | 0.866240452 |
| A ubiquitin ligase c | IBA | 1058 | 0.870510397 |
| A semiautonomous | IBA | 1107.9 | 0.91858471 |
| A lipid bilayer alon | IEA; IEA | 755.8 | 0.757740143 |
| | | 1062.5 | 0.742305882 |
| A membrane-boun | IC | 500.7 | 0.879768324 |
| | | 818.6 | 0.823356951 |
| A membrane-boun | IEA; IEA; IEA; IBA; IE | 1043 | 0.841418984 |
| A membrane-boun | IEA | 994.5 | 0.773755656 |

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|---|---|---|---|
| | | 786 | 0.908778626 |
| | | 1596 | 0.94122807 |
| | | 1543.5 | 0.870489148 |
| A membrane-boun | IEA; IEA | 724.7 | 0.821029391 |
| A lipid bilayer alon | IEA; IEA | 1118.3 | 0.9107574 |
| A membrane-boun | IEA | 698.2 | 0.83428817 |
| A membrane-boun | IBA; IEA | 1042.7 | 0.761676417 |
| The membrane sur | IEA | 1360.6 | 0.833308834 |
| A lipid bilayer alon | IEA; IEA | 608.3 | 0.92832484 |
| That part of the nu | IEA; IBA | 1144.9 | 0.740326666 |
| | | 927.3 | 0.841259571 |
| The membrane sur | IBA; IEA; IEA | 893.9 | 0.894954693 |
| | | 259.4 | 0.81688512 |
| | | 908.6 | 0.825005503 |
| | | 1178 | 0.919269949 |
| | | 602.1 | 0.906992194 |
| A semiautonomous | IBA | 1940.6 | 0.850716273 |
| A membrane-boun | IEA; IEA; IEA | 1519.4 | 0.819468211 |
| | | 1180.2 | 0.873157092 |
| | | 372.6 | 0.83870102 |
| The lipid bilayer su | IBA; IEA; IBA; IEA | 1267.2 | 0.863557449 |
| A membrane-boun | IEA | 167 | 0.825748503 |
| | | 1352.8 | 0.910851567 |

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|---|---|---|---|
| A highly compacted | IBA; IEA; IEA | 1032.4 | 0.760654785 |
|  |  | 624.6 | 0.749439641 |
| A membrane-boun | IBA | 1132.1 | 0.856991432 |
| A membrane-boun | IEA | 1023 | 0.753861193 |
|  |  | 451.7 | 0.847907903 |
| A chlorophyll-cont | IEA; IEA | 520 | 0.877115385 |
| A vacuole to which | IBA; IBA; IEA; IEA; IB | 937.1 | 0.940134457 |
|  |  | 687 | 0.892576419 |
|  |  | 303.7 | 0.936450445 |
| A lipid bilayer alon | IEA; IEA | 932.6 | 0.883873043 |
|  |  | 569.2 | 0.894764582 |
| A lipid bilayer alon | IEA; IEA | 1150.4 | 0.744697497 |
| The contents of a c | IBA | 2211.8 | 0.801293064 |
|  |  | 1810.5 | 0.768572218 |
| A membrane-boun | IEA | 662.1 | 0.872828878 |
| A membrane-boun | IBA | 544.3 | 0.795884622 |
|  |  | 457.5 | 0.914754098 |
| The membrane sur | IBA; IBA; IBA | 2057.7 | 0.79739515 |

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|---|---|---|---|
| A lipid bilayer alon | IBA; IBA | 1256.3 | 0.841757542 |
| | | 1442.6 | 0.934978511 |
| A lipid bilayer alon | IEA; IEA | 755.8 | 0.927626356 |
| The membrane sur | IEA; IBA; IEA | 795.9 | 0.930518909 |
| A lipid bilayer alon | IEA; IEA | 1350.3 | 0.794638229 |
| | | 249 | 0.786746988 |
| | | 1688.9 | 0.793593463 |
| | | 968 | 0.765805785 |
| | | 140.2 | 0.89871612 |
| The irregular netwo | IBA; IBA; IBA | 351.7 | 0.924367359 |
| | | 846.1 | 0.941378088 |
| The membrane sur | IBA; IEA; IEA | 360.1 | 0.90002777 |
| A membrane-boun | IEA | 1802.2 | 0.924037288 |
| The membrane sur | IEA; IEA; IEA | 1136.3 | 0.912259087 |
| | | 572.2 | 0.911045089 |
| | | 1187.5 | 0.874273684 |
| The contents of a c | IEA; IEA; IEA | 3866.2 | 0.903083131 |
| A protein complex | IBA; IEA; IEA; IEA; IB | 1843.5 | 0.968321128 |
| A lipid bilayer alon | IEA; IEA | 628.8 | 0.761609415 |
| | | 363 | 0.872176309 |
| A lipid bilayer alon | IEA; IEA | 1517.6 | 0.920927781 |
| A membrane-boun | IEA | 697.2 | 0.907917384 |
| The lipid bilayer su | IEA; IEA | 1072.2 | 0.772617049 |
| A membrane-boun | IEA | 951.2 | 0.75567704 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA | 2666.5 | 0.966435402 |
| | | 445.6 | 0.94008079 |
| The lipid bilayer su | IEA; IBA; IEA; IBA; IE | 981.6 | 0.917379788 |
| | | 1292.7 | 0.946545989 |
| | | 2712.8 | 0.797589207 |
| Complex that trans | IEA; IEA; IEA | 235.2 | 0.87372449 |
| The lipid bilayer su | IBA; IEA | 821.4 | 0.919771122 |
| The membrane surr | IBA; IEA | 763 | 0.817300131 |
| | | 1964.5 | 0.893917027 |
| | | 1328.8 | 0.833157736 |
| The inner, i.e. lume | IBA; IBA | 1725.7 | 0.932780901 |
| | | 971.3 | 0.803356327 |
| A lipid bilayer along | IEA; IEA | 1370.2 | 0.920157641 |
| | | 1051.7 | 0.891318817 |
| The space external | IEA; IEA; IEA | 1338 | 0.894469357 |
| | | 1119 | 0.894191242 |
| A membrane-boun | IEA; IBA; IBA | 605.7 | 0.91959716 |
| | | 440.4 | 0.920072661 |
| The membrane surr | IBA; IEA; IEA; IBA; IE | 656.4 | 0.851462523 |

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|---|---|---|---|
| | | 1151.1 | 0.854400139 |
| | | 960.4 | 0.809246147 |
| A closed structure, | IBA | 1117.7 | 0.886821151 |
| The membrane surr | IEA; IBA; IEA | 1192.7 | 0.929152343 |
| A membrane-boun | IC; IEA | 715.4 | 0.79829466 |
| The contents of a c | IBA | 1228.3 | 0.956932346 |
| A membrane-boun | IBA | 582.5 | 0.743862661 |
| A lipid bilayer alon | IBA; IEA | 406.1 | 0.838217188 |
| The irregular netwo | IBA; IBA; IEA; IEA | 460.5 | 0.972855592 |
| A membrane-boun | IEA | 2416 | 0.931663907 |
| A membrane-boun | IEA | 2529.7 | 0.906826896 |
| The membrane surr | IBA; IBA | 931.8 | 0.897724834 |

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|---|---|---|---|
| A prelysosomal end | IEA; IBA; IEA; IBA | 1335.5 | 0.879820292 |
| The irregular netwo | IBA; IBA; IEA; IEA | 1606.8 | 0.902352502 |
|  |  | 1313.6 | 0.764387942 |
|  |  | 2281.2 | 0.907899351 |
|  |  | 517.5 | 0.754589372 |
| An RNA polymerase | IEA; IBA; IBA | 1486.3 | 0.943483819 |
| A membrane-boun | IBA; IBA | 395 | 0.861012658 |
| A membrane-boun | IEA; IEA | 795.6 | 0.90925088 |
| Any member of a fa | IEA; IEA; IEA | 1204.5 | 0.772768784 |
|  |  | 1319.3 | 0.895399075 |
|  |  | 2239.1 | 0.862668036 |
| The space external | IEA; IBA | 824.2 | 0.878427566 |
|  |  | 842.5 | 0.784451039 |

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|---|---|---|---|
| The space external | IEA; IEA | 860.4 | 0.740237099 |
|  |  | 1517.8 | 0.809724601 |
| The irregular netwo | IBA | 839.4 | 0.849773648 |
|  |  | 706.5 | 0.868931352 |
| A membrane-boun | IEA | 603.8 | 0.925968864 |
| The membrane surr | IBA; IEA; IEA; IBA | 399.6 | 0.755255255 |
| A membrane-boun | IBA | 319.9 | 0.843075961 |
| A membrane-boun | IEA | 632.3 | 0.755337656 |
|  |  | 255.8 | 0.80218921 |
| A small, dense bod | IBA; IBA | 1110.6 | 0.797136683 |
| A semiautonomous | IBA | 2426.2 | 0.938628308 |
| The membrane surr | IBA | 795.2 | 0.876257545 |
| A lipid bilayer alon | IEA; IEA | 1107.5 | 0.879819413 |
| The contents of a c | IEA | 409.9 | 0.868016589 |
|  |  | 644.3 | 0.913083967 |
|  |  | 1172.5 | 0.921535181 |
|  |  | 1013.4 | 0.887408723 |
| A semiautonomous | IBA | 715.7 | 0.90275255 |
| A protein complex | IBA; IBA | 1823.7 | 0.776662828 |
|  |  | 1675.8 | 0.904821578 |
| The contents of a c | IBA | 642.1 | 0.865597259 |
| A lipid bilayer alon | IEA; IEA | 1579 | 0.884863838 |
| Any complex forme | IBA; IBA | 2694.9 | 0.895766077 |
|  |  | 1202 | 0.76921797 |
| The large subunit o | IBA | 1978.1 | 0.777109347 |
| A lipid bilayer alon | IEA; IEA | 181 | 0.793370166 |

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|---|---|---|---|
| A chlorophyll-conta | IEA; IEA | 300.7 | 0.910542069 |
| The inner, i.e. lume | IBA | 514 | 0.855058366 |
| A lipid bilayer alon | IEA; IEA | 1321.9 | 0.929495423 |
| The contents of a c | IEA; IBA; IEA; IEA | 2015 | 0.833548387 |
| The part of the cyto | IEA | 1735.9 | 0.839218849 |
| | | 1201.8 | 0.89482443 |
| The part of the cyto | IEA; IBA | 1424.9 | 0.935784967 |
| | | 1176.9 | 0.842127623 |
| | | 776.8 | 0.879634398 |
| | | 1660.1 | 0.840491537 |
| | | 779.3 | 0.775311177 |
| The contents of a c | IBA; IEA | 1232.4 | 0.861814346 |
| A semiautonomous | IBA | 188 | 0.778191489 |
| The double lipid bil | IEA; IEA; IBA | 767.6 | 0.865033872 |
| | | 520.2 | 0.876778162 |
| The part of the cyto | IEA; IBA | 1002.5 | 0.843690773 |
| | | 427.3 | 0.893283407 |
| A macromolecular | IBA | 1059.6 | 0.919592299 |
| A membrane-boun | IC | 435 | 0.78137931 |
| A membrane-boun | IBA | 941.1 | 0.784401233 |
| The membrane surr | IBA; IBA | 322.3 | 0.813838039 |
| A membrane-boun | IBA | 3981.6 | 0.805856942 |
| | | 469.3 | 0.75964202 |
| A membrane-boun | IEA; IEA; IBA | 837.7 | 0.840157574 |
| | | 271.5 | 0.811049724 |
| A membrane-boun | IEA; IEA | 2424.5 | 0.809651475 |
| | | 723.9 | 0.813924575 |
| A membrane-boun | IBA; IBA | 1824.7 | 0.918342741 |
| The contents of a c | IEA | 586.9 | 0.793150452 |
| A semiautonomous | IBA | 1214.1 | 0.849353431 |
| The component of | IEA | 1179.7 | 0.850046622 |
| | | 588.1 | 0.881142663 |
| A membrane-boun | IEA; IEA | 1327.4 | 0.974235347 |
| | | 573.3 | 0.828187685 |
| A membrane-boun | IEA; IEA | 1544.8 | 0.845287416 |
| | | 271.8 | 0.793966152 |

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|---|---|---|---|
| Cyclin-dependent p | IBA; IBA; IBA | 979 | 0.743820225 |
| The contents of a c | IBA | 1525 | 0.829442623 |
| | | 379.8 | 0.822801474 |
| The membrane surr | IEA; IEA; IEA | 382 | 0.771204188 |
| A membrane-boun | IBA | 1714.1 | 0.875678198 |
| A membrane-boun | IEA; IEA; IEA | 1156.5 | 0.841158668 |
| | | 4119.6 | 0.93557627 |
| The membrane surr | IEA; IEA; IEA | 431.6 | 0.954819277 |
| | | 1813.1 | 0.741327009 |
| | | 227.9 | 0.764809127 |
| Organized structur | IBA | 1478.1 | 0.824436777 |
| The contents of a c | IBA; IBA | 607.2 | 0.85342556 |
| | | 274.2 | 0.741429613 |
| A semiautonomous | IEA | 457.1 | 0.813826296 |
| | | 402.1 | 0.919920418 |
| The contents of a c | IEA; IBA; IEA | 1799.8 | 0.896099567 |
| A protein complex | IEA | 1445.1 | 0.869490001 |
| A ribonucleoprotei | IEA | 883.4 | 0.8182024 |
| The membrane surr | IBA; IEA; IEA | 1511.7 | 0.89283588 |
| A semiautonomous | IEA; IBA | 1032.6 | 0.931725741 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA; IE | 353.4 | 0.850028297 |
| | | 689.3 | 0.74916582 |
| A lipid bilayer alon | IEA; IEA | 713.7 | 0.935547149 |
| | | 906.6 | 0.767482903 |
| The part of a cell e | IBA | 329 | 0.841337386 |
| | | 1872.7 | 0.941528275 |
| Organized structur | IBA | 1502.2 | 0.875782186 |
| A membrane-boun | IEA | 1163.6 | 0.756445514 |
| A membrane-boun | IBA | 2324 | 0.786359725 |
| | | 984.2 | 0.957630563 |
| A heterotrimeric tra | IEA | 1215.6 | 0.80207305 |
| The contents of a c | IEA; IEA; IEA; IEA; IE | 1707.6 | 0.904134458 |
| A protein complex | IBA | 1426.5 | 0.841009464 |
| | | 706.7 | 0.88665629 |
| A membrane-boun | IEA | 915.1 | 0.86045241 |

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|---|---|---|---|
| A lipid bilayer along | IEA; IEA | 1621.6 | 0.925752343 |
| A semiautonomous | IBA | 1688.8 | 0.761842729 |
| A protein complex t | IBA | 578.2 | 0.859910066 |
| | | 748.2 | 0.864474739 |
| | | 672.8 | 0.918549346 |
| | | 1910.8 | 0.889941386 |
| | | 343.3 | 0.778327993 |
| | | 1779.7 | 0.953700062 |
| A membrane-bound | IBA | 604.5 | 0.753349876 |
| | | 1863.7 | 0.745237967 |
| A semiautonomous | IBA; IEA; IEA | 580.3 | 0.910218852 |
| A lipid bilayer along | IEA; IEA | 1408.3 | 0.929844493 |
| | | 1334 | 0.845202399 |
| A membrane-bound | IEA | 1436 | 0.818593315 |
| | | 1003.8 | 0.82825264 |
| A lipid bilayer along | IEA; IEA | 1536.9 | 0.815082309 |
| A lipid bilayer along | IBA; IEA | 1168.2 | 0.904040404 |
| | | 794.8 | 0.905007549 |
| | | 1479.6 | 0.824209246 |
| A lipid bilayer along | IEA | 1790.5 | 0.840379782 |
| | | 1058.7 | 0.772740153 |
| | | 1394.3 | 0.878863946 |
| | | 785.6 | 0.858706721 |
| A chlorophyll-conta | IEA | 963.7 | 0.919477016 |
| A protein complex t | IEA; IEA; IBA | 444.5 | 0.880089989 |
| A membrane-bound | IEA; IEA; IEA; IEA | 1301.4 | 0.808283387 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA; IEA; IBA | 2274.7 | 0.953971952 |
| | | 446.1 | 0.76216095 |
| | | 1162.4 | 0.946834136 |
| | | 767.1 | 0.75479077 |
| A lipid bilayer alon | IEA | 1067.6 | 0.827088797 |
| | | 227.3 | 0.827980642 |

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|---|---|---|---|
| | | 742.2 | 0.766774454 |
| A membrane-boun | IBA; IBA | 738.6 | 0.884375846 |
| | | 821.2 | 0.933511934 |
| | | 831.1 | 0.770906028 |
| | | 1521.1 | 0.90296496 |
| The membrane surr | IBA | 1621.6 | 0.832696103 |
| A complex that is c | IBA | 2111 | 0.91814306 |
| A lipid bilayer alon | IEA; IEA | 1136.8 | 0.871393385 |
| | | 911.6 | 0.777095217 |
| | | 1209.8 | 0.923375765 |
| A protein complex | IBA; IEA; IEA; IEA | 611.4 | 0.833660451 |
| A lipid bilayer alon | IEA; IEA | 1389.1 | 0.823698798 |
| | | 2322.5 | 0.948159311 |
| | | 2519.5 | 0.826433816 |
| | | 545.8 | 0.92616343 |
| A closed structure, | IEA | 958.1 | 0.921615698 |
| A lipid bilayer alon | IEA | 1096.3 | 0.814010763 |
| The Y-shaped regi | IEA; IEA | 713.4 | 0.825904121 |
| A chlorophyll-cont | IEA; IEA; IEA; IEA | 1332.6 | 0.842488369 |
| A membrane-boun | IEA; IBA; IBA; IEA; IE | 489 | 0.896523517 |
| A membrane-boun | IBA | 2025.3 | 0.823976695 |
| The membrane surr | IBA; IEA; IEA; IBA | 386.4 | 0.813405797 |
| The membrane surr | IEA | 689.7 | 0.825431347 |
| A lipid bilayer alon | IEA; IEA | 748.3 | 0.865962849 |
| A lipid bilayer alon | IEA; IEA | 219.1 | 0.884984026 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA; IEA | 2529.3 | 0.832167003 |
|  |  | 982.4 | 0.858713355 |
| A lipid bilayer alon | IEA; IEA; IEA | 405.4 | 0.931179082 |
|  |  | 997.5 | 0.904461153 |
|  |  | 1295 | 0.882857143 |
|  |  | 1352.6 | 0.864335354 |
| The membrane surr | IEA | 2307 | 0.953315995 |
| The network of inte | IBA; IEA; IEA | 578.4 | 0.955567082 |
|  |  | 958 | 0.869624217 |
| A membrane-boun | IEA | 3968.6 | 0.908809152 |
|  |  | 1185.4 | 0.948456217 |
| A lipid bilayer alon | IEA; IEA | 178.2 | 0.853535354 |
|  |  | 556.4 | 0.918583753 |
| The contents of a c | IEA; IEA; IEA; IEA; IB | 1014 | 0.783234714 |
| A membrane-boun | IEA | 769.5 | 0.88317089 |
| The outer, i.e. cyto | IEA; IEA; IEA | 2454.9 | 0.748625199 |
|  |  | 1294.2 | 0.844768969 |
| A multisubunit com | IEA | 1202.1 | 0.930288662 |
| A membrane-boun | IBA; IBA | 779 | 0.901155327 |
| A membrane-boun | IEA; IEA | 1096 | 0.910492701 |
| A membrane-boun | IEA; IEA | 623.5 | 0.805613472 |

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|---|---|---|---|
| A chlorophyll-conta | IEA | 2116.5 | 0.789936215 |
| A part of a cellular | IEA | 2505 | 0.906986028 |
|  |  | 2938.7 | 0.886854732 |

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|---|---|---|---|
| The membrane surr | IBA; IBA | 899 | 0.930367075 |
|  |  | 1725.5 | 0.740423066 |
| A lipid bilayer alon | IEA; IEA | 513.3 | 0.863822326 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1918 | 0.886183525 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 673 | 0.816344725 |
|  |  | 1496.9 | 0.749081435 |
|  |  | 306.9 | 0.892798957 |
|  |  | 615 | 0.755121951 |

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|---|---|---|---|
| A membrane-boun | IEA | 1161.8 | 0.806507144 |
| A membrane-boun | IEA; IEA | 2519.1 | 0.823587789 |
| The lipid bilayer su | IBA; IEA; IBA | 851.7 | 0.88493601 |
|  |  | 993.4 | 0.804207771 |
| A semiautonomous | IBA; IEA | 1758.9 | 0.902495878 |
| The pigmented me | IBA | 401.1 | 0.852904513 |
| The lipid bilayer su | IEA; IEA; IBA | 1765.9 | 0.918285294 |
|  |  | 434.9 | 0.887790297 |
|  |  | 1608.4 | 0.796568018 |
| A lipid bilayer alon | IEA; IEA | 813.6 | 0.947394297 |
|  |  | 294.9 | 0.806375042 |

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|---|---|---|---|
| A lipid bilayer along | IEA | 1397.2 | 0.81219582 |
| A membrane-bound | IEA | 2154.8 | 0.932569148 |
| | | 550 | 0.874 |
| Any microtubule in | IBA | 2708.9 | 0.7929787 |
| | | 996.2 | 0.83798434 |
| The larger of the tw | IBA | 307 | 0.878501629 |
| A small, dense body | IEA; IEA | 526.8 | 0.92350038 |
| The contents of a c | IEA; IBA; IBA | 1919.8 | 0.924262944 |
| The outer, i.e. cytop | IBA | 2361.2 | 0.908139929 |
| | | 151.6 | 0.863456464 |
| A heterotrimeric tra | IBA | 274.5 | 0.844444444 |
| A membrane-bound | IEA; IBA; IEA | 1632 | 0.753921569 |
| | | 608.4 | 0.844345825 |

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|---|---|---|---|
| A membrane-boun | IBA | 1259.5 | 0.896546249 |

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| | | 966.5 | 0.863010864 |
| A lipid bilayer alon | IEA; IEA | 238.2 | 0.742653233 |
| A semiautonomous | IEA | 888.8 | 0.824932493 |
| | | 660.5 | 0.754579864 |
| A lipid bilayer alon | IEA; IEA | 885.3 | 0.919010505 |
| | | 1085.2 | 0.854496867 |
| | | 203.6 | 0.765717092 |
| A chlorophyll-cont | IEA; IBA | 1088.4 | 0.909132672 |

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|---|---|---|---|
| | | 1903.9 | 0.842008509 |

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|---|---|---|---|
| | | 4927.1 | 0.797446774 |
| | | 708 | 0.854661017 |
| | | 1205.1 | 0.740851382 |
| A membrane-boun | IEA; IEA; IEA | 1842.1 | 0.910699745 |
| A lipid bilayer alon | IEA; IEA | 1122.6 | 0.893461607 |
| The component of | IEA | 1133.2 | 0.948464525 |
| A membrane-boun | IEA | 726.9 | 0.958866419 |
| | | 1575.8 | 0.887612641 |
| Organized structur | IBA | 1495.9 | 0.868173006 |
| The contents of a c | IBA | 1606.1 | 0.750326879 |
| The double lipid bil | IEA; IEA; IEA; IEA; IE | 902.7 | 0.860972638 |
| | | 1788 | 0.925727069 |

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|---|---|---|---|
| | | 375.7 | 0.929997338 |
| | | 752.2 | 0.860941239 |
| A lipid bilayer alon | IEA; IEA | 681.4 | 0.953478133 |
| | | 329.9 | 0.823279782 |
| | | 479.8 | 0.780533556 |
| | | 1461.7 | 0.860299651 |
| A membrane-boun | IEA | 2075.6 | 0.802225862 |
| A lipid bilayer alon | IEA; IBA | 1212 | 0.940264026 |
| A membrane-boun | IBA | 975.7 | 0.801065901 |
| | | 784.6 | 0.91282182 |
| A membrane-boun | IEA | 421.2 | 0.75617284 |
| The contents of a c | IBA; IBA | 1389.8 | 0.951431861 |
| | | 1069.8 | 0.937651898 |
| A ubiquitin ligase c | IBA | 1092.5 | 0.870755149 |
| | | 3096.2 | 0.923906724 |
| | | 1596.3 | 0.748982021 |
| The irregular netwo | IEA; IEA; IEA | 531.5 | 0.913828786 |
| A membrane-boun | IBA; IBA | 995.4 | 0.902250352 |
| The end of a linear | IEA; IBA; IBA; IBA | 349 | 0.85530086 |
| | | 3828.1 | 0.871032627 |
| | | 1742.4 | 0.800906795 |
| | | 1299.1 | 0.789546609 |

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|  |  | 731.6 | 0.947102242 |
|  |  | 1265.1 | 0.858351118 |
| A semiautonomous | IBA | 1134 | 0.887654321 |
| A membrane-boun | IBA | 1123.5 | 0.758878505 |
| The membrane sur | IBA | 640.2 | 0.841611996 |
|  |  | 1437.3 | 0.919084394 |
| A membrane-boun | IBA; IBA | 643.3 | 0.82838489 |
| The lipid bilayer su | IEA; IEA | 1416.5 | 0.838545711 |
| The inner, i.e. lume | IBA; IBA; IEA | 472.1 | 0.784155899 |
| Cyclin-dependent p | IBA; IBA | 1448.2 | 0.888206049 |
|  |  | 1284 | 0.80288162 |
|  |  | 582.7 | 0.836451004 |
|  |  | 662.8 | 0.878998189 |
|  |  | 974.2 | 0.849312256 |
|  |  | 1182.4 | 0.801251691 |
| The membrane sur | IBA; IBA | 1934.5 | 0.946394417 |
| A membrane-boun | IBA; IBA; IEA | 1006.7 | 0.762491308 |
| A membrane-boun | IEA; IEA; IEA | 1026.7 | 0.816207266 |
| A membrane-boun | IBA; IBA | 1519.1 | 0.743400698 |
|  |  | 1022.2 | 0.868225396 |
|  |  | 254.1 | 0.826446281 |
| A membrane-boun | IEA; IBA; IBA | 3670.3 | 0.869710923 |
|  |  | 141 | 0.780851064 |
| The contents of a c | IBA | 529.9 | 0.814304586 |

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|---|---|---|---|
| | | 1195.7 | 0.745337459 |
| Organized structure | IBA | 1007.1 | 0.811637375 |
| The lipid bilayer su | IEA; IEA | 624.1 | 0.861560647 |
| Organized structure | IBA | 1069.2 | 0.907875047 |
| A lipid bilayer along | IEA; IEA | 715.4 | 0.936678781 |
| | | 1105.5 | 0.851922207 |
| | | 1695.7 | 0.912189656 |
| A membrane-boun | IBA | 623.8 | 0.901090093 |
| | | 702 | 0.848860399 |
| Organized structure | IEA | 1629.3 | 0.957589149 |
| The array of microt | IEA; IEA; IBA; IBA | 1573.3 | 0.878090638 |
| | | 1067.6 | 0.83270888 |
| A membrane-boun | IEA | 898.7 | 0.780794481 |
| The membrane surr | IBA; IBA | 1014.5 | 0.917693445 |
| The space external | IEA | 855.1 | 0.884224067 |
| The contents of a c | IEA; IEA | 351.2 | 0.933940774 |
| The contents of a c | IBA; IEA; IEA | 3182.2 | 0.812142543 |
| A protein complex | IBA | 1485.4 | 0.804901037 |
| A protein complex | IEA; IEA; IBA | 509.6 | 0.795918367 |
| | | 1711.5 | 0.812445223 |
| | | 814.3 | 0.931106472 |
| The membrane surr | IBA; IBA; IEA; IEA; IB | 467.6 | 0.865269461 |
| The irregular netwo | IEA; IEA; IEA | 1265.2 | 0.930287702 |
| | | 537.8 | 0.911863146 |
| A structure lying ex | IEA | 789.2 | 0.872782565 |
| The contents of a c | IEA | 1010.2 | 0.873490398 |
| A membrane-boun | IEA; IBA | 1805.3 | 0.92782363 |

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|---|---|---|---|
| | | 1015.2 | 0.836189913 |
| | | 775.1 | 0.871629467 |
| | | 878.1 | 0.848764378 |
| The lipid bilayer su | IEA; IEA | 1090 | 0.873669725 |
| The irregular netwo | IEA; IBA; IEA; IEA; IE | 476.4 | 0.804156171 |
| The component of | IEA | 206.8 | 0.912959381 |
| A membrane-boun | IBA | 1057.2 | 0.909950813 |
| | | 1308.3 | 0.878773982 |
| | | 453.6 | 0.797398589 |
| | | 1237.3 | 0.923219914 |
| | | 1901.5 | 0.770602156 |
| The larger of the tw | IBA; IEA | 324.5 | 0.783975347 |
| A membrane-boun | IBA | 772.6 | 0.783717318 |
| A lipid bilayer alon | IEA | 1035.7 | 0.948151009 |
| A membrane-boun | IEA; IBA; IEA | 1172.5 | 0.929808102 |
| | | 177.2 | 0.75 |
| | | 2493.4 | 0.887342584 |
| | | 565.1 | 0.925322952 |
| | | 1460.2 | 0.903917272 |
| | | 1805 | 0.822105263 |
| | | 1079.3 | 0.739924025 |

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|---|---|---|---|
| | | 1343.9 | 0.964208646 |
| | | 1111.2 | 0.942764579 |
| A membrane-boun | IBA; IBA | 1710.7 | 0.834629099 |
| | | 829.5 | 0.898613623 |
| The contents of a c | IEA | 747.2 | 0.838998929 |
| A lipid bilayer alon | IEA; IEA | 752.4 | 0.962519936 |
| A lipid bilayer alon | IEA; IEA | 1486.9 | 0.914452889 |
| | | 1387.9 | 0.882700483 |
| The membrane surr | IBA; IEA; IEA | 871.5 | 0.914974182 |
| | | 594.1 | 0.934691129 |
| | | 1192.2 | 0.86176816 |
| | | 1126.2 | 0.871426034 |
| A membrane-boun | IBA | 617 | 0.794165316 |
| | | 1780.5 | 0.850098287 |
| | | 674.3 | 0.899599585 |
| | | 698.7 | 0.827966223 |
| A membrane-boun | IBA; IBA | 1143 | 0.866579178 |
| The smaller of the t | IBA; IEA; IEA; IEA | 699.4 | 0.866599943 |
| A lipid bilayer alon | IEA; IEA | 419.7 | 0.91922802 |
| | | 1456.6 | 0.968007689 |
| The contents of a c | IBA | 1085.2 | 0.895134537 |
| | | 499.6 | 0.783626902 |
| Any dynein comple | IBA; IEA; IEA | 367 | 0.870572207 |
| | | 1997.5 | 0.795594493 |
| A membrane-boun | IEA | 1112.1 | 0.855138926 |

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|---|---|---|---|
| The space external | IEA | 918.2 | 0.777063821 |
| A membrane-boun | IEA | 774.4 | 0.879261364 |
|  |  | 249.7 | 0.757308771 |
| A membrane-boun | IEA | 498.2 | 0.901043758 |
| A membrane-boun | IEA; IEA; IBA | 1001 | 0.901698302 |
| A small, dense bod | IEA | 811.4 | 0.892038452 |
| A membrane-boun | IEA; IEA | 928.1 | 0.799375067 |
| A semiautonomous | IEA; IEA | 863.2 | 0.920064875 |
| A lipid bilayer alon | IEA; IEA | 418.6 | 0.859531773 |
|  |  | 865.4 | 0.800554657 |
| The membrane surr | IBA; IEA | 734.1 | 0.866230759 |
| A lipid bilayer alon | IEA; IEA | 799.3 | 0.864631553 |
|  |  | 1215.8 | 0.89545978 |
| A lipid bilayer alon | IEA; IEA | 1072 | 0.920522388 |
|  |  | 1093.2 | 0.822173436 |
|  |  | 1374 | 0.765720524 |
| A chlorophyll-cont | IEA; IEA | 697.6 | 0.887184633 |

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|---|---|---|---|
| | | 331.9 | 0.872853269 |
| | | 1356.3 | 0.861387599 |
| | | 837 | 0.810991637 |
| A membrane-boun | IBA | 1345.9 | 0.913143621 |
| | | 783.8 | 0.968614442 |
| | | 881.7 | 0.860496768 |
| | | 780.9 | 0.964656166 |
| | | 1385.2 | 0.807248051 |
| | | 1911 | 0.768969126 |
| The contents of a c | IBA | 586.2 | 0.768509041 |
| A membrane-boun | IBA | 758.6 | 0.898233588 |
| A lipid bilayer alon | IEA; IEA | 1358.3 | 0.808805124 |
| A membrane-boun | IBA; IEA; IEA; IEA; IB | 1153 | 0.945706852 |
| The space external | IEA; IEA; IEA | 625.9 | 0.908292059 |
| The membrane surr | IBA | 1053.1 | 0.886145665 |
| | | 314.7 | 0.743247537 |
| A membrane-boun | IBA | 374.4 | 0.937232906 |
| The contents of a c | IBA; IEA | 1851.8 | 0.860190085 |
| | | 1748.2 | 0.801052511 |
| | | 567.1 | 0.90142832 |
| A closed structure, | IEA; IEA; IEA | 772.8 | 0.867883023 |
| | | 819.9 | 0.853762654 |
| A membrane-boun | IBA; IEA | 4055.4 | 0.823593234 |
| A membrane-boun | IBA | 2759.1 | 0.81744047 |
| Punctate structures | IBA; IBA; IEA; IBA; IB | 1305.4 | 0.822200092 |
| A membrane-boun | IEA; IEA | 3983.3 | 0.827303994 |
| The membrane surr | IBA; IBA | 389.7 | 0.829612522 |
| A semiautonomous | IEA; IEA; IEA; IEA | 1851.9 | 0.90615044 |
| The membrane surr | IBA; IEA; IEA | 781 | 0.784507042 |
| A membrane-boun | IBA; IBA | 839 | 0.879737783 |
| | | 1678.4 | 0.856410867 |
| The irregular netwo | IBA; IBA; IBA; IEA | 413.9 | 0.884754772 |
| A membrane-boun | IBA; IEA; IEA | 1418.4 | 0.888395375 |
| The double lipid bil | IBA; IEA; IEA | 418.6 | 0.903726708 |
| | | 717.8 | 0.785316244 |

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|---|---|---|---|
| The membrane surr | ISS; ISS; IBA; IEA | 627.5 | 0.900398406 |
| | | 1380.2 | 0.94522533 |
| The component of | IEA | 1068.5 | 0.777632195 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA | 1542.1 | 0.79865119 |
| | | 458.1 | 0.864876664 |
| The membrane surr | IEA; IEA; IEA | 1636.3 | 0.900323901 |
| | | 620.3 | 0.835724649 |
| The lipid bilayer su | IBA; IEA; IEA; IEA | 802.2 | 0.778359511 |
| The membrane surr | IBA; IEA; IEA | 680.3 | 0.96854329 |
| The part of the cyto | IBA | 676.3 | 0.876977673 |
| A small, dense bod | IEA; IEA | 597 | 0.861809045 |
| The irregular netwo | IEA | 503.5 | 0.858192651 |
| | | 821.8 | 0.899732295 |
| A protein complex | IEA | 377.9 | 0.96030696 |
| The contents of a c | IBA | 2061.6 | 0.804617773 |
| The lipid bilayer su | IBA | 3524.5 | 0.803830331 |
| That part of the nu | IBA; IBA; IBA | 799.2 | 0.773773774 |
| A membrane-boun | IEA | 2665.8 | 0.782391777 |
| | | 1263.4 | 0.847475067 |
| | | 220.7 | 0.741277753 |
| | | 619.8 | 0.9386899 |
| The contents of a c | IBA | 2595.8 | 0.94664458 |
| The membrane surr | IEA; IEA; IEA; IDA | 660.5 | 0.942013626 |

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|---|---|---|---|
| A membrane-boun | IEA | 328.1 | 0.954891801 |
| A membrane-boun | IEA | 1408.6 | 0.748331677 |
| Cyclin-dependent p | IBA; IBA | 630.9 | 0.767792043 |
| | | 1563.8 | 0.948139148 |
| | | 835.5 | 0.859126272 |
| | | 1852.8 | 0.79722582 |
| A membrane-boun | IEA; IEA | 605.2 | 0.796926636 |
| A membrane-boun | IBA | 1579.9 | 0.740046838 |
| The lipid bilayer su | IEA; IEA; IEA; IEA; IE | 1117.6 | 0.850930565 |
| The component of t | IBA; IEA; IEA | 1022.3 | 0.913821774 |
| A membrane-boun | IEA; IEA | 968.9 | 0.8403344 |
| A more or less rigid | IEA; IEA | 939.9 | 0.857857219 |
| The contents of a c | IBA | 1410.7 | 0.818884242 |
| A ribosome found i | IBA; IEA | 581.8 | 0.920763149 |

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|---|---|---|---|
| Any complex forme | IBA | 1804.4 | 0.88178896 |
| A membrane-boun | IEA; IEA; IBA; IEA | 2005.7 | 0.896345416 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 715.2 | 0.789988814 |
| A lipid bilayer alon | IEA; IEA | 987.4 | 0.815373709 |
| A membrane-boun | IEA; IEA | 717.1 | 0.905591968 |
| The membrane surr | IBA; IEA; IEA | 1557.6 | 0.937724705 |
| The contents of a c | IBA; IBA; IBA; IBA; IE | 1543.7 | 0.948759474 |
| The membrane surr | IBA | 1441.7 | 0.843240619 |
| A lipid bilayer alon | IEA; IEA | 1220.1 | 0.888205885 |
|  |  | 1862.8 | 0.829074511 |
|  |  | 647.6 | 0.848517603 |
|  |  | 702.5 | 0.867615658 |
|  |  | 888.1 | 0.928499043 |

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|---|---|---|---|
| A membrane-boun | IMP | 1645.9 | 0.771006744 |
| | | 426.9 | 0.930194425 |
| | | 937.5 | 0.80064 |
| A membrane-boun | IEA | 2357.4 | 0.856494443 |
| | | 1900.7 | 0.909243963 |
| OBSOLETE. The bas | IEA; IEA; IEA | 637.7 | 0.802728556 |
| A semiautonomous | IBA | 2020.5 | 0.815639693 |
| An intracellular org | IEA; IEA | 341.1 | 0.851070067 |
| The component of | IEA | 985.7 | 0.943796287 |
| The membrane surr | IBA; IEA; IEA | 1918.8 | 0.813946216 |
| | | 1283.9 | 0.865176416 |
| The contents of a c | IEA; IEA; IEA; IEA; IE | 369.9 | 0.943227899 |
| The component of | IEA | 675.6 | 0.863972765 |
| A lipid bilayer along | IEA | 717.9 | 0.768491433 |
| | | 409.2 | 0.823069404 |
| | | 1502.8 | 0.884349215 |
| The membrane surr | IBA; IBA | 404.3 | 0.792480831 |
| | | 906.9 | 0.811666115 |
| The lipid bilayer su | IBA; IBA; IEA; IEA; IE | 1309.5 | 0.931882398 |
| | | 950.2 | 0.819511682 |
| | | 1159.3 | 0.873803157 |
| | | 641.9 | 0.94251441 |
| A heterotetrameric | IEA; IEA | 453.1 | 0.984109468 |
| A membrane-boun | IBA | 2106 | 0.889933523 |
| | | 670.1 | 0.83211461 |
| | | 718.7 | 0.861833867 |
| | | 4286.2 | 0.862652233 |
| | | 816.8 | 0.945763957 |
| The lipid bilayer su | ISS; IEA; IEA; IEA | 1153.7 | 0.855161654 |
| The membrane surr | IBA | 634.2 | 0.774203721 |
| The irregular netwo | IEA; IEA; IEA; IEA | 475.6 | 0.884146341 |
| The lipid bilayer su | IEA; IBA; IEA; IEA; IE | 910.4 | 0.849516696 |

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|---|---|---|---|
| A lipid bilayer along | IEA | 1053.9 | 0.926653383 |
| | | 2220.7 | 0.759625343 |
| A lipid bilayer along | IEA; IEA | 804.3 | 0.907124207 |
| A membrane-boun | IEA | 814 | 0.819164619 |
| | | 1832.3 | 0.906620095 |
| A lipid bilayer along | IEA; IEA | 1008.8 | 0.953211737 |
| A membrane-boun | IEA | 845.6 | 0.789735099 |
| The contents of a c | IBA; IEA | 2168.3 | 0.946363511 |
| A lipid bilayer along | IEA; IEA; IBA | 1055.6 | 0.90403562 |
| The contents of a c | IBA | 1570.2 | 0.827601579 |
| The membrane surr | IEA; IEA; IEA | 324.3 | 0.902251002 |
| | | 689.6 | 0.840632251 |
| The end of a linear | IBA; IBA; IBA; IBA; IB | 583.9 | 0.820174687 |
| OBSOLETE. The bas | IEA | 1302 | 0.932718894 |
| | | 545.1 | 0.941295175 |
| A membrane-boun | IBA; IEA; IBA | 1775.1 | 0.884231874 |
| | | 1692.6 | 0.836996337 |
| | | 548.9 | 0.874294043 |
| A membrane-boun | IBA | 649.8 | 0.780701754 |
| Organized structure | IBA | 1533.7 | 0.864249853 |
| | | 455.6 | 0.8118964 |

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|---|---|---|---|
| The membrane surr | IEA; IEA | 1175.7 | 0.82129795 |
| Organized structure | IBA | 1005.7 | 0.75439992 |
| | | 1286.6 | 0.844551531 |
| A semiautonomous | IBA; IEA | 1462.8 | 0.77372163 |
| The contents of a c | IBA | 322 | 0.868944099 |
| | | 172.2 | 0.87630662 |
| A lipid bilayer along | IEA; IEA | 2347.2 | 0.872869802 |
| | | 694.9 | 0.906749173 |
| A small organelle e | IEA | 892.4 | 0.897803675 |
| | | 580.5 | 0.828251507 |
| Organized structure | IBA | 976.4 | 0.817697665 |
| | | 1167 | 0.915681234 |
| A large complex of | IEA; IBA; IEA; IEA; IE | 735.6 | 0.930668842 |
| | | 270.1 | 0.896334691 |
| The space external | IEA; IEA | 357.2 | 0.895856663 |
| A chlorophyll-conta | IEA; IEA; IBA | 1397.4 | 0.863890082 |
| The membrane surr | IBA; IEA; IEA | 1513.2 | 0.949577055 |
| The contents of a c | IEA; IEA; IBA; IEA; IE | 318 | 0.894339623 |
| A lipid bilayer along | IEA; IEA | 1621.8 | 0.94136145 |
| Either of the ends o | IEA; IBA; IBA; IEA; IB | 2288 | 0.863024476 |
| | | 430.1 | 0.825389444 |
| A lipid bilayer along | IEA; IEA | 524.4 | 0.779176201 |

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|---|---|---|---|
| A membrane-boun | IBA | 1010 | 0.784851485 |
|  |  | 184.7 | 0.807255008 |

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|---|---|---|---|
| A membrane-boun | IEA | 1531.5 | 0.825073457 |
| The lipid bilayer su | IBA; IBA; IEA; IEA | 746.4 | 0.74624866 |
| A closed structure, | IBA | 1346 | 0.891753343 |
| A lipid bilayer alon | IEA; IEA | 1452.4 | 0.782360231 |
|  |  | 1225.9 | 0.940533486 |

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|---|---|---|---|
| A membrane-boun | IEA | 313.9 | 0.914303918 |
| The membrane surr | IBA; IEA; IEA | 721.9 | 0.904141848 |
| A membrane-boun | IEA; IEA | 483.4 | 0.792097642 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1030.7 | 0.90511303 |
| The double lipid bil | IEA; IEA; IEA | 530.6 | 0.847342631 |
| Organized structur | IBA | 1433.6 | 0.830426897 |
| The irregular netwo | IEA; IEA; IEA | 1063.1 | 0.96011664 |
| The contents of a c | IBA | 1533.5 | 0.894946201 |
|  |  | 1584.6 | 0.749905339 |
| The membrane surr | IBA; IEA; IEA; IBA; IE | 713.3 | 0.757184915 |
| The contents of a c | IBA | 1138.2 | 0.812247408 |
|  |  | 1192.3 | 0.923257569 |
|  |  | 1255.8 | 0.932552954 |
|  |  | 1066.9 | 0.845533789 |
| A membrane-boun | IEA; IEA; IEA | 1283.8 | 0.921483097 |
|  |  | 187.7 | 0.819925413 |

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|---|---|---|---|
| A membrane-boun | IEA | 543.9 | 0.900717044 |
| A membrane-boun | IEA; IEA; IBA | 394.2 | 0.828006088 |
| The contents of a c | IBA | 1331.8 | 0.895179456 |
| A lipid bilayer alon | IEA; IEA | 634.3 | 0.870093016 |
| | | 1662.3 | 0.914215244 |
| | | 664.9 | 0.867348473 |
| | | 420.1 | 0.742918353 |
| A complex possessi | IEA | 2060.9 | 0.872774031 |
| A membrane-boun | IEA | 1046.2 | 0.854616708 |
| | | 1024.8 | 0.857045277 |
| A membrane-boun | IBA; IBA | 357.8 | 0.922861934 |
| The lipid bilayer su | IEA | 1353.1 | 0.85160003 |
| A membrane-boun | IEA; IEA; IEA; IEA; IE | 437.2 | 0.870997255 |
| The contents of a c | IBA; IBA | 1533.1 | 0.955710652 |
| A lipid bilayer alon | IEA; IEA | 434.2 | 0.879548595 |
| A membrane-boun | IEA | 790.1 | 0.753322364 |
| | | 282.3 | 0.859723698 |
| A membrane-boun | IBA | 666.6 | 0.742724272 |
| A semiautonomous | IBA | 1137.2 | 0.929739712 |
| | | 450.9 | 0.822133511 |
| | | 756.6 | 0.899947132 |
| A lipid bilayer alon | IEA; IEA | 149.8 | 0.85246996 |

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|---|---|---|---|
| A closed structure, | IEA; IEA; IBA; IEA; IE | 748.6 | 0.960593107 |
| A chlorophyll-conta | IBA | 792.5 | 0.937791798 |
| A chlorophyll-conta | IDA; IDA; IDA; IDA | 1519.7 | 0.887477792 |
| An intracellular org | IEA; IEA | 459.9 | 0.813437704 |
| A membrane-bound | IEA; IEA | 293.9 | 0.825110582 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 1295.1 | 0.920083391 |
| A small organelle e | IEA | 633.6 | 0.922979798 |
|  |  | 554.5 | 0.77006312 |
|  |  | 677.3 | 0.828584084 |
|  |  | 238.4 | 0.819630872 |
| The contents of a c | IEA; IBA; IEA; IEA; IE | 1296.4 | 0.853131749 |
| The irregular netwo | IEA; IBA; IEA | 854.8 | 0.93086102 |
| A semiautonomous | IBA | 889.8 | 0.87300517 |
| A lipid bilayer along | IEA; IEA | 791.4 | 0.915339904 |

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|---|---|---|---|
| The membrane surr | IBA; IBA | 728.1 | 0.860733416 |
| That part of a multi | IEA | 341.8 | 0.775014628 |
| | | 1694.2 | 0.746192893 |
| A membrane-boun | IEA | 1839.3 | 0.882346545 |
| | | 936.3 | 0.907935491 |
| | | 1227.7 | 0.786511363 |
| A membrane-boun | IEA; IEA; IEA | 1377.6 | 0.844294425 |
| A membrane-boun | IEA | 922.7 | 0.875690907 |
| An enzyme comple | IEA; IEA; IEA | 387.8 | 0.826972666 |
| That part of a multi | IEA | 809.6 | 0.766304348 |
| A membrane-boun | IBA | 1982.9 | 0.824449039 |
| | | 1161.9 | 0.862552715 |
| Organized structure | IBA | 958.3 | 0.769070229 |
| The irregular netwo | IEA; IEA; IEA; IEA | 417 | 0.909832134 |
| | | 1006 | 0.769880716 |
| | | 1316.9 | 0.786088541 |
| A membrane-boun | IBA; IBA | 1751.8 | 0.874186551 |
| A membrane-boun | IEA | 410.2 | 0.858361775 |
| A semiautonomous | IBA | 1540.8 | 0.808605919 |
| | | 792.6 | 0.80229624 |
| The membrane surr | IBA; IEA; IEA; IBA | 368.3 | 0.781699701 |
| A lipid bilayer along | IEA; IEA | 1502.2 | 0.821927839 |
| A membrane-boun | IEA; IBA; IEA | 1513.9 | 0.809828919 |
| The contents of a c | IBA | 1028.8 | 0.902118974 |
| | | 341.7 | 0.854550776 |
| Cyclin-dependent p | IBA; IBA; IBA | 697.2 | 0.84595525 |
| A vacuole to which | IEA; IEA; IEA | 1047.2 | 0.900305577 |
| The membrane surr | ISS; ISS; IBA; IEA | 483.4 | 0.945800579 |
| | | 1375.6 | 0.874309392 |
| A membrane-boun | IEA | 974 | 0.85 |
| | | 575.9 | 0.826879667 |

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|---|---|---|---|
| | | 801.4 | 0.807836286 |
| A chlorophyll-cont | IEA; IEA | 2256.3 | 0.949075921 |
| A membrane-boun | IEA; IEA | 1604.4 | 0.785153328 |
| A membrane-boun | IEA; IEA; IEA | 806.6 | 0.903917679 |
| | | 1238 | 0.880936995 |
| A lipid bilayer alon | IEA | 1070 | 0.857196262 |
| The component of | IEA | 1267.7 | 0.92127475 |
| A small, dense bod | IBA | 534.6 | 0.885895997 |
| The membrane sur | IBA; IBA | 461.5 | 0.777031419 |
| | | 884.6 | 0.883902329 |
| Any complex that i | IBA; IBA | 1868.3 | 0.86276294 |
| | | 968.8 | 0.874380677 |
| A semiautonomous | IBA; IBA | 531 | 0.833521657 |
| | | 1251 | 0.916946443 |
| A semiautonomous | IBA; IEA; IEA | 840.1 | 0.896321866 |
| A semiautonomous | IBA | 1297.7 | 0.797719041 |
| The contents of a c | IBA; IBA | 1074.5 | 0.861796184 |
| A ubiquitin ligase c | IBA | 1421.1 | 0.8307649 |
| | | 816 | 0.796446078 |
| The membrane sur | IBA; IEA; IEA | 1899.5 | 0.803316662 |
| A membrane-boun | IEA; IBA; IBA | 2664 | 0.89039039 |
| OBSOLETE. The bas | IEA; IEA | 708.3 | 0.821544543 |
| The part of the cyto | IBA | 666.9 | 0.894586895 |
| | | 679.4 | 0.955401825 |
| | | 309 | 0.809061489 |
| A membrane-boun | IBA | 1022.7 | 0.806688178 |
| | | 266 | 0.809774436 |
| | | 797.7 | 0.934937947 |

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|---|---|---|---|
| An intracellular org | IEA; IEA; IEA; IEA | 637.2 | 0.885436284 |
| | | 1987.2 | 0.813305153 |
| | | 1370.2 | 0.883082762 |
| A membrane-boun | IEA | 576.9 | 0.831513261 |
| The irregular netwo | IBA | 835.3 | 0.880043098 |
| | | 1458.1 | 0.922158974 |
| The membrane surr | IBA; IEA; IEA | 2036.2 | 0.773057656 |
| Organized structur | IBA | 989.7 | 0.814388198 |
| The membrane surr | IBA | 1714 | 0.793523921 |
| A membrane-boun | IBA; IBA | 2408.6 | 0.836253425 |
| The membrane surr | IEA; IEA; IEA | 394.7 | 0.928806689 |
| The component of | IEA | 906.4 | 0.879964695 |
| | | 1113.2 | 0.877919511 |
| | | 652.4 | 0.778816677 |
| A small organelle e | IEA; IEA; IEA | 838.3 | 0.853513062 |
| | | 697.1 | 0.928274279 |
| | | 745.9 | 0.845287572 |
| A membrane-boun | IEA; IEA | 1493.7 | 0.93840798 |
| The part of the cyto | IBA | 884 | 0.872511312 |
| | | 217.1 | 0.897282358 |
| The contents of a c | IBA; IBA; IBA | 1750.6 | 0.94396207 |
| The space external | IEA | 932.7 | 0.860726922 |
| A membrane-boun | IEA; IEA | 868 | 0.833294931 |
| A chlorophyll-cont | IEA; IEA | 970.1 | 0.935779817 |
| The part of the cyto | IBA | 677.4 | 0.777531739 |
| The membrane surr | IEA; IEA; IEA | 427 | 0.815222482 |

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|---|---|---|---|
| | | 1262.3 | 0.875861523 |
| A membrane-boun | IBA; IBA | 1350.6 | 0.900636754 |
| The membrane surr | IBA; IEA; IEA | 1583.3 | 0.829722731 |
| | | 1682.9 | 0.899994058 |
| The membrane surr | IBA; IEA; IEA | 1395 | 0.865878136 |
| | | 634.7 | 0.890814558 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1008.2 | 0.847351716 |
| | | 332.1 | 0.890093345 |
| | | 369.3 | 0.832114812 |
| Organized structure | IBA | 1752.4 | 0.901392376 |
| | | 1416 | 0.789971751 |
| | | 2114.5 | 0.907543154 |
| | | 1721.9 | 0.793774319 |
| A membrane-boun | IBA | 2748.6 | 0.78050644 |
| The membrane surr | IBA; IBA | 1103.9 | 0.901893287 |
| The membrane surr | ISS; ISS; IEA; IBA; IE | 608.2 | 0.860078921 |
| The contents of a c | IBA; IEA; IEA | 1324.1 | 0.781965108 |
| | | 1072.5 | 0.765501166 |
| A membrane-boun | IEA; IEA; IEA | 745.8 | 0.835344596 |
| | | 1301.9 | 0.937245564 |
| A lipid bilayer alon | IBA; IEA | 1207.8 | 0.923000497 |
| A semiautonomous | IEA | 710 | 0.906760563 |
| A lipoprotein partic | IEA | 242.3 | 0.845645894 |
| A lipid bilayer alon | IEA; IEA | 1512.8 | 0.844526705 |
| A lipid bilayer alon | IEA | 1022.6 | 0.81459026 |

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|---|---|---|---|
| | | 1185.1 | 0.846088938 |
| A lipid bilayer alon | IEA; IEA | 2142.5 | 0.786884481 |
| An organelle consis | IBA | 1451.9 | 0.959156967 |
| | | 281.8 | 0.852732434 |
| A membrane-boun | IBA; IEA | 931.8 | 0.873363383 |
| A semiautonomous | IBA | 1296.8 | 0.918954349 |
| The contents of a c | IBA; IBA; IBA | 1008.3 | 0.804026579 |
| A protein complex | IBA; IBA; IEA; IEA; IE | 1956.8 | 0.818785773 |
| | | 1531.7 | 0.833910035 |
| | | 195.7 | 0.786918753 |
| The contents of a c | IEA | 969.8 | 0.892452052 |
| The contents of a c | IEA | 279.2 | 0.897206304 |
| | | 1164.2 | 0.897612094 |
| | | 2427 | 0.951133086 |
| Organized structur | IEA | 1392.5 | 0.794039497 |
| The irregular netwo | IBA; IEA; IEA | 641.6 | 0.829021197 |
| | | 1224.9 | 0.757776145 |
| A membrane-boun | IEA; IEA; IEA; IEA | 1126.4 | 0.855379972 |
| | | 1841.2 | 0.899467738 |
| | | 1369.3 | 0.879062295 |
| | | 338.8 | 0.954250295 |
| A lipid bilayer alon | IEA; IEA | 883.5 | 0.899603848 |
| A membrane-boun | IEA | 743.3 | 0.803444101 |
| A lipid bilayer alon | IEA; IBA | 1219.7 | 0.895466098 |
| | | 263.7 | 0.901023891 |
| | | 1365.1 | 0.901032891 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 959.2 | 0.92910759 |
| | | 835.5 | 0.919928187 |
| A membrane-boun | IEA | 2193.1 | 0.87592905 |
| | | 690 | 0.745217391 |
| | | 1124.6 | 0.823670638 |
| A membrane-boun | IEA; IEA | 2174.4 | 0.863134658 |
| A membrane-boun | IEA | 1934.6 | 0.93719632 |
| The contents of a c | IBA | 1539.5 | 0.876063657 |
| A membrane-boun | IEA; IBA; IBA | 1096.4 | 0.912714338 |
| The contents of a c | IBA | 2470.2 | 0.819731196 |
| | | 2425.5 | 0.751020408 |
| A vacuole to which | IEA; IEA | 1538.3 | 0.829227069 |
| A membrane-boun | IBA | 1582.8 | 0.911549153 |
| | | 1480.2 | 0.740778273 |
| A lipid bilayer alon | IEA; IEA | 1202.3 | 0.905348083 |
| Protein translocon | IEA; IEA; IEA | 1440.2 | 0.957505902 |
| The membrane sur | IBA; IEA; IEA | 1557 | 0.933204881 |
| The contents of a c | IEA; IBA | 1449.9 | 0.854748603 |

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|---|---|---|---|
| The membrane surr | IBA | 1111.3 | 0.899037164 |
| | | 401.3 | 0.882382258 |
| | | 613.8 | 0.886608016 |
| The contents of a c | IBA | 1420.8 | 0.844664977 |
| A membrane-boun | IEA; IEA; IBA | 3952.1 | 0.927709319 |
| | | 2267.9 | 0.957493717 |
| A membrane-boun | IBA; IBA; IEA | 985.8 | 0.907486306 |
| A lipid bilayer along | IEA | 1185.8 | 0.861190757 |
| A membrane-boun | IEA; IEA | 1064.5 | 0.910474401 |
| | | 894.8 | 0.901765758 |
| The membrane surr | IBA; IEA | 520.4 | 0.912759416 |
| | | 738.8 | 0.849891716 |
| | | 1807.5 | 0.843208852 |
| The membrane surr | IBA; IEA | 1714.8 | 0.813447632 |
| A lipid bilayer along | IEA; IEA | 1506.3 | 0.922127066 |
| The membrane surr | IBA | 1215.3 | 0.878301654 |
| | | 295 | 0.899322034 |
| The membrane surr | IBA | 1365.4 | 0.8122162 |
| The lipid bilayer su | IEA; IEA | 1794.6 | 0.87111334 |
| Organized structure | IEA | 1582.5 | 0.908436019 |
| | | 980.9 | 0.902028749 |
| | | 1073 | 0.913233924 |
| | | 350.8 | 0.924458381 |
| A lipid bilayer along | IEA | 1118 | 0.938550984 |
| The contents of a c | IBA; IBA; IBA | 1667.1 | 0.800671825 |
| Organized structure | IEA | 1333.8 | 0.880566802 |
| A membrane-boun | IC | 549.5 | 0.823657871 |
| Any of a series of ri | IBA; IEA | 1509.5 | 0.775488572 |
| | | 1292.8 | 0.928759282 |
| A lipid bilayer along | IEA; IEA; IBA | 2174.3 | 0.947661316 |
| | | 1321.5 | 0.802345819 |
| A protein complex | IEA; IBA | 1545.8 | 0.925928322 |
| The part of the cyto | IEA; IEA | 3168.6 | 0.938458625 |
| A membrane-boun | IEA | 554.9 | 0.815642458 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA | 1566.3 | 0.877928877 |
| The component of | IEA | 1006.2 | 0.941860465 |
| Organized structur | IBA | 947.5 | 0.906279683 |
| A lipid bilayer alon | IEA; IEA | 876.5 | 0.893896178 |
| A membrane-boun | IEA | 969.2 | 0.766714816 |
| | | 1740.1 | 0.885983564 |
| A lipid bilayer alon | IEA; IEA | 506.3 | 0.785502666 |
| A lipid bilayer alon | IEA; IEA | 1533.5 | 0.861493316 |
| The contents of a c | IBA | 1310.4 | 0.846916972 |
| The inner, i.e. lume | IBA; IEA; IEA | 883 | 0.810532276 |
| Sac-like membrano | IEA; IEA | 798.9 | 0.919013644 |
| The lipid bilayer su | IBA; IEA; IEA | 932.3 | 0.880510565 |
| The membrane sur | IBA; IEA; IEA | 1268.4 | 0.96499527 |
| A membrane-boun | IBA; IBA | 2800.9 | 0.907351209 |
| The contents of a c | IEA; IEA; IEA | 566.8 | 0.944424841 |
| | | 1328.5 | 0.865788483 |
| A membrane-boun | IBA; IBA; IBA | 849.9 | 0.84468761 |
| A discrete extra-nu | IBA | 1910.2 | 0.925662234 |
| | | 873.9 | 0.874814052 |
| | | 1089.3 | 0.878821261 |
| A membrane-boun | IBA | 844.7 | 0.935953593 |

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|---|---|---|---|
| A chlorophyll-conta | IEA | 1106.9 | 0.902610895 |
| A lipid bilayer alon | IEA; IEA | 1051.1 | 0.823898773 |
| Any microtubule th | IEA; IEA | 1811.7 | 0.926257107 |
| A membrane-boun | IEA; IEA | 650.4 | 0.902367774 |
| A membrane-boun | IDA | 684.5 | 0.836815194 |
|  |  | 1407.4 | 0.932428592 |
| A collection of mem | IBA; IEA | 1927.5 | 0.926848249 |
| The contents of a c | IBA | 787.9 | 0.800609214 |
| A membrane-boun | IBA | 829.8 | 0.755121716 |
|  |  | 1975.9 | 0.899843109 |
|  |  | 682.5 | 0.844835165 |
| A lipid bilayer alon | IBA; IEA | 478 | 0.867364017 |
|  |  | 696.3 | 0.900043085 |
| The irregular netwo | IEA | 373.6 | 0.866702355 |
| The contents of a c | IBA; IDA | 449.9 | 0.895310069 |
|  |  | 1077.8 | 0.858044164 |
| A fine cytoplasmic | IEA; IEA | 1329.2 | 0.921005116 |
| A membrane-boun | IBA; IBA | 930.3 | 0.744491024 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1258.4 | 0.963127781 |
| A semiautonomous | IBA | 768.2 | 0.754881541 |
| The contents of a c | IBA | 952.9 | 0.869661035 |
| The irregular netwo | IBA; IEA | 695.6 | 0.926682001 |
| A membrane-boun | IBA | 693 | 0.751948052 |
| A semiautonomous | IEA; IEA; IEA; IEA | 496.8 | 0.887681159 |
|  |  | 430.1 | 0.844687282 |
| A vacuole to which | IBA; IBA; IBA; IBA | 230.8 | 0.76559792 |
|  |  | 495 | 0.745858586 |
| The rigid or semi-ri | IEA | 756 | 0.928439153 |
| A membrane-boun | IBA | 828.5 | 0.849487025 |

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|---|---|---|---|
| | | 377.4 | 0.947800742 |
| | | 813 | 0.924354244 |
| The contents of a c | IBA; IBA; IBA | 284.6 | 0.869992973 |

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|---|---|---|---|
| | | 394.2 | 0.744038559 |
| | | 533.7 | 0.743863594 |
| The membrane surr | IBA; IEA; IEA | 2183.2 | 0.958913521 |
| A lipid bilayer along | IEA; IEA | 523.7 | 0.953599389 |
| The contents of a c | IBA | 454.1 | 0.912794539 |
| | | 383.5 | 0.761408083 |
| A membrane-boun | IEA | 730.9 | 0.767957313 |
| | | 1232.8 | 0.805564568 |
| | | 750.6 | 0.880895284 |
| | | 860.7 | 0.905193447 |
| A lipid bilayer along | IEA | 1192 | 0.895469799 |
| | | 2436.5 | 0.882495383 |
| The space external | IEA; IEA; IEA | 768.6 | 0.916601613 |
| The component of t | IBA | 385.5 | 0.739818418 |
| | | 451.8 | 0.843293493 |
| The membrane surr | IBA; IBA | 1043.7 | 0.928715148 |

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|---|---|---|---|
| A membrane-boun | IBA | 2281.3 | 0.817516328 |
| A semiautonomous | IEA | 1210 | 0.909586777 |
| | | 649.5 | 0.908545035 |
| A lipid bilayer along | IEA; IEA | 2106.5 | 0.782387847 |
| The membrane surr | IBA | 885.2 | 0.870876638 |
| | | 309.6 | 0.822674419 |
| The membrane surr | IBA; IEA; IEA | 813.3 | 0.911717693 |

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|---|---|---|---|
| A membrane-boun | IEA; IEA; IBA | 1018.7 | 0.833415137 |
| The contents of a c | IBA | 487.1 | 0.914185999 |
| A vacuole to which | IBA; IBA | 1136.8 | 0.882389163 |
| The membrane surr | IBA; IBA | 1134.3 | 0.802521379 |
| Organized structure | IBA | 2124.5 | 0.89771711 |

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|---|---|---|---|
| A ubiquitin ligase c | IBA | 723.2 | 0.881084071 |
| | | 845 | 0.904260355 |
| The part of the cyto | IBA | 1066.6 | 0.777892368 |
| | | 2398.9 | 0.883613323 |
| | | 852.1 | 0.744748269 |
| A spliceosomal com | IBA; IBA; IEA; IBA | 1697.3 | 0.89889825 |
| | | 726.4 | 0.88160793 |
| The membrane surr | IBA | 1014.9 | 0.891910533 |
| A chlorophyll-conta | IBA | 573.7 | 0.884782988 |
| | | 808 | 0.799876238 |
| Organized structure | IEA | 1380.1 | 0.939497138 |
| | | 739 | 0.887415426 |
| A chlorophyll-conta | IEA; IEA | 278 | 0.920143885 |
| The contents of a c | IBA | 1603.9 | 0.864081302 |
| A lipid bilayer along | IBA; IEA | 462.9 | 0.756966948 |
| The membrane surr | IBA; IBA; IEA; IEA | 1720.1 | 0.916865299 |
| | | 1232.2 | 0.783882487 |
| A membrane-bound | IBA; IBA; IBA | 1298.3 | 0.748825387 |
| That part of a multi | IBA; IBA | 700.4 | 0.873215306 |
| A membrane-bound | IBA; IBA | 1765.9 | 0.855767597 |
| A lipid bilayer along | IEA; IEA | 529.6 | 0.77907855 |

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|---|---|---|---|
| The irregular netwo | IDA | 914.9 | 0.914307575 |
| A membrane-boun | IEA | 673.6 | 0.868171021 |
| A membrane-boun | IEA | 2011.5 | 0.77648521 |
| | | 1094.8 | 0.942272561 |
| A chlorophyll-conta | IEA | 1775.7 | 0.916371009 |
| | | 811.4 | 0.976460439 |
| A lipid bilayer alon | IEA; IEA | 213.2 | 0.920731707 |
| A membrane-boun | IEA | 1051 | 0.760894386 |
| The membrane sur | IBA | 827.5 | 0.947311178 |
| | | 1645.1 | 0.901829676 |
| The contents of a c | IBA | 2349.2 | 0.898901754 |
| The membrane sur | IBA; IEA; IEA; IBA | 363.9 | 0.804341852 |
| A membrane-boun | IBA | 539.9 | 0.747545842 |
| | | 273.5 | 0.92321755 |
| The lipid bilayer su | IBA | 4107.8 | 0.889405521 |

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|---|---|---|---|
| A membrane-boun | IEA | 1456.9 | 0.75928341 |
| A closed structure, | IEA; IBA; IBA | 717.5 | 0.758606272 |
| A semiautonomous | IBA | 674.2 | 0.876742806 |
| | | 353.6 | 0.958144796 |
| A membrane-boun | IBA | 1845.1 | 0.792477373 |
| A membrane-boun | IBA; IEA | 1089.4 | 0.941160272 |
| | | 1027.2 | 0.830023364 |
| A lipid bilayer alon | IEA; IEA | 483.5 | 0.913133402 |
| The contents of a c | IBA | 785.8 | 0.924917282 |
| A lipid bilayer alon | IEA; IEA | 945.5 | 0.928503437 |
| A chlorophyll-conta | IEA | 895.1 | 0.775667523 |
| The component of t | IBA | 1764.3 | 0.835175424 |
| A heterotetrameric | IBA; IEA | 438.9 | 0.961038961 |
| A vacuole to which | IBA; IBA | 506.6 | 0.87465456 |
| The membrane surr | IBA; IEA; IEA | 2062.3 | 0.836444746 |
| | | 474 | 0.919620253 |
| | | 1787.6 | 0.892481539 |
| | | 1023.9 | 0.941595859 |
| That part of a multi | IEA; IEA | 1027 | 0.856183057 |
| The lipid bilayer su | IEA; IEA; IEA | 1053.6 | 0.766799544 |
| | | | |
| | | | |
| The contents of a c | IBA; IBA; IBA; IEA; IE | 1783 | 0.863825014 |
| A lipid bilayer alon | IEA; IEA | 667.4 | 0.745879533 |
| | | 327.9 | 0.824641659 |
| | | 367.5 | 0.928707483 |
| A lipid bilayer alon | IEA; IEA | 831.4 | 0.946716382 |
| A lipid bilayer alon | IEA; IEA | 523.9 | 0.799389196 |
| The membrane surr | IBA; IBA | 753 | 0.879946879 |
| The irregular netwo | IEA; IBA; IEA; IBA | 2144.5 | 0.860760084 |
| A semiautonomous | IBA | 394.5 | 0.854499366 |
| A prelysosomal end | IBA; IBA; IBA; IBA | 3281.3 | 0.925425898 |
| A membrane-boun | IBA; IBA | 617.3 | 0.920622064 |
| | | 1043.2 | 0.759010736 |
| The contents of a c | IBA; IBA | 475.3 | 0.820955186 |
| | | 1508.5 | 0.910043089 |
| A chlorophyll-conta | IEA | 2235.3 | 0.920502841 |

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| | | 552.1 | 0.879731933 |
| A membrane-boun | IBA | 635.9 | 0.786287152 |
| | | 1084.5 | 0.783033656 |
| A membrane-boun | IEA; IBA; IBA | 956.4 | 0.889481389 |
| The membrane surr | IBA; IBA | 904.8 | 0.866931919 |
| The irregular netwo | IBA; IBA; IEA; IEA | 1044 | 0.934961686 |
| | | 1493.6 | 0.864890198 |
| | | 1403.5 | 0.786961169 |
| Organized structure | IBA | 1731.7 | 0.873938904 |
| The membrane surr | IBA; IBA; IEA | 2440.3 | 0.907880179 |
| The membrane surr | IBA | 1064.7 | 0.866065558 |
| | | 179.1 | 0.930764936 |
| The membrane surr | IBA; IBA; IEA | 1124.1 | 0.915132106 |
| A semiautonomous | IBA | 1346.7 | 0.833667483 |
| | | 2274.9 | 0.766275441 |
| A semiautonomous | IEA; IEA | 1131 | 0.824226348 |
| The irregular netwo | IBA; IBA; IEA; IEA | 963 | 0.850778816 |
| | | 667.3 | 0.844297917 |
| | | 449.8 | 0.928190307 |
| A large ribonucleop | IBA; IBA | 1824.4 | 0.928305196 |
| | | 285.1 | 0.773412838 |
| A chlorophyll-cont | IEA | 613 | 0.89233279 |
| A lipid bilayer alon | IEA; IEA | 488 | 0.860040984 |
| A membrane-boun | IBA | 1741.7 | 0.877361199 |
| A lipid bilayer alon | IBA | 1358.7 | 0.88120998 |
| | | 894.5 | 0.823029625 |
| A lipid bilayer alon | IEA; IEA | 429.3 | 0.916142558 |
| Any complex that i | IBA; IEA | 1973.1 | 0.853175207 |

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|---|---|---|---|
| A membrane-boun | IDA; IEA | 188.7 | 0.902490726 |
| A membrane-boun | IEA | 2533.2 | 0.881770093 |
| | | 1493.2 | 0.801433164 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 993.1 | 0.754908871 |
| | | 3547.4 | 0.817669279 |
| A chlorophyll-conta | IEA | 1070.9 | 0.897282659 |
| | | 383.7 | 0.798540526 |
| The lipid bilayer su | IBA; IBA | 1662.1 | 0.882377715 |
| | | 1571.9 | 0.83497678 |
| A highly compacted | IEA; IBA; IEA; IEA | 1408.6 | 0.785886696 |
| | | 741.1 | 0.805694238 |
| A lipid bilayer alon | IBA; IBA | 1088.2 | 0.967101636 |
| The membrane surr | IEA | 1240.7 | 0.850326429 |
| A closed structure, | IEA; IBA; IEA; IEA; IB | 441 | 0.74739229 |
| The lipid bilayer su | IEA; IEA; IBA; IBA; IE | 2555.4 | 0.911951162 |
| The space external | IEA | 223.4 | 0.840196956 |
| The contents of a c | IBA | 1468.1 | 0.837000204 |
| | | 2359.6 | 0.832598746 |
| Organized structure | IBA | 1087.8 | 0.888030888 |
| A closed structure, | IEA; IBA; IBA | 703.2 | 0.777872582 |
| | | 342 | 0.891812865 |
| The membrane surr | IBA; IEA; IEA | 1682.7 | 0.929874606 |

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|---|---|---|---|
| The part of the cyto | IEA | 1348.4 | 0.882008306 |
| | | 300.5 | 0.742762063 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 478.4 | 0.816889632 |
| The contents of a c | IEA; IEA; IEA; IEA | 929.6 | 0.766351119 |
| A semiautonomous | IEA | 742.3 | 0.900579281 |
| A semiautonomous | IBA | 1203.1 | 0.917546339 |
| | | 659.9 | 0.912259433 |
| The gel-like materi | IBA | 546.9 | 0.920460779 |
| The membrane surr | IEA; IEA; IEA | 939 | 0.928328009 |
| | | 833.9 | 0.824799137 |
| OBSOLETE. The bas | IEA | 437.9 | 0.810915734 |
| | | 532.7 | 0.837056505 |
| A lipid bilayer along | IBA | 852.7 | 0.912865017 |
| A lipid bilayer along | IEA; IEA | 765.8 | 0.85296422 |
| | | 321.6 | 0.763681592 |
| | | 764.6 | 0.927151452 |
| | | 1170.7 | 0.832066285 |
| The component of a | IEA | 934.2 | 0.916292015 |
| A protein complex t | IBA; IBA | 1174.5 | 0.935972754 |
| A semiautonomous | IEA; IEA | 410 | 0.867560976 |
| A ubiquitin ligase c | IBA | 1394.5 | 0.919971316 |
| A chlorophyll-conta | IEA | 612.3 | 0.818552997 |
| | | 553.1 | 0.840535165 |
| A lipid bilayer along | IEA; IEA | 222 | 0.882882883 |
| | | 536.3 | 0.906582137 |
| A lipid bilayer along | IBA; IEA | 576.7 | 0.95006069 |
| A membrane-boun | IEA | 1164.3 | 0.866271579 |
| A lipid bilayer along | IEA; IEA | 600.3 | 0.921872397 |
| A discrete extra-nu | IBA | 2043.7 | 0.743112981 |
| | | 413.6 | 0.760396518 |
| A lipid bilayer along | IEA; IEA | 1352.5 | 0.908983364 |
| A semiautonomous | IEA | 1486.3 | 0.912265357 |
| | | 1361.8 | 0.960126303 |
| A membrane-boun | IBA | 4986.8 | 0.909922195 |
| A lipid bilayer along | IEA; IEA | 242.7 | 0.901936547 |
| | | 1182.5 | 0.952727273 |
| | | 749.2 | 0.792578751 |
| A ribonucleoprotei | IBA; IBA; IBA | 1742.3 | 0.931642082 |
| A semiautonomous | IBA | 787.5 | 0.88152381 |
| A lipid bilayer along | IEA; IEA | 1510.1 | 0.941195947 |

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|---|---|---|---|
| | | 688.1 | 0.846243279 |
| A membrane-boun | IEA; IEA | 1123 | 0.931255565 |
| | | 433.4 | 0.826488233 |
| The membrane surr | IBA; IBA; IEA; IEA | 1023.2 | 0.947713057 |
| The contents of a c | IEA; IEA; IBA; IEA | 2041.5 | 0.897722263 |
| | | 786.1 | 0.830810329 |
| A protein complex | IBA; IBA | 1143.2 | 0.827151854 |
| The contents of a c | IBA | 8369.8 | 0.955411121 |
| | | 1578.3 | 0.793068491 |
| The part of the cyto | IBA | 1319.7 | 0.883155263 |
| A semiautonomous | IBA; IBA | 1597.5 | 0.93827856 |
| The membrane surr | IBA; IEA; IEA | 2100.7 | 0.926357881 |
| A membrane-boun | IBA | 760.9 | 0.879353397 |
| The membrane surr | IBA; IEA; IEA | 763.4 | 0.821325648 |
| | | 2062.5 | 0.752678788 |
| A membrane-boun | IEA; IEA | 736.1 | 0.89566635 |
| A semiautonomous | IBA | 1085.2 | 0.780040546 |
| | | 1070.3 | 0.823040269 |
| A lipid bilayer along | IEA; IEA | 317.6 | 0.960642317 |
| | | 1446.6 | 0.901216646 |
| A semiautonomous | IEA; IEA; IEA; IEA; IB | 588.8 | 0.944293478 |
| The membrane surr | IBA | 186.1 | 0.758731865 |
| A fine cytoplasmic | IBA; IEA; IEA | 602.7 | 0.840550854 |
| The lipid bilayer su | IEA; IBA; IEA; IEA; IE | 1020.5 | 0.848211661 |
| | | 324.4 | 0.825524044 |

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|---|---|---|---|
| Any complex that ir | IBA; IEA; IBA | 2163.7 | 0.830799094 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1390.4 | 0.798331415 |
| A semiautonomous | IBA | 689.2 | 0.829947766 |
| | | 327.1 | 0.8083155 |
| | | 590.4 | 0.909214092 |
| The membrane surr | IBA; IEA | 842.5 | 0.934599407 |
| A membrane-boun | IEA; IEA | 4016.6 | 0.839117662 |
| The contents of a c | IBA | 345.9 | 0.860653368 |
| A lipid bilayer alon | IEA; IEA | 736.1 | 0.7546529 |
| Cyclin-dependent p | IBA; IBA; IBA | 732.7 | 0.871707384 |
| | | 1267.6 | 0.884269486 |
| | | 1221.3 | 0.892491607 |
| Organized structur | IBA | 815.1 | 0.844804318 |
| An endosomal sorti | IEA; IEA; IBA | 521.1 | 0.924966417 |
| The lipid bilayer su | IEA; IEA; IEA | 802.5 | 0.883239875 |
| A protein complex | IBA | 1294.6 | 0.82573768 |
| A membrane-boun | IEA | 512.3 | 0.750341597 |
| A semiautonomous | IBA | 1098.1 | 0.881249431 |
| A membrane-boun | IBA; IBA | 763.5 | 0.856057629 |
| | | 799.6 | 0.946098049 |
| | | 666.7 | 0.922303885 |
| The portion of the | IBA | 1180.5 | 0.930792037 |
| A semiautonomous | IBA | 1155.8 | 0.814500779 |
| The end of a linear | IBA; IBA; IBA; IBA | 2073.4 | 0.856178258 |
| A membrane-boun | IEA; IEA; IBA; IBA | 2972.8 | 0.923405544 |
| | | 1051.2 | 0.850171233 |
| The membrane surr | IBA; IEA; IEA | 1952.4 | 0.905449703 |
| The space external | IEA | 262.7 | 0.875142748 |
| A multisubunit gua | IBA | 1652.7 | 0.939553458 |
| The gel-like materi | IBA | 1051.7 | 0.894741847 |
| | | 343.8 | 0.940372309 |
| A membrane-boun | IBA; IBA | 909.5 | 0.747993403 |
| | | 1214.7 | 0.871079279 |

|  |  |  |  |
|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1122.9 | 0.883961172 |
| A membrane-boun | IDA; IEA | 1698.7 | 0.805792665 |
| A membrane-boun | IBA | 778.3 | 0.892457921 |
| A protein complex | IBA; IEA | 878.3 | 0.843447569 |
| Cyclin-dependent | IBA; IBA | 1529.4 | 0.865175886 |
| Organized structur | IEA | 1119.8 | 0.788890873 |
| The membrane surr | IBA; IEA; IEA | 1648.2 | 0.929498847 |
| The contents of a c | IEA | 1070.8 | 0.906331715 |
| A small organelle e | IEA | 316.4 | 0.845448799 |
|  |  | 590.3 | 0.881924445 |
| A membrane-boun | IBA; IBA | 571.7 | 0.888752842 |
|  |  | 646.8 | 0.781539889 |
| A lipid bilayer alon | IEA; IEA | 1069.3 | 0.838024876 |
|  |  | 1226.1 | 0.920316451 |
| A lipid bilayer alon | IBA; IEA | 1269 | 0.935303388 |
|  |  | 662.7 | 0.944922288 |
|  |  | 844.8 | 0.939630682 |
|  |  | 542 | 0.879889299 |

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|---|---|---|---|
| The membrane surr | IBA; IEA; IEA | 1899.8 | 0.814033056 |
| A vacuole that is m | IBA; IBA; IEA; IEA | 1044.6 | 0.826153552 |
|  |  | 852.7 | 0.943825495 |
| A membrane-boun | IBA | 2489.6 | 0.897212404 |
| The part of the cyto | IBA; IBA; IBA | 808.9 | 0.945357893 |
| A small, dense bod | IBA; IBA | 680.1 | 0.910895457 |
| The contents of a c | IBA | 606.1 | 0.915030523 |
|  |  | 1598.8 | 0.899612209 |
| The membrane surr | IBA | 1700.7 | 0.80602105 |
| A lipid bilayer alon | IEA; IEA | 551.9 | 0.95886936 |
| The gel-like materi | IEA | 225.9 | 0.913235945 |
| A lipid bilayer alon | IBA; IEA | 1060.6 | 0.889213653 |
| A semiautonomous | IBA | 1673.1 | 0.904548443 |
|  |  | 186.1 | 0.8323482 |
|  |  | 951.7 | 0.808342965 |
|  |  | 999.9 | 0.820582058 |
| A ubiquitin ligase c | IBA | 1353.3 | 0.957363482 |
| A lipid bilayer alon | IEA; IEA | 1105.8 | 0.876017363 |

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|---|---|---|---|
| A membrane-boun | IEA | 1953 | 0.861495136 |
| A lipid bilayer alon | IEA; IEA | 2202 | 0.859718438 |
| A chlorophyll-cont | IBA; IEA | 796.6 | 0.822872207 |
| The lipid bilayer su | IBA; IEA; IEA | 1299.5 | 0.879261254 |
|  |  | 2884.7 | 0.775713246 |
| OBSOLETE. The bas | IEA | 881.8 | 0.908369245 |
|  |  | 1746.2 | 0.908830604 |
| The contents of a c | IBA; IBA; IBA | 1702.8 | 0.932992718 |
| A membrane-boun | IEA | 743.7 | 0.944735781 |
| A membrane-boun | IBA | 809.4 | 0.775636274 |
| The Golgi cisterna | IEA; IEA; IEA; IEA; IE | 1294.5 | 0.963460796 |
|  |  | 1032 | 0.8125 |
| A semiautonomous | IBA | 879.7 | 0.806752302 |
| Organized structur | IBA | 1612.3 | 0.822241518 |
|  |  | 732.5 | 0.905392491 |
| A semiautonomous | IEA | 1473.5 | 0.818187988 |
|  |  | 505 | 0.951683168 |
| The contents of a c | IEA; IEA; IEA | 1710.4 | 0.907273152 |
|  |  | 1731 | 0.857423455 |
| The contents of a c | IBA | 1205 | 0.934190871 |
| A membrane-boun | IEA; IEA | 1316.1 | 0.801002963 |
| A membrane-boun | IEA | 1336.3 | 0.759934147 |
| The contents of a c | IBA | 607.7 | 0.823926279 |
| The irregular netwo | IBA; IBA; IEA; IEA | 384.4 | 0.847814776 |
| The irregular netwo | IEA; IEA; IEA; IEA | 2001.8 | 0.943350984 |
| The space external | IEA | 623.1 | 0.880276039 |
| A chlorophyll-cont | IEA | 572.7 | 0.854723241 |

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|---|---|---|---|
| | | 1088.9 | 0.850583157 |
| | | 493.1 | 0.829243561 |
| A membrane-boun | IEA; IEA | 1046.1 | 0.925341746 |
| A lipid bilayer alon | IEA; IEA | 804.8 | 0.915382704 |
| A lipid bilayer alon | IBA; IBA | 1237 | 0.797089733 |
| | | 855.2 | 0.896515435 |
| | | 676.5 | 0.859866962 |
| A semiautonomous | IBA | 1195.4 | 0.860716078 |
| Organized structur | IBA | 1577.1 | 0.78650688 |
| A lipid bilayer alon | IEA; IEA | 664.9 | 0.878929162 |
| | | 1485.9 | 0.888283195 |
| A small organelle e | IEA; IBA | 302.7 | 0.863230922 |

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|---|---|---|---|
| | | 773.2 | 0.949172271 |
| A membrane-boun | IEA | 375.3 | 0.844924061 |
| | | 667.7 | 0.796165943 |
| The lipid bilayer su | IBA; IEA; IEA; IEA | 930.5 | 0.930360021 |
| A subcomplex of th | IBA; IEA | 1677.6 | 0.964473057 |
| Organized structur | IBA | 1813.9 | 0.88268372 |
| | | 321.4 | 0.887990044 |
| A lipid bilayer along | IEA; IEA; IEA | 2407.2 | 0.874459953 |
| The contents of a c | IBA; IEA; IEA; IEA | 553.3 | 0.875474426 |
| A semiautonomous | IBA | 1100.8 | 0.918332122 |
| | | 1829.2 | 0.916958233 |
| | | 1014.1 | 0.859284094 |
| A transmembrane p | IEA | 462.3 | 0.933376595 |
| | | 1201.4 | 0.875894789 |
| The membrane surr | IEA; IEA; IEA | 1370.7 | 0.892025972 |
| The membrane surr | IEA; IEA; IEA | 1072.4 | 0.87383439 |
| The contents of a c | IBA | 4640 | 0.913706897 |
| | | 1217.8 | 0.850303827 |

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|---|---|---|---|
| | | 795.6 | 0.867144294 |
| A chlorophyll-conta | IBA; IEA; IEA; IEA; IE | 235.5 | 0.759235669 |
| A membrane-boun | IEA; IEA; IBA; IEA | 1537.7 | 0.943096833 |
| | | 827.4 | 0.888324873 |
| | | 1490.2 | 0.840625419 |
| The membrane surr | IBA; IEA | 2700.1 | 0.920188141 |
| A semiautonomous | IBA | 1025.2 | 0.854857589 |
| | | 1227.1 | 0.899437699 |
| A closed structure t | IBA; IBA; IEA; IEA | 3298.9 | 0.883688502 |
| The component of | IEA | 510.8 | 0.797768207 |
| A chlorophyll-conta | IBA | 1639.3 | 0.93887635 |
| | | 548.8 | 0.832908163 |
| A lipid bilayer alon | IEA; IEA | 202.6 | 0.854392892 |
| | | 1395.1 | 0.87635295 |

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|---|---|---|---|
| A membrane-bound | IBA | 801.9 | 0.803840878 |
| A semiautonomous | IEA; IEA; IEA; IEA | 778.2 | 0.908763814 |
| A protein complex | IBA | 4276.2 | 0.740096347 |
|  |  | 818.3 | 0.85213247 |
|  |  | 635.7 | 0.829479314 |
| A membrane-bound | IEA; IEA; IBA | 4190.7 | 0.920132675 |
| That part of a multi | IBA; IEA; IEA | 962.8 | 0.933215621 |
|  |  | 273.1 | 0.740388136 |
|  |  | 523.8 | 0.93890798 |
| A multisubunit com | IBA; IBA; IEA; IEA; IB | 665.7 | 0.838515848 |
| A membrane-bound | IBA | 975.4 | 0.766249744 |
| A membrane-bound | IBA | 865 | 0.820578035 |
| The membrane surr | IBA; IEA; IEA | 2356.8 | 0.857264087 |

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|---|---|---|---|
| The membrane surr | IBA; IBA | 245.6 | 0.903908795 |
| The membrane surr | IEA | 904 | 0.872123894 |
| The component of | IEA | 987.8 | 0.930046568 |
| The space external | IEA; IBA; IEA; IEA | 1715.6 | 0.922767545 |
| A protein complex | IBA | 595.7 | 0.867047171 |
| A semiautonomous | IBA; IEA | 1680.8 | 0.774928605 |
| | | 629.3 | 0.747338312 |
| Organized structur | IBA | 1689.2 | 0.832346673 |
| A lipid bilayer alon | IBA; IEA | 1129.1 | 0.853777345 |
| A semiautonomous | IBA; IBA; IEA; IEA; IE | 1038.3 | 0.852643745 |
| | | 722.4 | 0.928571429 |
| A lipid bilayer alon | IEA; IEA | 454.1 | 0.773838362 |
| The irregular netwo | IBA | 1235.9 | 0.825956793 |
| | | 788.5 | 0.84032974 |
| A membrane-boun | IEA; IBA; IBA | 1457.3 | 0.889590338 |
| | | 863.6 | 0.889532191 |
| A semiautonomous | IEA | 1371.9 | 0.817187842 |
| A membrane-boun | IEA | 1098.2 | 0.740848661 |
| A lipid bilayer alon | IEA; IEA; IBA | 752.3 | 0.946829722 |
| The component of | IEA | 1159 | 0.871095772 |
| | | 1214.5 | 0.92070811 |
| A membrane-boun | IBA; IEA; IBA | 1062.9 | 0.855395616 |
| A membrane-boun | IEA | 1323.1 | 0.890106568 |
| | | 1908.1 | 0.815313663 |
| A part of a cellular | IEA | 1266.7 | 0.899344754 |

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|---|---|---|---|
| The lipid bilayer su | IBA; IEA; IEA; IEA | 626.3 | 0.778540635 |
| | | 978.1 | 0.758204683 |
| A chlorophyll-conta | IBA | 967.6 | 0.894377842 |
| The membrane surr | IEA; IBA; IEA; IEA | 1256.2 | 0.967361885 |
| | | 1043.8 | 0.881394903 |
| | | 1445.1 | 0.95868798 |
| | | 592.5 | 0.908523207 |
| A membrane-boun | IBA; IEA; IEA | 1340.1 | 0.920379076 |
| A lipid bilayer along | IBA; IEA | 1034.3 | 0.914918302 |
| The lipid bilayer su | IEA; IEA; IEA | 1059.5 | 0.938461538 |
| | | 837.1 | 0.922709354 |
| A lipid bilayer along | IEA; IEA | 1096.8 | 0.802242888 |
| Organized structure | IBA | 1519.4 | 0.827563512 |
| Organized structure | IBA | 2116.1 | 0.809602571 |
| | | 918.4 | 0.858885017 |
| | | 1191 | 0.91125105 |
| A membrane-boun | IEA | 677.2 | 0.762847017 |
| The membrane surr | IBA | 1461.6 | 0.823617953 |
| A chlorophyll-conta | IEA; IEA | 979 | 0.950868233 |
| A semiautonomous | IBA | 1113.5 | 0.78688819 |
| A closed structure, | IEA; IEA; IEA; IBA; IE | 1707.1 | 0.954367055 |
| A membrane-boun | IEA | 569.4 | 0.842817 |
| | | 1288.9 | 0.863759795 |
| A membrane-boun | IBA | 1019.8 | 0.758678172 |
| | | 678.1 | 0.778203805 |
| | | 997.9 | 0.783645656 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA | 825.8 | 0.912932914 |
| | | 942.7 | 0.82985043 |
| | | 1614.1 | 0.879003779 |
| The contents of a c | IBA | 469.6 | 0.884582624 |
| | | 827.9 | 0.941055683 |
| | | 1654 | 0.934159613 |
| The subcomplex of | IBA; IBA | 1298.9 | 0.865116637 |
| The pigmented mer | IBA; IEA; IEA | 666.7 | 0.832908355 |
| The space enclosed | IEA | 889.2 | 0.837831759 |
| Arrays of microtubu | IEA | 1995 | 0.806015038 |
| A membrane-boun | IBA; IBA; IBA | 1401.6 | 0.911743721 |
| | | 869.3 | 0.888070862 |
| That part of a multi | IDA | 170.9 | 0.908718549 |
| A membrane-boun | IEA; IBA | 1084.5 | 0.879944675 |
| A semiautonomous | IEA; IEA | 1359.7 | 0.934103111 |
| The contents of a c | IBA | 788.3 | 0.89915007 |
| | | 740.7 | 0.861617389 |
| | | 405.9 | 0.870904164 |
| | | 1450.8 | 0.879101186 |
| A lipid bilayer along | IEA; IEA | 1770.8 | 0.925175062 |

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|---|---|---|---|
| An RNA polymerase | IEA; IBA; IEA | 1270 | 0.822519685 |
| A lipid bilayer alon | IEA | 1734.5 | 0.914384549 |
|  |  | 764.4 | 0.807430665 |
| A lipid bilayer alon | IEA; IEA | 1066.8 | 0.909448819 |
|  |  | 531.1 | 0.950103559 |
|  |  | 1481.2 | 0.80920875 |
|  |  | 735.1 | 0.851312747 |
| The lipid bilayer su | IEA; IEA; IEA; IEA | 1290.4 | 0.936608803 |
| The part of the cyt | IBA; IBA | 2148.8 | 0.895057707 |
| A membrane-boun | IEA; IEA; IBA | 1537.3 | 0.805438106 |
| The membrane sur | IBA; IEA; IEA | 1260.9 | 0.945039258 |
| A membrane-boun | IEA | 448.6 | 0.826125724 |
| A ribonuclease com | IBA; IBA; IEA | 673.8 | 0.96645889 |
|  |  | 1308.7 | 0.872392451 |
|  |  | 993.7 | 0.748314381 |
| The part of the cyt | IBA | 712.5 | 0.896421053 |
| A membrane-boun | IEA; IEA; IEA; IEA | 1202.6 | 0.832363213 |
|  |  | 2769.6 | 0.838604853 |
| An intracellular org | IEA; IEA; IBA; IEA; IE | 516.9 | 0.889920681 |
| A membrane-boun | IEA; IBA | 1672 | 0.864533493 |
|  |  | 639.6 | 0.79518449 |
|  |  | 1151.7 | 0.880090301 |
| A membrane-boun | IBA; IBA | 779.7 | 0.831858407 |
|  |  | 646.8 | 0.888682746 |
|  |  | 481 | 0.84968815 |
| The membrane sur | IEA; IEA; IEA | 1891.9 | 0.778053808 |
|  |  | 755.1 | 0.914978149 |
| A lipid bilayer alon | IEA; IEA | 434.3 | 0.880036841 |
| The component of | IEA | 2031.4 | 0.822388501 |
| The lipid bilayer su | IEA; IEA; IEA | 2095.8 | 0.873699781 |

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|---|---|---|---|
| The contents of a c | IEA | 1327.5 | 0.871487759 |
|  |  | 2002.7 | 0.773256104 |
|  |  |  |  |
| A membrane-boun | IBA; IBA; IBA; IEA | 1264.4 | 0.934356216 |
|  |  | 519.7 | 0.923609775 |
|  |  |  |  |
| The space external | IEA; IEA; IEA | 1299 | 0.933025404 |
| A membrane-boun | IEA | 623.6 | 0.89913406 |
|  |  |  |  |
| A lipid bilayer along | IBA; IEA | 1095.6 | 0.813891931 |
| A lipid bilayer along | IEA; IEA | 803.1 | 0.887436185 |
|  |  | 916.2 | 0.840537001 |
|  |  | 612.5 | 0.836571429 |
|  |  | 1538.5 | 0.768150796 |
| A chlorophyll-conta | IBA | 603.7 | 0.8416432 |
|  |  | 2188.5 | 0.839570482 |
| A lipid bilayer along | IEA | 909.4 | 0.923795909 |
| Organized structure | IBA | 1239.9 | 0.850633116 |
|  |  |  |  |
|  |  | 199.8 | 0.853853854 |
| A lipid bilayer along | IEA; IEA | 919.9 | 0.87933471 |
| The space external | IEA; IEA; IEA | 584.8 | 0.946819425 |
| A membrane-boun | IBA; IBA; IBA | 761.1 | 0.878465379 |

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|---|---|---|---|
| A ubiquitin ligase c | IBA | 1347 | 0.957089829 |
| | | 1200.4 | 0.927440853 |
| A membrane-boun | IEA; IEA; IEA; IEA; IB | 1654.5 | 0.952432759 |
| A membrane-boun | IEA; IEA | 797.7 | 0.840792278 |
| | | 3340 | 0.768742515 |
| A membrane-boun | IEA; IEA; IEA; IBA | 540.8 | 0.909578402 |
| | | 1708.2 | 0.784392928 |
| The component of | IEA | 419.9 | 0.864729698 |
| OBSOLETE. The bas | IEA | 1571 | 0.939465309 |
| A part of a cellular | IEA | 289.3 | 0.773591428 |
| | | 1041.4 | 0.888419435 |
| | | 1172.1 | 0.9501749 |
| | | 1671.9 | 0.900711765 |
| A semiautonomous | IBA; IEA; IEA | 1540.6 | 0.891211216 |
| | | 1795.1 | 0.920505821 |
| A lipid bilayer alon | IEA; IEA | 781.5 | 0.777095329 |
| A ubiquitin ligase c | IEA | 973 | 0.865878726 |
| The lipid bilayer su | IBA | 517.8 | 0.904982619 |
| A membrane-boun | IBA; IBA; IBA; IBA; IB | 1250.2 | 0.878579427 |
| | | 182.2 | 0.957189901 |
| | | 2185.9 | 0.840660597 |
| | | 888.1 | 0.876252674 |
| | | 1262.9 | 0.848760789 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 745.7 | 0.971436234 |

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|---|---|---|---|
| | | 929.8 | 0.784577328 |
| A protein complex | IEA | 1706 | 0.912602579 |
| | | 798 | 0.929699248 |
| A membrane-boun | IBA | 1261.4 | 0.977088949 |
| | | 333.9 | 0.878406709 |
| A lipid bilayer alon | IEA | 1127.7 | 0.939434247 |
| A membrane-boun | IEA; IEA | 1454.6 | 0.777808332 |
| A membrane-boun | IEA; IEA | 895.5 | 0.785706309 |
| | | 1535.9 | 0.875773162 |
| A lipid bilayer alon | IEA; IEA | 1087.2 | 0.913539367 |
| A membrane-boun | IEA | 470.6 | 0.925839354 |
| | | 1002.2 | 0.920674516 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1142.1 | 0.943700201 |
| A lipid bilayer alon | IEA; IEA | 459.8 | 0.897129187 |
| | | 984 | 0.921646341 |
| | | 764.9 | 0.777095045 |
| | | 581.7 | 0.91559223 |
| Any microtubule in | IBA | 735 | 0.908163265 |
| | | 317.4 | 0.758664146 |
| The contents of a c | IBA | 1545.3 | 0.872516663 |
| The membrane surr | IEA | 608.2 | 0.977967774 |
| | | 775.2 | 0.943369453 |

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|---|---|---|---|
| A membrane-boun | IEA | 710.3 | 0.800084471 |
| A membrane-boun | IEA | 722.6 | 0.914198727 |
| The part of the cyto | IBA | 662.2 | 0.911960133 |
| | | 750.9 | 0.911839126 |
| A vacuole to which | IEA; IEA; IEA | 2469.5 | 0.795424175 |
| A lipid bilayer alon | IEA; IEA | 1025.8 | 0.882823162 |
| The irregular netwo | IEA; IEA; IEA; IEA | 1080.6 | 0.898667407 |
| | | 915.1 | 0.910829418 |
| | | 140.6 | 0.890469417 |
| A membrane-boun | IEA | 1081.8 | 0.742281383 |
| | | 1395.1 | 0.820729697 |
| | | 1293.6 | 0.925401979 |
| A ubiquitin ligase c | IBA | 1193 | 0.759765298 |

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|---|---|---|---|
| A membrane-boun | IEA | 717.4 | 0.791051018 |
| A membrane-boun | IEA | 528.1 | 0.933156599 |
| A lipid bilayer alon | IEA; IEA | 2425.4 | 0.968953575 |
| A lipid bilayer alon | IEA; IEA | 940.6 | 0.905911121 |
| | | 620.3 | 0.914557472 |
| The membrane sur | IBA | 1262.4 | 0.953976553 |
| A membrane-boun | IBA; IBA; IBA | 457.1 | 0.922992781 |
| A membrane-boun | IEA; IEA | 807 | 0.834820322 |
| | | 896 | 0.894977679 |
| The membrane sur | IEA; IBA; IEA | 1077.3 | 0.954144621 |
| The membrane sur | IBA; IEA; IEA | 2097.5 | 0.904123957 |
| | | 1621.9 | 0.768728035 |
| The part of the cyt | IEA; IBA | 623.1 | 0.883806773 |
| A membrane-boun | IBA; IBA | 634 | 0.849369085 |
| | | 300.9 | 0.775008308 |
| A lipid bilayer alon | IEA; IEA | 373.8 | 0.791867309 |
| | | 1106.2 | 0.934912312 |
| | | 1163.3 | 0.855153443 |
| The irregular netwo | IEA; IEA; IBA; IEA; IE | 744.5 | 0.947212895 |
| The lipid bilayer su | ISS; IEA; IEA; IEA | 1262.8 | 0.812242635 |
| The lipid bilayer su | IEA; IEA; IEA | 974.8 | 0.922035289 |
| The part of the cyt | IBA; IBA; IBA | 1682.9 | 0.918711748 |
| | | 521.2 | 0.975249424 |
| A membrane-boun | IBA; IBA | 951.1 | 0.825254968 |
| | | 557.6 | 0.902080344 |
| The contents of a c | IBA; IEA; IEA; IBA; IE | 1145.7 | 0.81295278 |

|  |  |  |  |
|---|---|---|---|
| A membrane-boun | IEA | 504.4 | 0.813441713 |
| A chlorophyll-conta | IEA | 639.5 | 0.76825645 |
|  |  | 906.8 | 0.913983238 |
|  |  | 1015.4 | 0.870395903 |
| The membrane surr | IBA; IBA; IBA | 1339.4 | 0.922801254 |
| The outer, i.e. cytop | IEA; IEA | 2002.2 | 0.855858556 |
| A lipid bilayer along | IEA; IEA | 1250.3 | 0.936655203 |
|  |  | 1714.8 | 0.851761138 |
| A lipid bilayer along | IEA | 1028.6 | 0.783686564 |
|  |  | 902.9 | 0.829992247 |
| A protein complex p | IEA | 1817.3 | 0.966323667 |
| A chlorophyll-conta | IEA | 972 | 0.945781893 |
|  |  | 1104.8 | 0.926955105 |
|  |  | 643.4 | 0.891513833 |
| The membrane surr | IEA; IEA; IEA | 908.2 | 0.865007708 |
| A lipid bilayer along | IEA; IEA | 1140.5 | 0.892240246 |
| The space external | IEA | 731.4 | 0.866010391 |
| The volume enclose | IEA | 454.5 | 0.920352035 |
| A membrane-boun | IBA | 688.7 | 0.770001452 |
|  |  | 578.4 | 0.88208852 |
| A protein complex t | IBA | 3148.7 | 0.963794582 |
|  |  | 982.2 | 0.786703319 |
|  |  | 1252.8 | 0.857998084 |
|  |  | 506.2 | 0.942710391 |
| A membrane-boun | IBA; IBA | 629.9 | 0.928083823 |
| A membrane-boun | IEA; IEA; IBA; IEA | 1374.8 | 0.950029095 |
| A lipid bilayer along | IBA; IBA | 1170.6 | 0.861609431 |
| A membrane-boun | IEA | 1488.8 | 0.949758195 |
|  |  | 283.1 | 0.941363476 |
| A membrane-boun | IEA | 860.4 | 0.779521153 |
|  |  | 366.1 | 0.838295548 |

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|---|---|---|---|
| A membrane-boun | IBA | 1367.6 | 0.883737935 |
| A membrane-boun | IEA | 584.4 | 0.791581109 |
| A membrane-boun | IBA; IBA | 1067.7 | 0.751709282 |
| The contents of a c | IBA | 454.1 | 0.899141158 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA | 1328.7 | 0.937457665 |
| The membrane surr | IBA; IEA; IEA | 788.7 | 0.895777862 |
| A complex with me | IBA; IEA; IBA; IBA | 449.6 | 0.934386121 |
| | | 1676.9 | 0.908223508 |
| The irregular netwo | IBA; IBA; IEA | 965.6 | 0.955157415 |
| The gel-like materi | IBA; IEA; IEA; IBA | 625.7 | 0.919769858 |
| A small, dense bod | IEA | 421.9 | 0.903057597 |
| A membrane-boun | IBA; IBA | 1010.7 | 0.742455724 |
| | | 693.9 | 0.813373685 |
| The membrane surr | IBA; IEA; IEA | 1728.9 | 0.918907976 |
| | | 2456.9 | 0.856770727 |
| The contents of a c | IBA | 604.1 | 0.818407548 |
| A membrane-boun | IBA | 378.3 | 0.785884219 |
| The contents of a c | IBA | 1279.7 | 0.745252794 |
| A membrane-boun | IBA | 1946.9 | 0.755046484 |
| A lipid bilayer alon | IEA; IEA | 156.8 | 0.797831633 |
| | | 477 | 0.874633124 |
| | | 183.6 | 0.916122004 |
| A chlorophyll-conta | IEA | 605.8 | 0.865797293 |

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|---|---|---|---|
| A lipid bilayer alon | IBA | 954.7 | 0.89284592 |
| A membrane-boun | IBA | 1016 | 0.882185039 |
| | | 561.6 | 0.86235755 |
| | | 707.8 | 0.867617971 |
| A lipid bilayer alon | IEA; IEA | 1028.6 | 0.911044138 |
| | | 836.7 | 0.962830166 |
| The membrane sur | IBA | 814.4 | 0.890103143 |
| A membrane-boun | IBA; IBA | 1547.4 | 0.79649735 |
| The double lipid bil | IBA; IEA | 923.1 | 0.757556061 |
| The contents of a c | IEA | 239.7 | 0.818940342 |
| The space external | IEA; IBA | 971.4 | 0.90107062 |
| | | 1497.3 | 0.811193482 |
| A membrane-boun | IEA | 779.1 | 0.904120139 |
| A membrane-boun | IEA; IEA | 707.3 | 0.88420755 |
| | | 731.2 | 0.782685996 |
| | | 808.5 | 0.969325912 |
| The contents of a c | IBA; IBA | 308.8 | 0.906088083 |
| OBSOLETE. The bas | IEA | 326.5 | 0.902603369 |
| Organized structur | IEA | 844.2 | 0.770670457 |
| | | 1255.4 | 0.887127609 |
| A membrane-boun | IEA; IEA; IEA | 959.6 | 0.898082534 |
| A membrane-boun | IBA | 476 | 0.792226891 |
| The lipid bilayer su | IBA | 1134.7 | 0.888076143 |

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|---|---|---|---|
| The component of | IEA | 1720.2 | 0.955470294 |
|  |  | 1113 | 0.89640611 |
|  |  | 689.2 | 0.863174695 |
| A membrane-boun | IEA | 326.6 | 0.749234538 |
| A lipid bilayer alon | IEA; IEA | 160.6 | 0.843711083 |
|  |  | 712.4 | 0.858085345 |
| A semiautonomous | IBA; IBA | 1447.4 | 0.862719359 |
|  |  | 288.5 | 0.805199307 |
| The irregular netwo | IEA; IEA; IEA; IEA | 573.8 | 0.965318926 |
| A lipid bilayer alon | IEA; IEA | 1492.6 | 0.970856224 |
| The space external | IEA | 335.5 | 0.79076006 |
|  |  | 692.4 | 0.956961294 |
|  |  | 1266.5 | 0.937149625 |
|  |  | 459.7 | 0.914509463 |
| A membrane-boun | IEA | 893.7 | 0.864943493 |
| A membrane-boun | IEA; IEA; IBA | 2922.9 | 0.862191659 |
| The lipid bilayer su | IBA; IEA; IEA; IEA; IE | 1070.2 | 0.875256961 |
|  |  | 1387.7 | 0.883404194 |
| A lipid bilayer alon | IEA; IEA | 1246 | 0.88105939 |
| The contents of a c | IBA | 1410.3 | 0.769127136 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA; IEA; IE | 460.8 | 0.770399306 |
| | | 1857.1 | 0.929944537 |
| Organized structure | IBA | 1362.4 | 0.773341163 |
| The membrane surr | IEA | 840.5 | 0.855800119 |
| A membrane-bound | IEA | 675.4 | 0.876517619 |
| | | 563.1 | 0.786716391 |
| | | 783 | 0.909961686 |
| The space external | IEA | 867.9 | 0.860352575 |
| | | 933.2 | 0.898521217 |
| A membrane-bound | IEA; IEA | 1044.3 | 0.745092406 |
| A membrane-bound | IBA; IBA | 1493.5 | 0.953598929 |
| | | 522 | 0.756130268 |
| A lipid bilayer along | IEA; IEA; IEA | 1337.8 | 0.966362685 |
| OBSOLETE. The bas | IEA | 1908 | 0.916352201 |
| A ubiquitin ligase c | IBA | 910.8 | 0.961572244 |
| The membrane surr | IBA; IEA; IEA | 1864.7 | 0.74928943 |

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|---|---|---|---|
| | | 1486.6 | 0.764294363 |
| The space external | IEA; IEA | 1192.9 | 0.887081901 |
| A membrane-boun | IEA | 1040.7 | 0.837417123 |
| A membrane-boun | IEA | 666.6 | 0.741224122 |
| The contents of a c | IBA | 1986.3 | 0.848864723 |
| Organized structure | IBA | 1471.2 | 0.747009244 |
| A membrane-boun | IBA; IBA | 587.9 | 0.845381868 |
| A membrane-boun | IBA; IEA | 1118.5 | 0.914170764 |
| A membrane-boun | IEA | 2035.1 | 0.944720161 |
| A lipid bilayer along | IEA; IEA | 1083.8 | 0.761210555 |
| A membrane-boun | IBA; IBA; IEA | 883.3 | 0.749915091 |
| | | 346.8 | 0.796424452 |
| | | 435.1 | 0.924155367 |
| The irregular netwo | IEA; IBA | 785.7 | 0.95481736 |
| | | 1240.4 | 0.835617543 |
| | | 1000.1 | 0.849415058 |
| The contents of a c | IBA | 397.9 | 0.901231465 |
| A lipid bilayer along | IEA; IEA | 1814.4 | 0.828317901 |
| The space external | IEA | 685.6 | 0.844224037 |
| The lipid bilayer su | IEA; IEA; IEA; IEA; IE | 1753.1 | 0.934173749 |
| A membrane-boun | IEA; IBA | 223.5 | 0.873378076 |
| | | 872.3 | 0.874240514 |
| | | 568.2 | 0.799718409 |
| Cyclin-dependent p | IBA; IBA; IBA | 1032.1 | 0.84003488 |
| | | 241.8 | 0.748138958 |
| The irregular netwo | IEA; IEA; IEA; IEA | 498.9 | 0.915013029 |
| A membrane-boun | IBA | 1275.2 | 0.802697616 |
| | | 437 | 0.764759725 |
| | | 511.1 | 0.880649579 |
| A semiautonomous | IEA; IEA; IEA; IEA | 621.6 | 0.959298584 |

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|---|---|---|---|
| | | 359.4 | 0.803561491 |
| | | 993.4 | 0.917455204 |
| | | 978.9 | 0.946470528 |
| The membrane surr | IEA; IEA | 1403.4 | 0.940430383 |
| | | 1139.3 | 0.788554375 |
| A lipid bilayer alon | IBA; IEA | 1286.8 | 0.87589369 |
| | | 1600.8 | 0.941591704 |
| An intracellular org | IEA; IBA; IEA | 598.5 | 0.930994152 |
| A membrane-boun | IBA | 1140.7 | 0.822915753 |
| A membrane-boun | IBA | 609.6 | 0.793143045 |
| The contents of a c | IBA; IBA | 341.7 | 0.950541411 |
| A multisubunit prot | IEA; IEA | 768 | 0.930338542 |
| Organized structure | IEA | 862.4 | 0.886943414 |
| A membrane-boun | IEA | 1561 | 0.937027546 |
| A membrane-boun | IBA; IBA; IBA | 604.7 | 0.844551017 |
| A lipid bilayer alon | IBA; IEA | 1053.2 | 0.923376377 |
| | | 976.6 | 0.904054884 |
| The contents of a c | IEA; IEA; IEA; IEA | 1548.7 | 0.928456124 |
| A highly compacted | IBA; IBA; IEA | 3234.6 | 0.813021703 |
| The double lipid bil | IEA; IEA | 998.5 | 0.868402604 |
| A membrane-boun | IBA | 709.9 | 0.774334413 |
| A semiautonomous | IBA; IBA | 480.7 | 0.926357395 |
| | | 1092.9 | 0.845182542 |
| | | 1236.5 | 0.934573393 |
| A membrane-boun | IEA; IEA; IEA | 1046.4 | 0.793291284 |
| | | 1623.5 | 0.744748999 |
| A membrane-boun | IEA; IEA; IEA | 510.7 | 0.901116115 |
| A membrane-boun | IBA | 892 | 0.88867713 |
| | | 1011.4 | 0.89242634 |
| A semiautonomous | IBA | 595.5 | 0.949118388 |

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|---|---|---|---|
|  |  | 2106.9 | 0.938487826 |
| A lipid bilayer alon | IEA; IEA | 721.3 | 0.857479551 |
| The gel-like materi | IBA | 1287.3 | 0.8746213 |
| A lipid bilayer alon | IEA; IEA | 536.1 | 0.876329043 |
| A small, dense bod | IBA | 467.4 | 0.938596491 |
|  |  | 1022.5 | 0.926356968 |
|  |  | 976.2 | 0.915181315 |
|  |  | 991.6 | 0.855385236 |
|  |  | 548.1 | 0.915891261 |
| The membrane surr | ISS; ISS; IBA; IEA | 544 | 0.959926471 |
| A semiautonomous | IBA | 1971 | 0.850380518 |
|  |  | 1023.4 | 0.861051397 |
| A lipid bilayer alon | IEA; IEA | 483.2 | 0.91763245 |
|  |  | 489.6 | 0.865808824 |
| A membrane-boun | IEA | 618.5 | 0.75763945 |
| A chlorophyll-cont | IEA | 538.6 | 0.848124768 |
|  |  | 774.1 | 0.777289756 |
|  |  | 791.5 | 0.967782691 |
|  |  | 1678.1 | 0.874679697 |
| That part of a multi | IEA | 1058.3 | 0.853822168 |

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|---|---|---|---|
|  |  | 935.7 | 0.91268569 |
| A lipid bilayer along | IEA; IEA | 1656.7 | 0.852960705 |
|  |  | 1112.8 | 0.818386053 |
|  |  | 808.4 | 0.940623454 |
| The pigmented me | IBA; IEA | 1532.3 | 0.876656007 |
| A lipid bilayer along | IEA; IEA | 2068.9 | 0.844990091 |
| A lipid bilayer along | IEA; IEA | 556.6 | 0.912863816 |
|  |  | 1200.8 | 0.903897402 |
|  |  | 255.1 | 0.821638573 |
|  |  | 1337 | 0.896634256 |
| An intracellular org | IEA; IEA | 379.7 | 0.818540953 |
| A lipid bilayer along | IEA; IEA | 1603 | 0.929507174 |
|  |  | 681.3 | 0.770732423 |
| The membrane surr | IBA; IEA; IEA; IBA | 1058.7 | 0.941154246 |
|  |  | 679.5 | 0.89874908 |
| A membrane-boun | IEA | 785 | 0.769426752 |
| A lipid bilayer along | IEA; IEA | 603.5 | 0.754598177 |
|  |  | 1523.1 | 0.903420655 |
| The network of inte | IBA | 3795.2 | 0.949488828 |
| A membrane-boun | IEA | 490.9 | 0.883071909 |
| A membrane-boun | IBA | 789.7 | 0.874129416 |
|  |  | 1668.8 | 0.79524209 |
| A spliceosomal com | IBA | 1618.9 | 0.82815492 |
| A membrane-boun | IEA | 756.7 | 0.872208273 |
| A heterohexameric | IEA | 539 | 0.816141002 |
| A semiautonomous | IEA; IEA; IEA | 1032.9 | 0.877432472 |
| A semiautonomous | IBA | 1129.8 | 0.746238272 |
|  |  | 3870.8 | 0.94546347 |

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|---|---|---|---|
| The irregular netwo | IBA; IEA; IEA | 429 | 0.863636364 |
| A lipid bilayer alonç | IEA; IEA | 1099.3 | 0.93313927 |
| | | 550.1 | 0.910925286 |
| Cyclin-dependent p | IBA; IBA | 1577.3 | 0.90483738 |
| A multisubunit com | IBA; IBA | 1615.8 | 0.740500062 |
| | | 699.5 | 0.820872051 |
| | | 256.9 | 0.830673414 |
| | | 452.7 | 0.762756793 |
| That part of a multi | IEA | 694.9 | 0.906893078 |
| | | 656.8 | 0.888398295 |
| The membrane surr | IBA | 954.1 | 0.919924536 |
| A membrane-bound | IEA | 644.1 | 0.946592144 |
| | | 1102.7 | 0.885553641 |
| A lipid bilayer alonç | IBA; IBA | 1182.8 | 0.886117687 |
| Organized structure | IBA | 1059.1 | 0.750637334 |
| | | 776.5 | 0.909980683 |
| The contents of a c | IBA | 1039 | 0.958036574 |
| That part of a multi | IEA | 855.6 | 0.92484806 |
| The irregular netwo | IEA; IEA; IEA | 2205.9 | 0.915907339 |
| The lipid bilayer su | IEA; IBA; IEA; IEA | 1282.6 | 0.861219398 |
| A membrane-bound | IEA; IEA; IEA; IEA; IE | 888.8 | 0.87950045 |
| A membrane-bound | IBA | 3786.5 | 0.845107619 |
| A multisubunit prot | IEA; IEA; IEA | 1473.1 | 0.833276763 |
| | | 1706.9 | 0.911184018 |
| | | 1042.3 | 0.877770316 |
| Organized structure | IEA | 1608.7 | 0.9738298 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 1104 | 0.846557971 |
| A lipid bilayer alon | IEA; IEA | 432.7 | 0.929974578 |
| A membrane-boun | IEA | 842.8 | 0.827123873 |
| A chlorophyll-cont | IBA | 648.6 | 0.911655874 |
| A lipid bilayer alon | IEA; IEA | 207 | 0.870048309 |
| | | 730.5 | 0.925119781 |
| The ordered and or | IBA; IEA | 1787.3 | 0.787164997 |
| OBSOLETE. The bas | IEA; IEA | 924 | 0.910064935 |
| | | 586.4 | 0.824693042 |
| | | 666.7 | 0.865906705 |
| The membrane surr | IBA; IEA; IBA | 1367.2 | 0.940462259 |
| | | 674.5 | 0.84017791 |
| The component of | IEA | 1424.8 | 0.941325098 |
| Organized structure | IBA | 1751.7 | 0.93828852 |
| A membrane-boun | IBA | 2293.8 | 0.902258261 |
| | | 881.1 | 0.866530473 |
| | | 915 | 0.886666667 |
| A focus in the cyto | IBA; IEA; IEA | 1356.3 | 0.927007299 |
| | | 332 | 0.760843373 |
| | | 804.3 | 0.774462265 |
| A lipid bilayer alon | IBA; IEA | 1321 | 0.882664648 |
| | | 877.2 | 0.929662563 |
| A lipid bilayer alon | IBA; IEA | 1163.9 | 0.853251998 |
| | | 158.2 | 0.804677623 |
| | | 1340.3 | 0.87084981 |
| | | 545.2 | 0.805759354 |
| The membrane surr | IBA | 947.3 | 0.853689433 |
| A membrane-boun | IEA; IBA | 916.9 | 0.874359254 |
| | | 1190 | 0.835042017 |
| The irregular netwo | IEA; IEA; IBA | 1215.5 | 0.86631016 |
| | | 765.8 | 0.85949334 |

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|---|---|---|---|
|  |  | 236.3 | 0.743123149 |
| The lipid bilayer su | IBA; IEA; IEA | 1157.7 | 0.940571823 |
| A chlorophyll-conta | IEA | 2365.2 | 0.776974463 |
|  |  | 2178.3 | 0.822751687 |
|  |  | 1017.8 | 0.922774612 |
| The space enclosed | IBA | 946.4 | 0.751373626 |
|  |  | 2898.7 | 0.790354297 |
|  |  | 613.5 | 0.798370008 |
| A membrane-boun | IBA; IBA | 648.5 | 0.802621434 |
| The gel-like materi | IEA | 522.4 | 0.84992343 |
|  |  | 934.7 | 0.888306408 |
| The component of | IEA | 642.1 | 0.954679956 |
|  |  | 1163.8 | 0.862347482 |
|  |  | 966.2 | 0.859656386 |
|  |  | 1255.6 | 0.847722205 |
| A membrane-boun | IEA; IEA; IEA; IBA | 389 | 0.968894602 |
| A lipid bilayer alon | IEA | 2316.3 | 0.940810776 |
| A lipid bilayer alon | IEA; IEA | 1168.7 | 0.868743048 |
|  |  | 876.1 | 0.920785298 |
|  |  | 1059.1 | 0.858275895 |
| The part of the cyto | IBA | 931.1 | 0.937600687 |
| A membrane-boun | IEA | 1006.3 | 0.891483653 |

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|---|---|---|---|
| The space external | IEA; IBA; IEA | 473.8 | 0.809624314 |
| A lipid bilayer alon | IEA; IEA; IEA; IEA | 1164.3 | 0.933006957 |
| A chlorophyll-conta | IBA | 1103.9 | 0.957967207 |
| | | 1427.2 | 0.82504204 |
| A chlorophyll-conta | IEA | 1269.4 | 0.887348354 |
| | | 391.1 | 0.767578624 |
| A semiautonomous | IEA; IEA; IEA; IBA | 949.4 | 0.964819886 |
| | | 1022.1 | 0.957831915 |
| A membrane-boun | IEA; IEA; IBA | 658 | 0.956990881 |
| A lipid bilayer alon | IBA; IBA | 1081.3 | 0.904466845 |
| A lipid bilayer alon | IEA; IEA | 2156.5 | 0.774542082 |
| A membrane-boun | IEA; IEA | 1196.2 | 0.752466143 |
| The contents of a c | IBA | 670.3 | 0.858570789 |
| | | 1190.7 | 0.914504073 |
| A semiautonomous | IBA; IBA; IEA; IEA; IE | 1073.8 | 0.918979326 |
| That part of a multi | IBA | 766 | 0.963446475 |
| A membrane-boun | IEA; IBA | 2950.6 | 0.844099505 |
| The membrane surr | IBA; IEA; IEA | 1577.9 | 0.943152291 |
| A lipid bilayer alon | IEA; IEA | 1135.6 | 0.900845368 |
| A membrane-boun | IBA; IEA; IEA; IEA; IE | 694.3 | 0.903211868 |

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|---|---|---|---|
| A protein complex | IEA; IBA | 2195.9 | 0.912200009 |
| The component of | IEA; IBA | 737.6 | 0.776030369 |
| A semiautonomous | IBA | 562.9 | 0.923432226 |
| A lipid bilayer along | IEA; IEA | 1569.5 | 0.944950621 |
| | | 988.9 | 0.931034483 |
| The pigmented me | IBA; IBA; IEA; IEA | 736.7 | 0.913261843 |
| The contents of a c | IBA; IBA | 848.3 | 0.900153248 |
| | | 613.3 | 0.954997554 |
| | | 513.1 | 0.763983629 |
| The contents of a c | IBA; IBA; IBA; IBA | 1217.7 | 0.903835099 |
| | | 497.1 | 0.828404748 |
| | | 876.8 | 0.853216241 |
| A part of a cellular | IEA | 1187.9 | 0.867581446 |
| | | 873.8 | 0.921149004 |
| | | 496.1 | 0.950010079 |
| | | 533.3 | 0.876617289 |
| | | | |
| | | 520.9 | 0.806680745 |
| The component of | IEA | 1439.6 | 0.803070297 |
| | | 409.1 | 0.780004889 |
| A semiautonomous | IEA | 381.5 | 0.923722149 |
| | | 814.4 | 0.803167976 |
| | | 579 | 0.859240069 |
| | | 463.6 | 0.825711821 |
| The contents of a c | IBA; IBA; IBA | 2778.5 | 0.869245996 |
| A lipid bilayer along | IEA; IEA | 349 | 0.846131805 |
| | | | |
| A protein complex | IBA; IEA; IEA; IBA; IB | 768.6 | 0.921935988 |
| A lipid bilayer along | IEA; IEA | 1158.4 | 0.881474448 |
| The contents of a c | IEA | 277 | 0.916606498 |
| | | 379.5 | 0.874571805 |
| The contents of a c | IBA | 909.8 | 0.928006155 |
| | | | |
| The membrane surr | IEA; IBA; IEA | 1573.4 | 0.897419601 |
| | | | |
| A lipid bilayer along | IEA | 1688.3 | 0.914707102 |

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| The membrane surr | IEA; IEA | 538.4 | 0.860141159 |
| Organized structure | IBA | 959.8 | 0.767555741 |
| | | | |
| A semiautonomous | IEA; IEA; IEA; IEA | 571.9 | 0.878824969 |
| A lipid bilayer along | IEA | 1066.6 | 0.77648603 |
| A membrane-bound | IBA; IBA | 609 | 0.850574713 |
| The irregular netwo | IBA; IEA; IEA; IEA | 1710.6 | 0.870396352 |
| The irregular netwo | IEA | 778.2 | 0.950526857 |
| A small, dense body | IBA | 364.7 | 0.888401426 |
| | | | |
| A protein complex t | IEA | 1069.9 | 0.917842789 |
| | | 626.6 | 0.846473029 |
| The lipid bilayer su | IEA; IEA; IEA; IBA; IB | 1484.5 | 0.929067026 |
| A membrane-bound | IBA; IEA; IEA | 850.6 | 0.941335528 |
| A chlorophyll-conta | IBA | 701.1 | 0.760519184 |
| A semiautonomous | IEA; IEA; IEA | 761.5 | 0.888115561 |
| | | | |
| | | 222.3 | 0.887089519 |
| | | | |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 593.5 | 0.824262848 |
| Organized structure | IBA | 1796.7 | 0.958702065 |
| | | | |
| A membrane-bound | IEA | 256.2 | 0.81459797 |
| A protein complex t | IBA; IBA | 1435.8 | 0.91384594 |
| A protein complex t | IBA; IBA | 3824.4 | 0.865103023 |
| Organized structure | IBA | 961.8 | 0.804221252 |
| A lipid bilayer along | IEA; IEA | 346.8 | 0.893886967 |

|  |  |  |  |
|---|---|---|---|
| The membrane surr | IEA; IBA; IEA | 573.6 | 0.807182706 |
| The membrane surr | IBA; IEA; IEA | 434.3 | 0.871977895 |
| A membrane-bound | IEA; IBA | 324.2 | 0.860271437 |
|  |  | 201 | 0.937810945 |
|  |  | 1156.8 | 0.916926003 |
| The membrane surr | IBA | 1005.9 | 0.910229645 |
|  |  | 807.6 | 0.833580981 |
| The irregular netwo | IEA; IEA; IEA; IEA | 461.4 | 0.927828349 |
| The membrane surr | IBA; IBA; IEA; IEA; IE | 1911.3 | 0.833987338 |
| The contents of a c | IBA; IBA; IBA | 453.5 | 0.780374862 |
| The membrane surr | IBA; IBA | 867.7 | 0.919787945 |
| A macromolecular c | IBA | 365.3 | 0.869969888 |
| A membrane-bound | IEA; IEA; IEA; IEA; IE | 785 | 0.757707006 |
| OBSOLETE. The bas | IEA | 1819.5 | 0.836878263 |
| The pigmented mer | IBA; IBA | 894.3 | 0.921167393 |
| A semiautonomous | IBA | 333.1 | 0.840588412 |
|  |  | 763 | 0.894757536 |
| A membrane-bound | IEA; IEA; IBA | 851.2 | 0.91600094 |
|  |  | 741.4 | 0.838278932 |
| The contents of a c | IBA; IBA; IEA; IBA | 2794 | 0.902612742 |
| The irregular netwo | IEA | 1090.9 | 0.930149418 |
| The lipid bilayer su | IEA; IEA; IEA; IEA; IE | 308.4 | 0.822957198 |
| The lipid bilayer su | IEA; IBA; IEA; IEA; IE | 1363.6 | 0.918231153 |
| A lipid bilayer along | IEA; IEA | 1201.5 | 0.848106533 |
| The rigid or semi-ri | IBA; IBA; IEA | 1855.7 | 0.889044565 |

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|---|---|---|---|
| A chlorophyll-conta | IBA | 809.6 | 0.854249012 |
| The space external | IEA | 330.8 | 0.899032648 |
| A semiautonomous | IEA | 580.1 | 0.950008619 |
|  |  | 1416.5 | 0.949947053 |
| A membrane-bound | IEA | 758.7 | 0.821668644 |
|  |  | 968.8 | 0.767857143 |
|  |  | 1491.8 | 0.864324977 |
| A lipid bilayer along | IEA; IEA | 745.8 | 0.904129794 |
| The space enclosed | IEA; IBA | 584.5 | 0.927459367 |
| A semiautonomous | IBA | 1644.1 | 0.903594672 |
| The membrane surr | IBA; IEA; IEA; IBA | 1067.8 | 0.894736842 |
|  |  |  |  |
|  |  |  |  |
| The lipid bilayer sur | IEA; IEA; IEA | 881.7 | 0.873766587 |
| A membrane-bound | IBA; IBA; IEA | 1184.1 | 0.952875602 |
|  |  |  |  |
|  |  |  |  |
| The contents of a c | IBA | 1833.9 | 0.758492829 |
| A membrane-bound | IBA; IBA; IEA | 572 | 0.940734266 |
|  |  |  |  |
|  |  |  |  |
| The rigid or semi-ri | IEA | 1281 | 0.809445746 |
| A membrane-bound | IEA | 644.4 | 0.875853507 |
|  |  |  |  |
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|  |  |  |  |
|  |  |  |  |
|  |  | 979.2 | 0.924223856 |
|  |  | 177.1 | 0.865612648 |
| The part of the cyto | IEA; IEA | 547.6 | 0.953798393 |
| The contents of a c | IEA; IEA; IEA | 1575.8 | 0.85061556 |

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|---|---|---|---|
| The membrane surr | IBA; IEA; IEA | 2105 | 0.941662708 |
| | | 876.9 | 0.829170943 |
| | | 1390.8 | 0.853034225 |
| A membrane-boun | IBA | 1027.8 | 0.799961082 |
| A membrane-boun | IBA; IBA | 745.1 | 0.831834653 |
| | | 1225.4 | 0.894483434 |
| | | 772.8 | 0.869694617 |

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|---|---|---|---|
| The membrane surr | IEA; IEA | 1447.6 | 0.787164963 |
| | | 671.8 | 0.79220006 |
| A membrane-boun | IEA; IEA | 772.8 | 0.775232919 |
| | | 1013.1 | 0.947389201 |
| | | 790 | 0.925316456 |
| | | 1679.9 | 0.81606048 |
| | | 212 | 0.958962264 |
| | | 747.1 | 0.930129835 |
| | | 503.9 | 0.93014487 |
| A small organelle e | IEA | 581.1 | 0.937016004 |
| The part of the cyto | IEA; IEA | 3298.4 | 0.937181664 |
| The part of the cyto | IBA | 1420.1 | 0.812407577 |
| A semiautonomous | IEA | 1946.3 | 0.90828752 |
| A semiautonomous | IEA | 392.7 | 0.7820219 |
| A membrane-boun | IEA | 536.6 | 0.818859486 |
| | | 335.6 | 0.81227652 |
| A lipid bilayer along | IEA; IEA | 1645 | 0.912401216 |
| The membrane surr | IBA; IBA; IEA | 669.7 | 0.951769449 |
| The contents of a c | IBA; IEA; IEA; IBA; IE | 2441.5 | 0.79479828 |

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|---|---|---|---|
| | | 570.7 | 0.806378132 |
| That part of a multi | IBA; IEA | 457.9 | 0.808473466 |
| | | 222.2 | 0.895589559 |
| | | 954.6 | 0.882149591 |
| A chlorophyll-conta | IEA | 578.3 | 0.908524987 |
| A chlorophyll-conta | IBA | 743.7 | 0.882613957 |
| | | 1378.9 | 0.862861701 |
| The contents of a c | IBA | 2950.7 | 0.903649981 |
| A semiautonomous | IBA | 616.8 | 0.825064851 |
| A small, dense bod | IBA | 1802.2 | 0.884918433 |
| The part of the cyto | IEA | 1422.7 | 0.927743024 |
| A chlorophyll-conta | IEA; IEA; IEA | 1040.9 | 0.743202997 |
| | | 309.7 | 0.893122376 |
| The irregular netwo | IEA; IEA; IBA; IEA | 337.4 | 0.857439241 |
| | | 716.1 | 0.896941768 |
| A membrane-boun | IBA | 415.4 | 0.766971594 |
| The part of the cyto | IBA | 711.2 | 0.926040495 |
| | | 355.5 | 0.758649789 |
| The region of a chr | IBA; IBA; IBA; IEA | 892.7 | 0.861095553 |
| | | 1013.7 | 0.897405544 |
| A lipid bilayer alon | IBA; IEA | 1207 | 0.881938691 |
| A chlorophyll-conta | IEA; IEA; IEA | 1528.9 | 0.914513703 |

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|---|---|---|---|
| | | 501.1 | 0.82857713 |
| A semiautonomous | IBA; IBA | 1940.1 | 0.775166229 |
| A lipid bilayer alon | IEA; IEA | 873.6 | 0.789949634 |
| | | 800.6 | 0.797401949 |
| The outer, i.e. cyto | IBA | 1358.2 | 0.786040348 |
| | | 406.1 | 0.905688254 |
| The inner, i.e. lume | IBA; IBA; IEA; IEA; IE | 231.8 | 0.815358067 |
| | | 451.5 | 0.850055371 |

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|---|---|---|---|
| | | 457.1 | 0.908991468 |
| A chlorophyll-conta | IEA | 1145 | 0.781222707 |
| A semiautonomous | IEA; IEA | 336.7 | 0.783486783 |
| | | 890.8 | 0.928378985 |
| | | 678 | 0.867846608 |
| | | 821.7 | 0.915906048 |
| | | 1339.5 | 0.84695782 |

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|---|---|---|---|
| | | 973.3 | 0.872598377 |

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|---|---|---|---|
| A closed structure, | IEA; IBA; IBA | 769.9 | 0.831926224 |
| A semiautonomous | IBA | 674.5 | 0.85841364 |
| | | 805.3 | 0.892089904 |
| The membrane surr | IBA | 1065.5 | 0.927170343 |
| A semiautonomous | IBA | 1795.2 | 0.855670677 |
| A lipid bilayer alon | IEA; IEA | 742.3 | 0.865687727 |
| The membrane surr | IBA; IEA; IEA | 1840.1 | 0.928916907 |
| OBSOLETE. The bas | IEA | 1056.3 | 0.94897283 |
| The space external | IEA; IEA; IEA | 594.6 | 0.970063909 |
| The part of the cyt | IBA | 1481.3 | 0.946668467 |
| | | 620.6 | 0.905736384 |
| Organized structur | IBA | 1622.3 | 0.924551563 |
| A membrane-boun | IBA | 2772.6 | 0.957621006 |
| | | 197.6 | 0.79757085 |
| The space enclosed | IEA | 404.1 | 0.908438505 |
| | | 1033.1 | 0.850450102 |

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|---|---|---|---|
| The irregular netwo | IEA; IEA | 1134.5 | 0.949405024 |
| The smaller of the t | IBA; IEA; IEA | 561.2 | 0.775481112 |
| The membrane surr | IBA; IEA; IEA | 1136.6 | 0.784532817 |
| The irregular netwo | IBA; IEA; IEA; IEA; IE | 1204.4 | 0.943872468 |
| The membrane surr | IEA; IEA; IEA | 1120.8 | 0.857958601 |
| | | 555.3 | 0.919142806 |
| | | 830.2 | 0.857142857 |
| | | 536.8 | 0.77552161 |
| OBSOLETE. The bas | IEA | 1587.8 | 0.825229878 |
| | | 725.6 | 0.934123484 |
| | | 462.3 | 0.93770279 |

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|---|---|---|---|
| | | 1080.7 | 0.943925234 |
| The space external | IEA | 583.4 | 0.91755228 |
| | | 806.7 | 0.856700136 |
| An RNA polymerase | IEA | 750.9 | 0.860300972 |
| | | 1465.8 | 0.913221449 |
| A chlorophyll-conta | IEA; IEA; IEA; IEA; IE | 459.1 | 0.895229797 |
| A membrane-boun | IBA; IBA; IEA | 286.4 | 0.817039106 |
| The membrane surr | ISS; ISS; IBA; IEA | 603.1 | 0.892720942 |
| | | 598.8 | 0.830995324 |
| A ubiquitin ligase c | IBA | 810.5 | 0.786428131 |
| A membrane-boun | IBA | 577.2 | 0.74982675 |
| | | 689.2 | 0.874056878 |
| The part of the cyto | IBA | 843.5 | 0.905749852 |
| The contents of a c | IEA | 886.8 | 0.947338746 |
| The irregular netwo | IEA; IEA; IBA; IEA; IE | 1839.1 | 0.939318145 |
| | | 391.8 | 0.870597243 |
| A membrane-boun | IBA; IBA | 1209.3 | 0.947572976 |
| The component of a | IEA | 1358.2 | 0.960830511 |
| | | 1366.8 | 0.864940006 |

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|---|---|---|---|
| A lipid bilayer alon | IEA; IEA | 329.5 | 0.95660091 |
| A closed structure, | IEA | 884.9 | 0.892869251 |
| | | 587.7 | 0.850093585 |
| | | 462.4 | 0.934256055 |
| The contents of a c | IBA | 635.6 | 0.895217118 |
| A protein complex | IBA | 1467.3 | 0.926054658 |
| A membrane-boun | IBA | 2628.3 | 0.965605144 |
| | | 1033.6 | 0.742356811 |
| | | 949.1 | 0.828890528 |
| The component of t | IEA; IEA; IEA; IEA; IE | 4865.4 | 0.906688042 |
| A membranous cell | IBA; IBA | 705.8 | 0.973788609 |
| | | 1265.8 | 0.90946437 |
| A membrane-boun | IEA; IEA | 944.9 | 0.872261615 |
| Organized structur | IBA | 1410.1 | 0.812850152 |
| The irregular netwo | IBA; IEA; IEA | 909.4 | 0.886848472 |
| | | 815.7 | 0.925830575 |
| | | 1357.7 | 0.793768874 |
| A semiautonomous | IEA | 1098.7 | 0.927368708 |
| The membrane surr | IBA; IEA; IEA | 1620.3 | 0.762513115 |
| Organized structur | IEA | 1635 | 0.948318043 |
| Any complex that i | IBA; IEA | 1272.5 | 0.862632613 |
| The contents of a c | IBA | 679.2 | 0.902385159 |
| | | 221 | 0.931221719 |
| | | 1020.7 | 0.933281082 |
| | | 499.9 | 0.849569914 |
| | | 740.8 | 0.896598272 |
| The membrane surr | IBA; IEA; IEA | 1753.2 | 0.798882044 |
| A membrane-boun | IEA | 1015.5 | 0.767897587 |
| | | 1239.7 | 0.787932564 |
| The contents of a c | IBA; IBA; IBA; IBA | 1302.8 | 0.863140927 |

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|---|---|---|---|
| Organized structur | IBA | 1886.2 | 0.859930018 |
| | | 720.8 | 0.898307436 |
| A membrane-boun | IEA | 618.7 | 0.848715048 |
| The membrane surr | IBA; IBA | 894.3 | 0.793469753 |
| | | 483 | 0.949275362 |
| A semiautonomous | IEA; IEA; IEA; IEA; IE | 1527.8 | 0.896648776 |
| Organized structur | IBA | 1092.4 | 0.920450384 |
| A lipid bilayer alon | IEA; IEA | 1113.5 | 0.885675797 |
| A semiautonomous | IEA; IEA; IBA; IBA; IB | 369.5 | 0.948037889 |
| | | 951.3 | 0.907179649 |
| The contents of a c | IEA | 658 | 0.763981763 |
| The lipid bilayer su | IBA; IBA; IEA; IEA | 551.9 | 0.951078094 |
| A ribonuclease com | IBA; IBA; IBA | 593.6 | 0.988544474 |
| A membrane-boun | IEA; IEA; IBA | 873.7 | 0.941169738 |
| A chlorophyll-conta | IEA | 656.2 | 0.911002743 |
| The lipid bilayer su | IBA | 581 | 0.915146299 |
| A membrane-boun | IEA | 628.7 | 0.74757436 |
| | | 2229.1 | 0.87838141 |
| The pigmented mer | IEA; IEA; IEA; IEA | 394.2 | 0.863267377 |
| The contents of a c | IEA | 223.9 | 0.924519875 |
| The space enclosed | IEA | 785.7 | 0.925162276 |
| | | 563 | 0.762699822 |
| | | 749.4 | 0.767547371 |
| The contents of a c | IBA; IEA | 1266.9 | 0.905438472 |
| A lipid bilayer alon | IEA; IEA | 743.9 | 0.911009544 |
| A ubiquitin ligase c | IEA | 207.1 | 0.842105263 |
| The membrane surr | IBA; IBA; IBA | 1325.4 | 0.903199034 |
| A lipid bilayer alon | IEA; IEA | 956.2 | 0.85431918 |
| The pigmented mer | IEA | 458.9 | 0.843538897 |
| A membrane-boun | IBA | 2305.3 | 0.779291199 |
| A lipid bilayer alon | IEA; IEA | 810.9 | 0.846343569 |
| A small organelle e | IEA; IBA; IEA; IEA; IB | 576.8 | 0.842059639 |
| | | 1195.2 | 0.946452477 |
| The lipid bilayer su | IEA; IEA; IBA | 1804.8 | 0.885472074 |
| | | 619.7 | 0.762142972 |
| | | 1042.5 | 0.867529976 |

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|---|---|---|---|
| The membrane surr | IEA; IEA; IEA | 1299.7 | 0.902285143 |
| The irregular netwo | IEA; IEA | 1161.9 | 0.838626388 |
|  |  | 800.3 | 0.858927902 |
| A membrane-boun | IBA; IEA | 905.5 | 0.902484815 |
| The space external | IEA; IBA; IBA; IEA | 1899.2 | 0.898483572 |
|  |  | 1266.2 | 0.772152898 |
|  |  | 1311.7 | 0.915605703 |

|  |  |  |  |
|---|---|---|---|
| The space external | IEA; IEA | 1322.8 | 0.899304506 |
| The membrane surr | IBA; IEA; IEA | 763.3 | 0.91065112 |
| Organized structur | IBA | 1303.5 | 0.884004603 |
| The portion of the | IBA | 1114.9 | 0.953897211 |
| The component of | IEA | 515 | 0.881553398 |
| A vacuole to which | IEA; IBA; IEA; IEA; IE | 1194.6 | 0.855767621 |
| The contents of a c | IEA | 730.1 | 0.892754417 |
|  |  | 1061.5 | 0.867451719 |
|  |  | 523.8 | 0.874379534 |

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|---|---|---|---|
|  |  | 3700.6 | 0.802518511 |
| The contents of a c | IBA; IEA; IEA; IEA | 526 | 0.842965779 |
|  |  | 613.8 | 0.853372434 |
|  |  | 458.4 | 0.822207679 |
|  |  | 670.8 | 0.789505069 |
| A membrane-bound | IBA | 1020.7 | 0.818457921 |
|  |  | 861.2 | 0.936483976 |

group HMM details

| avgrp_relscore | maxgrp_relscore | n_mem | n_multid | Brachypodium_dist | Hordeum_ |
|---|---|---|---|---|---|
| 0.944315789 | 0.965473684 | 16 | 0 | KQJ99091 0.908 −1 | HORVU.M |
| 0.929742363 | 0.95505618 | 16 | 0 | KQK03265 0.871 − | HORVU.M |
| 0.949244919 | 0.972294766 | 16 | 0 | KQJ81997 0.938 −0 | HORVU.M |
| 0.922019421 | 0.972738602 | 16 | 0 | KQK18555 0.901 − | HORVU.M |
| 0.936920173 | 0.972815534 | 16 | 0 | KQK13552 0.924 − | HORVU.M |
| 0.912588968 | 0.976706567 | 16 | 0 | KQJ83155 0.838 −1 | HORVU.M |
| 0.912436069 | 0.951528537 | 16 | 2 | KQK13415 0.896 − | HORVU.M |
| 0.909130688 | 0.962660443 | 16 | 0 | PNT68966 0.824 − | HORVU.M |
| 0.930002654 | 0.987261146 | 16 | 0 | KQJ97464 0.799 −2 | HORVU.M |
| 0.894153226 | 1.002932551 | 16 | 0 | KQJ97520 0.870 −0 | genblast_ |
| 0.947791699 | 0.981714396 | 16 | 0 | KQJ93432 0.918 −1 | HORVU.M |
| 0.888605236 | 0.919520029 | 16 | 1 | KQJ95251 0.915 1. | HORVU.M |
| 0.91468069 | 0.96165948 | 16 | 0 | KQK19761 0.888 − | HORVU.M |
| 0.919411001 | 0.960457979 | 16 | 3 | KQK19767 0.948 1 | HORVU.M |
| 0.878234618 | 0.927544566 | 16 | 0 | KQJ90691 0.845 −0 | HORVU.M |
| 0.939621976 | 0.981180171 | 16 | 1 | PNT62494 0.911 − | HORVU.M |
| 0.967038843 | 1.013347023 | 16 | 0 | KQK02337 0.960 − | HORVU.M |
| 0.953735497 | 0.974663027 | 16 | 0 | KQK16623 0.940 − | HORVU.M |
| 0.921041748 | 0.958154924 | 16 | 0 | KQK06441 0.917 − | HORVU.M |
| 0.925503465 | 0.952446947 | 16 | 0 | KQK04899 0.940 0 | HORVU.M |
| 0.839809289 | 0.937727037 | 16 | 0 | KQK17561 0.826 − | HORVU.M |
| 0.910264824 | 0.987801112 | 16 | 1 | KQK01126 0.907 − | HORVU.M |
| 0.944264847 | 0.977650064 | 16 | 0 | KQJ90143 0.966 0. | HORVU.M |
| 0.908632748 | 0.9775096 | 16 | 1 | KQJ91153 0.931 0. | genblast_ |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| 0.903042492 | 0.94669967 | 16 | 0 | KQK17737 0.910 0 | HORVU.M |
| 0.854785929 | 0.920098173 | 16 | 1 | KQK12241 0.739 − | HORVU.M |
| 0.895486052 | 0.973124681 | 16 | 3 | KQJ94475 0.933 0. | HORVU.M |
| 0.868791467 | 0.977699963 | 16 | 1 | KQJ88961 0.930 0. | HORVU.M |
| | | | | | |
| 0.949674115 | 0.997113594 | 16 | 0 | KQJ89556 0.975 0. | HORVU.M |
| 0.892220511 | 0.964084507 | 16 | 1 | PNT72712 0.855 − | HORVU.M |
| | | | | | |
| | | | | | |
| | | | | | |
| 0.904638411 | 0.983847066 | 16 | 2 | KQK14848 0.877 − | HORVU.M |
| 0.944024101 | 0.984943411 | 16 | 0 | KQK17580 0.976 0 | HORVU.M |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 0.881651987 | 0.93281442 | 16 | 0 | KQK23477 | 0.739 | – | HORVU.MC |
| 0.926963048 | 0.97278126 | 16 | 0 | KQK16066 | 0.972 | 0. | HORVU.MC |
| 0.886167731 | 0.975343811 | 16 | 2 | KQK17401 | 0.959 | 1. | HORVU.MC |
| 0.884065745 | 0.934731935 | 16 | 1 | KQJ90249 | 0.839 | –0 | HORVU.MC |
| 0.814028168 | 0.894762927 | 16 | 0 | KQJ99660 | 0.824 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.93256042 | 0.986310025 | 16 | 1 | KQK12244 | 0.939 | 0. | HORVU.MC |
| 0.900415539 | 0.97734828 | 16 | 2 | KQK22341 | 0.861 | – | HORVU.MC |
| 0.95229124 | 0.981562774 | 16 | 1 | KQJ90421 | 0.961 | 0. | HORVU.MC |
| 0.874063389 | 0.945854299 | 16 | 2 | KQJ94792 | 0.867 | –0 | HORVU.MC |
| 0.91967097 | 0.969143577 | 16 | 0 | KQJ99227 | 0.854 | –1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.92115937 | 0.970242716 | 16 | 1 | KQJ82208 | 0.949 | 0. | HORVU.MC |
| 0.869941366 | 0.974706829 | 16 | 0 | KQJ86323 | 0.754 | –1 | HORVU.MC |
| 0.917644671 | 0.991733097 | 16 | 0 | KQK23655 | 0.923 | 0. | HORVU.MC |
| 0.919411288 | 0.994301994 | 16 | 0 | KQJ93724 | 0.928 | 0. | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.890155579 | 0.968049595 | 16 | 0 | KQJ85024 | 0.860 | –0 | HORVU.MC |
| 0.903031541 | 0.986234898 | 16 | 1 | genblast_Os05t044 | | | HORVU.MC |
| 0.896473521 | 0.987741092 | 16 | 1 | KQK18700 | 0.926 | 0. | HORVU.MC |
| 0.925220335 | 0.969905417 | 16 | 1 | KQK03328 | 0.935 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.951054217 | 0.992609092 | 16 | 2 | KQK05138 | 0.954 | 0 | HORVU.MC |
| 0.9497141 | 0.986682108 | 16 | 0 | KQK11009 | 0.923 | – | HORVU.MC |
| 0.910591624 | 0.974074895 | 16 | 0 | KQK00028 | 0.932 | 0 | HORVU.MC |
| 0.879695247 | 0.941366674 | 16 | 1 | KQK17983 | 0.878 | – | HORVU.MC |
| 0.919789031 | 0.966140795 | 16 | 1 | KQK04090 | 0.957 | 0 | HORVU.MC |
| 0.915259173 | 0.964181712 | 16 | 1 | KQJ99139 | 0.847 | –1 | HORVU.MC |

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| 0.838554438 | 0.930848455 | 16 | 0 | KQJ88511 | 0.738 | –1 | HORVU.MC |
| 0.869464448 | 0.973013063 | 16 | 6 | genblast_Os11t019 |  |  | HORVU.MC |
| 0.940709503 | 0.992979719 | 16 | 2 | KQK12197 | 0.957 | 0 | HORVU.MC |
| 0.925536323 | 0.985636682 | 16 | 0 | KQJ96087 | 0.974 | 0. | HORVU.MC |
| 0.875907522 | 0.927041181 | 16 | 2 | KQJ88175 | 0.891 | 0. | HORVU.MC |
| 0.855432203 | 0.910305085 | 16 | 0 | KQK05993 | 0.897 | 0 | HORVU.MC |

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| 0.847191564 | 0.946187806 | 16 | 1 | KQK19280 | 0.804 | – | HORVU.MC |
| 0.897148854 | 0.978937574 | 16 | 5 | KQK05256 | 0.923 | 0 | genblast_C |
| 0.84519406 | 0.941245845 | 16 | 1 | PNT74870 | 0.772 | – | HORVU.MC |
| 0.956691241 | 1.002847825 | 16 | 3 | KQJ93992 | 0.980 | 0. | HORVU.MC |
| 0.916143836 | 0.960148716 | 16 | 1 | KQJ93640 | 0.930 | 0. | HORVU.MC |
| 0.940150407 | 0.987048256 | 16 | 0 | KQJ97022 | 0.910 | –0 | HORVU.MC |
| 0.929433791 | 0.992161254 | 16 | 0 | KQJ82280 | 0.930 | 0. | genblast_C |
| 0.916154372 | 1.007058288 | 16 | 2 | genblast_Os03t064 |  |  | genblast_C |
| 0.855783655 | 0.929440524 | 16 | 3 | KQK01353 | 0.776 | – | genblast_C |
| 0.959463248 | 0.991844225 | 16 | 1 | KQK01927 | 0.974 | 0 | HORVU.MC |
| 0.950747181 | 0.987925357 | 16 | 0 | KQK01167 | 0.975 | 0 | HORVU.MC |
| 0.81912985 | 0.901995963 | 16 | 1 | KQK03287 | 0.758 | – | HORVU.MC |
| 0.971848362 | 1.01884253 | 16 | 0 | KQK04498 | 0.999 | 0 | HORVU.MC |
| 0.875709374 | 0.958472426 | 16 | 0 | KQK04755 | 0.826 | – | HORVU.MC |

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| 0.96901278 | 0.998251603 | 16 | 1 | KQJ88946 | 0.993 | 0. | HORVU.MC |
| 0.930982549 | 0.98646434 | 16 | 1 | KQK11556 | 0.944 | 0 | HORVU.MC |
| 0.949375565 | 0.993997677 | 16 | 1 | KQK10623 | 0.961 | 0 | HORVU.MC |
| 0.943322433 | 0.996800602 | 16 | 0 | genblast_Os08t054 |  |  | HORVU.MC |
| 0.866817216 | 0.936875664 | 16 | 1 | KQK01771 | 0.829 | – | HORVU.MC |
| 0.952539855 | 0.9831148 | 16 | 1 | KQJ89752 | 0.964 | 0. | HORVU.MC |
| 0.94628508 | 0.986807388 | 16 | 1 | KQJ84826 | 0.955 | 0. | HORVU.MC |
| 0.933119946 | 0.988509008 | 16 | 0 | KQJ97807 | 0.953 | 0. | HORVU.MC |
| 0.921254139 | 0.974958609 | 16 | 0 | KQK13678 | 0.914 | – | HORVU.MC |
| 0.946948636 | 0.990203866 | 16 | 1 | KQK18442 | 0.884 | – | HORVU.MC |
| 0.861123296 | 0.916317992 | 16 | 0 | KQK06123 | 0.852 | – | HORVU.MC |
| 0.927731143 | 0.980557088 | 16 | 2 | KQK15939 | 0.972 | 0 | HORVU.MC |
| 0.857983461 | 0.945110869 | 16 | 0 | KQK12723 | 0.895 | 0 | HORVU.MC |
| 0.886383084 | 0.961088092 | 16 | 3 | KQJ84682 | 0.878 | –0 | HORVU.MC |

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| 0.841890193 | 0.952500699 | 16 | 0 | KQK15922 0.786 – | HORVU.MC |
| 0.970109559 | 1.002222928 | 16 | 0 | KQJ90214 0.999 0. | HORVU.MC |
| 0.889329538 | 0.962635419 | 16 | 0 | KQJ86843 0.737 –1 | genblast_C |
| 0.915628095 | 0.981181908 | 16 | 1 | PNT73942 0.939 0. | HORVU.MC |
| 0.887029474 | 0.943181818 | 16 | 0 | KQK12998 0.783 – | HORVU.MC |
| 0.928484694 | 0.966677962 | 16 | 0 | KQJ99423 0.928 –0 | HORVU.MC |
| 0.830096366 | 0.921718458 | 16 | 2 | KQK01698 0.788 – | HORVU.MC |
| 0.867855754 | 0.941679627 | 16 | 0 | KQK19066 0.894 0 | HORVU.MC |
| 0.936195827 | 0.977849117 | 16 | 0 | KQK04921 0.889 – | genblast_C |
| 0.929640508 | 0.995864662 | 16 | 1 | genblast_Os01t057 | HORVU.MC |
| 0.880437245 | 0.95061169 | 16 | 0 | KQK15613 0.825 – | genblast_C |
| 0.918600463 | 0.988099712 | 16 | 0 | KQJ95513 0.969 0. | HORVU.MC |
| 0.907725495 | 0.983341003 | 16 | 2 | PNT69747 0.853 – | HORVU.MC |
| 0.875542443 | 0.943797629 | 16 | 0 | KQJ98245 0.860 –0 | HORVU.MC |
| 0.927446972 | 0.98563779 | 16 | 2 | KQK21732 0.955 0 | HORVU.MC |
| 0.976778564 | 0.999906881 | 16 | 1 | KQK11460 0.991 0 | HORVU.MC |
| 0.921706601 | 0.978637413 | 16 | 0 | PNT77653 0.939 0. | HORVU.MC |
| 0.887652619 | 0.982276487 | 16 | 0 | KQJ81440 0.814 –1 | HORVU.MC |
| 0.90309466 | 0.94776699 | 16 | 0 | KQK02231 0.922 0 | HORVU.MC |
| 0.90139414 | 0.962003781 | 16 | 0 | KQK03595 0.890 – | HORVU.MC |
| 0.874939399 | 0.964555053 | 16 | 1 | PNT66435 0.876 0. | HORVU.MC |
| 0.944968615 | 0.997724598 | 16 | 2 | KQK16229 0.982 0 | HORVU.MC |
| 0.930915257 | 0.979210712 | 16 | 1 | genblast_Os01t095 | HORVU.MC |
| 0.92240018 | 0.992555831 | 16 | 3 | PNT73294 0.923 0. | HORVU.MC |
| 0.872757746 | 0.947454249 | 16 | 0 | KQJ98977 0.845 –0 | HORVU.MC |
| 0.939394837 | 0.979725249 | 16 | 0 | KQJ93467 0.924 –0 | HORVU.MC |
| 0.854836025 | 0.925170634 | 16 | 3 | KQK07453 0.880 0 | HORVU.MC |
| 0.893249365 | 0.958679388 | 16 | 1 | KQK08563 0.868 – | HORVU.MC |
| 0.926220101 | 0.982242087 | 16 | 0 | genblast_Os09t045 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.848019148 | 0.972533925 | 16 | 2 | KQK14461 | 0.773 | –( | HORVU.MC |
| 0.87577317 | 0.939498411 | 16 | 1 | KQK00335 | 0.866 | –( | HORVU.MC |
| 0.872435084 | 0.947022832 | 16 | 3 | PNT69831 | 0.854 | –( | HORVU.MC |
| 0.892699905 | 0.980009519 | 16 | 0 | KQK01359 | 0.851 | –( | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.935139086 | 0.994519744 | 16 | 2 | KQK08656 | 0.947 | 0 | HORVU.MC |
| 0.926631858 | 0.969359696 | 16 | 0 | KQK09507 | 0.962 | 0 | HORVU.MC |
| 0.926650281 | 0.996067416 | 16 | 0 | KQK06626 | 0.946 | 0 | HORVU.MC |
| 0.929666752 | 0.966292135 | 16 | 0 | KQK18814 | 0.928 | –( | HORVU.MC |
| 0.846712252 | 0.93068565 | 16 | 0 | genblast_Os06t060 | | | HORVU.MC |
| 0.950371688 | 1.009603147 | 16 | 1 | KQK19115 | 1.003 | 0 | HORVU.MC |
| 0.86596546 | 0.994826537 | 16 | 1 | KQK10872 | 0.773 | – | HORVU.MC |
| 0.92286323 | 0.977191077 | 16 | 0 | KQK08701 | 0.863 | – | HORVU.MC |
| 0.951215799 | 0.999673212 | 16 | 1 | KQJ84278 | 0.979 | 0. | HORVU.MC |
| 0.910682434 | 0.964754566 | 16 | 0 | KQJ83199 | 0.947 | 0. | HORVU.MC |
| 0.828515129 | 0.908379179 | 16 | 1 | KQJ94809 | 0.865 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.96167243 | 0.990334061 | 16 | 0 | KQJ94406 | 0.970 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.837876894 | 0.905327293 | 16 | 0 | KQK22739 | 0.841 | 0 | HORVU.MC |
| 0.82541825 | 0.928538326 | 16 | 2 | KQK18157 | 0.766 | – | HORVU.MC |
| 0.930388787 | 0.971821439 | 16 | 1 | KQJ84161 | 0.945 | 0. | HORVU.MC |
| 0.9065491 | 0.98085758 | 16 | 0 | KQJ85647 | 0.736 | –1 | HORVU.MC |
| 0.871222834 | 0.936290563 | 16 | 1 | KQK15757 | 0.849 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.951926411 | 0.978082952 | 16 | 1 | KQJ90477 | 0.950 | –0 | HORVU.MC |
| 0.925016472 | 0.965737952 | 16 | 0 | KQK07115 | 0.925 | – | HORVU.MC |
| 0.871519303 | 0.95518083 | 16 | 0 | KQK13881 | 0.889 | 0 | HORVU.MC |
| 0.919149616 | 0.971873926 | 16 | 7 | PNT70811 | 0.966 | 0. | HORVU.MC |
| 0.942865282 | 0.991896683 | 16 | 0 | KQK10184 | 0.970 | 0 | HORVU.MC |
| 0.947219634 | 0.985092326 | 16 | 1 | KQJ97392 | 0.960 | 0. | HORVU.MC |
| 0.950134302 | 1.025865499 | 16 | 0 | KQK17880 | 1.015 | 0 | HORVU.MC |
| 0.85897179 | 0.935566597 | 16 | 1 | KQJ99053 | 0.864 | 0. | HORVU.MC |
| 0.871049546 | 0.932816801 | 16 | 3 | KQK14367 | 0.862 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.932119243 | 0.989474631 | 16 | 0 | KQK11478 | 0.976 | 0 | HORVU.MC |
| 0.950597472 | 0.992099546 | 16 | 0 | KQJ81670 | 0.979 | 0. | HORVU.MC |
| 0.870031723 | 0.943921408 | 16 | 1 | KQJ96494 | 0.735 | –2 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.889662792 | 0.938802959 | 16 | 2 | KQK03395 | 0.873 | − | genblast_C |
| 0.934715671 | 1.002096436 | 16 | 0 | KQK12388 | 0.970 | 0 | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.866985701 | 0.934732472 | 16 | 1 | KQK00041 | 0.882 | 0 | HORVU.MC |
| 0.954188543 | 0.981061316 | 16 | 1 | KQK12026 | 0.959 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.916623062 | 0.992008372 | 16 | 2 | KQK20996 | 0.977 | 0 | HORVU.MC |
| 0.922142396 | 1.009041007 | 16 | 1 | KQK05387 | 0.941 | 0 | HORVU.MC |
| 0.973415 | 1.00232 | 16 | 2 | KQJ97086 | 0.986 | 0. | HORVU.MC |
| 0.878404692 | 0.95260574 | 16 | 3 | KQK05198 | 0.884 | 0 | genblast_C |
| 0.888045758 | 0.965779468 | 16 | 0 | KQJ85514 | 0.910 | 0. | HORVU.MC |
| 0.920407954 | 0.972939729 | 16 | 1 | KQJ91651 | 0.957 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.88055067 | 0.954165751 | 16 | 1 | KQK01604 | 0.735 | − | HORVU.MC |
| 0.929768439 | 0.981068081 | 16 | 1 | KQJ93336 | 0.924 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.960613905 | 1.009204471 | 16 | 0 | KQJ91580 | 0.920 | −0 | HORVU.MC |
| 0.857848929 | 0.937933207 | 16 | 1 | KQJ98572 | 0.818 | −0 | HORVU.MC |
| 0.885116566 | 0.983699773 | 16 | 0 | KQJ90934 | 0.922 | 0. | HORVU.MC |
| 0.843028391 | 0.889968454 | 16 | 0 | PNT76349 | 0.777 | − | HORVU.MC |
| 0.949289909 | 0.994566954 | 16 | 2 | KQK16151 | 0.967 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.8125 | 0.885527392 | 16 | 0 | PNT66081 | 0.765 | –1 | HORVU.MC |
| 0.861843076 | 0.927369353 | 16 | 0 | KQK04548 | 0.863 | 0. | HORVU.MC |
| 0.970235827 | 0.995733008 | 16 | 0 | KQK01726 | 0.978 | 0. | HORVU.MC |
| 0.839199444 | 0.948467695 | 16 | 5 | KQK17272 | 0.811 | – | HORVU.MC |
| 0.853407148 | 0.94124487 | 16 | 2 | PNT73386 | 0.752 | –1 | HORVU.MC |
| 0.960556166 | 0.995128475 | 16 | 1 | KQJ92368 | 0.940 | –0 | HORVU.MC |
| 0.957654761 | 1.007680207 | 16 | 0 | KQJ85379 | 0.992 | 0. | HORVU.MC |
| 0.872118238 | 0.954043978 | 16 | 3 | KQK15789 | 0.786 | – | HORVU.MC |
| 0.95366718 | 0.995678932 | 16 | 1 | KQJ91924 | 0.962 | 0. | HORVU.MC |
| 0.920535515 | 0.969271877 | 16 | 0 | PNT69176 | 0.908 | – | HORVU.MC |
| 0.854075642 | 0.926269798 | 16 | 1 | KQK13885 | 0.835 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.83873552 | 0.920338017 | 16 | 5 | KQJ83532 | 0.885 | 0. | HORVU.MC |
| 0.917557329 | 0.973669048 | 16 | 2 | KQK06394 | 0.945 | 0. | HORVU.MC |
| 0.867475901 | 0.963741921 | 16 | 1 | KQK05006 | 0.766 | − | HORVU.MC |
| 0.911807046 | 0.971459227 | 16 | 2 | KQK15891 | 0.940 | 0. | HORVU.MC |
| 0.89588364 | 0.950573498 | 16 | 4 | PNT69890 | 0.734 | − | HORVU.MC |
| 0.965149648 | 0.998591549 | 16 | 2 | PNT77590 | 0.983 | 0. | HORVU.MC |
| 0.920561665 | 0.973116872 | 16 | 1 | KQJ94454 | 0.954 | 0. | genblast_C |
| 0.93993946 | 0.991729636 | 16 | 0 | KQJ92501 | 0.903 | −0 | HORVU.MC |
| 0.838349126 | 0.937808621 | 16 | 0 | KQK04546 | 0.751 | − | genblast_C |
| 0.908430022 | 0.96142132 | 16 | 1 | KQK13425 | 0.936 | 0 | HORVU.MC |
| 0.951674632 | 0.991719485 | 16 | 1 | KQJ83048 | 0.969 | 0. | HORVU.MC |
| 0.955280043 | 0.982489806 | 16 | 0 | KQJ84644 | 0.976 | 0. | HORVU.MC |
| 0.961831131 | 1.000527753 | 16 | 3 | KQJ97502 | 0.974 | 0. | HORVU.MC |
| 0.955871166 | 0.995374878 | 16 | 1 | KQK14765 | 0.946 | − | HORVU.MC |
| 0.887722263 | 0.939525838 | 16 | 2 | KQJ94431 | 0.921 | 0. | HORVU.MC |
| 0.867810249 | 0.935626307 | 16 | 0 | KQJ97699 | 0.777 | −1 | HORVU.MC |
| 0.974262965 | 0.999289605 | 16 | 0 | KQJ92779 | 0.986 | 0. | genblast_C |
| 0.863240796 | 0.938364402 | 16 | 6 | KQJ94740 | 0.897 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.948879578 | 0.985069392 | 16 | 0 | KQK04126 | 0.979 | 0 | HORVU.MC |
| 0.937166853 | 0.998276412 | 16 | 3 | KQK09541 | 0.985 | 0 | HORVU.MC |
| 0.892369902 | 0.952883263 | 16 | 1 | KQK13704 | 0.913 | 0 | HORVU.MC |
| 0.876053873 | 1.000762123 | 16 | 2 | PNT77927 | 0.849 | – | HORVU.MC |
| 0.954800962 | 1.002099738 | 16 | 0 | KQK08693 | 0.971 | 0 | HORVU.MC |
| 0.929496989 | 0.997290517 | 16 | 2 | KQJ82341 | 0.972 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.9722583 | 1.00646224 | 16 | 1 | KQJ92333 | 1.002 | 0. | HORVU.MC |
| 0.909719839 | 0.983696585 | 16 | 1 | KQK18035 | 0.885 | – | genblast_C |
| 0.793309753 | 0.875978326 | 16 | 0 | KQK07795 | 0.734 | – | genblast_C |
| 0.904213324 | 0.967035732 | 16 | 3 | KQK04337 | 0.898 | – | HORVU.MC |
| 0.869539821 | 0.91974807 | 16 | 0 | KQJ98947 | 0.849 | –0 | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.936013228 | 0.986808952 | 16 | 1 | KQK04157 | 0.957 | 0 | HORVU.MC |
| 0.926308236 | 0.975601678 | 16 | 0 | KQK11605 | 0.883 | – | HORVU.MC |
| 0.872504506 | 0.964577846 | 16 | 3 | KQJ93304 | 0.876 | 0. | HORVU.MC |
| 0.863547291 | 0.944918064 | 16 | 2 | PNT63061 | 0.927 | 0. | HORVU.MC |
| 0.855606687 | 0.922614576 | 16 | 0 | KQK11747 | 0.870 | 0 | HORVU.MC |
| 0.89799773 | 0.973022049 | 16 | 2 | KQJ90901 | 0.891 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.86461558 | 0.938289774 | 16 | 10 | KQK18080 | 0.733 | – | HORVU.MC |
| 0.898085144 | 0.984646253 | 16 | 0 | KQJ85260 | 0.733 | –2 | HORVU.MC |
| 0.927677349 | 0.971601277 | 16 | 0 | KQJ82865 | 0.949 | 0. | HORVU.MC |
| 0.848091943 | 0.942998082 | 16 | 0 | KQK19148 | 0.812 | – | HORVU.MC |
| 0.868250292 | 0.972458688 | 16 | 1 | KQJ99294 | 0.841 | –0 | HORVU.MC |
| 0.939569612 | 0.987961947 | 16 | 2 | KQJ87391 | 0.963 | 0. | HORVU.MC |
| 0.887072179 | 0.937648255 | 16 | 1 | KQK12384 | 0.815 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.956117882 | 0.99191113 | 16 | 0 | PNT76283 | 0.883 | – | HORVU.MC |
| 0.903915929 | 0.96079646 | 16 | 1 | KQK03370 | 0.948 | 0 | HORVU.MC |
| 0.944749628 | 0.983454434 | 16 | 0 | KQK16199 | 0.979 | 0 | HORVU.MC |
| 0.86626518 | 0.945251842 | 16 | 1 | KQK02985 | 0.733 | – | HORVU.MC |
| 0.926884624 | 0.983911744 | 16 | 1 | KQK07278 | 0.948 | 0 | HORVU.MC |
| 0.860869024 | 0.931648406 | 16 | 9 | KQJ82170 | 0.906 | 0. | HORVU.MC |
| 0.952265111 | 0.987498389 | 16 | 0 | KQK01705 | 0.953 | 0 | HORVU.MC |
| 0.874009488 | 0.9506308 | 16 | 6 | KQK00721 | 0.933 | 0 | HORVU.MC |
| 0.930331869 | 0.984545307 | 16 | 0 | KQJ86868 | 0.974 | 0. | HORVU.MC |
| 0.889045578 | 0.943140794 | 16 | 1 | KQJ94207 | 0.895 | 0. | HORVU.MC |
| 0.878644378 | 0.962639665 | 16 | 0 | KQK21316 | 0.873 | – | HORVU.MC |
| 0.901645697 | 0.960247994 | 16 | 0 | PNT71705 | 0.891 | – | HORVU.MC |
| 0.903004328 | 0.996005326 | 16 | 0 | KQK06624 | 0.940 | 0 | HORVU.MC |

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| 0.894227937 | 0.974078002 | 16 | 1 KQK22792 0.877 – | HORVU.MC |
| 0.937243534 | 0.979234021 | 16 | 0 PNT65814 0.898 – | HORVU.MC |
| 0.870176811 | 0.934205537 | 16 | 0 KQK19923 0.804 – | HORVU.MC |
| 0.916966105 | 0.966903464 | 16 | 1 PNT65801 0.732 – | HORVU.MC |
| 0.856752977 | 0.900036088 | 16 | 0 KQK17530 0.732 – | HORVU.MC |
| 0.903984806 | 0.975515339 | 16 | 6 KQK03038 0.907 0 | HORVU.MC |
| 0.954622099 | 0.987304106 | 16 | 0 KQK12927 0.939 – | genblast_C |
| 0.867244983 | 0.938628763 | 16 | 0 KQK07700 0.732 – | HORVU.MC |
| 0.969976319 | 0.999791818 | 16 | 0 KQJ92509 0.985 0. | HORVU.MC |
| 0.925057461 | 0.98903819 | 16 | 0 KQJ83484 0.741 –2 | genblast_C |
| 0.884185168 | 0.954916916 | 16 | 0 KQJ91115 0.855 –0 | HORVU.MC |
| 0.941707422 | 0.994361335 | 16 | 1 KQK15406 0.924 – | HORVU.MC |
| 0.79556728 | 0.882034632 | 16 | 0 PNT66002 0.732 – | HORVU.MC |
| 0.921066506 | 0.967613166 | 16 | 1 KQK09140 0.950 0 | HORVU.MC |
| 0.888635684 | 0.971309026 | 16 | 0 KQK13126 0.732 – | HORVU.MC |
| 0.911621927 | 0.980027313 | 16 | 3 KQJ88171 0.894 –0 | HORVU.MC |
| 0.916959897 | 0.978887399 | 16 | 1 KQK13808 0.909 – | HORVU.MC |
| 0.859857748 | 0.941369438 | 16 | 5 PNT72801 0.732 – | genblast_C |
| 0.867946264 | 0.928824614 | 16 | 0 KQK16997 0.789 – | HORVU.MC |
| 0.883133562 | 0.928455174 | 16 | 2 KQJ98986 0.884 0. | HORVU.MC |
| 0.924096785 | 0.973815048 | 16 | 1 KQK01205 0.873 – | HORVU.MC |
| 0.947066293 | 0.992898979 | 16 | 0 KQK03195 0.950 0 | HORVU.MC |
| 0.952995665 | 0.992768145 | 16 | 1 KQK12976 0.974 0 | HORVU.MC |
| 0.894585482 | 0.976437921 | 16 | 1 PNT64786 0.871 – | HORVU.MC |
| 0.912907853 | 0.961703304 | 16 | 1 KQK05793 0.941 0 | HORVU.MC |
| 0.898049438 | 0.94470478 | 16 | 0 KQJ86376 0.882 –0 | HORVU.MC |

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| 0.912251737 | 0.973583798 | 16 | 1 | KQK02135 | 0.887 | – | HORVU.MC |
| 0.859075485 | 0.947969996 | 16 | 0 | KQJ97012 | 0.731 | –1 | HORVU.MC |
| 0.905485826 | 0.977710452 | 16 | 0 | KQK01158 | 0.861 | – | HORVU.MC |
| 0.903279049 | 0.94375 | 16 | 0 | KQK22498 | 0.914 | 0 | HORVU.MC |
| 0.883002485 | 0.954323002 | 16 | 4 | KQJ90080 | 0.919 | 0. | HORVU.MC |
| 0.874210184 | 0.965062256 | 16 | 0 | KQK15455 | 0.731 | – | HORVU.MC |
| 0.94608349 | 0.988492808 | 16 | 3 | PNT75563 | 0.959 | 0. | genblast_C |
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| 0.838026636 | 0.902681058 | 16 | 1 | KQK18074 | 0.821 | – | HORVU.MC |
| 0.941015898 | 0.982995574 | 16 | 1 | KQK12580 | 0.929 | – | HORVU.MC |
| 0.935458176 | 0.99264046 | 16 | 1 | KQK03774 | 0.976 | 0 | HORVU.MC |
| 0.86638959 | 0.934062851 | 16 | 0 | PNT61234 | 0.857 | – | HORVU.MC |
| 0.895107835 | 1.01134415 | 16 | 1 | KQJ97779 | 0.924 | 0. | HORVU.MC |
| 0.898432563 | 0.979568911 | 16 | 5 | KQJ92446 | 0.938 | 0. | genblast_C |
| 0.918752051 | 1.00590745 | 16 | 0 | KQK12052 | 0.921 | 0 | HORVU.MC |
| 0.879484649 | 0.952631579 | 16 | 0 | KQJ95438 | 0.858 | –0 | HORVU.MC |
| 0.884197389 | 0.931182796 | 16 | 0 | KQK03466 | 0.842 | – | HORVU.MC |
| 0.819360857 | 0.950890708 | 16 | 0 | KQK22989 | 0.805 | – | HORVU.MC |
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| 0.910774222 | 0.958827478 | 16 | 0 | KQJ97834 | 0.872 | –0 | HORVU.MC |
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| 0.952978034 | 0.99426474 | 16 | 0 | KQK16483 | 0.962 | 0 | HORVU.MC |
| 0.959537841 | 0.998263027 | 16 | 0 | KQK05363 | 0.968 | 0 | HORVU.MC |
| 0.897361498 | 0.987619932 | 16 | 1 | KQK13192 | 0.755 | – | HORVU.MC |
| 0.963883715 | 1.000212879 | 16 | 0 | KQK02468 | 0.984 | 0 | HORVU.MC |
| 0.918386027 | 0.995520331 | 16 | 1 | KQK01951 | 0.934 | 0 | HORVU.MC |
| 0.932884144 | 0.980924046 | 16 | 1 | KQJ91117 | 0.939 | 0. | HORVU.MC |
| 0.867070747 | 0.944780074 | 16 | 0 | KQJ89583 | 0.827 | –0 | HORVU.MC |
| 0.882288851 | 1.009508716 | 16 | 2 | KQJ81460 | 0.919 | 0. | HORVU.MC |
| 0.840375346 | 0.939391319 | 16 | 8 | KQJ81391 | 0.735 | –1 | HORVU.MC |
| 0.954085152 | 0.987333835 | 16 | 0 | KQJ84543 | 0.975 | 0. | HORVU.MC |
| 0.927863979 | 0.981350831 | 16 | 2 | KQJ98707 | 0.968 | 0. | HORVU.MC |
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| 0.911035236 | 0.97034931 | 16 | 0 | KQK15524 | 0.803 | – | HORVU.MC |
| 0.904198045 | 0.969745013 | 16 | 3 | KQJ82828 | 0.867 | –0 | HORVU.MC |
| 0.961647456 | 0.997643762 | 16 | 2 | KQK13610 | 0.974 | 0 | HORVU.MC |

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| 0.926106976 | 0.972625205 | 16 | 1 | KQJ96985 0.941 0. | HORVU.MC |
| 0.872836562 | 0.940166842 | 16 | 1 | genblast_Os04t032 | HORVU.MC |
| 0.897228207 | 0.973317865 | 16 | 0 | KQK10259 0.840 – | HORVU.MC |
| 0.879508487 | 0.935502122 | 16 | 0 | KQK13653 0.897 0 | HORVU.MC |
| 0.881207697 | 0.959389265 | 16 | 2 | KQK20893 0.859 – | HORVU.MC |
| 0.82987988 | 0.962162162 | 16 | 0 | KQJ90157 0.788 –0 | HORVU.MC |
| 0.846673019 | 0.93076068 | 16 | 1 | KQJ91837 0.794 –0 | HORVU.MC |
| 0.826109748 | 0.924829878 | 16 | 0 | KQJ91096 0.806 –0 | HORVU.MC |
| 0.88241206 | 0.963819095 | 16 | 0 | KQK22971 0.865 – | genblast_C |
| 0.889346061 | 0.966315558 | 16 | 2 | KQK23995 0.905 0 | HORVU.MC |
| 0.953952865 | 0.991672506 | 16 | 1 | KQJ97066 0.975 0. | HORVU.MC |
| 0.877245893 | 0.976386037 | 16 | 2 | KQK23073 0.844 – | HORVU.MC |
| 0.872189526 | 0.953058923 | 16 | 1 | PNT74065 0.872 – | HORVU.MC |
| 0.897696451 | 0.963654681 | 16 | 2 | KQJ84858 0.912 0. | HORVU.MC |
| 0.949773212 | 1.00298826 | 16 | 0 | KQK04331 0.930 – | HORVU.MC |
| 0.868484982 | 0.938515901 | 16 | 0 | KQK05440 0.730 – | HORVU.MC |
| 0.917411335 | 0.966759388 | 16 | 2 | KQK02123 0.903 – | HORVU.MC |
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| 0.906189438 | 0.980481728 | 16 | 0 | KQJ86903 0.729 –2 | HORVU.MC |
| 0.925343613 | 0.994860245 | 16 | 2 | PNT69108 0.956 0. | HORVU.MC |
| 0.892706829 | 0.966877522 | 16 | 4 | PNT62482 0.945 0. | HORVU.MC |
| 0.830911594 | 0.942184154 | 16 | 0 | KQJ93198 0.774 –0 | HORVU.MC |
| 0.904640036 | 0.963183475 | 16 | 4 | KQJ85908 0.925 0. | HORVU.MC |
| 0.891787673 | 0.970709211 | 16 | 1 | KQK04864 0.903 0 | HORVU.MC |
| 0.876340996 | 0.950063857 | 16 | 0 | KQJ91587 0.872 –0 | HORVU.MC |
| 0.936619416 | 0.987285223 | 16 | 0 | genblast_Os03t041 | genblast_C |
| | | | | | |
| 0.927377518 | 0.986030975 | 16 | 1 | PNT61346 0.956 0. | HORVU.MC |
| 0.841571291 | 0.927485584 | 16 | 0 | KQK12708 0.745 – | HORVU.MC |

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| 0.929155856 | 0.981011912 | 16 | 0 | KQK10544 | 0.919 | - | HORVU.MC |
| 0.862264954 | 0.931755552 | 16 | 0 | KQJ82401 | 0.887 | 0. | HORVU.MC |
| 0.947073894 | 0.989212513 | 16 | 1 | KQK10250 | 0.978 | 0 | HORVU.MC |
| 0.922708817 | 0.996906419 | 16 | 0 | KQK13599 | 0.915 | - | HORVU.MC |
| 0.946351796 | 1.010622155 | 16 | 0 | KQK01767 | 0.912 | - | HORVU.MC |
| 0.861075842 | 0.93956323 | 16 | 0 | KQJ84085 | 0.857 | -0 | HORVU.MC |
| 0.937188405 | 0.985204246 | 16 | 1 | KQJ94453 | 0.920 | -0 | HORVU.MC |
| 0.919004612 | 1.010376633 | 16 | 0 | KQK20413 | 0.972 | 0 | genblast_C |
| 0.931303855 | 0.98122449 | 16 | 0 | KQK04455 | 0.933 | 0 | HORVU.MC |
| 0.927350736 | 0.982549755 | 16 | 0 | KQK05341 | 0.953 | 0 | HORVU.MC |
| 0.922392788 | 0.985136452 | 16 | 0 | KQJ98815 | 0.970 | 0. | HORVU.MC |
| 0.906954612 | 0.965739385 | 16 | 0 | PNT70760 | 0.729 | - | HORVU.MC |
| 0.941393826 | 0.992703461 | 16 | 0 | KQK03594 | 0.937 | - | HORVU.MC |
| 0.902354027 | 0.959433082 | 16 | 0 | KQK15854 | 0.862 | - | HORVU.MC |
| 0.989735025 | 1.026647651 | 16 | 0 | KQK17920 | 1.018 | 0 | HORVU.MC |
| 0.829510206 | 0.932559536 | 16 | 0 | PNT70656 | 0.791 | - | HORVU.MC |

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|---|---|---|---|---|
| 0.963290944 | 0.995322549 | 16 | 4 KQK16632 0.978 0 | HORVU.MC |
| 0.938003892 | 0.995273839 | 16 | 1 KQJ97995 0.973 0. | HORVU.MC |
| 0.910148185 | 0.97247075 | 16 | 2 KQJ94009 0.962 0. | HORVU.MC |
| 0.944735702 | 0.993067591 | 16 | 0 KQJ98757 0.988 0. | HORVU.MC |

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| 0.877593561 | 0.950467804 | 16 | 7 PNT67634 0.823 – | HORVU.MC |
| 0.858032078 | 0.909694935 | 16 | 1 KQJ87525 0.910 0. | HORVU.MC |
| 0.939762797 | 0.983770287 | 16 | 3 KQJ99827 0.976 0. | HORVU.MC |

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| 0.930832918 | 0.962300797 | 16 | 1 genblast_Os05t027 | HORVU.MC |

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| 0.904853092 | 0.969919911 | 16 | 0 KQJ88406 0.728 –2 | HORVU.MC |
| 0.897397899 | 0.976559683 | 16 | 3 KQK19243 0.871 – | HORVU.MC |
| 0.946873011 | 0.991979631 | 16 | 0 KQK03300 0.974 0 | HORVU.MC |
| 0.943689512 | 0.989140221 | 16 | 1 KQJ82488 0.963 0. | HORVU.MC |
| 0.91502947 | 0.975301712 | 16 | 1 KQK03733 0.956 0 | HORVU.MC |
| 0.967817661 | 1.005682827 | 16 | 1 KQJ90241 0.996 0. | HORVU.MC |
| 0.848784641 | 0.917801785 | 16 | 0 KQK02194 0.811 – | HORVU.MC |
| 0.916126943 | 0.960749521 | 16 | 1 PNT68096 0.903 – | HORVU.MC |
| 0.90937736 | 0.984840565 | 16 | 2 genblast_Os04t052 | HORVU.MC |
| 0.875524182 | 0.953312832 | 16 | 0 KQK09884 0.788 – | HORVU.MC |
| 0.910657713 | 0.985766758 | 16 | 2 KQJ93701 0.873 –0 | HORVU.MC |
| 0.868900795 | 0.961680386 | 16 | 6 KQJ85137 0.921 0. | HORVU.MC |
| 0.939815424 | 0.996751822 | 16 | 3 KQJ91765 0.975 0. | HORVU.MC |

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| 0.834217793 | 0.909369178 | 16 | 1 KQK06867 0.800 – | HORVU.MC |
| 0.902305294 | 0.967621965 | 16 | 1 KQJ96983 0.922 0. | HORVU.MC |
| 0.931807573 | 0.97966805 | 16 | 0 KQK21451 0.976 0 | genblast_C |
| 0.875695832 | 0.960319726 | 16 | 0 KQJ85965 0.857 –0 | HORVU.MC |
| 0.841822163 | 0.924600152 | 16 | 2 KQJ91808 0.835 –0 | HORVU.MC |

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| 0.897150014 | 0.951793722 | 16 | 0 KQK17456 0.913 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.847403944 | 0.896249885 | 16 | 0 | KQJ92966 | 0.743 | −2 | HORVU.MC |
| 0.948258416 | 0.992307112 | 16 | 3 | KQK21199 | 0.968 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.847051732 | 0.941253836 | 16 | 5 | KQJ93270 | 0.869 | 0. | HORVU.MC |
| 0.886774259 | 0.96589525 | 16 | 0 | KQK24124 | 0.727 | − | HORVU.MC |
| 0.926814645 | 0.975058623 | 16 | 1 | KQJ89423 | 0.946 | 0. | HORVU.MC |
| 0.914900907 | 0.984863186 | 16 | 3 | PNT68493 | 0.727 | − | HORVU.MC |
| 0.913571509 | 0.97327596 | 16 | 0 | PNT76146 | 0.918 | 0. | HORVU.MC |
| 0.880951264 | 0.953203203 | 16 | 3 | KQK17939 | 0.917 | 0. | HORVU.MC |
| 0.877439223 | 0.959021059 | 16 | 5 | genblast_Os10t045 | | | HORVU.MC |
| 0.935368799 | 0.982869205 | 16 | 0 | PNT67030 | 0.956 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.858769846 | 0.921818619 | 16 | 0 | KQJ84394 | 0.813 | −0 | HORVU.MC |
| 0.850484914 | 0.920946442 | 16 | 2 | KQK07734 | 0.832 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.937118709 | 0.99093374 | 16 | 2 | KQK07118 | 0.959 | 0. | HORVU.MC |
| 0.899790427 | 0.955508782 | 16 | 0 | KQK12404 | 0.813 | − | HORVU.MC |
| 0.884677194 | 0.953046395 | 16 | 1 | KQJ99360 | 0.798 | −1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.94582129 | 0.995946098 | 16 | 2 | KQJ97713 | 0.929 | −0 | HORVU.MC |
| 0.953501467 | 0.995600251 | 16 | 0 | KQK03432 | 0.963 | 0. | HORVU.MC |
| 0.916766092 | 0.980910426 | 16 | 3 | KQJ93639 | 0.948 | 0. | HORVU.MC |
| 0.82578534 | 0.899057592 | 16 | 0 | KQJ90947 | 0.744 | −1 | HORVU.MC |
| 0.949319649 | 0.992158672 | 16 | 0 | PNT68406 | 0.959 | 0. | HORVU.MC |
| 0.842521456 | 0.879844961 | 16 | 0 | KQK17613 | 0.767 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.847110656 | 0.948087432 | 16 | 1 | PNT74484 | 0.726 | − | HORVU.MC |
| 0.942759901 | 1.001980198 | 16 | 0 | KQJ87968 | 0.907 | −0 | HORVU.MC |
| 0.92221471 | 0.97231944 | 16 | 1 | PNT63889 | 0.923 | 0. | HORVU.MC |
| 0.917327293 | 0.986329073 | 16 | 1 | KQK13777 | 0.928 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.929875188 | 0.975225225 | 16 | 1 | KQJ89512 | 0.926 | –0 | HORVU.MC |
| 0.958258751 | 0.993078759 | 16 | 0 | KQJ95400 | 0.967 | 0. | HORVU.MC |
| 0.902661009 | 0.956958545 | 16 | 0 | KQK07145 | 0.840 | – | HORVU.MC |
| 0.947461208 | 0.987598062 | 16 | 0 | KQJ91573 | 0.966 | 0. | HORVU.MC |
| 0.853463357 | 0.926713948 | 16 | 2 | KQJ89570 | 0.860 | 0. | HORVU.MC |
| 0.878884946 | 0.967626905 | 16 | 4 | KQK02843 | 0.886 | 0 | HORVU.MC |
| 0.882870269 | 0.949264221 | 16 | 0 | KQJ90086 | 0.884 | 0. | HORVU.MC |
| 0.899105408 | 0.937661917 | 16 | 1 | KQK16401 | 0.915 | 0 | HORVU.MC |
| 0.931500608 | 0.990886999 | 16 | 0 | KQK19263 | 0.991 | 0 | HORVU.MC |
| 0.952764858 | 0.992868217 | 16 | 1 | KQJ83254 | 0.983 | 0. | HORVU.MC |
| 0.895561156 | 0.97893907 | 16 | 4 | KQJ84904 | 0.900 | 0. | HORVU.MC |
| 0.947084202 | 0.979847116 | 16 | 0 | KQJ99772 | 0.951 | 0. | HORVU.MC |
| 0.87473492 | 0.950282752 | 16 | 2 | KQK23470 | 0.864 | – | genblast_C |
| 0.91217459 | 0.986606301 | 16 | 1 | KQK18023 | 0.927 | 0 | HORVU.MC |
| 0.88202745 | 0.972550382 | 16 | 1 | KQK04640 | 0.855 | – | HORVU.MC |

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| 0.812366382 | 0.945483699 | 16 | 0 | KQK15993 | 0.760 | – | HORVU.MC |
| 0.858473048 | 0.948641766 | 16 | 0 | KQK12400 | 0.833 | – | HORVU.MC |
| 0.896418948 | 0.951791436 | 16 | 1 | PNT72604 | 0.807 | – | HORVU.MC |
| 0.828825224 | 0.880665813 | 16 | 0 | KQJ85679 | 0.841 | 0. | HORVU.MC |
| 0.896716002 | 0.970115377 | 16 | 1 | KQJ89240 | 0.930 | 0. | genblast_C |
| 0.855411687 | 0.934661355 | 16 | 1 | KQK02819 | 0.745 | – | HORVU.MC |
| 0.933135961 | 0.989673824 | 16 | 1 | KQK21744 | 0.962 | 0 | HORVU.MC |
| 0.881023752 | 0.965399109 | 16 | 1 | KQJ97237 | 0.912 | 0. | HORVU.MC |
| 0.949945055 | 0.990901099 | 16 | 1 | KQJ96380 | 0.969 | 0. | HORVU.MC |
| 0.93601654 | 0.990656213 | 16 | 1 | KQJ88730 | 0.929 | –0 | HORVU.MC |
| 0.919494183 | 0.967039234 | 16 | 0 | KQK02131 | 0.935 | 0 | HORVU.MC |
| 0.862777892 | 0.944421573 | 16 | 0 | KQK04852 | 0.725 | – | genblast_C |
| | | | | | | | |
| 0.919727795 | 0.985683338 | 16 | 2 | KQJ88971 | 0.965 | 0. | HORVU.MC |
| 0.90314075 | 0.948665298 | 16 | 0 | KQK03361 | 0.912 | 0 | HORVU.MC |
| 0.939002214 | 0.98369527 | 16 | 2 | KQK09601 | 0.950 | 0 | HORVU.MC |
| 0.927093437 | 0.983834465 | 16 | 1 | KQJ91952 | 0.925 | –0 | genblast_C |
| | | | | | | | |
| 0.901633498 | 0.955179762 | 16 | 1 | KQK00216 | 0.916 | 0 | HORVU.MC |
| | | | | | | | |
| 0.934127231 | 0.98519441 | 16 | 1 | KQK11109 | 0.910 | – | HORVU.MC |
| 0.942090599 | 0.971243793 | 16 | 0 | PNT76457 | 0.946 | 0. | HORVU.MC |
| 0.899175663 | 0.958208636 | 16 | 0 | KQJ91208 | 0.882 | –0 | HORVU.MC |
| 0.886781475 | 0.99069118 | 16 | 0 | KQJ89789 | 0.960 | 0. | HORVU.MC |
| 0.945093289 | 0.984090252 | 16 | 0 | KQK15864 | 0.963 | 0 | HORVU.MC |
| 0.861966442 | 0.947404812 | 16 | 5 | KQK03864 | 0.891 | 0 | HORVU.MC |
| 0.900449922 | 0.965884194 | 16 | 0 | PNT73136 | 0.887 | – | HORVU.MC |
| 0.945553422 | 0.999455799 | 16 | 1 | KQK18012 | 0.994 | 0 | HORVU.MC |
| 0.946955424 | 0.991753164 | 16 | 0 | KQK09594 | 0.943 | – | HORVU.MC |
| 0.882478313 | 0.958271014 | 16 | 0 | KQK17871 | 0.791 | – | genblast_Z |
| 0.93499972 | 0.990363066 | 16 | 0 | KQK08700 | 0.960 | 0 | HORVU.MC |
| 0.933935361 | 0.983168568 | 16 | 1 | KQK06772 | 0.969 | 0 | HORVU.MC |
| | | | | | | | |
| 0.869118081 | 0.967057039 | 16 | 4 | KQK23174 | 0.865 | – | HORVU.MC |
| 0.834639893 | 0.890812092 | 16 | 0 | PNT77221 | 0.839 | 0. | HORVU.MC |
| 0.790552746 | 0.842244701 | 16 | 4 | KQK02589 | 0.771 | – | HORVU.MC |
| 0.802313883 | 0.903995401 | 16 | 0 | KQJ90243 | 0.742 | –1 | HORVU.MC |
| 0.829331783 | 0.938536191 | 16 | 0 | KQK11197 | 0.738 | – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.958823347 | 0.996368738 | 16 | 1 | KQK22276 0.942 – | HORVU.MC |
| 0.957679256 | 0.991710704 | 16 | 1 | KQK06467 0.963 0 | HORVU.MC |
| 0.918694131 | 0.979254512 | 16 | 0 | KQJ82265 0.891 –0 | HORVU.MC |
| 0.92309138 | 0.985499499 | 16 | 2 | KQK15663 0.925 0 | HORVU.MC |
| 0.856155961 | 0.909722222 | 16 | 2 | KQK07545 0.903 0 | HORVU.MC |
| 0.899262775 | 0.938194304 | 16 | 1 | KQJ92685 0.803 –1 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.926173816 | 0.98255755 | 16 | 1 | genblast_Os05t013 | HORVU.MC |
| 0.899630928 | 0.970360237 | 16 | 1 | KQK01871 0.892 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.92073241 | 0.996731341 | 16 | 3 | KQK16625 0.960 0 | HORVU.MC |
| 0.874734419 | 0.957034939 | 16 | 1 | KQK11279 0.883 0 | HORVU.MC |
| 0.88066859 | 0.957485575 | 16 | 1 | KQJ92237 0.938 0. | HORVU.MC |
| 0.893047006 | 0.954252938 | 16 | 1 | KQJ98868 0.876 –0 | HORVU.MC |
| 0.930262636 | 0.972889177 | 16 | 0 | PNT76512 0.923 – | HORVU.MC |
| 0.867281753 | 0.920408847 | 16 | 1 | KQK03131 0.724 – | HORVU.MC |
| 0.91060872 | 0.965638278 | 16 | 2 | KQK07501 0.921 0 | HORVU.MC |
| 0.847547863 | 0.925083241 | 16 | 0 | KQK15074 0.731 – | HORVU.MC |
| 0.960089667 | 0.993080383 | 16 | 1 | KQK06307 0.972 0 | HORVU.MC |
| 0.836856583 | 0.900098987 | 16 | 1 | KQJ81796 0.724 –2 | HORVU.MC |
| 0.837891297 | 0.889232886 | 16 | 1 | KQJ88940 0.793 –0 | HORVU.MC |
| 0.913926973 | 0.958589815 | 16 | 1 | KQJ83672 0.939 0. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.852541303 | 0.9279486 | 16 | 0 | genblast_Os01t083 | genblast_C |
| 0.919915873 | 0.990626921 | 16 | 5 | KQK10480 0.964 0 | HORVU.MC |
| 0.865860377 | 0.945913462 | 16 | 4 | KQK09040 0.850 – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.928512533 | 0.978726913 | 16 | 2 | KQK02564 | 0.932 | 0 | HORVU.MC |
| 0.815850113 | 0.88079032 | 16 | 8 | KQJ99943 | 0.821 | 0. | HORVU.MC |
| 0.883950206 | 0.932154107 | 16 | 0 | KQJ98671 | 0.833 | –1 | HORVU.MC |
| 0.917522122 | 0.97086896 | 16 | 0 | KQJ84110 | 0.904 | –0 | HORVU.MC |
| 0.8596511 | 0.940978483 | 16 | 2 | KQK09804 | 0.844 | – | HORVU.MC |
| 0.870670573 | 0.918452381 | 16 | 1 | KQK16977 | 0.853 | – | HORVU.MC |
| 0.869381034 | 0.924728479 | 16 | 4 | KQJ84775 | 0.892 | 0. | HORVU.MC |
| 0.829717332 | 0.947681627 | 16 | 0 | KQK02850 | 0.723 | – | HORVU.MC |
| 0.932081202 | 0.988491049 | 16 | 0 | KQK12967 | 0.909 | – | HORVU.MC |
| 0.906864685 | 1.013113272 | 16 | 0 | KQK04839 | 0.863 | – | HORVU.MC |
| 0.880360301 | 0.969053935 | 16 | 0 | KQK01068 | 0.723 | – | HORVU.MC |
| 0.927313536 | 0.979494263 | 16 | 0 | KQJ82749 | 0.952 | 0. | genblast_C |
| 0.884568487 | 0.977509823 | 16 | 1 | KQK12501 | 0.903 | 0 | HORVU.MC |
| 0.839342949 | 0.904428904 | 16 | 0 | KQK04006 | 0.881 | 0 | HORVU.MC |
| 0.856106671 | 0.939541348 | 16 | 0 | KQK17238 | 0.900 | 0 | HORVU.MC |
| 0.940989445 | 1.000115354 | 16 | 2 | KQK10202 | 0.908 | – | HORVU.MC |
| 0.929863946 | 0.959727891 | 16 | 0 | KQK03069 | 0.931 | 0 | HORVU.MC |
| 0.980662033 | 1.009860531 | 16 | 0 | KQK04806 | 0.995 | 0 | HORVU.MC |
| 0.834176247 | 0.901313825 | 16 | 1 | PNT78341 | 0.739 | – | HORVU.MC |
| 0.923926117 | 0.981596029 | 16 | 3 | KQK21604 | 0.958 | 0 | HORVU.MC |
| 0.905816875 | 0.951489951 | 16 | 0 | KQK14888 | 0.879 | – | HORVU.MC |
| 0.899996216 | 0.969421738 | 16 | 2 | KQJ85923 | 0.860 | –0 | HORVU.MC |
| 0.940836113 | 0.986958829 | 16 | 1 | PNT65836 | 0.971 | 0. | HORVU.MC |
| 0.868310908 | 0.937962202 | 16 | 1 | KQK06029 | 0.778 | – | HORVU.MC |
| 0.900248232 | 0.973068553 | 16 | 3 | KQK02797 | 0.913 | 0 | HORVU.MC |
| 0.907791746 | 0.978494624 | 16 | 0 | KQK18810 | 0.899 | – | HORVU.MC |
| 0.900833105 | 0.962973121 | 16 | 1 | KQK06711 | 0.903 | 0 | HORVU.MC |
| 0.928911911 | 0.972204568 | 16 | 2 | KQK01842 | 0.943 | 0 | HORVU.MC |
| 0.926093327 | 0.976014427 | 16 | 1 | KQK09021 | 0.949 | 0 | HORVU.MC |
| 0.835451007 | 0.893642072 | 16 | 3 | KQK17543 | 0.770 | – | HORVU.MC |
| 0.820195638 | 0.93780507 | 16 | 3 | PNT67525 | 0.785 | – | HORVU.MC |
| 0.859528664 | 0.95010794 | 16 | 1 | KQK13334 | 0.763 | – | HORVU.MC |
| 0.937453455 | 0.990169794 | 16 | 1 | KQJ90491 | 0.927 | –0 | HORVU.MC |
| 0.934269497 | 0.984529985 | 16 | 1 | KQK16429 | 0.963 | 0 | HORVU.MC |
| 0.939777654 | 0.972111554 | 16 | 1 | KQK22159 | 0.944 | 0 | HORVU.MC |
| 0.926913382 | 0.982584785 | 16 | 0 | KQJ91143 | 0.902 | –0 | HORVU.MC |
| 0.871298528 | 0.930014525 | 16 | 0 | KQJ87622 | 0.764 | –1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.804178446 | 0.909880714 | 16 | 3 | KQK01053 | 0.773 | – | HORVU.MC |
| 0.888273903 | 0.97191745 | 16 | 1 | KQK12853 | 0.898 | 0 | HORVU.MC |
| 0.927685787 | 0.987799081 | 16 | 0 | KQJ96964 | 0.929 | 0. | HORVU.MC |
| 0.860301115 | 0.949157151 | 16 | 0 | PNT75576 | 0.859 | – | HORVU.MC |
| 0.907106164 | 0.946917808 | 16 | 0 | KQJ86491 | 0.928 | 0. | HORVU.MC |
| 0.942804458 | 0.990902002 | 16 | 0 | KQK16370 | 0.977 | 0 | genblast_C |
| 0.901487361 | 0.984956843 | 16 | 5 | KQK15989 | 0.962 | 0 | HORVU.MC |
| 0.922836046 | 0.973475141 | 16 | 2 | KQJ93013 | 0.937 | 0. | HORVU.MC |
| 0.920949662 | 0.989678511 | 16 | 0 | KQK18984 | 0.966 | 0 | HORVU.MC |
| 0.932676406 | 1.006300205 | 16 | 1 | genblast_Os08t053 | | | HORVU.MC |
| 0.898208901 | 0.946839401 | 16 | 1 | KQK20271 | 0.899 | 0 | HORVU.MC |
| 0.849978599 | 0.932515337 | 16 | 9 | KQK17507 | 0.722 | – | HORVU.MC |
| 0.883576884 | 0.93220553 | 16 | 0 | KQJ90847 | 0.885 | 0. | HORVU.MC |
| 0.92072016 | 0.997078238 | 16 | 1 | KQJ91559 | 0.988 | 0. | HORVU.MC |
| 0.90842422 | 0.960887552 | 16 | 0 | KQK21055 | 0.894 | – | HORVU.MC |
| 0.919942908 | 0.967879688 | 16 | 0 | KQK00337 | 0.857 | – | HORVU.MC |
| 0.92856512 | 0.996624274 | 16 | 0 | KQK20011 | 0.924 | – | HORVU.MC |
| 0.96176732 | 0.987167259 | 16 | 1 | KQK23114 | 0.982 | 0 | HORVU.MC |
| 0.850228922 | 0.945749827 | 16 | 0 | KQK21473 | 0.860 | 0 | HORVU.MC |
| 0.843126961 | 0.921727894 | 16 | 1 | KQJ84970 | 0.761 | –1 | HORVU.MC |
| 0.910807626 | 0.972750643 | 16 | 0 | KQJ86004 | 0.827 | –1 | HORVU.MC |
| 0.846981814 | 0.928504011 | 16 | 8 | PNT64058 | 0.865 | 0. | HORVU.MC |
| 0.957294185 | 0.99628859 | 16 | 1 | PNT71083 | 0.891 | – | HORVU.MC |
| 0.855454545 | 0.958518519 | 16 | 0 | PNT71096 | 0.721 | – | HORVU.MC |
| 0.873802607 | 0.995288945 | 16 | 0 | KQJ97998 | 0.843 | –0 | genblast_C |
| 0.884065254 | 0.951136539 | 16 | 0 | KQJ95786 | 0.901 | 0. | HORVU.MC |
| 0.892064654 | 0.971840505 | 16 | 2 | KQJ99084 | 0.937 | 0. | HORVU.MC |
| 0.886170879 | 0.963797814 | 16 | 0 | KQK14752 | 0.875 | – | HORVU.MC |
| 0.944468341 | 0.985203028 | 16 | 1 | KQK22318 | 0.975 | 0 | HORVU.MC |
| 0.81993016 | 0.96564925 | 16 | 8 | KQJ89520 | 0.881 | 0. | HORVU.MC |
| 0.865460877 | 0.94761397 | 16 | 1 | KQK00867 | 0.813 | – | HORVU.MC |
| 0.873828443 | 0.939871412 | 16 | 2 | KQJ98661 | 0.848 | –0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.927182856 | 0.958156405 | 16 | 1 | KQK13901 0.944 0 | HORVU.MC |
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| 0.863906327 | 0.926021664 | 16 | 1 | KQK19730 0.720 – | HORVU.MC |
| 0.934898915 | 0.99566075 | 16 | 0 | KQJ85162 0.940 0. | HORVU.MC |
| 0.873044301 | 0.987506447 | 16 | 4 | genblast_Os10t034 | HORVU.MC |
| 0.898318334 | 0.972849298 | 16 | 0 | KQK15972 0.914 0 | HORVU.MC |
| 0.91559422 | 0.971194945 | 16 | 0 | KQK22211 0.959 0 | genblast_C |
| 0.867977437 | 0.934186708 | 16 | 2 | KQK13595 0.857 – | HORVU.MC |
| 0.900204918 | 0.947131148 | 16 | 0 | KQJ99063 0.815 –1 | HORVU.MC |
| 0.835486306 | 0.90082504 | 16 | 2 | PNT75479 0.856 0. | HORVU.MC |
| 0.920034879 | 0.982765696 | 16 | 0 | PNT65200 0.953 0. | HORVU.MC |
| 0.936392171 | 0.987444609 | 16 | 0 | KQK11291 0.939 0 | HORVU.MC |
| 0.826937998 | 0.883146674 | 16 | 3 | KQK05747 0.823 – | HORVU.MC |
| 0.932421957 | 0.984412319 | 16 | 1 | KQJ90669 0.922 –0 | HORVU.MC |
| 0.938247193 | 0.980026243 | 16 | 2 | KQJ97406 0.967 0. | HORVU.MC |
|  |  |  |  |  |  |
| 0.955317554 | 0.99325548 | 16 | 0 | KQK20600 0.983 0 | HORVU.MC |
| 0.831054688 | 0.919921875 | 16 | 4 | KQK17501 0.769 – | genblast_C |
| 0.877064512 | 0.985883682 | 16 | 2 | KQK12732 0.780 – | HORVU.MC |
| 0.960569551 | 0.99890471 | 16 | 0 | KQK07769 0.974 0 | HORVU.MC |
| 0.855201659 | 0.918495956 | 16 | 0 | genblast_Zm00001 | HORVU.MC |
|  |  |  |  |  |  |
| 0.893205411 | 0.960679459 | 16 | 0 | KQK14077 0.891 – | HORVU.MC |
| 0.870274465 | 0.945168429 | 16 | 1 | KQK16124 0.785 – | HORVU.MC |
|  |  |  |  |  |  |
| 0.836001252 | 0.918881797 | 16 | 3 | genblast_Os07t068 | HORVU.MC |
| 0.841811201 | 0.906402812 | 16 | 2 | KQJ88436 0.869 0. | genblast_C |
| 0.821044138 | 0.928033111 | 16 | 5 | KQK22840 0.928 1 | HORVU.MC |
| 0.859597518 | 0.921131154 | 16 | 2 | KQJ83527 0.887 0. | HORVU.MC |

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| 0.906910261 | 0.978084963 | 16 | 1 | PNT76075 0.875 -( | HORVU.MC |
| 0.872247114 | 0.941980559 | 16 | 0 | KQK11025 0.877 0. | HORVU.MC |
| 0.840214592 | 0.961373391 | 16 | 0 | KQK22274 0.818 -( | HORVU.MC |
| 0.932851201 | 0.982542525 | 16 | 0 | KQJ99205 0.922 -0 | HORVU.MC |
| 0.903719728 | 0.963205488 | 16 | 1 | KQJ85345 0.813 -1 | HORVU.MC |
| 0.914460375 | 0.955756883 | 16 | 2 | KQK08862 0.935 0. | HORVU.MC |

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| 0.916690314 | 0.958254509 | 16 | 2 | KQK13422 0.902 -( | HORVU.MC |
| 0.901039706 | 0.969890854 | 16 | 0 | genblast_Os01t025 | genblast_C |
| 0.864075307 | 0.962704918 | 16 | 8 | KQK00285 0.915 0. | HORVU.MC |
| 0.925318222 | 0.993657883 | 16 | 1 | genblast_Os04t067 | HORVU.MC |
| 0.833165666 | 0.892374847 | 16 | 0 | KQK10405 0.719 -. | HORVU.MC |
| 0.842411629 | 0.932786885 | 16 | 4 | PNT61749 0.876 0. | HORVU.MC |
| 0.880540381 | 0.944920027 | 16 | 2 | KQJ89009 0.915 0. | HORVU.MC |
| 0.934592407 | 0.966204751 | 16 | 0 | KQJ83006 0.962 1. | HORVU.MC |
| 0.957259659 | 0.995907609 | 16 | 1 | KQJ91227 0.973 0. | HORVU.MC |
| 0.85272694 | 0.915080527 | 16 | 0 | PNT61984 0.767 -1 | HORVU.MC |
| 0.872010251 | 0.957099468 | 16 | 0 | KQK19170 0.808 - | HORVU.MC |

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| 0.780434019 | 0.853798358 | 16 | 16 | PNT73418 0.854 2. | HORVU.MC |

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| 0.940759721 | 0.994336433 | 16 | 1 | KQK18461 0.973 0. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.933267711 | 0.967493902 | 16 | 0 | KQK06923 0.947 0. | HORVU.MC |
| 0.92222742 | 0.98041829 | 16 | 2 | KQJ86320 0.949 0. | genblast_C |
| 0.929163559 | 0.964558473 | 16 | 1 | KQK22918 0.911 -( | HORVU.MC |
| 0.848785015 | 0.945029486 | 16 | 1 | KQJ87527 0.788 -0 | HORVU.MC |
| 0.851076345 | 0.921337266 | 16 | 0 | KQK05321 0.831 -( | HORVU.MC |
| 0.859501008 | 0.942876344 | 16 | 0 | KQK15105 0.783 - | HORVU.MC |
| 0.888683032 | 0.949010883 | 16 | 2 | KQJ87321 0.802 -1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.812827427 | 0.912788906 | 16 | 0 | KQK21483 | 0.798 | – | HORVU.MC |
| 0.879885011 | 0.965583789 | 16 | 0 | KQK12795 | 0.852 | – | HORVU.MC |
| 0.949798371 | 0.983829026 | 16 | 1 | KQJ95996 | 0.970 | 0. | HORVU.MC |
| 0.865405569 | 0.924293785 | 16 | 1 | KQK15300 | 0.795 | – | HORVU.MC |
| 0.894093111 | 0.979978471 | 16 | 0 | PNT76212 | 0.966 | 0. | HORVU.MC |
| 0.889062993 | 0.961053295 | 16 | 3 | KQJ96083 | 0.898 | 0. | HORVU.MC |
| 0.961688381 | 0.993745042 | 16 | 1 | KQJ85913 | 0.967 | 0. | HORVU.MC |
| 0.867995883 | 0.916577157 | 16 | 1 | KQK22358 | 0.863 | – | HORVU.MC |
| 0.935213632 | 0.993855387 | 16 | 3 | KQJ97598 | 0.923 | –0 | HORVU.MC |
| 0.955109073 | 1.00434122 | 16 | 1 | KQK04354 | 0.998 | 0 | HORVU.MC |
| 0.904561513 | 0.956497645 | 16 | 2 | KQK00825 | 0.866 | – | HORVU.MC |
| 0.849294628 | 0.901790559 | 16 | 0 | KQK09388 | 0.889 | 0 | HORVU.MC |
| 0.833020014 | 0.916705229 | 16 | 4 | KQJ96102 | 0.717 | –1 | HORVU.MC |
| 0.851262098 | 0.927020664 | 16 | 2 | KQK21988 | 0.814 | – | HORVU.MC |
| 0.948550113 | 0.994629245 | 16 | 1 | KQJ85338 | 0.980 | 0. | HORVU.MC |
| 0.93929928 | 0.990403838 | 16 | 1 | KQJ86717 | 0.901 | –0 | HORVU.MC |
| 0.894109018 | 0.995058678 | 16 | 2 | KQJ90712 | 0.909 | 0. | HORVU.MC |
| 0.939808153 | 0.97793765 | 16 | 0 | KQK10914 | 0.956 | 0 | HORVU.MC |
| 0.916467723 | 0.9763178 | 16 | 2 | PNT73127 | 0.908 | – | HORVU.MC |
| 0.945494758 | 1.006422018 | 16 | 0 | KQK14403 | 0.966 | 0 | HORVU.MC |
| 0.961366164 | 1.004201681 | 16 | 2 | KQK14736 | 0.986 | 0 | HORVU.MC |
| 0.920185553 | 0.967929139 | 16 | 2 | KQK17834 | 0.890 | – | HORVU.MC |
| 0.80018276 | 0.871459031 | 16 | 2 | KQJ90464 | 0.778 | –0 | HORVU.MC |
| 0.877332485 | 0.922815946 | 16 | 1 | PNT61169 | 0.807 | – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.923431316 | 0.980540897 | 16 | 0 | KQJ88471 0.922 -0 | HORVU.MC |
| 0.925008978 | 0.991919555 | 16 | 0 | KQK11174 0.827 - | HORVU.MC |
| 0.877514472 | 0.95918958 | 16 | 1 | KQK02845 0.767 - | HORVU.MC |
| 0.912879545 | 0.991610068 | 16 | 0 | KQK13757 0.953 0 | HORVU.MC |
| 0.897431361 | 0.969902821 | 16 | 0 | KQK13092 0.905 0 | HORVU.MC |
| 0.890392995 | 0.965353992 | 16 | 1 | KQK19054 0.868 - | HORVU.MC |

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|---|---|---|---|---|---|
| 0.948541321 | 0.999367939 | 16 | 0 | KQK14010 0.964 0 | HORVU.MC |
| 0.873553666 | 0.974581252 | 16 | 4 | genblast_Os02t065 | HORVU.MC |
| 0.889229955 | 0.970052707 | 16 | 2 | KQK07308 0.854 - | HORVU.MC |
| 0.885879663 | 0.955838216 | 16 | 2 | KQK17672 0.895 0 | HORVU.MC |
| 0.858207034 | 0.927310182 | 16 | 0 | KQK00804 0.865 0 | HORVU.MC |
| 0.832199952 | 0.930923407 | 16 | 1 | KQK00538 0.828 - | HORVU.MC |
| 0.935311711 | 0.991219405 | 16 | 2 | PNT72475 0.968 0. | HORVU.MC |
| 0.905153203 | 1.004735376 | 16 | 0 | KQK23019 1.003 0 | HORVU.MC |
| 0.930642661 | 0.989042676 | 16 | 1 | KQK11992 0.977 0 | HORVU.MC |
| 0.939625451 | 0.98746278 | 16 | 1 | KQK00145 0.946 0 | HORVU.MC |
| 0.850767875 | 0.926485398 | 16 | 0 | KQK00819 0.926 1 | HORVU.MC |
| 0.930484557 | 0.993112355 | 16 | 0 | KQJ88590 0.963 0. | HORVU.MC |

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| 0.855442917 | 0.957883745 | 16 | 0 | KQJ90655 0.939 1. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.866885809 | 0.909263208 | 16 | 0 | KQK08897 0.868 0 | HORVU.MC |
| 0.88105649 | 0.936885978 | 16 | 0 | PNT77825 0.928 0. | HORVU.MC |
| 0.865518691 | 0.931764241 | 16 | 0 | KQK16753 0.892 0 | HORVU.MC |
| 0.925029487 | 0.986829172 | 16 | 1 | KQJ90391 0.947 0. | HORVU.MC |
| 0.824531382 | 0.882055602 | 16 | 0 | KQK00971 0.779 - | HORVU.MC |
| 0.851643921 | 0.974937965 | 16 | 0 | PNT71548 0.716 -1 | HORVU.MC |
| 0.883938394 | 0.950678401 | 16 | 1 | KQJ94309 0.949 0. | HORVU.MC |
| 0.941031885 | 0.984471194 | 16 | 1 | genblast_Os04t032 | HORVU.MC |
| 0.844766452 | 0.935649449 | 16 | 4 | KQK12961 0.774 - | HORVU.MC |
| 0.934093291 | 0.986792453 | 16 | 1 | KQJ99675 0.973 0. | genblast_C |
| 0.924098573 | 0.984475419 | 16 | 0 | KQK16187 0.944 0 | HORVU.MC |
| 0.847717683 | 0.916762562 | 16 | 1 | KQJ84651 0.838 -0 | HORVU.MC |
| 0.92490233 | 0.982877538 | 16 | 4 | KQK04739 0.968 0 | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.875905148 | 0.967163751 | 16 | 1 | KQK12491 | 0.884 | 0 | HORVU.MC |
| 0.903311472 | 0.96656198 | 16 | 0 | KQJ94524 | 0.715 | –2 | HORVU.MC |
| | | | | | | | |
| 0.889389852 | 0.964839961 | 16 | 3 | KQK00154 | 0.837 | – | genblast_C |
| 0.907563376 | 0.997998666 | 16 | 0 | KQK17601 | 0.899 | – | HORVU.MC |
| 0.951779769 | 1.005866498 | 16 | 0 | KQJ81879 | 0.951 | –0 | HORVU.MC |
| 0.92471727 | 0.963101399 | 16 | 0 | KQJ94990 | 0.937 | 0. | HORVU.MC |
| 0.803148896 | 0.85687491 | 16 | 0 | KQK17314 | 0.715 | – | HORVU.MC |
| 0.889981442 | 0.956178161 | 16 | 1 | KQJ96323 | 0.926 | 0. | HORVU.MC |
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| 0.909184727 | 0.958278048 | 16 | 1 | KQJ86841 | 0.895 | –0 | HORVU.MC |
| 0.927373607 | 0.966958599 | 16 | 2 | KQK05513 | 0.938 | 0 | HORVU.MC |
| 0.821811716 | 0.956846673 | 16 | 0 | KQK11546 | 0.783 | – | HORVU.MC |
| 0.911340384 | 0.941430049 | 16 | 0 | KQJ84011 | 0.883 | –1 | HORVU.MC |
| 0.883090839 | 0.977649923 | 16 | 1 | PNT70935 | 0.896 | 0. | HORVU.MC |
| 0.892575954 | 1.003705076 | 16 | 1 | KQK01729 | 0.930 | 0 | HORVU.MC |
| 0.86363417 | 0.961776062 | 16 | 0 | KQK01000 | 0.715 | – | HORVU.MC |
| 0.882058971 | 0.948858904 | 16 | 2 | PNT65620 | 0.906 | 0. | HORVU.MC |
| 0.89868149 | 0.961291458 | 16 | 2 | PNT67767 | 0.918 | 0. | HORVU.MC |
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| 0.87307145 | 0.95416417 | 16 | 1 | KQK16273 | 0.768 | – | HORVU.MC |
| 0.872645349 | 0.922325581 | 16 | 0 | KQJ84622 | 0.832 | –0 | HORVU.MC |
| 0.93553684 | 0.975478748 | 16 | 1 | KQK14891 | 0.962 | 0 | HORVU.MC |
| 0.922851925 | 0.961990838 | 16 | 1 | KQK00278 | 0.929 | 0 | genblast_C |
| 0.933976447 | 0.97870208 | 16 | 1 | KQJ94086 | 0.943 | 0. | HORVU.MC |
| 0.894253954 | 0.960712006 | 16 | 2 | KQK13774 | 0.869 | – | HORVU.MC |
| 0.942527376 | 0.997161011 | 16 | 0 | KQJ94631 | 0.959 | 0. | HORVU.MC |
| 0.937601857 | 0.983644724 | 16 | 1 | PNT77591 | 0.942 | 0. | HORVU.MC |
| | | | | | | | |
| 0.838683577 | 0.918259822 | 16 | 0 | KQJ82241 | 0.808 | –0 | HORVU.MC |
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| 0.88909409 | 0.984836703 | 16 | 0 | KQJ87731 | 0.842 | –0 | HORVU.MC |
| 0.946276545 | 0.97704228 | 16 | 0 | genblast_Os09t052 | | | HORVU.MC |
| 0.911799708 | 0.977617185 | 16 | 5 | KQJ94873 | 0.958 | 0. | HORVU.MC |
| 0.818418457 | 0.998684787 | 16 | 0 | KQJ91961 | 0.799 | –0 | HORVU.MC |

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| 0.903167147 | 0.954841643 | 16 | 1 | KQK16852 | 0.936 | 0 | HORVU.MC |
| 0.845941004 | 0.940327362 | 16 | 8 | KQK00310 | 0.823 | – | genblast_C |
| 0.908247333 | 0.974374314 | 16 | 3 | PNT76750 | 0.907 | –( | HORVU.MC |
| 0.891115791 | 0.959023415 | 16 | 1 | KQK02300 | 0.808 | – | HORVU.MC |
| 0.966662971 | 1.000266075 | 16 | 1 | KQK07908 | 0.987 | 0 | genblast_C |
| 0.969820791 | 0.996966092 | 16 | 2 | KQJ83708 | 0.984 | 0. | HORVU.MC |
| 0.92213183 | 0.990337628 | 16 | 0 | KQK03834 | 0.944 | 0 | HORVU.MC |
| 0.897592164 | 0.976061283 | 16 | 4 | KQK02086 | 0.967 | 0 | HORVU.MC |
| 0.864206665 | 0.952975515 | 16 | 0 | genblast_Os06t032 | | | HORVU.MC |
| 0.860002074 | 0.963704241 | 16 | 0 | KQK20066 | 0.819 | – | HORVU.MC |
| 0.874221782 | 0.952134541 | 16 | 2 | KQK11085 | 0.894 | 0 | HORVU.MC |
| 0.934815263 | 0.991121872 | 16 | 2 | KQK11417 | 0.946 | 0 | HORVU.MC |
| 0.888337375 | 0.989693847 | 16 | 2 | KQJ97878 | 0.714 | –1 | genblast_C |
| 0.925654479 | 0.989506707 | 16 | 1 | KQJ91286 | 0.946 | 0. | HORVU.MC |
| 0.946093709 | 0.993316004 | 16 | 1 | KQK06571 | 0.984 | 0 | HORVU.MC |
| 0.872384587 | 0.958749069 | 16 | 1 | KQK05309 | 0.839 | – | genblast_C |
| 0.861694054 | 0.935331534 | 16 | 0 | KQJ87828 | 0.793 | –1 | HORVU.MC |
| 0.956602022 | 0.988545699 | 16 | 0 | KQK22351 | 0.981 | 0 | HORVU.MC |
| 0.908087216 | 0.968801997 | 16 | 1 | KQK04917 | 0.915 | 0 | HORVU.MC |
| 0.888564184 | 0.921721741 | 16 | 10 | KQK03852 | 0.900 | 0 | HORVU.MC |
| 0.954705666 | 0.990244554 | 16 | 1 | KQJ82766 | 0.951 | –0 | HORVU.MC |
| 0.933315094 | 0.98881323 | 16 | 0 | KQJ81517 | 0.903 | –0 | HORVU.MC |
| 0.81294991 | 0.871425715 | 16 | 0 | KQK09356 | 0.811 | – | HORVU.MC |
| 0.915877954 | 0.966743359 | 16 | 1 | KQK20287 | 0.895 | – | HORVU.MC |
| 0.818119878 | 0.866250658 | 16 | 11 | KQK14283 | 0.794 | – | HORVU.MC |
| 0.862750664 | 0.957922701 | 16 | 2 | KQK12952 | 0.830 | – | HORVU.MC |

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| 0.91166422 | 0.971312401 | 16 | 1 PNT77835 0.920 0.HORVU.MC |
| 0.859773496 | 0.90672115 | 16 | 0 KQJ95429 0.713 –3HORVU.MC |
| 0.840147259 | 0.964725911 | 16 | 6 KQJ88434 0.912 0.HORVU.MC |
| 0.842152104 | 0.926860841 | 16 | 0 KQK11294 0.713 –HORVU.MC |
| 0.849594171 | 0.963546611 | 16 | 0 KQK09233 0.877 0HORVU.MC |
| 0.903902306 | 0.984703489 | 16 | 3 KQJ83553 0.784 –1HORVU.MC |
| 0.871039318 | 0.95245431 | 16 | 2 KQJ94950 0.852 –0HORVU.MC |
| 0.926617723 | 1.000831601 | 16 | 3 KQJ91479 0.979 0. HORVU.MC |
| 0.854039965 | 0.950695048 | 16 | 2 KQK05074 0.753 – HORVU.MC |
| 0.901280845 | 0.963697198 | 16 | 1 PNT67824 0.900 –HORVU.MC |
| 0.864907644 | 0.927276952 | 16 | 2 KQJ87103 0.775 –1HORVU.MC |
| 0.903589215 | 0.942593981 | 16 | 1 KQJ95203 0.884 –0HORVU.MC |
| 0.919144661 | 0.968771527 | 16 | 0 KQJ86430 0.960 0.HORVU.MC |
| 0.902162143 | 0.956973722 | 16 | 3 KQJ94249 0.903 0.HORVU.MC |
| 0.893269819 | 0.94322008 | 16 | 0 KQK07787 0.855 –HORVU.MC |
| 0.895742803 | 0.954372624 | 16 | 1 KQK06153 0.922 0HORVU.MC |
| 0.824347908 | 0.883364974 | 16 | 4 KQK22246 0.831 0HORVU.MC |
| 0.952563892 | 0.991700222 | 16 | 1 KQK15352 0.954 0HORVU.MC |
| 0.880229186 | 0.949081203 | 16 | 0 KQJ85787 0.773 –1genblast_C |

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| 0.828146777 | 0.947909408 | 16 | 1 KQK03874 0.726 – | HORVU.MC |
| 0.943681144 | 0.980959052 | 16 | 0 PNT70505 0.903 – | HORVU.MC |
| 0.834600028 | 0.961613897 | 16 | 0 KQK05680 0.769 – | HORVU.MC |
| 0.974276192 | 1.004582379 | 16 | 0 KQJ85531 1.001 0. | HORVU.MC |
| 0.867393443 | 0.935081967 | 16 | 0 PNT67848 0.782 – | HORVU.MC |
| 0.908097409 | 0.977543186 | 16 | 0 KQK15291 0.921 0 | HORVU.MC |
| 0.850994875 | 0.928549894 | 16 | 1 PNT64350 0.808 – | HORVU.MC |
| 0.856191899 | 0.921115538 | 16 | 1 KQK22579 0.846 – | HORVU.MC |
| 0.904692918 | 0.979558314 | 16 | 0 KQK04149 0.980 1 | HORVU.MC |
| 0.896693187 | 0.964893088 | 16 | 0 PNT71038 0.818 – | HORVU.MC |

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| 0.965682755 | 0.997054709 | 16 | 0 KQK07484 0.981 0 | HORVU.MC |
| 0.914803505 | 0.980499431 | 16 | 3 KQJ92311 0.905 –0 | HORVU.MC |

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| 0.952130229 | 0.984252729 | 16 | 0 KQK23903 0.963 0 | HORVU.MC |
| 0.852406103 | 0.948356808 | 16 | 0 KQK05689 0.712 – | HORVU.MC |
| 0.913007766 | 0.982078853 | 16 | 0 KQK04417 0.944 0 | HORVU.MC |
| 0.960227273 | 0.994539995 | 16 | 0 KQJ84026 0.971 0. | HORVU.MC |

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| 0.785271318 | 0.871035941 | 16 | 0 PNT73763 0.712 – | HORVU.MC |
| 0.958432744 | 1.000386897 | 16 | 0 KQK17819 0.982 0 | HORVU.MC |
| 0.821234441 | 0.904836931 | 16 | 2 KQK17057 0.849 0 | HORVU.MC |
| 0.912767243 | 0.96881596 | 16 | 3 KQK15898 0.938 0 | HORVU.MC |

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| 0.934471972 | 0.995995996 | 16 | 1 KQK00777 0.954 0 | HORVU.MC |

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| 0.911400189 | 0.989025544 | 16 | 0 | KQK13148 | 0.900 | –( | HORVU.MC |
| 0.905203245 | 0.989881368 | 16 | 0 | KQJ85348 | 0.884 | –0 | HORVU.MC |
| 0.801459468 | 0.879007864 | 16 | 0 | KQJ91985 | 0.752 | –0 | HORVU.MC |

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| 0.904779536 | 0.951591063 | 16 | 0 | KQJ88024 | 0.917 | 0.: | genblast_C |
| 0.884294069 | 0.945071011 | 16 | 0 | KQJ93687 | 0.825 | –1 | genblast_C |
| 0.860435052 | 0.946497518 | 16 | 0 | KQJ91257 | 0.815 | –0 | HORVU.MC |
| 0.827514734 | 0.914544002 | 16 | 9 | KQK21169 | 0.731 | – | HORVU.MC |
| 0.907596553 | 0.977338015 | 16 | 0 | KQK00288 | 0.898 | –( | genblast_C |
| 0.822718922 | 0.907532149 | 16 | 0 | KQK08903 | 0.746 | – | HORVU.MC |
| 0.954957018 | 1.001972943 | 16 | 0 | PNT72757 | 0.979 | 0. | HORVU.MC |
| 0.867362648 | 0.944630872 | 16 | 2 | KQK13228 | 0.880 | 0 | HORVU.MC |
| 0.946296739 | 0.976736775 | 16 | 1 | KQK23179 | 0.972 | 0 | HORVU.MC |
| 0.91093977 | 0.97723656 | 16 | 1 | PNT70046 | 0.861 | –( | HORVU.MC |
| 0.834749865 | 0.933807637 | 16 | 1 | KQJ83954 | 0.777 | –0 | HORVU.MC |
| 0.95510856 | 0.996883441 | 16 | 1 | KQJ85369 | 0.903 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.861569929 | 0.948903983 | 16 | 1 | KQJ97384 | 0.804 | –0 | HORVU.MC |
| 0.94750342 | 0.993342453 | 16 | 0 | PNT73219 | 0.973 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.945503499 | 0.978438662 | 16 | 2 | PNT69106 | 0.925 | –( | HORVU.MC |
| 0.893051197 | 0.970013947 | 16 | 0 | KQJ97902 | 0.918 | 0. | HORVU.MC |

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| 0.928719176 | 0.970149254 | 16 | 0 KQK12285 0.954 0. | HORVU.MC |
| 0.915327712 | 0.961925973 | 16 | 0 genblast_Os03t019 | HORVU.MC |
| 0.95509195 | 0.991811242 | 16 | 0 KQK17529 0.966 0. | HORVU.MC |
|  |  |  |  |  |
| 0.838200634 | 0.911381556 | 16 | 0 PNT69819 0.821 – | HORVU.MC |
| 0.922947132 | 0.96287964 | 16 | 0 KQJ90447 0.878 –0 | HORVU.MC |
| 0.9282791 | 0.96484885 | 16 | 0 KQJ90247 0.946 0. | HORVU.MC |
| 0.947669778 | 0.979123173 | 16 | 0 PNT66780 0.955 0. | HORVU.MC |
| 0.952831482 | 0.992982969 | 16 | 0 KQJ95791 0.963 0. | HORVU.MC |
|  |  |  |  |  |
| 0.887187407 | 0.98987794 | 16 | 2 KQJ93926 0.902 0. | HORVU.MC |
| 0.904247573 | 0.980906149 | 16 | 0 KQK13902 0.902 – | HORVU.MC |
| 0.850075248 | 0.968541653 | 16 | 6 genblast_Os02t077 | HORVU.MC |
| 0.911901846 | 0.981537302 | 16 | 0 KQJ96930 0.710 –2 | HORVU.MC |
| 0.85448288 | 0.940169432 | 16 | 0 KQK23106 0.804 – | HORVU.MC |
| 0.904202949 | 0.99234778 | 16 | 3 PNT67066 0.886 – | HORVU.MC |
| 0.836689331 | 0.919979079 | 16 | 0 KQJ91069 0.770 –1 | HORVU.MC |
| 0.817125451 | 0.8877858 | 16 | 0 KQK05562 0.726 – | genblast_C |
| 0.953254572 | 0.996024083 | 16 | 1 KQK08523 0.989 0. | HORVU.MC |
| 0.934942991 | 0.993829645 | 16 | 1 KQJ96871 0.931 –0 | HORVU.MC |
| 0.838906267 | 0.926138243 | 16 | 5 KQK24103 0.832 – | HORVU.MC |
| 0.830152124 | 0.917336395 | 16 | 0 KQJ95109 0.762 –0 | HORVU.MC |
|  |  |  |  |  |
| 0.879782549 | 0.941508395 | 16 | 2 KQK05019 0.892 0. | HORVU.MC |
| 0.932960364 | 0.98035274 | 16 | 1 KQJ97029 0.931 –0 | HORVU.MC |
| 0.901518723 | 0.986395474 | 16 | 0 KQK21468 0.918 0. | genblast_C |
| 0.962667195 | 1.006599789 | 16 | 1 KQK01093 0.954 – | HORVU.MC |
|  |  |  |  |  |
| 0.963686754 | 0.998626113 | 16 | 1 KQK08736 0.980 0. | HORVU.MC |
|  |  |  |  |  |
| 0.822580353 | 0.926017084 | 16 | 1 PNT77542 0.719 –1 | HORVU.MC |
| 0.931875946 | 0.986588795 | 16 | 0 KQJ94320 0.947 0. | genblast_C |
| 0.863361418 | 0.964582332 | 16 | 3 KQJ98302 0.866 0. | genblast_C |

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| 0.929855005 | 0.987197285 | 16 | 1 KQK19929 0.911 – | HORVU.MC |
| 0.966701717 | 0.989685043 | 16 | 1 KQK22526 0.947 – | HORVU.MC |
| 0.879214418 | 0.966845407 | 16 | 1 KQK17960 0.900 0 | HORVU.MC |
| 0.906660441 | 0.975780214 | 16 | 0 PNT60617 0.931 0. | HORVU.MC |
| 0.818925439 | 0.922631579 | 16 | 4 KQK01724 0.858 0 | genblast_C |
| 0.931526446 | 0.987472935 | 16 | 1 KQJ81427 0.932 0. | HORVU.MC |
| 0.931798205 | 0.972612879 | 16 | 0 KQK05930 0.932 0 | HORVU.MC |

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| 0.878550794 | 0.986037554 | 16 | 1 KQJ87107 0.845 –0 | HORVU.MC |
| 0.868763934 | 0.96872614 | 16 | 5 genblast_Os07t057 | HORVU.MC |
| 0.958953901 | 1.002304965 | 16 | 0 KQK19461 0.986 0 | HORVU.MC |
| 0.82871975 | 0.898726998 | 16 | 5 KQJ99828 0.811 –0 | HORVU.MC |
| 0.945938581 | 0.98105548 | 16 | 0 KQK09282 0.964 0 | HORVU.MC |

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| 0.841974374 | 0.912106538 | 16 | 0 KQK23909 0.756 – | HORVU.MC |
| 0.930182954 | 0.978950197 | 16 | 2 KQK00171 0.926 – | genblast_C |

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| 0.895944878 | 0.978035413 | 16 | 0 KQJ99486 0.933 0. | HORVU.MC |
| 0.949204665 | 0.991327765 | 16 | 1 KQJ85257 0.962 0. | HORVU.MC |
| 0.951587282 | 0.987094868 | 16 | 1 KQJ98946 0.954 0. | HORVU.MC |
| 0.926997168 | 0.974195289 | 16 | 0 PNT77346 0.943 0. | HORVU.MC |
| 0.929147761 | 0.972482436 | 16 | 0 KQJ88842 0.940 0. | HORVU.MC |
| 0.919106942 | 0.964117979 | 16 | 0 KQK09203 0.902 – | HORVU.MC |
| 0.860005832 | 0.933339315 | 16 | 1 KQK14469 0.770 – | HORVU.MC |
| 0.800665212 | 0.908489371 | 16 | 1 KQJ81982 0.781 –0 | HORVU.MC |
| 0.866594944 | 0.929424422 | 16 | 2 KQJ98238 0.904 0. | HORVU.MC |
| 0.977223771 | 1.004054739 | 16 | 0 KQK05899 0.994 0 | HORVU.MC |
| 0.84037493 | 0.886215258 | 16 | 0 KQJ94147 0.886 1. | HORVU.MC |

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| 0.909100332 | 0.950580431 | 16 | 1 genblast_Os09t048 | HORVU.MC |
| 0.94600482 | 0.985446793 | 16 | 1 KQK20769 0.925 – | HORVU.MC |

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| 0.937051387 | 0.984339315 | 16 | 1 KQK22640 0.880 – | HORVU.MC |

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|---|---|---|---|---|
| 0.861047892 | 0.933900653 | 16 | 1 KQK21365 0.801 – | HORVU.MC |
| 0.922430214 | 0.975254534 | 16 | 1 PNT68172 0.963 0. | HORVU.MC |
| 0.902833333 | 0.975466667 | 16 | 0 KQK22287 0.975 0 | HORVU.MC |
| 0.930021994 | 0.979081134 | 16 | 0 KQK04606 0.914 – | HORVU.MC |
| 0.922882946 | 0.968801314 | 16 | 0 genblast_Os11t010 | HORVU.MC |
| 0.831349635 | 0.941947566 | 16 | 9 KQK02134 0.706 – | HORVU.MC |
| 0.774394763 | 0.89486166 | 16 | 0 KQJ94687 0.710 –1 | HORVU.MC |
| 0.915425139 | 0.962735675 | 16 | 1 KQK03357 0.958 0 | HORVU.MC |
| 0.915739105 | 0.984452297 | 16 | 1 KQK01513 0.949 0 | genblast_C |
| 0.925192141 | 0.977720626 | 16 | 4 KQK04270 0.964 0 | HORVU.MC |
| 0.858147131 | 1.006248817 | 16 | 0 KQK24084 0.773 – | HORVU.MC |
| 0.874676836 | 0.960186143 | 16 | 0 KQK13227 0.847 – | genblast_C |
| 0.877316795 | 0.964071856 | 16 | 4 KQJ92183 0.840 –0 | HORVU.MC |
| 0.927420457 | 0.978569867 | 16 | 2 KQJ82605 0.941 0. | HORVU.MC |
| 0.966990956 | 0.998095918 | 16 | 0 KQJ98563 0.968 0. | HORVU.MC |
| 0.829309857 | 0.929313715 | 16 | 1 KQJ97809 0.742 –1 | HORVU.MC |
| 0.851386586 | 0.931663467 | 16 | 2 PNT65760 0.823 –( | genblast_C |
| 0.924199595 | 0.996072364 | 16 | 1 KQJ83378 0.928 0. | HORVU.MC |
| 0.87655095 | 0.960665259 | 16 | 1 KQJ99290 0.735 –1 | HORVU.MC |
| 0.841549556 | 0.891863905 | 16 | 0 KQK10466 0.810 – | HORVU.MC |
| 0.849512079 | 0.959236624 | 16 | 6 genblast_Os10t054 | HORVU.MC |
| 0.925203646 | 0.988828549 | 16 | 0 KQK14762 0.966 0 | HORVU.MC |
| 0.876229546 | 0.989887847 | 16 | 2 KQK14722 0.865 – | HORVU.MC |
| 0.845441376 | 0.926026384 | 16 | 0 KQK23679 0.790 – | HORVU.MC |

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| 0.969207756 | 1.002241255 | 16 | 2 | PNT64610 | 0.982 0. | HORVU.MC |
| 0.955988746 | 0.987485878 | 16 | 0 | KQK13001 | 0.951 –( | HORVU.MC |

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| 0.896728905 | 0.983922463 | 16 | 1 | KQK16841 | 0.881 –( | HORVU.MC |

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| 0.819355822 | 0.892089706 | 16 | 2 | KQK17908 | 0.777 –( | HORVU.MC |
| 0.840242578 | 0.942070963 | 16 | 0 | KQK02190 | 0.789 –( | HORVU.MC |
| 0.9168992 | 0.990418807 | 16 | 1 | KQK12386 | 0.892 –( | genblast_C |

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| 0.836005577 | 0.928546532 | 16 | 0 | PNT61174 | 0.812 –( | HORVU.MC |
| 0.885999588 | 0.956964114 | 16 | 2 | KQK17365 | 0.894 0. | HORVU.MC |

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| 0.958790735 | 0.998895333 | 16 | 0 | KQJ83757 | 0.989 0. | HORVU.MC |
| 0.917691304 | 0.973073224 | 16 | 1 | KQK20859 | 0.936 0. | HORVU.MC |
| 0.916979362 | 0.981238274 | 16 | 1 | PNT69567 | 0.935 0. | HORVU.MC |
| 0.924928257 | 0.974372664 | 16 | 0 | KQJ93127 | 0.940 0. | HORVU.MC |
| 0.949095514 | 0.99880091 | 16 | 3 | KQJ82123 | 0.978 0. | HORVU.MC |
| 0.901581701 | 0.947196621 | 16 | 0 | KQJ97405 | 0.923 0. | HORVU.MC |
| 0.954965693 | 0.987051372 | 16 | 2 | PNT60923 | 0.935 –( | HORVU.MC |

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| 0.836399168 | 0.959839357 | 16 | 1 | KQK05022 | 0.728 | – | HORVU.MC |
| 0.850356831 | 0.943280977 | 16 | 1 | KQK08622 | 0.747 | – | genblast_C |
| 0.843534185 | 0.912724448 | 16 | 7 | KQK15655 | 0.848 | 0 | genblast_C |
| 0.813983299 | 0.874011134 | 16 | 1 | PNT72100 | 0.740 | – | HORVU.MC |
| 0.882636436 | 0.942745767 | 16 | 0 | KQK15152 | 0.920 | 0. | HORVU.MC |

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| 0.929464186 | 0.969061764 | 16 | 1 | KQK17701 | 0.873 | – | HORVU.MC |
| 0.88399576 | 0.966613672 | 16 | 0 | PNT74401 | 0.872 | – | HORVU.MC |
| 0.836502621 | 0.900291206 | 16 | 0 | KQJ89215 | 0.705 | –2 | HORVU.MC |
| 0.945170391 | 0.976644958 | 16 | 0 | KQJ91634 | 0.960 | 0. | HORVU.MC |
| 0.791535505 | 0.883078504 | 16 | 11 | PNT64454 | 0.727 | – | HORVU.MC |
| 0.916549174 | 0.967349362 | 16 | 0 | KQK10721 | 0.912 | – | HORVU.MC |
| 0.831631918 | 0.944369716 | 16 | 8 | PNT72797 | 0.710 | – | HORVU.MC |
| 0.911330487 | 0.962646745 | 16 | 0 | KQK16492 | 0.935 | 0 | genblast_Z |

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| 0.969115109 | 1.004514073 | 16 | 0 | KQJ92978 | 0.960 | –0 | HORVU.MC |
| 0.834754189 | 0.942629887 | 16 | 1 | PNT69111 | 0.855 | 0. | HORVU.MC |

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| 0.800617799 | 0.946735395 | 16 | 2 | KQK05598 | 0.736 | – | HORVU.MC |

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| 0.940234023 | 0.983618362 | 16 | 0 KQJ89764 0.951 0. | HORVU.MC |
| 0.920129981 | 0.951000513 | 16 | 0 KQK07336 0.900 – | HORVU.MC |
| 0.916469675 | 0.953677173 | 16 | 0 genblast_Os07t025 | HORVU.MC |
| 0.879089027 | 0.960248447 | 16 | 0 KQK13827 0.882 0 | HORVU.MC |
| 0.857875067 | 0.930863425 | 16 | 3 KQJ89164 0.878 0. | HORVU.MC |
| 0.913911938 | 0.981798715 | 16 | 0 KQK10892 0.940 0 | HORVU.MC |
| 0.923643124 | 0.980024147 | 16 | 1 KQK09146 0.951 0 | HORVU.MC |
| 0.895788405 | 0.953824686 | 16 | 1 KQJ94889 0.841 –1 | HORVU.MC |
| 0.848976904 | 0.916855754 | 16 | 7 PNT69893 0.913 1. | HORVU.MC |
| 0.841668135 | 0.931265421 | 16 | 0 KQK12814 0.817 – | HORVU.MC |
| 0.917372881 | 0.981155219 | 16 | 0 KQJ85889 0.939 0. | HORVU.MC |
| 0.894559391 | 0.964209556 | 16 | 0 KQK14050 0.927 0 | HORVU.MC |

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| 0.85938358 | 0.95332235 | 16 | 0 | KQK01523 0.779 – | HORVU.MC |
| 0.907426512 | 0.968682872 | 16 | 1 | KQK05859 0.928 0 | HORVU.MC |
| 0.908764368 | 0.966091954 | 16 | 1 | KQK20293 0.906 – | HORVU.MC |
| 0.932511376 | 0.988193334 | 16 | 0 | KQJ98224 0.965 0. | genblast_C |
| 0.905514904 | 0.971269528 | 16 | 0 | KQK09979 0.941 0 | HORVU.MC |
| 0.923607112 | 0.991265956 | 16 | 2 | KQK00113 0.950 0 | HORVU.MC |
| 0.868305806 | 0.943228943 | 16 | 1 | genblast_Os06t072 | HORVU.MC |
| 0.904883519 | 0.961798213 | 16 | 1 | KQJ89010 0.938 0. | HORVU.MC |
| 0.96286831 | 1.013229104 | 16 | 0 | KQJ99154 0.984 0. | genblast_C |
| 0.908182106 | 1.016037139 | 16 | 0 | KQJ93284 0.907 –0 | HORVU.MC |
| 0.897792465 | 0.949727939 | 16 | 1 | KQK17564 0.889 – | HORVU.MC |
| 0.906443974 | 0.980405781 | 16 | 4 | KQK09298 0.960 0 | HORVU.MC |
| 0.925644479 | 0.967423368 | 16 | 0 | KQK04063 0.942 0 | HORVU.MC |
| 0.84994195 | 0.928018576 | 16 | 1 | KQJ88837 0.703 –2 | HORVU.MC |
| 0.923040404 | 0.972437242 | 16 | 3 | KQJ90398 0.880 –0 | HORVU.MC |
| 0.839527027 | 0.92194781 | 16 | 2 | KQJ88151 0.872 0. | HORVU.MC |
| 0.953037938 | 0.993772534 | 16 | 0 | PNT73444 0.940 – | HORVU.MC |

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| 0.907471555 | 0.969962073 | 16 | 2 | KQJ95949 0.903 –0 | HORVU.MC |
| 0.917331407 | 0.944867629 | 16 | 0 | KQJ97723 0.909 –0 | HORVU.MC |
| 0.851730118 | 0.916518793 | 16 | 0 | KQJ89130 0.834 –0 | HORVU.MC |
| 0.915006499 | 0.973663389 | 16 | 0 | KQJ85740 0.915 0. | HORVU.MC |

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| 0.881971369 | 0.933492395 | 16 | 5 | KQK20602 0.863 – | HORVU.MC |
| 0.935878254 | 1.002271536 | 16 | 3 | KQJ89165 0.955 0. | HORVU.MC |
| 0.937073541 | 0.987869598 | 16 | 1 | genblast_Os06t014 | HORVU.MC |

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| 0.92566165 | 0.977685522 | 16 | 0 | KQK09515 0.929 0 | HORVU.MC |
| 0.885291582 | 0.931637142 | 16 | 2 | KQK20063 0.878 – | HORVU.MC |
| 0.895100352 | 0.970734048 | 16 | 3 | KQK20873 0.706 – | HORVU.MC |
| 0.892838515 | 0.974337576 | 16 | 1 | KQK05383 0.869 – | HORVU.MC |
| 0.841713367 | 0.944746831 | 16 | 7 | KQK22859 0.807 – | HORVU.MC |
| 0.84805778 | 0.931183726 | 16 | 0 | KQK10195 0.702 – | HORVU.MC |
| 0.80097716 | 0.986578761 | 16 | 1 | KQK02309 0.731 – | HORVU.MC |

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| 0.913958574 | 0.964719491 | 16 | 1 | KQK02840 0.891 – | HORVU.MC |
| 0.810570266 | 0.93684506 | 16 | 11 | genblast_Os12t011 | HORVU.MC |
| 0.919189816 | 0.969401876 | 16 | 0 | KQJ85359 0.921 0. | HORVU.MC |

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| 0.91481838 | 0.980917308 | 16 | 0 | KQJ90007 | 0.873 | –0 | HORVU.MC |
| 0.875289271 | 0.937868163 | 16 | 0 | KQJ96122 | 0.923 | 0. | HORVU.MC |
| 0.910160879 | 0.971083195 | 16 | 1 | PNT70976 | 0.933 | 0. | HORVU.MC |
| 0.848091844 | 0.907253699 | 16 | 0 | PNT75365 | 0.701 | –2 | HORVU.MC |
| 0.799077851 | 0.889164746 | 16 | 0 | KQJ85141 | 0.703 | –1 | HORVU.MC |
| 0.94972083 | 1.013217867 | 16 | 0 | KQK03773 | 0.920 | – | HORVU.MC |
| 0.85554356 | 0.924521217 | 16 | 0 | KQK20185 | 0.881 | 0. | HORVU.MC |
| 0.858460231 | 0.958900059 | 16 | 0 | KQK03190 | 0.796 | – | HORVU.MC |
| 0.859462564 | 0.934767989 | 16 | 0 | KQK22649 | 0.770 | – | HORVU.MC |
| 0.939843332 | 1.000357079 | 16 | 2 | KQK13698 | 0.999 | 0 | HORVU.MC |
| 0.894650959 | 0.96490327 | 16 | 2 | KQK19268 | 0.830 | – | HORVU.MC |
| 0.861225252 | 0.934752833 | 16 | 1 | KQK10102 | 0.843 | – | HORVU.MC |
| 0.954321702 | 0.996393886 | 16 | 3 | KQJ94656 | 0.972 | 0. | HORVU.MC |

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| 0.958870609 | 0.996146435 | 16 | 0 | KQK18873 0.974 0 | HORVU.MC |
| 0.836262759 | 0.914182111 | 16 | 1 | KQJ82028 0.701 -2 | HORVU.MC |
| 0.894208967 | 0.968695143 | 16 | 2 | KQK20780 0.906 0 | genblast_C |
| 0.812183198 | 0.950625782 | 16 | 9 | PNT71230 0.849 0. | genblast_C |
| 0.95850271 | 1.003899795 | 16 | 0 | KQJ94492 0.962 0. | HORVU.MC |
| 0.933875845 | 0.991462113 | 16 | 0 | genblast_Os01t075 | HORVU.MC |
| 0.923137851 | 0.963662227 | 16 | 0 | KQJ92221 0.950 0. | HORVU.MC |
| 0.869981347 | 0.919079766 | 16 | 0 | KQK21562 0.836 - | HORVU.MC |
| 0.875743978 | 0.983503609 | 16 | 2 | KQK03427 0.873 - | HORVU.MC |
| 0.89249625 | 0.979998333 | 16 | 4 | KQJ85417 0.866 -0 | HORVU.MC |
| 0.958308195 | 0.989341378 | 16 | 1 | KQK14517 0.981 0 | HORVU.MC |
| 0.904693046 | 0.957670567 | 16 | 0 | KQK00723 0.945 0 | HORVU.MC |
| 0.952978774 | 0.986437 | 16 | 0 | KQK15624 0.974 0 | HORVU.MC |
| 0.952066442 | 0.996770647 | 16 | 1 | KQJ81920 0.982 0. | HORVU.MC |
| 0.803441737 | 0.902517753 | 16 | 1 | KQK01812 0.713 - | genblast_C |
| 0.842085535 | 0.928602028 | 16 | 0 | KQJ85668 0.794 -0 | HORVU.MC |
| 0.897037602 | 0.948720094 | 16 | 3 | KQJ96023 0.946 0. | HORVU.MC |
| 0.945237933 | 0.987819289 | 16 | 0 | KQK11014 0.953 0 | HORVU.MC |
| 0.872710022 | 0.935395503 | 16 | 2 | KQK20509 0.864 - | genblast_C |
| 0.881781238 | 0.958871915 | 16 | 0 | KQK23638 0.700 - | HORVU.MC |
| 0.862877788 | 0.9375 | 16 | 0 | KQJ89567 0.700 -2 | HORVU.MC |

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| 0.871061394 | 0.951599805 | 16 | 0 | KQK14788 | 0.700 | – | HORVU.MC |
| 0.859680375 | 0.929967427 | 16 | 0 | KQJ84169 | 0.700 | –2 | HORVU.MC |
| 0.911733432 | 0.972978984 | 16 | 2 | KQK07346 | 0.943 | 0. | HORVU.MC |
| 0.838217845 | 0.909112482 | 16 | 0 | KQJ97960 | 0.775 | –1 | genblast_C |
| 0.896174531 | 0.982825779 | 16 | 4 | KQK04945 | 0.931 | 0. | HORVU.MC |
| 0.878260453 | 0.962025316 | 16 | 0 | KQK22354 | 0.898 | 0. | HORVU.MC |
| 0.892690418 | 0.958498995 | 16 | 12 | KQJ90286 | 0.884 | –0 | HORVU.MC |

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| 0.81855168 | 0.904495256 | 16 | 3 | PNT76831 | 0.836 | 0. | HORVU.MC |
| 0.845653422 | 0.903582912 | 16 | 5 | KQK16875 | 0.870 | 0. | HORVU.MC |
| 0.864708907 | 0.936746561 | 16 | 1 | KQK14165 | 0.837 | – | HORVU.MC |
| 0.895317883 | 0.964453492 | 16 | 0 | KQK06102 | 0.893 | – | HORVU.MC |
| 0.90396954 | 0.967465975 | 16 | 0 | PNT75463 | 0.891 | – | HORVU.MC |
| 0.909440793 | 1.004546802 | 16 | 4 | KQJ91336 | 0.932 | 0. | HORVU.MC |
| 0.803557633 | 0.865883807 | 16 | 1 | KQK16869 | 0.699 | – | HORVU.MC |
| 0.938244674 | 0.996509809 | 16 | 0 | PNT68733 | 0.955 | 0. | HORVU.MC |

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| 0.894638781 | 0.945078555 | 16 | 0 | KQK21440 | 0.911 | 0 | HORVU.MC |
| 0.923695718 | 0.965451223 | 16 | 0 | KQK06087 | 0.919 | – | HORVU.MC |
| 0.924907197 | 0.969101365 | 16 | 2 | PNT64147 | 0.952 | 0. | HORVU.MC |
| 0.955858748 | 1 | 16 | 0 | KQJ90999 | 0.990 | 0. | genblast_C |
| 0.901713872 | 0.991792726 | 16 | 1 | KQK07071 | 0.914 | 0 | HORVU.MC |
| 0.825302971 | 0.934844931 | 16 | 4 | PNT71733 | 0.845 | 0. | HORVU.MC |
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| 0.798763736 | 0.896367521 | 16 | 0 | KQK11758 | 0.811 | 0 | HORVU.MC |

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| 0.91528587 | 0.993687788 | 16 | 1 | KQK23431 | 0.970 | 0 | HORVU.MC |
| 0.912391653 | 0.972489165 | 16 | 1 | KQK04549 | 0.927 | 0 | HORVU.MC |
| 0.940359125 | 0.992848335 | 16 | 0 | KQK03055 | 0.933 | – | HORVU.MC |
| 0.931476563 | 0.983875 | 16 | 2 | KQJ83669 | 0.961 | 0. | HORVU.MC |
| 0.858041432 | 0.976342962 | 16 | 4 | KQJ91701 | 0.824 | –0 | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.859180606 | 0.968271921 | 16 | 7 | PNT66672 | 0.851 | –( | HORVU.MC |
| 0.829331754 | 0.97100201 | 16 | 0 | KQJ90625 | 0.699 | –1 | HORVU.MC |
| 0.900122479 | 0.969921385 | 16 | 1 | genblast_Zm00001 |  |  | HORVU.MC |
| 0.907408009 | 0.968924717 | 16 | 0 | KQK23882 | 0.850 | – | HORVU.MC |
| 0.85844002 | 0.907200453 | 16 | 0 | KQK03217 | 0.835 | – | HORVU.MC |

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| 0.940563289 | 0.985411848 | 16 | 0 | KQK06589 | 0.973 | 0 | HORVU.MC |
| 0.936825288 | 0.993299417 | 16 | 1 | KQJ99315 | 0.971 | 0. | HORVU.MC |
| 0.954795391 | 0.994654749 | 16 | 1 | KQK20978 | 0.934 | – | HORVU.MC |
| 0.900040636 | 0.94759137 | 16 | 0 | PNT61679 | 0.894 | –( | HORVU.MC |
| 0.937703508 | 0.982017317 | 16 | 0 | KQK17323 | 0.979 | 0 | HORVU.MC |
| 0.895723915 | 0.94047619 | 16 | 0 | KQK20029 | 0.891 | – | HORVU.MC |

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| 0.85785349 | 0.978657181 | 16 | 3 | PNT61952 | 0.863 | 0. | HORVU.MC |
| 0.905382272 | 0.961050383 | 16 | 1 | PNT61130 | 0.837 | – | HORVU.MC |
| 0.916389844 | 0.98011522 | 16 | 2 | KQK09949 | 0.929 | 0 | HORVU.MC |
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| 0.944979606 | 0.989586045 | 16 | 1 | KQK22730 | 0.981 | 0 | genblast_C |
| 0.882021761 | 0.95951417 | 16 | 0 | PNT71245 | 0.896 | 0. | HORVU.MC |
| | | | | | | | |
| 0.854596427 | 0.952686096 | 16 | 0 | KQK01707 | 0.698 | – | HORVU.MC |
| 0.889582699 | 0.976545842 | 16 | 0 | KQK01584 | 0.698 | – | HORVU.MC |
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| 0.923362655 | 0.990981668 | 16 | 0 | KQK19728 | 0.945 | 0 | HORVU.MC |
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| 0.863887223 | 0.963697809 | 16 | 1 | KQJ84208 | 0.856 | –0 | HORVU.MC |
| 0.897244479 | 0.97374091 | 16 | 1 | KQJ94209 | 0.935 | 0. | genblast_C |
| 0.944405634 | 0.982025527 | 16 | 1 | KQJ98476 | 0.962 | 0. | HORVU.MC |
| | | | | | | | |
| 0.853654427 | 0.934161085 | 16 | 4 | KQK23112 | 0.832 | – | genblast_C |
| 0.921601423 | 0.977224199 | 16 | 2 | PNT70978 | 0.921 | – | HORVU.MC |
| 0.905739331 | 0.999159585 | 16 | 0 | KQK11183 | 0.873 | – | HORVU.MC |
| 0.821941827 | 0.954331279 | 16 | 0 | KQK20490 | 0.697 | – | HORVU.MC |
| 0.935801397 | 0.996925358 | 16 | 3 | KQK09984 | 0.980 | 0 | HORVU.MC |
| 0.937325545 | 0.97502286 | 16 | 0 | KQK03517 | 0.975 | 0 | HORVU.MC |
| 0.938297125 | 0.985948984 | 16 | 0 | KQJ97655 | 0.856 | –1 | HORVU.MC |
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| 0.93482467 | 1.004586279 | 16 | 1 | KQJ87177 | 0.877 | –0 | HORVU.MC |
| 0.891879252 | 0.976643991 | 16 | 1 | KQK09755 | 0.904 | 0 | HORVU.MC |
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| 0.936007795 | 0.980519673 | 16 | 2 | KQJ81850 | 0.970 | 0. | HORVU.MC |
| 0.932509968 | 0.984976077 | 16 | 2 | KQJ89166 | 0.936 | 0. | genblast_C |

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| 0.860984026 | 0.94633995 | 16 | 1 KQJ88720 0.697 –2 | HORVU.MC |
| 0.935998601 | 0.988416388 | 16 | 1 KQK10527 0.960 0 | HORVU.MC |
| 0.894140305 | 0.966730297 | 16 | 0 KQK02342 0.906 0 | HORVU.MC |
| 0.903967218 | 0.967724331 | 16 | 1 KQK02411 0.950 0 | HORVU.MC |
| | | | | |
| 0.865048017 | 0.954460967 | 16 | 3 KQJ88915 0.771 –1 | HORVU.MC |
| 0.896894244 | 0.959379441 | 16 | 0 KQK13435 0.882 – | HORVU.MC |
| 0.925901657 | 0.9789264 | 16 | 0 PNT71481 0.946 0. | HORVU.MC |
| | | | | |
| 0.954845494 | 0.987506247 | 16 | 1 KQK12535 0.973 0 | HORVU.MC |
| 0.924302539 | 0.975943869 | 16 | 0 KQK21323 0.934 0 | HORVU.MC |
| 0.810045346 | 0.900764503 | 16 | 0 KQK14319 0.697 – | HORVU.MC |
| 0.877696527 | 0.979211282 | 16 | 2 KQK19009 0.957 0 | genblast_C |
| 0.816248087 | 0.921524976 | 16 | 0 KQJ87858 0.753 –0 | HORVU.MC |
| 0.942446099 | 0.988659023 | 16 | 1 KQK01341 0.943 0 | HORVU.MC |
| 0.9427429 | 0.989158663 | 16 | 1 KQJ98790 0.898 –0 | HORVU.MC |
| 0.908111979 | 0.981458333 | 16 | 5 KQK15235 0.909 0 | HORVU.MC |
| | | | | |
| 0.910976936 | 0.965709312 | 16 | 2 KQK00973 0.872 – | HORVU.MC |
| | | | | |
| 0.875165822 | 0.950533577 | 16 | 6 genblast_Os06t012 | HORVU.MC |
| 0.911640664 | 0.974572093 | 16 | 2 KQJ87110 0.926 0. | HORVU.MC |
| 0.810409043 | 0.871406168 | 16 | 0 KQJ92040 0.777 –0 | genblast_C |
| 0.917309756 | 0.964014526 | 16 | 2 KQK23601 0.950 0 | HORVU.MC |
| 0.946587028 | 0.9875587 | 16 | 0 KQK22599 0.970 0 | HORVU.MC |
| 0.868048511 | 0.960680084 | 16 | 4 KQJ91751 0.728 –2 | HORVU.MC |
| | | | | |
| 0.909879867 | 0.983595692 | 16 | 0 KQK04515 0.884 – | HORVU.MC |
| 0.887426594 | 0.960151007 | 16 | 1 KQK17536 0.893 0 | HORVU.MC |
| 0.819293015 | 0.945826235 | 16 | 1 genblast_Os07t066 | HORVU.MC |
| | | | | |
| 0.942507264 | 0.99211291 | 16 | 0 KQJ82539 0.966 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.845393465 | 0.889791183 | 16 | 0 | KQJ89282 | 0.813 | -0 | HORVU.MC |
| 0.858848222 | 0.905060368 | 16 | 1 | KQK18773 | 0.866 | 0 | genblast_C |
| 0.903856499 | 0.96294802 | 16 | 0 | KQK08784 | 0.909 | 0 | HORVU.MC |
| 0.906710914 | 0.969174041 | 16 | 1 | KQJ85243 | 0.880 | -0 | HORVU.MC |
| 0.840506023 | 0.921921475 | 16 | 1 | KQJ88916 | 0.767 | -1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.948913704 | 0.99680948 | 16 | 4 | KQK00883 | 0.966 | 0 | HORVU.MC |
| 0.893187229 | 0.961069878 | 16 | 3 | KQJ82644 | 0.891 | -0 | HORVU.MC |
| 0.935530701 | 0.98666936 | 16 | 0 | KQK09276 | 0.903 | - | HORVU.MC |
| 0.904657123 | 0.985224461 | 16 | 3 | KQK03081 | 0.875 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.927675823 | 0.987018201 | 16 | 0 | KQK13520 | 0.930 | 0 | HORVU.MC |
| 0.875228549 | 0.937704062 | 16 | 1 | KQK13249 | 0.870 | - | HORVU.MC |
| 0.834844987 | 0.913258575 | 16 | 0 | KQJ88522 | 0.695 | -2 | HORVU.MC |
| 0.914193645 | 0.97146283 | 16 | 0 | KQK10317 | 0.841 | - | HORVU.MC |
| 0.821240844 | 0.896771568 | 16 | 9 | KQJ95318 | 0.695 | -1 | HORVU.MC |
| 0.879790088 | 0.998737374 | 16 | 1 | PNT64691 | 0.967 | 0. | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.946028435 | 1.000618142 | 16 | 0 | KQJ86466 | 0.945 | -0 | HORVU.MC |
| 0.88282649 | 0.965592223 | 16 | 1 | KQJ96119 | 0.863 | -0 | HORVU.MC |
| 0.938476563 | 0.985383065 | 16 | 1 | KQK00095 | 0.940 | 0 | HORVU.MC |
| 0.932198365 | 0.970020723 | 16 | 1 | KQK18000 | 0.928 | - | HORVU.MC |
| 0.956188177 | 0.992557701 | 16 | 2 | KQK02979 | 0.951 | - | HORVU.MC |
| 0.898264189 | 0.981129358 | 16 | 0 | KQK16691 | 0.874 | - | HORVU.MC |
| 0.901076667 | 0.974133333 | 16 | 8 | KQJ81687 | 0.929 | 0. | HORVU.MC |
| 0.949215937 | 0.99287943 | 16 | 1 | KQJ89697 | 0.977 | 0. | HORVU.MC |
| 0.906450486 | 0.975993377 | 16 | 0 | KQK18777 | 0.894 | - | HORVU.MC |
| 0.929064617 | 0.994788953 | 16 | 0 | KQK09628 | 0.976 | 0 | HORVU.MC |
| 0.902198917 | 0.974289581 | 16 | 1 | KQJ95629 | 0.917 | 0. | HORVU.MC |
| 0.908188528 | 0.980692576 | 16 | 0 | KQJ92348 | 0.921 | 0. | HORVU.MC |
| 0.941603435 | 0.994129393 | 16 | 3 | KQK13657 | 0.975 | 0 | HORVU.MC |
| 0.915782637 | 0.985278199 | 16 | 0 | KQK08938 | 0.892 | - | HORVU.MC |
| 0.913689875 | 0.986526543 | 16 | 2 | KQK09631 | 0.951 | 0 | HORVU.MC |
| 0.932964478 | 0.98526273 | 16 | 1 | KQK18483 | 0.975 | 0 | HORVU.MC |
| 0.930912672 | 0.965087752 | 16 | 1 | KQJ86793 | 0.940 | 0. | HORVU.MC |
| 0.809422025 | 0.909712722 | 16 | 0 | KQK02721 | 0.754 | - | genblast_C |
| 0.867026016 | 0.964362081 | 16 | 0 | KQK09253 | 0.904 | 0 | HORVU.MC |
| 0.944499298 | 0.991984085 | 16 | 1 | KQJ92048 | 0.907 | -0 | HORVU.MC |
| 0.787126643 | 0.871923536 | 16 | 0 | PNT76052 | 0.707 | - | HORVU.MC |
| 0.898276892 | 0.967840996 | 16 | 1 | KQJ86683 | 0.940 | 0. | HORVU.MC |
| 0.83463841 | 0.900095785 | 16 | 4 | KQK13151 | 0.862 | 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.947312255 | 0.991869318 | 16 | 1 | KQK01566 0.971 0 | HORVU.MC |
| 0.911142467 | 0.970193301 | 16 | 1 | KQJ90764 0.897 –0 | HORVU.MC |
| 0.916623996 | 0.95588467 | 16 | 0 | genblast_Os04t060 | HORVU.MC |
| 0.951130282 | 0.997212621 | 16 | 1 | KQK14406 0.994 0 | HORVU.MC |
| 0.918780771 | 0.968955142 | 16 | 0 | KQJ93088 0.893 –0 | HORVU.MC |
| 0.903070175 | 0.986329825 | 16 | 5 | KQJ83509 0.960 0. | HORVU.MC |
| 0.865073425 | 0.922725977 | 16 | 0 | KQK00858 0.694 – | HORVU.MC |
| 0.942923938 | 1.005712497 | 16 | 2 | KQK20641 0.975 0 | genblast_C |
| 0.869145143 | 0.967232074 | 16 | 0 | KQJ98537 0.848 –0 | HORVU.MC |
| 0.897114959 | 0.978756362 | 16 | 2 | KQJ94142 0.928 0. | HORVU.MC |
| 0.910830684 | 0.979014308 | 16 | 0 | KQJ86820 0.974 0. | HORVU.MC |
| 0.845758851 | 0.944292065 | 16 | 9 | KQK06588 0.830 – | HORVU.MC |
| 0.811949891 | 0.922178649 | 16 | 1 | KQK04815 0.693 – | HORVU.MC |
| 0.934974137 | 0.990473355 | 16 | 1 | KQK22086 0.959 0 | HORVU.MC |
| 0.920609396 | 0.994282447 | 16 | 2 | KQK03949 0.982 0 | HORVU.MC |
| 0.931587838 | 0.980894688 | 16 | 0 | KQJ82716 0.947 0. | HORVU.MC |
| 0.861579604 | 0.935866053 | 16 | 3 | KQJ98594 0.929 0. | HORVU.MC |
| 0.872688291 | 0.960521273 | 16 | 3 | KQK12121 0.886 0 | HORVU.MC |
| 0.856675219 | 0.940546757 | 16 | 0 | KQJ91415 0.764 –1 | HORVU.MC |
| 0.943751181 | 0.986352474 | 16 | 2 | KQK13027 0.838 – | HORVU.MC |
| 0.875434028 | 0.94593254 | 16 | 1 | KQK01052 0.900 0 | HORVU.MC |
| 0.864012192 | 0.95604877 | 16 | 5 | genblast_Os07t010 | genblast_C |
| 0.881737282 | 0.958351347 | 16 | 0 | KQK17111 0.693 – | HORVU.MC |
| 0.930346734 | 0.97446336 | 16 | 0 | KQK05688 0.902 – | HORVU.MC |
| 0.883520115 | 0.93908046 | 16 | 0 | KQJ99971 0.848 –1 | genblast_C |
| 0.911754307 | 0.969400874 | 16 | 0 | genblast_Os05t034 | HORVU.MC |
| 0.866629857 | 0.957941233 | 16 | 4 | KQK10137 0.900 0 | HORVU.MC |

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|---|---|---|---|---|
| 0.872704384 | 0.929079215 | 16 | 1 KQJ94307 0.821 –1 | HORVU.MC |
| 0.783171375 | 0.864577871 | 16 | 7 KQJ91511 0.812 0. | HORVU.MC |
| 0.844036067 | 0.924935921 | 16 | 0 KQK02524 0.692 – | HORVU.MC |
| 0.910844622 | 0.992642765 | 16 | 2 KQK12471 0.841 – | HORVU.MC |
| 0.846560078 | 0.950581395 | 16 | 3 KQK15484 0.692 – | HORVU.MC |
| 0.852622453 | 0.932162982 | 16 | 1 KQK09283 0.827 – | HORVU.MC |
| 0.956544164 | 0.995803902 | 16 | 2 KQK08398 0.990 0 | HORVU.MC |
| 0.873766312 | 0.950104178 | 16 | 0 KQK22852 0.692 – | HORVU.MC |
| 0.859539141 | 0.938282828 | 16 | 2 KQJ86818 0.889 0. | HORVU.MC |
| 0.92551306 | 0.979850746 | 16 | 2 KQJ83919 0.960 0. | HORVU.MC |
| 0.874161571 | 0.950735716 | 16 | 3 KQJ83106 0.857 –0 | HORVU.MC |
| 0.863892013 | 0.933633296 | 16 | 1 KQK14438 0.863 – | HORVU.MC |
| 0.932908394 | 0.982490975 | 16 | 2 KQK11359 0.941 0 | HORVU.MC |
| 0.927089837 | 0.988831079 | 16 | 2 KQK06761 0.961 0 | HORVU.MC |
| 0.901078501 | 0.960278171 | 16 | 1 KQK21685 0.895 – | HORVU.MC |
| 0.92847129 | 0.974884969 | 16 | 1 KQK05701 0.957 0 | HORVU.MC |
| 0.861351732 | 0.957964008 | 16 | 0 genblast_Os10t016 | HORVU.MC |
| 0.92133659 | 0.980461812 | 16 | 1 KQK15441 0.917 – | HORVU.MC |
| 0.797695122 | 0.897365854 | 16 | 0 KQK09494 0.746 – | HORVU.MC |
| 0.865491071 | 0.926607143 | 16 | 0 KQK16243 0.900 0 | HORVU.MC |
| 0.941354714 | 0.97767633 | 16 | 1 KQK21206 0.921 – | HORVU.MC |
| 0.841591697 | 0.921198838 | 16 | 6 KQJ92844 0.898 0. | genblast_C |
| 0.85222421 | 0.945072698 | 16 | 2 KQJ98889 0.866 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.892123003 | 0.950066578 | 16 | 0 | KQJ86242 | 0.865 | −0 | HORVU.MC |
| 0.871384634 | 0.947857259 | 16 | 1 | KQJ83755 | 0.861 | −0 | HORVU.MC |
| 0.801949985 | 0.855611789 | 16 | 1 | KQK16661 | 0.691 | − | HORVU.MC |
| 0.849020992 | 0.906702676 | 16 | 0 | KQK17917 | 0.837 | − | genblast_C |
| 0.93235202 | 0.979120994 | 16 | 0 | KQJ97744 | 0.940 | 0. | HORVU.MC |
| 0.902219977 | 0.965054114 | 16 | 0 | KQK00695 | 0.945 | 0 | HORVU.MC |
| 0.921624575 | 0.979237494 | 16 | 1 | KQK01242 | 0.898 | − | HORVU.MC |
| 0.861170732 | 0.960292683 | 16 | 3 | KQJ88124 | 0.903 | 0. | HORVU.MC |
| 0.928378939 | 0.986318408 | 16 | 1 | KQK17356 | 0.962 | 0 | HORVU.MC |
| 0.945917751 | 0.994129159 | 16 | 1 | KQK00596 | 0.941 | − | HORVU.MC |
| 0.833771832 | 0.925660546 | 16 | 0 | KQK12903 | 0.766 | − | HORVU.MC |
| 0.911451453 | 0.985468956 | 16 | 2 | KQK11016 | 0.912 | 0 | HORVU.MC |
| 0.877027702 | 0.981781882 | 16 | 1 | KQK05515 | 0.690 | − | HORVU.MC |
| 0.906036865 | 0.977069614 | 16 | 1 | KQJ99072 | 0.900 | −0 | HORVU.MC |
| 0.935815311 | 0.993104529 | 16 | 0 | KQJ86170 | 0.690 | −3 | HORVU.MC |
| 0.884232435 | 0.944803611 | 16 | 14 | KQK02787 | 0.945 | 1 | HORVU.MC |
| 0.792883384 | 0.8639789 | 16 | 1 | KQJ85651 | 0.704 | −1 | HORVU.MC |
| 0.918347193 | 0.967567568 | 16 | 0 | KQJ86944 | 0.899 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.961919557 | 1.00420198 | 16 | 1 | KQK10394 | 0.965 | 0 | HORVU.MC |
| 0.84118524 | 0.913695819 | 16 | 0 | KQK01781 | 0.690 | − | genblast_C |
| 0.901404088 | 0.981416477 | 16 | 0 | KQK06111 | 0.966 | 0 | HORVU.MC |
| 0.858795849 | 0.987837838 | 16 | 2 | KQK14971 | 0.747 | − | HORVU.MC |
| 0.779627303 | 0.845896147 | 16 | 0 | KQK17036 | 0.721 | − | HORVU.MC |
| 0.935338568 | 0.975946265 | 16 | 1 | KQJ85805 | 0.923 | −0 | HORVU.MC |
| 0.913303115 | 0.996087872 | 16 | 3 | KQK06731 | 0.964 | 0 | HORVU.MC |
| 0.822748415 | 0.945818851 | 16 | 0 | KQK02056 | 0.792 | − | HORVU.MC |
| 0.878489026 | 0.970680923 | 16 | 9 | PNT74452 | 0.873 | − | HORVU.MC |
| 0.920037229 | 0.990030288 | 16 | 3 | PNT65510 | 0.964 | 0. | HORVU.MC |
| 0.849100316 | 0.90525266 | 16 | 0 | PNT68397 | 0.689 | − | HORVU.MC |
| 0.888200965 | 0.953445311 | 16 | 0 | PNT61473 | 0.868 | − | HORVU.MC |
| 0.946832622 | 0.983239372 | 16 | 0 | KQJ83187 | 0.975 | 0. | HORVU.MC |
| 0.861071942 | 0.955971223 | 16 | 4 | KQK19084 | 0.897 | 0 | HORVU.MC |
| 0.96871641 | 1.009315657 | 16 | 0 | KQK10949 | 0.974 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.899896205 | 0.986408127 | 16 | 0 | KQJ88348 | 0.874 | −0 | HORVU.MC |
| 0.93580203 | 0.974843076 | 16 | 1 | KQJ94827 | 0.945 | 0. | HORVU.MC |
| 0.917434312 | 0.993225906 | 16 | 4 | KQK22913 | 0.978 | 0 | HORVU.MC |
| 0.852150262 | 0.935256515 | 16 | 6 | genblast_Os07t053 | | | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.916133835 | 0.992018865 | 16 | 3 | genblast_Os01t066 | | | HORVU.MC |

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|---|---|---|---|---|
| 0.839452418 | 0.922931403 | 16 | 1 KQK23194 0.792 − | HORVU.M |
| 0.913069826 | 0.977858177 | 16 | 3 KQK08242 0.947 0 | HORVU.M |
| 0.862647996 | 0.980115361 | 16 | 1 KQJ99628 0.888 0. | HORVU.M |
| 0.950434337 | 0.997967818 | 16 | 1 KQK16145 0.981 0 | HORVU.M |
| 0.95392612 | 0.999461714 | 16 | 3 KQK19116 0.980 0 | HORVU.M |
| 0.882483646 | 0.978953356 | 16 | 0 KQK06450 0.902 0 | HORVU.M |
| 0.848250807 | 0.929601722 | 16 | 3 KQJ83111 0.907 0. | HORVU.M |
| 0.91144629 | 0.989384066 | 16 | 2 KQK17833 0.951 0 | HORVU.M |
| 0.857043944 | 0.958641064 | 16 | 0 genblast_Os10t013 | HORVU.M |
| 0.929014484 | 0.970025189 | 16 | 0 KQJ96794 0.964 0. | genblast_ |
| 0.784929898 | 0.864217142 | 16 | 2 KQJ99403 0.750 −0 | HORVU.M |
| 0.799284229 | 0.908509277 | 16 | 1 KQJ82506 0.688 −1 | HORVU.M |
| 0.861240268 | 0.987456747 | 16 | 0 KQJ99293 0.767 −1 | HORVU.M |
| 0.893985643 | 0.948074601 | 16 | 1 genblast_Os03t069 | HORVU.M |
| 0.90742139 | 0.96383947 | 16 | 3 KQJ90285 0.921 0. | HORVU.M |
| 0.919354235 | 0.979946124 | 16 | 1 KQK12298 0.936 0 | HORVU.M |
| 0.893237793 | 0.96644102 | 16 | 2 KQJ82744 0.870 −0 | HORVU.M |
| 0.871404487 | 0.950729425 | 16 | 1 KQK17386 0.821 − | HORVU.M |
| 0.904949693 | 0.984993179 | 16 | 1 KQK10575 0.856 − | HORVU.M |
| 0.899041946 | 0.966841819 | 16 | 1 KQJ94507 0.928 0. | HORVU.M |
| 0.954578343 | 1.005588822 | 16 | 0 KQK11303 0.980 0 | HORVU.M |
| 0.824514208 | 0.960300878 | 16 | 1 KQK18104 0.747 − | HORVU.M |

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|---|---|---|---|---|
| 0.855167441 | 0.980716253 | 16 | 0 KQK16972 0.835 - | HORVU.MC |
| 0.86794675 | 0.9112852 | 16 | 0 genblast_Os10t033 | HORVU.MC |
| 0.941835192 | 0.993951994 | 16 | 3 KQK09655 0.979 0 | HORVU.MC |
| 0.913859845 | 0.961147297 | 16 | 2 KQJ91962 0.943 0. | HORVU.MC |
| 0.912879597 | 0.962424864 | 16 | 1 KQK00964 0.932 0 | HORVU.MC |
| 0.939987245 | 0.99 | 16 | 2 KQK13118 0.951 0 | HORVU.MC |
| 0.832399103 | 0.889974375 | 16 | 2 KQK14586 0.687 - | HORVU.MC |
| 0.939288176 | 1 | 16 | 1 KQK05658 0.947 0 | HORVU.MC |
| 0.94147131 | 0.993260807 | 16 | 2 KQK10875 0.932 - | HORVU.MC |
| 0.865434179 | 0.931958763 | 16 | 2 PNT72699 0.914 0. | HORVU.MC |
| 0.892499754 | 0.97236428 | 16 | 0 KQK13942 0.867 - | HORVU.MC |
| 0.944297043 | 0.986453613 | 16 | 2 KQJ92683 0.963 0. | HORVU.MC |
| 0.925195715 | 0.984706882 | 16 | 1 KQK08992 0.871 - | HORVU.MC |
| 0.857032782 | 0.949845895 | 16 | 1 KQK05068 0.820 - | HORVU.MC |
| 0.863599631 | 0.922188871 | 16 | 0 KQK00532 0.873 0 | HORVU.MC |
| 0.900839705 | 0.973238667 | 16 | 0 KQK21117 0.686 - | HORVU.MC |
| 0.881760524 | 0.944521885 | 16 | 0 KQK10581 0.861 - | HORVU.MC |
| 0.814911151 | 0.899986788 | 16 | 5 KQJ92488 0.686 -2 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.95299676 | 1.001727862 | 16 | 0 | KQK19482 | 0.977 | 0. | HORVU.MC |
| 0.82693978 | 0.914302258 | 16 | 0 | KQK06131 | 0.686 | – | HORVU.MC |
| 0.918314889 | 0.983259557 | 16 | 1 | KQK03151 | 0.936 | 0. | HORVU.MC |
| 0.851620586 | 0.992332714 | 16 | 1 | KQJ97250 | 0.844 | –0 | HORVU.MC |
| 0.800051318 | 0.906370017 | 16 | 2 | KQK13946 | 0.754 | – | HORVU.MC |
| 0.874296118 | 0.928715238 | 16 | 2 | KQK12560 | 0.895 | 0. | HORVU.MC |
| 0.887282149 | 0.954313993 | 16 | 2 | PNT76078 | 0.910 | 0. | HORVU.MC |
| 0.868035267 | 0.939065109 | 16 | 1 | KQK16454 | 0.844 | – | HORVU.MC |
| 0.835105526 | 0.946877635 | 16 | 4 | PNT75157 | 0.877 | 0. | HORVU.MC |
| 0.886470013 | 0.963401735 | 16 | 3 | KQK11296 | 0.895 | 0. | HORVU.MC |
| 0.848516949 | 0.967984934 | 16 | 0 | KQJ98994 | 0.778 | –0 | HORVU.MC |
| 0.861936672 | 0.91851933 | 16 | 2 | KQJ92005 | 0.861 | –0 | HORVU.MC |
| 0.904881246 | 0.943656179 | 16 | 0 | KQK17322 | 0.900 | – | HORVU.MC |
| 0.897559744 | 0.954182068 | 16 | 1 | KQK10687 | 0.916 | 0. | HORVU.MC |
| 0.887098782 | 0.958556764 | 16 | 1 | KQK03387 | 0.890 | 0. | HORVU.MC |
| 0.911481968 | 0.992834965 | 16 | 3 | PNT74205 | 0.967 | 0. | HORVU.MC |

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|---|---|---|---|---|
| 0.954681379 | 0.995593173 | 16 | 2 KQK20547 0.949 – | HORVU.M |
| 0.846858297 | 0.921913701 | 16 | 2 PNT68174 0.819 – | genblast_ |
| 0.936957046 | 0.977009477 | 16 | 1 KQK01613 0.936 – | HORVU.M |
| 0.88487392 | 0.927556422 | 16 | 0 KQJ96236 0.887 0. | HORVU.M |
| 0.922335133 | 0.973764055 | 16 | 1 KQK04067 0.945 0 | HORVU.M |
| 0.925979419 | 0.974544142 | 16 | 0 KQK00638 0.923 – | HORVU.M |
| 0.941614506 | 0.993171671 | 16 | 1 KQK11717 0.984 0 | HORVU.M |
| 0.859808037 | 0.953211607 | 16 | 2 KQK05911 0.905 0 | HORVU.M |
| 0.896737191 | 0.964035964 | 16 | 3 KQK06310 0.931 0 | HORVU.M |
| 0.921505096 | 0.974024551 | 16 | 2 KQK07224 0.925 0 | HORVU.M |
| 0.935927893 | 0.985466741 | 16 | 0 KQK12597 0.946 0 | HORVU.M |
| 0.873373288 | 0.953530032 | 16 | 2 KQK13737 0.862 – | HORVU.M |
| 0.932699254 | 0.992655911 | 16 | 1 KQK03072 0.933 0 | HORVU.M |
| 0.825990887 | 0.949494949 | 16 | 2 KQK13908 0.787 – | HORVU.M |
| 0.809767233 | 0.888374486 | 16 | 0 PNT63653 0.763 – | HORVU.M |
| 0.903325165 | 0.994826765 | 16 | 3 KQJ84057 0.967 0. | HORVU.M |
| 0.97446465 | 1.001699524 | 16 | 0 KQK15863 0.994 0 | HORVU.M |
| 0.934002559 | 0.980112113 | 16 | 4 KQK20786 0.954 0 | HORVU.M |
| 0.938553114 | 0.981318681 | 16 | 1 KQK20383 0.941 0 | HORVU.M |
| 0.903842894 | 0.949959317 | 16 | 2 KQJ98782 0.950 0. | HORVU.M |
| 0.951251716 | 0.984578008 | 16 | 1 KQJ90501 0.911 –0 | HORVU.M |

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| 0.968962731 | 1.002337895 | 16 | 1 | KQK02914 | 0.984 | 0. | HORVU.MC |
| 0.851580602 | 0.917576961 | 16 | 0 | KQK18634 | 0.799 | − | HORVU.MC |
| 0.823687738 | 0.897267382 | 16 | 0 | KQJ88206 | 0.845 | 0. | HORVU.MC |
| 0.881855986 | 0.966608954 | 16 | 4 | KQK16600 | 0.896 | 0. | HORVU.MC |
| 0.862078231 | 0.929390307 | 16 | 3 | KQK09239 | 0.887 | 0. | HORVU.MC |
| 0.827709773 | 0.926603718 | 16 | 0 | KQK11405 | 0.766 | − | HORVU.MC |

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| 0.939719324 | 0.997415773 | 16 | 1 | PNT66468 | 0.969 | 0. | genblast_C |
| 0.926523716 | 0.970758245 | 16 | 1 | KQK13650 | 0.922 | − | HORVU.MC |
| 0.959535728 | 1.004220652 | 16 | 1 | KQK19214 | 0.995 | 0. | HORVU.MC |
| 0.965435066 | 1.001466515 | 16 | 0 | PNT73647 | 1.000 | 0. | HORVU.MC |
| 0.788509895 | 0.84683948 | 16 | 10 | KQK23642 | 0.822 | 0. | HORVU.MC |

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| 0.917397425 | 0.985223442 | 16 | 1 | PNT65541 | 0.838 | − | HORVU.MC |
| 0.915904336 | 0.954594017 | 16 | 2 | KQJ86451 | 0.931 | 0. | HORVU.MC |
| 0.767009494 | 1.010456797 | 16 | 0 | KQK11760 | 0.715 | − | HORVU.MC |
| 0.917042699 | 1.008351293 | 16 | 0 | KQJ84465 | 0.838 | −0 | HORVU.MC |
| 0.82931496 | 0.957472478 | 16 | 0 | PNT78181 | 0.791 | − | HORVU.MC |
| 0.872171201 | 0.913615848 | 16 | 1 | KQK08315 | 0.848 | − | HORVU.MC |
| 0.953840993 | 0.990472996 | 16 | 0 | KQK07946 | 0.965 | 0. | HORVU.MC |
| 0.826896067 | 0.926516854 | 16 | 2 | KQK17346 | 0.683 | − | HORVU.MC |
| 0.924629796 | 0.991246012 | 16 | 2 | KQJ89205 | 0.979 | 0. | HORVU.MC |
| 0.915453906 | 0.965159056 | 16 | 0 | KQJ98329 | 0.929 | 0. | HORVU.MC |
| 0.808636364 | 0.915636364 | 16 | 2 | KQK23889 | 0.719 | − | HORVU.MC |
| 0.921783473 | 0.973779637 | 16 | 3 | KQK01442 | 0.902 | − | HORVU.MC |

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| 0.853275037 | 0.951415148 | 16 | 5 | KQK02012 | 0.928 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.799204976 | 0.875267754 | 16 | 0 | KQK02751 | 0.819 | 0 | HORVU.MC |
| 0.816260255 | 0.904284412 | 16 | 0 | KQJ94466 | 0.848 | 0. | HORVU.MC |
| 0.941808094 | 0.977806789 | 16 | 0 | KQK06962 | 0.918 | – | HORVU.MC |
| 0.908745613 | 0.967859122 | 16 | 2 | PNT70618 | 0.951 | 0. | genblast_C |
| 0.871555974 | 0.972737819 | 16 | 0 | KQK12414 | 0.683 | – | HORVU.MC |
| 0.891706146 | 0.946016706 | 16 | 0 | PNT76171 | 0.823 | – | HORVU.MC |
| 0.953571646 | 0.986286341 | 16 | 0 | KQK11652 | 0.980 | 0 | HORVU.MC |
| 0.934623304 | 0.984738372 | 16 | 1 | KQJ82867 | 0.981 | 0. | HORVU.MC |
| 0.844919305 | 0.944078947 | 16 | 0 | KQJ96966 | 0.749 | –1 | HORVU.MC |
| 0.912036704 | 0.982186467 | 16 | 3 | KQK10630 | 0.939 | 0 | HORVU.MC |
| 0.824507685 | 0.921549792 | 16 | 2 | KQK14710 | 0.713 | – | HORVU.MC |
| 0.780332128 | 0.879575237 | 16 | 0 | KQK06940 | 0.766 | – | HORVU.MC |
| 0.919368149 | 0.973835625 | 16 | 1 | KQK20457 | 0.960 | 0 | HORVU.MC |
| 0.933875092 | 0.97966683 | 16 | 2 | KQK00402 | 0.953 | 0 | HORVU.MC |
| 0.866241728 | 0.946671857 | 16 | 3 | KQK16447 | 0.682 | – | HORVU.MC |
| 0.849718536 | 0.919983916 | 16 | 0 | genblast_Os07t022 | | | HORVU.MC |
| 0.896754468 | 0.973032299 | 16 | 0 | KQK14664 | 0.682 | – | HORVU.MC |
| 0.910016649 | 0.976174843 | 16 | 1 | KQK18795 | 0.897 | – | HORVU.MC |
| 0.907766112 | 0.977914555 | 16 | 1 | KQK05144 | 0.923 | 0 | HORVU.MC |
| 0.923118077 | 0.974488083 | 16 | 0 | KQJ94564 | 0.941 | 0. | HORVU.MC |
| 0.800144933 | 0.902805611 | 16 | 2 | KQK14443 | 0.778 | – | HORVU.MC |
| 0.899649942 | 0.967244541 | 16 | 0 | KQK11816 | 0.935 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.932717848 | 0.983472294 | 16 | 2 | KQK01839 | 0.954 | 0 | HORVU.MC |
| 0.908044884 | 0.956162039 | 16 | 3 | KQJ83775 | 0.931 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.915017689 | 0.981132075 | 16 | 0 | KQK17345 | 0.895 | – | HORVU.MC |
| 0.89313163 | 0.964710976 | 16 | 0 | KQK13682 | 0.926 | 0 | HORVU.MC |
| 0.972345725 | 1.000428541 | 16 | 0 | KQK02871 | 0.986 | 0 | HORVU.MC |
| 0.924510502 | 0.959658358 | 16 | 1 | KQK12328 | 0.905 | – | HORVU.MC |
| 0.92227655 | 0.960695389 | 16 | 1 | KQK13489 | 0.897 | – | HORVU.MC |
| 0.900864521 | 0.973321532 | 16 | 1 | KQJ91914 | 0.900 | –0 | HORVU.MC |
| 0.913842063 | 0.968166691 | 16 | 1 | KQJ90062 | 0.927 | 0. | HORVU.MC |
| 0.939016332 | 0.983193277 | 16 | 2 | KQJ83143 | 0.968 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.878034279 | 0.981138265 | 16 | 0 | KQJ90576 | 0.861 | –0 | HORVU.MC |
| 0.934233449 | 1.015415479 | 16 | 4 | KQJ81720 | 0.984 | 0. | HORVU.MC |
| 0.875246157 | 0.949307585 | 16 | 1 | KQJ97488 | 0.783 | –1 | HORVU.MC |
| 0.762359551 | 0.834670947 | 16 | 3 | PNT69035 | 0.782 | 0. | HORVU.MC |
| 0.913776511 | 1.005665311 | 16 | 2 | KQK06896 | 0.959 | 0 | genblast_C |
| 0.883272389 | 0.964992207 | 16 | 2 | KQK09384 | 0.826 | – | HORVU.MC |
| 0.945157385 | 0.993220339 | 16 | 1 | KQK17168 | 0.983 | 0 | HORVU.MC |
| 0.90650464 | 0.971933001 | 16 | 2 | KQK21025 | 0.929 | 0 | HORVU.MC |
| 0.937301997 | 0.984012378 | 16 | 1 | KQJ93876 | 0.978 | 0. | HORVU.MC |
| 0.840366242 | 0.911889597 | 16 | 1 | KQJ89874 | 0.828 | –0 | HORVU.MC |
| 0.909208139 | 0.94681182 | 16 | 1 | KQK21320 | 0.947 | 0 | HORVU.MC |
| 0.848483212 | 0.922231823 | 16 | 0 | KQK19008 | 0.681 | – | HORVU.MC |

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| 0.964891425 | 0.999524489 | 16 | 1 | KQJ83000 | 0.981 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.94479374 | 0.983366512 | 16 | 2 | KQK13102 | 0.978 | 0 | HORVU.MC |
| 0.926915206 | 0.996137883 | 16 | 0 | KQJ99777 | 0.950 | 0. | genblast_C |
| 0.861347919 | 0.92944101 | 16 | 1 | PNT76043 | 0.898 | 0. | HORVU.MC |
| 0.901670772 | 0.974729816 | 16 | 1 | PNT72403 | 0.964 | 0. | HORVU.MC |
| 0.829396186 | 0.891031073 | 16 | 1 | KQJ95319 | 0.844 | 0. | HORVU.MC |
| 0.969359306 | 0.99704579 | 16 | 0 | KQK00224 | 0.994 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.89348962 | 0.966054145 | 16 | 1 | genblast_Os01t014 | | | HORVU.MC |
| 0.827752294 | 0.942507645 | 16 | 0 | KQK18736 | 0.893 | 0 | genblast_C |
| 0.927119402 | 0.978820406 | 16 | 1 | KQJ82560 | 0.944 | 0. | genblast_Z |
| 0.930685944 | 0.97313278 | 16 | 1 | KQK19839 | 0.922 | – | HORVU.MC |
| 0.87761011 | 0.940590294 | 16 | 1 | KQK17921 | 0.920 | 0 | HORVU.MC |
| 0.931840438 | 0.975230415 | 16 | 1 | KQK00434 | 0.942 | 0 | HORVU.MC |
| 0.948088164 | 0.998824018 | 16 | 3 | KQK04294 | 0.947 | – | HORVU.MC |
| 0.843399535 | 0.922903665 | 16 | 2 | PNT77532 | 0.795 | –1 | HORVU.MC |
| 0.781310186 | 0.922105714 | 16 | 1 | KQK08480 | 0.696 | – | HORVU.MC |
| 0.923684934 | 1.015945748 | 16 | 1 | KQK00021 | 0.958 | 0 | genblast_C |
| 0.911917985 | 0.977175898 | 16 | 2 | PNT67650 | 0.900 | – | HORVU.MC |
| 0.942459712 | 0.987303138 | 16 | 0 | KQJ87526 | 0.891 | –0 | HORVU.MC |
| 0.921943767 | 0.987135216 | 16 | 1 | KQJ96531 | 0.952 | 0. | HORVU.MC |
| 0.765452656 | 0.875275751 | 16 | 2 | PNT70966 | 0.786 | 0. | HORVU.MC |
| 0.867819695 | 0.926601322 | 16 | 0 | KQK01414 | 0.815 | – | HORVU.MC |
| 0.877668649 | 1 | 16 | 0 | KQK00303 | 0.916 | 0 | genblast_C |
| 0.83256262 | 0.907032755 | 16 | 3 | KQJ92728 | 0.898 | 0. | HORVU.MC |
| 0.796418919 | 0.882810811 | 16 | 0 | KQK02542 | 0.686 | – | HORVU.MC |
| 0.943779683 | 0.988707124 | 16 | 0 | KQJ84714 | 0.951 | 0. | HORVU.MC |
| 0.820623342 | 0.984084881 | 16 | 0 | KQJ93972 | 0.679 | –1 | HORVU.MC |
| 0.923447672 | 0.983975964 | 16 | 1 | KQK12081 | 0.882 | – | HORVU.MC |
| 0.948816138 | 1.001904762 | 16 | 1 | KQK03994 | 0.951 | 0 | genblast_C |

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|---|---|---|---|---|---|
| 0.867485461 | 0.915201515 | 16 | 1 | KQK15805 0.861 – | HORVU.MC |
| 0.866761962 | 0.945531147 | 16 | 0 | genblast_Os03t064 | HORVU.MC |
| 0.942521186 | 0.984881356 | 16 | 0 | KQK20464 0.933 – | HORVU.MC |
| 0.9081728 | 1.001725129 | 16 | 1 | KQK09766 0.954 0 | HORVU.MC |
| | | | | | |
| 0.948333481 | 1.000885269 | 16 | 1 | KQK10520 0.801 – | genblast_C |
| 0.905578538 | 0.961554293 | 16 | 1 | KQJ99108 0.816 –1 | HORVU.MC |
| 0.865935497 | 0.978098291 | 16 | 0 | KQK08156 0.679 – | HORVU.MC |
| 0.87294279 | 0.961990596 | 16 | 1 | KQJ83361 0.864 –0 | HORVU.MC |
| | | | | | |
| 0.878244484 | 0.946091644 | 16 | 1 | KQJ84985 0.895 0. | HORVU.MC |
| 0.886248309 | 0.972259811 | 16 | 0 | KQK07511 0.858 – | HORVU.MC |
| | | | | | |
| 0.910342052 | 0.950181087 | 16 | 1 | KQK10837 0.930 0 | HORVU.MC |
| 0.844886529 | 0.961012511 | 16 | 0 | KQJ98266 0.903 0. | genblast_C |
| 0.831811065 | 0.925539318 | 16 | 0 | KQJ82906 0.859 0. | genblast_C |
| 0.873950037 | 0.995114116 | 16 | 2 | KQK02756 0.878 0 | genblast_C |
| 0.94565392 | 0.990574122 | 16 | 0 | KQJ97589 0.975 0. | HORVU.MC |
| 0.944800301 | 0.996483296 | 16 | 0 | KQK07813 0.989 0 | HORVU.MC |
| | | | | | |
| 0.93720569 | 0.9981845 | 16 | 3 | KQJ95610 0.987 0. | HORVU.MC |
| 0.914040274 | 0.982396871 | 16 | 0 | PNT67842 0.847 – | HORVU.MC |
| | | | | | |
| 0.879656699 | 0.97494153 | 16 | 0 | KQK15233 0.891 0 | HORVU.MC |
| 0.822618533 | 0.886596825 | 16 | 8 | KQK12942 0.885 1 | HORVU.MC |
| 0.966064365 | 1.004314995 | 16 | 1 | KQK08644 0.992 0 | HORVU.MC |
| 0.919803079 | 1.003966755 | 16 | 2 | KQK13333 0.903 – | HORVU.MC |
| 0.808580388 | 0.99049791 | 16 | 2 | KQK00905 0.678 – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.800516917 | 0.918831169 | 16 | 4 | KQK02752 | 0.849 | 0 | HORVU.MC |
| 0.869057989 | 0.982578397 | 16 | 0 | KQK09530 | 0.818 | − | HORVU.MC |
| 0.899322126 | 0.976572668 | 16 | 3 | KQK18083 | 0.933 | 0 | HORVU.MC |
| 0.885789087 | 0.973521995 | 16 | 2 | KQJ84584 | 0.919 | 0. | HORVU.MC |
| 0.89655252 | 0.976555289 | 16 | 4 | PNT60769 | 0.895 | − | genblast_C |
| 0.947772821 | 0.992635083 | 16 | 0 | PNT73252 | 0.970 | 0. | HORVU.MC |
| 0.804210875 | 0.921898025 | 16 | 0 | KQJ87996 | 0.712 | −0 | genblast_C |
| 0.954770571 | 0.992899338 | 16 | 0 | KQK05790 | 0.967 | 0 | HORVU.MC |
| 0.798186528 | 0.908186528 | 16 | 0 | KQJ86746 | 0.743 | −0 | genblast_C |
| 0.932295029 | 0.989670755 | 16 | 1 | KQK16655 | 0.955 | 0 | HORVU.MC |
| 0.932659783 | 0.99821969 | 16 | 0 | KQK07749 | 0.913 | − | HORVU.MC |
| 0.929266448 | 0.970365733 | 16 | 0 | KQK22405 | 0.918 | − | HORVU.MC |
| 0.89099655 | 0.965302432 | 16 | 4 | KQK04213 | 0.926 | 0 | HORVU.MC |
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| 0.906367292 | 0.969705094 | 16 | 3 | KQJ86774 | 0.930 | 0. | genblast_C |
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| 0.884235224 | 0.92591853 | 16 | 0 | KQK09795 | 0.873 | − | HORVU.MC |
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| 0.857852697 | 0.94846473 | 16 | 1 | KQK10549 | 0.842 | − | HORVU.MC |
| 0.965397616 | 0.998043053 | 16 | 0 | KQK03076 | 0.986 | 0 | HORVU.MC |
| 0.826869159 | 0.895327103 | 16 | 0 | KQJ97137 | 0.677 | −2 | HORVU.MC |
| 0.838895427 | 0.930060525 | 16 | 6 | KQK10732 | 0.863 | 0 | genblast_C |
| 0.952599552 | 0.998185118 | 16 | 1 | KQK10539 | 0.914 | − | HORVU.MC |

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| 0.917256722 | 0.981724237 | 16 | 3 | KQK14391 | 0.926 | 0. | HORVU.MC |
| 0.813243065 | 0.872102798 | 16 | 4 | KQJ84562 | 0.844 | 0. | HORVU.MC |
| 0.915156811 | 0.995253976 | 16 | 3 | KQK15029 | 0.973 | 0. | HORVU.MC |
| 0.906472066 | 0.975496202 | 16 | 2 | KQK12269 | 0.928 | 0. | HORVU.MC |
| 0.896170435 | 0.994213459 | 16 | 1 | KQJ94020 | 0.897 | 0. | HORVU.MC |
| 0.844305203 | 0.927918782 | 16 | 0 | KQK06743 | 0.702 | – | HORVU.MC |
| 0.848735541 | 0.979659964 | 16 | 1 | PNT68820 | 0.676 | – | HORVU.MC |
| 0.794141181 | 0.940611664 | 16 | 4 | KQK10464 | 0.701 | – | HORVU.MC |
| 0.919136757 | 0.989108911 | 16 | 1 | KQJ98400 | 0.909 | –0 | HORVU.MC |
| 0.941890111 | 0.983728658 | 16 | 0 | KQK08960 | 0.966 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.944017741 | 0.979013414 | 16 | 0 | KQJ99725 | 0.959 | 0. | HORVU.MC |
| 0.939087467 | 0.981516814 | 16 | 1 | KQJ90511 | 0.960 | 0. | HORVU.MC |
| 0.906296059 | 0.966228773 | 16 | 0 | KQJ84008 | 0.903 | –0 | HORVU.MC |
| 0.858058832 | 0.949096961 | 16 | 3 | KQJ97825 | 0.866 | 0. | HORVU.MC |
| 0.854925473 | 0.932870111 | 16 | 0 | KQK17214 | 0.873 | 0 | HORVU.MC |
| 0.890219926 | 0.961601041 | 16 | 3 | KQK09206 | 0.905 | 0 | HORVU.MC |
| 0.819051669 | 0.977035935 | 16 | 0 | KQK19806 | 0.710 | – | HORVU.MC |
| 0.948336896 | 0.991116751 | 16 | 1 | KQK04767 | 0.974 | 0 | HORVU.MC |
| 0.802627304 | 0.886224008 | 16 | 0 | KQK00670 | 0.844 | 0 | HORVU.MC |
| 0.923176633 | 1.007431732 | 16 | 0 | KQK11839 | 0.884 | – | HORVU.MC |
| 0.843858658 | 0.915855355 | 16 | 0 | genblast_Os07t068 | | | HORVU.MC |
| 0.868811088 | 0.949206858 | 16 | 1 | PNT69481 | 0.820 | – | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.900901733 | 0.971923697 | 16 | 1 | KQK01748 | 0.930 | 0 | HORVU.MC |
| 0.880478868 | 0.94805726 | 16 | 1 | KQJ93061 | 0.835 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.882618308 | 0.94956979 | 16 | 1 | KQK06181 | 0.869 | – | HORVU.MC |
| 0.859019087 | 0.988025569 | 16 | 6 | KQK09666 | 0.924 | 0 | HORVU.MC |
| 0.806541036 | 0.914202561 | 16 | 3 | KQK17074 | 0.740 | – | HORVU.MC |
| 0.91036758 | 0.989078774 | 16 | 1 | KQJ85793 | 0.916 | 0. | HORVU.MC |
| 0.930781186 | 0.988940789 | 16 | 3 | KQK22484 | 0.956 | 0 | HORVU.MC |
| 0.892058373 | 0.974693555 | 16 | 5 | KQJ91337 | 0.713 | –1 | genblast_C |
| 0.871065237 | 0.944160584 | 16 | 2 | KQK11661 | 0.783 | – | HORVU.MC |
| 0.889993261 | 0.968425106 | 16 | 1 | KQK00705 | 0.873 | – | HORVU.MC |

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| 0.931500318 | 0.973776224 | 16 | 0 | genblast_Os01t010 | | | HORVU.MC |

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|---|---|---|---|---|---|
| 0.821466134 | 0.908498107 | 16 | 0 | KQJ97295 0.694 -1 | HORVU.MC |
| 0.924274158 | 0.966814421 | 16 | 9 | KQK18575 0.933 0 | HORVU.MC |
| 0.921346154 | 0.975621302 | 16 | 0 | KQK21134 0.929 0 | HORVU.MC |
| 0.823531067 | 0.901395768 | 16 | 0 | KQJ87737 0.779 -0 | genblast_C |
| 0.945282015 | 1.008158922 | 16 | 0 | KQK15109 1.006 0 | genblast_C |
| 0.821301981 | 0.961332338 | 16 | 10 | KQK15525 0.844 0 | HORVU.MC |
| 0.904444814 | 0.95854836 | 16 | 1 | KQK07210 0.913 0 | HORVU.MC |
| 0.875033154 | 0.959987875 | 16 | 4 | KQK10380 0.906 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.875764492 | 0.968799858 | 16 | 0 | KQK21493 0.853 - | HORVU.MC |
| 0.904267916 | 0.970345964 | 16 | 1 | PNT70975 0.830 - | HORVU.MC |
| 0.908315071 | 0.980950775 | 16 | 1 | PNT69805 0.945 0. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.895227964 | 0.96668693 | 16 | 1 | genblast_Os11t065 | HORVU.MC |
| 0.925879481 | 0.985152488 | 16 | 1 | KQK14951 0.884 - | HORVU.MC |
| 0.923483678 | 0.990245316 | 16 | 1 | KQK20720 0.921 - | HORVU.MC |

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|---|---|---|---|---|---|
| 0.903406331 | 0.957415803 | 16 | 1 | KQJ91553 0.903 -0 | HORVU.MC |
| 0.953944155 | 0.998697493 | 16 | 1 | KQK11761 0.969 0 | HORVU.MC |
| 0.887870013 | 0.932607933 | 16 | 2 | KQK02803 0.854 - | HORVU.MC |
| 0.835726853 | 0.951415974 | 16 | 5 | KQK13559 0.895 0 | HORVU.MC |

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| 0.823394823 | 0.92996331 | 16 | 10 | genblast_Os03t071 | HORVU.MC |
| 0.862634001 | 0.954089956 | 16 | 2 | KQJ93634 0.890 0. | HORVU.MC |
| 0.879923021 | 0.940369143 | 16 | 1 | KQK18413 0.873 - | HORVU.MC |
| 0.888093915 | 0.96248958 | 16 | 1 | PNT77546 0.912 0. | HORVU.MC |
| 0.921522022 | 0.987079473 | 16 | 3 | KQJ97470 0.935 0. | HORVU.MC |
| 0.915169093 | 0.974623395 | 16 | 5 | KQJ94284 0.909 -0 | HORVU.MC |
| 0.89938151 | 0.97625 | 16 | 2 | PNT63359 0.910 0. | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.919875 | 0.992 | 16 | 0 | KQK12521 | 0.855 | – | genblast_C |
| 0.819586507 | 0.920348205 | 16 | 2 | KQK15097 | 0.703 | – | HORVU.MC |
| 0.929041302 | 0.979649891 | 16 | 0 | KQJ97263 | 0.964 | 0. | HORVU.MC |
| 0.820778348 | 0.917888563 | 16 | 3 | PNT77476 | 0.831 | 0. | genblast_Z |
| 0.911321019 | 0.969628977 | 16 | 1 | KQK14667 | 0.834 | – | HORVU.MC |
| 0.921914266 | 0.992654166 | 16 | 1 | KQK13150 | 0.949 | 0 | HORVU.MC |
| 0.959457605 | 0.996707217 | 16 | 1 | KQK16981 | 0.980 | 0 | HORVU.MC |
| 0.947682584 | 0.997015449 | 16 | 0 | KQK14440 | 0.948 | 0 | HORVU.MC |
| 0.901394456 | 0.953239813 | 16 | 1 | KQJ92297 | 0.673 | –3 | HORVU.MC |
| 0.927394439 | 0.990988671 | 16 | 1 | KQK23216 | 0.927 | – | HORVU.MC |
| 0.941990503 | 0.990846867 | 16 | 2 | KQK15196 | 0.948 | 0 | genblast_C |
| 0.893119091 | 0.960094549 | 16 | 0 | KQK22871 | 0.784 | – | HORVU.MC |
| 0.872504558 | 0.968824066 | 16 | 2 | PNT64439 | 0.951 | 0. | HORVU.MC |
| 0.860371023 | 0.942199714 | 16 | 2 | PNT77426 | 0.903 | 0. | HORVU.MC |

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|---|---|---|---|---|
| 0.838708815 | 0.906718015 | 16 | 1 KQK00617 0.880 0 | HORVU.MC |
| 0.906075264 | 0.983225348 | 16 | 3 KQJ94768 0.868 -0 | HORVU.MC |
| 0.861635056 | 0.923440322 | 16 | 0 KQJ90775 0.795 -1 | HORVU.MC |

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|---|---|---|---|---|
| 0.85436282 | 0.926866652 | 16 | 0 KQJ92701 0.874 0. | HORVU.MC |
| 0.905774879 | 0.969937802 | 16 | 3 genblast_Os04t039 | HORVU.MC |
| 0.862818347 | 0.938669439 | 16 | 0 KQK18064 0.879 0 | HORVU.MC |
| 0.930841961 | 0.982252271 | 16 | 2 KQK17407 0.968 0 | HORVU.MC |
| 0.84160596 | 0.960596026 | 16 | 6 KQJ82725 0.932 0. | HORVU.MC |
| 0.924501351 | 0.979950135 | 16 | 2 KQJ98503 0.962 0. | HORVU.MC |
| 0.749546756 | 0.984351145 | 16 | 1 KQJ89429 0.671 -1 | HORVU.MC |
| 0.796249055 | 0.870899471 | 16 | 1 PNT73838 0.859 0. | HORVU.MC |
| 0.856733937 | 0.946128501 | 16 | 0 KQK12451 0.812 - | HORVU.MC |
| 0.931342758 | 0.988229273 | 16 | 0 KQK03454 0.942 0 | HORVU.MC |
| 0.893668273 | 0.987474191 | 16 | 1 KQJ93016 0.952 0. | HORVU.MC |
| 0.865697285 | 0.980221254 | 16 | 0 PNT76159 0.671 - | HORVU.MC |
| 0.951447353 | 0.985468804 | 16 | 1 PNT68810 0.963 0. | HORVU.MC |
| 0.95788809 | 0.995531378 | 16 | 0 KQJ93525 0.955 -0 | HORVU.MC |
| 0.912062615 | 0.985573972 | 16 | 0 KQJ99759 0.933 0. | HORVU.MC |
| 0.84101994 | 0.914646392 | 16 | 1 KQJ81604 0.801 -0 | HORVU.MC |
| 0.783763791 | 0.880942828 | 16 | 1 KQK17968 0.739 - | HORVU.MC |
| 0.957119094 | 1.001263371 | 16 | 0 KQK02731 0.968 0 | HORVU.MC |
| 0.84619397 | 0.921523758 | 16 | 1 KQJ86079 0.752 -1 | HORVU.MC |
| 0.875676533 | 0.967526393 | 16 | 3 PNT66891 0.753 - | HORVU.MC |
| 0.926509276 | 0.969600125 | 16 | 7 KQJ92010 0.963 0. | HORVU.MC |
| 0.822438364 | 0.914007538 | 16 | 9 KQK17450 0.867 0 | HORVU.MC |
| 0.873068274 | 0.91523469 | 16 | 3 KQK19496 0.852 - | HORVU.MC |
| 0.877727593 | 0.95823557 | 16 | 0 KQJ93506 0.920 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.935181306 | 0.985523437 | 16 | 1 | KQK16712 | 0.919 | – | HORVU.MC |
| 0.825772069 | 0.881388357 | 16 | 0 | KQK14753 | 0.670 | – | HORVU.MC |
| 0.912210707 | 0.989699898 | 16 | 1 | KQK07366 | 0.874 | – | HORVU.MC |
| 0.931931882 | 0.990074442 | 16 | 2 | KQK10257 | 0.951 | 0 | HORVU.MC |
| 0.917868208 | 0.972712107 | 16 | 0 | KQK09954 | 0.943 | 0 | HORVU.MC |
| 0.960484365 | 0.991477621 | 16 | 0 | KQK13072 | 0.972 | 0 | HORVU.MC |
| 0.894272246 | 0.951934927 | 16 | 0 | KQK12344 | 0.919 | 0 | genblast_C |
| 0.886579549 | 0.954903816 | 16 | 0 | KQK23207 | 0.785 | – | HORVU.MC |
| 0.96307743 | 0.997209735 | 16 | 1 | KQK16090 | 0.985 | 0 | HORVU.MC |
| 0.914396216 | 0.985707325 | 16 | 0 | KQK21687 | 0.967 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.824778224 | 0.908613341 | 16 | 5 | PNT73510 | 0.807 | - | HORVU.MC |
| 0.874398776 | 0.949278531 | 16 | 1 | KQK11008 | 0.826 | - | HORVU.MC |
| 0.900952903 | 0.975889158 | 16 | 4 | PNT72185 | 0.932 | 0. | HORVU.MC |
| 0.891748813 | 0.954849702 | 16 | 0 | KQJ88696 | 0.915 | 0. | HORVU.MC |
| 0.849524242 | 0.948515477 | 16 | 0 | KQK13082 | 0.670 | - | HORVU.MC |
| 0.871149289 | 0.967113126 | 16 | 3 | PNT69952 | 0.866 | - | HORVU.MC |
| 0.937898301 | 0.995397415 | 16 | 1 | KQJ93434 | 0.969 | 0. | HORVU.MC |
| 0.894935155 | 0.97965248 | 16 | 3 | KQJ98321 | 0.900 | 0. | genblast_C |
| 0.811105747 | 0.915762136 | 16 | 0 | KQJ89455 | 0.815 | 0. | HORVU.MC |
| 0.944390545 | 0.989945317 | 16 | 3 | KQK00003 | 0.969 | 0 | HORVU.MC |
| 0.900555003 | 0.976408217 | 16 | 1 | KQK15650 | 0.953 | 0 | HORVU.MC |
| 0.87108448 | 0.959025471 | 16 | 0 | KQK15164 | 0.669 | - | HORVU.MC |
| 0.908515199 | 0.959257422 | 16 | 1 | KQK06265 | 0.931 | 0 | HORVU.MC |
| 0.876033549 | 0.963347227 | 16 | 4 | KQK17873 | 0.899 | 0 | HORVU.MC |
| 0.851383669 | 0.937137 | 16 | 0 | KQJ85074 | 0.738 | -1 | HORVU.MC |
| 0.893163223 | 0.956999522 | 16 | 0 | PNT78237 | 0.926 | 0. | HORVU.MC |
| 0.828869723 | 0.932364957 | 16 | 1 | KQK13727 | 0.728 | - | genblast_C |
| 0.907321123 | 0.949228792 | 16 | 0 | KQK22017 | 0.928 | 0 | HORVU.MC |
| 0.898042812 | 0.96563893 | 16 | 1 | KQJ99173 | 0.885 | -0 | HORVU.MC |
| 0.912664145 | 0.954324864 | 16 | 1 | KQK04445 | 0.936 | 0 | HORVU.MC |
| 0.903807663 | 0.974075486 | 16 | 1 | KQK18076 | 0.932 | 0 | genblast_C |
| 0.907544809 | 0.962988827 | 16 | 2 | KQK12268 | 0.847 | - | HORVU.MC |
| 0.787856196 | 0.901921803 | 16 | 0 | KQJ98978 | 0.813 | 0. | HORVU.MC |
| 0.943869033 | 0.987261934 | 16 | 0 | KQJ97539 | 0.956 | 0. | HORVU.MC |
| 0.967648678 | 0.996182085 | 16 | 1 | KQJ86559 | 0.982 | 0. | HORVU.MC |
| 0.922354317 | 0.995854554 | 16 | 0 | KQJ84433 | 0.894 | -0 | genblast_C |
| 0.820553302 | 0.907763615 | 16 | 1 | KQK20423 | 0.749 | - | HORVU.MC |
| 0.96709392 | 1.001451906 | 16 | 0 | KQK07357 | 0.972 | 0 | HORVU.MC |
| 0.931676421 | 0.991991375 | 16 | 1 | KQK11128 | 0.915 | - | HORVU.MC |
| 0.909038535 | 0.969305331 | 16 | 1 | KQJ98447 | 0.926 | 0. | HORVU.MC |
| 0.905671296 | 0.988271605 | 16 | 0 | KQK23398 | 0.889 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.869973951 | 0.988244723 | 16 | 0 | PNT61627 | 0.912 | 0. | HORVU.MC |
| 0.943815753 | 0.993540052 | 16 | 1 | KQK09437 | 0.972 | 0. | HORVU.MC |
| 0.85874015 | 0.942255602 | 16 | 1 | KQK17694 | 0.793 | – | HORVU.MC |
| 0.928193311 | 0.986955745 | 16 | 1 | KQJ83014 | 0.855 | –0 | HORVU.MC |
| 0.873404158 | 0.961882181 | 16 | 1 | KQK01647 | 0.869 | – | HORVU.MC |
| 0.869376858 | 0.959787201 | 16 | 0 | KQJ81955 | 0.891 | 0. | HORVU.MC |
| 0.895486854 | 0.969428309 | 16 | 6 | PNT76744 | 0.893 | – | genblast_C |
| 0.960666611 | 0.994128725 | 16 | 0 | KQK01659 | 0.940 | – | HORVU.MC |
| 0.838917599 | 0.914040438 | 16 | 1 | KQJ88137 | 0.850 | 0. | HORVU.MC |
| 0.959631118 | 0.992966844 | 16 | 1 | KQJ85719 | 0.980 | 0. | HORVU.MC |
| 0.948522385 | 0.989781666 | 16 | 0 | KQK15185 | 0.987 | 0 | HORVU.MC |
| 0.852497936 | 0.907720892 | 16 | 0 | KQK10114 | 0.814 | – | HORVU.MC |
| 0.796647135 | 0.855208333 | 16 | 0 | KQK13867 | 0.855 | 1 | genblast_C |
| 0.800823957 | 0.895764781 | 16 | 0 | KQK07639 | 0.705 | – | HORVU.MC |
| 0.931475524 | 0.995079485 | 16 | 7 | KQJ94906 | 0.967 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.961383419 | 1.000570776 | 16 | 1 | KQJ91917 | 0.936 | −0 | HORVU.MC |
| | | | | | | | |
| 0.909526739 | 0.960986735 | 16 | 1 | PNT70184 | 0.944 | 0. | HORVU.MC |
| 0.892676829 | 0.964585366 | 16 | 0 | KQK06829 | 0.904 | 0 | genblast_C |
| 0.855301742 | 0.955580233 | 16 | 7 | KQJ94374 | 0.919 | 0. | HORVU.MC |
| | | | | | | | |
| 0.758484916 | 0.88176575 | 16 | 0 | KQK14329 | 0.695 | − | genblast_C |
| 0.892324777 | 0.965772836 | 16 | 0 | KQK16994 | 0.882 | − | HORVU.MC |
| | | | | | | | |
| 0.925588211 | 0.976634373 | 16 | 0 | KQK04130 | 0.910 | − | HORVU.MC |
| 0.854917641 | 0.939723084 | 16 | 3 | KQJ81462 | 0.816 | −0 | HORVU.MC |
| 0.831100104 | 0.916162669 | 16 | 0 | KQJ91599 | 0.848 | 0. | HORVU.MC |
| 0.869098542 | 0.990811153 | 16 | 0 | KQJ94949 | 0.754 | −1 | HORVU.MC |
| 0.96179966 | 1 | 16 | 0 | KQK15103 | 0.973 | 0 | HORVU.MC |
| 0.797333044 | 0.87753686 | 16 | 1 | PNT69169 | 0.751 | − | HORVU.MC |
| 0.881961715 | 0.974301002 | 16 | 2 | KQK02638 | 0.954 | 0 | HORVU.MC |
| 0.868651933 | 0.951667134 | 16 | 0 | KQK03405 | 0.841 | − | HORVU.MC |
| 0.826002331 | 0.932851449 | 16 | 5 | KQJ98355 | 0.885 | 0. | genblast_C |
| 0.925678315 | 0.980731174 | 16 | 1 | KQJ82859 | 0.944 | 0. | HORVU.MC |
| 0.910327351 | 0.94131328 | 16 | 2 | KQJ82863 | 0.860 | −1 | genblast_C |
| 0.92635458 | 0.983050847 | 16 | 0 | KQJ98384 | 0.936 | 0. | HORVU.MC |
| 0.907970288 | 0.99580751 | 16 | 2 | KQK01324 | 0.959 | 0 | HORVU.MC |
| 0.83378218 | 0.942669345 | 16 | 2 | KQJ98103 | 0.743 | −0 | HORVU.MC |
| | | | | | | | |
| 0.814290926 | 0.911912974 | 16 | 1 | KQJ86765 | 0.881 | 0. | HORVU.MC |
| 0.951787833 | 1.005083884 | 16 | 0 | KQJ86919 | 0.941 | −0 | HORVU.MC |
| 0.819996433 | 0.928462244 | 16 | 2 | KQJ86530 | 0.859 | 0. | HORVU.MC |
| 0.832927077 | 0.953077392 | 16 | 0 | KQK00498 | 0.666 | − | HORVU.MC |

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|---|---|---|---|---|
| 0.864127271 | 0.974848626 | 16 | 0 KQJ91728 0.717 -1 | HORVU.MC |
| 0.923200076 | 0.978635274 | 16 | 1 KQK02011 0.817 – | HORVU.MC |
| 0.904288065 | 0.981714007 | 16 | 1 KQJ90976 0.938 0. | HORVU.MC |
| 0.920777713 | 0.986070807 | 16 | 2 KQK01435 0.941 0 | HORVU.MC |
| 0.843951731 | 0.968896714 | 16 | 0 KQK15476 0.786 – | HORVU.MC |
| 0.844305397 | 0.930050546 | 16 | 1 PNT76253 0.792 – | HORVU.MC |
| 0.790852446 | 0.890475076 | 16 | 2 KQK09913 0.741 – | HORVU.MC |
| 0.907260963 | 0.974299065 | 16 | 0 genblast_Os05t053 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.947471835 | 0.991201717 | 16 | 1 | KQK08793 0.971 0 | HORVU.MC |
| 0.924849562 | 0.988402626 | 16 | 1 | KQK12689 0.921 − | HORVU.MC |
| 0.873975534 | 0.937469645 | 16 | 1 | genblast_Os02t058 | HORVU.MC |
| 0.904352693 | 0.983405768 | 16 | 0 | KQJ98981 0.909 0. | HORVU.MC |
| 0.940585763 | 0.989040221 | 16 | 2 | KQK01684 0.971 0 | HORVU.MC |
| 0.800639103 | 0.852484675 | 16 | 1 | genblast_Os07t024 | HORVU.MC |
| 0.832989023 | 0.937345831 | 16 | 0 | KQK01522 0.801 − | HORVU.MC |
| 0.907107434 | 0.976208132 | 16 | 3 | genblast_Os07t054 | genblast_C |
| 0.927362962 | 0.986671673 | 16 | 0 | KQJ99121 0.976 0. | HORVU.MC |
| 0.793525759 | 0.930491669 | 16 | 3 | KQK18399 0.844 0 | HORVU.MC |
| 0.808724959 | 0.939750824 | 16 | 11 | PNT75007 0.851 0. | HORVU.MC |
| 0.827810292 | 0.936598751 | 16 | 4 | KQK14417 0.764 − | HORVU.MC |
| 0.875352327 | 0.972760891 | 16 | 7 | KQJ96888 0.951 0. | HORVU.MC |
| 0.842917201 | 0.943138093 | 16 | 2 | PNT68321 0.665 − | HORVU.MC |
| 0.836894244 | 0.91480056 | 16 | 1 | KQJ84638 0.743 −1 | HORVU.MC |

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|---|---|---|---|---|
| 0.894104777 | 0.947488133 | 16 | 3 KQJ98399 0.857 −0 | genblast_C |
| 0.92548445 | 0.992166333 | 16 | 4 KQJ82233 0.961 0. | HORVU.MC |
| 0.851607736 | 0.967939095 | 16 | 8 KQK07803 0.711 − | genblast_Z |
| 0.934375 | 1.003872054 | 16 | 1 KQJ88671 0.949 0. | HORVU.MC |
| 0.922493325 | 0.978844311 | 16 | 0 KQJ94670 0.887 −0 | HORVU.MC |
| 0.928482711 | 0.96899841 | 16 | 0 PNT65594 0.896 − | HORVU.MC |
| 0.85618777 | 0.925103533 | 16 | 2 KQJ99235 0.925 1. | HORVU.MC |
| 0.940595629 | 0.983448391 | 16 | 2 KQK02069 0.974 0 | HORVU.MC |
| 0.831201664 | 0.909229673 | 16 | 1 KQJ85119 0.785 −0 | HORVU.MC |
| 0.887437064 | 0.935118435 | 16 | 0 KQJ85066 0.857 −0 | HORVU.MC |
| 0.935287055 | 1.011951301 | 16 | 1 genblast_Os01t090 | HORVU.MC |
| 0.88074535 | 0.946901163 | 16 | 2 KQK22486 0.858 − | HORVU.MC |
| 0.859000785 | 0.926187672 | 16 | 0 KQJ85182 0.856 −0 | HORVU.MC |
| 0.817325228 | 0.913880446 | 16 | 0 KQK13240 0.732 − | HORVU.MC |
| 0.919572032 | 0.977737973 | 16 | 0 KQK09094 0.922 0 | genblast_C |
| 0.943094042 | 0.998163453 | 16 | 1 KQJ99714 0.975 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.931946343 | 0.977881066 | 16 | 6 | KQK05622 | 0.942 | 0 | HORVU.MC |
| 0.860552764 | 0.96289138 | 16 | 1 | KQK15814 | 0.920 | 0 | HORVU.MC |
| 0.892274247 | 0.966153846 | 16 | 2 | PNT64635 | 0.753 | − | HORVU.MC |
| 0.940023491 | 0.993580798 | 16 | 1 | KQK18047 | 0.947 | 0 | HORVU.MC |
| 0.873451683 | 0.935514372 | 16 | 0 | KQJ96675 | 0.777 | −1 | HORVU.MC |
| 0.94185817 | 0.988864143 | 16 | 2 | KQK17355 | 0.924 | − | HORVU.MC |
| 0.889316934 | 0.975344615 | 16 | 0 | KQJ90183 | 0.953 | 0. | HORVU.MC |
| 0.958873495 | 0.994470386 | 16 | 1 | KQK08682 | 0.974 | 0 | HORVU.MC |
| 0.881938468 | 0.938037866 | 16 | 1 | KQJ99306 | 0.866 | −0 | genblast_C |
| 0.915969837 | 0.961027326 | 16 | 0 | KQJ82448 | 0.903 | −0 | HORVU.MC |
| 0.779256257 | 0.876277758 | 16 | 1 | KQK07088 | 0.710 | − | HORVU.MC |
| 0.887082886 | 0.969135802 | 16 | 1 | KQK09143 | 0.969 | 0 | HORVU.MC |
| 0.887195122 | 0.974954984 | 16 | 0 | KQJ86062 | 0.902 | 0. | HORVU.MC |
| 0.912400218 | 0.976342525 | 16 | 1 | KQJ97288 | 0.954 | 0. | HORVU.MC |
| 0.888657248 | 0.955372153 | 16 | 4 | KQK09006 | 0.939 | 1 | HORVU.MC |
| 0.917183558 | 0.971930193 | 16 | 1 | KQJ83453 | 0.949 | 0. | HORVU.MC |
| 0.943814111 | 0.973329997 | 16 | 0 | KQK01343 | 0.939 | − | HORVU.MC |
| 0.788010486 | 0.851545254 | 16 | 3 | PNT72612 | 0.816 | 0. | HORVU.MC |
| 0.912564658 | 0.974376167 | 16 | 1 | KQK23686 | 0.886 | − | HORVU.MC |
| 0.811398635 | 0.899984124 | 16 | 0 | PNT74568 | 0.712 | − | HORVU.MC |
| 0.824857796 | 0.864597502 | 16 | 1 | KQK11264 | 0.773 | − | HORVU.MC |
| 0.856054698 | 0.904880241 | 16 | 6 | KQK03627 | 0.888 | 0 | HORVU.MC |
| 0.919603625 | 0.977663859 | 16 | 0 | KQK01626 | 0.881 | − | HORVU.MC |
| 0.832840237 | 0.920274058 | 16 | 0 | KQK02176 | 0.826 | − | HORVU.MC |
| 0.883714634 | 0.964261541 | 16 | 1 | KQK16890 | 0.705 | − | HORVU.MC |
| 0.934679335 | 0.99538913 | 16 | 1 | KQJ97410 | 0.941 | 0. | HORVU.MC |
| 0.913409538 | 1.005703048 | 16 | 1 | KQJ83937 | 0.978 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.952898682 | 0.993468985 | 16 | 2 | KQK20551 | 0.980 | 0 | HORVU.MC |
| 0.963194687 | 0.999651203 | 16 | 1 | KQK00162 | 0.973 | 0 | HORVU.MC |
| 0.842672829 | 0.911804352 | 16 | 1 | KQJ90193 | 0.828 | −0 | HORVU.MC |
| 0.906941489 | 0.970851064 | 16 | 0 | KQK15841 | 0.951 | 0 | HORVU.MC |
| 0.962381544 | 1.00150122 | 16 | 2 | KQJ84559 | 0.992 | 0. | HORVU.MC |
| 0.835519514 | 0.947531662 | 16 | 2 | KQK00044 | 0.694 | − | genblast_C |
| 0.762606444 | 0.832486019 | 16 | 0 | KQK01281 | 0.662 | − | HORVU.MC |
| 0.78947187 | 0.869277441 | 16 | 0 | KQJ82973 | 0.820 | 0. | genblast_C |
| 0.928779776 | 1.006562956 | 16 | 2 | KQJ82834 | 0.984 | 0. | HORVU.MC |
| 0.860714571 | 0.951855406 | 16 | 1 | KQK01436 | 0.813 | − | HORVU.MC |
| 0.83527027 | 0.921891892 | 16 | 1 | KQK16645 | 0.758 | − | HORVU.MC |
| 0.916404155 | 0.957104558 | 16 | 0 | PNT65674 | 0.903 | − | HORVU.MC |
| 0.788209977 | 0.869730243 | 16 | 1 | KQJ92487 | 0.662 | −2 | HORVU.MC |
| 0.928518444 | 0.983159583 | 16 | 0 | KQJ83652 | 0.945 | 0. | HORVU.MC |
| 0.855952606 | 0.932527694 | 16 | 3 | PNT61937 | 0.864 | 0. | HORVU.MC |
| 0.920253679 | 0.994076056 | 16 | 3 | KQJ95447 | 0.942 | 0. | HORVU.MC |
| 0.884144771 | 0.941524987 | 16 | 0 | KQK00957 | 0.850 | − | HORVU.MC |
| 0.828470667 | 0.920734438 | 16 | 8 | KQJ98265 | 0.918 | 1. | HORVU.MC |
| 0.831855121 | 0.909297448 | 16 | 4 | KQJ98581 | 0.887 | 0. | HORVU.MC |
| 0.939179224 | 0.981093184 | 16 | 2 | KQJ94112 | 0.971 | 0. | HORVU.MC |
| 0.881895557 | 0.9406809 | 16 | 0 | KQK03847 | 0.825 | − | HORVU.MC |

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|---|---|---|---|---|
| 0.924752452 | 0.97363729 | 16 | 1 KQK22394 0.959 0 | HORVU.MC |
| 0.921385497 | 0.971974777 | 16 | 1 KQK05286 0.962 0 | HORVU.MC |
| 0.890759587 | 0.949262537 | 16 | 1 KQJ94096 0.910 0. | HORVU.MC |
| 0.815269936 | 0.946365561 | 16 | 1 KQJ90325 0.685 −1 | HORVU.MC |
| 0.909072137 | 0.964977974 | 16 | 0 KQJ83127 0.930 0. | HORVU.MC |
| 0.935260943 | 0.987259658 | 16 | 2 KQK19815 0.972 0 | HORVU.MC |
| 0.876591883 | 0.951519479 | 16 | 0 KQJ88748 0.878 0. | HORVU.MC |
| 0.858913297 | 0.914463453 | 16 | 1 KQK09832 0.864 0 | HORVU.MC |
| 0.811819596 | 0.869880767 | 16 | 1 KQJ93345 0.660 −2 | HORVU.MC |
| 0.880358174 | 0.93818602 | 16 | 3 KQJ93794 0.909 0. | HORVU.MC |
| 0.920299728 | 1.001467198 | 16 | 2 PNT68470 0.871 − | HORVU.MC |
| 0.884800928 | 0.976844162 | 16 | 0 genblast_Os05t035 | HORVU.MC |
| 0.955838877 | 0.99883856 | 16 | 0 KQJ99659 0.978 0. | HORVU.MC |
| 0.866084265 | 0.932268371 | 16 | 0 PNT77571 0.884 0. | HORVU.MC |
| 0.837406508 | 0.913922057 | 16 | 3 KQJ88005 0.908 0. | HORVU.MC |
| 0.919247231 | 0.984318803 | 16 | 0 KQK03846 0.925 0 | HORVU.MC |
| 0.844972425 | 0.954982686 | 16 | 0 KQJ86353 0.719 −1 | HORVU.MC |
| 0.871269651 | 0.957633893 | 16 | 0 KQK20448 0.879 0 | HORVU.MC |
| 0.931870695 | 0.984959086 | 16 | 2 KQK05853 0.944 0 | HORVU.MC |
| 0.894884393 | 0.944739884 | 16 | 0 KQK15683 0.890 − | HORVU.MC |
| 0.84588101 | 0.927264314 | 16 | 3 genblast_Os05t014 | HORVU.MC |
| 0.793566425 | 0.925033796 | 16 | 3 KQK04827 0.727 − | HORVU.MC |
| 0.8864493 | 0.99472982 | 16 | 3 KQK17949 0.807 − | HORVU.MC |
| 0.806774888 | 0.88984595 | 16 | 0 KQK21803 0.754 − | HORVU.MC |
| 0.922956142 | 0.971684054 | 16 | 0 KQK21912 0.929 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.891021574 | 0.990433424 | 16 | 0 | KQK22883 | 0.961 | 0 | HORVU.MC |
| 0.835103068 | 0.948034516 | 16 | 1 | KQK03313 | 0.769 | – | HORVU.MC |
| 0.815189005 | 0.940332861 | 16 | 1 | KQJ98829 | 0.701 | –1 | HORVU.MC |
| 0.801208651 | 0.91198242 | 16 | 2 | PNT77180 | 0.831 | 0. | genblast_C |
| 0.81914794 | 0.933707865 | 16 | 3 | KQK02670 | 0.756 | – | HORVU.MC |
| 0.943104844 | 0.982421359 | 16 | 2 | KQJ99568 | 0.972 | 0. | HORVU.MC |
| 0.921355811 | 0.991129154 | 16 | 1 | KQJ85279 | 0.906 | –0 | HORVU.MC |
| 0.907897967 | 0.985956987 | 16 | 2 | KQK10663 | 0.965 | 0 | HORVU.MC |
| 0.901013562 | 0.946087878 | 16 | 3 | KQK09428 | 0.881 | – | HORVU.MC |
| 0.90735962 | 0.970639508 | 16 | 0 | KQJ97398 | 0.904 | –0 | genblast_C |
| 0.89365596 | 0.932807199 | 16 | 2 | KQK22075 | 0.879 | – | HORVU.MC |
| 0.913600618 | 0.96545429 | 16 | 0 | KQK24168 | 0.958 | 0 | HORVU.MC |
| 0.866543897 | 0.929262559 | 16 | 3 | KQJ87392 | 0.808 | –0 | HORVU.MC |
| 0.928690124 | 0.99873391 | 16 | 0 | KQK08787 | 0.985 | 0 | HORVU.MC |
| 0.832769744 | 0.931628596 | 16 | 4 | KQK21809 | 0.911 | 1 | HORVU.MC |

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| 0.894509476 | 0.999721293 | 16 | 0 KQK13888 0.860 – | HORVU.MC |
| 0.762179786 | 0.913295997 | 16 | 3 KQK06675 0.780 0 | HORVU.MC |
| 0.799067496 | 0.860568384 | 16 | 1 KQK16700 0.754 – | HORVU.MC |
| 0.89880151 | 0.977991103 | 16 | 1 KQJ93897 0.779 –1 | HORVU.MC |
|  |  |  |  |  |
| 0.917914452 | 0.968928863 | 16 | 1 KQJ91066 0.896 –0 | HORVU.MC |
| 0.874789326 | 0.953370787 | 16 | 0 KQJ90014 0.874 –0 | HORVU.MC |
| 0.825428341 | 0.913550672 | 16 | 4 PNT68924 0.864 0. | genblast_C |
| 0.861921981 | 0.944045608 | 16 | 2 KQK14666 0.754 – | HORVU.MC |
| 0.934286632 | 0.985960055 | 16 | 2 KQK00397 0.963 0 | HORVU.MC |
|  |  |  |  |  |
| 0.866515246 | 0.97048176 | 16 | 1 PNT72870 0.864 – | genblast_C |
|  |  |  |  |  |
| 0.858356185 | 0.949928905 | 16 | 0 KQJ90138 0.794 –0 | HORVU.MC |
| 0.924795757 | 0.960492623 | 16 | 0 KQK18610 0.926 0 | HORVU.MC |
|  |  |  |  |  |
| 0.8892019 | 0.970385547 | 16 | 1 KQJ83320 0.831 –0 | HORVU.MC |
| 0.918760378 | 0.979550817 | 16 | 2 KQK14874 0.860 – | HORVU.MC |
| 0.906259292 | 0.965011399 | 16 | 0 PNT69503 0.924 0. | HORVU.MC |
| 0.887661255 | 0.973105936 | 16 | 2 KQJ86513 0.938 0. | genblast_C |
| 0.896403037 | 0.978812233 | 16 | 3 KQK17227 0.897 0 | HORVU.MC |
| 0.885488754 | 0.939220701 | 16 | 2 KQJ92850 0.884 –0 | HORVU.MC |
| 0.896183823 | 0.963311472 | 16 | 1 PNT72015 0.917 0. | HORVU.MC |

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| 0.863434198 | 0.956339341 | 16 | 0 KQK13806 0.780 – | HORVU.MC |
| 0.896279158 | 0.963995943 | 16 | 1 KQK09396 0.876 – | HORVU.MC |
| 0.961545555 | 1.013463667 | 16 | 0 genblast_Os01t081 | HORVU.MC |
| 0.883073004 | 0.959413944 | 16 | 1 KQK14200 0.867 – | HORVU.MC |
| 0.797997025 | 0.899261387 | 16 | 1 KQK21883 0.818 0 | HORVU.MC |
| 0.913093788 | 0.98319123 | 16 | 0 KQK02081 0.863 – | HORVU.MC |
| 0.941053142 | 0.992179984 | 16 | 3 KQJ82662 0.966 0. | HORVU.MC |
| 0.932643381 | 0.9898232 | 16 | 0 KQJ85270 0.948 0. | HORVU.MC |
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| 0.922894646 | 0.98705576 | 16 | 2 KQK20636 0.973 0 | HORVU.MC |
| 0.77384549 | 0.885196375 | 16 | 1 PNT67502 0.765 – | HORVU.MC |
| 0.807449063 | 0.910367263 | 16 | 3 KQJ99914 0.810 0. | HORVU.MC |
| 0.925554901 | 0.975446867 | 16 | 0 KQK09767 0.947 0 | HORVU.MC |
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| 0.829269126 | 0.911885246 | 16 | 3 KQJ98817 0.836 0. | HORVU.MC |
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| 0.85184937 | 0.967300992 | 16 | 1 KQK09009 0.906 0 | HORVU.MC |
| 0.956226431 | 0.988687007 | 16 | 1 KQJ86512 0.963 0. | HORVU.MC |
| 0.858462705 | 0.936188437 | 16 | 4 KQK12638 0.873 0 | HORVU.MC |
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| 0.940437302 | 0.989041096 | 16 | 1 KQK00979 0.947 0 | HORVU.MC |
| 0.906603577 | 0.972435265 | 16 | 2 KQK09139 0.877 – | HORVU.MC |
| 0.859375882 | 0.964658725 | 16 | 5 KQJ88382 0.965 1. | HORVU.MC |
| 0.883764271 | 0.965480188 | 16 | 2 KQK11604 0.836 – | HORVU.MC |
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| 0.852108535 | 0.985215054 | 16 | 0 KQJ93777 0.687 –1 | HORVU.MC |
| 0.884781871 | 0.993379732 | 16 | 0 KQK14585 0.883 – | HORVU.MC |
| 0.921693427 | 0.979882544 | 16 | 0 KQJ99728 0.979 0. | HORVU.MC |
| | | | | |
| 0.896505018 | 0.971602434 | 16 | 1 PNT64827 0.841 – | HORVU.MC |
| 0.886152656 | 0.976276431 | 16 | 0 genblast_Zm00001 | HORVU.MC |
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| 0.971823479 | 1 | 16 | 0 KQK00424 0.978 0 | HORVU.MC |
| 0.885372738 | 0.93375051 | 16 | 0 KQJ90024 0.864 –0 | HORVU.MC |
| 0.914270194 | 0.989263804 | 16 | 0 KQK14946 0.945 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.888046614 | 0.966899484 | 16 | 1 | KQJ84101 | 0.885 | −0 | HORVU.MC |
| 0.922834967 | 0.979738562 | 16 | 1 | KQK16469 | 0.954 | 0. | HORVU.MC |
| 0.798295455 | 0.866761364 | 16 | 1 | KQJ96570 | 0.745 | −0 | HORVU.MC |
| 0.885074455 | 0.943851704 | 16 | 7 | KQK10258 | 0.873 | − | HORVU.MC |
| 0.93816896 | 0.988850663 | 16 | 1 | KQK15369 | 0.926 | − | HORVU.MC |
| 0.80896669 | 0.894440535 | 16 | 0 | KQK11348 | 0.655 | − | HORVU.MC |
| 0.800027233 | 0.923747277 | 16 | 1 | KQK09557 | 0.780 | − | HORVU.MC |
| 0.94133452 | 0.980355872 | 16 | 1 | KQJ85344 | 0.963 | 0. | HORVU.MC |
| 0.893516914 | 0.983086095 | 16 | 2 | KQJ89794 | 0.944 | 0. | HORVU.MC |
| 0.830154072 | 0.976522377 | 16 | 1 | PNT66668 | 0.810 | − | HORVU.MC |
| 0.868267276 | 0.965447154 | 16 | 3 | KQJ97141 | 0.911 | 0. | HORVU.MC |
| 0.744456658 | 0.820603015 | 16 | 10 | KQK24128 | 0.760 | 0. | HORVU.MC |
| 0.914665542 | 0.979750779 | 16 | 1 | KQK19881 | 0.929 | 0. | genblast_C |
| 0.859616397 | 0.921769663 | 16 | 2 | KQJ88022 | 0.869 | 0. | HORVU.MC |
| 0.773026764 | 1.011304822 | 16 | 2 | KQJ97937 | 0.806 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.910048149 | 1.000186986 | 16 | 3 | KQJ87576 | 0.939 | 0. | HORVU.MC |
| 0.883561644 | 0.963992172 | 16 | 1 | KQJ93496 | 0.889 | 0. | HORVU.MC |
| 0.812423219 | 0.894553645 | 16 | 0 | KQJ98210 | 0.774 | –0 | HORVU.MC |
| 0.792705294 | 0.891281963 | 16 | 1 | KQJ81660 | 0.813 | 0. | HORVU.MC |
| 0.961184686 | 0.995208823 | 16 | 1 | KQJ91766 | 0.970 | 0. | HORVU.MC |
| 0.907838368 | 0.948010456 | 16 | 0 | KQJ84757 | 0.831 | –1 | HORVU.MC |
| 0.935135313 | 0.967536638 | 16 | 0 | KQK08778 | 0.940 | 0 | HORVU.MC |
| 0.843705357 | 0.938571429 | 16 | 3 | genblast_Os06t027 | | | HORVU.MC |
| 0.917582948 | 0.995811287 | 16 | 1 | KQK14930 | 0.914 | – | HORVU.MC |
| 0.802793454 | 0.921218962 | 16 | 1 | KQK02553 | 0.740 | – | HORVU.MC |
| 0.96700223 | 0.998268625 | 16 | 1 | KQK01220 | 0.995 | 0 | HORVU.MC |
| 0.856647685 | 0.976231741 | 16 | 0 | KQK23531 | 0.654 | – | HORVU.MC |
| 0.897539003 | 0.966450366 | 16 | 2 | KQK01499 | 0.885 | – | genblast_C |
| 0.88696494 | 0.953884356 | 16 | 2 | KQK01934 | 0.654 | – | HORVU.MC |
| 0.901619318 | 0.974545455 | 16 | 0 | KQK06525 | 0.867 | – | HORVU.MC |
| 0.799215643 | 0.892178524 | 16 | 0 | KQJ90762 | 0.801 | 0. | HORVU.MC |
| 0.946235191 | 0.997038134 | 16 | 0 | KQJ90931 | 0.965 | 0. | HORVU.MC |
| 0.837221372 | 0.920454545 | 16 | 0 | KQJ90123 | 0.819 | –0 | HORVU.MC |
| 0.874701476 | 0.976335215 | 16 | 2 | KQK12332 | 0.891 | 0 | HORVU.MC |
| 0.825752919 | 0.917639828 | 16 | 4 | KQK18601 | 0.869 | 0 | HORVU.MC |
| 0.929555441 | 0.978774491 | 16 | 2 | KQK15965 | 0.971 | 0 | HORVU.MC |
| 0.873635123 | 0.956505914 | 16 | 1 | PNT75064 | 0.796 | – | genblast_C |

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| 0.811101196 | 0.975303878 | 16 | 1 KQK15041 0.714 – | HORVU.M |
| 0.876459568 | 0.949111189 | 16 | 0 PNT64464 0.845 – | HORVU.M |
| 0.833300531 | 0.959752017 | 16 | 9 PNT72785 0.785 – | HORVU.M |
| 0.936463004 | 0.974887892 | 16 | 0 KQJ84976 0.941 0. | HORVU.M |
| 0.838236408 | 0.936846888 | 16 | 4 PNT66810 0.897 0. | HORVU.M |
| 0.846966255 | 0.942209516 | 16 | 2 KQJ85885 0.737 –1 | HORVU.M |
| 0.956968712 | 1.000430367 | 16 | 0 KQJ98047 0.991 0. | genblast_ |
| 0.82726147 | 0.867570386 | 16 | 1 KQK15997 0.818 – | HORVU.M |
| 0.904285616 | 0.967151615 | 16 | 0 KQJ92414 0.891 –0 | HORVU.M |
| 0.936052484 | 0.979379903 | 16 | 1 KQJ83256 0.961 0. | HORVU.M |
| 0.888894158 | 0.972938796 | 16 | 0 KQK02928 0.894 0 | HORVU.M |
| 0.857920969 | 0.942074161 | 16 | 1 KQK04562 0.896 0 | HORVU.M |
| 0.802250765 | 0.888442403 | 16 | 0 KQK12154 0.759 – | genblast_ |
| 0.820514887 | 0.940921346 | 16 | 2 KQK17149 0.680 – | HORVU.M |
| 0.907601781 | 0.956155803 | 16 | 0 KQK09598 0.921 0 | HORVU.M |
| 0.913678923 | 0.960534829 | 16 | 0 KQK15462 0.863 – | HORVU.M |
| 0.835341713 | 0.906826568 | 16 | 2 KQK06036 0.852 0 | HORVU.M |
| 0.93475688 | 0.987416389 | 16 | 2 KQJ81989 0.976 0. | HORVU.M |
| 0.904076177 | 0.97453423 | 16 | 0 KQK11613 0.867 – | HORVU.M |
| 0.860897075 | 0.98200225 | 16 | 0 KQK23920 0.796 – | HORVU.M |
| 0.859563746 | 0.936835977 | 16 | 1 KQJ95651 0.937 1. | HORVU.M |
| 0.836475202 | 0.963450292 | 16 | 2 genblast_Os10t055 | HORVU.M |
| 0.894842153 | 0.941689322 | 16 | 0 KQK22280 0.850 – | HORVU.M |

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|---|---|---|---|---|---|
| 0.945904241 | 1.004320607 | 16 | 1 | KQK08835 0.964 0 | genblast_C |
| 0.884214092 | 0.950677507 | 16 | 2 | KQJ82498 0.840 -0 | HORVU.MC |
| 0.909325759 | 0.97408084 | 16 | 1 | genblast_Os01t082 | HORVU.MC |
| 0.895299057 | 0.945695655 | 16 | 2 | genblast_Os12t026 | HORVU.MC |
| 0.882507757 | 0.951573582 | 16 | 0 | KQJ98896 0.823 -0 | HORVU.MC |
| 0.92746339 | 0.98414619 | 16 | 3 | PNT75774 0.958 0. | HORVU.MC |
| 0.761385178 | 0.865138112 | 16 | 2 | KQJ91164 0.651 -1 | HORVU.MC |
| 0.868627583 | 0.958411591 | 16 | 3 | KQK09644 0.907 0 | HORVU.MC |
| 0.886176647 | 0.941001832 | 16 | 2 | KQJ94021 0.895 0. | HORVU.MC |
| 0.908695652 | 0.979198636 | 16 | 1 | PNT71040 0.888 - | HORVU.MC |
| 0.942142134 | 0.977717758 | 16 | 0 | KQK10340 0.960 0 | HORVU.MC |
| 0.89937231 | 0.955236729 | 16 | 0 | KQK12540 0.859 - | HORVU.MC |
| 0.903163921 | 0.995145631 | 16 | 1 | KQK10873 0.940 0 | genblast_C |
| 0.898236024 | 0.975172193 | 16 | 1 | KQK03010 0.905 0 | HORVU.MC |
| 0.951647918 | 1.010953227 | 16 | 0 | genblast_Os03t028 | HORVU.MC |
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| 0.927795994 | 0.975717831 | 16 | 0 | KQK15836 0.937 0 | HORVU.MC |
| 0.882211538 | 0.957702403 | 16 | 1 | KQJ86358 0.930 0. | genblast_C |
| 0.909732663 | 0.998120654 | 16 | 4 | KQK12436 0.933 0 | HORVU.MC |
| 0.834349971 | 0.951201387 | 16 | 1 | KQK16566 0.882 0 | HORVU.MC |
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| 0.856746728 | 0.943079051 | 16 | 3 | KQJ94281 0.931 1. | genblast_C |
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| 0.917293367 | 0.968779655 | 16 | 0 | KQJ81713 0.899 -0 | genblast_C |
| 0.877525503 | 0.933544617 | 16 | 2 | PNT71923 0.842 - | HORVU.MC |
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| 0.871362434 | 0.944550265 | 16 | 2 | KQJ82846 0.918 0. | HORVU.MC |

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| 0.806956811 | 0.92287234 | 16 | 1 | KQJ85166 | 0.651 | -1 | HORVU.MC |
| 0.796989137 | 0.860086158 | 16 | 6 | KQK20256 | 0.804 | 0. | HORVU.MC |
| 0.943949423 | 1.001357773 | 16 | 0 | KQK11110 | 0.988 | 0. | genblast_C |
| 0.822736135 | 0.969361228 | 16 | 6 | KQK23483 | 0.650 | - | HORVU.MC |
| 0.934855041 | 0.992903505 | 16 | 1 | KQJ99419 | 0.954 | 0. | genblast_C |
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| 0.95384578 | 0.997160638 | 16 | 1 | KQK20229 | 0.982 | 0. | genblast_C |
| 0.807906459 | 0.888641425 | 16 | 0 | KQK17031 | 0.804 | - | HORVU.MC |
| 0.913929213 | 0.965429512 | 16 | 0 | KQK01875 | 0.887 | - | genblast_C |
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| 0.944797161 | 0.982353324 | 16 | 0 | KQK05512 | 0.893 | - | HORVU.MC |
| 0.835601719 | 0.917283884 | 16 | 6 | KQK13121 | 0.770 | - | HORVU.MC |
| 0.892121011 | 0.946194763 | 16 | 1 | KQJ99434 | 0.817 | -2 | HORVU.MC |
| 0.881303442 | 0.928085946 | 16 | 1 | KQJ81573 | 0.840 | -1 | HORVU.MC |
| 0.892482427 | 0.940045483 | 16 | 1 | KQK07175 | 0.922 | 0. | HORVU.MC |
| 0.908013063 | 0.985611511 | 16 | 1 | KQK15970 | 0.969 | 1. | HORVU.MC |
| 0.882252136 | 0.931849791 | 16 | 0 | KQK15438 | 0.864 | - | HORVU.MC |
| 0.893074638 | 0.963906424 | 16 | 3 | KQK16327 | 0.862 | - | HORVU.MC |
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| 0.899215043 | 0.950618007 | 16 | 0 | KQK04842 | 0.857 | - | HORVU.MC |
| 0.900656325 | 0.949403341 | 16 | 0 | KQK15953 | 0.867 | - | HORVU.MC |
| 0.945808775 | 0.986902423 | 16 | 0 | KQJ83200 | 0.967 | 0. | HORVU.MC |
| 0.858737641 | 0.944729591 | 16 | 0 | PNT70770 | 0.824 | - | HORVU.MC |
| 0.850696969 | 0.905423088 | 16 | 1 | KQK08376 | 0.839 | - | HORVU.MC |
| 0.878021243 | 0.933999394 | 16 | 1 | PNT66052 | 0.774 | -2 | HORVU.MC |
| 0.937812277 | 0.98608137 | 16 | 1 | KQK23369 | 0.939 | 0. | HORVU.MC |
| 0.870883364 | 0.943878883 | 16 | 1 | KQK10939 | 0.897 | 0. | HORVU.MC |

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| 0.908814674 | 0.965655665 | 16 | 0 | KQK01988 0.881 − | HORVU.M |
| 0.884192024 | 0.941724297 | 16 | 1 | KQK12990 0.918 1 | HORVU.M |
| 0.933420023 | 0.966978431 | 16 | 0 | KQJ90359 0.926 −0 | HORVU.M |
| 0.90520063 | 0.940619008 | 16 | 5 | PNT77471 0.861 − | HORVU.M |
| 0.908843687 | 0.975100604 | 16 | 1 | PNT65087 0.891 − | HORVU.M |
| 0.94454251 | 0.987045574 | 16 | 0 | KQJ99279 0.901 −1 | HORVU.M |
| 0.87016333 | 0.934129803 | 16 | 2 | genblast_Os01t072 | HORVU.M |
| 0.897598002 | 0.976492091 | 16 | 3 | KQK12880 0.846 − | HORVU.M |
| 0.955085986 | 0.983534577 | 16 | 0 | KQJ90641 0.946 −0 | HORVU.M |
| 0.948587913 | 0.990314291 | 16 | 0 | KQK06669 0.914 − | HORVU.M |
| 0.923645572 | 0.967336683 | 16 | 1 | KQK21039 0.938 0 | HORVU.M |

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| 0.920556575 | 0.955305323 | 16 | 2 | KQK15358 0.920 − | HORVU.M |
| 0.948436715 | 0.966800603 | 16 | 0 | KQJ83569 0.934 −1 | HORVU.M |
| 0.921948064 | 0.946569567 | 16 | 4 | KQK03527 0.901 − | HORVU.M |
| 0.905432118 | 0.950291143 | 16 | 0 | KQK04636 0.871 − | HORVU.M |
| 0.963521853 | 0.98133239 | 16 | 0 | KQK08587 0.960 − | HORVU.M |

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| 0.928004986 | 0.973053257 | 16 | 0 | KQJ89441 0.867 −1 | HORVU.M |
| 0.875042 | 0.938211785 | 16 | 2 | KQK09942 0.767 − | HORVU.M |
| 0.950770195 | 0.987871528 | 16 | 0 | KQK13057 0.931 − | HORVU.M |

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| 0.955185813 | 0.973570958 | 16 | 0 | KQJ92159 0.956 0. | HORVU.M |
| 0.876140649 | 0.954449472 | 16 | 2 | PNT60755 0.789 − | HORVU.M |
| 0.924150617 | 0.984202554 | 16 | 0 | KQK20238 0.895 − | HORVU.M |
| 0.922208722 | 0.982222791 | 16 | 1 | PNT68888 0.911 − | HORVU.M |
| 0.889041508 | 0.942610715 | 16 | 0 | KQK21456 0.840 − | HORVU.M |
| 0.925319549 | 0.971428571 | 16 | 0 | KQK03623 0.851 − | HORVU.M |
| 0.903040421 | 0.951542371 | 16 | 0 | KQJ85912 0.921 0. | HORVU.M |
| 0.935953988 | 0.957903098 | 16 | 0 | KQK18069 0.938 0 | HORVU.M |
| 0.909305073 | 0.941071041 | 16 | 2 | KQK12651 0.902 − | HORVU.M |
| 0.89261979 | 0.930423367 | 16 | 0 | KQJ89703 0.871 −1 | HORVU.M |
| 0.922978325 | 0.980158129 | 16 | 4 | KQK11289 0.915 − | HORVU.M |
| 0.859972678 | 0.917039245 | 16 | 0 | KQJ82122 0.917 1. | HORVU.M |
| 0.912403985 | 0.965242439 | 16 | 0 | KQK23164 0.870 − | HORVU.M |

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| 0.962100704 | 0.99043494 | 16 | 0 | KQK00251 0.988 1 | HORVU.M |

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| 0.909445028 | 0.979516807 | 16 | 2 | KQJ83002 0.878 –0 | HORVU.MC |
| 0.934384751 | 0.969042536 | 16 | 1 | KQK00188 0.941 0 | HORVU.MC |
| 0.94510504 | 0.979700224 | 16 | 0 | KQJ90061 0.933 –0 | HORVU.MC |
| 0.941076916 | 0.998559631 | 16 | 3 | KQK04118 0.957 0 | HORVU.MC |
| 0.867492546 | 0.931421269 | 16 | 0 | PNT61575 0.853 – | HORVU.MC |
| 0.882652228 | 0.943682216 | 16 | 0 | KQJ94603 0.891 0. | HORVU.MC |
| 0.852357356 | 0.916590284 | 16 | 3 | KQJ95241 0.798 –1 | HORVU.MC |
| 0.867717252 | 0.913356164 | 16 | 0 | KQJ85075 0.864 –0 | HORVU.MC |
| 0.913747097 | 0.98017149 | 16 | 1 | KQJ90700 0.853 –1 | HORVU.MC |
| 0.892083051 | 0.937902952 | 16 | 1 | KQJ96493 0.858 –0 | HORVU.MC |
| 0.864217712 | 0.920314406 | 16 | 0 | KQK17899 0.821 – | HORVU.MC |
| 0.937220465 | 0.961280429 | 16 | 0 | PNT67851 0.939 0. | HORVU.MC |
| 0.944080526 | 0.97457085 | 16 | 0 | KQJ94285 0.956 0. | HORVU.MC |
| 0.95345332 | 0.980494725 | 16 | 0 | KQK23316 0.941 – | HORVU.MC |
| 0.854573942 | 0.8850046 | 16 | 0 | KQK00114 0.843 – | HORVU.MC |
| 0.90996696 | 0.94948605 | 16 | 2 | KQJ99758 0.903 –0 | HORVU.MC |
| 0.931460049 | 0.963044532 | 16 | 0 | KQK21194 0.930 – | HORVU.MC |
| 0.869728037 | 0.919492107 | 16 | 0 | genblast_Os06t012 | HORVU.MC |
| 0.874788749 | 0.90535973 | 16 | 0 | KQK09550 0.849 – | HORVU.MC |
| 0.886462969 | 0.937698665 | 16 | 0 | KQK23283 0.840 – | HORVU.MC |
| 0.952296836 | 0.97228176 | 16 | 1 | KQK06788 0.965 0 | HORVU.MC |
| 0.857703473 | 0.93979142 | 16 | 3 | KQJ99990 0.763 –1 | genblast_C |
| 0.962125564 | 0.987660625 | 16 | 1 | KQJ89721 0.942 –1 | HORVU.MC |
| 0.875952425 | 0.93644304 | 16 | 1 | KQK10348 0.853 – | HORVU.MC |
| 0.945492221 | 0.989280463 | 16 | 2 | KQJ97361 0.954 0. | HORVU.MC |
| 0.967240353 | 0.986660314 | 16 | 0 | KQK10543 0.912 – | HORVU.MC |
| 0.853117917 | 0.91196469 | 16 | 2 | KQJ94570 0.866 0. | HORVU.MC |
| 0.954417934 | 0.979444153 | 16 | 1 | KQK22566 0.916 – | HORVU.MC |
| 0.882507123 | 0.963939097 | 16 | 2 | KQJ82898 0.904 0. | genblast_C |
| 0.939417864 | 0.972314332 | 16 | 1 | KQK23699 0.924 – | HORVU.MC |
| 0.908030567 | 0.941413058 | 16 | 0 | KQK10367 0.941 0 | HORVU.MC |
| 0.955097321 | 0.977259588 | 16 | 0 | KQJ92949 0.933 –1 | HORVU.MC |

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| 0.947439049 | 0.982843383 | 16 | 0 | KQK19168 0.930 – | HORVU.MC |
| 0.937141148 | 0.960446571 | 16 | 0 | KQJ86608 0.933 –0 | HORVU.MC |
| 0.851154859 | 0.90689325 | 16 | 0 | KQJ90375 0.821 –0 | HORVU.MC |
| 0.85180798 | 0.91446384 | 16 | 0 | KQK17769 0.812 – | genblast_C |
| 0.918314961 | 0.965863632 | 16 | 2 | KQK14792 0.911 – | HORVU.MC |
| 0.928186963 | 0.977278529 | 16 | 1 | KQJ85833 0.939 0. | HORVU.MC |
| 0.876845882 | 0.928868552 | 16 | 1 | KQJ92530 0.824 –1 | HORVU.MC |
| 0.923769651 | 0.97949419 | 16 | 0 | KQJ95432 0.871 –1 | HORVU.MC |
| 0.919981414 | 0.949672498 | 16 | 1 | KQJ86266 0.930 0. | HORVU.MC |
| 0.915936748 | 0.986894892 | 16 | 0 | KQK04128 0.865 – | genblast_C |
| 0.910122921 | 0.95285611 | 16 | 0 | KQK00610 0.937 0 | HORVU.MC |
| 0.936906922 | 0.989813006 | 16 | 0 | KQK06021 0.930 – | HORVU.MC |
| 0.911796312 | 0.961314476 | 16 | 0 | KQK00579 0.880 – | HORVU.MC |
| 0.868569332 | 0.917931111 | 16 | 0 | KQK17373 0.861 – | HORVU.MC |
| 0.930415714 | 0.974451944 | 16 | 1 | KQK00889 0.929 – | HORVU.MC |
| 0.939301153 | 0.992622478 | 16 | 0 | KQK13033 0.919 – | HORVU.MC |
| 0.858865894 | 0.928476821 | 16 | 0 | KQJ99102 0.781 –1 | HORVU.MC |
| 0.873628792 | 0.942578548 | 16 | 0 | KQJ87479 0.849 –0 | HORVU.MC |
| 0.938198103 | 0.987355111 | 16 | 1 | PNT68556 0.957 0. | HORVU.MC |
| 0.948418278 | 0.985588752 | 16 | 0 | genblast_Os07t067 | HORVU.MC |
| 0.895877651 | 0.927275145 | 16 | 0 | KQJ85225 0.907 0. | HORVU.MC |
| 0.907351328 | 0.974813731 | 16 | 2 | KQK20043 0.892 – | HORVU.MC |
| 0.825299157 | 0.930921947 | 16 | 1 | KQK06924 0.768 – | HORVU.MC |
| 0.96108602 | 0.986451003 | 16 | 0 | KQJ90747 0.936 –1 | HORVU.MC |
| 0.886098998 | 0.936815736 | 16 | 0 | KQK22500 0.898 0 | HORVU.MC |

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| 0.919972959 | 0.95859562 | 16 | 3 | KQJ99427 0.866 –1 | HORVU.MC |
| 0.941038134 | 0.991563317 | 16 | 0 | KQJ99136 0.917 –0 | HORVU.MC |

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| 0.902305095 | 0.952052922 | 16 | 2 | PNT69129 0.911 0. | HORVU.MC |
| 0.90188427 | 0.978613315 | 16 | 0 | KQK11164 0.865 – | HORVU.MC |
| 0.927001397 | 0.968903918 | 16 | 1 | KQJ86182 0.912 –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.983943812 | 1.00056899 | 16 | 0 | KQK22066 | 0.987 | 0. | HORVU.MC |
| 0.846453287 | 0.873611364 | 16 | 1 | KQJ96999 | 0.851 | 0. | genblast_C |
| 0.932553058 | 0.966485199 | 16 | 2 | KQK00977 | 0.940 | 0. | HORVU.MC |
| 0.87624708 | 0.933004988 | 16 | 2 | KQJ86271 | 0.869 | -0 | HORVU.MC |
| 0.922313222 | 0.958284233 | 16 | 0 | KQK21415 | 0.908 | - | HORVU.MC |
| 0.896195903 | 0.972739874 | 16 | 0 | KQK22960 | 0.814 | - | HORVU.MC |

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| 0.983730297 | 1.005331479 | 16 | 0 | KQK09551 | 0.985 | 0. | HORVU.MC |
| 0.829973556 | 0.963222132 | 16 | 4 | KQK22237 | 0.769 | - | HORVU.MC |
| 0.907786352 | 0.956646146 | 16 | 0 | KQJ97234 | 0.882 | -0 | genblast_C |
| 0.959451467 | 0.97688252 | 16 | 1 | KQK19090 | 0.977 | 0. | HORVU.MC |
| 0.934660812 | 0.995760145 | 16 | 0 | KQJ90311 | 0.958 | 0. | HORVU.MC |
| 0.968599342 | 0.98979071 | 16 | 0 | KQJ85581 | 0.922 | -1 | HORVU.MC |
| 0.894788691 | 0.966835925 | 16 | 2 | KQK16586 | 0.864 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.937467837 | 0.979994854 | 16 | 1 | PNT69189 | 0.954 | 0. | HORVU.MC |
| 0.890269486 | 0.957197567 | 16 | 1 | KQK07991 | 0.915 | 0. | HORVU.MC |
| 0.95295433 | 0.99243141 | 16 | 0 | KQK00533 | 0.957 | 0. | HORVU.MC |
| 0.924878049 | 0.985528455 | 16 | 0 | KQJ95425 | 0.888 | -1 | HORVU.MC |
| 0.909173387 | 0.971646859 | 16 | 2 | KQK10411 | 0.922 | 0. | HORVU.MC |
| 0.932337022 | 0.960208031 | 16 | 0 | PNT76659 | 0.919 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.95915189 | 0.990938916 | 16 | 0 | KQJ97945 | 0.952 | -0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.930217504 | 0.985844985 | 16 | 0 | KQK08550 | 0.954 | 0. | HORVU.MC |
| 0.943270663 | 0.965003723 | 16 | 0 | KQK22715 | 0.964 | 1. | genblast_C |

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| 0.934329804 | 0.983599751 | 16 | 1 KQJ84989 0.930 -0HORVU.MC |

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| 0.932524157 | 0.973442409 | 16 | 1 KQK00734 0.927 -HORVU.MC |
| 0.872544932 | 0.941448953 | 16 | 0 KQK17506 0.802 - HORVU.MC |
| 0.957519779 | 0.985191196 | 16 | 0 KQK19620 0.893 -HORVU.MC |
| 0.938991341 | 0.980115459 | 16 | 0 KQK17747 0.947 0HORVU.MC |
| 0.883963744 | 0.949372629 | 16 | 0 KQK23047 0.869 -HORVU.MC |
| 0.8672688 | 0.950323974 | 16 | 0 KQJ90531 0.757 -1HORVU.MC |
| 0.945461108 | 0.970698882 | 16 | 0 KQK07624 0.898 - HORVU.MC |

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| 0.959807707 | 0.992546488 | 16 | 0 KQK06274 0.949 -HORVU.MC |
| 0.920083462 | 0.99205899 | 16 | 0 KQK23737 0.890 -genblast_C |
| 0.944647494 | 0.993565139 | 16 | 0 KQK10719 0.964 0HORVU.MC |

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|---|---|---|---|
| 0.891203282 | 0.942023701 | 16 | 2 genblast_Os09t030genblast_C |
| 0.97174856 | 0.987351831 | 16 | 0 PNT72990 0.965 -HORVU.MC |
| 0.942655736 | 0.983603767 | 16 | 0 KQJ94885 0.911 -1HORVU.MC |
| 0.92167998 | 0.955455705 | 16 | 3 KQJ89227 0.887 -1HORVU.MC |
| 0.843051934 | 0.90890917 | 16 | 7 KQK09398 0.906 1HORVU.MC |
| 0.95473788 | 0.99512874 | 16 | 0 KQK03365 0.953 -HORVU.MC |
| 0.855615155 | 0.915164683 | 16 | 3 KQJ81972 0.881 0.HORVU.MC |
| 0.875679068 | 0.932471462 | 16 | 0 KQK15629 0.910 0HORVU.MC |
| 0.871486442 | 0.918154762 | 16 | 0 KQK20175 0.882 0genblast_C |
| 0.872793676 | 0.968754694 | 16 | 1 KQK05831 0.852 -HORVU.MC |
| 0.909075699 | 0.95687091 | 16 | 0 KQK05238 0.852 - HORVU.MC |

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| 0.900529204 | 0.951130276 | 16 | 0 KQK04026 0.825 -HORVU.MC |
| 0.955601358 | 0.991755577 | 16 | 0 KQK13932 0.970 0HORVU.MC |
| 0.931579405 | 0.962656816 | 16 | 0 KQK23238 0.944 0HORVU.MC |
| 0.906337535 | 0.933457828 | 16 | 0 KQK04232 0.868 - HORVU.MC |
| 0.946493497 | 0.977485666 | 16 | 0 KQK13407 0.934 -HORVU.MC |
| 0.938377383 | 0.971577123 | 16 | 0 KQK14035 0.882 - HORVU.MC |
| 0.903025645 | 0.961907618 | 16 | 1 KQJ99760 0.900 -0HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.912870566 | 0.968866286 | 16 | 0 | KQK01268 | 0.882 | – | HORVU.MC |
| 0.950320513 | 0.986425339 | 16 | 0 | KQK15809 | 0.947 | – | HORVU.MC |
| 0.919193837 | 0.941406777 | 16 | 0 | KQK15129 | 0.917 | – | HORVU.MC |
| 0.931258591 | 0.967332417 | 16 | 1 | KQJ94584 | 0.934 | 0. | HORVU.MC |
| 0.938598776 | 0.969114032 | 16 | 0 | KQJ88881 | 0.959 | 0. | HORVU.MC |
| 0.890518579 | 0.932580395 | 16 | 2 | KQK15475 | 0.872 | – | HORVU.MC |
| 0.884218117 | 0.975054568 | 16 | 0 | KQK15657 | 0.875 | – | HORVU.MC |
| 0.895282729 | 0.95021512 | 16 | 0 | KQK13358 | 0.821 | – | HORVU.MC |
| 0.913634107 | 0.970673591 | 16 | 0 | KQJ82196 | 0.926 | 0. | HORVU.MC |
| 0.929403109 | 0.971402981 | 16 | 0 | KQK24102 | 0.932 | 0 | HORVU.MC |
| 0.853674451 | 0.931868132 | 16 | 1 | KQJ96845 | 0.876 | 0. | HORVU.MC |
| 0.963687349 | 0.998580151 | 16 | 0 | KQJ99776 | 0.971 | 0. | HORVU.MC |
| 0.923393009 | 0.941584999 | 16 | 0 | KQJ89305 | 0.908 | –1 | HORVU.MC |
| 0.910306894 | 0.954937138 | 16 | 0 | KQK00869 | 0.900 | – | HORVU.MC |
| 0.914681692 | 0.959196753 | 16 | 0 | KQK14890 | 0.903 | – | HORVU.MC |
| 0.953355973 | 0.971234519 | 16 | 0 | KQK17419 | 0.953 | – | HORVU.MC |
| 0.90613023 | 0.978281699 | 16 | 0 | KQK17637 | 0.885 | – | HORVU.MC |
| 0.899141558 | 0.968783931 | 16 | 0 | KQJ83435 | 0.955 | 1. | HORVU.MC |
| 0.915734694 | 0.951673469 | 16 | 0 | KQK03563 | 0.849 | – | HORVU.MC |
| 0.941834507 | 0.977974005 | 16 | 0 | KQJ89976 | 0.925 | –0 | HORVU.MC |

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| 0.848344738 | 0.938598114 | 16 | 0 | KQK05745 | 0.907 | 0 | HORVU.MC |
| 0.894082217 | 0.948789974 | 16 | 0 | KQJ82213 | 0.928 | 0. | genblast_C |
| 0.907544487 | 0.949533256 | 16 | 0 | KQK09549 | 0.797 | – | HORVU.MC |
| 0.85970937 | 0.926980914 | 16 | 0 | KQJ99986 | 0.817 | –1 | HORVU.MC |
| 0.911758728 | 0.966284443 | 16 | 3 | KQK11766 | 0.911 | – | HORVU.MC |
| 0.968807894 | 1.004107934 | 16 | 0 | KQK17224 | 0.948 | – | HORVU.MC |
| 0.978381362 | 1.007405094 | 16 | 1 | KQJ83208 | 0.983 | 0. | HORVU.MC |
| 0.916773327 | 0.958530654 | 16 | 3 | KQK21215 | 0.850 | – | HORVU.MC |
| 0.929072366 | 0.968048688 | 16 | 0 | KQK09615 | 0.898 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.934363508 | 0.965445909 | 16 | 0 | KQJ94580 | 0.927 | –0 | HORVU.MC |
| 0.944088855 | 0.97241598 | 16 | 0 | KQK11407 | 0.944 | 0 | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.838825378 | 0.928584442 | 16 | 1 | KQJ92547 | 0.781 | –1 | HORVU.MC |
| 0.851002931 | 0.929657446 | 16 | 0 | PNT77654 | 0.889 | 0. | HORVU.MC |
| 0.851775027 | 0.926550598 | 16 | 0 | KQK08866 | 0.829 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.962825673 | 0.989409024 | 16 | 0 | KQK04919 | 0.936 | – | HORVU.MC |
| 0.904550011 | 0.946900737 | 16 | 2 | PNT70088 | 0.851 | – | HORVU.MC |
| 0.894344359 | 0.984642646 | 16 | 0 | KQK21964 | 0.890 | – | HORVU.MC |
| 0.928997748 | 0.967807808 | 16 | 0 | KQK02189 | 0.905 | – | HORVU.MC |
| 0.91466825 | 0.970272755 | 16 | 1 | PNT71384 | 0.832 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.881885067 | 0.948896401 | 16 | 3 | KQK07729 | 0.894 | 0 | HORVU.MC |
| 0.95400393 | 0.978874969 | 16 | 0 | KQJ88762 | 0.936 | –0 | HORVU.MC |
| 0.915569106 | 0.971382114 | 16 | 0 | KQK00709 | 0.905 | – | HORVU.MC |
| 0.89598135 | 0.952930728 | 16 | 0 | KQK04708 | 0.768 | – | genblast_C |
| 0.926847051 | 0.967919637 | 16 | 0 | KQJ94919 | 0.866 | –1 | genblast_C |
| 0.940783287 | 0.989343029 | 16 | 0 | KQK05494 | 0.922 | – | HORVU.MC |
| 0.882102172 | 0.955918772 | 16 | 2 | KQJ86419 | 0.904 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.936020051 | 0.971355824 | 16 | 0 | KQJ95322 | 0.907 | –1 | HORVU.MC |
| 0.92968029 | 0.951746869 | 16 | 0 | KQJ90772 | 0.907 | –1 | HORVU.MC |
| 0.938721525 | 0.968418328 | 16 | 0 | KQK05621 | 0.929 | – | HORVU.MC |
| 0.907350619 | 0.96129868 | 16 | 0 | KQJ96694 | 0.876 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.953534019 | 0.978900256 | 16 | 0 | PNT78115 | 0.950 | – | HORVU.MC |
| 0.890169001 | 0.947256712 | 16 | 1 | KQK19710 | 0.918 | 0 | HORVU.MC |
| 0.858715986 | 0.915646259 | 16 | 0 | KQK13174 | 0.831 | – | HORVU.MC |
| 0.949980567 | 0.981343928 | 16 | 0 | KQK00332 | 0.967 | 0 | genblast_C |
| 0.849225453 | 0.888274547 | 16 | 1 | PNT72613 | 0.825 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.990322782 | 1.000199402 | 16 | 0 | KQK07636 | 0.983 | – | HORVU.MC |
| 0.824766887 | 0.880941551 | 16 | 0 | KQK14927 | 0.778 | – | HORVU.MC |
| 0.953364996 | 0.98410132 | 16 | 0 | KQK03226 | 0.927 | – | HORVU.MC |
| 0.913434735 | 0.978318584 | 16 | 1 | KQK10333 | 0.925 | 0 | genblast_C |
| 0.973058464 | 1.008726003 | 16 | 0 | KQJ94136 | 0.991 | 0. | HORVU.MC |
| 0.94300062 | 0.979039892 | 16 | 0 | KQJ88506 | 0.940 | –0 | HORVU.MC |
| 0.939478093 | 0.980154639 | 16 | 0 | KQK04943 | 0.923 | – | HORVU.MC |

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| 0.906261836 | 0.951395026 | 16 | 1 | KQK13236 | 0.918 | 0 | HORVU.MC |
| 0.891802051 | 0.937375204 | 16 | 4 | KQJ95891 | 0.872 | −0 | HORVU.MC |
| 0.870228413 | 0.926802873 | 16 | 7 | KQJ97601 | 0.909 | 0. | HORVU.MC |
| 0.893790688 | 0.955612547 | 16 | 0 | KQJ90868 | 0.878 | −0 | HORVU.MC |
| 0.897239454 | 0.990818859 | 16 | 1 | KQK23749 | 0.885 | − | HORVU.MC |
| 0.889136905 | 0.957806932 | 16 | 0 | KQJ96701 | 0.874 | −0 | HORVU.MC |
| 0.965741521 | 0.994417527 | 16 | 0 | KQJ90283 | 0.988 | 1. | HORVU.MC |
| 0.93226946 | 0.970352008 | 16 | 0 | KQJ84370 | 0.968 | 0. | HORVU.MC |
| 0.891541377 | 0.947067594 | 16 | 0 | KQJ94637 | 0.841 | −1 | HORVU.MC |
| 0.898344793 | 0.955029389 | 16 | 1 | genblast_Os03t024 |  |  | HORVU.MC |
| 0.873879212 | 0.959223301 | 16 | 1 | KQK13573 | 0.793 | − | HORVU.MC |
| 0.91509269 | 0.989856593 | 16 | 0 | KQK16963 | 0.912 | − | HORVU.MC |
| 0.935940471 | 0.996910646 | 16 | 0 | KQJ84635 | 0.920 | −0 | HORVU.MC |
| 0.950674716 | 0.97711039 | 16 | 0 | KQK05197 | 0.946 | − | HORVU.MC |
| 0.975947084 | 1.001975775 | 16 | 0 | KQK05204 | 0.969 | − | HORVU.MC |
| 0.920857405 | 0.951418067 | 16 | 0 | KQJ86074 | 0.856 | −2 | HORVU.MC |
| 0.874771929 | 0.930260846 | 16 | 1 | KQJ94744 | 0.848 | −0 | HORVU.MC |
| 0.974777783 | 0.995912159 | 16 | 0 | KQK17473 | 0.934 | − | HORVU.MC |
| 0.825027981 | 0.894688645 | 16 | 0 | KQJ94199 | 0.785 | −0 | HORVU.MC |
| 0.964585547 | 0.983846971 | 16 | 1 | KQJ92173 | 0.953 | −0 | HORVU.MC |
| 0.858251634 | 0.927720108 | 16 | 0 | KQJ99035 | 0.772 | −1 | HORVU.MC |
| 0.914879989 | 0.97472646 | 16 | 0 | KQK09606 | 0.863 | − | HORVU.MC |
| 0.957795631 | 0.979925776 | 16 | 0 | KQJ90809 | 0.957 | −0 | HORVU.MC |
| 0.941465736 | 0.986584482 | 16 | 1 | KQK18896 | 0.944 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.891335724 | 0.935094472 | 16 | 0 | KQJ93272 | 0.877 | -0 | HORVU.MC |
| 0.947567324 | 0.972970267 | 16 | 2 | KQJ93226 | 0.944 | -0 | HORVU.MC |
| 0.952187388 | 0.989938915 | 16 | 0 | KQJ84256 | 0.918 | -1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.875797687 | 0.940804999 | 16 | 5 | PNT71349 | 0.902 | 0. | HORVU.MC |
| 0.942095238 | 0.976380952 | 16 | 0 | KQJ97186 | 0.926 | -0 | HORVU.MC |
| 0.958010836 | 0.972405438 | 16 | 0 | PNT61632 | 0.959 | 0. | HORVU.MC |
| 0.87688734 | 0.960859466 | 16 | 0 | KQK01253 | 0.812 | - | HORVU.MC |
| 0.885756419 | 0.9462873 | 16 | 0 | KQK12831 | 0.890 | 0 | HORVU.MC |
| 0.876534837 | 0.910908053 | 16 | 0 | KQJ82219 | 0.879 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.96427078 | 0.99047342 | 16 | 0 | KQK15507 | 0.936 | - | HORVU.MC |
| 0.922668607 | 0.958621074 | 16 | 0 | KQK04832 | 0.916 | - | HORVU.MC |
| 0.878770445 | 0.940026906 | 16 | 6 | KQK18768 | 0.846 | - | HORVU.MC |
| 0.830639667 | 0.874261923 | 16 | 0 | KQJ91707 | 0.859 | 0. | HORVU.MC |
| 0.894550577 | 0.981858164 | 16 | 1 | KQK16239 | 0.934 | 0 | genblast_C |
| 0.923175072 | 0.979805782 | 16 | 0 | KQJ82364 | 0.924 | 0. | HORVU.MC |
| 0.875565504 | 0.909573604 | 16 | 2 | KQK09342 | 0.871 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.82166634 | 0.903270022 | 16 | 0 | KQK10353 | 0.765 | - | HORVU.MC |
| 0.924722088 | 0.960229234 | 16 | 1 | KQK13235 | 0.885 | - | HORVU.MC |
| 0.90452895 | 0.983916561 | 16 | 0 | KQJ93306 | 0.804 | -1 | HORVU.MC |
| 0.872746973 | 0.940974133 | 16 | 2 | KQJ86030 | 0.891 | 0. | HORVU.MC |
| 0.924175476 | 0.952097787 | 16 | 0 | KQK09064 | 0.892 | - | HORVU.MC |
| 0.848475804 | 0.939032155 | 16 | 0 | KQJ88574 | 0.757 | -1 | HORVU.MC |
| 0.930038088 | 0.963364752 | 16 | 0 | KQK20630 | 0.919 | - | HORVU.MC |
| 0.914602102 | 0.966966967 | 16 | 0 | KQK23274 | 0.895 | - | HORVU.MC |
| 0.956734795 | 0.9949754 | 16 | 0 | KQK03008 | 0.973 | 0 | HORVU.MC |
| 0.969510937 | 0.99449718 | 16 | 0 | KQK10851 | 0.965 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.949775207 | 0.983734088 | 16 | 1 | KQK07413 | 0.951 | 0 | HORVU.MC |
| 0.847322741 | 0.881375099 | 16 | 1 | KQJ96457 | 0.803 | -1 | HORVU.MC |
| 0.844308849 | 0.918002384 | 16 | 2 | KQK20107 | 0.897 | 0 | HORVU.MC |
| 0.864398269 | 0.959035872 | 16 | 0 | KQK01362 | 0.849 | - | HORVU.MC |
| 0.968459773 | 0.993634561 | 16 | 2 | KQK03728 | 0.960 | - | HORVU.MC |
| 0.880113491 | 0.913311105 | 16 | 2 | KQJ92167 | 0.854 | -0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.894781068 | 0.937718023 | 16 | 1 | KQK01474 0.927 0 | HORVU.MC |
| 0.959088404 | 0.991005291 | 16 | 0 | KQJ87282 0.933 –1 | HORVU.MC |
| 0.938480871 | 0.973168439 | 16 | 0 | KQK02032 0.910 – | HORVU.MC |
| 0.922908396 | 0.968578427 | 16 | 2 | KQK17281 0.951 0 | HORVU.MC |
| 0.932347599 | 0.953569172 | 16 | 0 | KQK22344 0.927 – | HORVU.MC |
| 0.962318908 | 0.983036157 | 16 | 3 | KQK14588 0.948 – | HORVU.MC |
| 0.843216532 | 0.913746631 | 16 | 0 | KQJ86815 0.818 –0 | HORVU.MC |
| 0.91561057 | 0.959774243 | 16 | 0 | KQK01128 0.831 – | HORVU.MC |
| 0.921742585 | 0.981652542 | 16 | 3 | KQJ86193 0.931 0. | HORVU.MC |
| 0.928801298 | 0.984356366 | 16 | 1 | PNT73211 0.916 – | genblast_C |
| 0.973302836 | 0.98591689 | 16 | 0 | KQK09166 0.976 0 | HORVU.MC |
| 0.958704415 | 0.971407144 | 16 | 0 | KQJ97865 0.943 –1 | HORVU.MC |
| 0.879143308 | 0.935564121 | 16 | 5 | genblast_Os04t043 | HORVU.MC |
| 0.939514566 | 0.978511298 | 16 | 0 | KQK22530 0.925 – | HORVU.MC |
| 0.958455583 | 0.97799511 | 16 | 0 | KQK05640 0.954 – | HORVU.MC |
| 0.911684416 | 0.978161229 | 16 | 0 | PNT72506 0.895 – | HORVU.MC |
| 0.969775398 | 0.985241439 | 16 | 0 | KQK03473 0.952 – | HORVU.MC |
| 0.875403838 | 0.915561212 | 16 | 3 | KQJ87187 0.889 0. | HORVU.MC |
| 0.91714499 | 0.96084937 | 16 | 2 | KQK06251 0.924 0 | HORVU.MC |
| 0.944469809 | 0.971122018 | 16 | 0 | KQJ82439 0.903 –1 | HORVU.MC |
| 0.96308679 | 1.030021834 | 16 | 0 | KQK14259 1.019 0 | HORVU.MC |
| 0.90554884 | 0.960667138 | 16 | 2 | KQK19096 0.897 – | genblast_C |
| 0.866757349 | 0.938606464 | 16 | 1 | KQK16825 0.760 – | HORVU.MC |

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|---|---|---|---|
| 0.949650814 | 0.991036463 | 16 | 0 KQK20472 0.923 – HORVU.MC |
| 0.926095585 | 0.969769465 | 16 | 0 KQK10633 0.873 – HORVU.MC |
| 0.869801997 | 0.941160915 | 16 | 3 KQK13051 0.860 – HORVU.MC |
| 0.889203407 | 0.970340681 | 16 | 0 KQK07089 0.784 – HORVU.MC |
| 0.904065798 | 0.956300435 | 16 | 1 KQK05435 0.909 0 HORVU.MC |
| 0.948019177 | 0.984944066 | 16 | 0 KQK17152 0.962 0 HORVU.MC |
| 0.94582505 | 0.971689861 | 16 | 0 KQK06486 0.955 0 HORVU.MC |
| 0.904364137 | 0.949642625 | 16 | 1 KQK21391 0.901 – HORVU.MC |
| 0.915617274 | 0.97342398 | 16 | 0 KQJ93375 0.956 0. HORVU.MC |
| 0.965928483 | 0.998293515 | 16 | 0 KQJ97768 0.947 –0 HORVU.MC |
| 0.897791957 | 0.948586118 | 16 | 0 KQK10616 0.899 0 HORVU.MC |
| 0.853013834 | 0.906549972 | 16 | 2 KQJ86482 0.856 0. HORVU.MC |
| 0.906489595 | 0.953450164 | 16 | 0 KQJ87912 0.919 0. HORVU.MC |
| 0.925993106 | 0.985374771 | 16 | 1 KQJ91622 0.922 –0 HORVU.MC |
| 0.933491967 | 0.980288916 | 16 | 0 KQK17862 0.918 – HORVU.MC |
| 0.857068663 | 0.903620891 | 16 | 3 KQK06629 0.874 0 HORVU.MC |
| 0.92638192 | 0.958238912 | 16 | 0 KQK03159 0.915 – HORVU.MC |
| 0.890351948 | 0.974818192 | 16 | 0 KQK04877 0.863 – HORVU.MC |
| 0.888257882 | 0.946429534 | 16 | 1 KQK00351 0.868 – HORVU.MC |
| 0.911312458 | 0.946896706 | 16 | 1 KQJ84870 0.900 –0 HORVU.MC |
| 0.951629168 | 0.990259352 | 16 | 2 KQK00944 0.948 – HORVU.MC |
| 0.870676819 | 0.955050826 | 16 | 6 KQK23104 0.809 – HORVU.MC |
| 0.840528351 | 0.967139175 | 16 | 0 KQK21538 0.816 – genblast_C |
| 0.851902504 | 0.949428641 | 16 | 0 KQK23091 0.748 – HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.96059261 | 0.983423486 | 16 | 0 | KQJ84656 | 0.966 | 0. | HORVU.MC |
| 0.873521695 | 0.979793233 | 16 | 0 | KQK23744 | 0.810 | – | HORVU.MC |
| 0.90159282 | 0.940018855 | 16 | 0 | KQK23225 | 0.844 | – | HORVU.MC |
| 0.878097474 | 0.946195479 | 16 | 0 | KQK02297 | 0.920 | 0 | HORVU.MC |
| 0.902009193 | 0.964768683 | 16 | 1 | KQJ88129 | 0.914 | 0. | HORVU.MC |
| 0.871771574 | 0.942880709 | 16 | 1 | KQK00682 | 0.858 | – | HORVU.MC |
| 0.852551424 | 0.931962025 | 16 | 1 | KQK13023 | 0.802 | – | HORVU.MC |
| 0.895568071 | 0.9611492 | 16 | 0 | KQJ84254 | 0.927 | 0. | HORVU.MC |
| 0.854498662 | 0.900314063 | 16 | 0 | KQK16912 | 0.758 | – | HORVU.MC |
| 0.960710762 | 0.987462271 | 16 | 0 | KQK13287 | 0.956 | – | HORVU.MC |
| 0.909479718 | 0.977601411 | 16 | 1 | KQK13285 | 0.868 | – | HORVU.MC |
| 0.922104121 | 0.951879319 | 16 | 0 | KQK00585 | 0.929 | 0 | HORVU.MC |
| 0.918805247 | 0.96578272 | 16 | 0 | KQK07777 | 0.912 | – | HORVU.MC |
| 0.957566594 | 0.98050444 | 16 | 0 | KQK22345 | 0.964 | 0 | HORVU.MC |
| 0.884771493 | 0.939681072 | 16 | 6 | KQJ93599 | 0.894 | 0. | HORVU.MC |
| 0.932779807 | 0.963105113 | 16 | 0 | KQK04786 | 0.927 | – | HORVU.MC |
| 0.875490119 | 0.955144291 | 16 | 0 | KQJ94328 | 0.810 | –1 | HORVU.MC |
| 0.94170881 | 0.971120575 | 16 | 0 | KQK12680 | 0.942 | 0 | HORVU.MC |
| 0.886648425 | 0.946399345 | 16 | 0 | KQK11225 | 0.880 | – | HORVU.MC |
| 0.9050793 | 0.978671042 | 16 | 1 | KQK21173 | 0.904 | – | genblast_C |
| 0.918743532 | 0.952627343 | 16 | 1 | KQJ90244 | 0.931 | 0. | HORVU.MC |
| 0.875319916 | 0.922392844 | 16 | 1 | KQK16729 | 0.886 | 0 | HORVU.MC |
| 0.889311745 | 0.948688047 | 16 | 2 | KQK14459 | 0.912 | 0 | HORVU.MC |
| 0.926945882 | 0.959982751 | 16 | 0 | KQK21800 | 0.937 | 0 | HORVU.MC |

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| 0.955728492 | 0.984581498 | 16 | 0 KQK06264 0.935 – | HORVU.MC |
| 0.912065996 | 0.952225546 | 16 | 0 KQK01175 0.930 0 | HORVU.MC |
| 0.891625545 | 0.955290337 | 16 | 5 KQJ89763 0.858 –0 | HORVU.MC |
| 0.854076158 | 0.913806586 | 16 | 0 PNT66187 0.768 – | HORVU.MC |
| 0.860538564 | 0.911901596 | 16 | 0 KQK21756 0.828 – | HORVU.MC |
| 0.957684077 | 0.990193634 | 16 | 0 KQJ95247 0.946 –0 | HORVU.MC |
| 0.926044264 | 0.973732336 | 16 | 0 KQJ93139 0.856 –2 | HORVU.MC |
| 0.940302615 | 0.974748382 | 16 | 0 KQK06255 0.918 – | HORVU.MC |
| 0.891521475 | 0.962560778 | 16 | 1 KQK09275 0.863 – | HORVU.MC |
| 0.950748642 | 0.973842196 | 16 | 0 KQJ90949 0.922 –1 | HORVU.MC |
| 0.909515328 | 0.980713874 | 16 | 0 PNT61702 0.818 – | HORVU.MC |
| 0.963428493 | 0.994970662 | 16 | 0 KQK22809 0.945 – | HORVU.MC |
| 0.886430623 | 0.967956469 | 16 | 0 KQJ89786 0.814 –1 | HORVU.MC |
| 0.904560572 | 0.96037362 | 16 | 0 KQK24060 0.880 – | HORVU.MC |
| 0.928308063 | 0.982612296 | 16 | 0 KQJ85012 0.872 –1 | HORVU.MC |
| 0.879465483 | 0.936421354 | 16 | 0 PNT66501 0.869 – | HORVU.MC |
| 0.9030327 | 0.968565401 | 16 | 0 KQK04103 0.904 0 | HORVU.MC |
| 0.937040501 | 0.971828237 | 16 | 1 KQK08641 0.937 0 | HORVU.MC |
| 0.89915164 | 0.968069121 | 16 | 0 KQK10415 0.866 – | HORVU.MC |
| 0.870175873 | 0.920421139 | 16 | 8 KQJ90814 0.906 0. | HORVU.MC |
| 0.941212828 | 0.991874136 | 16 | 2 KQK24088 0.952 0 | HORVU.MC |
| 0.962808339 | 0.993669504 | 16 | 0 KQK08964 0.945 – | HORVU.MC |
| 0.931264552 | 0.972976787 | 16 | 0 PNT74667 0.927 – | HORVU.MC |
| 0.896671807 | 0.93093336 | 16 | 0 KQK21655 0.930 0 | HORVU.MC |
| 0.93457216 | 0.962835206 | 16 | 0 KQK06838 0.912 – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.893907269 | 0.949673812 | 16 | 0 | KQJ83857 | 0.798 | –2 | HORVU.MC |
| 0.887007982 | 0.977153867 | 16 | 0 | KQK13009 | 0.838 | – | HORVU.MC |
| | | | | | | | |
| 0.913727915 | 0.955759717 | 16 | 0 | KQJ93670 | 0.873 | –1 | HORVU.MC |
| 0.953057035 | 0.987325634 | 16 | 1 | KQJ90048 | 0.938 | –0 | HORVU.MC |
| 0.953995363 | 0.981324168 | 16 | 1 | KQK00211 | 0.957 | 0. | HORVU.MC |
| 0.906161571 | 0.962191479 | 16 | 1 | KQK15591 | 0.829 | – | HORVU.MC |
| 0.926860487 | 0.96941518 | 16 | 1 | KQJ84993 | 0.887 | –1 | HORVU.MC |
| | | | | | | | |
| 0.864862304 | 0.912582112 | 16 | 0 | KQK13294 | 0.874 | 0. | HORVU.MC |
| | | | | | | | |
| 0.820464076 | 0.901239204 | 16 | 0 | KQK08395 | 0.770 | – | HORVU.MC |
| 0.917659501 | 0.972804973 | 16 | 1 | KQK04604 | 0.933 | 0. | HORVU.MC |
| 0.921042022 | 0.966609751 | 16 | 0 | KQK07926 | 0.888 | – | HORVU.MC |
| 0.959625362 | 0.980333012 | 16 | 0 | KQK12124 | 0.945 | – | HORVU.MC |
| 0.968366564 | 0.98696319 | 16 | 0 | KQJ91123 | 0.983 | 0. | HORVU.MC |
| | | | | | | | |
| 0.977083545 | 0.990660847 | 16 | 0 | KQJ94214 | 0.976 | –0 | HORVU.MC |
| 0.879907801 | 0.926014184 | 16 | 0 | KQK04685 | 0.877 | – | HORVU.MC |
| 0.956186319 | 0.98121418 | 16 | 0 | KQK07360 | 0.947 | – | HORVU.MC |
| 0.966427453 | 0.994363257 | 16 | 1 | KQK08721 | 0.973 | 0. | HORVU.MC |
| 0.923659208 | 0.962884035 | 16 | 0 | KQK02658 | 0.913 | – | HORVU.MC |

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|---|---|---|---|
| 0.909480633 | 0.960607655 | 16 | 2 KQJ89340 0.898 −0genblast_C |
| 0.888299722 | 0.922577654 | 16 | 0 KQK15843 0.833 −genblast_C |
| 0.957888927 | 0.995923913 | 16 | 1 KQJ89099 0.907 −2HORVU.MC |
| 0.965711195 | 1.002163332 | 16 | 0 KQJ91471 0.954 −0HORVU.MC |
| 0.966120261 | 0.996146675 | 16 | 0 KQK14681 0.946 −HORVU.MC |
| 0.931969237 | 0.985947588 | 16 | 0 KQJ83308 0.937 0. HORVU.MC |
| 0.977359185 | 0.989814701 | 16 | 0 KQK19535 0.955 −HORVU.MC |
| 0.864674139 | 0.938148609 | 16 | 0 KQJ81685 0.799 −1HORVU.MC |
| 0.96053991 | 0.978189332 | 16 | 0 KQK11088 0.949 −HORVU.MC |
| 0.926449732 | 0.968379031 | 16 | 1 KQJ82516 0.921 −0HORVU.MC |
| 0.936130303 | 0.981107633 | 16 | 0 KQK09074 0.908 −HORVU.MC |
| 0.911395582 | 0.963855422 | 16 | 0 KQK15072 0.832 −HORVU.MC |
| 0.927154741 | 0.97142417 | 16 | 0 KQK07166 0.905 −genblast_C |
| 0.924039958 | 0.969901401 | 16 | 0 KQK23538 0.840 − HORVU.MC |
| 0.949917219 | 0.986944182 | 16 | 0 KQK23918 0.943 −HORVU.MC |
| 0.856979351 | 0.919045213 | 16 | 0 KQK09696 0.769 − HORVU.MC |
| 0.967378576 | 0.996324854 | 16 | 0 KQK06294 0.971 0HORVU.MC |
| 0.923653762 | 0.957117789 | 16 | 0 KQK22746 0.920 −HORVU.MC |
| 0.954497787 | 0.975753665 | 16 | 0 KQJ93195 0.919 −2HORVU.MC |
| 0.925421232 | 0.97497274 | 16 | 3 genblast_Os11t015HORVU.MC |
| 0.848740602 | 0.905263158 | 16 | 1 KQK18078 0.768 − HORVU.MC |
| 0.966105632 | 0.984777015 | 16 | 0 KQJ90125 0.976 0.HORVU.MC |
| 0.907952006 | 0.980169444 | 16 | 1 KQJ99684 0.802 −1HORVU.MC |
| 0.970904057 | 0.98882219 | 16 | 0 KQJ82559 0.940 −2HORVU.MC |
| 0.846816939 | 0.9067276 | 16 | 3 genblast_Os02t083HORVU.MC |
| 0.915243855 | 0.989032358 | 16 | 1 KQJ81490 0.922 0. HORVU.MC |
| 0.833771256 | 0.897142182 | 16 | 1 KQK08358 0.749 − HORVU.MC |
| 0.907441771 | 0.964849416 | 16 | 0 KQJ93980 0.916 0.HORVU.MC |
| 0.945112216 | 0.975173158 | 16 | 0 KQJ95167 0.901 −1HORVU.MC |
| 0.922930422 | 0.96515998 | 16 | 1 KQK05555 0.921 −HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.949091589 | 0.976948795 | 16 | 0 | KQJ95418 | 0.935 | −0 | HORVU.MC |
| 0.980942698 | 0.995229941 | 16 | 1 | KQK19554 | 0.969 | − | HORVU.MC |
| 0.924989287 | 0.991429388 | 16 | 1 | KQK10448 | 0.920 | − | genblast_C |
| 0.861140167 | 0.964136282 | 16 | 0 | KQJ87625 | 0.846 | −0 | HORVU.MC |
| 0.913291418 | 0.972634541 | 16 | 4 | KQK18217 | 0.865 | − | HORVU.MC |
| 0.933565329 | 0.982844451 | 16 | 0 | KQJ84182 | 0.926 | −0 | HORVU.MC |
| 0.848381198 | 0.892712002 | 16 | 0 | genblast_Os05t036 | | | HORVU.MC |
| 0.909572279 | 0.956628093 | 16 | 0 | KQJ95126 | 0.883 | −0 | HORVU.MC |
| 0.824578278 | 0.88635691 | 16 | 0 | PNT75632 | 0.757 | − | HORVU.MC |
| 0.954104899 | 0.990753769 | 16 | 0 | KQJ93084 | 0.961 | 0. | HORVU.MC |
| 0.923943193 | 0.953289693 | 16 | 3 | KQK02860 | 0.948 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.885176809 | 0.950383772 | 16 | 0 | KQJ90626 | 0.810 | −1 | HORVU.MC |
| 0.930202004 | 0.977993102 | 16 | 0 | KQK11214 | 0.906 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.922491698 | 0.961385199 | 16 | 0 | KQK17470 | 0.877 | − | HORVU.MC |
| 0.871898202 | 0.921062915 | 16 | 0 | KQK17757 | 0.838 | − | HORVU.MC |
| 0.881460188 | 0.944609298 | 16 | 1 | KQJ90896 | 0.881 | −0 | HORVU.MC |
| 0.93974714 | 0.982567641 | 16 | 0 | KQK07433 | 0.896 | − | HORVU.MC |
| 0.938930615 | 0.975282149 | 16 | 0 | KQJ99395 | 0.931 | −0 | HORVU.MC |
| 0.908219704 | 0.972006502 | 16 | 0 | PNT65051 | 0.899 | − | HORVU.MC |
| 0.951840491 | 0.989723926 | 16 | 0 | PNT76064 | 0.948 | − | HORVU.MC |
| 0.943719503 | 0.975676475 | 16 | 0 | PNT64542 | 0.926 | − | HORVU.MC |
| 0.933212532 | 0.975253765 | 16 | 0 | KQJ99161 | 0.907 | −0 | HORVU.MC |
| 0.948297294 | 0.995143386 | 16 | 0 | KQK23912 | 0.919 | − | HORVU.MC |
| 0.928803178 | 0.967460116 | 16 | 1 | KQK20921 | 0.912 | − | HORVU.MC |
| 0.96129863 | 0.991842711 | 16 | 0 | KQK08713 | 0.972 | 0 | HORVU.MC |
| 0.875492989 | 0.92258253 | 16 | 0 | KQK20654 | 0.878 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.960589789 | 0.981690141 | 16 | 0 | KQK15658 | 0.967 | 0 | HORVU.MC |
| 0.919398118 | 0.959525906 | 16 | 1 | KQK13453 | 0.925 | 0 | HORVU.MC |
| 0.913859807 | 0.966161252 | 16 | 6 | KQJ92070 | 0.930 | 0. | HORVU.MC |
| 0.909774241 | 0.97721598 | 16 | 0 | KQJ93454 | 0.918 | 0. | HORVU.MC |
| 0.915267465 | 0.950838115 | 16 | 0 | KQK14922 | 0.910 | − | HORVU.MC |

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| 0.866195341 | 0.946139443 | 16 | 0 | KQJ84799 | 0.771 | −1 | HORVU.MC |
| 0.959663437 | 0.986201473 | 16 | 0 | KQK19797 | 0.934 | − | HORVU.MC |
| 0.909859776 | 0.994116493 | 16 | 0 | KQK11579 | 0.815 | − | HORVU.MC |
| 0.889463623 | 0.936637899 | 16 | 6 | PNT65458 | 0.883 | −( | HORVU.MC |
| 0.940649421 | 0.973592024 | 16 | 0 | KQK00702 | 0.935 | −( | HORVU.MC |
| 0.969017348 | 0.999287072 | 16 | 0 | KQJ82543 | 0.973 | 0. | HORVU.MC |
| 0.942278812 | 0.97039389 | 16 | 1 | KQJ98966 | 0.970 | 0. | HORVU.MC |
| 0.90077698 | 0.943714822 | 16 | 0 | KQK12035 | 0.866 | − | HORVU.MC |
| 0.942665562 | 0.972274542 | 16 | 0 | KQJ95619 | 0.928 | −0 | HORVU.MC |
| 0.946721167 | 0.979746835 | 16 | 0 | KQK05684 | 0.928 | −( | HORVU.MC |
| 0.927424473 | 0.992383854 | 16 | 0 | KQK01016 | 0.917 | −( | HORVU.MC |
| 0.963341264 | 0.996872876 | 16 | 0 | KQK22529 | 0.918 | − | HORVU.MC |
| 0.862443182 | 0.963939394 | 16 | 2 | KQJ90971 | 0.815 | −0 | HORVU.MC |
| 0.92341735 | 0.965228396 | 16 | 1 | KQK15463 | 0.922 | −( | HORVU.MC |
| 0.949309737 | 0.969022342 | 16 | 0 | KQJ98818 | 0.938 | −0 | HORVU.MC |
| 0.963980638 | 0.989179954 | 16 | 0 | KQJ83314 | 0.943 | −1 | HORVU.MC |
| 0.963594771 | 0.982222222 | 16 | 0 | KQJ86186 | 0.958 | −0 | HORVU.MC |
| 0.956457284 | 1.004617968 | 16 | 0 | PNT69181 | 0.987 | 0. | HORVU.MC |
| 0.892939541 | 0.979886417 | 16 | 3 | KQK09173 | 0.917 | 0 | genblast_C |
| 0.902021859 | 0.976216323 | 16 | 1 | KQK08175 | 0.874 | −( | HORVU.MC |
| 0.943250721 | 0.968622795 | 16 | 0 | KQK09553 | 0.920 | − | HORVU.MC |
| 0.929070017 | 0.983161512 | 16 | 0 | KQK23448 | 0.908 | −( | HORVU.MC |
| 0.941949218 | 0.983814053 | 16 | 0 | KQK15445 | 0.933 | −( | HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.926699185 | 0.982204117 | 16 | 2 | KQK03706 | 0.933 0 | genblast_C |
| 0.944532766 | 0.973533568 | 16 | 1 | KQK18642 | 0.932 – | HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.906096059 | 0.972632731 | 16 | 2 | KQK15091 | 0.888 – | HORVU.MC |
| 0.950714432 | 0.983358341 | 16 | 0 | KQK12387 | 0.910 – | HORVU.MC |
| 0.945232753 | 0.963833157 | 16 | 1 | KQK04073 | 0.955 0 | HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.94627944 | 0.979872627 | 16 | 0 | KQJ93372 | 0.924 –1 | HORVU.MC |
| 0.854496256 | 0.918183946 | 16 | 3 | KQK21791 | 0.865 0 | HORVU.MC |
| 0.944887776 | 0.986486486 | 16 | 1 | KQJ87108 | 0.921 –0 | HORVU.MC |
| 0.843585699 | 0.900893796 | 16 | 1 | KQJ93799 | 0.865 0. | HORVU.MC |
| 0.901442051 | 0.944876853 | 16 | 0 | KQK22439 | 0.837 – | HORVU.MC |
| 0.901446324 | 0.95512591 | 16 | 4 | KQJ97284 | 0.913 0. | HORVU.MC |
| 0.876407967 | 0.938461538 | 16 | 0 | KQK15073 | 0.813 – | HORVU.MC |
| 0.915064423 | 0.957251298 | 16 | 1 | KQK16804 | 0.907 – | HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.977675225 | 0.988130935 | 16 | 0 | KQJ88487 | 0.977 –0 | HORVU.MC |
| 0.913619811 | 0.979606701 | 16 | 1 | PNT69295 | 0.909 – | HORVU.MC |
| 0.936719766 | 0.97503251 | 16 | 0 | PNT69208 | 0.914 – | HORVU.MC |
| 0.928878348 | 0.976339286 | 16 | 0 | KQK12243 | 0.897 – | HORVU.MC |
| 0.892838786 | 0.951925984 | 16 | 5 | KQK03030 | 0.897 0 | HORVU.MC |
| 0.955515274 | 0.997979318 | 16 | 0 | KQK22645 | 0.953 – | HORVU.MC |
| 0.870641402 | 0.961277299 | 16 | 0 | KQJ89069 | 0.821 –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.932197784 | 0.991400695 | 16 | 0 | KQK11976 | 0.944 | 0. | HORVU.MC |
| 0.943946188 | 0.964700471 | 16 | 0 | genblast_Os02t064 | | | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.860179744 | 0.943311441 | 16 | 0 | KQK23311 | 0.845 | − | HORVU.MC |
| 0.916517461 | 0.972654632 | 16 | 2 | KQK22255 | 0.912 | − | HORVU.MC |
| 0.912823954 | 0.968770332 | 16 | 1 | KQJ97030 | 0.905 | −0 | HORVU.MC |
| 0.927071196 | 0.949195992 | 16 | 1 | KQJ97087 | 0.947 | 1. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.986596894 | 1.001215395 | 16 | 0 | KQK17269 | 0.991 | 0. | HORVU.MC |
| 0.920085858 | 0.948015354 | 16 | 0 | KQJ86017 | 0.916 | −0 | HORVU.MC |
| 0.919793575 | 0.958516905 | 16 | 1 | KQK04722 | 0.916 | − | HORVU.MC |
| 0.880593029 | 0.934440239 | 16 | 1 | KQJ85386 | 0.858 | −0 | HORVU.MC |
| 0.931783082 | 0.969871031 | 16 | 0 | KQJ82191 | 0.853 | −2 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.971445635 | 0.99142562 | 16 | 2 | KQK15830 | 0.968 | − | HORVU.MC |
| 0.844148492 | 0.951018949 | 16 | 5 | KQJ93513 | 0.891 | 0. | HORVU.MC |
| 0.891296697 | 0.96783974 | 16 | 2 | KQJ84716 | 0.885 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.956878828 | 0.978827647 | 16 | 0 | KQJ88292 | 0.950 | −0 | HORVU.MC |
| 0.870484839 | 0.92958893 | 16 | 0 | KQK18043 | 0.812 | − | HORVU.MC |
| 0.866887417 | 0.924881741 | 16 | 0 | KQK01328 | 0.807 | − | HORVU.MC |
| 0.922673651 | 0.955516931 | 16 | 0 | KQJ90957 | 0.946 | 0. | HORVU.MC |
| 0.928185887 | 0.969668246 | 16 | 0 | KQK01318 | 0.928 | − | HORVU.MC |

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| 0.93408926 | 1.003193033 | 16 | 0 | KQK15768 | 0.937 | 0. | HORVU.MC |
| 0.939667051 | 0.981561279 | 16 | 0 | KQJ89712 | 0.929 | –0 | HORVU.MC |
| 0.943655303 | 0.96596098 | 16 | 0 | KQJ98998 | 0.938 | –0 | HORVU.MC |
| 0.923087559 | 0.973630652 | 16 | 2 | KQK02433 | 0.860 | – | HORVU.MC |
| 0.884575826 | 0.957440772 | 16 | 1 | KQK18903 | 0.797 | – | genblast_C |
| 0.969870072 | 0.984714316 | 16 | 0 | KQK01439 | 0.969 | – | HORVU.MC |
| 0.961022294 | 0.988266354 | 16 | 0 | KQK03417 | 0.953 | – | HORVU.MC |
| 0.962337134 | 0.99259698 | 16 | 0 | KQK23346 | 0.939 | – | HORVU.MC |
| 0.925756142 | 0.985763201 | 16 | 1 | genblast_Os09t054 |  |  | HORVU.MC |
| 0.888863264 | 0.932144321 | 16 | 8 | KQJ87822 | 0.860 | –0 | HORVU.MC |
| 0.829405163 | 0.929453263 | 16 | 2 | KQK14138 | 0.772 | – | HORVU.MC |
| 0.910613664 | 0.956682515 | 16 | 1 | KQK04565 | 0.871 | – | HORVU.MC |
| 0.873905551 | 0.951937407 | 16 | 0 | KQK07737 | 0.797 | – | HORVU.MC |
| 0.936536852 | 0.966120282 | 16 | 1 | KQK06179 | 0.939 | 0. | HORVU.MC |
| 0.970968163 | 0.995012758 | 16 | 0 | KQJ94250 | 0.967 | –0 | HORVU.MC |
| 0.874705228 | 0.956025693 | 16 | 2 | KQJ91571 | 0.873 | –0 | HORVU.MC |
| 0.856771417 | 0.947718276 | 16 | 4 | KQJ95840 | 0.869 | 0. | HORVU.MC |
| 0.892259065 | 0.940267176 | 16 | 0 | KQJ99163 | 0.835 | –1 | HORVU.MC |
| 0.976204357 | 0.997611193 | 16 | 0 | KQK18109 | 0.965 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.956821014 | 0.978471817 | 16 | 0 | KQJ91359 | 0.957 | −0 | HORVU.MC |
| 0.888076301 | 0.949851712 | 16 | 0 | KQJ88957 | 0.853 | −0 | HORVU.MC |
| 0.880897637 | 0.950351428 | 16 | 0 | PNT69179 | 0.841 | − | HORVU.MC |
| 0.956544803 | 0.977807152 | 16 | 1 | KQK13788 | 0.932 | − | HORVU.MC |
| 0.920177296 | 0.974527527 | 16 | 0 | KQK16092 | 0.902 | − | HORVU.MC |
| 0.982321522 | 1.003022408 | 16 | 0 | KQK15465 | 0.978 | − | HORVU.MC |
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| 0.940664813 | 0.973979702 | 16 | 0 | KQJ84513 | 0.900 | −1 | HORVU.MC |
| 0.915092274 | 0.963349766 | 16 | 0 | KQJ93988 | 0.896 | −0 | HORVU.MC |
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| 0.916282019 | 0.985528942 | 16 | 0 | KQJ85433 | 0.907 | −0 | HORVU.MC |
| 0.888932695 | 0.92734441 | 16 | 1 | KQK00143 | 0.888 | − | HORVU.MC |
| 0.940061364 | 0.995156199 | 16 | 7 | KQJ98786 | 0.873 | −1 | HORVU.MC |
| | | | | | | | |
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| 0.971756169 | 0.987483609 | 16 | 0 | KQK07046 | 0.965 | − | HORVU.MC |
| 0.911453069 | 0.988545246 | 16 | 0 | KQJ84308 | 0.928 | 0. | genblast_C |
| 0.884007509 | 0.948286303 | 16 | 3 | KQK11537 | 0.895 | 0 | HORVU.MC |
| 0.887190017 | 0.926780704 | 16 | 0 | KQJ81425 | 0.841 | −1 | HORVU.MC |
| 0.887096445 | 0.928075194 | 16 | 0 | KQJ85712 | 0.898 | 0. | HORVU.MC |
| 0.927733842 | 0.957367512 | 16 | 0 | KQK08934 | 0.927 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.929734567 | 0.952796088 | 16 | 0 | KQK18285 | 0.900 | – | HORVU.MC |
| 0.918223616 | 0.956411138 | 16 | 0 | KQK19286 | 0.911 | – | HORVU.MC |
| 0.938032704 | 0.958204432 | 16 | 0 | KQK03409 | 0.944 | 0 | HORVU.MC |
| 0.923561151 | 0.972482014 | 16 | 0 | KQK03433 | 0.871 | – | HORVU.MC |
| 0.890907488 | 0.963136207 | 16 | 5 | KQK15543 | 0.831 | – | HORVU.MC |
| 0.889848962 | 0.987768718 | 16 | 0 | KQJ84255 | 0.901 | 0. | HORVU.MC |
| 0.842211788 | 1.025582902 | 16 | 1 | genblast_Os06t053 | | | HORVU.MC |
| 0.897138124 | 0.955561331 | 16 | 0 | KQJ94140 | 0.903 | 0. | HORVU.MC |
| 0.870121711 | 0.922538681 | 16 | 0 | KQK03732 | 0.903 | 0 | HORVU.MC |
| 0.922026887 | 0.99131334 | 16 | 0 | KQK23097 | 0.872 | – | HORVU.MC |
| 0.874101181 | 0.973908577 | 16 | 7 | KQK13591 | 0.903 | 0 | HORVU.MC |
| 0.879717521 | 0.952881976 | 16 | 0 | KQK10148 | 0.823 | – | HORVU.MC |
| 0.884947959 | 0.960185438 | 16 | 2 | KQK15469 | 0.862 | – | HORVU.MC |
| 0.898132865 | 0.931691214 | 16 | 3 | KQK10843 | 0.895 | – | HORVU.MC |
| 0.946961223 | 0.964951529 | 16 | 0 | PNT61693 | 0.927 | – | HORVU.MC |
| 0.914624275 | 0.948949627 | 16 | 1 | KQK01645 | 0.911 | – | HORVU.MC |
| 0.929984709 | 0.971009174 | 16 | 0 | KQJ98258 | 0.923 | –0 | HORVU.MC |
| 0.904767919 | 0.951028171 | 16 | 0 | KQK23177 | 0.899 | – | HORVU.MC |
| 0.913187041 | 0.966121772 | 16 | 0 | KQK10727 | 0.899 | – | HORVU.MC |

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| 0.909272951 | 0.960772232 | 16 | 0 | KQJ94491 | 0.866 | –1 | HORVU.MC |
| 0.915180006 | 0.972249009 | 16 | 1 | KQK14564 | 0.900 | – | HORVU.MC |
| 0.970640132 | 1.001518806 | 16 | 0 | KQK18612 | 0.957 | – | HORVU.MC |
| 0.95107833 | 0.974465148 | 16 | 0 | KQK12296 | 0.929 | – | HORVU.MC |
| 0.870942243 | 0.94688027 | 16 | 0 | KQJ99344 | 0.840 | –0 | HORVU.MC |
| 0.95153692 | 0.995907231 | 16 | 0 | KQK23016 | 0.970 | 0 | HORVU.MC |
| 0.961736076 | 0.98553403 | 16 | 0 | KQK16756 | 0.963 | 0 | HORVU.MC |
| 0.862252781 | 0.969097651 | 16 | 0 | KQK04008 | 0.863 | 0 | HORVU.MC |
| 0.843668577 | 0.884314747 | 16 | 0 | KQJ96088 | 0.880 | 0. | HORVU.MC |
| 0.956340264 | 0.975622247 | 16 | 3 | KQK23959 | 0.941 | – | HORVU.MC |
| 0.909619349 | 0.982131949 | 16 | 0 | KQK04766 | 0.876 | – | HORVU.MC |
| 0.906012908 | 0.967228662 | 16 | 2 | KQK14963 | 0.858 | – | HORVU.MC |
| 0.819353376 | 0.884765625 | 16 | 3 | PNT71338 | 0.813 | – | HORVU.MC |
| 0.908342634 | 0.969419643 | 16 | 3 | KQK07938 | 0.916 | 0 | HORVU.MC |
| 0.984258105 | 0.997350374 | 16 | 0 | KQK22357 | 0.977 | – | HORVU.MC |
| 0.941192535 | 0.9712335 | 16 | 0 | KQK09185 | 0.944 | 0 | HORVU.MC |
| 0.945247183 | 0.976372228 | 16 | 0 | KQK11169 | 0.934 | – | HORVU.MC |
| 0.885905377 | 0.949130206 | 16 | 1 | KQK23827 | 0.755 | – | HORVU.MC |
| 0.915598488 | 0.972334932 | 16 | 0 | KQK17081 | 0.897 | – | HORVU.MC |
| 0.889964326 | 0.960039822 | 16 | 7 | KQK20995 | 0.883 | – | HORVU.MC |
| 0.831861958 | 0.894060995 | 16 | 0 | PNT65129 | 0.798 | – | HORVU.MC |
| 0.88141261 | 0.9624423 | 16 | 0 | PNT67437 | 0.889 | 0. | HORVU.MC |

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| 0.873719928 | 0.929778934 | 16 | 0 | KQK00791 | 0.824 | – | HORVU.MC |
| 0.964983842 | 0.983905715 | 16 | 0 | KQK15945 | 0.966 | 0 | HORVU.MC |
| 0.951485363 | 0.978913421 | 16 | 0 | KQK00918 | 0.971 | 0 | HORVU.MC |
| 0.941127594 | 0.98540856 | 16 | 0 | KQJ89779 | 0.917 | –0 | HORVU.MC |
| 0.976362574 | 0.987204724 | 16 | 0 | KQJ89761 | 0.978 | 0. | HORVU.MC |
| 0.882982373 | 0.931813384 | 16 | 0 | KQJ83517 | 0.859 | –0 | HORVU.MC |
| 0.924332109 | 0.978450241 | 16 | 2 | KQK00449 | 0.905 | – | HORVU.MC |
| 0.960060751 | 0.98460972 | 16 | 0 | PNT65758 | 0.946 | – | HORVU.MC |
| 0.896764706 | 0.968663102 | 16 | 4 | KQJ87966 | 0.828 | –1 | HORVU.MC |
| 0.95917223 | 0.982474442 | 16 | 0 | KQK17829 | 0.952 | – | HORVU.MC |
| 0.9454709 | 0.973421578 | 16 | 1 | KQK17830 | 0.945 | 0 | HORVU.MC |
| 0.897718454 | 0.957473227 | 16 | 0 | KQK13863 | 0.923 | 0 | HORVU.MC |
| 0.929744078 | 0.967963668 | 16 | 0 | KQK16679 | 0.928 | – | HORVU.MC |
| 0.973728153 | 0.996549037 | 16 | 0 | KQJ86731 | 0.977 | 0. | HORVU.MC |
| 0.924081146 | 0.957633556 | 16 | 0 | KQJ81479 | 0.932 | 0. | genblast_C |
| 0.948106116 | 0.972719273 | 16 | 0 | KQJ83858 | 0.958 | 0. | HORVU.MC |
| 0.953751455 | 0.980256112 | 16 | 1 | KQJ85161 | 0.956 | 0. | HORVU.MC |
| 0.930490311 | 0.975631239 | 16 | 0 | KQK20539 | 0.965 | 0 | HORVU.MC |
| 0.968830891 | 0.994667633 | 16 | 0 | PNT61808 | 0.959 | – | HORVU.MC |
| 0.932797906 | 0.9696439 | 16 | 0 | KQK22776 | 0.904 | – | HORVU.MC |
| 0.970318477 | 0.991885939 | 16 | 0 | KQK18108 | 0.967 | – | HORVU.MC |
| 0.957424497 | 0.990149383 | 16 | 0 | KQK05685 | 0.940 | – | HORVU.MC |
| 0.951981554 | 1.004020909 | 16 | 0 | KQK04923 | 0.921 | – | HORVU.MC |
| 0.863024802 | 0.912221571 | 16 | 1 | KQK11457 | 0.884 | 0 | HORVU.MC |
| 0.903681079 | 0.956623031 | 16 | 1 | KQK18546 | 0.925 | 0 | HORVU.MC |

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| 0.945276797 | 0.973618612 | 16 | 4 | KQK09735 0.953 0 | HORVU.MC |
| 0.924176776 | 0.958058925 | 16 | 0 | KQJ90600 0.899 -0 | HORVU.MC |
| 0.914101776 | 0.975612365 | 16 | 0 | KQJ90628 0.835 -1 | HORVU.MC |
| 0.94866572 | 0.971894155 | 16 | 0 | KQK10327 0.934 - | HORVU.MC |
| 0.864241508 | 0.962867012 | 16 | 1 | KQK01770 0.815 - | HORVU.MC |
| 0.942500551 | 0.973330395 | 16 | 0 | KQK13028 0.960 0 | HORVU.MC |
| 0.885973831 | 0.969410309 | 16 | 0 | KQJ82253 0.791 -1 | HORVU.MC |
| 0.86075772 | 0.952530404 | 16 | 5 | genblast_Os01t019 | HORVU.MC |
| 0.888090293 | 0.952557936 | 16 | 0 | KQK00550 0.826 - | HORVU.MC |
| 0.896396961 | 0.95507682 | 16 | 2 | PNT69254 0.898 0. | genblast_C |
| 0.947105051 | 0.991223357 | 16 | 0 | KQK15661 0.953 0 | genblast_C |
| 0.925645049 | 0.975360298 | 16 | 0 | KQJ87823 0.921 -0 | HORVU.MC |
| 0.936082785 | 0.979404267 | 16 | 0 | KQJ89486 0.906 -0 | HORVU.MC |
| 0.860604362 | 0.912759886 | 16 | 0 | KQJ92179 0.793 -2 | HORVU.MC |
| 0.881770906 | 0.928381963 | 16 | 0 | KQK21550 0.906 0 | HORVU.MC |

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| 0.937117369 | 0.99772608 | 16 | 2 | PNT65680 | 0.966 | 0. | HORVU.MC |
| 0.926652187 | 0.983014447 | 16 | 0 | KQJ90401 | 0.946 | 0. | HORVU.MC |
| 0.941986943 | 0.966965027 | 16 | 0 | KQK03228 | 0.949 | 0 | HORVU.MC |
| 0.953512397 | 0.989987285 | 16 | 0 | KQK23767 | 0.880 | – | HORVU.MC |
| 0.925882384 | 0.965761386 | 16 | 0 | KQK23432 | 0.940 | 0 | HORVU.MC |
| 0.883496835 | 0.95443038 | 16 | 2 | KQJ93350 | 0.893 | 0. | HORVU.MC |
| 0.945652326 | 0.996188341 | 16 | 3 | KQJ94907 | 0.938 | –0 | HORVU.MC |
| 0.869379985 | 0.950326323 | 16 | 0 | KQK19617 | 0.886 | 0 | HORVU.MC |
| 0.907936753 | 0.947095179 | 16 | 1 | KQK17329 | 0.940 | 0 | HORVU.MC |
| 0.904379977 | 0.968373151 | 16 | 0 | KQK21668 | 0.893 | – | HORVU.MC |
| 0.922064615 | 0.97106807 | 16 | 1 | KQK01742 | 0.954 | 0 | HORVU.MC |
| 0.858193169 | 0.94153426 | 16 | 5 | KQJ98124 | 0.856 | –0 | genblast_C |
| 0.893182249 | 0.945761426 | 16 | 0 | KQJ94476 | 0.846 | –1 | HORVU.MC |
| 0.976079689 | 0.997831587 | 16 | 0 | KQK10622 | 0.970 | – | HORVU.MC |
| 0.920558866 | 0.955548397 | 16 | 0 | KQK15461 | 0.814 | – | HORVU.MC |
| 0.936465606 | 0.968244117 | 16 | 1 | KQJ87671 | 0.934 | –0 | HORVU.MC |

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| 0.864220331 | 0.929982335 | 16 | 0 | KQK09586 | 0.804 | – | HORVU.MC |
| 0.908362662 | 0.975609756 | 16 | 3 | KQK18531 | 0.889 | – | HORVU.MC |
| 0.938810412 | 0.988628287 | 16 | 0 | PNT69398 | 0.954 | 0. | HORVU.MC |

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| 0.935718717 | 0.960581354 | 16 | 0 | KQJ89079 | 0.934 | –0 | HORVU.MC |
| 0.89885395 | 0.955667034 | 16 | 6 | KQK09911 | 0.840 | – | HORVU.MC |
| 0.90516607 | 0.968257757 | 16 | 0 | KQK03144 | 0.916 | 0. | HORVU.MC |
| 0.948137933 | 0.978941586 | 16 | 0 | KQK07191 | 0.916 | – | genblast_C |
| 0.937345185 | 0.962534833 | 16 | 0 | KQK00930 | 0.906 | – | HORVU.MC |
| 0.914457577 | 0.962600253 | 16 | 3 | KQK09280 | 0.894 | – | HORVU.MC |
| 0.870268334 | 0.948013441 | 16 | 3 | KQJ98134 | 0.771 | –1 | HORVU.MC |
| 0.903614411 | 0.967383107 | 16 | 0 | KQJ84051 | 0.868 | –0 | HORVU.MC |
| 0.93888539 | 0.985894207 | 16 | 1 | PNT75834 | 0.808 | – | HORVU.MC |
| 0.929707659 | 0.972748442 | 16 | 0 | KQJ98970 | 0.942 | 0. | HORVU.MC |
| 0.956298062 | 0.987366604 | 16 | 0 | KQJ89908 | 0.945 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.977468449 | 1.001448226 | 16 | 1 | KQK03085 | 0.954 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.957304273 | 0.9932082 | 16 | 0 | KQK02988 | 0.896 | – | HORVU.MC |
| 0.892535764 | 0.970004615 | 16 | 0 | KQK11726 | 0.784 | – | HORVU.MC |
| 0.9217373 | 0.961094791 | 16 | 0 | KQK15885 | 0.892 | – | HORVU.MC |
| 0.910173458 | 0.978288232 | 16 | 0 | KQK23924 | 0.849 | – | HORVU.MC |
| 0.922787153 | 0.972539152 | 16 | 4 | PNT62411 | 0.938 | 0. | HORVU.MC |

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| 0.948877038 | 0.986668034 | 16 | 0 | KQJ96422 | 0.924 | –1 | HORVU.MC |
| 0.960964663 | 0.986598394 | 16 | 0 | KQJ99218 | 0.928 | –1 | HORVU.MC |
| 0.932494995 | 0.984317651 | 16 | 0 | KQJ85983 | 0.873 | –1 | HORVU.MC |
| 0.943561552 | 0.985980411 | 16 | 0 | KQK23361 | 0.883 | – | HORVU.MC |
| 0.888067497 | 0.924628365 | 16 | 1 | KQK02432 | 0.862 | – | HORVU.MC |
| 0.859234761 | 0.921278983 | 16 | 0 | KQJ97811 | 0.806 | –1 | HORVU.MC |
| 0.895950751 | 0.967928073 | 16 | 1 | KQK19397 | 0.918 | 0. | HORVU.MC |
| 0.914264148 | 0.962387854 | 16 | 0 | KQK07206 | 0.893 | – | HORVU.MC |
| 0.934754288 | 0.975754505 | 16 | 0 | KQK05481 | 0.932 | – | HORVU.MC |
| 0.927141764 | 0.965323814 | 16 | 0 | KQK13506 | 0.949 | 0. | HORVU.MC |
| 0.907498231 | 0.957934007 | 16 | 1 | KQK15917 | 0.910 | 0. | HORVU.MC |
| 0.889525835 | 0.949574601 | 16 | 0 | KQJ91111 | 0.907 | 0. | HORVU.MC |
| 0.923090645 | 0.972198732 | 16 | 0 | KQK21857 | 0.941 | 0. | HORVU.MC |
| 0.870598592 | 0.932550319 | 16 | 1 | KQK19285 | 0.797 | – | HORVU.MC |
| 0.920170708 | 0.966588273 | 16 | 1 | KQK10230 | 0.912 | – | HORVU.MC |
| 0.920772883 | 0.9528092 | 16 | 1 | KQK01722 | 0.913 | – | HORVU.MC |
| 0.952197438 | 0.998233216 | 16 | 0 | KQK13647 | 0.939 | – | HORVU.MC |
| 0.946117051 | 0.98368036 | 16 | 0 | KQJ93196 | 0.949 | 0. | HORVU.MC |
| 0.882225327 | 0.925871452 | 16 | 1 | KQK08811 | 0.823 | – | HORVU.MC |
| 0.895129298 | 0.923890685 | 16 | 0 | KQK06286 | 0.922 | 0. | HORVU.MC |
| 0.885936271 | 0.944107404 | 16 | 2 | KQK19469 | 0.858 | – | HORVU.MC |
| 0.920728431 | 0.959471907 | 16 | 0 | KQJ83034 | 0.912 | –0 | HORVU.MC |
| 0.86477882 | 0.914804885 | 16 | 0 | KQK13464 | 0.810 | – | HORVU.MC |
| 0.936715355 | 0.975857074 | 16 | 0 | KQJ98155 | 0.936 | –0 | HORVU.MC |
| 0.945640072 | 0.992939387 | 16 | 1 | KQK23935 | 0.958 | 0. | HORVU.MC |

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| 0.912548607 | 0.976992871 | 16 | 0 | PNT64722 | 0.782 | – | HORVU.MC |
| 0.9566005 | 0.984896161 | 16 | 1 | KQK06690 | 0.929 | – | HORVU.MC |
| 0.89362817 | 0.964996856 | 16 | 0 | KQJ95901 | 0.908 | 0. | HORVU.MC |
| 0.980163172 | 1.010131951 | 16 | 0 | KQK12487 | 0.970 | – | HORVU.MC |
| 0.915627899 | 0.9682282 | 16 | 0 | KQK22737 | 0.933 | 0 | HORVU.MC |
| 0.940001624 | 0.987524366 | 16 | 0 | KQK10946 | 0.957 | 0 | HORVU.MC |
| | | | | | | | |
| 0.909013477 | 0.971078134 | 16 | 0 | KQJ93591 | 0.878 | –0 | HORVU.MC |
| 0.886898356 | 0.963412248 | 16 | 0 | KQK05284 | 0.787 | – | HORVU.MC |
| 0.937743033 | 0.980557356 | 16 | 1 | KQK19104 | 0.959 | 0 | genblast_Z |
| 0.869883802 | 0.911550468 | 16 | 0 | KQK01661 | 0.815 | – | HORVU.MC |
| 0.895589536 | 0.946183154 | 16 | 2 | KQK19859 | 0.883 | – | HORVU.MC |
| 0.973850182 | 0.992106861 | 16 | 0 | KQK10867 | 0.970 | – | HORVU.MC |
| 0.933170766 | 0.974083498 | 16 | 1 | PNT70155 | 0.952 | 0. | HORVU.MC |
| 0.876470588 | 0.946300974 | 16 | 0 | KQK02444 | 0.810 | – | HORVU.MC |
| 0.881546781 | 0.952716298 | 16 | 8 | KQK11394 | 0.843 | – | HORVU.MC |
| 0.908993837 | 0.949394464 | 16 | 1 | PNT69492 | 0.925 | 0. | HORVU.MC |
| 0.939161491 | 0.98310559 | 16 | 0 | KQK13603 | 0.938 | – | HORVU.MC |
| 0.849683126 | 0.936097175 | 16 | 0 | KQJ99586 | 0.831 | –0 | genblast_C |
| 0.909372305 | 0.957989405 | 16 | 1 | KQK00582 | 0.910 | 0 | HORVU.MC |
| 0.974387564 | 1.000609172 | 16 | 0 | KQJ83881 | 0.966 | –0 | HORVU.MC |
| 0.957136534 | 0.98435963 | 16 | 1 | KQJ93484 | 0.949 | –0 | HORVU.MC |
| 0.922123809 | 0.981901899 | 16 | 1 | genblast_Os06t048 | | | HORVU.MC |
| | | | | | | | |
| 0.966805465 | 0.983063535 | 16 | 0 | KQK03490 | 0.957 | – | HORVU.MC |
| 0.935898245 | 0.987627825 | 16 | 0 | KQK23652 | 0.836 | – | HORVU.MC |
| 0.933517849 | 0.990962494 | 16 | 0 | KQK19854 | 0.900 | – | HORVU.MC |
| 0.892074468 | 0.953333333 | 16 | 0 | KQK13040 | 0.849 | – | HORVU.MC |
| | | | | | | | |
| 0.941964286 | 0.989718615 | 16 | 0 | KQJ84919 | 0.906 | –1 | HORVU.MC |
| 0.892309266 | 0.947228472 | 16 | 0 | KQK08542 | 0.897 | 0 | HORVU.MC |

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| 0.883530099 | 0.944473275 | 16 | 0 | KQK01240 0.879 – | HORVU.MC |
| 0.90128606 | 0.963483659 | 16 | 0 | KQK12526 0.910 0 | HORVU.MC |
| 0.959403086 | 0.984337827 | 16 | 0 | KQJ84700 0.954 –0 | HORVU.MC |
| 0.974187745 | 0.990187527 | 16 | 0 | KQK13339 0.984 0 | HORVU.MC |

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| 0.910482043 | 0.978045579 | 16 | 0 | KQJ98913 0.926 0. | HORVU.MC |
| 0.903711133 | 0.93781344 | 16 | 1 | KQK06656 0.873 – | HORVU.MC |
| 0.950790285 | 0.992135698 | 16 | 0 | KQK05290 0.920 – | HORVU.MC |
| 0.92681068 | 0.969200042 | 16 | 0 | KQK15495 0.856 – | HORVU.MC |
| 0.843685056 | 0.893822029 | 16 | 0 | KQJ81624 0.752 –2 | HORVU.MC |
| 0.893377393 | 0.944170601 | 16 | 2 | KQJ84216 0.883 –0 | HORVU.MC |
| 0.958377032 | 1.002097535 | 16 | 0 | KQK23020 0.933 – | HORVU.MC |

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| 0.907258316 | 0.947624797 | 16 | 1 | PNT64270 0.883 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.897663752 | 0.936362333 | 16 | 0 | KQJ85742 0.916 0. | HORVU.MC |
| 0.943154147 | 0.983618654 | 16 | 0 | KQJ94521 0.953 0. | HORVU.MC |
| 0.930289007 | 0.980694981 | 16 | 0 | PNT69315 0.932 0. | HORVU.MC |

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| 0.908644873 | 0.961040476 | 16 | 2 | KQK14589 0.899 – | HORVU.MC |
| 0.945999171 | 0.988444872 | 16 | 0 | KQK04628 0.924 – | HORVU.MC |
| 0.920856354 | 0.973357888 | 16 | 1 | KQK00689 0.924 0 | HORVU.MC |
| 0.94978183 | 0.977092099 | 16 | 1 | KQK13779 0.956 0 | HORVU.MC |
| 0.905711341 | 0.951119993 | 16 | 0 | KQJ96423 0.853 –2 | HORVU.MC |
| 0.871340606 | 0.92274783 | 16 | 0 | KQK11434 0.825 – | HORVU.MC |
| 0.898340576 | 0.971696011 | 16 | 4 | PNT61074 0.925 0. | genblast_C |
| 0.925694805 | 0.954909091 | 16 | 1 | KQK22372 0.891 – | HORVU.MC |

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| 0.912354002 | 0.954895072 | 16 | 1 KQJ85480 0.892 −0 | HORVU.M |
| 0.893310093 | 0.952988048 | 16 | 0 KQK15878 0.833 − | HORVU.M |
| 0.914116194 | 0.990979381 | 16 | 0 KQJ81968 0.890 −0 | HORVU.M |
| 0.879626471 | 0.953948491 | 16 | 0 KQJ96956 0.843 −0 | HORVU.M |
| 0.836504536 | 0.907762097 | 16 | 0 KQK11318 0.801 − | HORVU.M |
| 0.892894553 | 0.927374302 | 16 | 1 genblast_Os07t010 | HORVU.M |
| 0.888126566 | 0.940350877 | 16 | 0 KQK13883 0.842 − | genblast_ |
| 0.876361386 | 0.945544554 | 16 | 0 PNT61190 0.811 − | HORVU.M |
| 0.933567425 | 0.97818109 | 16 | 1 KQJ93715 0.948 0. | HORVU.M |
| 0.884949449 | 0.934926471 | 16 | 0 KQK11319 0.868 − | HORVU.M |

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|---|---|---|---|---|
| 0.913382755 | 0.970347249 | 16 | 0 KQK02807 0.847 − | HORVU.M |
| 0.977669797 | 0.994977069 | 16 | 0 KQK08885 0.968 − | HORVU.M |
| 0.893369269 | 0.95750471 | 16 | 2 genblast_Os05t049 | HORVU.M |

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|---|---|---|---|---|
| 0.836563135 | 0.905271036 | 16 | 0 KQK00809 0.820 − | HORVU.M |
| 0.952466412 | 0.985511064 | 16 | 3 KQK22502 0.929 − | HORVU.M |
| 0.934880464 | 0.971791537 | 16 | 0 KQJ94716 0.923 −0 | HORVU.M |
| 0.933091463 | 0.958298645 | 16 | 0 KQJ86386 0.907 −1 | HORVU.M |
| 0.82380394 | 0.948968105 | 16 | 1 KQK13964 0.847 0 | HORVU.M |
| 0.926748317 | 0.988863957 | 16 | 2 KQJ97202 0.929 0. | genblast_ |
| 0.915570438 | 0.954556326 | 16 | 0 KQJ92385 0.865 −1 | HORVU.M |
| 0.914457662 | 0.971364342 | 16 | 2 KQJ94583 0.890 −0 | HORVU.M |

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|---|---|---|---|---|
| 0.922521014 | 0.963908589 | 16 | 2 KQK16335 0.914 − | HORVU.M |
| 0.950361715 | 0.986572291 | 16 | 1 genblast_Os05t017 | HORVU.M |
| 0.956274488 | 0.987483674 | 16 | 0 PNT72500 0.950 − | HORVU.M |
| 0.937530181 | 0.953158954 | 16 | 0 KQK21364 0.930 − | HORVU.M |
| 0.961330203 | 0.988595524 | 16 | 0 KQK01510 0.945 − | HORVU.M |
| 0.936754996 | 0.982119902 | 16 | 0 KQJ93030 0.919 −0 | HORVU.M |

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| 0.870925027 | 0.965554948 | 16 | 0 KQK00941 0.821 − | HORVU.M |

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|---|---|---|---|---|---|---|---|
| 0.96187837 | 0.987916916 | 16 | 3 | KQK15828 | 0.973 | 0 | HORVU.MC |
| 0.923059611 | 0.968036304 | 16 | 4 | KQJ91213 | 0.911 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.93290619 | 0.964354794 | 16 | 0 | KQJ91339 | 0.908 | −1 | HORVU.MC |
| 0.983496878 | 1.004205429 | 16 | 0 | KQK22446 | 0.993 | 0 | HORVU.MC |
| 0.941476368 | 0.969528083 | 16 | 0 | KQJ87742 | 0.910 | −1 | HORVU.MC |
| 0.957268884 | 0.995772836 | 16 | 0 | KQK16719 | 0.934 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.92483916 | 0.973923935 | 16 | 0 | KQK12704 | 0.896 | − | HORVU.MC |
| 0.930802357 | 0.961559383 | 16 | 0 | KQK18465 | 0.948 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.942611039 | 0.976897854 | 16 | 0 | KQK23816 | 0.924 | − | HORVU.MC |
| 0.962462481 | 0.989252517 | 16 | 0 | KQK13463 | 0.975 | 0 | HORVU.MC |
| 0.916713351 | 0.957424225 | 16 | 1 | KQK12108 | 0.917 | 0 | HORVU.MC |
| 0.93897185 | 0.9671816 | 16 | 1 | KQJ82574 | 0.949 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.93122577 | 0.99245052 | 16 | 3 | KQJ92793 | 0.925 | −0 | HORVU.MC |
| 0.957919958 | 0.98612984 | 16 | 0 | KQK00478 | 0.931 | − | HORVU.MC |
| 0.93165851 | 0.978370698 | 16 | 1 | genblast_Os08t041 | | | HORVU.MC |
| 0.86473455 | 0.93405226 | 16 | 0 | KQK11238 | 0.848 | − | HORVU.MC |
| 0.925354647 | 0.991133827 | 16 | 0 | KQK01412 | 0.877 | − | genblast_C |
| 0.96629709 | 0.983963144 | 16 | 0 | KQJ86898 | 0.946 | −1 | HORVU.MC |
| 0.938948342 | 0.963952366 | 16 | 0 | KQK22347 | 0.945 | 0 | HORVU.MC |
| 0.972830641 | 1.003504495 | 16 | 0 | KQJ84393 | 0.976 | 0. | HORVU.MC |
| 0.931998465 | 0.989423405 | 16 | 0 | KQJ99975 | 0.875 | −1 | HORVU.MC |
| 0.947401316 | 0.977192982 | 16 | 0 | KQK15474 | 0.937 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.962360387 | 0.981236039 | 16 | 0 | KQJ94920 | 0.928 | –2 | HORVU.MC |
| 0.93435066 | 0.975361628 | 16 | 0 | KQJ84554 | 0.938 | 0. | HORVU.MC |
| 0.934573738 | 0.989476895 | 16 | 0 | KQJ97842 | 0.927 | –0 | HORVU.MC |
| | | | | | | | |
| 0.927854378 | 0.976173198 | 16 | 1 | KQJ91061 | 0.886 | –1 | HORVU.MC |
| 0.957875135 | 0.983650095 | 16 | 0 | KQK19134 | 0.971 | 0 | HORVU.MC |
| 0.957978324 | 0.990727979 | 16 | 0 | KQK04989 | 0.919 | – | HORVU.MC |
| 0.958497684 | 0.98426822 | 16 | 0 | KQK14627 | 0.932 | – | HORVU.MC |
| 0.941364673 | 0.982513938 | 16 | 1 | KQK15947 | 0.913 | – | HORVU.MC |
| 0.922591339 | 0.971661721 | 16 | 0 | KQK11943 | 0.950 | 0 | HORVU.MC |
| 0.939645249 | 0.976663876 | 16 | 2 | KQK15916 | 0.878 | – | HORVU.MC |
| 0.908642211 | 0.969430646 | 16 | 4 | KQK23831 | 0.828 | – | HORVU.MC |
| 0.900959133 | 0.971226022 | 16 | 0 | KQJ84679 | 0.869 | –0 | HORVU.MC |
| 0.912507263 | 0.977106334 | 16 | 5 | KQK01454 | 0.835 | – | HORVU.MC |
| 0.900634456 | 0.969741337 | 16 | 1 | KQJ90500 | 0.908 | 0. | HORVU.MC |
| 0.881190096 | 0.948010456 | 16 | 1 | KQK23222 | 0.790 | – | genblast_C |
| 0.962561817 | 0.983492373 | 16 | 0 | KQJ98909 | 0.919 | –2 | HORVU.MC |
| | | | | | | | |
| 0.913420738 | 0.96869078 | 16 | 1 | KQJ91367 | 0.892 | –0 | HORVU.MC |
| 0.931563661 | 0.991547225 | 16 | 2 | KQK11629 | 0.935 | 0 | HORVU.MC |
| 0.930082307 | 0.975394267 | 16 | 1 | KQK17066 | 0.935 | 0 | HORVU.MC |
| 0.932426798 | 1.005189029 | 16 | 0 | KQK11996 | 0.836 | – | HORVU.MC |
| 0.882446208 | 0.967459158 | 16 | 4 | KQK00848 | 0.888 | 0 | HORVU.MC |
| 0.944425653 | 0.972940062 | 16 | 0 | KQK16136 | 0.946 | 0 | HORVU.MC |
| 0.973754678 | 0.989030843 | 16 | 0 | KQJ92882 | 0.967 | –0 | HORVU.MC |
| 0.925562443 | 0.96735027 | 16 | 1 | KQK13031 | 0.868 | – | HORVU.MC |
| 0.911573816 | 0.947918328 | 16 | 0 | KQK12338 | 0.926 | 0 | HORVU.MC |
| 0.952786057 | 0.97817318 | 16 | 1 | KQJ99005 | 0.924 | –1 | HORVU.MC |
| | | | | | | | |
| 0.969540663 | 0.998995984 | 16 | 0 | KQJ87687 | 0.989 | 1. | HORVU.MC |
| 0.99570802 | 1.007017544 | 16 | 0 | KQK13838 | 1.003 | 0 | HORVU.MC |
| 0.924901985 | 0.973405714 | 16 | 1 | KQJ87251 | 0.901 | –0 | HORVU.MC |
| | | | | | | | |
| 0.889020537 | 0.959221959 | 16 | 4 | KQK07364 | 0.925 | 0 | HORVU.MC |
| 0.929174921 | 0.97591828 | 16 | 2 | PNT77958 | 0.937 | 0. | HORVU.MC |
| 0.976965797 | 1.006205924 | 16 | 0 | KQK14867 | 0.988 | 0 | HORVU.MC |
| 0.934431697 | 0.974273999 | 16 | 0 | PNT64179 | 0.882 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.920283909 | 0.974973332 | 16 | 0 | KQK14947 | 0.907 | – | HORVU.MC |
| 0.899311915 | 0.97608707 | 16 | 2 | PNT73703 | 0.892 | – | HORVU.MC |
| 0.953875566 | 0.971674697 | 16 | 0 | KQJ88096 | 0.964 | 0. | HORVU.MC |
| 0.968383937 | 0.988824559 | 16 | 0 | PNT69118 | 0.960 | – | HORVU.MC |
| 0.908588587 | 0.954098946 | 16 | 0 | KQJ90944 | 0.798 | –2 | HORVU.MC |
| 0.991084835 | 1.009438009 | 16 | 0 | KQK09885 | 0.998 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.914931922 | 0.969227137 | 16 | 2 | KQK05949 | 0.895 | – | HORVU.MC |
| 0.914276376 | 0.975084589 | 16 | 3 | KQK12468 | 0.924 | 0. | HORVU.MC |
| 0.922233868 | 0.970543201 | 16 | 3 | KQK02356 | 0.893 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.950469667 | 0.985519729 | 16 | 1 | KQK10070 | 0.942 | – | HORVU.MC |
| 0.862371941 | 0.911781446 | 16 | 0 | KQK16903 | 0.828 | – | HORVU.MC |
| 0.947037052 | 0.97603008 | 16 | 0 | KQK23504 | 0.884 | – | HORVU.MC |
| 0.922651796 | 0.958637147 | 16 | 0 | KQK05014 | 0.847 | – | HORVU.MC |
| 0.953172356 | 0.971127772 | 16 | 0 | KQK00892 | 0.959 | 0. | HORVU.MC |
| 0.945482919 | 0.975305254 | 16 | 1 | KQJ92141 | 0.934 | –0 | HORVU.MC |

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| 0.907554878 | 0.942317014 | 16 | 0 KQJ83115 0.918 0.HORVU.MC |
| 0.874860123 | 0.945408041 | 16 | 5 KQK02866 0.945 1.HORVU.MC |
| 0.913347301 | 0.968026387 | 16 | 1 KQK21479 0.861 – HORVU.MC |
| 0.878001744 | 0.962167964 | 16 | 0 KQJ87926 0.877 –0HORVU.MC |
| 0.918045949 | 0.976482213 | 16 | 0 KQJ99246 0.844 –1HORVU.MC |

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|---|---|---|---|
| 0.861835071 | 0.952597345 | 16 | 6 KQK11021 0.902 0.genblast_C |

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| 0.948530298 | 0.981929888 | 16 | 0 KQJ92249 0.867 –2HORVU.MC |
| 0.946286878 | 0.987325594 | 16 | 0 KQJ90726 0.912 –0HORVU.MC |
| 0.947080999 | 0.976099654 | 16 | 1 KQK01459 0.947 –HORVU.MC |
| 0.935243867 | 0.959929907 | 16 | 0 KQK08380 0.949 0.HORVU.MC |
| 0.827494566 | 0.881401983 | 16 | 0 PNT64690 0.747 –HORVU.MC |
| 0.98098881 | 1.002055264 | 16 | 0 KQJ89940 0.966 –0HORVU.MC |

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|---|---|---|---|
| 0.935974124 | 0.969787047 | 16 | 0 KQJ84855 0.920 –0HORVU.MC |
| 0.941767183 | 0.991275982 | 16 | 1 KQK18761 0.935 –HORVU.MC |
| 0.948808948 | 0.972175521 | 16 | 0 KQK22836 0.946 –HORVU.MC |
| 0.946061525 | 0.987876254 | 16 | 0 KQK23337 0.969 0.HORVU.MC |

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|---|---|---|---|
| 0.944844989 | 0.976001648 | 16 | 0 KQK07558 0.937 –HORVU.MC |
| 0.902676178 | 0.962236691 | 16 | 2 KQK03471 0.911 0.HORVU.MC |
| 0.9276162 | 0.963413971 | 16 | 1 KQK23874 0.891 – HORVU.MC |
| 0.908622139 | 0.954222165 | 16 | 0 KQK01278 0.865 – HORVU.MC |
| 0.927680273 | 0.965117983 | 16 | 0 KQK02874 0.895 – HORVU.MC |
| 0.896905824 | 0.96324821 | 16 | 0 KQJ90886 0.885 –0HORVU.MC |
| 0.916958697 | 0.962091158 | 16 | 0 KQK06504 0.938 0.HORVU.MC |
| 0.94814956 | 0.989329268 | 16 | 0 KQJ94822 0.947 –0HORVU.MC |
| 0.889006102 | 0.929109322 | 16 | 1 KQK14426 0.905 0.HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.977105372 | 1 | 16 | 0 | KQJ89842 | 0.973 | −0 | HORVU.MC |
| 0.958012008 | 0.969923984 | 16 | 1 | KQJ99020 | 0.964 | 0. | HORVU.MC |
| 0.907188373 | 0.950593575 | 16 | 0 | KQK18566 | 0.901 | − | HORVU.MC |
| 0.941765193 | 0.965801433 | 16 | 2 | KQJ84384 | 0.936 | −0 | HORVU.MC |
| 0.967827082 | 0.987669817 | 16 | 0 | KQK09420 | 0.953 | − | HORVU.MC |
| 0.96556563 | 0.991256477 | 16 | 0 | KQK00835 | 0.886 | − | HORVU.MC |
| 0.889193317 | 1.004671218 | 16 | 1 | KQK01885 | 0.842 | − | HORVU.MC |
| 0.876010963 | 0.949676492 | 16 | 0 | KQK13044 | 0.790 | − | HORVU.MC |
| 0.914526551 | 0.948306595 | 16 | 0 | KQK01970 | 0.901 | − | HORVU.MC |
| 0.950068074 | 0.97431155 | 16 | 0 | PNT71630 | 0.965 | 0. | HORVU.MC |
| 0.954624407 | 0.993379107 | 16 | 0 | PNT64970 | 0.934 | − | HORVU.MC |
| 0.945991508 | 0.985728557 | 16 | 0 | KQK19564 | 0.922 | − | HORVU.MC |
| 0.917002961 | 0.955638137 | 16 | 1 | KQK11566 | 0.922 | 0 | HORVU.MC |
| 0.900976834 | 0.979277383 | 16 | 4 | KQJ96452 | 0.902 | 0. | HORVU.MC |
| 0.9475 | 0.983697813 | 16 | 0 | KQK09763 | 0.941 | − | HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.892413964 | 0.935804103 | 16 | 0 | KQK06341 | 0.889 | –HORVU.MC |
| 0.87014485 | 0.907725322 | 16 | 0 | KQK16304 | 0.787 | –HORVU.MC |
| 0.952197039 | 0.985982084 | 16 | 0 | KQJ99096 | 0.959 | 0.HORVU.MC |
| 0.925992311 | 0.973607648 | 16 | 0 | KQJ98441 | 0.935 | 0.HORVU.MC |
| 0.953892378 | 0.993850152 | 16 | 1 | KQJ97320 | 0.958 | 0. HORVU.MC |
| 0.944488259 | 0.987765403 | 16 | 6 | KQK22208 | 0.930 | –HORVU.MC |
| 0.90378105 | 0.96643682 | 16 | 0 | KQK03368 | 0.899 | –HORVU.MC |
| 0.983598571 | 1.006495615 | 16 | 0 | KQK19021 | 0.973 | –HORVU.MC |
| 0.968063702 | 1.009548493 | 16 | 0 | KQK20032 | 0.925 | – HORVU.MC |
| 0.94127086 | 0.975726456 | 16 | 0 | KQK09981 | 0.906 | – HORVU.MC |

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| 0.865148643 | 0.939744613 | 16 | 0 | KQJ84066 | 0.940 | 1.HORVU.MC |
| 0.951118392 | 0.983160053 | 16 | 0 | KQK15286 | 0.884 | –HORVU.MC |
| 0.938318808 | 0.98179194 | 16 | 0 | KQK03995 | 0.940 | 0HORVU.MC |
| 0.893168605 | 0.950166113 | 16 | 2 | KQK23089 | 0.847 | – HORVU.MC |
| 0.876708394 | 0.931543299 | 16 | 0 | KQJ97563 | 0.830 | –1HORVU.MC |
| 0.942706094 | 0.987959948 | 16 | 1 | KQK17861 | 0.929 | –HORVU.MC |
| 0.963257724 | 0.987407118 | 16 | 0 | KQJ92219 | 0.966 | 0. HORVU.MC |
| 0.954178182 | 0.985874405 | 16 | 0 | KQJ94896 | 0.920 | –1HORVU.MC |
| 0.956030243 | 0.988117269 | 16 | 0 | KQK01920 | 0.960 | 0HORVU.MC |
| 0.968106113 | 1.000137363 | 16 | 0 | KQJ97269 | 0.949 | –0HORVU.MC |
| 0.958353474 | 0.975895849 | 16 | 0 | KQK17116 | 0.957 | –HORVU.MC |
| 0.920699138 | 0.967793177 | 16 | 0 | KQJ91871 | 0.913 | –0genblast_C |

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|---|---|---|---|---|---|---|
| 0.913339646 | 0.967272727 | 16 | 0 | KQK17436 | 0.880 | – HORVU.MC |
| 0.989109281 | 1.016167665 | 16 | 0 | KQK16855 | 0.983 | –HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.96890277 | 0.999456817 | 16 | 0 | KQK16114 | 0.976 | 0HORVU.MC |
| 0.971213774 | 1.001869741 | 16 | 1 | KQK15075 | 0.978 | 0HORVU.MC |
| 0.945601931 | 0.989043347 | 16 | 0 | KQJ90090 | 0.903 | –1HORVU.MC |
| 0.898356052 | 0.969349458 | 16 | 3 | KQK06159 | 0.900 | 0HORVU.MC |

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|---|---|---|---|---|---|---|
| 0.980075703 | 0.997876976 | 16 | 0 | KQK14348 | 0.985 | 0HORVU.MC |
| 0.856875418 | 0.914658635 | 16 | 0 | PNT69182 | 0.830 | –HORVU.MC |

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|---|---|---|---|
| 0.888780659 | 0.956566173 | 16 | 1 KQK03377 0.844 –(HORVU.MC |
| 0.975927714 | 0.998620499 | 16 | 0 KQJ81694 0.973 –0HORVU.MC |
| 0.918197682 | 0.946924799 | 16 | 0 PNT66473 0.917 –(HORVU.MC |
| 0.956065786 | 0.972086924 | 16 | 0 KQK04253 0.921 –:HORVU.MC |
| 0.950662474 | 0.985681615 | 16 | 0 KQK23906 0.937 –(HORVU.MC |
| 0.925167874 | 0.963766689 | 16 | 0 KQJ97182 0.899 –0HORVU.MC |
| 0.980720367 | 0.997815718 | 16 | 0 KQK03472 0.987 0 HORVU.MC |
| 0.920453631 | 0.968443085 | 16 | 0 KQK23783 0.859 –:HORVU.MC |
| 0.970309252 | 1.001386001 | 16 | 0 KQK08294 0.969 –(HORVU.MC |
| 0.958531475 | 0.98417708 | 16 | 0 KQK15232 0.950 –(HORVU.MC |
| 0.874506876 | 0.951532913 | 16 | 0 KQK21208 0.895 0 HORVU.MC |
| 0.928011248 | 0.973434321 | 16 | 1 KQK10201 0.885 – HORVU.MC |
| 0.926800351 | 0.955035129 | 16 | 0 KQJ99490 0.900 –1HORVU.MC |
| 0.999079378 | 1.014320786 | 16 | 3 PNT74744 0.991 –(HORVU.MC |
| 0.934646332 | 0.980947197 | 16 | 0 PNT68039 0.934 –(HORVU.MC |
| 0.970448714 | 1.000337633 | 16 | 0 KQJ85628 0.982 0.:HORVU.MC |
| 0.943855189 | 0.968326321 | 16 | 0 KQK12852 0.963 0 HORVU.MC |
| 0.955364924 | 0.992810458 | 16 | 0 KQJ85806 0.933 –0HORVU.MC |
| 0.880870001 | 0.930896249 | 16 | 8 KQK20091 0.806 – HORVU.MC |
| 0.908400583 | 0.928715535 | 16 | 0 KQK03222 0.918 0 genblast_C |
| 0.889333129 | 0.961070735 | 16 | 3 KQJ95851 0.874 –0HORVU.MC |
| 0.904943034 | 0.969426017 | 16 | 0 KQK24057 0.807 – HORVU.MC |
| 0.962230861 | 0.996889952 | 16 | 0 KQK07781 0.951 –(genblast_C |
| 0.930886453 | 0.955138766 | 16 | 0 KQJ88928 0.924 –0HORVU.MC |
| 0.899783886 | 0.982600022 | 16 | 1 KQJ96412 0.839 –0HORVU.MC |
| 0.875146622 | 0.960118861 | 16 | 0 KQJ83955 0.873 –0HORVU.MC |
| 0.882707911 | 0.925219743 | 16 | 0 KQJ84327 0.809 –2HORVU.MC |
| 0.955062549 | 0.981860829 | 16 | 0 KQK15844 0.956 0 HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.905239586 | 0.974366443 | 16 | 0 | KQK04783 | 0.909 | 0 | HORVU.MC |
| 0.924116458 | 0.97209181 | 16 | 0 | KQK15260 | 0.943 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.944844021 | 0.985355286 | 16 | 1 | KQJ97812 | 0.937 | –0 | HORVU.MC |
| 0.963805757 | 0.992661075 | 16 | 0 | KQK22588 | 0.957 | – | HORVU.MC |
| 0.925678539 | 0.968588062 | 16 | 1 | KQK23032 | 0.902 | – | HORVU.MC |
| 0.949428105 | 0.983267974 | 16 | 1 | KQK23460 | 0.907 | – | HORVU.MC |
| 0.910915536 | 0.960009695 | 16 | 0 | KQK10128 | 0.873 | – | HORVU.MC |
| 0.95712488 | 0.999041227 | 16 | 0 | KQJ97966 | 0.942 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.915668428 | 0.990011581 | 16 | 0 | KQJ93579 | 0.893 | –0 | HORVU.MC |
| 0.959541967 | 0.978806026 | 16 | 0 | KQK18409 | 0.962 | 0 | HORVU.MC |

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| 0.950559296 | 0.963727194 | 16 | 0 | KQK17750 | 0.955 | 0 | HORVU.MC |
| 0.850622463 | 0.922814614 | 16 | 11 | KQK14382 | 0.897 | 1 | HORVU.MC |
| 0.942662703 | 1.002002503 | 16 | 1 | PNT71562 | 0.968 | 0. | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.900492756 | 0.972052659 | 16 | 1 | KQJ91171 | 0.899 | –0 | HORVU.MC |

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| 0.916859926 | 0.94887652 | 16 | 0 | KQK14217 | 0.872 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.877947945 | 0.941539338 | 16 | 1 | KQK13744 | 0.900 | 0 | HORVU.MC |
| 0.909872698 | 0.961646804 | 16 | 0 | KQJ83100 | 0.855 | –1 | genblast_C |
| 0.925843007 | 0.951271278 | 16 | 1 | KQJ86799 | 0.943 | 0. | HORVU.MC |
| 0.912070358 | 1.005287897 | 16 | 1 | KQK23040 | 0.847 | – | HORVU.MC |
| 0.969479683 | 0.98968968 | 16 | 0 | KQK01556 | 0.916 | – | HORVU.MC |
| 0.923801828 | 0.963352653 | 16 | 0 | KQJ83168 | 0.891 | –1 | HORVU.MC |

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| 0.912769292 | 0.968780428 | 16 | 1 | KQK13043 | 0.916 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.874121714 | 0.956255666 | 16 | 1 | KQK12892 | 0.791 | – | HORVU.MC |
| 0.94409652 | 0.989026855 | 16 | 0 | KQK05796 | 0.922 | – | HORVU.MC |
| 0.966704679 | 0.989010989 | 16 | 0 | KQJ83001 | 0.936 | –1 | HORVU.MC |
| 0.950784332 | 0.987272496 | 16 | 0 | KQJ91347 | 0.905 | –1 | HORVU.MC |
| 0.883463938 | 0.968350578 | 16 | 0 | KQK15144 | 0.830 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.875944857 | 0.967365837 | 16 | 4 | KQK21108 | 0.859 | – | genblast_C |
| 0.940754961 | 0.972981789 | 16 | 0 | KQJ83119 | 0.926 | –0 | HORVU.MC |
| 0.973741725 | 0.990861995 | 16 | 0 | KQK01598 | 0.962 | – | HORVU.MC |
| 0.971289436 | 0.999840663 | 16 | 0 | KQK11300 | 0.944 | – | HORVU.MC |
| 0.967462335 | 0.990282486 | 16 | 0 | KQK19758 | 0.981 | 0. | HORVU.MC |
| 0.947155649 | 0.981824661 | 16 | 0 | KQJ98356 | 0.954 | 0. | HORVU.MC |

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| 0.888055302 | 0.931994523 | 16 | 0 | genblast_Os06t064 | | | HORVU.MC |
| 0.945978156 | 0.980931692 | 16 | 0 | KQJ91480 | 0.954 | 0. | genblast_C |

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| 0.926873602 | 0.974418831 | 16 | 0 | KQK14578 | 0.871 | – | HORVU.MC |
| 0.904817748 | 0.964164872 | 16 | 0 | KQJ92876 | 0.889 | –0 | HORVU.MC |
| 0.859428571 | 0.917714286 | 16 | 0 | KQK23185 | 0.858 | – | HORVU.MC |
| 0.901061486 | 0.978369718 | 16 | 0 | KQJ91150 | 0.813 | –1 | HORVU.MC |
| 0.958825667 | 0.985846076 | 16 | 0 | genblast_Os10t037 | | | HORVU.MC |
| 0.916246598 | 0.95739599 | 16 | 3 | KQK06383 | 0.922 | 0. | HORVU.MC |

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| 0.920750064 | 0.967589034 | 16 | 1 | KQK12930 | 0.881 | – | HORVU.MC |
| 0.938416207 | 0.982888957 | 16 | 0 | KQK23039 | 0.915 | – | genblast_C |
| 0.932593103 | 0.974344828 | 16 | 1 | KQK11274 | 0.916 | – | HORVU.MC |
| 0.957968418 | 0.991507431 | 16 | 0 | KQK01427 | 0.992 | 1 | HORVU.MC |
| 0.929527229 | 0.972895686 | 16 | 0 | KQK12706 | 0.881 | – | HORVU.MC |
| 0.871191944 | 0.937339281 | 16 | 0 | PNT64944 | 0.855 | – | HORVU.MC |
| 0.910177894 | 0.963254593 | 16 | 0 | KQK15949 | 0.915 | 0 | HORVU.MC |
| 0.92097973 | 0.983063063 | 16 | 0 | KQK13679 | 0.956 | 0 | HORVU.MC |
| 0.936111772 | 0.970172934 | 16 | 0 | KQJ90514 | 0.857 | –2 | HORVU.MC |
| 0.973207701 | 0.997471555 | 16 | 0 | KQK22140 | 0.969 | – | genblast_C |
| 0.948101032 | 1.005408063 | 16 | 0 | KQK07199 | 0.942 | – | HORVU.MC |
| 0.966785882 | 1.002579737 | 16 | 1 | KQJ93086 | 0.947 | –0 | HORVU.MC |
| 0.967875583 | 1.016322452 | 16 | 0 | KQJ91157 | 0.944 | –0 | HORVU.MC |
| 0.965320522 | 0.985820453 | 16 | 0 | KQJ95295 | 0.932 | –1 | HORVU.MC |
| 0.895100309 | 0.991975309 | 16 | 2 | KQK11328 | 0.881 | – | HORVU.MC |
| 0.979002545 | 0.9952733 | 16 | 0 | KQK04968 | 0.972 | – | genblast_C |
| 0.944041087 | 0.981531049 | 16 | 0 | KQJ90111 | 0.893 | –1 | HORVU.MC |
| 0.92805777 | 0.986528284 | 16 | 1 | KQK05760 | 0.921 | – | HORVU.MC |
| 0.906893896 | 0.956961294 | 16 | 1 | KQK06568 | 0.889 | – | HORVU.MC |
| 0.892260731 | 0.945904512 | 16 | 0 | KQK21749 | 0.896 | 0 | HORVU.MC |
| 0.917792136 | 0.96631688 | 16 | 0 | KQK13444 | 0.841 | – | HORVU.MC |

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| 0.935874077 | 0.963376384 | 16 | 1 KQJ89202 0.913 –0HORVU.MC |
| 0.817935818 | 0.887633316 | 16 | 0 KQK10046 0.774 – HORVU.MC |
| 0.870357356 | 0.981937799 | 16 | 2 KQK11254 0.811 – HORVU.MC |
| 0.893106754 | 0.957323107 | 16 | 0 KQK10685 0.789 –HORVU.MC |
| 0.914762473 | 0.967255382 | 16 | 0 KQK03326 0.909 –genblast_C |
| 0.920964223 | 0.981500873 | 16 | 0 KQK08424 0.895 –HORVU.MC |
| 0.83593793 | 0.929197201 | 16 | 8 KQK23269 0.819 –HORVU.MC |
| 0.965040973 | 0.99444885 | 16 | 0 KQJ90521 0.953 –0HORVU.MC |
| 0.971789424 | 0.994216242 | 16 | 0 KQK09334 0.951 – HORVU.MC |
| 0.975095156 | 0.992724333 | 16 | 0 KQK10363 0.955 – HORVU.MC |
| 0.961899082 | 0.98236502 | 16 | 0 KQK08899 0.949 –HORVU.MC |
| 0.97178948 | 0.991470205 | 16 | 0 KQK07042 0.964 –HORVU.MC |
| 0.895462087 | 0.947154971 | 16 | 0 PNT76621 0.898 0.HORVU.MC |
| 0.936110463 | 0.966106965 | 16 | 1 KQK05350 0.907 – HORVU.MC |
| 0.952586726 | 0.983076589 | 16 | 1 KQK11843 0.946 –HORVU.MC |
| 0.859399275 | 0.912998446 | 16 | 0 KQK22763 0.865 0HORVU.MC |
| 0.914981061 | 0.978787879 | 16 | 0 KQJ86143 0.849 –1HORVU.MC |
| 0.914230035 | 0.963026867 | 16 | 0 KQJ84301 0.919 0. HORVU.MC |
| 0.830499918 | 0.959446093 | 16 | 0 PNT73727 0.815 –HORVU.MC |
| 0.871639493 | 0.955289855 | 16 | 1 PNT77994 0.796 –HORVU.MC |
| 0.933563784 | 0.977649399 | 16 | 0 KQK21532 0.903 –HORVU.MC |
| 0.93670276 | 0.971893918 | 16 | 0 KQK04846 0.933 –HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.98878991 | 0.998434891 | 16 | 0 | KQK08990 | 0.984 | -0 | HORVU.MC |
| 0.923709266 | 0.962570344 | 16 | 0 | KQK22192 | 0.914 | -0 | HORVU.MC |
| 0.93709256 | 0.964357839 | 16 | 1 | KQJ94698 | 0.908 | -1 | genblast_C |
| 0.954747666 | 0.990373396 | 16 | 0 | KQK11650 | 0.941 | -0 | HORVU.MC |
| 0.933440615 | 0.960963455 | 16 | 0 | KQJ82650 | 0.938 | 0. | HORVU.MC |
| 0.945411584 | 0.977781005 | 16 | 1 | PNT71391 | 0.937 | -0 | HORVU.MC |

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| 0.94001507 | 0.991528185 | 16 | 0 | KQJ99151 | 0.909 | -0 | HORVU.MC |
| 0.971882405 | 0.993938392 | 16 | 0 | KQK09943 | 0.966 | -0 | HORVU.MC |
| 0.887724223 | 0.962811725 | 16 | 0 | KQK23726 | 0.809 | - | HORVU.MC |
| 0.935963909 | 0.995425647 | 16 | 0 | KQK20696 | 0.941 | 0. | HORVU.MC |

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| 0.902055417 | 0.947990007 | 16 | 0 | KQK05181 | 0.831 | -2 | HORVU.MC |
| 0.927479859 | 0.960322256 | 16 | 0 | KQJ86990 | 0.905 | -0 | HORVU.MC |
| 0.968234699 | 0.984825493 | 16 | 0 | KQJ94854 | 0.956 | -0 | HORVU.MC |
| 0.879905486 | 0.978015204 | 16 | 0 | KQK12337 | 0.807 | - | genblast_C |
| 0.929379562 | 0.981021898 | 16 | 1 | KQK02315 | 0.912 | -0 | HORVU.MC |
| 0.928731919 | 0.957030419 | 16 | 0 | PNT77162 | 0.909 | -1 | HORVU.MC |
| 0.976239895 | 1.008302381 | 16 | 0 | KQK13519 | 0.970 | -0 | genblast_C |
| 0.94439402 | 0.965865812 | 16 | 0 | KQJ93197 | 0.936 | -0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.950488273 | 0.979822368 | 16 | 0 | KQK05709 | 0.922 | – | genblast_C |
| 0.939782932 | 0.995261969 | 16 | 1 | PNT73166 | 0.925 | –0 | HORVU.MC |
| 0.938280232 | 0.963308728 | 16 | 1 | KQK07359 | 0.932 | –0 | HORVU.MC |
| 0.969372252 | 0.990690458 | 16 | 0 | KQK12936 | 0.960 | –0 | HORVU.MC |
| 0.888755101 | 0.953592104 | 16 | 1 | KQJ91429 | 0.887 | –0 | HORVU.MC |
| 0.890399485 | 0.944501718 | 16 | 0 | KQJ90962 | 0.898 | 0. | HORVU.MC |
| 0.901480441 | 0.953197359 | 16 | 1 | KQJ89823 | 0.869 | –0 | HORVU.MC |
| 0.871938514 | 0.928936979 | 16 | 0 | KQK13974 | 0.927 | 1. | HORVU.MC |
| 0.960232904 | 0.988107037 | 16 | 0 | KQK08876 | 0.968 | 0. | genblast_C |
| 0.925797522 | 0.981802236 | 16 | 0 | KQK19700 | 0.911 | –0 | HORVU.MC |
| 0.92956648 | 0.989672978 | 16 | 1 | PNT73040 | 0.915 | –0 | HORVU.MC |
| 0.897922324 | 0.955574124 | 16 | 2 | KQJ95961 | 0.917 | 0. | HORVU.MC |
| 0.944785434 | 0.976205213 | 16 | 0 | KQK16048 | 0.933 | –0 | HORVU.MC |
| 0.958752447 | 0.996411483 | 16 | 0 | KQJ82913 | 0.947 | –0 | HORVU.MC |
| 0.961896186 | 0.987627119 | 16 | 0 | KQK23768 | 0.940 | – | HORVU.MC |
| 0.875664192 | 0.947731384 | 16 | 3 | KQK09509 | 0.890 | 0. | HORVU.MC |
| 0.922238598 | 0.973937325 | 16 | 0 | KQK18710 | 0.789 | – | HORVU.MC |
| 0.939759518 | 0.975365255 | 16 | 0 | KQK07668 | 0.910 | – | HORVU.MC |
| 0.876784674 | 0.931818182 | 16 | 0 | PNT77706 | 0.805 | –1 | HORVU.MC |
| 0.920087336 | 0.959097525 | 16 | 0 | KQK20866 | 0.911 | –0 | HORVU.MC |

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| 0.940561224 | 0.982089552 | 16 | 1 KQK22635 0.927 – | HORVU.MC |
| 0.900966942 | 0.950143472 | 16 | 0 KQK00839 0.820 – | HORVU.MC |
| 0.892227801 | 0.955207718 | 16 | 0 KQJ93783 0.899 0. | HORVU.MC |
| 0.966171051 | 0.992773522 | 16 | 0 KQK21932 0.975 0 | HORVU.MC |
| 0.935000907 | 0.963278629 | 16 | 0 KQK18844 0.935 – | HORVU.MC |
| 0.977539575 | 0.991079237 | 16 | 0 KQK18875 0.981 0 | HORVU.MC |
| 0.953465058 | 0.987634257 | 16 | 0 KQK00297 0.973 0 | HORVU.MC |
| 0.914980197 | 0.973145286 | 16 | 0 KQJ96037 0.857 –1 | HORVU.MC |
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| 0.969143314 | 0.985154905 | 16 | 0 KQK15023 0.948 – | HORVU.MC |
| 0.966521764 | 0.991616766 | 16 | 0 KQJ83812 0.962 –0 | HORVU.MC |
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| 0.950372048 | 0.992818385 | 16 | 0 KQK22458 0.916 – | HORVU.MC |
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| 0.895426339 | 0.959204781 | 16 | 0 KQK00899 0.863 – | HORVU.MC |
| 0.840469943 | 0.909669211 | 16 | 0 KQJ84200 0.783 –1 | HORVU.MC |
| 0.866408321 | 0.939424842 | 16 | 0 KQJ81412 0.872 0. | HORVU.MC |
| 0.91190941 | 0.935650137 | 16 | 1 KQJ98919 0.917 0. | HORVU.MC |
| 0.919518381 | 0.977270636 | 16 | 4 KQK17145 0.933 0 | HORVU.MC |
| 0.868025927 | 0.93190023 | 16 | 3 KQK17775 0.824 – | HORVU.MC |
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| 0.959172094 | 0.974935859 | 16 | 0 KQJ83690 0.969 0. | HORVU.MC |
| 0.946084219 | 0.970877607 | 16 | 0 KQK06621 0.942 – | HORVU.MC |
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| 0.876828889 | 0.938312055 | 16 | 0 KQJ99120 0.888 0. | HORVU.MC |
| 0.955780561 | 0.975378425 | 16 | 0 KQK12559 0.939 – | HORVU.MC |
| 0.959624576 | 0.976036298 | 16 | 0 KQK22622 0.973 0 | HORVU.MC |
| 0.961495108 | 0.984772437 | 16 | 0 KQK02799 0.964 0 | HORVU.MC |
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| 0.887403923 | 0.941493633 | 16 | 0 KQK13611 0.784 – | HORVU.MC |
| 0.954748403 | 0.981358363 | 16 | 1 KQJ88641 0.965 0. | HORVU.MC |
| 0.942299674 | 0.983928436 | 16 | 0 KQJ97983 0.953 0. | HORVU.MC |
| 0.93527072 | 0.984129529 | 16 | 1 KQK07836 0.929 – | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.91786979 | 0.962135658 | 16 | 0 | KQK02058 | 0.858 | – | HORVU.MC |
| 0.922247522 | 0.976694348 | 16 | 0 | KQK15443 | 0.923 | 0. | HORVU.MC |
| 0.883933151 | 0.962728672 | 16 | 2 | KQJ96068 | 0.807 | –1 | HORVU.MC |
| 0.972854921 | 0.998902305 | 16 | 0 | KQK22560 | 0.995 | 1. | HORVU.MC |
| 0.955636433 | 0.989107667 | 16 | 1 | KQK08397 | 0.891 | – | HORVU.MC |
| 0.822241664 | 0.907989934 | 16 | 0 | KQJ89877 | 0.777 | –0 | HORVU.MC |
| 0.955736902 | 0.990614233 | 16 | 0 | KQJ90894 | 0.954 | –0 | HORVU.MC |
| 0.936770927 | 0.981540828 | 16 | 0 | KQJ99106 | 0.982 | 1. | HORVU.MC |
| 0.946254038 | 0.973629984 | 16 | 0 | KQJ98350 | 0.927 | –1 | HORVU.MC |
| 0.900276394 | 0.96966677 | 16 | 0 | KQK10906 | 0.878 | – | HORVU.MC |
| 0.873896196 | 0.930344572 | 16 | 0 | KQK17144 | 0.750 | – | HORVU.MC |
| 0.911382592 | 0.960008554 | 16 | 0 | KQK14300 | 0.892 | – | HORVU.MC |
| 0.960901219 | 0.989099587 | 16 | 0 | KQK03631 | 0.972 | 0. | HORVU.MC |
| 0.883261777 | 0.983771861 | 16 | 0 | KQJ85708 | 0.806 | –1 | HORVU.MC |
| 0.953216725 | 0.981214644 | 16 | 0 | KQJ86522 | 0.846 | –3 | HORVU.MC |
| 0.957198209 | 0.988924403 | 16 | 0 | KQJ90425 | 0.931 | –1 | HORVU.MC |
| 0.84852415 | 0.896839595 | 16 | 0 | KQJ90745 | 0.768 | –1 | HORVU.MC |
| 0.890431394 | 0.938176601 | 16 | 1 | KQK13183 | 0.902 | 0. | HORVU.MC |
| 0.966018916 | 0.990638251 | 16 | 0 | KQJ86920 | 0.961 | –0 | HORVU.MC |
| 0.906228398 | 0.966403982 | 16 | 0 | PNT72490 | 0.865 | – | HORVU.MC |
| 0.94005994 | 1.004551005 | 16 | 0 | KQK19118 | 0.925 | – | HORVU.MC |
| 0.906808236 | 0.960829328 | 16 | 4 | KQK07807 | 0.914 | 0. | HORVU.MC |
| 0.93684432 | 0.965794867 | 16 | 0 | KQK01246 | 0.938 | 0. | HORVU.MC |
| 0.92035791 | 0.975771319 | 16 | 2 | PNT65725 | 0.870 | – | genblast_C |
| 0.936960072 | 0.971871049 | 16 | 0 | KQK00451 | 0.961 | 0. | HORVU.MC |
| 0.911770396 | 0.96175105 | 16 | 0 | KQK21224 | 0.962 | 1. | HORVU.MC |
| 0.967722155 | 0.993888219 | 16 | 0 | KQK00913 | 0.980 | 0. | HORVU.MC |

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| 0.951816136 | 0.989287308 | 16 | 0 | KQK15471 0.856 – | HORVU.MC |
| 0.929996882 | 0.977798566 | 16 | 0 | KQK16960 0.899 – | HORVU.MC |
| 0.955934388 | 0.980725462 | 16 | 0 | KQJ90409 0.956 –0 | HORVU.MC |
| 0.898584751 | 0.944243778 | 16 | 4 | KQK08470 0.943 0 | HORVU.MC |
| 0.897034402 | 0.948991407 | 16 | 3 | KQJ81761 0.887 –0 | HORVU.MC |
| 0.879467167 | 0.915617941 | 16 | 0 | KQK08617 0.854 – | HORVU.MC |
| 0.912288085 | 0.97366839 | 16 | 2 | KQJ82894 0.949 0. | HORVU.MC |
| | | | | | |
| 0.943824405 | 0.968915344 | 16 | 0 | KQK19105 0.917 – | HORVU.MC |
| 0.956469096 | 0.994926199 | 16 | 1 | KQJ89951 0.924 –1 | HORVU.MC |
| 0.96291806 | 0.988762542 | 16 | 0 | KQK00258 0.957 – | HORVU.MC |
| 0.931534372 | 0.969266638 | 16 | 1 | KQJ94090 0.940 0. | HORVU.MC |
| 0.896496098 | 0.949579832 | 16 | 0 | KQJ98276 0.930 0. | HORVU.MC |
| | | | | | |
| 0.874715023 | 0.956083513 | 16 | 0 | KQK11736 0.862 – | HORVU.MC |
| 0.93689117 | 0.980740873 | 16 | 1 | KQJ82278 0.920 –0 | HORVU.MC |
| 0.93060686 | 0.978891821 | 16 | 0 | KQK08747 0.933 0 | HORVU.MC |
| 0.88400227 | 0.985279956 | 16 | 1 | KQJ83008 0.896 0. | HORVU.MC |
| 0.940844701 | 0.975515915 | 16 | 0 | KQJ90493 0.937 –0 | HORVU.MC |
| 0.921939491 | 0.958065049 | 16 | 0 | KQK07106 0.940 0 | HORVU.MC |
| 0.932389476 | 0.952660407 | 16 | 0 | KQJ89994 0.938 0. | HORVU.MC |
| 0.956827067 | 0.978041988 | 16 | 0 | KQJ95920 0.962 0. | HORVU.MC |
| 0.938558226 | 0.974248693 | 16 | 1 | KQK12215 0.948 0 | HORVU.MC |
| 0.897939801 | 0.963657616 | 16 | 3 | KQK02006 0.875 – | HORVU.MC |
| 0.932089552 | 0.97217484 | 16 | 1 | KQK09422 0.906 – | HORVU.MC |
| 0.991499205 | 1 | 16 | 0 | KQK01039 0.976 – | HORVU.MC |
| 0.888222622 | 0.947141663 | 16 | 12 | KQK15307 0.886 – | HORVU.MC |
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| 0.964017161 | 0.996942278 | 16 | 0 | KQJ94171 0.949 –0 | HORVU.MC |
| 0.914975214 | 0.981779207 | 16 | 0 | KQK13000 0.855 – | HORVU.MC |
| 0.909448959 | 0.95901055 | 16 | 0 | PNT71974 0.806 – | HORVU.MC |

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| 0.948893611 | 0.98461313 | 16 | 0 | KQK17141 | 0.922 | – | HORVU.MC |
| 0.915235019 | 0.967564596 | 16 | 0 | KQK08330 | 0.858 | – | HORVU.MC |
| 0.928170678 | 0.962645799 | 16 | 0 | KQK17783 | 0.930 | 0. | HORVU.MC |

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| 0.881037879 | 0.944242424 | 16 | 0 | PNT68392 | 0.812 | –1 | HORVU.MC |
| 0.913470205 | 0.973560341 | 16 | 0 | genblast_Os03t068 | | | HORVU.MC |
| 0.938101626 | 0.962186809 | 16 | 1 | KQJ82404 | 0.921 | –0 | HORVU.MC |

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| 0.934153176 | 0.969115816 | 16 | 0 | KQK09964 | 0.876 | – | HORVU.MC |
| 0.922628536 | 0.975785118 | 16 | 1 | KQK09724 | 0.906 | – | HORVU.MC |
| 0.856889631 | 0.932022809 | 16 | 3 | KQK23035 | 0.782 | – | HORVU.MC |
| 0.945515775 | 0.972546609 | 16 | 0 | KQJ86562 | 0.926 | –1 | HORVU.MC |
| 0.93823337 | 0.971123228 | 16 | 1 | KQK00082 | 0.931 | – | HORVU.MC |
| 0.849682588 | 0.922007255 | 16 | 0 | KQJ92276 | 0.843 | –0 | HORVU.MC |
| 0.949616587 | 0.988088148 | 16 | 0 | KQJ84314 | 0.946 | –0 | HORVU.MC |
| 0.947820544 | 0.974814404 | 16 | 1 | KQK22630 | 0.946 | – | HORVU.MC |
| 0.964129762 | 0.993260899 | 16 | 0 | KQJ98616 | 0.970 | 0. | HORVU.MC |
| 0.959905 | 0.992 | 16 | 0 | KQK13262 | 0.946 | – | HORVU.MC |
| 0.890851277 | 0.945121951 | 16 | 3 | KQK21222 | 0.879 | – | HORVU.MC |
| 0.890403683 | 0.940332861 | 16 | 0 | PNT63475 | 0.936 | 0. | HORVU.MC |
| 0.953748381 | 0.981766006 | 16 | 3 | KQK02885 | 0.962 | 0 | HORVU.MC |
| 0.871225827 | 0.904678727 | 16 | 1 | KQJ90761 | 0.849 | –0 | HORVU.MC |
| 0.915784932 | 0.97463605 | 16 | 0 | KQK21876 | 0.831 | – | HORVU.MC |
| 0.956740623 | 0.979606477 | 16 | 0 | PNT64036 | 0.928 | – | HORVU.MC |
| 0.920502036 | 0.998499786 | 16 | 0 | KQJ82036 | 0.813 | –1 | HORVU.MC |
| 0.965020394 | 0.993615889 | 16 | 0 | KQK00524 | 0.929 | – | HORVU.MC |
| 0.880617198 | 0.99001387 | 16 | 2 | KQK10414 | 0.884 | 0 | HORVU.MC |
| 0.963839239 | 0.995072859 | 16 | 1 | KQK08722 | 0.985 | 0 | HORVU.MC |
| 0.887803404 | 0.954678215 | 16 | 1 | KQJ88100 | 0.894 | 0. | HORVU.MC |
| 0.949355313 | 0.981568017 | 16 | 0 | KQK22378 | 0.952 | 0 | HORVU.MC |
| 0.940403527 | 0.995252628 | 16 | 0 | KQK02783 | 0.939 | – | HORVU.MC |
| 0.929054831 | 0.952607362 | 16 | 0 | KQK03251 | 0.859 | – | HORVU.MC |

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|---|---|---|---|
| 0.970513268 | 0.99301676 | 16 | 0 KQK15227 0.972 0 HORVU.MC |
| 0.922666459 | 0.972433855 | 16 | 0 KQK05862 0.882 – HORVU.MC |
| 0.921250255 | 0.956140351 | 16 | 0 KQK04960 0.884 – HORVU.MC |
| 0.941550641 | 0.968210941 | 16 | 0 KQK13890 0.906 – HORVU.MC |
| 0.960245464 | 0.990699802 | 16 | 0 PNT66571 0.947 – HORVU.MC |

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|---|---|---|---|
| 0.937895179 | 0.965718238 | 16 | 0 KQK09608 0.963 1 HORVU.MC |
| 0.955033052 | 0.978988373 | 16 | 0 KQJ97373 0.963 0. HORVU.MC |
| 0.961674075 | 0.982989999 | 16 | 0 KQK02747 0.963 0 HORVU.MC |
| 0.981398159 | 0.992001 | 16 | 0 KQK15115 0.976 – HORVU.MC |
| 0.947633051 | 0.982245132 | 16 | 2 KQJ84068 0.957 0. HORVU.MC |
| 0.924824277 | 0.969515085 | 16 | 0 KQJ86688 0.933 0. HORVU.MC |
| 0.890732978 | 0.951480323 | 16 | 2 KQK19313 0.758 – HORVU.MC |
| 0.929870463 | 1.004683841 | 16 | 2 KQK08286 0.947 0 HORVU.MC |
| 0.927807677 | 0.975142161 | 16 | 2 KQJ83169 0.922 –0 HORVU.MC |
| 0.959516903 | 0.98779756 | 16 | 1 KQK18312 0.939 – HORVU.MC |
| 0.900028111 | 0.971176912 | 16 | 7 KQK16641 0.936 0 genblast_C |
| 0.941980235 | 0.971764435 | 16 | 0 KQK08880 0.937 – HORVU.MC |
| 0.947219456 | 0.985219351 | 16 | 0 KQJ98157 0.964 0. HORVU.MC |
| 0.950443129 | 0.988499387 | 16 | 2 KQK02075 0.952 0 HORVU.MC |
| 0.950314623 | 0.987597799 | 16 | 3 KQK02705 0.960 0 HORVU.MC |
| 0.938018525 | 0.984827821 | 16 | 2 KQK01564 0.929 – HORVU.MC |
| 0.964770798 | 0.98576466 | 16 | 0 KQJ93096 0.962 –0 HORVU.MC |
| 0.915424687 | 0.952065035 | 16 | 0 KQJ86679 0.904 –0 HORVU.MC |
| 0.955749459 | 0.990692641 | 16 | 0 KQK16042 0.965 0 HORVU.MC |

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|---|---|---|---|
| 0.824572435 | 0.878604963 | 16 | 0 KQJ90394 0.820 –0 HORVU.MC |
| 0.957992221 | 0.994988929 | 16 | 0 genblast_Zm00001 HORVU.MC |
| 0.888429752 | 0.976387249 | 16 | 1 KQJ84328 0.787 –1 HORVU.MC |

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| 0.929506699 | 0.962850183 | 16 | 0 KQK24134 0.924 – HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.95097349 | 0.977762672 | 16 | 0 | KQK08252 | 0.907 | – | HORVU.MC |
| 0.948690044 | 0.98483068 | 16 | 1 | KQK19253 | 0.935 | – | HORVU.MC |
| 0.942550011 | 0.966025928 | 16 | 0 | KQK04211 | 0.938 | – | HORVU.MC |
| 0.937007709 | 0.975364505 | 16 | 0 | KQK03833 | 0.902 | – | HORVU.MC |
| 0.90970923 | 0.963829124 | 16 | 1 | KQJ83559 | 0.864 | –1 | HORVU.MC |
| 0.910271299 | 0.968373196 | 16 | 1 | KQK07963 | 0.902 | – | HORVU.MC |
| 0.930006448 | 0.958511422 | 16 | 4 | KQK09193 | 0.917 | – | HORVU.MC |
| 0.952295724 | 0.97006491 | 16 | 0 | KQJ89044 | 0.953 | 0. | HORVU.MC |
| 0.938315452 | 0.985024412 | 16 | 2 | KQK14307 | 0.913 | – | HORVU.MC |
| 0.964487674 | 0.980684514 | 16 | 1 | KQJ91709 | 0.981 | 1. | HORVU.MC |
| 0.937945602 | 0.982037037 | 16 | 0 | KQJ89597 | 0.871 | –2 | HORVU.MC |
| 0.932011323 | 0.969521992 | 16 | 2 | KQK10984 | 0.926 | – | HORVU.MC |
| 0.96438694 | 0.999375112 | 16 | 1 | KQJ99656 | 0.981 | 0. | HORVU.MC |
| 0.827423727 | 0.888048411 | 16 | 0 | KQJ99570 | 0.813 | –0 | HORVU.MC |
| 0.932196624 | 0.974756691 | 16 | 1 | KQK13708 | 0.903 | – | HORVU.MC |
| 0.959844685 | 0.988230754 | 16 | 0 | KQK07842 | 0.940 | – | HORVU.MC |
| 0.848225363 | 0.920506912 | 16 | 6 | KQJ99244 | 0.909 | 1. | HORVU.MC |
| 0.945165516 | 0.989521315 | 16 | 0 | KQK15919 | 0.923 | – | HORVU.MC |
| 0.928957058 | 0.969055105 | 16 | 0 | KQJ89377 | 0.935 | 0. | HORVU.MC |
| 0.926337905 | 0.980408332 | 16 | 0 | KQK22243 | 0.926 | – | HORVU.MC |
| 0.921390433 | 0.972205968 | 16 | 0 | KQJ84145 | 0.921 | –0 | HORVU.MC |
| 0.959356065 | 0.989118338 | 16 | 0 | KQK21868 | 0.978 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.924161357 | 0.96844078 | 16 | 0 | KQK19660 | 0.840 | – | HORVU.MC |
| 0.965026189 | 0.994471119 | 16 | 0 | KQK06514 | 0.944 | – | HORVU.MC |
| 0.952112551 | 0.991478786 | 16 | 0 | KQK03170 | 0.948 | – | HORVU.MC |
| 0.915370734 | 0.966535826 | 16 | 1 | KQK23951 | 0.875 | – | HORVU.MC |
| 0.90274867 | 0.944542963 | 16 | 5 | KQK05673 | 0.867 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.922918692 | 0.949173726 | 16 | 0 | KQK23795 | 0.913 | - | HORVU.MC |
| 0.923884207 | 0.987515605 | 16 | 1 | KQK07395 | 0.877 | - | HORVU.MC |
| 0.915888969 | 0.957765016 | 16 | 1 | KQK00615 | 0.904 | - | HORVU.MC |
| 0.975615085 | 0.993546652 | 16 | 5 | KQJ91882 | 0.963 | -0 | HORVU.MC |
| 0.959469387 | 1.001562268 | 16 | 1 | KQK22031 | 0.915 | - | HORVU.MC |
| 0.930827794 | 0.951705934 | 16 | 1 | KQJ90322 | 0.929 | -0 | HORVU.MC |
| 0.94507166 | 0.988642509 | 16 | 0 | KQJ93717 | 0.926 | -0 | HORVU.MC |
| 0.901858916 | 0.945001139 | 16 | 0 | KQK15688 | 0.846 | - | HORVU.MC |
| 0.947191959 | 0.975666409 | 16 | 1 | KQK05932 | 0.976 | 0. | HORVU.MC |
| 0.943230541 | 0.977132806 | 16 | 0 | KQK22885 | 0.925 | - | HORVU.MC |
| 0.941141773 | 0.982765696 | 16 | 0 | KQJ84359 | 0.933 | -0 | HORVU.MC |
| 0.914411036 | 0.955648317 | 16 | 1 | KQK12019 | 0.933 | 0. | HORVU.MC |
| 0.932968137 | 0.968236637 | 16 | 0 | KQJ89970 | 0.936 | 0. | genblast_C |
| 0.915430473 | 0.973843523 | 16 | 4 | KQK23695 | 0.932 | 0. | HORVU.MC |
| 0.934144213 | 0.986038622 | 16 | 1 | KQK12937 | 0.942 | 0. | HORVU.MC |
| 0.862313111 | 0.915085298 | 16 | 0 | KQK19635 | 0.810 | - | HORVU.MC |

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| 0.9526603 | 0.977950774 | 16 | 1 | KQJ93058 | 0.944 | −0 | HORVU.MC |
| 0.919046135 | 0.958354115 | 16 | 0 | KQK02671 | 0.941 | 0. | HORVU.MC |
| 0.939533035 | 0.979326298 | 16 | 4 | KQK04607 | 0.952 | 0 | HORVU.MC |
| 0.920070563 | 0.961874308 | 16 | 1 | KQK12980 | 0.919 | − | HORVU.MC |
| 0.939228947 | 0.972184013 | 16 | 0 | PNT67576 | 0.925 | −( | genblast_C |
| 0.915294179 | 0.963952766 | 16 | 0 | KQJ89321 | 0.942 | 0. | HORVU.MC |
| 0.968493132 | 0.989292667 | 16 | 0 | KQK09932 | 0.957 | − | HORVU.MC |
| 0.953234044 | 0.991752316 | 16 | 0 | KQJ83357 | 0.903 | −1 | genblast_C |
| 0.926806816 | 0.977710573 | 16 | 0 | KQJ86967 | 0.894 | −0 | HORVU.MC |
| 0.905596026 | 0.956291391 | 16 | 0 | KQK03451 | 0.860 | − | HORVU.MC |
| 0.970463539 | 0.993569813 | 16 | 0 | KQJ93906 | 0.964 | −0 | HORVU.MC |
| 0.965700653 | 1.000148522 | 16 | 0 | PNT76442 | 0.956 | −( | HORVU.MC |
| 0.930329007 | 0.975076398 | 16 | 1 | KQK22714 | 0.911 | − | HORVU.MC |
| 0.919400913 | 0.958115183 | 16 | 1 | KQK22652 | 0.922 | 0 | HORVU.MC |
| 0.891667925 | 0.979915433 | 16 | 0 | PNT66629 | 0.897 | 0. | HORVU.MC |
| 0.930850053 | 0.95880833 | 16 | 1 | KQJ90508 | 0.915 | −0 | HORVU.MC |
| 0.944151779 | 0.973507406 | 16 | 0 | KQJ88770 | 0.942 | −0 | HORVU.MC |
| 0.910804568 | 0.968967922 | 16 | 1 | KQK02313 | 0.835 | − | HORVU.MC |
| 0.89285291 | 0.961597724 | 16 | 2 | KQK00346 | 0.848 | − | HORVU.MC |
| 0.940118963 | 0.962035124 | 16 | 1 | PNT70992 | 0.949 | 0. | HORVU.MC |
| 0.83350061 | 0.920317416 | 16 | 11 | PNT78276 | 0.796 | −( | genblast_C |
| 0.940775681 | 0.965758211 | 16 | 1 | KQJ81838 | 0.913 | −1 | HORVU.MC |
| 0.940651425 | 0.966280405 | 16 | 1 | KQJ97941 | 0.928 | −0 | HORVU.MC |
| 0.941647385 | 0.975203004 | 16 | 0 | KQK22365 | 0.928 | − | HORVU.MC |
| 0.894632871 | 0.969608558 | 16 | 0 | KQK14273 | 0.908 | 0 | HORVU.MC |
| 0.97752052 | 1 | 16 | 1 | KQJ94943 | 0.973 | −0 | genblast_C |
| 0.949791323 | 0.981287837 | 16 | 0 | KQK15649 | 0.947 | − | HORVU.MC |
| 0.891128838 | 0.921936664 | 16 | 0 | KQK11618 | 0.809 | − | HORVU.MC |

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|---|---|---|---|
| 0.951405109 | 0.992467153 | 16 | 1 KQK07753 0.937 – HORVU.MC |
| 0.850211759 | 0.921773792 | 16 | 1 KQK10145 0.868 0 HORVU.MC |
| 0.957761774 | 0.989788142 | 16 | 1 KQK13986 0.935 – HORVU.MC |
| 0.934495919 | 0.998035067 | 16 | 3 PNT78038 0.941 0.HORVU.MC |
| 0.949335048 | 0.982267951 | 16 | 0 KQJ94802 0.941 –0HORVU.MC |
| 0.944082351 | 0.983240223 | 16 | 0 PNT64409 0.926 – HORVU.MC |
| 0.890705593 | 0.940522244 | 16 | 0 KQK11772 0.913 0 HORVU.MC |
| 0.955947703 | 0.993264103 | 16 | 0 KQK17325 0.972 0 HORVU.MC |
| 0.906434013 | 0.942798392 | 16 | 1 KQK05985 0.838 – HORVU.MC |
| 0.972663629 | 1.001605591 | 16 | 0 KQK16245 0.975 0 HORVU.MC |
| 0.932605237 | 0.96732746 | 16 | 0 KQJ97793 0.837 –3HORVU.MC |
| 0.865895626 | 0.908346402 | 16 | 1 KQK17523 0.852 – HORVU.MC |

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|---|---|---|---|
| 0.944654404 | 0.988116043 | 16 | 0 KQJ97718 0.924 –0HORVU.MC |
| 0.963611721 | 1.000754872 | 16 | 0 KQK02291 0.959 – genblast_C |

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| 0.96023417 | 0.988468541 | 16 | 0 KQK06380 0.947 – HORVU.MC |
| 0.913941522 | 0.967162089 | 16 | 1 KQJ88273 0.909 –0HORVU.MC |
| 0.963451226 | 1.038304392 | 16 | 0 KQK14911 0.895 – HORVU.MC |
| 0.86939422 | 0.930808656 | 16 | 0 KQJ82267 0.899 0.HORVU.MC |
| 0.875022426 | 0.963760316 | 16 | 3 KQK04942 0.884 0 HORVU.MC |
| 0.881888634 | 0.934557979 | 16 | 0 KQK16409 0.890 0 HORVU.MC |
| 0.973158534 | 0.995027752 | 16 | 1 KQK09322 0.954 – HORVU.MC |
| 0.93276047 | 0.968663661 | 16 | 1 KQK09438 0.922 – HORVU.MC |
| 0.914021047 | 0.950654404 | 16 | 0 KQJ92999 0.911 –0HORVU.MC |
| 0.936540864 | 0.979942898 | 16 | 0 genblast_Os03t086HORVU.MC |

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|---|---|---|---|
| 0.872916271 | 0.932370821 | 16 | 1 KQJ84349 0.820 –0HORVU.MC |
| 0.92465238 | 0.968272171 | 16 | 0 KQK21766 0.908 – HORVU.MC |
| 0.946033851 | 0.973285335 | 16 | 0 KQK00208 0.920 – HORVU.MC |
| 0.90363957 | 0.939955107 | 16 | 1 KQJ89527 0.901 –0HORVU.MC |

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|---|---|---|---|
| 0.970400528 | 0.990291751 | 16 | 1 KQK12393 0.969 – HORVU.MC |
| 0.951860876 | 0.985988701 | 16 | 0 KQJ85310 0.948 –0HORVU.MC |
| 0.93933796 | 0.964905717 | 16 | 0 KQK16706 0.927 – HORVU.MC |
| 0.868784041 | 0.953517869 | 16 | 0 KQK02525 0.785 – HORVU.MC |
| 0.965474783 | 1.001970055 | 16 | 1 KQK23617 0.958 – HORVU.MC |
| 0.953979867 | 0.981154006 | 16 | 1 KQK00580 0.944 – genblast_C |
| 0.948215424 | 1.000637349 | 16 | 0 KQK17296 0.834 – HORVU.MC |
| 0.9310116 | 0.98073142 | 16 | 0 PNT69744 0.957 0.HORVU.MC |
| 0.919397896 | 1.004988309 | 16 | 0 KQK00437 0.918 – HORVU.MC |

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| 0.835656118 | 0.915519068 | 16 | 0 KQK23310 0.800 – HORVU.MC |
| 0.954622573 | 0.976299854 | 16 | 1 KQJ90482 0.950 –0HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.887877349 | 0.936035465 | 16 | 0 | KQJ84981 | 0.818 | –1 | HORVU.MC |
| 0.940462095 | 0.968941968 | 16 | 1 | PNT78338 | 0.936 | – | HORVU.MC |
| | | | | | | | |
| 0.921198593 | 0.999458874 | 16 | 0 | KQK15448 | 0.920 | – | HORVU.MC |
| | | | | | | | |
| 0.943665264 | 0.98340346 | 16 | 1 | KQK17127 | 0.887 | – | HORVU.MC |
| 0.974787569 | 0.993398558 | 16 | 1 | KQK14609 | 0.976 | 0 | genblast_C |
| 0.947460324 | 0.989419739 | 16 | 1 | KQJ93158 | 0.934 | –0 | HORVU.MC |
| 0.93424821 | 0.979611319 | 16 | 1 | PNT65906 | 0.948 | 0. | HORVU.MC |
| 0.925469908 | 0.974516537 | 16 | 3 | KQJ87692 | 0.940 | 0. | HORVU.MC |
| | | | | | | | |
| 0.933013576 | 0.982767171 | 16 | 0 | KQK17832 | 0.946 | 0 | HORVU.MC |
| 0.958613291 | 0.97204512 | 16 | 0 | KQK22362 | 0.946 | – | HORVU.MC |
| 0.891004151 | 0.961047254 | 16 | 4 | KQK21383 | 0.877 | – | HORVU.MC |
| | | | | | | | |
| 0.881722585 | 0.9675589 | 16 | 0 | KQK12042 | 0.794 | – | HORVU.MC |
| | | | | | | | |
| 0.947309837 | 0.981857523 | 16 | 0 | KQK02112 | 0.937 | – | HORVU.MC |
| 0.967443895 | 0.995058678 | 16 | 0 | KQK03147 | 0.957 | – | HORVU.MC |
| 0.941711092 | 0.968730401 | 16 | 0 | PNT78187 | 0.934 | – | HORVU.MC |
| 0.885160789 | 0.96520586 | 16 | 4 | KQK23622 | 0.869 | – | HORVU.MC |
| 0.908998959 | 0.959461625 | 16 | 0 | KQJ86441 | 0.946 | 0. | HORVU.MC |
| 0.913947083 | 0.96653034 | 16 | 0 | PNT76226 | 0.896 | – | HORVU.MC |
| 0.951097992 | 0.986989547 | 16 | 0 | KQK13502 | 0.902 | – | HORVU.MC |
| 0.934831202 | 0.977587997 | 16 | 3 | KQK00909 | 0.907 | – | HORVU.MC |
| 0.917400235 | 0.97156013 | 16 | 0 | KQK10638 | 0.875 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.942305943 | 0.976228017 | 16 | 1 | KQK23805 | 0.885 | – | HORVU.MC |
| 0.932711528 | 0.97524644 | 16 | 3 | KQK02981 | 0.909 | – | HORVU.MC |
| 0.944102777 | 0.970117718 | 16 | 0 | KQK14078 | 0.942 | – | HORVU.MC |
| 0.879351052 | 0.948192121 | 16 | 3 | PNT64993 | 0.877 | – | genblast_C |
| 0.942896801 | 0.99611741 | 16 | 0 | KQK04720 | 0.944 | 0. | HORVU.MC |
| 0.95261871 | 0.985366582 | 16 | 1 | KQK08796 | 0.943 | – | HORVU.MC |
| 0.929251234 | 0.956555129 | 16 | 0 | KQK12027 | 0.917 | – | HORVU.MC |
| 0.890971299 | 0.966533688 | 16 | 0 | KQJ93587 | 0.751 | –2 | HORVU.MC |
| 0.945339912 | 0.988421053 | 16 | 1 | KQK13711 | 0.934 | – | HORVU.MC |
| 0.923014163 | 0.971574332 | 16 | 3 | KQK12629 | 0.935 | 0. | HORVU.MC |
| 0.949980281 | 0.974842245 | 16 | 0 | KQJ84968 | 0.959 | 0. | HORVU.MC |
| 0.947632243 | 0.976718309 | 16 | 1 | KQJ83451 | 0.961 | 0. | HORVU.MC |
| 0.975570276 | 0.986912442 | 16 | 0 | KQJ96885 | 0.968 | –1 | HORVU.MC |
| 0.959750895 | 0.979495822 | 16 | 0 | PNT77661 | 0.964 | 0. | HORVU.MC |

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| 0.977653749 | 0.998146588 | 16 | 0 | KQJ90103 | 0.977 | –0 | HORVU.MC |

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| 0.961105437 | 0.98570178 | 16 | 0 | KQJ89926 | 0.964 | 0. | HORVU.MC |
| 0.927284117 | 0.970591475 | 16 | 2 | KQK03141 | 0.912 | – | HORVU.MC |
| 0.899744603 | 0.942174248 | 16 | 0 | KQK01931 | 0.924 | 0. | HORVU.MC |
| 0.976538419 | 0.989725525 | 16 | 0 | KQK02853 | 0.967 | – | HORVU.MC |
| 0.886997516 | 0.948509485 | 16 | 0 | KQK07243 | 0.881 | – | HORVU.MC |

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| 0.918483336 | 0.970119236 | 16 | 0 | KQK19641 | 0.862 | – | HORVU.MC |
| 0.902204926 | 0.963738804 | 16 | 0 | KQJ91929 | 0.886 | –0 | HORVU.MC |
| 0.971205088 | 0.983912053 | 16 | 1 | KQK22179 | 0.977 | 0 | HORVU.MC |

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| 0.974622353 | 0.990608665 | 16 | 1 | KQK21990 | 0.981 | 0 | HORVU.MC |
| 0.963613392 | 0.989762511 | 16 | 0 | KQJ93138 | 0.956 | –0 | HORVU.MC |
| 0.928596491 | 0.993684211 | 16 | 0 | KQK00329 | 0.994 | 1 | HORVU.MC |

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| 0.969429648 | 0.984105374 | 16 | 0 | KQK22783 | 0.952 | – | HORVU.MC |
| 0.948815417 | 0.974540311 | 16 | 1 | KQK03695 | 0.949 | 0 | HORVU.MC |
| 0.946928246 | 0.975616921 | 16 | 0 | KQJ83383 | 0.934 | –0 | genblast_C |
| 0.909269735 | 0.976182375 | 16 | 2 | KQK13347 | 0.883 | – | HORVU.MC |
| 0.974594922 | 1.014034192 | 16 | 0 | KQK09395 | 0.992 | 0 | HORVU.MC |
| 0.96426206 | 0.985870405 | 16 | 0 | KQK05109 | 0.954 | – | HORVU.MC |

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| 0.884613854 | 0.944426752 | 16 | 0 | KQK00955 | 0.805 | – | HORVU.MC |

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| 0.891752782 | 0.96772655 | 16 | 1 | KQJ99166 | 0.846 | –0 | HORVU.MC |

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| 0.922585955 | 0.973109376 | 16 | 1 | KQK13399 | 0.928 | 0 | HORVU.MC |
| 0.963007354 | 0.985943027 | 16 | 0 | KQK00990 | 0.965 | 0 | HORVU.MC |
| 0.94017162 | 0.994085941 | 16 | 1 | KQK01998 | 0.944 | 0 | HORVU.MC |
| 0.966830205 | 0.995482835 | 16 | 3 | PNT62024 | 0.971 | 0. | HORVU.MC |
| 0.878699435 | 0.970999405 | 16 | 0 | KQJ88276 | 0.860 | –0 | HORVU.MC |
| 0.916527632 | 0.963011428 | 16 | 4 | KQK00808 | 0.911 | –0 | HORVU.MC |
| 0.970134041 | 0.993856465 | 16 | 0 | KQK19250 | 0.961 | –0 | HORVU.MC |
| 0.956345848 | 0.997095658 | 16 | 2 | KQJ90694 | 0.954 | –0 | HORVU.MC |
| 0.910714286 | 0.975019516 | 16 | 0 | KQK22042 | 0.897 | –0 | HORVU.MC |
| 0.959450652 | 1.000931099 | 16 | 0 | KQK21926 | 0.932 | – | HORVU.MC |

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| 0.88594041 | 0.960428305 | 16 | 2 | PNT72663 | 0.928 | 0. | HORVU.MC |
| 0.958444702 | 0.981705868 | 16 | 0 | KQK23065 | 0.956 | –0 | HORVU.MC |
| 0.952007513 | 0.981900673 | 16 | 0 | KQK15974 | 0.930 | – | HORVU.MC |
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| 0.947746456 | 0.963315658 | 16 | 0 | KQJ89126 | 0.946 | –0 | HORVU.MC |
| 0.953197467 | 0.985016054 | 16 | 0 | KQJ84780 | 0.943 | –0 | HORVU.MC |
| 0.934460083 | 0.972773419 | 16 | 0 | KQK22880 | 0.948 | 0 | HORVU.MC |
| 0.978113655 | 1 | 16 | 0 | KQK19137 | 0.980 | 0 | HORVU.MC |
| 0.85735779 | 0.923493459 | 16 | 2 | KQJ92228 | 0.842 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.963470441 | 0.994309012 | 16 | 0 | KQK21844 | 0.962 | –0 | genblast_C |
| 0.953236131 | 0.978947368 | 16 | 0 | KQK16885 | 0.911 | – | HORVU.MC |
| 0.922430857 | 0.975704989 | 16 | 1 | KQK18754 | 0.892 | –0 | HORVU.MC |
| 0.958497141 | 0.974777903 | 16 | 0 | KQK09649 | 0.962 | 0 | HORVU.MC |
| 0.892680514 | 0.944114738 | 16 | 0 | PNT72318 | 0.887 | –0 | HORVU.MC |
| 0.908401933 | 0.956900168 | 16 | 4 | KQK21762 | 0.928 | 0 | HORVU.MC |
| 0.937239092 | 0.964449232 | 16 | 0 | KQK18284 | 0.907 | – | HORVU.MC |
| 0.946795529 | 0.9815596 | 16 | 0 | KQK17318 | 0.928 | –0 | HORVU.MC |
| 0.932986379 | 0.977897713 | 16 | 0 | KQK02357 | 0.942 | 0 | HORVU.MC |
| 0.905037483 | 0.957201272 | 16 | 2 | KQJ91840 | 0.782 | –2 | HORVU.MC |

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|---|---|---|---|
| 0.934976819 | 0.954826438 | 16 | 1 KQJ88921 0.922 −1HORVU.MC |
| 0.99572284 | 1.0213858 | 16 | 0 KQJ84549 0.998 0. HORVU.MC |
| 0.947893412 | 0.982036239 | 16 | 1 KQK13257 0.921 − HORVU.MC |
| 0.905091304 | 0.940763835 | 16 | 0 KQJ92849 0.884 −0HORVU.MC |
| 0.966760083 | 0.996294238 | 16 | 0 PNT69116 0.949 −(HORVU.MC |
| 0.875581074 | 0.959933592 | 16 | 7 KQJ83880 0.861 −0HORVU.MC |
| 0.963431277 | 0.984886202 | 16 | 2 KQK02054 0.974 0HORVU.MC |
| 0.927925124 | 0.981999234 | 16 | 1 KQJ83650 0.893 −0genblast_C |
| | | | |
| 0.951733371 | 0.996134643 | 16 | 1 KQJ97767 0.929 −1HORVU.MC |
| | | | |
| 0.973975876 | 0.987437415 | 16 | 0 KQK15279 0.982 0HORVU.MC |
| 0.929039301 | 0.959355055 | 16 | 0 KQJ91246 0.931 0. HORVU.MC |
| 0.923794469 | 0.955716139 | 16 | 0 KQK15975 0.935 0HORVU.MC |
| | | | |
| 0.94009827 | 0.98490566 | 16 | 2 KQJ89034 0.947 0.HORVU.MC |
| 0.859635417 | 0.943382353 | 16 | 1 KQK10494 0.812 −HORVU.MC |
| 0.958795459 | 0.992766727 | 16 | 0 KQJ93644 0.927 −1HORVU.MC |
| | | | |
| 0.945805315 | 0.976304835 | 16 | 0 KQJ91844 0.910 −1genblast_C |
| 0.954019368 | 0.977759112 | 16 | 1 KQK13313 0.950 −HORVU.MC |
| 0.977736476 | 0.997785511 | 16 | 0 KQJ94843 0.994 0.HORVU.MC |
| 0.934036524 | 0.972027045 | 16 | 1 KQK00546 0.924 −HORVU.MC |
| 0.902827088 | 0.979801372 | 16 | 3 KQK01257 0.840 − HORVU.MC |
| 0.963855507 | 0.986900558 | 16 | 0 KQJ83400 0.950 −0HORVU.MC |
| 0.944812957 | 0.996999812 | 16 | 0 KQJ85886 0.929 −0HORVU.MC |
| 0.954832284 | 0.97844135 | 16 | 1 PNT73316 0.941 −(HORVU.MC |
| | | | |
| 0.87554492 | 0.96398787 | 16 | 1 KQK12443 0.855 −HORVU.MC |
| 0.928977641 | 0.96500324 | 16 | 0 KQJ82493 0.870 −1HORVU.MC |
| 0.951775783 | 0.982483599 | 16 | 0 KQK01533 0.937 −HORVU.MC |
| 0.87753317 | 0.922755362 | 16 | 0 KQJ83519 0.891 0.HORVU.MC |
| 0.865889438 | 0.935762817 | 16 | 0 PNT61055 0.785 −1HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.948620839 | 0.968305333 | 16 | 2 | KQK23540 | 0.957 | 0. | HORVU.MC |
| 0.959755791 | 0.979657603 | 16 | 0 | KQK22576 | 0.958 | – | HORVU.MC |
| 0.910114924 | 0.95604534 | 16 | 0 | KQK12691 | 0.916 | 0. | HORVU.MC |
| 0.927786011 | 0.966212211 | 16 | 2 | genblast_Os01t082 | | | HORVU.MC |
| 0.912640358 | 0.942561002 | 16 | 0 | KQK20876 | 0.925 | 0. | HORVU.MC |
| 0.921862724 | 0.951789158 | 16 | 0 | PNT70982 | 0.935 | 0. | HORVU.MC |
| 0.96435652 | 0.986518636 | 16 | 0 | KQK01943 | 0.946 | – | HORVU.MC |
| 0.932298714 | 0.974966171 | 16 | 0 | KQJ85687 | 0.905 | –0 | HORVU.MC |
| 0.949800042 | 0.996421806 | 16 | 0 | KQK00756 | 0.954 | 0. | HORVU.MC |
| 0.890635327 | 0.954064772 | 16 | 0 | KQK12335 | 0.857 | – | HORVU.MC |
| 0.899759391 | 0.945669047 | 16 | 0 | KQK06824 | 0.871 | – | HORVU.MC |
| 0.937894284 | 0.979353852 | 16 | 0 | KQJ84253 | 0.947 | 0. | HORVU.MC |
| 0.971940732 | 0.986853637 | 16 | 0 | KQJ90222 | 0.975 | 0. | HORVU.MC |
| 0.867991845 | 0.919215087 | 16 | 0 | KQJ97450 | 0.819 | –1 | HORVU.MC |
| 0.943609726 | 0.974563591 | 16 | 0 | KQJ81534 | 0.951 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.915564945 | 0.969060924 | 16 | 0 | KQK15207 | 0.872 | – | HORVU.MC |
| 0.954419679 | 0.996344435 | 16 | 0 | KQK07550 | 0.975 | 0. | HORVU.MC |
| 0.954279815 | 1.008118701 | 16 | 0 | KQK11102 | 0.896 | – | HORVU.MC |
| 0.894500591 | 0.942104819 | 16 | 4 | KQK03769 | 0.899 | 0. | HORVU.MC |
| 0.955322982 | 0.980614718 | 16 | 0 | KQK23344 | 0.938 | – | HORVU.MC |
| 0.873063633 | 0.960994388 | 16 | 3 | KQK16207 | 0.833 | – | HORVU.MC |
| 0.959029093 | 0.995696333 | 16 | 0 | KQJ97818 | 0.952 | –0 | HORVU.MC |
| 0.932524252 | 0.963706305 | 16 | 0 | KQJ91125 | 0.912 | –0 | HORVU.MC |
| 0.92834026 | 0.971238938 | 16 | 1 | KQK17885 | 0.928 | – | HORVU.MC |
| 0.980122156 | 1.00176398 | 16 | 0 | KQJ98138 | 0.975 | –0 | HORVU.MC |
| 0.913179398 | 0.957409929 | 16 | 2 | PNT77113 | 0.925 | 0. | HORVU.MC |
| 0.883381074 | 0.970931466 | 16 | 0 | KQK00371 | 0.872 | – | HORVU.MC |
| 0.938595079 | 0.971914455 | 16 | 1 | KQJ85857 | 0.960 | 0. | HORVU.MC |
| 0.903549687 | 0.972293518 | 16 | 3 | KQJ97184 | 0.929 | 0. | genblast_C |
| 0.918229028 | 0.959612134 | 16 | 1 | KQJ98599 | 0.935 | 0. | HORVU.MC |
| 0.930636206 | 0.968215159 | 16 | 0 | KQK23341 | 0.875 | – | HORVU.MC |
| 0.979847268 | 1.003691399 | 16 | 0 | KQJ86222 | 0.984 | 0. | HORVU.MC |
| 0.975137598 | 0.999394062 | 16 | 0 | KQK15496 | 0.970 | – | HORVU.MC |
| 0.870115519 | 0.944482405 | 16 | 2 | KQJ97924 | 0.882 | 0. | HORVU.MC |
| 0.940776925 | 0.962535459 | 16 | 0 | KQK10214 | 0.927 | – | HORVU.MC |
| 0.969810121 | 0.999623068 | 16 | 0 | KQK13798 | 0.970 | 0 | HORVU.MC |
| 0.930746425 | 0.970331364 | 16 | 2 | KQJ96371 | 0.939 | 0. | HORVU.MC |
| 0.850661744 | 0.916523973 | 16 | 0 | KQJ90027 | 0.800 | –1 | HORVU.MC |
| 0.949074242 | 0.971838124 | 16 | 1 | KQJ91226 | 0.962 | 0. | HORVU.MC |
| 0.953524483 | 0.982473575 | 16 | 0 | KQJ83150 | 0.947 | –0 | HORVU.MC |

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| 0.912119709 | 0.95952381 | 16 | 0 | KQK21869 0.956 1 | HORVU.MC |
| 0.90978759 | 1.006192717 | 16 | 0 | PNT64740 0.854 – | HORVU.MC |
| 0.96253401 | 0.989505393 | 16 | 0 | KQJ92646 0.946 –1 | HORVU.MC |
| 0.90879332 | 0.965501019 | 16 | 2 | KQJ97292 0.913 0. | HORVU.MC |
| 0.966592014 | 0.989556136 | 16 | 0 | KQK00768 0.977 0 | HORVU.MC |
| 0.948706575 | 0.996638028 | 16 | 0 | KQK13376 0.953 0 | HORVU.MC |

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| 0.95633873 | 0.978880676 | 16 | 0 | KQJ90979 0.940 –1 | HORVU.MC |
| 0.928052225 | 0.984058775 | 16 | 1 | KQK22543 0.954 0 | HORVU.MC |
| 0.937976556 | 0.962751972 | 16 | 0 | KQK13927 0.928 – | HORVU.MC |
| 0.949049192 | 0.974684288 | 16 | 0 | PNT68754 0.965 0. | HORVU.MC |
| 0.976293103 | 1.004756243 | 16 | 1 | KQK00238 0.954 – | HORVU.MC |
| 0.968065754 | 0.991201958 | 16 | 0 | KQJ85392 0.951 –1 | HORVU.MC |
| 0.953190213 | 0.976836394 | 16 | 0 | KQK09574 0.940 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.937058954 | 0.963909835 | 16 | 3 | KQK01959 0.934 – | HORVU.MC |
| 0.918925165 | 0.957635915 | 16 | 1 | KQK24155 0.891 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.939579459 | 0.981332231 | 16 | 1 | KQJ85696 0.945 0. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.962885466 | 0.983796131 | 16 | 0 | KQK01550 0.970 0 | HORVU.MC |
| 0.969562036 | 1.011707596 | 16 | 2 | KQK22339 0.989 0 | HORVU.MC |
| 0.942080548 | 0.973957265 | 16 | 0 | KQK02501 0.932 – | HORVU.MC |
| 0.974103796 | 0.990327651 | 16 | 0 | KQJ94036 0.960 –1 | HORVU.MC |
| 0.967490308 | 0.992494657 | 16 | 0 | KQK22575 0.959 – | HORVU.MC |
| 0.931020874 | 0.979915804 | 16 | 2 | KQK13621 0.922 – | genblast_C |
| 0.854589927 | 0.931458512 | 16 | 9 | PNT77125 0.879 0. | HORVU.MC |
| 0.959659028 | 0.984064183 | 16 | 0 | KQJ84220 0.944 –0 | HORVU.MC |
| 0.965792404 | 0.988246938 | 16 | 0 | KQJ88448 0.967 0. | HORVU.MC |
| 0.993500654 | 1.008502289 | 16 | 0 | KQK23362 0.992 – | HORVU.MC |
| 0.927875865 | 0.968511103 | 16 | 0 | KQK11219 0.905 – | HORVU.MC |
| 0.910030672 | 0.962144076 | 16 | 2 | genblast_Os07t068 | HORVU.MC |
| 0.93013544 | 0.967881329 | 16 | 2 | KQK21393 0.918 – | HORVU.MC |
| 0.941325104 | 0.967401726 | 16 | 0 | KQJ86449 0.955 0. | HORVU.MC |
| 0.906808036 | 0.979679803 | 16 | 0 | KQJ93048 0.848 –1 | genblast_C |

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| 0.915508991 | 0.982171799 | 16 | 1 | KQK05388 | 0.895 | – | HORVU.MC |
| 0.955209128 | 0.987192586 | 16 | 2 | KQK03051 | 0.961 | 0 | HORVU.MC |
| 0.975775284 | 1.014155336 | 16 | 0 | KQK09135 | 0.969 | – | HORVU.MC |
| 0.905514545 | 0.978511913 | 16 | 0 | KQJ91442 | 0.894 | –0 | HORVU.MC |
| 0.89854871 | 0.961020907 | 16 | 4 | KQK10037 | 0.892 | – | genblast_C |
| 0.958209296 | 0.996983409 | 16 | 0 | KQK01610 | 0.961 | 0 | HORVU.MC |
| 0.933430768 | 0.983795847 | 16 | 0 | KQK05587 | 0.894 | – | HORVU.MC |
| 0.914548558 | 0.962714069 | 16 | 0 | KQJ91431 | 0.919 | 0. | HORVU.MC |
| 0.919395482 | 0.956373411 | 16 | 0 | KQK20086 | 0.864 | – | HORVU.MC |
| 0.944993065 | 0.989446388 | 16 | 0 | KQK24008 | 0.920 | – | HORVU.MC |
| 0.957828283 | 0.983714698 | 16 | 1 | KQK03233 | 0.971 | 0 | HORVU.MC |
| 0.891953656 | 0.937393707 | 16 | 0 | KQK19743 | 0.850 | – | HORVU.MC |
| 0.928200664 | 0.95391825 | 16 | 0 | KQJ91493 | 0.894 | –1 | HORVU.MC |
| 0.938015953 | 0.980365908 | 16 | 0 | KQJ94497 | 0.896 | –1 | HORVU.MC |
| 0.95948002 | 0.979931125 | 16 | 0 | KQJ97287 | 0.974 | 0. | HORVU.MC |
| 0.942585099 | 0.984864397 | 16 | 0 | KQJ99626 | 0.936 | –0 | HORVU.MC |
| 0.909480365 | 0.982268941 | 16 | 4 | KQK04781 | 0.824 | – | HORVU.MC |
| 0.960862216 | 0.982670662 | 16 | 0 | PNT61900 | 0.950 | – | HORVU.MC |
| 0.960187329 | 0.979595336 | 16 | 0 | KQK13669 | 0.971 | 0 | HORVU.MC |
| 0.944960202 | 0.991041704 | 16 | 2 | KQJ93837 | 0.968 | 0. | HORVU.MC |
| 0.958228997 | 0.983473144 | 16 | 1 | KQK18695 | 0.965 | 0 | HORVU.MC |
| 0.935767541 | 0.984469744 | 16 | 0 | KQK10431 | 0.947 | 0 | HORVU.MC |
| 0.853015654 | 0.915899325 | 16 | 1 | KQK15998 | 0.857 | 0 | HORVU.MC |
| 0.936505251 | 0.971203544 | 16 | 0 | KQK14941 | 0.932 | – | genblast_C |
| 0.865457215 | 0.929530201 | 16 | 1 | PNT77989 | 0.918 | 1. | HORVU.MC |
| 0.95308163 | 0.987383295 | 16 | 1 | KQJ97307 | 0.959 | 0. | HORVU.MC |
| 0.906097408 | 0.950169025 | 16 | 0 | KQK00496 | 0.869 | – | HORVU.MC |
| 0.928996354 | 0.977355594 | 16 | 0 | PNT61253 | 0.961 | 0. | HORVU.MC |
| 0.950657604 | 0.980492541 | 16 | 0 | KQK16453 | 0.956 | 0 | HORVU.MC |
| 0.9403047 | 0.989113117 | 16 | 0 | KQK23014 | 0.953 | 0 | HORVU.MC |
| 0.949359583 | 0.98066888 | 16 | 0 | KQK17886 | 0.918 | – | HORVU.MC |

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|---|---|---|---|
| 0.92485877 | 0.961844786 | 16 | 0 KQK02880 0.858 – HORVU.MC |
| 0.970609191 | 0.998218739 | 16 | 0 KQJ91079 0.982 0. HORVU.MC |
| 0.939151824 | 0.965527147 | 16 | 0 KQK15305 0.936 – HORVU.MC |
| 0.970345561 | 0.990455382 | 16 | 0 KQK06282 0.969 – HORVU.MC |
| 0.902544782 | 0.966164345 | 16 | 0 KQJ86871 0.904 0. HORVU.MC |
| 0.886788669 | 0.921141506 | 16 | 0 KQJ84302 0.871 –0 HORVU.MC |
| 0.938133691 | 0.958864426 | 16 | 1 KQJ82732 0.926 –0 HORVU.MC |

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| 0.925873107 | 0.967035327 | 16 | 0 KQK06300 0.926 0 HORVU.MC |
| 0.898637527 | 0.958790539 | 16 | 0 KQK12126 0.883 – HORVU.MC |
| 0.943949712 | 0.97365861 | 16 | 0 KQJ90350 0.928 –0 HORVU.MC |
| 0.91154893 | 0.970967338 | 16 | 1 KQJ97203 0.919 0. HORVU.MC |
| 0.932388377 | 0.976045358 | 16 | 1 KQK06235 0.927 – HORVU.MC |

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| 0.936861807 | 0.971134021 | 16 | 1 KQK05282 0.931 – HORVU.MC |
| 0.856708215 | 0.898223574 | 16 | 6 KQK13596 0.894 1 genblast_C |
| 0.910518484 | 0.942434211 | 16 | 0 KQK05808 0.923 0 HORVU.MC |
| 0.916376122 | 0.970773708 | 16 | 1 KQJ84291 0.904 –0 HORVU.MC |
| 0.917611499 | 0.975711983 | 16 | 0 KQK01999 0.880 – HORVU.MC |
| 0.958113364 | 0.982850177 | 16 | 1 KQJ95224 0.963 0. HORVU.MC |
| 0.96311054 | 0.982919166 | 16 | 0 KQJ91912 0.964 0. genblast_C |
| 0.955839706 | 0.987540815 | 16 | 0 KQK20321 0.945 – HORVU.MC |
| 0.897434106 | 0.95315265 | 16 | 0 KQK11451 0.917 0 HORVU.MC |

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| 0.924078164 | 0.957627119 | 16 | 0 KQJ93543 0.901 –0 HORVU.MC |
| 0.928783002 | 0.972083965 | 16 | 0 KQK14014 0.886 – HORVU.MC |
| 0.92422822 | 0.956060606 | 16 | 0 KQK17739 0.895 – HORVU.MC |
| 0.883999234 | 0.932346183 | 16 | 0 KQK09249 0.848 – HORVU.MC |
| 0.850728848 | 0.918933525 | 16 | 2 KQJ88226 0.793 –1 genblast_C |
| 0.903398341 | 0.971086208 | 16 | 3 KQK11724 0.920 0 HORVU.MC |
| 0.968210626 | 0.99433657 | 16 | 0 KQJ87232 0.968 –0 HORVU.MC |
| 0.970160996 | 0.984787363 | 16 | 0 KQJ85698 0.975 0. HORVU.MC |
| 0.911094558 | 0.976810791 | 16 | 1 KQJ97271 0.898 –0 HORVU.MC |
| 0.901726775 | 0.973595234 | 16 | 1 KQJ98279 0.943 0. HORVU.MC |
| 0.934118909 | 0.981554556 | 16 | 1 KQJ96008 0.867 –1 HORVU.MC |
| 0.917598898 | 0.95028102 | 16 | 1 KQK11709 0.914 – HORVU.MC |
| 0.970456172 | 0.989912071 | 16 | 0 KQJ98502 0.979 0. HORVU.MC |
| 0.959567941 | 0.981555154 | 16 | 1 KQK10117 0.955 – HORVU.MC |
| 0.861100311 | 0.934681182 | 16 | 1 KQK08364 0.802 – HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.889609582 | 0.988561008 | 16 | 5 | KQK20678 | 0.937 | 0 | HORVU.MC |
| 0.948344749 | 0.973515982 | 16 | 0 | PNT73835 | 0.963 | 0. | HORVU.MC |
| 0.913380834 | 0.964011835 | 16 | 1 | KQJ94976 | 0.915 | 0. | HORVU.MC |
| 0.932378725 | 0.982739826 | 16 | 0 | KQK07049 | 0.903 | – | HORVU.MC |
| 0.906452573 | 0.962958063 | 16 | 2 | KQK07183 | 0.923 | 0 | genblast_C |
| 0.881142823 | 0.961098762 | 16 | 1 | KQJ85957 | 0.863 | –0 | genblast_C |
| 0.92077834 | 0.957287979 | 16 | 0 | KQJ86905 | 0.947 | 0. | HORVU.MC |
| | | | | | | | |
| 0.977425453 | 0.995897624 | 16 | 0 | KQK20651 | 0.978 | 0 | HORVU.MC |
| 0.98862898 | 1.012345679 | 16 | 0 | KQK01192 | 0.995 | 0 | HORVU.MC |
| | | | | | | | |
| 0.972086166 | 0.990003998 | 16 | 0 | KQK19713 | 0.954 | – | HORVU.MC |
| 0.95976221 | 0.981006934 | 16 | 0 | KQK16787 | 0.947 | – | HORVU.MC |
| 0.95899465 | 0.979759251 | 16 | 0 | KQK10306 | 0.949 | – | HORVU.MC |
| | | | | | | | |
| 0.952402981 | 0.99139828 | 16 | 0 | KQJ83139 | 0.945 | –0 | HORVU.MC |
| 0.909368112 | 0.984423218 | 16 | 1 | KQJ81468 | 0.753 | –2 | HORVU.MC |
| 0.934737974 | 0.97392778 | 16 | 1 | KQJ98079 | 0.948 | 0. | HORVU.MC |
| 0.971094278 | 0.995945033 | 16 | 0 | KQK00696 | 0.965 | – | HORVU.MC |
| 0.955729167 | 0.994087838 | 16 | 0 | KQJ97451 | 0.965 | 0. | HORVU.MC |
| | | | | | | | |
| 0.956000617 | 0.972965947 | 16 | 0 | KQJ86500 | 0.935 | –1 | HORVU.MC |
| 0.943857582 | 0.958797414 | 16 | 0 | KQJ92885 | 0.943 | –0 | HORVU.MC |
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| 0.97245184 | 0.990032586 | 16 | 0 | KQK22522 | 0.969 | – | HORVU.MC |
| 0.946615256 | 0.984770263 | 16 | 0 | KQK07870 | 0.948 | 0 | HORVU.MC |
| 0.925086623 | 0.961762158 | 16 | 0 | KQK07041 | 0.915 | – | HORVU.MC |
| 0.941920566 | 0.992383025 | 16 | 0 | KQK05034 | 0.903 | – | HORVU.MC |
| 0.941070665 | 0.99358883 | 16 | 1 | KQK03192 | 0.942 | 0 | HORVU.MC |
| | | | | | | | |
| 0.866373048 | 0.914638576 | 16 | 0 | KQK18909 | 0.867 | 0 | HORVU.MC |
| 0.918526786 | 0.942956349 | 16 | 0 | PNT62596 | 0.925 | 0. | HORVU.MC |
| 0.924792389 | 0.965869684 | 16 | 0 | KQJ83782 | 0.932 | 0. | genblast_C |
| 0.946219476 | 0.989691753 | 16 | 0 | KQK08853 | 0.922 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.948923803 | 0.986418048 | 16 | 0 | KQK04590 | 0.911 | – | HORVU.MC |
| 0.924639264 | 0.967823972 | 16 | 1 | KQK13968 | 0.889 | – | HORVU.MC |
| 0.95405479 | 0.986695694 | 16 | 0 | PNT72790 | 0.939 | – | HORVU.MC |
| 0.954986437 | 0.994464128 | 16 | 3 | KQK13982 | 0.965 | 0 | HORVU.MC |
| 0.961816512 | 0.978712382 | 16 | 0 | KQK21051 | 0.963 | 0 | HORVU.MC |
| 0.904805672 | 0.965919701 | 16 | 3 | KQK08655 | 0.890 | – | HORVU.MC |
| 0.948057432 | 0.979854855 | 16 | 0 | KQK03098 | 0.958 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.931689104 | 0.971182162 | 16 | 0 | KQK13366 | 0.873 | – | HORVU.MC |
| 0.94399612 | 1.012796169 | 16 | 0 | PNT62784 | 0.906 | – | HORVU.MC |
| 0.925758471 | 0.973573485 | 16 | 1 | KQJ90866 | 0.947 | 0. | HORVU.MC |
| 0.955280503 | 0.972409565 | 16 | 0 | KQK21779 | 0.950 | – | HORVU.MC |
| 0.918975511 | 0.962944443 | 16 | 2 | KQJ96911 | 0.921 | 0. | HORVU.MC |
| 0.878942692 | 0.929216644 | 16 | 0 | KQJ90194 | 0.850 | –0 | HORVU.MC |
| 0.969367388 | 0.99594046 | 16 | 0 | KQJ97953 | 0.943 | –1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.945974099 | 0.978828829 | 16 | 0 | KQK00569 | 0.918 | – | HORVU.MC |
| 0.941983466 | 0.964848327 | 16 | 0 | KQK14038 | 0.942 | 0 | HORVU.MC |
| 0.950009685 | 0.989927686 | 16 | 0 | KQK06333 | 0.943 | – | HORVU.MC |
| 0.94215412 | 0.99145473 | 16 | 0 | KQK21318 | 0.913 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.926578163 | 0.982299287 | 16 | 2 | KQJ97133 | 0.897 | −0 | HORVU.MC |
| 0.92190216 | 0.966476285 | 16 | 0 | KQK19605 | 0.962 | 0 | HORVU.MC |
| 0.939383506 | 0.980233312 | 16 | 0 | KQJ86695 | 0.922 | −0 | HORVU.MC |
| 0.966867069 | 0.989085101 | 16 | 1 | KQK13286 | 0.948 | − | genblast_C |
| | | | | | | | |
| 0.916443009 | 0.978263751 | 16 | 0 | KQK19355 | 0.868 | − | HORVU.MC |
| 0.969160023 | 0.990643858 | 16 | 0 | KQK01746 | 0.954 | − | HORVU.MC |
| 0.956568595 | 0.979994978 | 16 | 0 | KQK14210 | 0.958 | 0 | HORVU.MC |
| 0.930172609 | 0.961625623 | 16 | 0 | KQJ84222 | 0.937 | 0. | HORVU.MC |
| 0.934505304 | 0.966715435 | 16 | 0 | KQK24094 | 0.932 | − | HORVU.MC |
| 0.925002763 | 0.962204376 | 16 | 2 | KQK10893 | 0.934 | 0 | HORVU.MC |
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| 0.92664705 | 0.988382758 | 16 | 1 | PNT72966 | 0.913 | − | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.907115134 | 0.966995983 | 16 | 3 | KQJ88294 | 0.891 | -0 | HORVU.MC |
| 0.932417423 | 0.981649604 | 16 | 0 | KQK17767 | 0.937 | 0. | HORVU.MC |
| 0.940443604 | 0.976016684 | 16 | 0 | KQK23122 | 0.918 | - | HORVU.MC |
| 0.938475787 | 0.982446855 | 16 | 1 | KQK17286 | 0.919 | - | HORVU.MC |
| 0.963192464 | 0.981262729 | 16 | 0 | KQJ97584 | 0.925 | -2 | HORVU.MC |
| 0.956436774 | 0.978232798 | 16 | 0 | KQJ94170 | 0.977 | 1. | HORVU.MC |
| 0.929207465 | 0.978381649 | 16 | 0 | KQK16736 | 0.845 | - | HORVU.MC |
| 0.890110703 | 0.943641961 | 16 | 1 | KQK14404 | 0.895 | 0. | HORVU.MC |
| 0.913371455 | 0.96910871 | 16 | 0 | KQK04586 | 0.874 | - | HORVU.MC |
| 0.97407648 | 0.991129134 | 16 | 0 | KQK21879 | 0.941 | - | HORVU.MC |
| 0.898360924 | 0.958832498 | 16 | 0 | KQK21635 | 0.911 | 0. | HORVU.MC |
| 0.925334273 | 0.977351283 | 16 | 0 | KQK21701 | 0.947 | 0. | HORVU.MC |
| 0.897615893 | 0.978630822 | 16 | 10 | genblast_Os01t019 | | | HORVU.MC |
| 0.958392857 | 0.991208791 | 16 | 0 | KQK08513 | 0.908 | - | HORVU.MC |
| 0.90167707 | 0.946902655 | 16 | 1 | KQK15364 | 0.903 | 0. | HORVU.MC |
| 0.95256587 | 0.986151961 | 16 | 0 | KQK09378 | 0.946 | - | genblast_C |
| 0.951966816 | 0.965548098 | 16 | 0 | PNT69484 | 0.963 | 0. | HORVU.MC |
| 0.916538379 | 0.954174424 | 16 | 1 | KQK22771 | 0.853 | - | genblast_C |
| 0.911947113 | 0.974295366 | 16 | 3 | KQK20542 | 0.891 | - | HORVU.MC |
| 0.83357343 | 0.902939311 | 16 | 1 | PNT64119 | 0.783 | -1 | genblast_C |
| 0.921553314 | 0.958705224 | 16 | 0 | KQK17510 | 0.889 | - | HORVU.MC |
| 0.947097567 | 0.978407992 | 16 | 0 | KQJ90031 | 0.933 | -0 | HORVU.MC |
| 0.92365871 | 0.970810683 | 16 | 0 | KQK05586 | 0.900 | - | HORVU.MC |
| 0.976708021 | 0.995273839 | 16 | 0 | KQJ99894 | 0.989 | 0. | HORVU.MC |
| 0.862090481 | 0.949943757 | 16 | 0 | KQJ93950 | 0.812 | -1 | HORVU.MC |
| 0.915744506 | 0.961199404 | 16 | 3 | KQK15161 | 0.901 | - | HORVU.MC |
| 0.910121114 | 0.965519962 | 16 | 0 | KQK00679 | 0.832 | - | HORVU.MC |

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|---|---|---|---|---|---|
| 0.954215686 | 0.978196078 | 16 | 0 | KQK12698 0.943 – | HORVU.M |
| 0.878754496 | 0.950359712 | 16 | 0 | KQK15267 0.779 – | genblast_ |
| 0.913307975 | 0.956728175 | 16 | 0 | KQJ97399 0.904 –0 | genblast_ |
| 0.931582994 | 0.954529749 | 16 | 0 | KQJ92498 0.924 –0 | HORVU.M |
| 0.883659233 | 0.953889248 | 16 | 0 | genblast_Os05t053 | HORVU.M |
| 0.936884648 | 0.962052246 | 16 | 0 | KQJ89011 0.926 –0 | HORVU.M |
| 0.935449758 | 0.963674033 | 16 | 0 | KQK08756 0.894 – | HORVU.M |
| 0.892635891 | 0.945186708 | 16 | 1 | KQK06982 0.896 0 | HORVU.M |
| 0.906492739 | 0.983076288 | 16 | 12 | KQK04790 0.853 – | genblast_ |
| 0.930430066 | 0.95743922 | 16 | 0 | KQK08172 0.907 – | HORVU.M |
| 0.906941934 | 0.965386353 | 16 | 0 | KQJ98123 0.942 0. | HORVU.M |
| 0.979193489 | 1.002942799 | 16 | 0 | KQK06901 0.975 – | HORVU.M |
| 0.922785909 | 0.970974944 | 16 | 0 | KQK02937 0.897 – | HORVU.M |
| 0.947154772 | 0.975337838 | 16 | 0 | KQJ91277 0.948 0. | HORVU.M |
| 0.902354111 | 0.959880637 | 16 | 0 | KQJ93803 0.892 –0 | genblast_ |
| 0.886172154 | 0.913806492 | 16 | 0 | KQK17101 0.896 0 | HORVU.M |
| 0.914076736 | 0.980360397 | 16 | 0 | KQJ92514 0.861 –1 | HORVU.M |
| 0.894544426 | 0.93747429 | 16 | 0 | KQK07299 0.901 0 | HORVU.M |
| 0.922366931 | 0.9599094 | 16 | 0 | KQJ83882 0.915 –0 | HORVU.M |
| 0.955895303 | 0.996607958 | 16 | 0 | KQJ97394 0.950 –0 | HORVU.M |
| 0.967753853 | 0.993033566 | 16 | 0 | KQJ92163 0.945 –0 | HORVU.M |
| 0.936881188 | 0.970832218 | 16 | 1 | KQK06570 0.921 – | HORVU.M |
| 0.94792201 | 0.997435371 | 16 | 1 | KQK15829 0.946 – | HORVU.M |
| 0.965175195 | 0.994563933 | 16 | 0 | genblast_Os06t018 | HORVU.M |
| 0.830081036 | 0.898658718 | 16 | 0 | KQJ96389 0.829 –0 | HORVU.M |
| 0.944799853 | 0.984675835 | 16 | 1 | KQK09611 0.956 0 | HORVU.M |
| 0.937735288 | 0.982299716 | 16 | 1 | KQJ94463 0.933 –0 | HORVU.M |

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|---|---|---|---|---|---|---|---|
| 0.919143625 | 0.982795699 | 16 | 0 | KQJ93472 | 0.956 | 0. | HORVU.MC |
| 0.878960958 | 0.939206635 | 16 | 3 | KQJ94197 | 0.881 | 0. | genblast_C |
| 0.956113001 | 0.97845805 | 16 | 0 | KQK07459 | 0.959 | 0 | HORVU.MC |
| 0.990341545 | 1.020156775 | 16 | 0 | KQK16113 | 0.971 | − | HORVU.MC |
| 0.903530411 | 0.950663216 | 16 | 0 | PNT77075 | 0.891 | − | HORVU.MC |
| 0.967335182 | 0.985227327 | 16 | 0 | KQJ84621 | 0.966 | −0 | HORVU.MC |
| 0.933398679 | 0.964919521 | 16 | 0 | KQK08565 | 0.866 | − | HORVU.MC |
| 0.902714718 | 0.981157775 | 16 | 1 | KQK04669 | 0.929 | 0 | HORVU.MC |
| 0.939536152 | 0.973591152 | 16 | 0 | KQK04938 | 0.897 | − | HORVU.MC |
| 0.955182443 | 0.982945531 | 16 | 2 | KQJ82243 | 0.967 | 0. | HORVU.MC |
| 0.957494493 | 0.99154185 | 16 | 0 | KQK05775 | 0.939 | − | HORVU.MC |
| 0.961290765 | 1.001370238 | 16 | 0 | KQJ93418 | 0.937 | −1 | genblast_C |
| 0.945683747 | 0.981984334 | 16 | 0 | KQK12714 | 0.922 | − | HORVU.MC |
| 0.967724807 | 0.988302183 | 16 | 0 | KQK22056 | 0.959 | − | HORVU.MC |
| 0.922763299 | 0.967224187 | 16 | 2 | KQK14181 | 0.941 | 0 | HORVU.MC |
| 0.912357996 | 0.967157006 | 16 | 0 | KQK07953 | 0.900 | − | HORVU.MC |
| 0.909017388 | 1.014557218 | 16 | 0 | PNT67692 | 0.927 | 0. | HORVU.MC |
| 0.960766676 | 0.994326045 | 16 | 0 | KQJ93358 | 0.981 | 0. | HORVU.MC |
| 0.956705326 | 0.98344781 | 16 | 0 | KQK00293 | 0.932 | − | HORVU.MC |
| 0.930163266 | 0.954787779 | 16 | 0 | KQK16183 | 0.942 | 0 | HORVU.MC |
| 0.912826256 | 0.963590247 | 16 | 1 | KQJ98000 | 0.853 | −1 | HORVU.MC |
| 0.966915513 | 0.990060318 | 16 | 0 | KQK19768 | 0.940 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.953987091 | 0.983321102 | 16 | 0 | KQJ90468 | 0.903 | -1 | HORVU.MC |
| 0.985241348 | 1.00007286 | 16 | 0 | KQK22113 | 0.985 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.935434298 | 0.974387528 | 16 | 2 | KQK08719 | 0.954 | 0 | HORVU.MC |
| 0.864195185 | 0.960090214 | 16 | 0 | KQJ86325 | 0.821 | -0 | HORVU.MC |
| 0.961843377 | 0.984276177 | 16 | 0 | KQK04957 | 0.962 | - | HORVU.MC |
| 0.952848179 | 0.990649606 | 16 | 2 | KQJ97421 | 0.960 | 0. | HORVU.MC |
| 0.950202057 | 0.994709772 | 16 | 0 | PNT71800 | 0.937 | - | HORVU.MC |
| 0.973804743 | 0.991341448 | 16 | 0 | KQK14768 | 0.968 | - | HORVU.MC |
| 0.897292123 | 0.977631899 | 16 | 1 | KQK12453 | 0.894 | - | HORVU.MC |
| 0.911054155 | 0.955459629 | 16 | 2 | KQJ95819 | 0.900 | -0 | genblast_C |
| 0.939957615 | 0.971648383 | 16 | 0 | KQK22003 | 0.943 | 0 | HORVU.MC |
| 0.910305871 | 0.95469947 | 16 | 0 | PNT77826 | 0.926 | 0. | HORVU.MC |
| 0.962643678 | 0.998612763 | 16 | 1 | KQK23782 | 0.908 | - | HORVU.MC |
| 0.96595598 | 0.994235714 | 16 | 1 | KQK10035 | 0.972 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.812670947 | 0.89206301 | 16 | 13 | KQJ87740 | 0.838 | 0. | HORVU.MC |
| 0.95808242 | 1.001258314 | 16 | 0 | KQK20328 | 0.961 | 0 | HORVU.MC |
| 0.991835586 | 1.017017017 | 16 | 0 | KQJ90520 | 1.012 | 0. | HORVU.MC |
| 0.948332739 | 0.977603424 | 16 | 0 | PNT64733 | 0.947 | - | HORVU.MC |
| 0.94162094 | 0.968669794 | 16 | 0 | KQK14751 | 0.909 | - | HORVU.MC |
| 0.944619972 | 0.999644001 | 16 | 1 | KQK00686 | 0.972 | 0 | HORVU.MC |
| 0.972117416 | 1.00160982 | 16 | 0 | KQK11111 | 0.936 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.904686309 | 0.954406909 | 16 | 1 | KQJ90509 | 0.863 | -1 | HORVU.MC |
| 0.939866286 | 0.983999399 | 16 | 1 | KQK05219 | 0.948 | 0 | HORVU.MC |
| 0.914342192 | 0.976279376 | 16 | 0 | KQJ93656 | 0.886 | -0 | HORVU.MC |
| 0.953743071 | 0.982993197 | 16 | 0 | KQJ84882 | 0.940 | -0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.893887739 | 0.946304639 | 16 | 0 | KQK09702 | 0.847 | – | HORVU.MC |
| 0.940854779 | 0.967307692 | 16 | 2 | KQJ90223 | 0.931 | –0 | HORVU.MC |
| 0.922655697 | 0.955838641 | 16 | 1 | KQJ93389 | 0.900 | –1 | HORVU.MC |
| 0.953336113 | 0.976825723 | 16 | 1 | KQK16988 | 0.967 | 0. | HORVU.MC |
| 0.92275939 | 0.95830566 | 16 | 0 | KQK22591 | 0.923 | 0. | HORVU.MC |
| 0.948029625 | 0.978035162 | 16 | 1 | KQK04922 | 0.946 | – | HORVU.MC |
| 0.866871905 | 0.926765702 | 16 | 0 | genblast_Os10t032 | | | HORVU.MC |
| 0.907780742 | 0.965650407 | 16 | 0 | KQJ85968 | 0.856 | –1 | HORVU.MC |
| 0.934073962 | 0.972591697 | 16 | 3 | KQK00479 | 0.912 | – | HORVU.MC |
| 0.904570798 | 0.967819189 | 16 | 0 | KQK20750 | 0.863 | – | HORVU.MC |
| 0.927210801 | 0.970185627 | 16 | 3 | KQJ86411 | 0.949 | 0. | HORVU.MC |
| 0.939685862 | 0.969407715 | 16 | 1 | genblast_Os12t050 | | | HORVU.MC |
| 0.954616707 | 0.995909745 | 16 | 1 | KQJ94212 | 0.953 | –0 | HORVU.MC |
| 0.916586229 | 0.955874242 | 16 | 0 | KQK00928 | 0.903 | – | HORVU.MC |
| 0.961929365 | 0.988167573 | 16 | 0 | KQK17515 | 0.943 | – | HORVU.MC |
| 0.91079931 | 0.944292346 | 16 | 0 | KQK09922 | 0.900 | – | HORVU.MC |
| 0.937462605 | 0.958316713 | 16 | 0 | KQJ83922 | 0.930 | –0 | HORVU.MC |
| 0.966017944 | 0.986328476 | 16 | 1 | KQK08635 | 0.985 | 0. | HORVU.MC |

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| 0.961061223 | 0.98216516 | 16 | 3 KQK02230 0.938 – | HORVU.MC |
| 0.852922535 | 0.941070423 | 16 | 1 PNT62327 0.740 – | HORVU.MC |
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| 0.940072613 | 0.986723382 | 16 | 5 KQK23188 0.954 0 | HORVU.MC |
| 0.910561505 | 0.959965562 | 16 | 0 KQK01062 0.833 – | HORVU.MC |
| 0.97591494 | 0.98723262 | 16 | 0 KQK13887 0.977 0 | HORVU.MC |
| 0.97472578 | 0.991377124 | 16 | 0 KQJ86780 0.973 –0 | HORVU.MC |
| | | | | |
| 0.860962492 | 0.926222122 | 16 | 4 KQK06143 0.839 – | HORVU.MC |
| 0.91029724 | 0.982085987 | 16 | 1 KQK16696 0.855 – | HORVU.MC |
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| 0.91935799 | 0.975642296 | 16 | 4 KQK14501 0.921 0 | HORVU.MC |
| 0.981909491 | 0.99812812 | 16 | 0 KQJ95771 0.979 –0 | HORVU.MC |
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| 0.898351876 | 0.941713716 | 16 | 1 KQK10385 0.871 – | HORVU.MC |
| 0.961099953 | 0.997069943 | 16 | 0 PNT69177 0.963 0. | HORVU.MC |
| 0.949442639 | 0.973102266 | 16 | 0 KQJ97322 0.970 1. | HORVU.MC |
| 0.889851813 | 0.952897592 | 16 | 0 KQK01730 0.903 0 | HORVU.MC |
| 0.880582353 | 0.932517647 | 16 | 1 KQJ88655 0.883 0. | HORVU.MC |
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| 0.949470741 | 0.997803076 | 16 | 0 KQJ92907 0.921 –0 | HORVU.MC |
| 0.90608203 | 0.959931591 | 16 | 1 KQK00384 0.877 – | HORVU.MC |
| 0.950059923 | 0.977948226 | 16 | 1 KQK18485 0.927 – | HORVU.MC |
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| 0.888260432 | 0.951231775 | 16 | 0 KQJ93258 0.915 0. | HORVU.MC |

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| 0.952298028 | 0.971501272 | 16 | 0 | KQK06280 | 0.909 | – | HORVU.MC |
| 0.966482613 | 0.98358396 | 16 | 0 | PNT69082 | 0.974 | 0. | HORVU.MC |
| 0.949995951 | 0.988467768 | 16 | 0 | KQK22482 | 0.931 | – | genblast_C |
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| 0.895439492 | 0.937491376 | 16 | 0 | KQJ96172 | 0.821 | –2 | HORVU.MC |
| 0.959033801 | 0.978807118 | 16 | 2 | KQK23733 | 0.911 | – | genblast_C |
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| 0.919444643 | 0.967487826 | 16 | 0 | KQJ85858 | 0.919 | –0 | HORVU.MC |
| 0.890878249 | 0.98244941 | 16 | 0 | KQK18273 | 0.872 | – | HORVU.MC |
| 0.95473045 | 0.994708217 | 16 | 0 | KQK00834 | 0.963 | 0 | HORVU.MC |
| 0.970933339 | 1.010027947 | 16 | 0 | KQK03175 | 0.968 | – | HORVU.MC |
| 0.870703773 | 0.94340117 | 16 | 2 | KQK18431 | 0.924 | 0 | HORVU.MC |
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| 0.90648927 | 0.951256336 | 16 | 0 | KQJ89303 | 0.841 | –1 | HORVU.MC |
| 0.956545755 | 1.007271507 | 16 | 0 | KQK11323 | 0.915 | – | HORVU.MC |
| 0.885866423 | 0.958750964 | 16 | 0 | KQK05605 | 0.864 | – | HORVU.MC |
| 0.914717698 | 0.971494607 | 16 | 0 | KQK19258 | 0.902 | – | HORVU.MC |
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| 0.951421902 | 0.973174873 | 16 | 1 | KQJ90974 | 0.955 | 0. | HORVU.MC |
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| 0.949198638 | 0.976415878 | 16 | 0 | KQJ95697 | 0.917 | –1 | HORVU.MC |
| 0.959477739 | 0.986086777 | 16 | 0 | KQJ86279 | 0.970 | 0. | HORVU.MC |
| 0.921210675 | 0.973015664 | 16 | 2 | KQJ97867 | 0.911 | –0 | HORVU.MC |
| 0.953747246 | 0.989239112 | 16 | 1 | KQJ96995 | 0.958 | 0. | HORVU.MC |
| 0.947933441 | 1.004294149 | 16 | 0 | KQJ92310 | 0.954 | 0. | HORVU.MC |
| 0.946866122 | 0.990924874 | 16 | 1 | KQJ86187 | 0.939 | –0 | HORVU.MC |
| 0.924775449 | 0.978443114 | 16 | 0 | KQJ90528 | 0.978 | 1. | HORVU.MC |
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| 0.956497635 | 0.982554701 | 16 | 1 | KQK00598 | 0.956 | – | HORVU.MC |

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| 0.893724574 | 0.974622239 | 16 | 5 | PNT75562 | 0.954 | 1. | HORVU.MC |
| 0.856708293 | 0.935158501 | 16 | 1 | KQK15487 | 0.771 | – | genblast_C |
| 0.918729573 | 0.966875718 | 16 | 0 | KQK23107 | 0.877 | – | HORVU.MC |
| 0.883669355 | 0.945552297 | 16 | 2 | KQJ96246 | 0.932 | 0. | HORVU.MC |
| 0.934234558 | 0.978082798 | 16 | 0 | KQK01375 | 0.946 | 0 | HORVU.MC |
| 0.936370192 | 0.989615385 | 16 | 0 | KQK22619 | 0.910 | – | HORVU.MC |
| 0.979257817 | 0.996158361 | 16 | 0 | KQK22981 | 0.970 | – | HORVU.MC |
| 0.957814774 | 0.987772926 | 16 | 0 | KQK19010 | 0.960 | 0 | genblast_C |
| 0.958614587 | 0.985512018 | 16 | 0 | KQK09504 | 0.936 | – | HORVU.MC |
| 0.945106423 | 0.976838945 | 16 | 0 | KQJ99969 | 0.967 | 0. | HORVU.MC |
| 0.942155657 | 0.982080112 | 16 | 0 | KQK11395 | 0.895 | – | HORVU.MC |
| 0.911481876 | 0.965229485 | 16 | 1 | KQK18445 | 0.921 | 0 | HORVU.MC |
| 0.912805746 | 0.940636586 | 16 | 2 | KQJ84597 | 0.801 | –3 | HORVU.MC |
| 0.927961889 | 0.974924054 | 16 | 2 | KQK03715 | 0.933 | 0 | HORVU.MC |
| 0.928419045 | 0.968131702 | 16 | 0 | KQJ90818 | 0.888 | –1 | HORVU.MC |
| 0.891110141 | 0.952048503 | 16 | 0 | KQJ83834 | 0.869 | –0 | HORVU.MC |
| 0.951844262 | 0.976393443 | 16 | 0 | KQJ82206 | 0.958 | 0. | HORVU.MC |
| 0.90118822 | 0.930067551 | 16 | 2 | genblast_Os05t051 |  |  | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.957180809 | 0.987582584 | 16 | 1 | KQJ84356 | 0.946 | −0 | HORVU.MC |
| 0.970301019 | 0.986967974 | 16 | 0 | KQK21951 | 0.974 | 0. | HORVU.MC |
| 0.957759989 | 0.984916645 | 16 | 0 | KQK00067 | 0.946 | − | HORVU.MC |

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| 0.963037128 | 0.983415002 | 16 | 0 | KQJ84550 | 0.955 | −0 | HORVU.MC |
| 0.917097127 | 0.965563208 | 16 | 0 | KQJ97260 | 0.858 | −1 | HORVU.MC |
| 0.892720884 | 0.956626506 | 16 | 1 | KQK17406 | 0.787 | − | genblast_Z |
| 0.882145923 | 0.94375037 | 16 | 2 | KQJ92508 | 0.802 | −1 | HORVU.MC |
| 0.897036415 | 0.96911157 | 16 | 0 | KQK07065 | 0.922 | 0. | HORVU.MC |
| 0.941422967 | 0.998573466 | 16 | 0 | KQK13341 | 0.899 | − | HORVU.MC |
| 0.96950526 | 1.003980665 | 16 | 0 | KQK01037 | 0.959 | − | HORVU.MC |
| 0.968842335 | 0.987708309 | 16 | 0 | KQK03304 | 0.971 | 0. | HORVU.MC |
| 0.952582616 | 1.004998611 | 16 | 0 | KQJ94051 | 0.923 | −0 | HORVU.MC |
| 0.946731772 | 0.966818333 | 16 | 0 | KQJ94847 | 0.925 | −1 | HORVU.MC |

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| 0.954138432 | 0.976238669 | 16 | 1 | KQK00017 | 0.942 | − | HORVU.MC |
| 0.960044565 | 0.993533729 | 16 | 0 | KQJ96848 | 0.947 | −0 | HORVU.MC |
| 0.940973684 | 0.961768421 | 16 | 0 | KQJ85143 | 0.928 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.952191428 | 0.9918266 | 16 | 3 | KQJ84949 | 0.951 | −0 | HORVU.MC |
| 0.990059669 | 1.003525902 | 16 | 0 | KQK04263 | 0.982 | − | HORVU.MC |
| 0.907711116 | 0.959446565 | 16 | 1 | KQJ92186 | 0.779 | −2 | HORVU.MC |
| 0.919438705 | 0.983471074 | 16 | 0 | KQK12617 | 0.904 | − | HORVU.MC |
| 0.965957762 | 0.986425936 | 16 | 0 | KQK01694 | 0.966 | − | HORVU.MC |

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| 0.942394578 | 0.969592656 | 16 | 0 | KQK05679 | 0.945 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.931391065 | 0.982839023 | 16 | 0 | KQJ92371 | 0.895 | −0 | HORVU.MC |
| 0.868679037 | 0.937026913 | 16 | 3 | KQJ82936 | 0.847 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.978492406 | 0.991749484 | 16 | 0 | KQK01011 | 0.972 | – | HORVU.MC |
| 0.976997307 | 1.002692998 | 16 | 1 | KQK23328 | 0.940 | – | HORVU.MC |
| 0.940696312 | 0.973105134 | 16 | 0 | KQK22016 | 0.917 | – | HORVU.MC |
| 0.973461553 | 0.99450762 | 16 | 0 | KQJ92133 | 0.979 | 0. | HORVU.MC |
| 0.921522504 | 0.990231495 | 16 | 1 | PNT65531 | 0.955 | 0. | HORVU.MC |
| 0.942867772 | 0.985119048 | 16 | 0 | KQK13024 | 0.939 | – | genblast_C |
| 0.961917154 | 0.980155832 | 16 | 0 | KQK24046 | 0.967 | 0. | HORVU.MC |
| 0.90819135 | 0.9491481 | 16 | 0 | KQJ89275 | 0.888 | –0 | HORVU.MC |
| 0.945873632 | 0.981471112 | 16 | 1 | KQJ86024 | 0.920 | –1 | HORVU.MC |
| 0.90774571 | 0.971101746 | 16 | 0 | KQJ81558 | 0.949 | 0. | HORVU.MC |
| 0.959530915 | 0.978791215 | 16 | 0 | KQJ93009 | 0.951 | –0 | HORVU.MC |
| 0.908408834 | 0.949655101 | 16 | 0 | KQJ83883 | 0.887 | –0 | HORVU.MC |
| 0.946723106 | 0.975915925 | 16 | 0 | KQK05349 | 0.922 | – | HORVU.MC |
| 0.950086764 | 0.986973472 | 16 | 0 | KQK00409 | 0.968 | 0. | HORVU.MC |
| 0.956894619 | 0.989237668 | 16 | 0 | KQK11711 | 0.947 | – | HORVU.MC |
| 0.957355898 | 0.997229669 | 16 | 0 | KQJ92913 | 0.925 | –1 | HORVU.MC |
| 0.951326977 | 0.979858016 | 16 | 0 | PNT74169 | 0.956 | 0. | HORVU.MC |
| 0.967316644 | 0.990463215 | 16 | 0 | KQK23934 | 0.956 | – | HORVU.MC |
| 0.924750533 | 0.98857404 | 16 | 0 | KQJ85320 | 0.851 | –1 | HORVU.MC |

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| 0.919332595 | 0.954738945 | 16 | 0 | KQJ94865 | 0.854 | –2 | HORVU.MC |
| 0.890195491 | 0.952519783 | 16 | 0 | KQJ92337 | 0.827 | –1 | HORVU.MC |
| 0.954756419 | 0.986042766 | 16 | 1 | KQK21463 | 0.963 | 0. | HORVU.MC |
| 0.959299279 | 0.975014673 | 16 | 0 | KQK14893 | 0.933 | – | HORVU.MC |
| | | | | | | | |
| 0.893765725 | 0.954710651 | 16 | 0 | KQK23774 | 0.804 | – | HORVU.MC |
| 0.980867866 | 0.99487096 | 16 | 0 | KQK06088 | 0.978 | – | HORVU.MC |
| | | | | | | | |
| 0.8525 | 0.899914163 | 16 | 0 | KQK00978 | 0.838 | – | HORVU.MC |
| 0.952443979 | 0.988672741 | 16 | 0 | KQK00650 | 0.983 | 0. | HORVU.MC |
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| 0.98805646 | 1.000434311 | 16 | 0 | KQK05788 | 0.977 | – | HORVU.MC |
| | | | | | | | |
| 0.977698158 | 0.995902318 | 16 | 6 | PNT76268 | 0.975 | – | genblast_C |
| 0.956939064 | 0.986559671 | 16 | 0 | KQK01688 | 0.957 | 0. | HORVU.MC |
| 0.948064231 | 0.988516849 | 16 | 0 | KQK22721 | 0.898 | – | HORVU.MC |

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| 0.93394796 | 0.956870086 | 16 | 0 | KQK22742 | 0.890 – | HORVU.MC |
| 0.958278877 | 0.982760767 | 16 | 5 | KQJ91503 | 0.969 0. | HORVU.MC |
| 0.882774437 | 0.945264921 | 16 | 0 | genblast_Os01t078 | | HORVU.MC |
| 0.950237265 | 0.992591618 | 16 | 2 | KQJ83073 | 0.963 0. | HORVU.MC |
| 0.871195652 | 0.979323671 | 16 | 1 | KQK18764 | 0.811 – | HORVU.MC |
| 0.974121981 | 0.996366817 | 16 | 0 | PNT73400 | 0.962 – | HORVU.MC |
| 0.977689873 | 1.000506329 | 16 | 0 | KQK22672 | 0.984 0 | HORVU.MC |
| 0.940068816 | 0.977501257 | 16 | 0 | KQJ96747 | 0.914 –1 | HORVU.MC |
| 0.896637609 | 0.96097966 | 16 | 2 | KQK19408 | 0.901 0 | HORVU.MC |
| 0.954805579 | 0.994390965 | 16 | 0 | KQK05511 | 0.924 – | HORVU.MC |
| 0.956235206 | 0.980706534 | 16 | 0 | KQJ97688 | 0.962 0. | HORVU.MC |
| 0.926565154 | 0.972822131 | 16 | 0 | KQK04485 | 0.933 0 | HORVU.MC |
| 0.896327893 | 0.958694362 | 16 | 0 | KQJ91133 | 0.872 –0 | HORVU.MC |

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| 0.878995235 | 0.933984193 | 16 | 4 | KQK11432 0.817 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.884508005 | 0.9465674 | 16 | 1 | KQJ98412 0.880 –0 | HORVU.MC |
| 0.92423904 | 0.964855849 | 16 | 0 | KQJ90707 0.913 –0 | HORVU.MC |
| 0.932041755 | 0.971974522 | 16 | 1 | KQK14956 0.869 – | HORVU.MC |
| 0.965023601 | 0.996853263 | 16 | 0 | KQK05647 0.975 0 | HORVU.MC |
| 0.890249625 | 0.956956957 | 16 | 0 | PNT63633 0.850 – | HORVU.MC |
| 0.911613004 | 0.950609565 | 16 | 0 | KQK22238 0.918 0 | HORVU.MC |
| 0.845761506 | 0.931361695 | 16 | 0 | KQJ99962 0.865 0. | HORVU.MC |
| 0.911454261 | 0.987099296 | 16 | 0 | KQK22865 0.884 – | HORVU.MC |
| 0.932153791 | 0.982081758 | 16 | 2 | KQJ82753 0.922 –0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.966653099 | 0.991303273 | 16 | 1 | genblast_Os10t042 | HORVU.MC |
| 0.931117958 | 0.974974849 | 16 | 0 | KQK09532 0.933 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.946241535 | 0.966772009 | 16 | 0 | KQK23732 0.940 – | genblast_C |
| 0.941403391 | 0.980970969 | 16 | 0 | KQK05552 0.868 – | HORVU.MC |
| 0.947927984 | 0.969268974 | 16 | 2 | KQJ83750 0.966 1. | HORVU.MC |
| 0.980031983 | 0.989936034 | 16 | 0 | KQJ82407 0.983 0. | HORVU.MC |
| 0.945307874 | 0.99003355 | 16 | 0 | KQJ92016 0.980 0. | HORVU.MC |
| 0.950127498 | 0.990778259 | 16 | 0 | KQK13752 0.947 – | HORVU.MC |
| 0.923935543 | 0.974392718 | 16 | 0 | KQJ86533 0.937 0. | HORVU.MC |
| 0.936892081 | 0.968074949 | 16 | 0 | KQJ85736 0.934 –0 | HORVU.MC |
| 0.907997197 | 0.945958573 | 16 | 0 | KQK20096 0.901 – | HORVU.MC |
| 0.943983534 | 0.9720076 | 16 | 0 | PNT62140 0.897 – | HORVU.MC |
| 0.935152974 | 0.965416156 | 16 | 1 | KQK03035 0.949 0 | HORVU.MC |
| 0.925821547 | 0.973960067 | 16 | 0 | KQK01378 0.941 0 | HORVU.MC |
| 0.864658637 | 0.944239422 | 16 | 7 | KQK10301 0.820 – | genblast_C |
| 0.91961326 | 0.996685083 | 16 | 0 | KQK02675 0.850 – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.942696209 | 0.98104423 | 16 | 0 | KQJ86487 | 0.918 | –1 | HORVU.MC |
| 0.926264591 | 0.994747082 | 16 | 0 | KQJ86662 | 0.855 | –2 | HORVU.MC |
| 0.97538108 | 0.993872456 | 16 | 0 | KQJ83214 | 0.969 | –0 | HORVU.MC |
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| | | | | | | | |
| 0.924798387 | 0.972952854 | 16 | 0 | PNT69411 | 0.935 | 0. | HORVU.MC |
| 0.907951207 | 0.960942451 | 16 | 1 | KQJ99238 | 0.881 | –0 | HORVU.MC |
| | | | | | | | |
| | | | | | | | |
| 0.969446871 | 0.991512731 | 16 | 0 | KQK00098 | 0.975 | 0 | HORVU.MC |
| 0.963650958 | 0.979437153 | 16 | 0 | KQJ91014 | 0.962 | –0 | HORVU.MC |
| 0.967717096 | 0.99745093 | 16 | 1 | KQJ96712 | 0.977 | 0. | HORVU.MC |
| 0.93327594 | 0.963182286 | 16 | 0 | KQK07599 | 0.917 | – | HORVU.MC |
| 0.956166044 | 0.985723752 | 16 | 0 | KQJ82282 | 0.968 | 0. | HORVU.MC |
| 0.930971705 | 0.981136918 | 16 | 3 | KQJ90538 | 0.944 | 0. | HORVU.MC |
| 0.933280591 | 0.973385265 | 16 | 0 | KQK01856 | 0.862 | – | HORVU.MC |
| 0.930452128 | 0.963829787 | 16 | 2 | KQK09772 | 0.912 | – | genblast_C |
| 0.967154117 | 0.984887962 | 16 | 0 | KQJ95837 | 0.971 | 0. | HORVU.MC |
| 0.970648308 | 1.005382545 | 16 | 0 | PNT65040 | 0.951 | – | HORVU.MC |
| 0.944975062 | 0.961895262 | 16 | 0 | KQK10755 | 0.951 | 0 | genblast_C |
| 0.938333723 | 0.979639597 | 16 | 0 | KQJ85195 | 0.944 | 0. | HORVU.MC |
| 0.978741978 | 0.988203096 | 16 | 0 | KQK15497 | 0.984 | 0 | HORVU.MC |
| 0.872844828 | 0.935172414 | 16 | 0 | KQK07328 | 0.839 | – | HORVU.MC |
| 0.906718202 | 0.976729359 | 16 | 3 | PNT70031 | 0.936 | 0. | HORVU.MC |
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| 0.885820664 | 0.944461682 | 16 | 2 | KQJ94996 | 0.848 | –1 | HORVU.MC |
| 0.901613045 | 0.978174603 | 16 | 3 | KQK09117 | 0.900 | – | HORVU.MC |
| 0.962404113 | 1.002983166 | 16 | 0 | KQK21887 | 0.975 | 0 | HORVU.MC |
| 0.928054494 | 0.965500776 | 16 | 0 | KQJ91251 | 0.930 | 0. | genblast_C |
| 0.926220074 | 0.986740331 | 16 | 0 | KQK01030 | 0.858 | – | HORVU.MC |
| 0.946648794 | 0.991544648 | 16 | 0 | KQK20617 | 0.961 | 0 | HORVU.MC |
| 0.903474237 | 0.977206797 | 16 | 0 | KQJ93125 | 0.889 | –0 | HORVU.MC |
| 0.974660218 | 0.988655669 | 16 | 0 | KQK11053 | 0.965 | – | HORVU.MC |
| 0.88930184 | 0.971715795 | 16 | 2 | KQJ85186 | 0.897 | 0. | HORVU.MC |
| 0.924491393 | 0.962276583 | 16 | 2 | PNT67575 | 0.938 | 0. | HORVU.MC |
| 0.944625752 | 0.993303382 | 16 | 2 | KQK02465 | 0.956 | 0 | HORVU.MC |
| 0.919507737 | 0.988437341 | 16 | 1 | KQJ97762 | 0.895 | –0 | HORVU.MC |
| 0.980346919 | 0.988549043 | 16 | 0 | KQK13184 | 0.975 | – | HORVU.MC |
| 0.913079976 | 0.969300541 | 16 | 0 | KQJ83233 | 0.857 | –1 | HORVU.MC |
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| 0.949261231 | 0.98213361 | 16 | 0 | KQJ89478 | 0.939 | –0 | HORVU.MC |
| 0.943754599 | 0.991537896 | 16 | 0 | KQK21754 | 0.940 | – | HORVU.MC |

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| 0.911018897 | 0.982124617 | 16 | 1 | PNT77839 | 0.949 | 0. | HORVU.MC |
| 0.90722541 | 0.967409836 | 16 | 0 | KQK05825 | 0.935 | 0. | HORVU.MC |
| 0.930802396 | 0.979989468 | 16 | 0 | KQJ83606 | 0.895 | –0 | HORVU.MC |
| 0.843242801 | 0.881937173 | 16 | 2 | KQK14505 | 0.820 | – | HORVU.MC |
| 0.96575827 | 0.985590106 | 16 | 1 | KQJ94840 | 0.951 | –0 | HORVU.MC |
| 0.937402724 | 0.990661479 | 16 | 1 | KQK21958 | 0.936 | – | HORVU.MC |
| 0.959152588 | 0.978395961 | 16 | 1 | KQK21360 | 0.947 | – | HORVU.MC |
| 0.989863299 | 1.016218721 | 16 | 0 | KQJ95816 | 0.986 | –0 | HORVU.MC |
| 0.840156362 | 0.910705422 | 16 | 2 | PNT64014 | 0.741 | – | HORVU.MC |
| 0.854541466 | 0.931987714 | 16 | 0 | KQK02944 | 0.784 | – | HORVU.MC |
| 0.936502097 | 0.987619241 | 16 | 0 | KQK12164 | 0.909 | – | HORVU.MC |
| 0.897953722 | 0.948616601 | 16 | 0 | KQK20198 | 0.897 | – | HORVU.MC |
| 0.881473377 | 0.936907367 | 16 | 1 | KQJ90368 | 0.847 | –0 | HORVU.MC |
| 0.92611026 | 0.984686064 | 16 | 0 | KQK01814 | 0.909 | – | HORVU.MC |

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| 0.954038175 | 0.985078339 | 16 | 0 | KQK01766 | 0.941 | – | HORVU.MC |
| 0.957297339 | 0.98360929 | 16 | 0 | KQK17586 | 0.937 | – | HORVU.MC |
| 0.953913224 | 0.989412497 | 16 | 1 | KQK11259 | 0.953 | – | HORVU.MC |
| 0.914329579 | 0.957210777 | 16 | 0 | KQJ90050 | 0.871 | –1 | HORVU.MC |
| 0.939112423 | 0.968247668 | 16 | 0 | KQJ82656 | 0.939 | 0. | HORVU.MC |
| 0.962098102 | 0.981406159 | 16 | 0 | KQK09757 | 0.957 | – | HORVU.MC |
| 0.920380589 | 0.965761177 | 16 | 0 | KQJ83654 | 0.910 | –0 | genblast_C |
| 0.950910344 | 0.994197011 | 16 | 1 | KQK23338 | 0.945 | – | HORVU.MC |
| 0.970479543 | 0.999299426 | 16 | 0 | PNT64693 | 0.938 | – | HORVU.MC |
| 0.847314141 | 0.929516876 | 16 | 2 | KQK19627 | 0.822 | – | HORVU.MC |
| 0.907598784 | 0.952279635 | 16 | 0 | KQJ97687 | 0.841 | –1 | HORVU.MC |
| 0.974024804 | 0.998291237 | 16 | 0 | KQJ92122 | 0.965 | –0 | HORVU.MC |
| 0.940612102 | 0.980828119 | 16 | 0 | KQK04677 | 0.876 | – | HORVU.MC |
| 0.838051091 | 0.909333104 | 16 | 0 | KQJ97586 | 0.779 | –1 | HORVU.MC |
| 0.888255701 | 0.949741824 | 16 | 3 | KQJ97177 | 0.885 | –0 | HORVU.MC |
| 0.977710323 | 0.992582808 | 16 | 0 | KQK15691 | 0.967 | – | HORVU.MC |
| 0.92910394 | 0.969973676 | 16 | 0 | KQJ82009 | 0.907 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.964211466 | 0.992211291 | 16 | 0 | KQK01419 | 0.971 | 0. | HORVU.MC |
| 0.929854539 | 0.984928146 | 16 | 0 | KQJ92115 | 0.841 | –2 | HORVU.MC |
| 0.940825315 | 0.978916089 | 16 | 0 | KQK11722 | 0.897 | – | HORVU.MC |
| 0.926408316 | 0.967325975 | 16 | 0 | KQK02563 | 0.860 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.952581555 | 0.986864825 | 16 | 1 | KQJ94221 | 0.943 | −0 | HORVU.MC |
| 0.921305069 | 0.973945997 | 16 | 0 | KQJ95952 | 0.931 | 0. | HORVU.MC |
| 0.934451747 | 0.966447596 | 16 | 0 | KQJ90904 | 0.946 | 0. | HORVU.MC |
| 0.926983093 | 0.962977813 | 16 | 1 | KQK16849 | 0.928 | 0 | HORVU.MC |
| 0.9655544 | 0.988406659 | 16 | 0 | KQJ84329 | 0.944 | −1 | HORVU.MC |
| 0.966434216 | 0.990527528 | 16 | 1 | KQJ86089 | 0.957 | −0 | HORVU.MC |
| 0.869574716 | 0.941450626 | 16 | 1 | KQJ92774 | 0.878 | 0. | HORVU.MC |
| 0.969692926 | 0.982974659 | 16 | 0 | KQK13638 | 0.965 | − | HORVU.MC |
| 0.881513648 | 0.936972705 | 16 | 0 | KQJ99272 | 0.791 | −1 | HORVU.MC |
| 0.923394994 | 0.979610452 | 16 | 0 | KQK13472 | 0.941 | 0 | HORVU.MC |
| 0.958458987 | 0.984663105 | 16 | 0 | KQJ83160 | 0.969 | 0. | HORVU.MC |
| 0.965849783 | 0.979265781 | 16 | 0 | KQK18550 | 0.976 | 0 | HORVU.MC |
| 0.938155922 | 0.974362819 | 16 | 0 | KQK15678 | 0.943 | 0 | HORVU.MC |
| 0.903064067 | 0.944916435 | 16 | 1 | KQK05398 | 0.864 | − | HORVU.MC |
| 0.947063658 | 0.983861327 | 16 | 0 | KQK17385 | 0.935 | − | HORVU.MC |
| 0.935979081 | 0.986466263 | 16 | 1 | KQJ84978 | 0.919 | −0 | HORVU.MC |
| 0.9519132 | 0.975089882 | 16 | 0 | KQK10378 | 0.946 | − | HORVU.MC |
| 0.942005851 | 0.979365878 | 16 | 0 | KQJ89290 | 0.924 | −0 | HORVU.MC |
| 0.928194275 | 0.966545012 | 16 | 1 | KQK08256 | 0.933 | 0 | HORVU.MC |
| 0.941130271 | 0.974755655 | 16 | 3 | KQK11041 | 0.937 | − | HORVU.MC |
| 0.921041135 | 0.972135638 | 16 | 1 | PNT66434 | 0.936 | 0. | HORVU.MC |
| 0.963619738 | 0.988237825 | 16 | 1 | KQK01178 | 0.964 | 0 | HORVU.MC |
| 0.928541879 | 0.995290224 | 16 | 0 | KQK23987 | 0.881 | − | HORVU.MC |
| 0.950834025 | 0.967105946 | 16 | 0 | PNT65832 | 0.919 | − | HORVU.MC |
| 0.961234533 | 0.981327334 | 16 | 0 | KQJ85262 | 0.978 | 0. | HORVU.MC |
| 0.925479292 | 0.96457661 | 16 | 2 | KQK01764 | 0.926 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.974645008 | 0.986108058 | 16 | 0 | KQK23395 | 0.978 | 0. | HORVU.MC |
| 0.873963237 | 0.925577225 | 16 | 0 | KQJ91780 | 0.889 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.985052478 | 0.997935306 | 16 | 0 | KQJ95027 | 0.990 | 0. | HORVU.MC |
| 0.917717703 | 0.967931169 | 16 | 0 | KQK06197 | 0.923 | 0 | HORVU.MC |
| 0.93809128 | 0.973960285 | 16 | 0 | KQJ90461 | 0.948 | 0. | genblast_C |
| 0.920974483 | 0.995600528 | 16 | 0 | KQK15675 | 0.860 | - | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.897669092 | 0.980732956 | 16 | 1 | KQK11698 | 0.916 | 0. | HORVU.MC |
| 0.942407934 | 0.980368264 | 16 | 0 | KQK14320 | 0.916 | – | HORVU.MC |
| 0.962052484 | 0.981612275 | 16 | 0 | KQJ83908 | 0.948 | –0 | HORVU.MC |
| 0.891386416 | 0.947058116 | 16 | 0 | KQK10500 | 0.813 | – | HORVU.MC |
| 0.947270889 | 0.967589245 | 16 | 0 | PNT78229 | 0.950 | 0. | HORVU.MC |
| 0.932616706 | 0.978539714 | 16 | 3 | KQJ89086 | 0.940 | 0. | HORVU.MC |
| 0.950488513 | 0.982567504 | 16 | 0 | PNT64614 | 0.934 | – | HORVU.MC |
| 0.941403501 | 1.001583392 | 16 | 0 | KQJ84175 | 0.930 | –0 | HORVU.MC |
| 0.896528082 | 0.954804739 | 16 | 0 | PNT64894 | 0.855 | – | HORVU.MC |
| 0.963867995 | 0.980988593 | 16 | 7 | KQJ82537 | 0.961 | –0 | HORVU.MC |
| 0.937530667 | 0.969741577 | 16 | 0 | KQK16650 | 0.956 | 0 | HORVU.MC |
| 0.931088475 | 0.977179469 | 16 | 1 | PNT65996 | 0.824 | – | HORVU.MC |
| 0.977451561 | 0.992249731 | 16 | 0 | KQJ98828 | 0.968 | –0 | HORVU.MC |
| 0.938990871 | 0.988172256 | 16 | 0 | KQK01448 | 0.940 | 0 | HORVU.MC |
| 0.962761085 | 0.998351044 | 16 | 0 | KQK15877 | 0.952 | – | HORVU.MC |
| 0.973880597 | 0.998747521 | 16 | 0 | KQJ88458 | 0.962 | –0 | HORVU.MC |
| 0.966951336 | 0.995256773 | 16 | 1 | KQK03062 | 0.990 | 0 | genblast_C |
| 0.898890875 | 0.96327446 | 16 | 0 | KQK10802 | 0.897 | – | HORVU.MC |
| 0.941955576 | 0.985141828 | 16 | 0 | KQK04181 | 0.936 | – | genblast_C |
| 0.940593047 | 0.979345603 | 16 | 0 | KQK22562 | 0.933 | – | HORVU.MC |
| 0.934309115 | 0.980151089 | 16 | 2 | KQK16165 | 0.927 | – | HORVU.MC |
| 0.866589027 | 0.912784679 | 16 | 1 | KQK03857 | 0.821 | – | HORVU.MC |
| 0.89681202 | 0.934174279 | 16 | 6 | KQJ94887 | 0.895 | –0 | HORVU.MC |
| 0.931260858 | 0.962715488 | 16 | 0 | KQK04963 | 0.887 | – | HORVU.MC |
| 0.915278412 | 0.955271565 | 16 | 0 | KQK06201 | 0.885 | – | HORVU.MC |

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| 0.942582928 | 0.969161428 | 16 | 1 | KQJ98959 0.951 0. | HORVU.MC |
| 0.94176252 | 0.985850977 | 16 | 0 | genblast_Os06t030 | HORVU.MC |
| 0.976967193 | 0.99802664 | 16 | 0 | KQJ82179 0.965 –0 | HORVU.MC |
| 0.978226817 | 0.999197995 | 16 | 0 | KQK17502 0.968 – | HORVU.MC |
| 0.929580116 | 0.975444015 | 16 | 2 | KQK01761 0.915 – | HORVU.MC |
| 0.941959005 | 0.990388881 | 16 | 3 | KQJ98841 0.953 0. | HORVU.MC |
| 0.983420026 | 0.997355873 | 16 | 0 | KQK09863 0.981 – | HORVU.MC |
| 0.978194156 | 0.995159059 | 16 | 0 | KQK22175 0.968 – | HORVU.MC |
| 0.947207724 | 0.975887265 | 16 | 1 | KQJ84480 0.903 –1 | HORVU.MC |
| 0.966104231 | 0.991432747 | 16 | 0 | KQJ93234 0.956 –0 | HORVU.MC |
| 0.978498819 | 0.992576346 | 16 | 2 | KQJ91349 0.976 –0 | HORVU.MC |
| 0.945180976 | 1.002244669 | 16 | 0 | KQK17657 0.974 0 | HORVU.MC |
| 0.952304996 | 0.975916607 | 16 | 0 | KQK17615 0.952 – | HORVU.MC |
| 0.878044872 | 0.937475345 | 16 | 3 | KQK22936 0.850 – | HORVU.MC |
| 0.943209877 | 0.977387914 | 16 | 0 | KQJ85974 0.883 –2 | HORVU.MC |
| 0.871387327 | 0.956087824 | 16 | 3 | KQK12284 0.895 0 | genblast_C |
| 0.910296902 | 0.948925977 | 16 | 1 | KQJ90552 0.903 –0 | HORVU.MC |
| 0.955660927 | 0.97479411 | 16 | 0 | KQK16072 0.930 – | HORVU.MC |
| 0.980616175 | 1.003979461 | 16 | 0 | KQK15466 0.969 – | HORVU.MC |
| 0.947559307 | 0.980109489 | 16 | 0 | KQJ91236 0.930 –0 | HORVU.MC |
| 0.913522454 | 0.949318364 | 16 | 1 | KQK07265 0.935 0 | HORVU.MC |

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| 0.915798488 | 0.956626506 | 16 | 2 | KQK09159 0.928 0. | HORVU.MC |
| 0.970830838 | 0.994251497 | 16 | 1 | KQK16410 0.977 0. | HORVU.MC |
| 0.949137799 | 0.989178889 | 16 | 3 | KQJ97970 0.950 0. | HORVU.MC |

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| 0.959489711 | 0.974304783 | 16 | 0 | KQJ84139 0.962 0. | HORVU.MC |
| 0.862072588 | 0.929527673 | 16 | 8 | PNT65897 0.916 0. | HORVU.MC |
| 0.929536821 | 0.967855056 | 16 | 1 | KQJ99897 0.916 -0 | HORVU.MC |

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| 0.937066606 | 0.963086548 | 16 | 0 | KQJ88573 0.900 -1 | HORVU.MC |
| 0.94259844 | 0.984695394 | 16 | 0 | KQJ93417 0.816 -2 | HORVU.MC |
| 0.89039014 | 0.960652014 | 16 | 0 | KQJ81469 0.870 -0 | HORVU.MC |
| 0.952997719 | 0.991854024 | 16 | 0 | KQK13892 0.931 - | HORVU.MC |
| 0.890762195 | 0.927317073 | 16 | 0 | KQK13012 0.885 - | HORVU.MC |

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| 0.954531761 | 0.996212773 | 16 | 1 | KQK00364 0.935 - | HORVU.MC |
| 0.923755012 | 0.992576714 | 16 | 7 | KQJ86104 0.919 -0 | HORVU.MC |
| 0.948345955 | 0.974521545 | 16 | 0 | KQJ87857 0.952 0. | HORVU.MC |
| 0.957821623 | 0.984497685 | 16 | 0 | KQJ98861 0.961 0. | HORVU.MC |
| 0.952203792 | 0.974302121 | 16 | 1 | KQK23492 0.928 - | HORVU.MC |
| 0.933012341 | 0.987035652 | 16 | 3 | KQK08518 0.921 - | HORVU.MC |
| 0.955858203 | 0.991562376 | 16 | 1 | KQK19159 0.957 0 | HORVU.MC |
| 0.931090481 | 0.966429064 | 16 | 0 | genblast_Os01t071 | HORVU.MC |
| 0.947669268 | 0.990673962 | 16 | 1 | KQJ91055 0.931 -0 | HORVU.MC |
| 0.972829093 | 0.984636185 | 16 | 0 | KQK13972 0.973 0 | HORVU.MC |
| 0.892399966 | 0.971515768 | 16 | 0 | KQJ90474 0.947 1. | HORVU.MC |

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| 0.902993487 | 0.967363298 | 16 | 2 | PNT76082 | 0.826 | -1 | HORVU.MC |
| 0.96828882 | 0.986541674 | 16 | 0 | KQK00494 | 0.933 | -2 | HORVU.MC |
| 0.94 | 0.968545455 | 16 | 1 | KQK22549 | 0.883 | -2 | HORVU.MC |
| 0.883142143 | 0.95607073 | 16 | 7 | KQK01342 | 0.867 | - | HORVU.MC |
| 0.941301947 | 0.969885565 | 16 | 1 | KQK03522 | 0.954 | 0. | HORVU.MC |
| 0.948717427 | 1.001302932 | 16 | 1 | KQJ94414 | 0.927 | -0 | genblast_C |
| 0.968216116 | 0.994115414 | 16 | 1 | PNT68523 | 0.955 | - | genblast_C |
| 0.97014663 | 0.981456402 | 16 | 0 | KQJ89214 | 0.957 | -0 | HORVU.MC |
| 0.947669617 | 0.983144164 | 16 | 2 | KQK14701 | 0.918 | - | HORVU.MC |
| 0.929543206 | 0.98878628 | 16 | 0 | KQK07450 | 0.934 | 0. | HORVU.MC |
| 0.928847905 | 0.995992714 | 16 | 0 | KQJ83724 | 0.907 | -0 | HORVU.MC |
| 0.898717065 | 0.966973039 | 16 | 5 | PNT62821 | 0.917 | 0. | HORVU.MC |
| 0.924556213 | 0.958086785 | 16 | 2 | KQK01301 | 0.917 | - | HORVU.MC |

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| 0.947930726 | 0.984200079 | 16 | 0 | KQK13847 | 0.909 | – | HORVU.MC |
| 0.925129333 | 0.975271599 | 16 | 0 | KQJ85078 | 0.904 | –0 | HORVU.MC |
| 0.873871746 | 0.965994962 | 16 | 0 | KQJ91890 | 0.861 | –0 | HORVU.MC |
| 0.925320657 | 0.967034203 | 16 | 0 | KQK02993 | 0.945 | 0. | HORVU.MC |
| 0.911004921 | 0.976381529 | 16 | 1 | KQK22196 | 0.881 | – | HORVU.MC |
| 0.9587075 | 0.988704394 | 16 | 0 | KQK03006 | 0.960 | 0. | HORVU.MC |
| 0.958314136 | 0.993457427 | 16 | 0 | KQK13688 | 0.972 | 0. | genblast_Z |
| 0.902873281 | 0.962671906 | 16 | 1 | PNT61725 | 0.897 | – | HORVU.MC |
| 0.962938717 | 0.987596472 | 16 | 0 | KQK01711 | 0.944 | – | HORVU.MC |
| 0.922451941 | 0.959083986 | 16 | 2 | KQK06929 | 0.917 | – | HORVU.MC |

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| 0.922656076 | 0.96636967 | 16 | 1 | KQK16131 | 0.943 | 0 | HORVU.MC |
| 0.936555438 | 0.98700565 | 16 | 0 | KQJ91116 | 0.936 | –0 | HORVU.MC |
| 0.876804829 | 0.968052444 | 16 | 2 | KQJ91623 | 0.895 | 0. | HORVU.MC |
| 0.937720536 | 0.957982737 | 16 | 1 | KQK21752 | 0.911 | – | HORVU.MC |
| 0.919077365 | 0.938446464 | 16 | 0 | KQK08403 | 0.896 | – | HORVU.MC |
| 0.964133648 | 0.978468055 | 16 | 0 | KQK08823 | 0.965 | 0 | genblast_C |
| 0.977687784 | 0.999312147 | 16 | 0 | KQK10435 | 0.971 | – | HORVU.MC |
| 0.937170802 | 0.980644752 | 16 | 2 | KQJ82124 | 0.955 | 0. | HORVU.MC |
| 0.949127615 | 0.985025737 | 16 | 0 | KQJ92605 | 0.937 | –0 | HORVU.MC |
| 0.910754312 | 0.965132931 | 16 | 2 | KQK21115 | 0.904 | – | HORVU.MC |
| 0.916140467 | 0.947269303 | 16 | 1 | KQK12843 | 0.887 | – | HORVU.MC |
| 0.956973574 | 0.978299776 | 16 | 0 | KQJ85864 | 0.950 | –0 | HORVU.MC |

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| 0.962653048 | 0.990684056 | 16 | 0 | KQK09895 0.970 0 | HORVU.MC |
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| 0.924396769 | 0.977399628 | 16 | 0 | KQK21446 0.877 – | HORVU.MC |
| 0.98639749 | 1.009832697 | 16 | 0 | KQK12962 0.978 –0 | HORVU.MC |
| 0.909688542 | 0.966050318 | 16 | 0 | KQJ96226 0.876 –0 | HORVU.MC |
| 0.905481451 | 0.971238016 | 16 | 0 | KQK11000 0.897 –0 | HORVU.MC |
| 0.924629712 | 0.962098926 | 16 | 1 | genblast_Os08t050 | HORVU.MC |
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| 0.910890225 | 0.96468491 | 16 | 1 | KQK15758 0.857 – | HORVU.MC |
| 0.970936469 | 0.993976898 | 16 | 2 | KQK10813 0.974 0 | HORVU.MC |
| 0.926142769 | 0.965153223 | 16 | 0 | KQJ95933 0.898 –0 | HORVU.MC |
| 0.949902817 | 0.967499363 | 16 | 1 | KQJ82956 0.948 –0 | HORVU.MC |
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| 0.84087132 | 0.911918329 | 16 | 0 | KQK09455 0.756 – | HORVU.MC |
| 0.975225752 | 0.993236437 | 16 | 0 | KQK22669 0.965 –0 | HORVU.MC |
| 0.965934053 | 0.979715835 | 16 | 0 | KQK14962 0.950 – | HORVU.MC |
| 0.955234554 | 0.99020595 | 16 | 0 | genblast_Zm00001 | HORVU.MC |
| 0.967100801 | 0.990439894 | 16 | 2 | KQK13177 0.960 –0 | HORVU.MC |
| 0.860145336 | 0.970995427 | 16 | 8 | KQK07321 0.917 0 | HORVU.MC |
| 0.957490593 | 0.995484478 | 16 | 0 | KQK13413 0.952 –0 | HORVU.MC |
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| 0.969007434 | 0.992063492 | 16 | 1 | KQJ97835 0.969 0. | HORVU.MC |
| 0.948334527 | 0.970487106 | 16 | 0 | KQK21566 0.943 –0 | HORVU.MC |
| 0.94011716 | 0.972727985 | 16 | 3 | KQK24179 0.940 –0 | HORVU.MC |
| 0.928263458 | 1.009641873 | 16 | 2 | KQK20523 0.950 0 | HORVU.MC |
| 0.916865522 | 0.977445924 | 16 | 0 | KQJ99620 0.905 –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.975029046 | 0.994805905 | 16 | 0 | KQK09810 | 0.947 | – | HORVU.MC |
| 0.947528851 | 0.977551182 | 16 | 0 | KQK22959 | 0.934 | – | HORVU.MC |
| 0.931679894 | 1.014109347 | 16 | 0 | KQK01149 | 0.901 | – | HORVU.MC |
| 0.900623053 | 0.964931019 | 16 | 4 | PNT65488 | 0.814 | – | HORVU.MC |
| 0.893958919 | 0.949859419 | 16 | 1 | KQK20849 | 0.890 | – | HORVU.MC |
| 0.958824706 | 0.982327976 | 16 | 0 | KQJ87838 | 0.925 | –1 | HORVU.MC |
| 0.923159879 | 0.959894295 | 16 | 1 | KQJ81544 | 0.908 | –0 | HORVU.MC |
| 0.947935051 | 0.972114366 | 16 | 0 | KQK21856 | 0.949 | 0 | HORVU.MC |
| 0.895811269 | 0.958271553 | 16 | 0 | KQK18514 | 0.937 | 0 | genblast_C |
| 0.940011739 | 0.959881232 | 16 | 0 | KQJ91857 | 0.921 | –1 | HORVU.MC |
| 0.906259735 | 0.959657321 | 16 | 3 | KQK09711 | 0.929 | 0 | HORVU.MC |
| 0.892783594 | 0.929637893 | 16 | 0 | KQK04595 | 0.836 | – | HORVU.MC |
| 0.950588413 | 0.996680748 | 16 | 1 | KQK18894 | 0.892 | – | HORVU.MC |
| 0.928819801 | 0.9785465 | 16 | 2 | PNT73053 | 0.880 | – | HORVU.MC |
| 0.946168809 | 0.984945873 | 16 | 1 | KQJ88557 | 0.949 | 0. | HORVU.MC |
| 0.972489661 | 0.989971569 | 16 | 1 | PNT61865 | 0.977 | 0. | HORVU.MC |
| 0.884064269 | 0.931061885 | 16 | 0 | KQK21245 | 0.884 | 0 | HORVU.MC |
| 0.951683793 | 0.98967566 | 16 | 0 | PNT66576 | 0.945 | – | HORVU.MC |
| 0.864191791 | 0.928246988 | 16 | 6 | KQK03474 | 0.921 | 0 | HORVU.MC |
| 0.944158433 | 0.972118959 | 16 | 0 | KQJ96210 | 0.913 | –1 | HORVU.MC |
| 0.880140693 | 0.916961826 | 16 | 0 | KQJ83946 | 0.896 | 0. | HORVU.MC |
| 0.953483026 | 0.984578917 | 16 | 2 | KQJ97187 | 0.968 | 0. | HORVU.MC |
| 0.869414894 | 0.958865248 | 16 | 0 | PNT64499 | 0.959 | 1. | HORVU.MC |
| 0.931319589 | 0.978297792 | 16 | 1 | KQJ97636 | 0.911 | –0 | HORVU.MC |

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| 0.861550765 | 0.914694321 | 16 | 4 | KQJ99389 | 0.823 | –0 | HORVU.MC |
| 0.914910386 | 0.963360143 | 16 | 0 | KQK03485 | 0.879 | – | HORVU.MC |
| 0.938170966 | 0.975644929 | 16 | 0 | KQJ88510 | 0.922 | –0 | HORVU.MC |
| 0.956562149 | 0.982603816 | 16 | 0 | KQJ99354 | 0.941 | –0 | HORVU.MC |
| 0.965779634 | 0.995387196 | 16 | 0 | KQK09373 | 0.958 | – | HORVU.MC |
| 0.926232474 | 0.982541836 | 16 | 0 | KQJ90754 | 0.894 | –0 | HORVU.MC |
| 0.94542077 | 0.981777437 | 16 | 1 | KQK13959 | 0.948 | 0 | HORVU.MC |
| 0.950885701 | 0.981083681 | 16 | 0 | KQJ98141 | 0.954 | 0. | HORVU.MC |
| 0.950712251 | 1.003418803 | 16 | 0 | KQJ93222 | 0.963 | 0. | HORVU.MC |
| 0.979427515 | 0.997851838 | 16 | 0 | KQJ97042 | 0.965 | –1 | HORVU.MC |
| 0.923127344 | 0.965550118 | 16 | 0 | KQK16088 | 0.951 | 0 | HORVU.MC |
| 0.923426377 | 0.974147621 | 16 | 1 | KQJ83173 | 0.903 | –0 | genblast_C |
| 0.877260209 | 0.951819295 | 16 | 0 | KQK18673 | 0.837 | – | HORVU.MC |
| 0.955187284 | 0.978018728 | 16 | 0 | KQJ87061 | 0.935 | –1 | HORVU.MC |
| 0.953835809 | 0.988188516 | 16 | 0 | KQK17685 | 0.988 | 1 | HORVU.MC |
| 0.976936219 | 0.996013667 | 16 | 0 | KQJ82471 | 0.967 | –0 | HORVU.MC |
| 0.934754258 | 0.976965621 | 16 | 3 | KQK18254 | 0.951 | 0 | HORVU.MC |
| 0.960330551 | 0.993335129 | 16 | 2 | KQK05789 | 0.977 | 0 | HORVU.MC |
| 0.885314462 | 0.974686028 | 16 | 0 | KQK06847 | 0.857 | – | HORVU.MC |
| 0.888420245 | 0.931931055 | 16 | 1 | PNT64438 | 0.883 | – | HORVU.MC |
| 0.966650804 | 0.985754636 | 16 | 0 | PNT77316 | 0.956 | – | HORVU.MC |
| 0.948339927 | 0.97433704 | 16 | 0 | KQJ94763 | 0.865 | –3 | HORVU.MC |
| 0.979741345 | 1.004742333 | 16 | 0 | KQJ85828 | 0.933 | –2 | HORVU.MC |
| 0.958825307 | 0.982893269 | 16 | 0 | KQK18778 | 0.966 | 0 | HORVU.MC |
| 0.938901736 | 0.975671566 | 16 | 0 | KQK01986 | 0.873 | – | HORVU.MC |
| 0.955503861 | 0.978222134 | 16 | 0 | KQJ86073 | 0.954 | –0 | HORVU.MC |
| 0.95938002 | 0.981942059 | 16 | 0 | KQK21286 | 0.928 | – | HORVU.MC |

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| 0.914173316 | 0.960894405 | 16 | 0 | KQK11990 | 0.873 | – | HORVU.MC |
| 0.941725261 | 0.980776674 | 16 | 0 | KQJ97810 | 0.930 | –0 | HORVU.MC |
| 0.950019929 | 0.976995786 | 16 | 0 | KQJ84286 | 0.897 | –1 | HORVU.MC |
| 0.969134174 | 0.997889908 | 16 | 0 | KQK01942 | 0.874 | – | HORVU.MC |
| 0.917952351 | 0.980058774 | 16 | 0 | KQJ86661 | 0.938 | 0. | HORVU.MC |
| 0.957628143 | 0.978723404 | 16 | 0 | KQJ95832 | 0.955 | –0 | HORVU.MC |
| 0.940154417 | 0.969731366 | 16 | 0 | KQK16331 | 0.933 | – | HORVU.MC |
| 0.954798211 | 0.987082473 | 16 | 1 | KQK22236 | 0.958 | 0 | HORVU.MC |
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| 0.958719136 | 1.000661376 | 16 | 0 | PNT73951 | 0.969 | 0. | HORVU.MC |
| 0.975147499 | 0.995150731 | 16 | 0 | KQK22322 | 0.972 | – | HORVU.MC |
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| 0.876350907 | 0.960925585 | 16 | 4 | KQJ98885 | 0.878 | 0. | HORVU.MC |
| 0.940427581 | 0.995993837 | 16 | 0 | KQK08379 | 0.868 | – | genblast_C |
| 0.894180365 | 0.972948486 | 16 | 0 | KQK05337 | 0.817 | – | HORVU.MC |
| 0.978106595 | 0.992758521 | 16 | 0 | KQK01305 | 0.956 | – | HORVU.MC |
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| 0.956855011 | 0.987547974 | 16 | 0 | KQK10595 | 0.942 | – | HORVU.MC |
| 0.827560666 | 0.889390519 | 16 | 0 | KQJ86016 | 0.760 | –1 | genblast_C |
| 0.952018328 | 0.984679554 | 16 | 0 | KQJ82144 | 0.956 | 0. | HORVU.MC |
| 0.959863299 | 0.991859848 | 16 | 0 | KQK10123 | 0.931 | – | HORVU.MC |
| 0.965214525 | 0.995411587 | 16 | 1 | PNT73850 | 0.949 | – | HORVU.MC |
| 0.910180055 | 0.99401662 | 16 | 5 | KQK20826 | 0.926 | 0 | HORVU.MC |
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| 0.88525549 | 0.968590753 | 16 | 3 | KQK15256 | 0.841 | – | HORVU.MC |

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| 0.98092306 | 0.992707791 | 16 | 0 | KQJ97532 | 0.970 | −1 | HORVU.MC |
| 0.967175126 | 0.979211663 | 16 | 0 | KQJ88691 | 0.967 | −0 | HORVU.MC |
| 0.937196762 | 0.977611504 | 16 | 1 | KQJ83284 | 0.935 | −0 | HORVU.MC |
| 0.966485835 | 1.000964436 | 16 | 1 | KQK23994 | 0.933 | − | HORVU.MC |
| 0.938152436 | 0.976311563 | 16 | 0 | KQJ99892 | 0.927 | −0 | HORVU.MC |
| 0.97266248 | 0.984449761 | 16 | 0 | KQK14945 | 0.974 | 0. | HORVU.MC |
| 0.949361928 | 0.974376219 | 16 | 0 | KQK08665 | 0.948 | − | HORVU.MC |
| 0.94103952 | 0.98616615 | 16 | 0 | KQJ97786 | 0.887 | −1 | HORVU.MC |
| 0.957458405 | 0.984165232 | 16 | 0 | KQK17489 | 0.956 | − | HORVU.MC |
| 0.961854065 | 0.983336139 | 16 | 0 | KQJ84065 | 0.944 | −1 | HORVU.MC |
| 0.944414737 | 0.986998826 | 16 | 0 | KQK19230 | 0.941 | − | HORVU.MC |
| 0.922965503 | 0.964659918 | 16 | 0 | KQK12220 | 0.888 | − | HORVU.MC |
| 0.915072934 | 0.964181524 | 16 | 1 | KQK20515 | 0.928 | 0. | HORVU.MC |
| 0.921229992 | 0.975344004 | 16 | 2 | KQJ81652 | 0.927 | 0. | HORVU.MC |
| 0.943561842 | 0.967818478 | 16 | 0 | KQK08434 | 0.907 | − | HORVU.MC |
| 0.935997209 | 0.98053528 | 16 | 0 | KQK20713 | 0.967 | 0. | HORVU.MC |
| 0.930479003 | 0.971566054 | 16 | 0 | KQK14102 | 0.934 | 0. | HORVU.MC |
| 0.943326423 | 0.981984558 | 16 | 0 | KQK03180 | 0.940 | − | genblast_C |
| 0.966047177 | 0.985704074 | 16 | 0 | KQK21549 | 0.957 | − | HORVU.MC |
| 0.982317555 | 0.992448167 | 16 | 0 | KQK04122 | 0.982 | 0. | HORVU.MC |
| 0.952785201 | 0.983136749 | 16 | 0 | KQJ85135 | 0.958 | 0. | HORVU.MC |
| 0.945819155 | 0.998398719 | 16 | 0 | KQK05126 | 0.971 | 0. | HORVU.MC |
| 0.902741826 | 0.93760218 | 16 | 1 | KQJ82999 | 0.916 | 0. | HORVU.MC |
| 0.902237171 | 0.959949937 | 16 | 3 | PNT70869 | 0.936 | 0. | HORVU.MC |
| 0.935010341 | 0.972034889 | 16 | 0 | KQK19803 | 0.958 | 0. | HORVU.MC |

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| 0.895086855 | 0.967654106 | 16 | 1 KQK12778 0.849 – | HORVU.MC |
| 0.953827157 | 0.997417355 | 16 | 0 KQK21797 0.960 0 | HORVU.MC |
| 0.868517221 | 0.956748098 | 16 | 1 KQK06028 0.889 0 | HORVU.MC |
| 0.961762344 | 1.000200723 | 16 | 0 KQJ99548 0.923 –1 | HORVU.MC |
| 0.963942308 | 0.981318681 | 16 | 0 KQJ92171 0.955 –0 | HORVU.MC |
| 0.94949316 | 0.988045354 | 16 | 0 KQK23900 0.898 – | HORVU.MC |
| 0.934092501 | 0.997090831 | 16 | 0 KQK06561 0.958 0 | HORVU.MC |
| 0.967352583 | 0.996177016 | 16 | 0 PNT72906 0.961 – | HORVU.MC |
| 0.930646799 | 0.980410893 | 16 | 0 KQK12620 0.940 0 | HORVU.MC |
| 0.876278311 | 0.965218396 | 16 | 0 KQK05132 0.801 – | HORVU.MC |
| 0.936393203 | 0.970439995 | 16 | 0 KQJ84605 0.957 0. | HORVU.MC |
| 0.937562555 | 0.970474165 | 16 | 1 KQJ84269 0.912 –1 | HORVU.MC |
| 0.956160553 | 0.994324724 | 16 | 0 KQJ85860 0.947 –0 | HORVU.MC |
| 0.969344683 | 0.994589552 | 16 | 0 KQK08195 0.921 – | HORVU.MC |
| 0.922555342 | 0.979509696 | 16 | 1 PNT71163 0.957 0. | HORVU.MC |
| 0.900786936 | 0.951091703 | 16 | 2 KQJ85883 0.912 0. | HORVU.MC |
| 0.947874857 | 0.979644495 | 16 | 0 KQJ85178 0.887 –2 | HORVU.MC |

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| 0.90074194 | 0.945766797 | 16 | 0 | KQK11157 | 0.888 | – | HORVU.MC |
| 0.953504018 | 0.99225835 | 16 | 1 | KQK08877 | 0.958 | 0. | HORVU.MC |
| 0.888045102 | 0.925328554 | 16 | 2 | KQK05343 | 0.841 | – | HORVU.MC |
| 0.963927483 | 0.987294747 | 16 | 0 | KQJ96374 | 0.962 | –0 | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.97709875 | 0.987879561 | 16 | 0 | KQK13941 | 0.988 | 2. | HORVU.MC |
| 0.949238687 | 0.977883634 | 16 | 0 | KQK06581 | 0.938 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.976837623 | 0.995774107 | 16 | 0 | KQK15532 | 0.989 | 1. | HORVU.MC |
| 0.912972856 | 0.98714987 | 16 | 1 | KQK17284 | 0.930 | 0. | HORVU.MC |
| 0.91626112 | 0.982836211 | 16 | 1 | KQK16456 | 0.949 | 0. | genblast_C |
| 0.930303224 | 0.991982259 | 16 | 1 | KQK16171 | 0.876 | – | HORVU.MC |
| 0.956614158 | 0.983785921 | 16 | 0 | KQK17658 | 0.964 | 0. | HORVU.MC |
| 0.917990319 | 0.97187661 | 16 | 3 | KQK16178 | 0.939 | 0. | HORVU.MC |
| 0.968061578 | 0.981613183 | 16 | 0 | KQK23557 | 0.977 | 0. | HORVU.MC |
| 0.937579885 | 0.963093146 | 16 | 0 | KQJ84412 | 0.925 | –0 | HORVU.MC |
| 0.943060963 | 0.978349634 | 16 | 0 | PNT61636 | 0.897 | –1 | HORVU.MC |
| 0.830910391 | 0.9116619 | 16 | 1 | PNT73986 | 0.746 | –1 | genblast_C |
| 0.969701522 | 0.996260684 | 16 | 0 | KQK00473 | 0.959 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.93249811 | 0.968841128 | 16 | 1 | KQJ94059 | 0.937 | 0. | HORVU.MC |
| 0.894566554 | 0.934160851 | 16 | 2 | KQK08132 | 0.920 | 0. | HORVU.MC |
| 0.947936872 | 0.970375595 | 16 | 0 | KQJ82511 | 0.955 | 0. | HORVU.MC |
| 0.928636128 | 0.9686853 | 16 | 0 | KQJ92366 | 0.896 | –1 | HORVU.MC |
| 0.938879741 | 0.972435663 | 16 | 0 | KQK10176 | 0.909 | – | HORVU.MC |
| 0.919177208 | 0.968585096 | 16 | 4 | KQK16557 | 0.947 | 0. | HORVU.MC |
| 0.901716139 | 0.950128665 | 16 | 6 | KQJ91341 | 0.937 | 0. | genblast_C |
| 0.916424085 | 0.978397426 | 16 | 0 | KQK23925 | 0.921 | 0. | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.923141616 | 0.977757136 | 16 | 3 | KQK04896 | 0.898 | – | HORVU.MC |
| 0.89966641 | 0.962022068 | 16 | 0 | KQK18975 | 0.854 | – | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.937047762 | 0.961606998 | 16 | 0 | KQJ88010 | 0.930 | –0 | genblast_C |
| 0.943149808 | 0.978104994 | 16 | 0 | KQJ90304 | 0.972 | 0. | HORVU.MC |
| 0.928084029 | 0.94624553 | 16 | 0 | KQK22386 | 0.929 | 0. | HORVU.MC |
| 0.909214133 | 0.956565777 | 16 | 0 | KQK07880 | 0.884 | – | HORVU.MC |
| 0.914849601 | 0.931384392 | 16 | 0 | KQK21920 | 0.921 | 0. | HORVU.MC |
| 0.961660145 | 0.981457981 | 16 | 0 | KQJ96945 | 0.959 | –0 | HORVU.MC |
| 0.944980291 | 0.989727664 | 16 | 0 | KQK23681 | 0.925 | – | HORVU.MC |
| 0.886031973 | 0.927835052 | 16 | 0 | KQJ86261 | 0.891 | 0. | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.945517928 | 0.977848606 | 16 | 0 | KQJ99611 | 0.949 | 0. | HORVU.MC |
| 0.977159107 | 1.003187944 | 16 | 0 | KQK23030 | 0.967 | − | HORVU.MC |
| 0.925590781 | 0.971455311 | 16 | 0 | KQJ99699 | 0.937 | 0. | HORVU.MC |
| 0.91742186 | 0.98534466 | 16 | 2 | KQJ96248 | 0.924 | 0. | genblast_C |
| 0.951402532 | 0.998471949 | 16 | 0 | KQK08623 | 0.961 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.973213194 | 0.998227709 | 16 | 1 | KQK23086 | 0.969 | − | HORVU.MC |
| 0.919927857 | 0.962115106 | 16 | 0 | KQJ82092 | 0.869 | −1 | HORVU.MC |
| 0.933386313 | 0.977561705 | 16 | 0 | KQK07841 | 0.956 | 0. | HORVU.MC |
| 0.98169925 | 0.998383066 | 16 | 0 | KQK13123 | 0.977 | − | HORVU.MC |
| 0.935993642 | 0.989945291 | 16 | 0 | KQJ95759 | 0.940 | 0. | HORVU.MC |
| 0.935437605 | 1.005025126 | 16 | 0 | KQK01563 | 0.864 | − | HORVU.MC |
| 0.948150447 | 0.989275074 | 16 | 0 | KQK20918 | 0.912 | − | HORVU.MC |
| 0.938062789 | 0.964346556 | 16 | 1 | KQJ99155 | 0.938 | −0 | HORVU.MC |
| 0.996030696 | 1.012966393 | 16 | 0 | KQK07235 | 0.979 | − | HORVU.MC |
| 0.90938167 | 0.978754366 | 16 | 2 | KQJ84427 | 0.943 | 0. | HORVU.MC |
| 0.921944602 | 0.960221308 | 16 | 1 | KQK18683 | 0.924 | 0. | HORVU.MC |
| 0.910347848 | 0.949074074 | 16 | 0 | KQJ94080 | 0.931 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.889789181 | 0.927151324 | 16 | 1 | KQJ88441 | 0.915 | 0. | HORVU.MC |
| 0.95967726 | 0.977520975 | 16 | 1 | KQK11204 | 0.970 | 0. | HORVU.MC |
| 0.8253285 | 0.920706842 | 16 | 0 | KQJ92510 | 0.741 | −1 | HORVU.MC |
| 0.992537915 | 1.005485641 | 16 | 0 | KQK16651 | 0.987 | − | HORVU.MC |
| 0.968651283 | 0.983511827 | 16 | 0 | KQK13498 | 0.966 | − | HORVU.MC |

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| 0.974148372 | 0.997577593 | 16 | 0 | KQK01944 | 0.969 | − | HORVU.MC |

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| 0.977160165 | 0.987808595 | 16 | 0 | KQJ83035 | 0.978 | 0. | HORVU.MC |
| 0.847321809 | 0.975223626 | 16 | 6 | KQJ98825 | 0.773 | −0 | HORVU.MC |
| 0.83962395 | 0.927088287 | 16 | 3 | KQK15573 | 0.827 | − | HORVU.MC |
| 0.966647749 | 0.980688068 | 16 | 0 | KQK16086 | 0.972 | 0 | HORVU.MC |
| 0.928022142 | 0.971633752 | 16 | 2 | KQJ85395 | 0.938 | 0. | HORVU.MC |
| 0.880468075 | 0.941439983 | 16 | 9 | KQK22506 | 0.897 | 0 | HORVU.MC |
| 0.934773629 | 0.985128883 | 16 | 2 | KQK04375 | 0.959 | 0 | HORVU.MC |
| 0.87201326 | 0.927527059 | 16 | 1 | KQJ83854 | 0.858 | −0 | HORVU.MC |
| 0.947991231 | 0.983625626 | 16 | 4 | KQJ85502 | 0.956 | 0. | HORVU.MC |
| 0.966038589 | 0.988066125 | 16 | 0 | KQJ86575 | 0.941 | −1 | HORVU.MC |
| 0.914793838 | 0.949220766 | 16 | 1 | KQK03779 | 0.888 | – | HORVU.MC |
| 0.962289871 | 0.983189701 | 16 | 1 | KQK23228 | 0.972 | 0 | genblast_C |
| 0.928173956 | 0.973063018 | 16 | 2 | KQK13560 | 0.962 | 0 | HORVU.MC |
| 0.951680131 | 0.973186662 | 16 | 0 | KQJ97061 | 0.939 | −0 | HORVU.MC |

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| 0.961708186 | 0.989137663 | 16 | 1 | KQJ97441 | 0.967 | 0. | HORVU.MC |
| 0.949908386 | 0.973326021 | 16 | 0 | KQK14277 | 0.942 | – | HORVU.MC |
| 0.929075783 | 0.972035794 | 16 | 0 | KQK17257 | 0.928 | – | HORVU.MC |
| 0.874607555 | 0.960299777 | 16 | 0 | KQJ81686 | 0.865 | –0 | HORVU.MC |
| 0.969007112 | 0.994561428 | 16 | 0 | KQJ90356 | 0.971 | 0. | HORVU.MC |
| 0.975109945 | 1.000321007 | 16 | 0 | KQJ85465 | 0.970 | –0 | HORVU.MC |
| 0.981809127 | 0.995206322 | 16 | 0 | KQK01836 | 0.978 | – | HORVU.MC |
| 0.89004734 | 0.943885691 | 16 | 0 | PNT65352 | 0.872 | – | HORVU.MC |
| 0.95535202 | 0.978034587 | 16 | 0 | KQK23785 | 0.927 | – | genblast_C |
| 0.906491572 | 0.980674254 | 16 | 1 | KQK11916 | 0.897 | – | HORVU.MC |
| 0.914810454 | 0.974058061 | 16 | 0 | KQK19618 | 0.916 | 0 | HORVU.MC |
| 0.938870107 | 0.975088968 | 16 | 0 | KQK10263 | 0.933 | – | HORVU.MC |
| 0.978767875 | 1.003152798 | 16 | 0 | KQK09883 | 0.972 | – | HORVU.MC |

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| 0.909973267 | 0.983048788 | 16 | 4 | PNT77772 0.776 – | HORVU.MC |
| 0.973398337 | 0.993675334 | 16 | 0 | KQK19407 0.976 0 | HORVU.MC |
| 0.89126 | 0.946453333 | 16 | 0 | KQK18490 0.912 0 | HORVU.MC |
| 0.931585115 | 0.983838127 | 16 | 4 | KQK09005 0.956 0 | HORVU.MC |
| 0.955993187 | 0.988214868 | 16 | 0 | KQK01989 0.951 – | HORVU.MC |
| 0.937705818 | 0.981025561 | 16 | 0 | KQK12596 0.917 – | HORVU.MC |
| 0.929788419 | 0.981242267 | 16 | 0 | KQK01451 0.816 – | HORVU.MC |
| 0.957637057 | 0.999413662 | 16 | 0 | KQK13351 0.938 – | genblast_C |
| 0.97186644 | 0.991478137 | 16 | 0 | KQJ83494 0.960 –0 | HORVU.MC |

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| 0.912748202 | 0.945017719 | 16 | 0 | PNT69563 0.900 – | HORVU.MC |
| 0.952955838 | 0.992522782 | 16 | 2 | PNT67306 0.960 0. | HORVU.MC |
| 0.973337388 | 1.007028927 | 16 | 0 | KQK12362 0.964 – | genblast_C |
| 0.946714032 | 0.982978094 | 16 | 0 | PNT64692 0.921 – | HORVU.MC |
| 0.934165622 | 0.976041231 | 16 | 0 | KQK22553 0.947 0 | HORVU.MC |
| 0.91090848 | 0.953323558 | 16 | 1 | KQK17511 0.865 – | HORVU.MC |
| 0.944362191 | 0.973383018 | 16 | 0 | genblast_Os06t022 | HORVU.MC |
| 0.886934207 | 0.965124907 | 16 | 0 | KQK12583 0.841 – | HORVU.MC |
| 0.935604808 | 0.978277649 | 16 | 0 | KQJ93075 0.951 0. | HORVU.MC |
| 0.960662467 | 0.982283314 | 16 | 0 | KQK04201 0.954 – | HORVU.MC |
| 0.918576352 | 0.950957693 | 16 | 0 | KQJ82185 0.904 –0 | HORVU.MC |
| 0.955894721 | 1.003019063 | 16 | 1 | KQK15033 0.943 – | genblast_C |
| 0.975541362 | 0.998286337 | 16 | 0 | KQK15239 0.943 – | HORVU.MC |
| 1.003586405 | 1.015449128 | 16 | 0 | KQJ86581 1.003 –0 | HORVU.MC |
| 0.935757953 | 0.974881292 | 16 | 3 | KQK19406 0.949 0 | HORVU.MC |
| 0.932808536 | 0.95597672 | 16 | 0 | KQJ99979 0.942 0. | HORVU.MC |

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| 0.930656046 | 0.964519271 | 16 | 0 | KQK03260 0.912 – | HORVU.MC |
| 0.94120958 | 0.987751388 | 16 | 2 | PNT74299 0.939 – | HORVU.MC |
| 0.971435786 | 0.994368266 | 16 | 0 | KQK16776 0.956 – | HORVU.MC |
| 0.938848921 | 0.982404438 | 16 | 0 | KQK10416 0.920 – | HORVU.MC |
| 0.912714838 | 0.967045096 | 16 | 2 | KQJ88899 0.946 0. | HORVU.MC |
| 0.949090622 | 0.975820017 | 16 | 0 | KQK05037 0.884 – | HORVU.MC |
| 0.930779053 | 0.98198594 | 16 | 1 | KQK14250 0.876 – | HORVU.MC |

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| 0.982671506 | 1.001233514 | 16 | 0 | KQJ97060 | 0.975 | –0 | HORVU.MC |
| 0.915099968 | 0.976628991 | 16 | 2 | PNT66979 | 0.760 | –2 | HORVU.MC |
| 0.939605868 | 0.964316797 | 16 | 0 | KQK23090 | 0.919 | – | HORVU.MC |
| 0.95867629 | 0.985012285 | 16 | 0 | PNT70158 | 0.939 | –0 | HORVU.MC |
| 0.941664847 | 0.965071222 | 16 | 1 | KQK01479 | 0.964 | 1. | HORVU.MC |
| 0.973762143 | 0.993259318 | 16 | 0 | KQJ93521 | 0.965 | –0 | HORVU.MC |
| 0.87309307 | 0.911069063 | 16 | 0 | KQJ96746 | 0.846 | –0 | HORVU.MC |
| 0.972198842 | 0.987640087 | 16 | 0 | KQK21437 | 0.972 | –0 | HORVU.MC |
| 0.944089854 | 0.970822281 | 16 | 0 | KQJ91581 | 0.904 | –2 | HORVU.MC |
| 0.917586136 | 0.975671889 | 16 | 4 | KQK23553 | 0.884 | –0 | HORVU.MC |
| 0.956232655 | 0.986740672 | 16 | 1 | KQK06953 | 0.951 | –0 | HORVU.MC |
| 0.952263994 | 0.986078886 | 16 | 3 | genblast_Os04t053 |  |  | HORVU.MC |
| 0.899672461 | 0.971570474 | 16 | 1 | KQK00456 | 0.877 | –0 | HORVU.MC |
| 0.972422235 | 0.991321045 | 16 | 0 | KQJ91146 | 0.953 | –1 | HORVU.MC |
| 0.969695927 | 0.997615116 | 16 | 0 | KQJ92331 | 0.965 | –0 | HORVU.MC |
| 0.949150752 | 0.980113796 | 16 | 1 | KQJ89380 | 0.923 | –1 | HORVU.MC |
| 0.892956842 | 0.950135886 | 16 | 1 | KQK21546 | 0.889 | –0 | HORVU.MC |
| 0.949808708 | 0.986882857 | 16 | 1 | KQJ85634 | 0.960 | 0. | HORVU.MC |
| 0.864458295 | 0.951831333 | 16 | 0 | PNT77340 | 0.801 | –1 | HORVU.MC |
| 0.945638 | 0.981026276 | 16 | 0 | PNT74784 | 0.949 | 0. | HORVU.MC |
| 0.93607331 | 0.970807726 | 16 | 0 | PNT72940 | 0.898 | –0 | HORVU.MC |

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| 0.932635876 | 0.965042103 | 16 | 0 | KQK04970 | 0.885 | – | HORVU.MC |
| 0.90988242 | 0.97136323 | 16 | 0 | PNT63431 | 0.779 | – | HORVU.MC |
| 0.90648803 | 0.953909529 | 16 | 0 | KQJ90748 | 0.894 | –0 | HORVU.MC |

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| 0.95972621 | 0.995214657 | 16 | 1 | KQK14550 | 0.959 | – | HORVU.MC |

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| 0.943206522 | 0.989440994 | 16 | 0 | KQK19886 | 0.892 | – | HORVU.MC |
| 0.940222125 | 0.977351916 | 16 | 1 | KQK14230 | 0.905 | – | HORVU.MC |
| 0.927149902 | 0.972009202 | 16 | 4 | PNT67104 | 0.904 | – | HORVU.MC |
| 0.951126061 | 0.99510721 | 16 | 0 | KQJ98916 | 0.907 | –1 | HORVU.MC |
| 0.957047008 | 0.990587181 | 16 | 0 | KQK17825 | 0.962 | 0 | HORVU.MC |
| 0.923697244 | 0.961412575 | 16 | 0 | KQJ97379 | 0.942 | 0. | HORVU.MC |
| 0.914750615 | 0.942748873 | 16 | 0 | KQK15478 | 0.867 | – | HORVU.MC |

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| 0.958381534 | 0.983376178 | 16 | 0 | KQK09953 | 0.945 | – | HORVU.MC |
| 0.957704595 | 0.977977162 | 16 | 0 | PNT76441 | 0.945 | – | HORVU.MC |
| 0.958371899 | 0.997038134 | 16 | 0 | KQJ93290 | 0.959 | 0. | HORVU.MC |
| 0.926739222 | 0.969484882 | 16 | 1 | KQJ89194 | 0.912 | –0 | HORVU.MC |
| 0.955390368 | 0.99463289 | 16 | 0 | KQK02304 | 0.937 | – | genblast_C |
| 0.969220856 | 0.995572297 | 16 | 0 | genblast_Os06t013 | | | HORVU.MC |
| 0.926985063 | 0.943710692 | 16 | 0 | KQK01587 | 0.900 | – | HORVU.MC |

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| 0.972160562 | 0.990442718 | 16 | 0 | KQJ91443 | 0.964 | –0 | HORVU.MC |
| 0.95111451 | 0.987543706 | 16 | 1 | KQJ85978 | 0.970 | 0. | HORVU.MC |
| 0.933518368 | 0.982794699 | 16 | 0 | KQK22972 | 0.931 | – | HORVU.MC |
| 0.924699657 | 0.99771167 | 16 | 0 | KQK05960 | 0.871 | – | HORVU.MC |

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| 0.904170792 | 0.95009901 | 16 | 1 | KQK04269 | 0.902 | – | HORVU.MC |
| 0.898484028 | 0.977260422 | 16 | 0 | KQJ95726 | 0.859 | –0 | HORVU.MC |

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| 0.916629938 | 0.969572315 | 16 | 1 | KQK09126 | 0.901 | – | HORVU.MC |
| 0.922117832 | 0.984324759 | 16 | 0 | KQK11424 | 0.911 | – | HORVU.MC |
| 0.946633544 | 0.962704309 | 16 | 1 | KQK03249 | 0.951 | 0 | HORVU.MC |
| 0.905600213 | 0.954626825 | 16 | 0 | KQK19135 | 0.822 | – | genblast_C |
| 0.965010401 | 0.977241211 | 16 | 0 | KQK10361 | 0.960 | – | HORVU.MC |

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| 0.968102899 | 0.99776999 | 16 | 0 | KQK16649 | 0.987 | 0 | HORVU.MC |
| 0.953239715 | 0.994320543 | 16 | 1 | KQJ92768 | 0.956 | 0. | HORVU.MC |
| 0.921196214 | 0.956557716 | 16 | 2 | KQJ95225 | 0.954 | 0. | HORVU.MC |

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| 0.956582905 | 0.989812749 | 16 | 0 | KQK00733 | 0.946 | – | HORVU.MC |
| 0.889865247 | 0.934602337 | 16 | 2 | KQK17498 | 0.865 | – | HORVU.MC |
| 0.945796422 | 0.981584821 | 16 | 1 | KQK00664 | 0.923 | – | HORVU.MC |
| 0.980693256 | 0.997272129 | 16 | 0 | KQK06074 | 0.977 | – | HORVU.MC |
| 0.947607597 | 0.979132703 | 16 | 1 | KQK00101 | 0.968 | 0 | HORVU.MC |
| 0.829795374 | 0.906664142 | 16 | 1 | KQJ86050 | 0.878 | 0. | HORVU.MC |
| 0.832968246 | 0.95429693 | 16 | 0 | KQK16387 | 0.757 | – | HORVU.MC |
| 0.927094316 | 0.981198383 | 16 | 2 | KQJ93636 | 0.969 | 0. | HORVU.MC |
| 0.966907448 | 0.990606391 | 16 | 0 | KQJ86973 | 0.971 | 0. | HORVU.MC |
| 0.965554826 | 0.981207199 | 16 | 0 | KQJ83175 | 0.964 | –0 | HORVU.MC |
| 0.916117959 | 0.947417752 | 16 | 0 | KQJ95841 | 0.846 | –2 | HORVU.MC |
| 0.972148115 | 0.994547437 | 16 | 0 | KQK00182 | 0.975 | 0 | HORVU.MC |
| 0.919619073 | 0.979754928 | 16 | 0 | genblast_Os10t050 | | | HORVU.MC |

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| 0.947830484 | 0.985475271 | 16 | 0 | PNT65319 | 0.949 | 0. | HORVU.MC |
| 0.925672248 | 0.9695586 | 16 | 0 | PNT73944 | 0.938 | 0. | HORVU.MC |
| 0.951273652 | 0.977323923 | 16 | 0 | KQK00730 | 0.948 | – | HORVU.MC |
| 0.93135149 | 0.966104367 | 16 | 1 | KQJ94399 | 0.921 | –0 | HORVU.MC |
| 0.94532425 | 0.96799615 | 16 | 0 | PNT72256 | 0.936 | – | HORVU.MC |
| 0.92191495 | 0.967363513 | 16 | 0 | KQJ99273 | 0.875 | –1 | HORVU.MC |
| 0.875029755 | 0.926922161 | 16 | 0 | KQJ82446 | 0.915 | 0. | HORVU.MC |
| 0.959880999 | 0.992770149 | 16 | 1 | KQJ85290 | 0.967 | 0. | HORVU.MC |
| 0.920049943 | 0.957560696 | 16 | 0 | KQJ85019 | 0.907 | –0 | HORVU.MC |
| 0.945574746 | 0.978044496 | 16 | 1 | KQJ86876 | 0.947 | 0. | HORVU.MC |
| 0.966828535 | 1.004471772 | 16 | 0 | KQK01581 | 0.953 | – | HORVU.MC |
| 0.936211293 | 0.979824108 | 16 | 0 | KQK14605 | 0.925 | – | HORVU.MC |
| 0.949765554 | 0.996569076 | 16 | 0 | KQJ94295 | 0.932 | –0 | genblast_C |
| 0.979787685 | 0.996282043 | 16 | 0 | KQK09227 | 0.968 | – | HORVU.MC |
| 0.941587978 | 0.984569323 | 16 | 0 | KQJ82584 | 0.917 | –0 | HORVU.MC |
| 0.886042906 | 0.948867232 | 16 | 0 | KQK00900 | 0.829 | – | HORVU.MC |
| 0.915603967 | 0.972724052 | 16 | 3 | KQJ91328 | 0.908 | –0 | HORVU.MC |
| 0.87594697 | 0.95709571 | 16 | 1 | KQK09372 | 0.865 | – | HORVU.MC |
| 0.966238349 | 0.986457967 | 16 | 0 | KQJ86532 | 0.960 | –0 | HORVU.MC |
| 0.905231204 | 0.976269683 | 16 | 0 | KQK05705 | 0.863 | – | HORVU.MC |
| 0.941415543 | 0.971054718 | 16 | 0 | KQJ91686 | 0.924 | –0 | HORVU.MC |
| 0.933995327 | 0.999332443 | 16 | 0 | KQJ85111 | 0.925 | –0 | HORVU.MC |

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| 0.974235239 | 0.991317125 | 16 | 0 | KQK13162 | 0.962 | – | HORVU.MC |
| 0.964921136 | 0.997223975 | 16 | 0 | PNT67158 | 0.947 | – | HORVU.MC |
| 0.97661545 | 0.998947161 | 16 | 0 | KQK16462 | 0.978 | 0 | HORVU.MC |
| 0.921708524 | 0.962165688 | 16 | 0 | KQK12179 | 0.881 | – | genblast_C |
| 0.89579789 | 0.95814903 | 16 | 0 | PNT72555 | 0.846 | – | HORVU.MC |
| 0.967883754 | 0.989884951 | 16 | 0 | KQJ86322 | 0.971 | 0. | HORVU.MC |
| 0.965159407 | 0.992582071 | 16 | 0 | KQK11298 | 0.975 | 0 | HORVU.MC |
| 0.902761497 | 0.959783589 | 16 | 1 | KQJ82034 | 0.876 | –0 | HORVU.MC |
| 0.918924406 | 0.984349624 | 16 | 0 | KQJ91217 | 0.937 | 0. | HORVU.MC |
| 0.954776636 | 1.000419463 | 16 | 0 | KQK10364 | 0.952 | – | HORVU.MC |
| 0.938454566 | 0.976936131 | 16 | 1 | KQK20535 | 0.963 | 0 | HORVU.MC |
| 0.961065454 | 0.971572298 | 16 | 0 | KQK08301 | 0.960 | – | HORVU.MC |
| 0.95225753 | 0.969880872 | 16 | 1 | KQJ82889 | 0.965 | 0. | HORVU.MC |
| 0.961492292 | 0.994187516 | 16 | 0 | PNT78259 | 0.939 | – | HORVU.MC |

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| 0.971827359 | 1.003021563 | 16 | 0 | KQK06584 | 0.983 | 0. | HORVU.MC |
| 0.929436074 | 0.968402575 | 16 | 0 | KQK03398 | 0.951 | 0. | HORVU.MC |
| 0.896872418 | 0.96151576 | 16 | 0 | PNT67785 | 0.826 | – | HORVU.MC |
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| 0.951527076 | 0.969879846 | 16 | 0 | KQK11324 | 0.960 | 0. | HORVU.MC |
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| 0.965963099 | 0.996582292 | 16 | 0 | KQK21408 | 0.969 | 0. | HORVU.MC |
| 0.93117211 | 0.989655453 | 16 | 2 | KQK03201 | 0.936 | 0. | HORVU.MC |
| 0.944314387 | 0.976771196 | 16 | 0 | KQK22067 | 0.942 | – | HORVU.MC |
| | | | | | | | |
| 0.922841931 | 0.950688198 | 16 | 0 | KQJ89669 | 0.927 | 0. | HORVU.MC |
| 0.927024239 | 0.982465188 | 16 | 0 | KQK02849 | 0.894 | – | HORVU.MC |
| 0.899101408 | 0.948369565 | 16 | 0 | PNT63973 | 0.842 | – | HORVU.MC |
| 0.912646881 | 0.962983509 | 16 | 0 | KQJ85555 | 0.929 | 0. | HORVU.MC |
| 0.931884198 | 0.972631035 | 16 | 0 | KQJ82678 | 0.946 | 0. | HORVU.MC |
| 0.928551863 | 0.966816237 | 16 | 0 | KQK19188 | 0.913 | – | HORVU.MC |
| 0.977128297 | 1.005515588 | 16 | 0 | KQJ85204 | 0.973 | –0 | HORVU.MC |
| 0.917414264 | 0.970576541 | 16 | 2 | PNT63797 | 0.944 | 0. | HORVU.MC |
| 0.91034342 | 0.970536867 | 16 | 1 | KQK19935 | 0.893 | – | HORVU.MC |
| 0.931081602 | 0.975682155 | 16 | 2 | KQK08262 | 0.921 | – | HORVU.MC |
| | | | | | | | |
| 0.922415895 | 0.962701121 | 16 | 2 | KQK14080 | 0.915 | – | HORVU.MC |
| 0.921704634 | 0.959436656 | 16 | 2 | PNT74579 | 0.909 | – | HORVU.MC |
| 0.912384873 | 0.987383295 | 16 | 1 | KQK00860 | 0.938 | 0. | HORVU.MC |
| 0.8578265 | 0.963888135 | 16 | 0 | KQK21230 | 0.839 | – | HORVU.MC |
| 0.944273399 | 0.98142724 | 16 | 4 | PNT70238 | 0.951 | 0. | HORVU.MC |
| 0.918682707 | 0.95858379 | 16 | 2 | KQK17516 | 0.921 | 0. | HORVU.MC |
| 0.94613263 | 0.984059098 | 16 | 0 | KQJ91003 | 0.939 | –0 | HORVU.MC |
| 0.934518584 | 0.969856599 | 16 | 0 | KQJ93091 | 0.944 | 0. | HORVU.MC |
| 0.91300918 | 0.95195066 | 16 | 0 | KQJ90110 | 0.916 | 0. | HORVU.MC |
| 0.943975602 | 0.981951872 | 16 | 0 | KQK15745 | 0.938 | – | HORVU.MC |
| 0.975990381 | 0.992966487 | 16 | 0 | KQK09359 | 0.978 | 0. | HORVU.MC |
| 0.956332691 | 0.988368712 | 16 | 0 | KQK22609 | 0.914 | – | HORVU.MC |
| 0.942485883 | 0.964476386 | 16 | 1 | KQK03692 | 0.907 | – | HORVU.MC |
| 0.905636829 | 0.965792672 | 16 | 0 | KQK09710 | 0.863 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.941656788 | 0.984402296 | 16 | 0 | KQK13323 | 0.935 | – | HORVU.MC |
| 0.966912091 | 0.981695696 | 16 | 0 | KQJ89091 | 0.966 | –0 | HORVU.MC |
| | | | | | | | |
| 0.92901552 | 0.978995263 | 16 | 2 | genblast_Os01t081 | | | HORVU.MC |
| 0.954802566 | 0.981403422 | 16 | 0 | KQJ90722 | 0.944 | –0 | HORVU.MC |
| 0.937858441 | 0.979806139 | 16 | 0 | KQK14286 | 0.894 | – | HORVU.MC |
| 0.927757009 | 0.958224299 | 16 | 2 | KQK14241 | 0.912 | – | genblast_C |
| 0.970325195 | 0.991796166 | 16 | 0 | KQK15617 | 0.965 | – | HORVU.MC |
| 0.940083707 | 0.978301534 | 16 | 0 | KQK14803 | 0.899 | – | HORVU.MC |
| 0.872982124 | 0.939111593 | 16 | 0 | KQJ86800 | 0.887 | 0. | HORVU.MC |
| 0.942205517 | 0.97592132 | 16 | 0 | KQK04148 | 0.884 | – | genblast_C |
| 0.936937992 | 0.973237703 | 16 | 2 | KQJ91154 | 0.957 | 0. | HORVU.MC |
| 0.914256038 | 0.940028902 | 16 | 1 | KQK12361 | 0.905 | – | HORVU.MC |
| 0.953872411 | 0.983427495 | 16 | 1 | KQJ85029 | 0.937 | –0 | HORVU.MC |
| 0.967176259 | 0.986330935 | 16 | 0 | KQJ98721 | 0.933 | –1 | HORVU.MC |
| 0.930521664 | 0.961909297 | 16 | 0 | KQK01609 | 0.899 | – | HORVU.MC |
| 0.937485551 | 0.966787393 | 16 | 0 | KQK12889 | 0.958 | 0 | HORVU.MC |
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| 0.951279665 | 0.986505351 | 16 | 0 | KQJ91087 | 0.943 | –0 | HORVU.MC |
| 0.96115685 | 0.990781789 | 16 | 2 | KQJ86395 | 0.963 | 0. | HORVU.MC |
| 0.952818627 | 0.990073529 | 16 | 0 | KQK00237 | 0.939 | – | HORVU.MC |
| | | | | | | | |
| 0.918876678 | 0.963727297 | 16 | 1 | KQJ90504 | 0.872 | –1 | HORVU.MC |
| 0.974899118 | 0.998160661 | 16 | 1 | KQJ97088 | 0.979 | 0. | HORVU.MC |
| 0.945494494 | 0.988422985 | 16 | 1 | KQK01838 | 0.968 | 0 | HORVU.MC |
| 0.967161493 | 1.00359874 | 16 | 0 | KQK20420 | 0.975 | 0 | HORVU.MC |
| 0.977415734 | 0.988224904 | 16 | 0 | KQJ90715 | 0.973 | –0 | HORVU.MC |
| 0.902144013 | 0.950485437 | 16 | 0 | PNT69117 | 0.939 | 0. | HORVU.MC |
| 0.872806053 | 0.922460154 | 16 | 0 | KQK08378 | 0.817 | – | HORVU.MC |
| 0.912077068 | 0.955263158 | 16 | 0 | KQK10764 | 0.953 | 0 | HORVU.MC |
| 0.965541557 | 0.982324182 | 16 | 0 | KQJ87466 | 0.961 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.94366957 | 0.990583804 | 16 | 0 | KQJ86303 | 0.917 | −0 | genblast_C |
| 0.931455062 | 0.980978261 | 16 | 1 | PNT67541 | 0.953 | 0. | HORVU.MC |
| 0.93534703 | 0.969931397 | 16 | 0 | KQK13304 | 0.923 | − | HORVU.MC |
| 0.911303952 | 0.971225516 | 16 | 0 | KQJ84388 | 0.859 | −1 | HORVU.MC |
| 0.953661858 | 0.988147971 | 16 | 0 | KQJ94079 | 0.944 | −0 | HORVU.MC |
| 0.967912009 | 0.991770112 | 16 | 0 | KQK11534 | 0.959 | − | HORVU.MC |
| 0.8932417 | 0.960858462 | 16 | 2 | KQJ90321 | 0.912 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.947724058 | 0.978377286 | 16 | 0 | KQK16104 | 0.975 | 0 | HORVU.MC |
| 0.921554113 | 0.98302217 | 16 | 3 | KQK15717 | 0.932 | 0 | HORVU.MC |
| 0.949680312 | 0.982147305 | 16 | 2 | KQJ88071 | 0.964 | 0. | HORVU.MC |
| 0.963279073 | 0.998733215 | 16 | 0 | KQK06828 | 0.953 | − | HORVU.MC |
| 0.958903354 | 0.989298323 | 16 | 0 | KQK17320 | 0.942 | − | HORVU.MC |
| 0.944046443 | 0.966492993 | 16 | 1 | KQK06461 | 0.954 | 0 | HORVU.MC |
| 0.940479384 | 1.002452483 | 16 | 0 | KQK10846 | 0.872 | − | genblast_C |
| 0.961760408 | 1.003101515 | 16 | 0 | KQJ93031 | 0.956 | −0 | HORVU.MC |
| 0.957215608 | 0.984937599 | 16 | 0 | KQJ95860 | 0.949 | −0 | HORVU.MC |
| 0.947655517 | 1.003619788 | 16 | 0 | KQJ98761 | 0.880 | −1 | HORVU.MC |
| 0.9581032 | 0.979313115 | 16 | 0 | KQK17113 | 0.941 | − | HORVU.MC |
| 0.966515837 | 1.002149321 | 16 | 0 | KQJ90296 | 0.962 | −0 | HORVU.MC |
| 0.947777522 | 1.006909258 | 16 | 0 | KQK12267 | 0.897 | − | HORVU.MC |

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| 0.97346981 | 0.992745344 | 16 | 0 | KQJ97462 | 0.963 | −0 | HORVU.MC |
| 0.927998017 | 0.969872413 | 16 | 1 | PNT77860 | 0.898 | − | HORVU.MC |

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| 0.90985023 | 0.953225806 | 16 | 0 | KQJ92336 | 0.904 | −0 | HORVU.MC |
| 0.973333935 | 0.995464385 | 16 | 0 | KQK17823 | 0.958 | − | HORVU.MC |
| 0.917294066 | 0.966194272 | 16 | 1 | KQK06120 | 0.939 | 0 | HORVU.MC |
| 0.919569672 | 0.982903981 | 16 | 0 | genblast_Os03t029 | | | HORVU.MC |

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| 0.968301909 | 0.997940268 | 16 | 0 | KQJ88780 | 0.953 | –0 | HORVU.MC |
| 0.94636643 | 0.976306827 | 16 | 0 | KQK14983 | 0.949 | 0 | HORVU.MC |
| 0.923968136 | 0.944230405 | 16 | 1 | KQK00999 | 0.922 | –0 | HORVU.MC |
| 0.955263236 | 0.994354982 | 16 | 0 | KQJ96039 | 0.976 | 0. | HORVU.MC |
| 0.952401434 | 0.983942652 | 16 | 0 | KQK04384 | 0.928 | –0 | HORVU.MC |
| 0.943585552 | 0.977627225 | 16 | 0 | KQJ84876 | 0.943 | –0 | HORVU.MC |
| 0.912982295 | 0.971731799 | 16 | 0 | KQJ85268 | 0.861 | –1 | HORVU.MC |
| 0.970340259 | 0.992472147 | 16 | 0 | KQK00875 | 0.982 | 0 | HORVU.MC |
| 0.912943406 | 0.977525047 | 16 | 0 | KQK08139 | 0.934 | 0 | HORVU.MC |
| 0.964459456 | 0.986247432 | 16 | 0 | KQK11645 | 0.970 | 0 | HORVU.MC |
| 0.910858051 | 0.965960452 | 16 | 0 | PNT76823 | 0.880 | –0 | HORVU.MC |
| 0.974252187 | 1.00264838 | 16 | 0 | KQJ86036 | 0.973 | –0 | HORVU.MC |
| 0.932055433 | 0.992392125 | 16 | 1 | PNT71309 | 0.940 | 0. | HORVU.MC |
| 0.910722732 | 0.964963982 | 16 | 7 | KQK10066 | 0.906 | –0 | HORVU.MC |
| 0.952769726 | 0.986683576 | 16 | 0 | KQK15551 | 0.963 | 0 | HORVU.MC |
| 0.91136756 | 0.947878987 | 16 | 0 | KQK21704 | 0.876 | – | HORVU.MC |
| 0.917184314 | 0.986103769 | 16 | 3 | KQK10855 | 0.943 | 0 | HORVU.MC |
| 0.860938228 | 0.934545455 | 16 | 6 | KQK13874 | 0.791 | – | HORVU.MC |
| 0.948419482 | 0.991552695 | 16 | 1 | KQK02459 | 0.935 | –0 | HORVU.MC |
| 0.977312006 | 0.999769568 | 16 | 0 | KQK22604 | 0.981 | 0 | HORVU.MC |
| 0.961940098 | 0.981453883 | 16 | 0 | KQK00755 | 0.965 | 0 | HORVU.MC |
| 0.957376761 | 0.989295775 | 16 | 0 | KQK22812 | 0.962 | 0 | HORVU.MC |
| 0.923261453 | 0.990094924 | 16 | 0 | KQJ83705 | 0.903 | –0 | genblast_C |
| 0.896987374 | 0.937070333 | 16 | 2 | KQK03637 | 0.845 | – | HORVU.MC |
| 0.906910082 | 0.946802269 | 16 | 0 | KQK16458 | 0.928 | 0 | genblast_C |

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| 0.940891064 | 1.000675049 | 16 | 0 | KQJ84922 0.937 -0 | HORVU.MC |
| 0.907537923 | 0.978529755 | 16 | 6 | PNT66733 0.956 0. | HORVU.MC |
| 0.976900957 | 0.990632964 | 16 | 0 | KQK22488 0.967 - | HORVU.MC |
| 0.90682665 | 0.951738822 | 16 | 0 | KQK06071 0.872 - | HORVU.MC |

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| 0.930926701 | 0.963726121 | 16 | 0 | KQJ83375 0.946 0. | HORVU.MC |
| 0.95681678 | 0.980027761 | 16 | 0 | KQK03956 0.949 - | HORVU.MC |
| 0.93523133 | 0.981949817 | 16 | 1 | KQJ95412 0.935 0. | HORVU.MC |
| 0.935871065 | 0.973068275 | 16 | 1 | KQK21721 0.938 0 | HORVU.MC |
| 0.946574884 | 0.988444212 | 16 | 1 | KQJ90113 0.959 0. | HORVU.MC |
| 0.924469852 | 1.017373531 | 16 | 0 | KQK14812 0.894 - | HORVU.MC |

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| 0.963929418 | 0.986904516 | 16 | 0 | KQJ94674 0.892 -3 | HORVU.MC |
| 0.954736748 | 0.98782235 | 16 | 0 | KQK05738 0.971 0 | HORVU.MC |
| 0.947410239 | 0.983422092 | 16 | 0 | KQJ88614 0.909 -1 | HORVU.MC |
| 0.970269365 | 0.998228265 | 16 | 0 | KQK20745 0.955 - | HORVU.MC |
| 0.925179533 | 0.978958707 | 16 | 1 | KQK23006 0.825 - | HORVU.MC |
| 0.950037017 | 1.013092269 | 16 | 0 | KQJ81612 0.829 -2 | genblast_C |
| 0.925463303 | 0.966609519 | 16 | 2 | KQK11150 0.923 - | HORVU.MC |
| 0.894314853 | 0.922940341 | 16 | 0 | PNT76228 0.886 - | HORVU.MC |
| 0.937096051 | 1.009613296 | 16 | 1 | PNT71613 0.902 - | HORVU.MC |
| 0.945798035 | 0.971153144 | 16 | 0 | genblast_Os02t069 | HORVU.MC |
| 0.982530254 | 1.000295159 | 16 | 0 | KQJ93393 0.954 -2 | HORVU.MC |
| 0.957265139 | 0.99909451 | 16 | 0 | KQK20156 0.967 0 | HORVU.MC |

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| 0.88968956 | 0.957890488 | 16 | 0 | KQK12943 0.803 - | HORVU.MC |
| 0.961055997 | 0.993604985 | 16 | 0 | KQJ83348 0.966 0. | HORVU.MC |
| 0.969093667 | 0.991657186 | 16 | 0 | KQJ84193 0.976 0. | HORVU.MC |

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| 0.942289026 | 0.979415427 | 16 | 0 | KQJ93169 0.938 -0 | HORVU.MC |

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| 0.976015169 | 0.997393661 | 16 | 0 | KQK17773 | 0.963 | – | HORVU.MC |

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| 0.959717235 | 0.98192699 | 16 | 0 | KQK07108 | 0.961 | 0 | HORVU.MC |

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| 0.941005312 | 0.977748393 | 16 | 2 | KQK03316 | 0.934 | – | HORVU.MC |
| 0.836630435 | 0.910434783 | 16 | 1 | KQK04743 | 0.805 | – | HORVU.MC |
| 0.918237596 | 0.972879246 | 16 | 3 | KQK12496 | 0.965 | 0 | HORVU.MC |
| 0.928681475 | 0.973188006 | 16 | 5 | KQK00173 | 0.935 | 0 | HORVU.MC |

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| 0.977650419 | 1.001188876 | 16 | 1 | PNT62115 | 0.975 | – | HORVU.MC |
| 0.942704612 | 0.984995128 | 16 | 0 | KQJ89648 | 0.928 | –0 | HORVU.MC |
| 0.951625775 | 0.979022255 | 16 | 0 | KQJ97638 | 0.959 | 0. | HORVU.MC |
| 0.918809712 | 0.96336329 | 16 | 0 | KQK19747 | 0.930 | 0 | HORVU.MC |
| 0.935010823 | 0.987672645 | 16 | 2 | PNT61682 | 0.957 | 0. | HORVU.MC |
| 0.946865046 | 0.981343041 | 16 | 0 | KQK08264 | 0.938 | – | HORVU.MC |
| 0.958692665 | 0.987237806 | 16 | 0 | KQJ83258 | 0.934 | –1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.918435853 | 0.964261586 | 16 | 0 | KQK15905 | 0.910 | – | HORVU.MC |
| 0.96409486 | 0.989935956 | 16 | 0 | PNT77601 | 0.956 | – | HORVU.MC |
| 0.973784023 | 0.990487432 | 16 | 0 | KQK16748 | 0.980 | 0 | HORVU.MC |
| 0.97659361 | 0.994797688 | 16 | 0 | KQJ86111 | 0.972 | –0 | HORVU.MC |
| 0.938784571 | 0.971239396 | 16 | 1 | KQJ84141 | 0.934 | –0 | HORVU.MC |

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| 0.947814497 | 0.980923243 | 16 | 0 KQK01035 0.951 0 HORVU.MC |
| 0.917907426 | 0.963369051 | 16 | 0 KQJ86605 0.931 0. HORVU.MC |
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| 0.948435973 | 0.98305637 | 16 | 0 KQJ96728 0.944 -0HORVU.MC |
| 0.941621798 | 0.971143018 | 16 | 1 KQK05989 0.950 0 HORVU.MC |
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| 0.962625882 | 0.984843501 | 16 | 1 KQJ89683 0.959 -0genblast_C |
| 0.988976586 | 0.998985846 | 16 | 0 KQJ93705 0.994 0. HORVU.MC |
| 0.956450345 | 0.981537837 | 16 | 0 KQK00367 0.932 - HORVU.MC |
| 0.962404073 | 0.994687131 | 16 | 0 KQK17261 0.966 0 HORVU.MC |
| 0.941721465 | 0.976232973 | 16 | 0 KQJ81630 0.915 -1HORVU.MC |
| 0.948927135 | 0.985918641 | 16 | 0 KQK09426 0.924 - HORVU.MC |
| 0.962144504 | 0.99923136 | 16 | 0 KQK22939 0.913 - HORVU.MC |
| 0.921485855 | 0.943015701 | 16 | 0 KQK05816 0.933 0 HORVU.MC |
| 0.932399723 | 0.96769018 | 16 | 1 KQK21594 0.911 - HORVU.MC |
| | | | |
| 0.900524114 | 0.949381852 | 16 | 3 KQJ91371 0.814 -2HORVU.MC |
| 0.966121457 | 0.989444334 | 16 | 0 KQK22829 0.964 - HORVU.MC |
| 0.950120341 | 0.981568337 | 16 | 0 KQK22473 0.960 0 HORVU.MC |
| 0.948707627 | 1.010169492 | 16 | 1 PNT65455 0.927 - HORVU.MC |
| 0.901462026 | 0.958253992 | 16 | 1 KQK15886 0.931 0 HORVU.MC |
| 0.936134793 | 0.98384041 | 16 | 2 KQK02059 0.941 0 HORVU.MC |
| 0.966635071 | 0.988815166 | 16 | 0 KQJ91424 0.978 0. HORVU.MC |
| 0.963477419 | 0.993271485 | 16 | 0 KQK12982 0.959 - HORVU.MC |
| 0.949941752 | 0.972972973 | 16 | 1 KQJ96559 0.959 0. HORVU.MC |
| 0.961445268 | 0.991448119 | 16 | 0 KQK22425 0.964 0 HORVU.MC |
| 0.963836091 | 0.985867621 | 16 | 0 KQK06319 0.943 - genblast_C |
| 0.93038435 | 0.980685022 | 16 | 3 KQK08454 0.963 0 HORVU.MC |
| 0.964129742 | 0.991902834 | 16 | 1 KQK01411 0.954 - HORVU.MC |
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| 0.960941765 | 1.002183803 | 16 | 0 KQJ94998 0.963 0. HORVU.MC |
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| 0.873203047 | 0.9279894 | 16 | 2 PNT68835 0.904 0.HORVU.MC |
| 0.965428721 | 0.988629332 | 16 | 0 KQJ81981 0.957 -0HORVU.MC |
| 0.972540013 | 0.985742538 | 16 | 0 KQK17864 0.964 - HORVU.MC |
| 0.965621453 | 0.993567915 | 16 | 0 KQJ87543 0.970 0. HORVU.MC |
| 0.955698506 | 0.980657265 | 16 | 0 KQJ98902 0.956 0. HORVU.MC |
| 0.969418671 | 0.985356309 | 16 | 0 KQK09492 0.975 0 HORVU.MC |
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| 0.904577401 | 0.94972067 | 16 | 0 KQJ83797 0.900 -0genblast_C |

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| 0.947399923 | 0.987167209 | 16 | 0 | KQK11317 | 0.959 | 0 | HORVU.MC |
| 0.971247018 | 0.992546213 | 16 | 0 | KQK05863 | 0.969 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.940072559 | 0.960527704 | 16 | 1 | KQK13113 | 0.936 | – | HORVU.MC |
| 0.930483457 | 0.969994295 | 16 | 0 | KQK11228 | 0.895 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.896957542 | 0.98153116 | 16 | 1 | KQK18628 | 0.806 | – | HORVU.MC |
| 0.949963364 | 0.99465548 | 16 | 0 | KQK19920 | 0.886 | – | HORVU.MC |
| 0.967027948 | 1.022713806 | 16 | 0 | KQK16555 | 0.980 | 0 | HORVU.MC |
| 0.95718536 | 0.988457776 | 16 | 0 | KQK23563 | 0.965 | 0 | HORVU.MC |
| 0.95806147 | 0.99023199 | 16 | 1 | KQJ98438 | 0.970 | 0. | HORVU.MC |
| 0.914531427 | 0.981540204 | 16 | 0 | KQJ97497 | 0.939 | 0. | HORVU.MC |
| 0.96211979 | 0.988358994 | 16 | 0 | KQK09148 | 0.955 | – | HORVU.MC |
| 0.944451893 | 0.979513032 | 16 | 0 | KQJ82561 | 0.960 | 0. | HORVU.MC |
| 0.986533231 | 1.002049827 | 16 | 0 | KQJ91090 | 0.982 | –0 | HORVU.MC |
| 0.952064515 | 0.982291406 | 16 | 0 | PNT69683 | 0.950 | – | HORVU.MC |

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| 0.978431546 | 0.994707128 | 16 | 0 | KQJ85261 | 0.982 | 0. | HORVU.MC |
| 0.957141513 | 0.996913813 | 16 | 0 | KQJ98915 | 0.949 | –0 | HORVU.MC |
| 0.914776738 | 0.940581245 | 16 | 0 | KQK08112 | 0.893 | – | HORVU.MC |
| 0.961538713 | 0.982462569 | 16 | 0 | KQK20076 | 0.964 | 0 | HORVU.MC |
| 0.942699394 | 0.980089255 | 16 | 0 | KQK09318 | 0.951 | 0 | HORVU.MC |
| 0.934344304 | 0.97301019 | 16 | 0 | KQJ92205 | 0.922 | –0 | HORVU.MC |
| 0.970507281 | 0.993607198 | 16 | 0 | KQK02001 | 0.978 | 0 | HORVU.MC |

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| 0.951621646 | 0.986629325 | 16 | 0 KQK15516 0.931 − | HORVU.MC |
| 0.944338074 | 0.986014651 | 16 | 2 KQK12435 0.935 − | HORVU.MC |
| 0.980177458 | 0.99812331 | 16 | 2 KQJ90122 0.984 0. | HORVU.MC |
| 0.939729397 | 0.988468635 | 16 | 0 KQK23466 0.907 − | HORVU.MC |
| | | | | |
| 0.890942294 | 0.918042367 | 16 | 0 KQK23798 0.871 − | HORVU.MC |
| 0.979452359 | 1.010515845 | 16 | 0 KQK15786 0.963 − | HORVU.MC |
| 0.96135214 | 0.98998703 | 16 | 1 KQK05704 0.938 − | HORVU.MC |
| 0.9300752 | 0.975377586 | 16 | 0 KQK06516 0.950 0 | HORVU.MC |
| 0.882690106 | 0.92769342 | 16 | 2 genblast_Os01t085 | HORVU.MC |
| 0.943842047 | 0.970747507 | 16 | 1 KQJ85733 0.941 −0 | HORVU.MC |
| 0.959679487 | 0.986813187 | 16 | 0 KQK01391 0.967 0 | HORVU.MC |
| 0.949307008 | 0.999790795 | 16 | 0 KQK10998 0.976 0 | HORVU.MC |
| | | | | |
| 0.946574752 | 0.972138446 | 16 | 0 KQJ99291 0.900 −2 | HORVU.MC |
| 0.935944192 | 0.975107066 | 16 | 0 KQK22059 0.922 − | HORVU.MC |
| 0.950127806 | 0.983329629 | 16 | 0 KQK05885 0.896 − | HORVU.MC |
| 0.944597792 | 0.978845797 | 16 | 1 KQK16750 0.933 − | genblast_C |
| 0.955137489 | 0.976602468 | 16 | 0 KQK20974 0.931 − | HORVU.MC |
| 0.903801193 | 0.949908632 | 16 | 1 KQK17581 0.897 − | HORVU.MC |
| 0.976339002 | 0.991020343 | 16 | 0 PNT77754 0.964 − | HORVU.MC |
| 0.910488805 | 0.989195522 | 16 | 0 genblast_Os05t048 | HORVU.MC |
| 0.922007818 | 0.954874593 | 16 | 0 KQK20284 0.942 0 | HORVU.MC |
| 0.969360983 | 0.996981024 | 16 | 0 KQJ82671 0.952 −0 | HORVU.MC |
| | | | | |
| 0.925992063 | 0.96998557 | 16 | 1 KQK12989 0.929 0 | HORVU.MC |
| 0.94971568 | 0.982487923 | 16 | 0 KQJ82575 0.941 −0 | HORVU.MC |
| 0.905036619 | 0.960706812 | 16 | 0 KQJ86308 0.845 −1 | HORVU.MC |
| 0.852361352 | 0.970103986 | 16 | 0 KQJ96853 0.796 −0 | HORVU.MC |
| 0.873005051 | 0.951313131 | 16 | 0 PNT73297 0.918 0. | HORVU.MC |
| | | | | |
| 0.959738757 | 0.982671958 | 16 | 0 KQK21980 0.946 − | HORVU.MC |
| | | | | |
| 0.905793603 | 0.957030779 | 16 | 0 KQK21735 0.874 − | HORVU.MC |

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|---|---|---|---|
| 0.979116985 | 0.998410175 | 16 | 1 KQJ84397 0.948 -1HORVU.MC |
| 0.946940344 | 0.959655597 | 16 | 0 KQK17496 0.949 0.HORVU.MC |
| 0.936929023 | 0.962403373 | 16 | 1 KQJ82533 0.937 0.HORVU.MC |

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|---|---|---|---|
| 0.873525495 | 0.921613394 | 16 | 0 KQK09637 0.883 0.HORVU.MC |
| 0.863394697 | 0.940041222 | 16 | 2 KQK15059 0.800 - HORVU.MC |
| 0.979345113 | 0.992946134 | 16 | 0 KQK21801 0.962 - HORVU.MC |
| 0.978172141 | 0.999809051 | 16 | 0 KQK06970 0.979 0.HORVU.MC |
| 0.95529619 | 0.988548778 | 16 | 0 KQK11382 0.931 -HORVU.MC |
| 0.875162973 | 0.944198175 | 16 | 0 KQJ90107 0.943 1. HORVU.MC |
| 0.912069024 | 0.959912437 | 16 | 0 KQJ92116 0.900 -0HORVU.MC |
| 0.926158947 | 0.98775146 | 16 | 1 PNT74947 0.870 -HORVU.MC |
| 0.964894751 | 0.987476685 | 16 | 0 PNT76692 0.972 0.HORVU.MC |
| 0.942946148 | 0.960613454 | 16 | 0 KQK18689 0.932 -HORVU.MC |
| 0.96010906 | 0.987667785 | 16 | 0 KQK08850 0.958 -genblast_C |
| 0.949982044 | 0.98046378 | 16 | 2 KQJ82746 0.954 0. HORVU.MC |
| 0.956178441 | 0.983866771 | 16 | 0 KQK00866 0.917 - HORVU.MC |
| 0.884225032 | 0.961867704 | 16 | 1 KQJ93474 0.849 -0HORVU.MC |
| 0.903414121 | 0.944001771 | 16 | 0 KQK15302 0.853 - HORVU.MC |
| 0.96844759 | 0.992334962 | 16 | 0 KQJ90891 0.960 -0HORVU.MC |

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|---|---|---|---|
| 0.928489239 | 0.964187086 | 16 | 2 KQK18942 0.900 -HORVU.MC |
| 0.964447314 | 0.992479339 | 16 | 0 genblast_Os05t043HORVU.MC |
| 0.966185527 | 0.996766744 | 16 | 0 KQJ85028 0.974 0.HORVU.MC |
| 0.887713624 | 0.947543318 | 16 | 6 KQJ81948 0.931 0.HORVU.MC |
| 0.949347605 | 0.99333484 | 16 | 0 KQK16711 0.921 -HORVU.MC |
| 0.919210271 | 0.974806202 | 16 | 0 KQJ98534 0.918 -0HORVU.MC |
| 0.954852146 | 0.982663224 | 16 | 0 KQK01727 0.912 -HORVU.MC |

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|---|---|---|---|
| 0.933266663 | 1.004221066 | 16 | 1 KQJ99767 0.967 0.HORVU.MC |
| 0.944300452 | 0.967357832 | 16 | 0 KQJ97546 0.917 -1HORVU.MC |
| 0.947913001 | 0.973434201 | 16 | 0 KQK04454 0.963 0 HORVU.MC |
| 0.888901746 | 0.925857357 | 16 | 0 KQK15882 0.848 - HORVU.MC |
| 0.955089433 | 0.978912685 | 16 | 2 KQJ83088 0.898 -2HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.953894151 | 0.998340708 | 16 | 0 | KQK01817 | 0.894 | – | HORVU.MC |
| 0.956397929 | 0.992662722 | 16 | 0 | KQK23981 | 0.925 | – | HORVU.MC |
| 0.921725577 | 0.968029252 | 16 | 0 | KQK14649 | 0.929 | 0. | HORVU.MC |
| 0.970291071 | 0.997582225 | 16 | 1 | KQJ98783 | 0.968 | –0 | HORVU.MC |
| | | | | | | | |
| 0.913207077 | 0.977232719 | 16 | 1 | PNT68561 | 0.917 | 0. | HORVU.MC |
| 0.942843045 | 0.964649738 | 16 | 0 | KQK22980 | 0.908 | – | HORVU.MC |
| 0.941440666 | 0.971090308 | 16 | 0 | KQJ90836 | 0.882 | –2 | HORVU.MC |
| 0.948098335 | 0.975859691 | 16 | 0 | KQJ90749 | 0.926 | –0 | HORVU.MC |
| | | | | | | | |
| 0.937107809 | 0.972633781 | 16 | 0 | KQJ88674 | 0.934 | –0 | genblast_C |
| 0.951160272 | 0.985148515 | 16 | 0 | KQK04642 | 0.947 | – | HORVU.MC |
| 0.972547279 | 0.993985943 | 16 | 0 | KQK11097 | 0.959 | – | HORVU.MC |
| | | | | | | | |
| 0.919561908 | 0.946549391 | 16 | 0 | KQK05396 | 0.922 | 0. | HORVU.MC |
| 0.952405576 | 0.975899281 | 16 | 0 | KQJ99285 | 0.949 | –0 | HORVU.MC |
| | | | | | | | |
| 0.957646206 | 0.997506079 | 16 | 0 | KQK15615 | 0.937 | – | HORVU.MC |
| 0.892228343 | 0.945344567 | 16 | 0 | KQK06760 | 0.945 | 1. | HORVU.MC |
| 0.950973054 | 0.978954712 | 16 | 0 | KQK20736 | 0.937 | – | HORVU.MC |
| 0.923049221 | 0.961451063 | 16 | 0 | KQK07435 | 0.932 | 0. | HORVU.MC |
| 0.870816645 | 0.975583455 | 16 | 8 | KQJ86172 | 0.813 | –0 | HORVU.MC |
| 0.921535908 | 0.95245574 | 16 | 0 | KQK12304 | 0.898 | – | HORVU.MC |
| 0.909023019 | 0.947788663 | 16 | 0 | KQK23653 | 0.863 | – | HORVU.MC |
| 0.954942409 | 1.007175227 | 16 | 0 | KQK16291 | 0.982 | 0. | HORVU.MC |

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|---|---|---|---|---|---|
| 0.948170565 | 0.978467592 | 16 | 0 | PNT78135 0.942 - | HORVU.MC |
| 0.908801588 | 0.945813539 | 16 | 0 | KQK10307 0.925 0 | HORVU.MC |
| 0.895898583 | 0.955903555 | 16 | 7 | KQJ90393 0.859 -0 | HORVU.MC |
| 0.980669985 | 1 | 16 | 0 | KQJ95809 0.985 0. | HORVU.MC |
| 0.964549192 | 0.978262094 | 16 | 0 | KQK00904 0.955 - | HORVU.MC |
| 0.991734964 | 1.006162189 | 16 | 0 | PNT68975 0.976 - | HORVU.MC |
| 0.961274625 | 0.988273921 | 16 | 0 | KQJ90077 0.950 -0 | HORVU.MC |
| 0.940045195 | 0.981731684 | 16 | 0 | KQJ93813 0.929 -0 | HORVU.MC |
| 0.968194864 | 0.997583082 | 16 | 0 | KQJ85319 0.970 0. | HORVU.MC |
| 0.958102851 | 0.98401313 | 16 | 1 | KQJ83113 0.968 0. | HORVU.MC |
| 0.942693257 | 0.972288439 | 16 | 0 | KQK16021 0.952 0 | HORVU.MC |
| 0.904231932 | 0.978015938 | 16 | 0 | genblast_Os03t011 | HORVU.MC |
| 0.888023245 | 0.965919615 | 16 | 1 | KQK18031 0.806 - | HORVU.MC |
| 0.965699269 | 0.98976234 | 16 | 0 | KQK17210 0.963 - | HORVU.MC |
| 0.949048152 | 0.969813525 | 16 | 1 | KQJ98517 0.952 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.938495264 | 0.983183472 | 16 | 1 | KQK21892 | 0.937 | – | HORVU.MC |
| 0.923832753 | 0.982996516 | 16 | 0 | genblast_Os01t069 | | | HORVU.MC |
| 0.939103753 | 0.984277662 | 16 | 0 | KQK14923 | 0.944 | 0 | HORVU.MC |
| 0.980892958 | 1.004242081 | 16 | 0 | KQK03577 | 0.972 | – | HORVU.MC |
| 0.893477996 | 0.9660723 | 16 | 4 | KQK16541 | 0.912 | 0 | HORVU.MC |
| 0.973752754 | 0.984486874 | 16 | 0 | KQK01583 | 0.973 | – | HORVU.MC |
| 0.952364437 | 0.995035047 | 16 | 0 | KQJ83319 | 0.952 | –0 | HORVU.MC |
| 0.944144261 | 0.962150982 | 16 | 0 | KQK22244 | 0.938 | – | HORVU.MC |
| 0.953733456 | 0.978238738 | 16 | 0 | KQK10838 | 0.944 | – | HORVU.MC |
| 0.991393443 | 1.013960867 | 16 | 0 | KQK06506 | 0.994 | 0 | HORVU.MC |
| 0.881388951 | 0.935649648 | 16 | 1 | KQK02820 | 0.913 | 0 | HORVU.MC |
| 0.945778779 | 0.991441365 | 16 | 0 | KQJ85273 | 0.930 | –0 | genblast_C |
| 0.982641262 | 0.99612668 | 16 | 0 | KQJ95879 | 0.981 | –0 | HORVU.MC |
| 0.957917983 | 0.986577181 | 16 | 0 | KQK10248 | 0.939 | – | HORVU.MC |
| 0.914115914 | 0.948504097 | 16 | 0 | PNT72250 | 0.887 | – | HORVU.MC |
| 0.973549578 | 1.00907173 | 16 | 0 | KQK17982 | 0.942 | – | HORVU.MC |
| 0.953597002 | 0.988140524 | 16 | 0 | KQK15081 | 0.939 | – | HORVU.MC |
| 0.972781766 | 0.998828011 | 16 | 0 | KQK22312 | 0.957 | – | HORVU.MC |
| 0.951649221 | 0.986562804 | 16 | 1 | KQJ90714 | 0.957 | 0. | HORVU.MC |
| 0.889889427 | 0.962129841 | 16 | 2 | KQK18816 | 0.883 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.94080903 | 0.976107684 | 16 | 1 | KQK01284 | 0.947 | 0 | HORVU.MC |
| 0.900228499 | 0.981570273 | 16 | 0 | KQJ91023 | 0.913 | 0. | HORVU.MC |
| 0.929608875 | 0.986886246 | 16 | 0 | KQK12057 | 0.950 | 0 | HORVU.MC |
| 0.9625 | 0.998639456 | 16 | 0 | KQJ90651 | 0.942 | –0 | HORVU.MC |
| 0.976477929 | 0.991941304 | 16 | 0 | KQK00826 | 0.971 | – | HORVU.MC |
| 0.938585608 | 0.97194121 | 16 | 0 | KQK04857 | 0.893 | – | genblast_C |
| 0.951809429 | 0.974900398 | 16 | 0 | KQK05606 | 0.952 | 0 | HORVU.MC |
| 0.952588016 | 0.973093961 | 16 | 2 | KQK02045 | 0.960 | 0 | HORVU.MC |
| 0.92382763 | 0.951330798 | 16 | 0 | KQK01395 | 0.948 | 0 | HORVU.MC |
| 0.959307287 | 0.979489836 | 16 | 0 | KQK01155 | 0.961 | 0 | HORVU.MC |
| 0.962801717 | 0.991252227 | 16 | 0 | KQK01259 | 0.956 | – | HORVU.MC |
| 0.890223591 | 0.979006902 | 16 | 0 | KQK00164 | 0.907 | 0 | genblast_C |
| 0.921720492 | 0.972228066 | 16 | 0 | KQK21583 | 0.938 | 0 | HORVU.MC |
| 0.948939344 | 0.969970169 | 16 | 0 | KQJ83505 | 0.916 | –2 | HORVU.MC |
| 0.959653067 | 0.97897374 | 16 | 2 | KQK03654 | 0.964 | 0 | HORVU.MC |

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|---|---|---|---|---|
| 0.911938508 | 0.954718348 | 16 | 0 KQK06964 0.881 – | HORVU.MC |
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| 0.902962337 | 0.973423494 | 16 | 0 genblast_Os06t063 | HORVU.MC |
| | | | | |
| 0.930590134 | 0.977408944 | 16 | 4 KQK10443 0.965 0. | HORVU.MC |
| 0.965541353 | 0.988707654 | 16 | 0 KQK13238 0.972 0. | HORVU.MC |
| 0.934419209 | 0.974358974 | 16 | 0 PNT71109 0.887 – | HORVU.MC |
| 0.983608716 | 1.000670498 | 16 | 0 KQJ90946 0.981 –0 | HORVU.MC |
| 0.941864455 | 0.977370112 | 16 | 2 KQJ91209 0.935 –0 | HORVU.MC |
| 0.906163164 | 0.979907374 | 16 | 3 KQK20911 0.934 0. | HORVU.MC |
| | | | | |
| 0.934121817 | 0.970837905 | 16 | 4 KQK01914 0.951 0. | HORVU.MC |
| 0.959774413 | 0.992091136 | 16 | 0 KQJ81755 0.959 –0 | HORVU.MC |
| 0.934036583 | 0.978021978 | 16 | 3 genblast_Os05t049 | HORVU.MC |
| 0.961823004 | 0.991066443 | 16 | 0 KQJ86756 0.935 –1 | genblast_Z |
| 0.947296726 | 0.982119029 | 16 | 0 KQJ84920 0.915 –1 | HORVU.MC |
| 0.922365783 | 0.971040321 | 16 | 0 KQK03401 0.847 – | HORVU.MC |
| 0.914795705 | 0.970064618 | 16 | 4 PNT66360 0.909 – | HORVU.MC |
| 0.919578912 | 0.956675508 | 16 | 3 KQK23811 0.947 0. | HORVU.MC |
| 0.916076064 | 0.954101765 | 16 | 0 KQJ88329 0.896 –0 | HORVU.MC |
| 0.918945752 | 0.949797692 | 16 | 0 KQK02499 0.844 – | HORVU.MC |
| 0.959968319 | 0.982881281 | 16 | 1 KQK13420 0.961 0. | HORVU.MC |
| | | | | |
| 0.957283902 | 0.983720675 | 16 | 0 KQK13345 0.964 0. | HORVU.MC |
| 0.876118029 | 0.957558751 | 16 | 0 KQJ85103 0.773 –1 | HORVU.MC |
| 0.929455546 | 0.975367047 | 16 | 0 KQK05651 0.902 – | HORVU.MC |
| 0.955801742 | 0.991393443 | 16 | 0 KQK13859 0.860 – | HORVU.MC |
| 0.951067922 | 0.981971637 | 16 | 1 KQJ83870 0.962 0. | HORVU.MC |
| 0.967491904 | 0.991977626 | 16 | 0 KQK22853 0.981 0. | HORVU.MC |
| 0.918550866 | 0.965902739 | 16 | 1 KQJ90168 0.936 0. | HORVU.MC |
| 0.961841952 | 1.004192872 | 16 | 0 KQK12912 0.948 – | HORVU.MC |
| 0.958380847 | 0.984187319 | 16 | 0 KQK00535 0.959 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.968600954 | 1.003709592 | 16 | 0 | KQK18885 | 0.923 | – | HORVU.MC |
| 0.947401015 | 0.982946471 | 16 | 2 | KQJ93247 | 0.947 | –0 | HORVU.MC |
| 0.925349083 | 0.970867935 | 16 | 0 | KQK15500 | 0.849 | – | HORVU.MC |
| 0.894478149 | 0.955794985 | 16 | 0 | KQK02437 | 0.856 | – | HORVU.MC |
| 0.938698061 | 0.979393359 | 16 | 2 | KQK15410 | 0.947 | 0 | HORVU.MC |
| 0.973853768 | 0.995424409 | 16 | 0 | KQK00223 | 0.980 | 0 | HORVU.MC |
| 0.853840891 | 0.939275476 | 16 | 1 | KQK23154 | 0.818 | – | HORVU.MC |
| 0.943091571 | 0.983033512 | 16 | 0 | KQJ96606 | 0.931 | –0 | HORVU.MC |
| 0.958251161 | 1 | 16 | 2 | KQJ87462 | 0.981 | 0. | HORVU.MC |
| 0.904466314 | 0.956836575 | 16 | 2 | KQK15986 | 0.931 | 0 | HORVU.MC |
| 0.911044393 | 0.970584267 | 16 | 3 | KQK10977 | 0.902 | – | genblast_C |
| 0.986525914 | 1.002389267 | 16 | 0 | KQJ84055 | 0.991 | 0. | HORVU.MC |
| 0.955519062 | 0.99056984 | 16 | 0 | KQK07036 | 0.974 | 0 | HORVU.MC |
| 0.83920068 | 0.928344671 | 16 | 0 | KQK09723 | 0.747 | – | HORVU.MC |
| 0.954772247 | 0.970806919 | 16 | 1 | KQK14881 | 0.961 | 0 | HORVU.MC |
| 0.914391226 | 0.990599821 | 16 | 0 | KQK01828 | 0.877 | – | HORVU.MC |
| 0.929368742 | 0.982971187 | 16 | 3 | KQJ85870 | 0.912 | –0 | HORVU.MC |
| 0.922394156 | 0.961222241 | 16 | 3 | KQK18836 | 0.956 | 0 | HORVU.MC |
| 0.953989704 | 0.975363118 | 16 | 0 | KQJ95970 | 0.973 | 0. | HORVU.MC |
| 0.941215159 | 0.98165529 | 16 | 0 | KQK10870 | 0.948 | 0 | HORVU.MC |
| 0.955445906 | 0.983040936 | 16 | 1 | KQK06893 | 0.939 | – | HORVU.MC |
| 0.976551821 | 0.995840019 | 16 | 1 | KQK13438 | 0.975 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.948860687 | 0.983758529 | 16 | 0 | KQJ90340 | 0.917 | −1 | HORVU.M |
| 0.849812812 | 0.962728785 | 16 | 0 | KQK01094 | 0.782 | − | HORVU.M |
| 0.94889214 | 0.995610368 | 16 | 0 | KQK12017 | 0.946 | − | genblast_ |
| 0.952714877 | 0.992254733 | 16 | 0 | KQJ89216 | 0.934 | −0 | HORVU.M |
| 0.944698909 | 0.97628991 | 16 | 0 | KQK16067 | 0.944 | − | HORVU.M |
| 0.96683048 | 0.98562048 | 16 | 0 | KQK19674 | 0.983 | 0 | HORVU.M |

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|---|---|---|---|---|---|---|---|
| 0.972439006 | 0.993483861 | 16 | 0 | KQJ83140 | 0.985 | 0. | HORVU.M |
| 0.948585208 | 0.985554946 | 16 | 0 | KQJ87445 | 0.936 | −0 | HORVU.M |
| 0.962320288 | 0.984132055 | 16 | 2 | KQK10382 | 0.941 | − | HORVU.M |
| 0.944350342 | 0.983331335 | 16 | 0 | KQJ93863 | 0.958 | 0. | HORVU.M |
| 0.919245261 | 0.97145467 | 16 | 0 | KQK14844 | 0.811 | − | genblast_ |
| 0.931492867 | 0.970152056 | 16 | 0 | KQJ96222 | 0.914 | −0 | HORVU.M |
| 0.966364196 | 0.98991439 | 16 | 0 | KQK13499 | 0.954 | − | HORVU.M |
| 0.909726756 | 0.933272395 | 16 | 0 | KQK16851 | 0.907 | − | HORVU.M |
| 0.90529773 | 0.972947761 | 16 | 0 | PNT63541 | 0.961 | 0. | HORVU.M |
| 0.966101556 | 0.994376144 | 16 | 2 | KQJ85107 | 0.930 | −1 | HORVU.M |
| 0.9279918 | 0.988639276 | 16 | 1 | KQK13086 | 0.925 | − | HORVU.M |
| 0.96564574 | 0.988760437 | 16 | 0 | KQJ91400 | 0.964 | −0 | HORVU.M |
| 0.970359728 | 0.98893146 | 16 | 0 | KQJ85680 | 0.969 | −0 | HORVU.M |
| 0.946570122 | 0.990731707 | 16 | 0 | genblast_Os01t078 | | | HORVU.M |
| 0.971114199 | 0.997131588 | 16 | 0 | KQK23778 | 0.940 | − | HORVU.M |
| 0.911215907 | 0.98448473 | 16 | 2 | KQK14556 | 0.900 | − | HORVU.M |
| 0.925420358 | 0.96872175 | 16 | 0 | PNT64181 | 0.841 | −2 | HORVU.M |
| 0.981475225 | 1.002702703 | 16 | 0 | KQJ85899 | 0.977 | −0 | HORVU.M |
| 0.941042793 | 0.968487787 | 16 | 0 | KQK12002 | 0.948 | 0 | HORVU.M |
| 0.98617132 | 1.005028611 | 16 | 0 | KQK06346 | 0.985 | − | HORVU.M |
| 0.928492442 | 0.965215151 | 16 | 1 | KQJ82478 | 0.899 | −0 | HORVU.M |
| 0.950628852 | 0.981842412 | 16 | 0 | KQK07001 | 0.946 | − | HORVU.M |
| 0.893749694 | 0.96418261 | 16 | 5 | KQK08150 | 0.897 | 0 | HORVU.M |
| 0.88393073 | 0.958655706 | 16 | 0 | PNT68034 | 0.831 | −1 | HORVU.M |
| 0.946432532 | 0.973678373 | 16 | 0 | KQK18288 | 0.911 | − | HORVU.M |
| 0.972561899 | 0.995424881 | 16 | 0 | KQK00425 | 0.964 | − | HORVU.M |
| | | | | | | | |
| 0.981371163 | 0.994566016 | 16 | 0 | KQJ85916 | 0.982 | 0. | HORVU.M |
| 0.940131948 | 0.968276249 | 16 | 2 | KQJ92873 | 0.949 | 0. | HORVU.M |
| 0.979578698 | 1.012772971 | 16 | 0 | KQK19893 | 0.902 | − | HORVU.M |
| 0.97877907 | 0.990443975 | 16 | 1 | KQJ96098 | 0.977 | −0 | HORVU.M |
| 0.903613855 | 0.951014415 | 16 | 1 | PNT64732 | 0.918 | 0. | HORVU.M |
| 0.954334787 | 0.975377375 | 16 | 0 | KQK03783 | 0.962 | 0 | HORVU.M |
| 0.946785714 | 0.972444444 | 16 | 0 | KQJ97889 | 0.953 | 0. | HORVU.M |
| | | | | | | | |
| 0.972692206 | 0.993775247 | 16 | 0 | KQK21179 | 0.969 | − | HORVU.M |

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|---|---|---|---|---|---|---|---|
| 0.896335925 | 0.929661386 | 16 | 0 | PNT65020 | 0.847 | –2 | HORVU.MC |
| 0.958370436 | 0.972751558 | 16 | 0 | KQJ94798 | 0.960 | 0. | HORVU.MC |
| 0.898621366 | 0.954083987 | 16 | 0 | KQK05124 | 0.857 | – | HORVU.MC |
| 0.971901876 | 0.985242377 | 16 | 0 | KQK23452 | 0.948 | – | HORVU.MC |
| 0.955795371 | 1.001861376 | 16 | 1 | KQK23598 | 0.969 | 0. | HORVU.MC |
| 0.931012276 | 0.966034856 | 16 | 0 | KQJ92454 | 0.920 | –0 | HORVU.MC |
| 0.911487491 | 0.942529741 | 16 | 1 | KQK14129 | 0.905 | – | HORVU.MC |
| 0.9747373 | 0.987968649 | 16 | 0 | KQJ86839 | 0.978 | 0. | HORVU.MC |
| 0.941939112 | 0.982005956 | 16 | 0 | KQJ85240 | 0.935 | –0 | HORVU.MC |
| 0.974601235 | 1.00378874 | 16 | 0 | KQJ91658 | 0.961 | –0 | HORVU.MC |
| 0.971600156 | 0.986917058 | 16 | 0 | KQJ88192 | 0.959 | –0 | HORVU.MC |
| 0.963446708 | 0.987147141 | 16 | 0 | KQJ92921 | 0.951 | –0 | HORVU.MC |
| 0.934091208 | 0.980549349 | 16 | 1 | KQJ91486 | 0.936 | 0. | HORVU.MC |
| 0.951000458 | 1.005763689 | 16 | 1 | KQK20015 | 0.934 | – | HORVU.MC |
| 0.881972727 | 0.954763636 | 16 | 12 | KQK23029 | 0.885 | 0 | HORVU.MC |
| 0.941983087 | 0.985735634 | 16 | 0 | KQJ92457 | 0.903 | –1 | HORVU.MC |
| 0.949289302 | 0.981478069 | 16 | 1 | KQK15394 | 0.964 | 0 | HORVU.MC |
| 0.888173876 | 0.928991871 | 16 | 0 | KQK16726 | 0.824 | – | HORVU.MC |
| 0.992738508 | 1.005352645 | 16 | 0 | KQJ82536 | 0.999 | 0. | genblast_C |
| 0.9692987 | 0.990667773 | 16 | 0 | PNT65583 | 0.969 | 0. | HORVU.MC |
| 0.977592137 | 1.000339674 | 16 | 0 | KQJ89492 | 0.948 | –1 | HORVU.MC |
| 0.847628963 | 0.910800645 | 16 | 0 | KQJ84661 | 0.852 | 0. | HORVU.MC |
| 0.93956363 | 0.980587357 | 16 | 0 | KQK23729 | 0.943 | 0 | HORVU.MC |
| 0.940745958 | 0.994512494 | 16 | 0 | KQK03892 | 0.943 | 0 | HORVU.MC |
| 0.94765336 | 1.003390875 | 16 | 0 | KQK01347 | 0.981 | 0 | HORVU.MC |

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|---|---|---|---|---|
| 0.936997389 | 0.979664464 | 16 | 1 KQK09695 0.964 0 | genblast_C |
| 0.873966125 | 0.949582854 | 16 | 0 KQK22001 0.900 0 | HORVU.MC |
| 0.93708285 | 0.984039466 | 16 | 0 KQK00587 0.933 − | HORVU.MC |
| 0.953301743 | 0.996637114 | 16 | 0 KQK18989 0.941 − | HORVU.MC |
| 0.941501524 | 0.966124661 | 16 | 0 KQK16754 0.937 − | HORVU.MC |
| 0.967744807 | 0.989554896 | 16 | 0 KQK06625 0.969 0 | HORVU.MC |
| 0.939247436 | 0.978240303 | 16 | 1 PNT75345 0.856 − | HORVU.MC |
| 0.931031367 | 0.965307892 | 16 | 0 KQJ83212 0.914 −0 | HORVU.MC |
| 0.919372368 | 0.992392338 | 16 | 0 KQJ96208 0.913 −0 | HORVU.MC |
| 0.904642077 | 0.960966289 | 16 | 0 KQJ90574 0.892 −0 | HORVU.MC |
| 0.933279426 | 0.969548754 | 16 | 2 PNT69623 0.938 0. | HORVU.MC |
| 0.941885696 | 0.975436011 | 16 | 0 KQJ88092 0.918 −0 | HORVU.MC |
| 0.897512575 | 0.956201693 | 16 | 1 KQK13543 0.897 − | HORVU.MC |
| 0.973793418 | 0.997697179 | 16 | 0 KQK23230 0.969 − | HORVU.MC |
| 0.924945483 | 0.948037383 | 16 | 0 KQK17037 0.907 − | HORVU.MC |
| 0.951954272 | 0.984473969 | 16 | 0 KQK02087 0.941 − | HORVU.MC |

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| 0.891286844 | 0.956080422 | 16 | 0 KQJ83893 0.894 0. | HORVU.MC |

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| 0.965542756 | 0.987797104 | 16 | 0 KQK17503 0.972 0 | HORVU.MC |
| 0.917992796 | 0.978781925 | 16 | 0 KQK05232 0.915 − | HORVU.MC |
| 0.981053027 | 0.992371186 | 16 | 0 KQJ94443 0.990 0. | HORVU.MC |
| 0.955461602 | 0.982750862 | 16 | 0 KQJ89937 0.943 −0 | HORVU.MC |
| 0.960980517 | 0.990088945 | 16 | 0 KQK18036 0.945 − | HORVU.MC |
| 0.943724044 | 0.988665859 | 16 | 1 KQK14712 0.872 − | HORVU.MC |
| 0.944966601 | 0.985193402 | 16 | 1 KQJ83245 0.949 0. | HORVU.MC |

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|---|---|---|---|---|
| 0.967955295 | 0.985131862 | 16 | 0 KQK15747 0.967 − | HORVU.MC |
| 0.947559932 | 0.977644597 | 16 | 0 KQK08447 0.975 0 | HORVU.MC |
| 0.945346112 | 0.972392952 | 16 | 0 KQJ89848 0.913 −1 | HORVU.MC |
| 0.903287971 | 0.937952037 | 16 | 0 KQK10204 0.888 − | HORVU.MC |
| 0.968150602 | 0.982815998 | 16 | 0 KQK01294 0.968 − | HORVU.MC |
| 0.948315822 | 0.982979937 | 16 | 0 KQK05220 0.930 − | genblast_C |
| 0.968222804 | 0.992437464 | 16 | 0 KQJ91967 0.950 −1 | HORVU.MC |
| 0.826580539 | 0.918856515 | 16 | 3 KQJ93064 0.876 0. | HORVU.MC |
| 0.937561744 | 0.98337038 | 16 | 0 KQK15556 0.903 − | HORVU.MC |

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|---|---|---|---|
| 0.960748954 | 0.989847716 | 16 | 2 KQJ97805 0.940 –0HORVU.MC |
| 0.929357744 | 0.980691117 | 16 | 1 genblast_Os11t018HORVU.MC |
| 0.949505332 | 0.988821791 | 16 | 0 KQJ96060 0.933 –0genblast_C |
| 0.966810885 | 1.000455425 | 16 | 0 KQK04587 0.954 –genblast_C |
| 0.919241206 | 0.961880476 | 16 | 0 KQJ99916 0.917 –0HORVU.MC |
| 0.933593052 | 0.97687087 | 16 | 1 KQK23443 0.948 0HORVU.MC |
| 0.953195152 | 0.978764713 | 16 | 0 KQJ82817 0.937 –1HORVU.MC |
| 0.954560842 | 0.993276055 | 16 | 0 KQJ85347 0.927 –1HORVU.MC |
| 0.956621365 | 1.006005057 | 16 | 0 KQJ82711 0.920 –0HORVU.MC |
| 0.933021345 | 0.965610706 | 16 | 0 KQK13655 0.922 –HORVU.MC |
| 0.957790362 | 0.983207976 | 16 | 0 KQJ93544 0.959 0. HORVU.MC |
| 0.920841064 | 0.968305504 | 16 | 1 KQJ97823 0.968 0.HORVU.MC |
| 0.92792598 | 0.980828579 | 16 | 1 KQK22118 0.925 –HORVU.MC |
| 0.958083558 | 0.979365468 | 16 | 0 KQJ84665 0.942 –0HORVU.MC |
| 0.981506107 | 1.002600473 | 16 | 0 KQK23658 0.935 – HORVU.MC |
| 0.979232684 | 0.989286253 | 16 | 0 KQJ82925 0.979 0.HORVU.MC |
| 0.980764678 | 0.99609375 | 16 | 0 PNT75065 0.975 –HORVU.MC |
| 0.955258303 | 0.984501845 | 16 | 2 KQJ82023 0.953 –0HORVU.MC |

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|---|---|---|---|---|---|
| 0.951688994 | 0.984261501 | 16 | 2 | KQK10098 0.939 – | HORVU.MC |
| 0.948377369 | 0.989756845 | 16 | 0 | KQK15111 0.962 0. | HORVU.MC |
| 0.981302041 | 1.000938196 | 16 | 0 | KQK13075 0.990 0. | HORVU.MC |
| 0.924631467 | 0.953928342 | 16 | 0 | KQJ81446 0.903 –1 | HORVU.MC |
| 0.97247033 | 0.995055013 | 16 | 0 | KQK01040 0.950 – | HORVU.MC |
| 0.960364285 | 0.993236289 | 16 | 0 | KQK12697 0.953 – | HORVU.MC |
| 0.966620607 | 0.987625804 | 16 | 0 | KQK23064 0.962 – | HORVU.MC |
| 0.952937359 | 0.984488366 | 16 | 1 | KQJ82212 0.951 –0 | HORVU.MC |
| 0.930330158 | 0.98188981 | 16 | 2 | KQK16944 0.943 0. | HORVU.MC |
| 0.981122033 | 0.992933502 | 16 | 0 | KQK19173 0.978 – | HORVU.MC |
| 0.967629482 | 0.995130589 | 16 | 0 | KQK06689 0.982 0. | HORVU.MC |
| 0.9612896 | 0.983499906 | 16 | 2 | KQK04171 0.971 0. | HORVU.MC |
| 0.96069422 | 0.997071305 | 16 | 0 | genblast_Os03t059 | HORVU.MC |
| 0.930413756 | 0.980118216 | 16 | 0 | KQK01763 0.888 – | HORVU.MC |
| 0.913470632 | 0.986445308 | 16 | 2 | PNT72992 0.940 0. | HORVU.MC |
| 0.946044604 | 0.9869987 | 16 | 1 | KQJ81739 0.934 –0 | HORVU.MC |
| 0.98152202 | 0.99763541 | 16 | 0 | KQK05982 0.985 0. | HORVU.MC |
| 0.950674851 | 0.986073431 | 16 | 2 | KQJ82919 0.976 0. | HORVU.MC |

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| 0.946594982 | 0.980645161 | 16 | 0 | KQJ97974 | 0.879 | –1 | HORVU.MC |
| 0.942657243 | 0.976294278 | 16 | 2 | KQJ93381 | 0.959 | 0. | HORVU.MC |
| 0.943556992 | 1.004393673 | 16 | 1 | PNT73961 | 0.922 | – | genblast_C |
| 0.950028857 | 0.971142747 | 16 | 2 | KQK18640 | 0.968 | 0. | HORVU.MC |
| 0.919820519 | 0.966651645 | 16 | 1 | KQK22975 | 0.907 | – | HORVU.MC |
| 0.956318043 | 0.987412112 | 16 | 0 | KQK10149 | 0.949 | – | HORVU.MC |
| 0.963205818 | 0.988145688 | 16 | 0 | KQK14961 | 0.951 | – | HORVU.MC |
| 0.971756078 | 0.993128964 | 16 | 0 | KQJ83855 | 0.973 | 0. | HORVU.MC |
| 0.976410179 | 0.99045314 | 16 | 0 | KQJ98801 | 0.974 | –0 | HORVU.MC |
| 0.926025451 | 0.994069681 | 16 | 1 | KQK14630 | 0.802 | – | HORVU.MC |
| 0.985897065 | 1.001544998 | 16 | 0 | KQJ84844 | 0.982 | –0 | HORVU.MC |
| 0.908412064 | 0.959593023 | 16 | 0 | KQK14095 | 0.906 | – | HORVU.MC |
| 0.950934978 | 0.988632488 | 16 | 0 | KQK16233 | 0.955 | 0. | HORVU.MC |
| 0.93927929 | 0.980028531 | 16 | 0 | KQK14723 | 0.868 | – | HORVU.MC |
| 0.967593857 | 0.997406143 | 16 | 1 | PNT69290 | 0.939 | – | HORVU.MC |
| 0.926094333 | 0.957651849 | 16 | 0 | KQJ86342 | 0.878 | –1 | HORVU.MC |
| 0.982735149 | 0.999405941 | 16 | 2 | genblast_Zm00001 | | | HORVU.MC |
| 0.961237138 | 0.982518709 | 16 | 1 | KQJ97719 | 0.972 | 0. | HORVU.MC |
| 0.927830734 | 0.96152513 | 16 | 2 | KQK17777 | 0.913 | – | HORVU.MC |
| 0.966467842 | 0.994605809 | 16 | 0 | KQK10831 | 0.964 | – | HORVU.MC |
| 0.89877289 | 0.967175747 | 16 | 3 | KQK11411 | 0.801 | – | HORVU.MC |
| 0.933066115 | 0.966474594 | 16 | 0 | KQJ90756 | 0.935 | 0. | HORVU.MC |
| 0.925960589 | 0.99358236 | 16 | 0 | KQJ98609 | 0.947 | 0. | HORVU.MC |
| 0.94367846 | 0.991935484 | 16 | 0 | KQK07100 | 0.943 | – | HORVU.MC |
| 0.970854356 | 0.988410431 | 16 | 0 | KQK11256 | 0.959 | – | HORVU.MC |
| 0.930077435 | 0.96742096 | 16 | 1 | KQK00631 | 0.884 | – | HORVU.MC |
| 0.946296054 | 0.971014493 | 16 | 0 | KQJ95812 | 0.936 | –0 | HORVU.MC |

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| 0.899078198 | 0.935255763 | 16 | 0 | KQK02887 | 0.851 | – | HORVU.MC |
| 0.899095011 | 0.956803894 | 16 | 0 | KQK20500 | 0.886 | – | HORVU.MC |
| 0.957054775 | 0.981263742 | 16 | 0 | KQK23488 | 0.925 | – | HORVU.MC |
| 0.944031126 | 0.975024851 | 16 | 0 | KQK23153 | 0.938 | – | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.95573464 | 0.991754244 | 16 | 1 | KQJ97999 | 0.955 | –0 | HORVU.MC |
| 0.950969072 | 0.994971936 | 16 | 0 | KQK11633 | 0.939 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.897366962 | 0.93466371 | 16 | 0 | KQJ85512 | 0.875 | –1 | HORVU.MC |
| 0.951067634 | 0.983352853 | 16 | 1 | KQK04428 | 0.961 | 0. | HORVU.MC |
| 0.950930505 | 0.98287997 | 16 | 0 | genblast_Os04t043 | | | HORVU.MC |
| 0.9479057 | 0.985110543 | 16 | 0 | PNT65556 | 0.879 | – | HORVU.MC |
| 0.947228952 | 0.978666128 | 16 | 0 | PNT62142 | 0.950 | 0. | HORVU.MC |
| 0.922592501 | 0.954410307 | 16 | 0 | KQK18711 | 0.929 | 0. | HORVU.MC |

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| 0.971886317 | 0.984997413 | 16 | 0 | KQJ93669 | 0.960 | –1 | HORVU.MC |
| | | | | | | | |
| 0.917599254 | 0.991207034 | 16 | 0 | KQK10731 | 0.904 | – | HORVU.MC |
| 0.920866407 | 0.996405571 | 16 | 0 | KQJ89493 | 0.851 | –1 | HORVU.MC |
| 0.976229178 | 0.999355185 | 16 | 0 | KQK00685 | 0.960 | – | HORVU.MC |
| | | | | | | | |
| 0.976249553 | 0.99076061 | 16 | 0 | KQK09703 | 0.971 | – | HORVU.MC |
| 0.963583301 | 0.98698936 | 16 | 0 | KQK15464 | 0.978 | 0. | HORVU.MC |
| | | | | | | | |
| 0.95681005 | 0.995332918 | 16 | 0 | KQK10521 | 0.965 | 0. | HORVU.MC |
| 0.957746552 | 0.983757062 | 16 | 1 | KQK11774 | 0.952 | – | HORVU.MC |
| 0.930327128 | 0.961503705 | 16 | 0 | KQJ86798 | 0.960 | 1. | HORVU.MC |
| 0.956866597 | 0.979287791 | 16 | 0 | KQJ97369 | 0.940 | –0 | HORVU.MC |
| 0.963156708 | 0.990159633 | 16 | 1 | KQK10786 | 0.961 | – | HORVU.MC |
| 0.915183414 | 0.973967064 | 16 | 0 | KQJ90289 | 0.889 | –0 | HORVU.MC |
| 0.970000541 | 0.988102963 | 16 | 0 | KQJ82064 | 0.965 | –0 | HORVU.MC |
| | | | | | | | |
| 0.933613909 | 0.95546862 | 16 | 0 | KQK04920 | 0.947 | 0. | HORVU.MC |
| 0.933236667 | 0.969942365 | 16 | 1 | KQK08799 | 0.924 | – | HORVU.MC |
| | | | | | | | |
| 0.915994498 | 0.958317792 | 16 | 0 | KQK19012 | 0.897 | – | HORVU.MC |
| 0.946756466 | 0.979461207 | 16 | 1 | KQJ86869 | 0.934 | –0 | HORVU.MC |
| 0.962062736 | 1.002874035 | 16 | 0 | KQJ82376 | 0.963 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.950226244 | 0.976747109 | 16 | 1 | KQJ81456 | 0.942 | -0 | HORVU.MC |
| 0.956449045 | 1.010191083 | 16 | 0 | KQK00435 | 0.995 | 0 | HORVU.MC |
| 0.972995383 | 0.989985043 | 16 | 0 | KQK22337 | 0.967 | - | HORVU.MC |
| 0.956920776 | 0.97486101 | 16 | 0 | KQK05177 | 0.947 | - | HORVU.MC |
| 0.935117769 | 0.984767145 | 16 | 0 | KQK02561 | 0.841 | - | HORVU.MC |
| 0.970329803 | 0.998111181 | 16 | 1 | KQJ89733 | 0.975 | 0. | HORVU.MC |
| 0.968542723 | 1.007608272 | 16 | 1 | KQJ91272 | 0.980 | 0. | HORVU.MC |
| 0.950686578 | 0.973025833 | 16 | 0 | KQJ90403 | 0.955 | 0. | HORVU.MC |
| 0.942111386 | 0.98772318 | 16 | 1 | KQJ81854 | 0.884 | -1 | HORVU.MC |
| 0.903203309 | 0.936178543 | 16 | 0 | KQK10586 | 0.936 | 1 | HORVU.MC |
| 0.97045614 | 0.996156896 | 16 | 0 | KQJ90431 | 0.968 | -0 | HORVU.MC |
| 0.94681578 | 0.983418367 | 16 | 0 | KQJ90555 | 0.920 | -0 | HORVU.MC |
| 0.954312685 | 0.987166831 | 16 | 1 | KQJ94119 | 0.977 | 0. | HORVU.MC |
| 0.944865063 | 0.985449072 | 16 | 0 | KQJ91406 | 0.953 | 0. | HORVU.MC |

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| 0.904274224 | 0.970819304 | 16 | 0 | KQK18616 | 0.907 | 0. | HORVU.MC |
| 0.948607363 | 0.968131586 | 16 | 0 | KQK01494 | 0.923 | – | genblast_C |
| 0.912426629 | 0.979654834 | 16 | 3 | KQK01979 | 0.914 | 0. | HORVU.MC |
| 0.937446536 | 0.972748381 | 16 | 0 | KQJ99000 | 0.872 | –1 | HORVU.MC |
| 0.874665723 | 0.905773163 | 16 | 0 | KQJ84300 | 0.846 | –1 | HORVU.MC |
| 0.957760637 | 0.983272484 | 16 | 1 | KQK18044 | 0.955 | – | HORVU.MC |
| 0.964043675 | 0.982758621 | 16 | 0 | KQJ92946 | 0.971 | 0. | HORVU.MC |
| 0.883856646 | 0.964481875 | 16 | 0 | KQK07874 | 0.799 | – | HORVU.MC |
| 0.97567058 | 1.010691103 | 16 | 0 | KQK11316 | 0.939 | – | HORVU.MC |
| 0.912338516 | 0.953732913 | 16 | 0 | PNT74105 | 0.902 | – | HORVU.MC |
| 0.925069202 | 0.974574534 | 16 | 2 | KQJ91636 | 0.932 | 0. | HORVU.MC |
| 0.942962428 | 0.970982659 | 16 | 1 | KQK03091 | 0.959 | 0. | HORVU.MC |
| 0.948850136 | 0.971232179 | 16 | 1 | KQJ98495 | 0.949 | –0 | HORVU.MC |

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| 0.938161645 | 0.971498371 | 16 | 0 KQK22494 0.945 0 | HORVU.MC |
| 0.963060011 | 0.994026549 | 16 | 1 KQJ94804 0.967 0. | HORVU.MC |
| 0.955836202 | 0.979550516 | 16 | 2 KQK17180 0.945 – | HORVU.MC |
| 0.960024918 | 0.987351364 | 16 | 1 genblast_Os11t029 | HORVU.MC |
| 0.9621139 | 0.984723854 | 16 | 3 KQJ86002 0.962 –0 | HORVU.MC |
|  |  |  |  |  |
| 0.955337488 | 0.983043789 | 16 | 0 KQJ92852 0.970 0. | HORVU.MC |
|  |  |  |  |  |
| 0.895667805 | 0.987446369 | 16 | 2 PNT72379 0.783 – | HORVU.MC |
| 0.961649745 | 0.984844897 | 16 | 0 genblast_Os06t050 | HORVU.MC |
| 0.946727482 | 0.986980781 | 16 | 0 KQJ91113 0.926 –0 | HORVU.MC |
|  |  |  |  |  |
| 0.955221275 | 1.000096311 | 16 | 2 KQK03604 0.962 0 | genblast_C |
|  |  |  |  |  |
| 0.960643342 | 0.984911406 | 16 | 0 KQK22073 0.973 0 | HORVU.MC |
| 0.95679641 | 0.997797842 | 16 | 0 KQJ87008 0.964 0. | HORVU.MC |
| 0.900654381 | 0.972651509 | 16 | 6 KQJ99260 0.871 –0 | HORVU.MC |
| 0.938348129 | 0.966518706 | 16 | 1 KQK19174 0.941 0 | HORVU.MC |
| 0.962494853 | 0.991628354 | 16 | 1 KQK21213 0.964 0 | HORVU.MC |
| 0.945171376 | 0.977072719 | 16 | 0 KQK13054 0.890 – | HORVU.MC |
| 0.933837197 | 0.975508419 | 16 | 0 genblast_Os05t013 | HORVU.MC |
|  |  |  |  |  |
| 0.930875524 | 0.982243671 | 16 | 0 KQJ86615 0.955 0. | HORVU.MC |
|  |  |  |  |  |
| 0.982071647 | 0.998803669 | 16 | 0 KQK22094 0.982 – | HORVU.MC |
| 0.952113891 | 0.988352028 | 16 | 1 KQK01887 0.936 – | HORVU.MC |
| 0.953664059 | 0.986661177 | 16 | 1 KQK19647 0.946 – | HORVU.MC |
| 0.931555179 | 0.987957475 | 16 | 5 KQK18240 0.857 – | HORVU.MC |
|  |  |  |  |  |
| 0.974897967 | 0.99009901 | 16 | 1 KQK15859 0.984 0 | HORVU.MC |
| 0.898455925 | 0.943556417 | 16 | 0 KQJ98275 0.926 0. | HORVU.MC |
|  |  |  |  |  |
| 0.956757717 | 0.985474066 | 16 | 0 KQK23061 0.924 – | HORVU.MC |

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| 0.857905556 | 0.933258822 | 16 | 0 | genblast_Os07t069 | | | HORVU.MC |
| 0.897959053 | 0.962682752 | 16 | 0 | KQK23547 | 0.945 | 0. | HORVU.MC |
| 0.932694295 | 0.978296817 | 16 | 0 | KQJ94478 | 0.968 | 1. | HORVU.MC |
| 0.983591387 | 0.999920395 | 16 | 0 | KQJ86120 | 0.984 | 0. | HORVU.MC |
| 0.973103085 | 0.994060165 | 16 | 0 | KQJ89821 | 0.978 | 0. | HORVU.MC |
| 0.977112311 | 0.991972874 | 16 | 0 | KQK10334 | 0.959 | – | HORVU.MC |
| 0.946413502 | 0.968438819 | 16 | 0 | KQK15773 | 0.955 | 0 | HORVU.MC |
| | | | | | | | |
| 0.963850645 | 0.987985971 | 16 | 1 | KQK15053 | 0.948 | – | HORVU.MC |
| 0.952649135 | 0.998743111 | 16 | 0 | KQJ96420 | 0.949 | –0 | HORVU.MC |
| 0.963019113 | 0.987446909 | 16 | 0 | KQK00575 | 0.966 | 0 | HORVU.MC |
| | | | | | | | |
| 0.954090013 | 0.979333413 | 16 | 0 | KQK22172 | 0.936 | – | HORVU.MC |
| 0.904774116 | 0.952133479 | 16 | 0 | KQJ86302 | 0.802 | –2 | HORVU.MC |
| 0.946578419 | 0.988284849 | 16 | 0 | KQK20128 | 0.934 | – | HORVU.MC |
| 0.914976253 | 0.980766504 | 16 | 1 | PNT71915 | 0.832 | –1 | HORVU.MC |
| 0.926883711 | 0.97114547 | 16 | 0 | KQK07141 | 0.919 | – | HORVU.MC |
| 0.962326826 | 0.986230059 | 16 | 0 | KQJ98354 | 0.911 | –2 | genblast_Z |
| | | | | | | | |
| 0.888889914 | 0.984642646 | 16 | 0 | KQK04553 | 0.781 | – | HORVU.MC |
| 0.912895115 | 0.97454844 | 16 | 1 | KQJ93433 | 0.928 | 0. | HORVU.MC |
| 0.979590143 | 0.998263534 | 16 | 0 | KQK19906 | 0.963 | – | HORVU.MC |
| 0.958374495 | 0.992096991 | 16 | 0 | KQK23433 | 0.957 | – | HORVU.MC |
| 0.977165222 | 0.992326167 | 16 | 0 | KQK12123 | 0.988 | 1 | HORVU.MC |
| 0.923494029 | 0.968914647 | 16 | 0 | KQK09802 | 0.923 | – | HORVU.MC |
| 0.953293506 | 0.992319032 | 16 | 1 | KQK21644 | 0.939 | – | HORVU.MC |
| 0.901034517 | 0.957932928 | 16 | 3 | KQJ90507 | 0.930 | 0. | HORVU.MC |
| | | | | | | | |
| 0.93155508 | 0.983925675 | 16 | 1 | KQJ99258 | 0.815 | –2 | HORVU.MC |
| 0.905520343 | 0.96823329 | 16 | 2 | KQK10157 | 0.905 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.955081436 | 0.975902155 | 16 | 0 | KQK19058 | 0.938 | -0 | HORVU.MC |
| 0.969575422 | 0.997029808 | 16 | 0 | KQK14076 | 0.976 | 0 | HORVU.MC |
| 0.929426615 | 0.964810111 | 16 | 0 | KQJ98891 | 0.929 | -0 | HORVU.MC |
| 0.946217526 | 0.981899489 | 16 | 0 | KQK13991 | 0.967 | 0 | HORVU.MC |
| 0.970271168 | 0.986592584 | 16 | 0 | KQK00640 | 0.962 | -0 | HORVU.MC |
| 0.972283102 | 0.991414752 | 16 | 1 | KQK21225 | 0.962 | -0 | HORVU.MC |
| 0.940127223 | 0.989067673 | 16 | 1 | KQK01995 | 0.912 | -0 | HORVU.MC |
| 0.943377831 | 0.980950952 | 16 | 0 | PNT65191 | 0.927 | -0 | genblast_C |
| 0.949413799 | 0.995614035 | 16 | 0 | KQJ84336 | 0.916 | -0 | genblast_C |
| 0.908192356 | 0.948220551 | 16 | 2 | KQK06031 | 0.928 | 0 | HORVU.MC |
| 0.959474886 | 0.989083904 | 16 | 1 | KQK09821 | 0.946 | -0 | HORVU.MC |
| 0.955006902 | 0.989531807 | 16 | 0 | KQK12721 | 0.960 | 0 | HORVU.MC |
| 0.952384435 | 0.980105325 | 16 | 0 | KQK00431 | 0.978 | 1 | HORVU.MC |
| 0.915150991 | 0.956569848 | 16 | 0 | KQK20473 | 0.957 | 1 | HORVU.MC |
| 0.967106715 | 0.988821063 | 16 | 0 | KQJ94710 | 0.954 | -0 | HORVU.MC |
| 0.970323798 | 0.993657237 | 16 | 0 | KQK01444 | 0.976 | 0 | HORVU.MC |
| 0.898508168 | 0.960712839 | 16 | 1 | KQK18776 | 0.905 | 0 | HORVU.MC |
| 0.94244272 | 0.97536339 | 16 | 0 | KQJ86338 | 0.871 | -2 | HORVU.MC |
| 0.942561862 | 0.982285636 | 16 | 0 | KQK13625 | 0.924 | -0 | HORVU.MC |
| 0.96130986 | 0.979274904 | 16 | 0 | KQK01681 | 0.969 | 0 | HORVU.MC |

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|---|---|---|---|---|
| 0.926166339 | 0.968188976 | 16 | 1 KQK14262 0.925 – | HORVU.MC |
| 0.97616388 | 1.003516864 | 16 | 0 KQJ82345 0.986 0. | HORVU.MC |
| 0.893331371 | 0.948979592 | 16 | 1 KQK03356 0.869 – | HORVU.MC |
| 0.96197155 | 0.992875891 | 16 | 0 KQK17125 0.945 – | HORVU.MC |
| 0.967249576 | 0.982489173 | 16 | 0 KQK03294 0.976 0 | HORVU.MC |
| 0.948027782 | 0.989940589 | 16 | 1 KQK13013 0.933 – | HORVU.MC |
| 0.885126173 | 0.917970344 | 16 | 0 KQK08279 0.881 – | HORVU.MC |
| 0.981652976 | 0.993567886 | 16 | 0 KQK18147 0.985 0 | HORVU.MC |
| 0.947973869 | 0.974543931 | 16 | 1 KQK23536 0.954 0 | HORVU.MC |
| 0.941301307 | 0.988681454 | 16 | 1 KQJ87581 0.940 –0 | HORVU.MC |
| 0.973129312 | 0.992782933 | 16 | 0 KQJ99228 0.953 –1 | HORVU.MC |
| 0.92521177 | 0.985287561 | 16 | 0 KQK04174 0.913 – | HORVU.MC |
| 0.982812036 | 0.988127041 | 16 | 0 KQJ88621 0.983 –0 | HORVU.MC |
| 0.95074788 | 0.979750898 | 16 | 1 PNT71313 0.955 0. | genblast_C |
| 0.933204186 | 0.982690953 | 16 | 0 KQK06934 0.916 – | HORVU.MC |
| 0.943429825 | 0.971368421 | 16 | 1 KQJ82855 0.937 –0 | HORVU.MC |
| 0.914679652 | 0.961749543 | 16 | 0 KQK19035 0.917 0 | HORVU.MC |
| 0.949112688 | 0.987146158 | 16 | 2 KQJ90873 0.977 0. | HORVU.MC |
| 0.952118398 | 0.982588508 | 16 | 0 KQJ89659 0.946 –0 | HORVU.MC |
| 0.937077602 | 0.973744019 | 16 | 0 KQK02064 0.957 0 | HORVU.MC |
| 0.864309725 | 0.928705441 | 16 | 1 KQJ85786 0.817 –1 | HORVU.MC |
| 0.940457584 | 0.980290006 | 16 | 0 KQJ91643 0.939 –0 | HORVU.MC |
| 0.939776517 | 0.982557394 | 16 | 0 KQK09524 0.945 0 | HORVU.MC |
| 0.955502087 | 0.983302412 | 16 | 0 KQK15158 0.938 – | HORVU.MC |
| 0.925233888 | 0.969230769 | 16 | 0 KQJ97760 0.916 –0 | HORVU.MC |
| 0.934549923 | 0.986415773 | 16 | 3 KQJ96909 0.960 0. | HORVU.MC |
| 0.959790094 | 0.987816183 | 16 | 0 KQK17157 0.956 – | HORVU.MC |
| 0.964957978 | 0.991250288 | 16 | 0 KQJ96369 0.971 0. | HORVU.MC |
| 0.903185611 | 0.954760264 | 16 | 4 KQK19388 0.897 – | genblast_C |
| 0.961273738 | 0.986449089 | 16 | 1 KQJ86448 0.972 0. | HORVU.MC |

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| 0.930786252 | 1.006403013 | 16 | 1 | KQJ91911 | 0.907 | -0 | HORVU.MC |
| 0.929208069 | 0.985669346 | 16 | 1 | KQJ93517 | 0.903 | -0 | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.966520682 | 0.988769377 | 16 | 0 | KQJ91801 | 0.936 | -1 | HORVU.MC |
| 0.962682798 | 0.991918414 | 16 | 0 | KQK03580 | 0.940 | - | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.963457467 | 0.98491147 | 16 | 0 | KQJ99739 | 0.975 | 0. | HORVU.MC |
| 0.95660279 | 0.993264913 | 16 | 0 | KQK00565 | 0.936 | - | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.926324617 | 0.976086163 | 16 | 1 | KQK21502 | 0.948 | 0 | HORVU.MC |
| 0.959134915 | 0.984310796 | 16 | 0 | KQK09200 | 0.956 | - | genblast_C |
| 0.936879229 | 0.984392054 | 16 | 0 | KQK03856 | 0.954 | 0 | HORVU.MC |
| 0.917908163 | 0.953469388 | 16 | 0 | KQJ93708 | 0.902 | -0 | HORVU.MC |
| 0.90389584 | 0.953136172 | 16 | 2 | KQK20360 | 0.941 | 0 | HORVU.MC |
| 0.91803669 | 0.958588703 | 16 | 1 | KQK02348 | 0.888 | - | HORVU.MC |
| 0.90729952 | 0.955494631 | 16 | 1 | PNT62986 | 0.927 | 0. | HORVU.MC |
| 0.950723004 | 0.969210468 | 16 | 0 | KQJ96804 | 0.924 | -1 | HORVU.MC |
| 0.945731511 | 0.981530769 | 16 | 1 | genblast_Os11t025 |  |  | HORVU.MC |
|  |  |  |  |  |  |  |  |
| 0.948917668 | 1.002502503 | 16 | 0 | KQJ84900 | 0.925 | -0 | HORVU.MC |
| 0.939218937 | 0.979345581 | 16 | 0 | KQK07220 | 0.937 | - | HORVU.MC |
| 0.982365766 | 0.996922025 | 16 | 0 | KQK17641 | 0.971 | - | HORVU.MC |
| 0.945720011 | 0.980160294 | 16 | 0 | KQJ99850 | 0.908 | -1 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.980795286 | 0.993615442 | 16 | 0 | KQK10625 0.966 – | HORVU.MC |
| 0.963710013 | 0.985171609 | 16 | 0 | KQK11203 0.950 – | HORVU.MC |
| 0.970383802 | 0.991236023 | 16 | 0 | KQJ82970 0.970 −0 | HORVU.MC |
| 0.940312774 | 0.989720446 | 16 | 1 | genblast_Os07t017 | genblast_C |
| 0.895093563 | 0.958862275 | 16 | 4 | KQK23468 0.873 – | HORVU.MC |
| 0.970298632 | 0.99556213 | 16 | 0 | KQK19007 0.975 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.893290452 | 0.940580728 | 16 | 0 | KQK23765 0.884 – | HORVU.MC |
| 0.919147416 | 0.956656347 | 16 | 0 | KQK14873 0.889 – | HORVU.MC |
| 0.964692075 | 0.994589433 | 16 | 0 | PNT76178 0.939 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.864586934 | 0.945039751 | 16 | 0 | PNT77567 0.878 0. | HORVU.MC |
| 0.948014692 | 0.988861148 | 16 | 0 | KQJ96341 0.888 −2 | genblast_C |
| 0.971397492 | 1.00196229 | 16 | 0 | PNT73796 0.962 – | HORVU.MC |
| 0.968206083 | 0.992164603 | 16 | 0 | KQK21418 0.971 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.956072309 | 0.989938985 | 16 | 0 | KQK22875 0.957 0 | HORVU.MC |
| 0.961297421 | 0.990028411 | 16 | 0 | KQK04814 0.945 – | HORVU.MC |
| 0.928222969 | 0.979142674 | 16 | 0 | KQK12996 0.961 0 | HORVU.MC |
| 0.954213772 | 0.987564234 | 16 | 0 | KQJ88704 0.954 −0 | HORVU.MC |
| 0.947892526 | 0.984356895 | 16 | 1 | KQK10426 0.949 0 | HORVU.MC |
| 0.94099944 | 0.986082227 | 16 | 0 | KQK02518 0.899 – | HORVU.MC |
| 0.98518112 | 1 | 16 | 0 | KQK15742 0.957 – | HORVU.MC |
| 0.955155771 | 0.991811153 | 16 | 1 | KQJ96636 0.973 0. | HORVU.MC |
| 0.922306047 | 0.948541831 | 16 | 0 | KQK14810 0.876 – | HORVU.MC |
| 0.941459142 | 0.972840288 | 16 | 0 | KQK04511 0.952 0 | HORVU.MC |
| 0.986371865 | 0.997049752 | 16 | 0 | KQK22641 0.985 – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.914927941 | 0.971391697 | 16 | 1 | PNT66518 | 0.896 | - | HORVU.MC |
| 0.973215856 | 0.992379836 | 16 | 0 | KQK15672 | 0.976 | 0 | HORVU.MC |
| 0.947000313 | 0.961654135 | 16 | 0 | KQJ82953 | 0.935 | -1 | HORVU.MC |
| 0.989609759 | 1.001506263 | 16 | 0 | KQK18218 | 0.993 | 0 | HORVU.MC |
| 0.948693471 | 1.007187781 | 16 | 0 | KQK00181 | 0.931 | - | HORVU.MC |
| | | | | | | | |
| 0.961453622 | 0.977387603 | 16 | 0 | KQJ84136 | 0.945 | -1 | genblast_C |
| 0.917855424 | 0.976900866 | 16 | 2 | KQK11064 | 0.924 | 0 | HORVU.MC |
| 0.939956728 | 0.97118928 | 16 | 1 | KQK06889 | 0.959 | 0 | HORVU.MC |
| 0.928791751 | 0.961781366 | 16 | 1 | KQJ90683 | 0.911 | -0 | HORVU.MC |
| | | | | | | | |
| 0.953803348 | 0.984455482 | 16 | 0 | KQK19726 | 0.914 | - | HORVU.MC |
| | | | | | | | |
| 0.98596207 | 1.001274968 | 16 | 0 | KQK10905 | 0.967 | - | HORVU.MC |
| 0.949816653 | 0.981540611 | 16 | 0 | KQJ95314 | 0.947 | -0 | HORVU.MC |
| 0.981180501 | 1.005516154 | 16 | 0 | KQK21859 | 0.978 | - | HORVU.MC |
| 0.927672358 | 0.995867769 | 16 | 0 | KQK03815 | 0.913 | - | HORVU.MC |
| 0.96687627 | 0.995020325 | 16 | 0 | KQK07718 | 0.976 | 0 | HORVU.MC |
| 0.866845339 | 0.926526343 | 16 | 1 | KQJ88814 | 0.858 | -0 | HORVU.MC |
| 0.955389376 | 0.977479801 | 16 | 1 | KQK09591 | 0.916 | - | HORVU.MC |
| 0.95662415 | 0.997959184 | 16 | 0 | KQJ99146 | 0.943 | -0 | HORVU.MC |
| 0.876378387 | 0.95463138 | 16 | 0 | KQK23541 | 0.853 | - | HORVU.MC |
| 0.938236103 | 0.986345693 | 16 | 1 | KQK01099 | 0.986 | 1 | HORVU.MC |
| 0.992734709 | 1.006576784 | 16 | 0 | KQJ82703 | 0.992 | -0 | HORVU.MC |
| 0.96848394 | 0.988519092 | 16 | 0 | KQK14160 | 0.956 | - | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.890715191 | 0.934675489 | 16 | 0 | KQJ82980 | 0.800 | –2 | HORVU.MC |
| 0.949254428 | 0.973567672 | 16 | 0 | KQK10600 | 0.914 | – | HORVU.MC |
| 0.945531939 | 0.971911809 | 16 | 0 | KQJ81655 | 0.925 | –1 | HORVU.MC |
| 0.94921927 | 0.97882541 | 16 | 0 | KQJ86339 | 0.942 | –0 | HORVU.MC |
| 0.943143855 | 0.971775663 | 16 | 0 | PNT70659 | 0.933 | – | HORVU.MC |
| 0.932168795 | 0.952232404 | 16 | 1 | KQK09487 | 0.935 | 0 | HORVU.MC |
| 0.970103415 | 0.989080141 | 16 | 0 | KQJ83430 | 0.961 | –0 | HORVU.MC |
| | | | | | | | |
| 0.939453338 | 0.961534259 | 16 | 0 | KQK07301 | 0.911 | – | HORVU.MC |
| 0.939322546 | 0.987197724 | 16 | 0 | KQJ86008 | 0.952 | 0. | genblast_C |
| | | | | | | | |
| 0.890789656 | 0.97550379 | 16 | 0 | KQK21317 | 0.815 | – | genblast_C |
| 0.925547452 | 0.978281127 | 16 | 0 | KQJ83781 | 0.919 | –0 | HORVU.MC |
| 0.974122604 | 0.995284477 | 16 | 0 | KQK00476 | 0.975 | 0 | HORVU.MC |
| 0.8876886 | 0.947778709 | 16 | 2 | KQJ91405 | 0.895 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.894985364 | 0.945218846 | 16 | 0 | KQJ98938 | 0.791 | –2 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.971406931 | 0.999621284 | 16 | 0 | KQJ98835 | 0.964 | –0 | HORVU.MC |
| 0.984618517 | 0.992454853 | 16 | 0 | KQK21033 | 0.978 | – | HORVU.MC |
| 0.964384435 | 0.984371678 | 16 | 0 | KQJ92257 | 0.972 | 0. | HORVU.MC |
| 0.957026842 | 0.991455747 | 16 | 1 | KQK01954 | 0.915 | – | HORVU.MC |
| 0.978938926 | 0.988989227 | 16 | 0 | KQK09729 | 0.979 | – | HORVU.MC |
| 0.969002953 | 0.997155983 | 16 | 0 | KQJ90265 | 0.972 | 0. | HORVU.MC |
| 0.937166976 | 0.975712515 | 16 | 1 | KQK13868 | 0.904 | – | HORVU.MC |
| 0.946526228 | 0.974665179 | 16 | 0 | KQJ90854 | 0.924 | –1 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.979810638 | 0.996287014 | 16 | 0 | KQK18009 | 0.962 | – | HORVU.MC |
| 0.957589392 | 0.975923719 | 16 | 0 | KQJ88871 | 0.904 | –2 | HORVU.MC |
| 0.877743696 | 0.937419076 | 16 | 1 | KQJ86999 | 0.896 | 0. | HORVU.MC |
| 0.965645563 | 0.984272187 | 16 | 0 | KQK12390 | 0.959 | – | HORVU.MC |
| 0.948393139 | 0.996529968 | 16 | 0 | KQK05065 | 0.898 | – | HORVU.MC |
| 0.834226487 | 0.888667331 | 16 | 0 | PNT66666 | 0.857 | 0. | HORVU.MC |
| 0.886286116 | 0.98047084 | 16 | 0 | KQK04860 | 0.841 | – | genblast_C |
| 0.965343066 | 0.976224914 | 16 | 0 | KQK08443 | 0.957 | – | HORVU.MC |

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| 0.952145835 | 0.995358033 | 16 | 0 | KQK08773 | 0.963 | 0 | HORVU.MC |
| 0.974168905 | 0.988985897 | 16 | 0 | KQJ89096 | 0.947 | –2 | HORVU.MC |
| 0.95443162 | 0.990180551 | 16 | 1 | KQK22160 | 0.909 | – | HORVU.MC |
| 0.948848482 | 0.994562987 | 16 | 0 | KQJ92052 | 0.922 | –1 | HORVU.MC |
| 0.961249926 | 0.984907006 | 16 | 0 | KQJ97748 | 0.954 | –0 | HORVU.MC |
| 0.98838018 | 0.999424405 | 16 | 0 | KQK12415 | 0.987 | – | HORVU.MC |

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| 0.933097203 | 0.964987909 | 16 | 0 | PNT60826 | 0.941 | 0. | HORVU.MC |
| 0.943474265 | 0.975251076 | 16 | 0 | KQK17990 | 0.966 | 1 | HORVU.MC |
| 0.897699005 | 0.94885223 | 16 | 2 | KQK22832 | 0.920 | 0 | HORVU.MC |

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| 0.959766554 | 1.000991277 | 16 | 0 | KQJ94842 | 0.954 | –0 | HORVU.MC |
| 0.911972244 | 0.978264269 | 16 | 0 | KQJ94545 | 0.909 | –0 | HORVU.MC |
| 0.968708646 | 0.986546096 | 16 | 0 | KQJ97491 | 0.958 | –0 | HORVU.MC |
| 0.929085828 | 0.984833563 | 16 | 0 | KQK04627 | 0.871 | – | HORVU.MC |
| 0.965502277 | 0.979169778 | 16 | 1 | KQK06270 | 0.971 | 0 | HORVU.MC |
| 0.952364899 | 0.986614724 | 16 | 2 | KQK06500 | 0.957 | 0 | HORVU.MC |
| 0.966608014 | 0.987443014 | 16 | 1 | KQJ83450 | 0.937 | –2 | genblast_C |
| 0.936698157 | 0.985770935 | 16 | 0 | PNT65516 | 0.924 | – | HORVU.MC |
| 0.92988042 | 0.959556679 | 16 | 0 | KQJ91095 | 0.952 | 0. | HORVU.MC |
| 0.910545188 | 0.979510466 | 16 | 0 | KQK12883 | 0.883 | – | HORVU.MC |
| 0.988279315 | 0.999944973 | 16 | 0 | KQK20447 | 0.988 | 0 | HORVU.MC |
| 0.975192901 | 0.993106996 | 16 | 0 | KQJ84592 | 0.964 | –0 | HORVU.MC |
| 0.964422294 | 0.987871108 | 16 | 0 | KQK01103 | 0.959 | – | HORVU.MC |
| 0.949642524 | 0.995337271 | 16 | 0 | KQK08274 | 0.903 | – | HORVU.MC |
| 0.966774939 | 0.991301475 | 16 | 1 | KQJ89699 | 0.953 | –0 | HORVU.MC |
| 0.954773126 | 0.978781236 | 16 | 0 | KQK10036 | 0.958 | 0 | HORVU.MC |
| 0.963118677 | 0.996445174 | 16 | 0 | KQK17328 | 0.934 | – | HORVU.MC |
| 0.955225523 | 0.974477448 | 16 | 1 | KQJ86515 | 0.920 | –2 | HORVU.MC |
| 0.922934514 | 0.973863801 | 16 | 1 | KQK01003 | 0.872 | – | HORVU.MC |
| 0.949742825 | 0.988070539 | 16 | 0 | KQJ84652 | 0.927 | –0 | HORVU.MC |
| 0.971778035 | 0.983167656 | 16 | 0 | KQJ93427 | 0.964 | –1 | HORVU.MC |
| 0.921890908 | 0.973936062 | 16 | 0 | KQJ81835 | 0.944 | 0. | HORVU.MC |
| 0.951069604 | 0.991698595 | 16 | 1 | KQK00518 | 0.972 | 0 | HORVU.MC |
| 0.97496049 | 0.993283287 | 16 | 0 | KQK00657 | 0.957 | – | HORVU.MC |
| 0.97171178 | 0.992379743 | 16 | 0 | KQK13017 | 0.953 | – | HORVU.MC |
| 0.969304626 | 0.987780041 | 16 | 0 | KQJ95059 | 0.970 | 0. | HORVU.MC |
| 0.948696181 | 0.976336921 | 16 | 1 | KQK10815 | 0.955 | 0 | HORVU.MC |
| 0.97077764 | 0.986767867 | 16 | 0 | KQJ99922 | 0.968 | –0 | HORVU.MC |
| 0.971344048 | 0.999293536 | 16 | 0 | KQK20336 | 0.952 | – | HORVU.MC |
| 0.84305265 | 0.909693166 | 16 | 0 | KQK15421 | 0.827 | – | HORVU.MC |
| 0.886950287 | 0.931439497 | 16 | 0 | KQJ90367 | 0.857 | –1 | HORVU.MC |

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| 0.952375512 | 0.984498391 | 16 | 0 | KQK09934 | 0.940 | – | HORVU.MC |
| 0.932826403 | 0.970910335 | 16 | 0 | KQK21191 | 0.899 | – | HORVU.MC |
| 0.959550904 | 0.988854547 | 16 | 1 | KQK15345 | 0.957 | – | HORVU.MC |
| 0.950024774 | 0.977097556 | 16 | 1 | KQK21409 | 0.918 | – | HORVU.MC |
| 0.959942049 | 0.979604124 | 16 | 0 | KQJ98117 | 0.952 | –0 | HORVU.MC |
| 0.962422341 | 0.995181945 | 16 | 1 | KQJ96433 | 0.952 | –0 | HORVU.MC |
| 0.971571953 | 0.997330961 | 16 | 0 | KQJ92502 | 0.934 | –2 | HORVU.MC |
| 0.940403423 | 0.9614169 | 16 | 0 | KQK13050 | 0.935 | – | HORVU.MC |
| 0.978814986 | 0.993889809 | 16 | 1 | KQK11299 | 0.978 | – | HORVU.MC |
| 0.963430957 | 0.992648234 | 16 | 0 | KQJ92649 | 0.920 | –2 | HORVU.MC |
| 0.963513273 | 0.990045034 | 16 | 0 | KQK06661 | 0.990 | 1 | HORVU.MC |
| 0.897923469 | 0.942712971 | 16 | 0 | KQJ88746 | 0.938 | 0. | HORVU.MC |
| 0.921575515 | 0.987173944 | 16 | 0 | KQJ93561 | 0.913 | –0 | HORVU.MC |
| 0.967515472 | 0.998322633 | 16 | 2 | KQJ85654 | 0.967 | –0 | genblast_C |
| 0.949099984 | 0.993121413 | 16 | 2 | KQK18609 | 0.932 | – | HORVU.MC |
| 0.935906721 | 0.975831816 | 16 | 1 | KQJ98427 | 0.904 | –0 | HORVU.MC |
| 0.915972773 | 0.98334655 | 16 | 0 | KQJ86689 | 0.786 | –2 | HORVU.MC |
| 0.881842424 | 0.969055247 | 16 | 0 | KQK12786 | 0.745 | – | HORVU.MC |
| 0.90396592 | 0.963018131 | 16 | 4 | KQK00758 | 0.912 | 0 | HORVU.MC |
| 0.904575893 | 0.982142857 | 16 | 1 | PNT62047 | 0.982 | 1. | HORVU.MC |
| 0.943802411 | 0.96918239 | 16 | 2 | KQJ97555 | 0.932 | –0 | HORVU.MC |
| 0.95751634 | 0.981481481 | 16 | 1 | KQK16399 | 0.980 | 1 | HORVU.MC |
| 0.948869264 | 0.999174645 | 16 | 0 | KQK13899 | 0.928 | – | HORVU.MC |

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| 0.93321855 | 0.955588143 | 16 | 2 | KQJ93739 | 0.904 | –1 | HORVU.MC |
| 0.935685285 | 0.968110236 | 16 | 0 | KQJ91847 | 0.919 | –0 | HORVU.MC |
| 0.962183939 | 0.986289174 | 16 | 0 | KQK12004 | 0.954 | – | HORVU.MC |
| 0.917234741 | 0.958462843 | 16 | 0 | KQK14954 | 0.912 | – | HORVU.MC |
| 0.958499417 | 0.993097414 | 16 | 0 | KQJ97660 | 0.951 | –0 | HORVU.MC |
| 0.976238496 | 0.993904625 | 16 | 0 | KQK09257 | 0.965 | – | HORVU.MC |
| 0.971175098 | 0.992632613 | 16 | 1 | KQK19438 | 0.974 | 0 | HORVU.MC |
| 0.908350297 | 0.963745638 | 16 | 4 | KQK16317 | 0.878 | – | HORVU.MC |
| 0.923220669 | 0.968259127 | 16 | 0 | KQK03816 | 0.929 | 0 | HORVU.MC |
| 0.944748644 | 0.992490613 | 16 | 0 | KQK03152 | 0.911 | – | HORVU.MC |
| 0.948148291 | 0.978587606 | 16 | 0 | KQK11791 | 0.964 | 0 | HORVU.MC |
| 0.935634141 | 0.979229279 | 16 | 1 | KQK15032 | 0.937 | 0 | HORVU.MC |
| 0.938141766 | 0.961108972 | 16 | 0 | KQK18384 | 0.904 | – | HORVU.MC |
| 0.945240704 | 0.977095999 | 16 | 0 | KQK09977 | 0.954 | 0 | HORVU.MC |
| 0.878538704 | 0.941876368 | 16 | 0 | KQJ82290 | 0.857 | –0 | HORVU.MC |
| 0.982537106 | 0.991218306 | 16 | 0 | KQJ84189 | 0.977 | –0 | genblast_C |
| 0.960633905 | 0.990608808 | 16 | 1 | KQK12440 | 0.906 | – | HORVU.MC |
| 0.938112557 | 0.975191424 | 16 | 0 | KQK12840 | 0.917 | – | HORVU.MC |
| 0.914889837 | 0.962331201 | 16 | 3 | KQJ86511 | 0.932 | 0. | HORVU.MC |
| 0.94711347 | 0.980962243 | 16 | 0 | KQJ89741 | 0.953 | 0. | HORVU.MC |
| 0.944410431 | 0.990516882 | 16 | 0 | KQK24080 | 0.935 | – | HORVU.MC |
| 0.875433298 | 0.934033613 | 16 | 0 | KQJ98652 | 0.862 | –0 | HORVU.MC |
| 0.965100908 | 0.996122323 | 16 | 0 | KQK13241 | 0.934 | – | HORVU.MC |

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| 0.982040606 | 0.995640042 | 16 | 0 | KQK05143 | 0.973 | – | HORVU.MC |
| 0.94077381 | 0.970350404 | 16 | 0 | KQK03244 | 0.896 | – | HORVU.MC |
| 0.931551074 | 0.96300058 | 16 | 0 | KQK22607 | 0.934 | 0. | HORVU.MC |
| 0.903991886 | 1.014696877 | 16 | 1 | KQK02982 | 0.912 | 0. | HORVU.MC |
| 0.946139477 | 1.01494396 | 16 | 1 | KQK12911 | 0.844 | – | HORVU.MC |
| 0.947369806 | 0.973048849 | 16 | 0 | KQJ84798 | 0.858 | –3 | HORVU.MC |
| 0.935539588 | 0.975473262 | 16 | 1 | KQJ85617 | 0.898 | –1 | HORVU.MC |
| 0.905654246 | 1 | 16 | 1 | KQJ91322 | 0.921 | 0. | HORVU.MC |
| 0.984195277 | 1.004705472 | 16 | 0 | KQK17548 | 0.982 | – | HORVU.MC |

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| 0.985080564 | 0.996918129 | 16 | 0 | KQK10880 | 0.980 | – | HORVU.MC |
| 0.859109538 | 0.935320417 | 16 | 2 | KQJ97229 | 0.851 | –0 | HORVU.MC |

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| 0.970131066 | 0.984546505 | 16 | 0 | KQJ89108 | 0.971 | 0. | HORVU.MC |
| 0.96672424 | 0.987445717 | 16 | 0 | KQK23713 | 0.960 | – | HORVU.MC |
| 0.945657494 | 0.976506417 | 16 | 0 | KQJ98560 | 0.932 | –1 | HORVU.MC |

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| 0.951423856 | 1.005930402 | 16 | 0 | KQK01529 | 0.919 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.932849225 | 0.985733347 | 16 | 2 | KQJ84273 | 0.960 | 0. | HORVU.MC |
| 0.937897122 | 0.977013642 | 16 | 0 | KQK11170 | 0.926 | – | HORVU.MC |
| 0.927370829 | 0.973841608 | 16 | 7 | KQJ88205 | 0.960 | 1. | HORVU.MC |
| 0.938959671 | 0.969983949 | 16 | 0 | KQJ97610 | 0.934 | –0 | HORVU.MC |
| 0.926097284 | 0.974544423 | 16 | 6 | KQJ99325 | 0.884 | –0 | HORVU.MC |

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| 0.891601563 | 0.956597222 | 16 | 0 | KQK18243 | 0.838 | – | HORVU.MC |
| 0.966543939 | 0.984545797 | 16 | 0 | KQK11371 | 0.968 | 0. | HORVU.MC |
| 0.947408984 | 0.985907223 | 16 | 2 | PNT64980 | 0.968 | 0. | HORVU.MC |
| 0.962395895 | 1.000237954 | 16 | 0 | KQK22415 | 0.958 | – | HORVU.MC |
| 0.946068996 | 0.978975422 | 16 | 0 | KQJ84295 | 0.877 | –2 | HORVU.MC |
| 0.916933049 | 0.958977091 | 16 | 0 | KQJ89419 | 0.787 | –3 | HORVU.MC |
| 0.955076628 | 0.97816092 | 16 | 0 | KQJ84438 | 0.968 | 0. | HORVU.MC |
| 0.941647943 | 0.974997119 | 16 | 1 | KQJ96034 | 0.975 | 1. | HORVU.MC |
| 0.952622696 | 0.973746249 | 16 | 0 | KQK22519 | 0.972 | 0. | HORVU.MC |
| 0.908341712 | 0.946662836 | 16 | 1 | KQJ99525 | 0.916 | 0. | HORVU.MC |
| 0.979527954 | 1.000803482 | 16 | 0 | KQJ93628 | 0.978 | –0 | HORVU.MC |
| 0.945174808 | 0.986590038 | 16 | 2 | genblast_Os02t014 | | | HORVU.MC |
| 0.981111713 | 0.992973539 | 16 | 1 | KQK13579 | 0.975 | – | HORVU.MC |
| 0.952676232 | 0.982232704 | 16 | 0 | KQK10463 | 0.956 | 0. | HORVU.MC |
| 0.982309508 | 1.001756697 | 16 | 0 | KQK09025 | 0.962 | – | HORVU.MC |
| 0.891922963 | 0.945245884 | 16 | 2 | KQK15839 | 0.903 | 0. | genblast_C |

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| 0.903992331 | 0.962935558 | 16 | 1 | KQJ88865 | 0.912 | 0. | HORVU.MC |

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| 0.973950038 | 1.000167659 | 16 | 0 | KQJ97164 | 0.977 | 0. | HORVU.MC |
| 0.914114298 | 0.96867493 | 16 | 2 | KQJ89601 | 0.837 | –1 | HORVU.MC |
| 0.891782928 | 0.945094509 | 16 | 0 | KQK05980 | 0.902 | 0 | HORVU.MC |
| 0.965180235 | 0.993606202 | 16 | 0 | KQK08049 | 0.971 | 0 | HORVU.MC |
| 0.912087072 | 0.988784666 | 16 | 1 | PNT66521 | 0.779 | – | HORVU.MC |
| 0.925231757 | 0.968191869 | 16 | 0 | KQK04812 | 0.866 | – | HORVU.MC |
| 0.946865221 | 0.970138578 | 16 | 0 | KQK11173 | 0.926 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.962081102 | 0.981278561 | 16 | 0 | KQJ85792 | 0.949 | –1 | HORVU.MC |
| 0.91201098 | 0.964107769 | 16 | 3 | KQK01676 | 0.931 | 0 | HORVU.MC |
| 0.859850843 | 0.908298426 | 16 | 1 | KQJ99233 | 0.881 | 0. | HORVU.MC |
| 0.867304642 | 0.938581315 | 16 | 0 | KQK18812 | 0.875 | 0 | HORVU.MC |
| 0.959262239 | 0.980694093 | 16 | 0 | KQK22433 | 0.964 | 0 | HORVU.MC |
| 0.976851852 | 0.991218022 | 16 | 0 | KQJ95286 | 0.972 | –0 | HORVU.MC |
| 0.931841543 | 0.964205095 | 16 | 0 | KQK19025 | 0.935 | 0 | HORVU.MC |
| 0.92409509 | 0.97270273 | 16 | 0 | KQK20113 | 0.849 | – | HORVU.MC |
| 0.949673285 | 0.979140488 | 16 | 0 | KQK09032 | 0.956 | 0 | HORVU.MC |
| 0.930993028 | 0.984126984 | 16 | 2 | KQK21256 | 0.936 | 0 | HORVU.MC |
| 0.941292299 | 0.983518086 | 16 | 0 | KQK17327 | 0.914 | – | HORVU.MC |
| 0.982662854 | 1.000798585 | 16 | 0 | KQK13273 | 0.971 | – | HORVU.MC |
| 0.940631991 | 0.991498881 | 16 | 2 | KQK23895 | 0.900 | – | HORVU.MC |
| 0.945496102 | 0.97466468 | 16 | 0 | PNT64513 | 0.918 | – | HORVU.MC |
| 0.885647659 | 0.967617036 | 16 | 0 | KQK18432 | 0.803 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.926042777 | 0.962309854 | 16 | 1 | KQJ86639 | 0.929 | 0. | HORVU.MC |
| 0.873268197 | 0.94375517 | 16 | 0 | PNT70250 | 0.748 | – | HORVU.MC |
| 0.953071758 | 0.98957707 | 16 | 0 | KQK21792 | 0.944 | – | HORVU.MC |
| 0.882067519 | 0.919855709 | 16 | 1 | KQJ87055 | 0.864 | –0 | HORVU.MC |
| 0.8763873 | 0.95583524 | 16 | 2 | KQK22072 | 0.914 | 0 | genblast_C |
| 0.951085893 | 0.988651927 | 16 | 0 | KQK20008 | 0.881 | – | HORVU.MC |

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| 0.986003861 | 1.000160875 | 16 | 0 | KQK08481 | 0.999 | 1 | HORVU.MC |

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| 0.953881469 | 0.989705064 | 16 | 0 | KQJ96519 0.978 0. | HORVU.MC |
| 0.940765301 | 0.958727602 | 16 | 0 | KQK22864 0.951 0 | HORVU.MC |
| 0.980916079 | 0.994177138 | 16 | 0 | KQJ82247 0.981 0. | HORVU.MC |
| 0.968874697 | 0.989169161 | 16 | 0 | KQK22173 0.966 – | HORVU.MC |
| 0.922644387 | 0.968840516 | 16 | 2 | KQK15597 0.918 – | HORVU.MC |
| 0.951769894 | 0.980338825 | 16 | 1 | KQJ86716 0.959 0. | HORVU.MC |
| | | | | | |
| 0.973763118 | 0.99643928 | 16 | 0 | KQK19731 0.957 – | HORVU.MC |
| 0.968065998 | 0.994152047 | 16 | 0 | KQK08552 0.967 – | genblast_C |
| 0.926602086 | 0.959936881 | 16 | 0 | KQK12029 0.952 0 | HORVU.MC |
| | | | | | |
| 0.890409695 | 0.958497375 | 16 | 0 | genblast_Os08t047 | genblast_C |
| 0.98024583 | 1.007901668 | 16 | 0 | KQJ97495 0.980 –0 | HORVU.MC |
| 0.96311849 | 0.979557292 | 16 | 0 | KQJ94758 0.934 –1 | HORVU.MC |
| 0.939065399 | 0.985273655 | 16 | 0 | KQJ93804 0.910 –1 | HORVU.MC |
| 0.96961483 | 0.996604741 | 16 | 0 | KQJ97130 0.972 0. | HORVU.MC |
| 0.958760542 | 0.99735406 | 16 | 0 | KQJ83146 0.967 0. | HORVU.MC |
| 0.96461973 | 0.992878845 | 16 | 0 | PNT68072 0.957 – | HORVU.MC |
| 0.956110485 | 0.998156871 | 16 | 0 | KQK03954 0.971 0 | HORVU.MC |
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| 0.967920675 | 0.983276296 | 16 | 0 | KQK00976 0.957 – | HORVU.MC |
| 0.930928476 | 0.968589625 | 16 | 3 | PNT77069 0.935 0. | HORVU.MC |
| 0.953054582 | 0.988683025 | 16 | 0 | KQK15118 0.918 – | HORVU.MC |
| 0.901544232 | 0.943654036 | 16 | 1 | KQJ89333 0.892 –0 | HORVU.MC |
| 0.96215155 | 0.985021843 | 16 | 0 | KQK21950 0.944 – | HORVU.MC |
| 0.975398024 | 1.001921493 | 16 | 1 | KQK21577 0.988 0 | HORVU.MC |
| 0.959275172 | 0.981641731 | 16 | 0 | KQK18471 0.966 0 | HORVU.MC |
| 0.903048547 | 0.955370795 | 16 | 3 | KQJ90494 0.914 0. | HORVU.MC |
| 0.941030182 | 0.987804127 | 16 | 0 | KQJ91273 0.931 –0 | HORVU.MC |
| 0.961241923 | 0.987663991 | 16 | 0 | KQJ90437 0.970 0. | genblast_C |
| 0.955640415 | 0.98396861 | 16 | 0 | KQJ92823 0.940 –0 | HORVU.MC |
| 0.964201849 | 0.992287918 | 16 | 0 | KQK22407 0.964 – | HORVU.MC |
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| 0.964084803 | 0.974979009 | 16 | 0 | KQJ98407 0.963 –0 | HORVU.MC |

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| 0.966182543 | 0.982865822 | 16 | 0 | KQJ82852 | 0.970 | 0. | HORVU.MC |
| 0.986716692 | 1.012200194 | 16 | 1 | KQJ97345 | 0.965 | −0 | HORVU.MC |
| 0.944238911 | 0.977705275 | 16 | 0 | KQJ92057 | 0.942 | −0 | HORVU.MC |
| 0.975097929 | 0.996642417 | 16 | 0 | KQK06837 | 0.985 | 0 | HORVU.MC |
| 0.978070175 | 1.001711596 | 16 | 0 | KQJ98239 | 0.968 | −0 | HORVU.MC |

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| 0.968459658 | 0.992176039 | 16 | 0 | KQK17716 | 0.948 | – | HORVU.MC |
| 0.970235351 | 0.992317148 | 16 | 0 | KQJ92942 | 0.964 | −0 | HORVU.MC |
| 0.9060357 | 0.966115369 | 16 | 1 | KQK16687 | 0.892 | − | HORVU.MC |
| 0.960009579 | 0.982667396 | 16 | 1 | KQJ96973 | 0.955 | −0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.981077665 | 0.994852941 | 16 | 0 | KQK17179 | 0.964 | – | HORVU.MC |
| 0.95803209 | 0.983561644 | 16 | 0 | KQJ85601 | 0.968 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.971357729 | 1.002442838 | 16 | 2 | KQJ98220 | 0.988 | 0. | HORVU.MC |
| 0.987712127 | 1.015728477 | 16 | 0 | KQJ97360 | 0.934 | −1 | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.940704146 | 0.990196078 | 16 | 3 | KQJ97554 | 0.946 | 0. | HORVU.MC |
| 0.873201293 | 0.94890865 | 16 | 0 | KQK10627 | 0.771 | – | HORVU.MC |
| 0.913618641 | 0.947827701 | 16 | 0 | KQK00760 | 0.848 | − | genblast_C |
| 0.88250872 | 0.957499031 | 16 | 2 | KQK15391 | 0.777 | – | HORVU.MC |
| 0.98603127 | 1.001389766 | 16 | 0 | KQK16073 | 0.981 | − | HORVU.MC |
| 0.968871045 | 0.994994339 | 16 | 0 | PNT69402 | 0.967 | − | HORVU.MC |
| 0.966869035 | 0.993291127 | 16 | 0 | KQK18484 | 0.972 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.963269477 | 0.991663995 | 16 | 0 | KQK23643 | 0.954 | – | HORVU.MC |
| 0.958626335 | 0.990945856 | 16 | 1 | KQK10995 | 0.959 | – | HORVU.MC |
| 0.934461494 | 0.976815241 | 16 | 0 | KQJ91269 | 0.932 | –0 | HORVU.MC |
| 0.966090426 | 0.988743196 | 16 | 0 | KQJ82503 | 0.978 | 0. | HORVU.MC |
| 0.951066208 | 0.982509952 | 16 | 0 | KQK09386 | 0.947 | – | genblast_C |

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|---|---|---|---|---|---|---|---|
| 0.946725917 | 0.976219247 | 16 | 3 | KQK07664 | 0.963 | 0 | HORVU.MC |
| 0.94953737 | 0.970355731 | 16 | 0 | PNT77473 | 0.913 | –1 | HORVU.MC |
| 0.963659644 | 0.992338441 | 16 | 1 | PNT63622 | 0.958 | – | HORVU.MC |
| 0.892836143 | 0.927087417 | 16 | 0 | KQK18650 | 0.822 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.956768886 | 0.98092745 | 16 | 0 | KQK10279 | 0.955 | – | HORVU.MC |
| 0.928249276 | 0.990255465 | 16 | 0 | KQJ82983 | 0.878 | –1 | genblast_C |
| 0.962332346 | 0.981659389 | 16 | 0 | KQJ99655 | 0.970 | 0. | HORVU.MC |
| 0.887714663 | 0.975488038 | 16 | 2 | KQK13601 | 0.883 | – | HORVU.MC |
| 0.971988051 | 0.994710494 | 16 | 0 | KQK17850 | 0.973 | 0 | genblast_C |
| 0.947682119 | 0.97218543 | 16 | 0 | KQK03736 | 0.932 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.85397293 | 0.915031847 | 16 | 0 | KQJ94471 | 0.828 | –0 | HORVU.MC |
| 0.881358741 | 0.966362883 | 16 | 0 | KQK22733 | 0.805 | – | HORVU.MC |
| 0.940466811 | 0.966778281 | 16 | 0 | KQK12221 | 0.925 | – | HORVU.MC |
| 0.972975733 | 0.987958474 | 16 | 0 | KQK17629 | 0.965 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.950295376 | 0.995111021 | 16 | 0 | KQK19480 | 0.979 | 0 | HORVU.MC |
| 0.935711346 | 0.963403824 | 16 | 0 | KQK03307 | 0.942 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.913496974 | 0.962667785 | 16 | 2 | KQJ84800 | 0.921 | 0. | HORVU.MC |
| 0.932577676 | 0.970535549 | 16 | 0 | PNT74171 | 0.828 | –2 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.929628651 | 0.973569446 | 16 | 0 | KQK19915 | 0.920 | – | HORVU.MC |
| 0.959172078 | 0.991280148 | 16 | 1 | KQK22215 | 0.953 | – | HORVU.MC |
| 0.96511642 | 0.99293252 | 16 | 4 | KQK15108 | 0.975 | 0 | HORVU.MC |
| 0.930916976 | 0.976101965 | 16 | 0 | PNT76556 | 0.949 | 0. | HORVU.MC |
| 0.977964826 | 0.992327168 | 16 | 2 | KQJ93806 | 0.985 | 0. | HORVU.MC |

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| 0.925393357 | 0.964801865 | 16 | 0 | KQK16987 0.901 – | HORVU.MC |
| 0.980624033 | 0.996907123 | 16 | 0 | KQJ91465 0.986 0. | HORVU.MC |
| 0.973425286 | 0.991456099 | 16 | 0 | KQK22088 0.989 0 | HORVU.MC |
| 0.953801591 | 0.978444177 | 16 | 0 | KQK15424 0.952 – | HORVU.MC |
| 0.892185759 | 0.964661468 | 16 | 1 | KQK13565 0.848 – | genblast_C |
| 0.899865976 | 0.965117941 | 16 | 1 | genblast_Os08t017 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.89837972 | 0.964577657 | 16 | 0 | KQK05633 0.903 0 | HORVU.MC |
| 0.942691076 | 0.981002872 | 16 | 0 | KQJ95971 0.957 0. | HORVU.MC |
| 0.950712333 | 0.974528709 | 16 | 0 | KQK01825 0.907 – | HORVU.MC |
| 0.95049863 | 0.993300853 | 16 | 0 | KQJ91121 0.943 –0 | HORVU.MC |
| 0.951950791 | 0.988994864 | 16 | 0 | KQK07863 0.920 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.961535476 | 0.980593076 | 16 | 0 | KQK17766 0.957 – | HORVU.MC |
| 0.947968622 | 0.971343067 | 16 | 1 | KQK10209 0.969 0 | genblast_C |
| 0.939898969 | 0.986557322 | 16 | 0 | KQJ91792 0.923 –0 | genblast_C |
| 0.927515107 | 0.963176282 | 16 | 0 | KQK16485 0.939 0 | HORVU.MC |
| 0.942087894 | 0.976046362 | 16 | 0 | KQK17563 0.948 0 | HORVU.MC |
| 0.981490616 | 1.002694899 | 16 | 0 | KQK00545 0.962 – | HORVU.MC |

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| 0.968114481 | 0.99684432 | 16 | 2 | KQK14206 0.957 – | HORVU.MC |

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|---|---|---|---|---|---|
| 0.972426221 | 0.999818668 | 16 | 1 | KQK02010 0.981 0 | HORVU.MC |

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|---|---|---|---|---|---|
| 0.966552316 | 1.002650865 | 16 | 0 | KQK15080 0.960 – | HORVU.MC |
| 0.947316607 | 0.97659766 | 16 | 0 | KQJ87817 0.941 –0 | HORVU.MC |
| 0.918904331 | 0.972639641 | 16 | 4 | KQJ84645 0.947 0. | HORVU.MC |
| 0.927601656 | 0.980992465 | 16 | 1 | PNT72148 0.938 0. | HORVU.MC |
| 0.96638277 | 0.994903041 | 16 | 0 | PNT67400 0.944 – | HORVU.MC |
| 0.935827017 | 0.966996066 | 16 | 0 | KQJ83866 0.928 –0 | HORVU.MC |
| 0.984607136 | 1.000186486 | 16 | 0 | KQJ86278 0.974 –1 | HORVU.MC |

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| 0.913903986 | 0.951449275 | 16 | 0 | KQK14611 | 0.856 | – | genblast_C |
| 0.970042755 | 1.001155535 | 16 | 0 | KQK18878 | 0.972 | 0 | HORVU.MC |
| 0.906561462 | 0.945064072 | 16 | 5 | KQK03965 | 0.912 | 0 | HORVU.MC |
| 0.942038622 | 0.964539007 | 16 | 0 | KQK21311 | 0.950 | 0 | HORVU.MC |
| 0.964673913 | 1.010628019 | 16 | 0 | KQK23339 | 0.939 | – | HORVU.MC |
| 0.967530801 | 0.994524298 | 16 | 0 | KQJ84762 | 0.960 | –0 | HORVU.MC |
| 0.872055615 | 0.928439546 | 16 | 4 | KQJ90129 | 0.875 | 0. | HORVU.MC |
| 0.963365801 | 0.984090909 | 16 | 0 | KQK07375 | 0.956 | – | HORVU.MC |
| 0.968206429 | 0.997783083 | 16 | 0 | KQK23377 | 0.974 | 0 | HORVU.MC |
| 0.942974726 | 1.00059997 | 16 | 0 | KQJ89695 | 0.961 | 0. | genblast_C |
| 0.966990016 | 0.992100644 | 16 | 0 | KQK00831 | 0.953 | – | HORVU.MC |
| 0.937472202 | 1.001779096 | 16 | 1 | KQK13637 | 0.906 | – | HORVU.MC |
| 0.969030741 | 0.992069062 | 16 | 0 | KQK14613 | 0.953 | – | HORVU.MC |
| 0.979502055 | 0.994805047 | 16 | 0 | PNT64399 | 0.975 | – | HORVU.MC |
| 0.955000981 | 0.982256518 | 16 | 3 | KQK12727 | 0.978 | 0 | HORVU.MC |
| 0.948494779 | 0.998751561 | 16 | 2 | KQK06505 | 0.934 | – | HORVU.MC |
| 0.954385246 | 0.993114754 | 16 | 0 | PNT77044 | 0.993 | 1. | HORVU.MC |
| 0.954646833 | 0.99078375 | 16 | 0 | KQJ85251 | 0.961 | 0. | HORVU.MC |
| 0.88313253 | 0.95753012 | 16 | 0 | KQK12770 | 0.761 | – | HORVU.MC |
| 0.961115256 | 0.9949024 | 16 | 0 | KQK00694 | 0.964 | 0 | HORVU.MC |
| 0.977190575 | 1.001059803 | 16 | 0 | KQJ83418 | 0.982 | 0. | HORVU.MC |
| 0.977741678 | 0.995212038 | 16 | 1 | KQK00773 | 0.984 | 0 | HORVU.MC |
| 0.952664533 | 0.982644557 | 16 | 1 | KQJ85597 | 0.958 | 0. | HORVU.MC |
| 0.886654551 | 0.923514539 | 16 | 0 | KQK12331 | 0.884 | – | HORVU.MC |
| 0.969698948 | 0.992315153 | 16 | 0 | KQK15018 | 0.962 | – | HORVU.MC |
| 0.945180668 | 0.995231108 | 16 | 0 | KQK22316 | 0.806 | – | HORVU.MC |
| 0.911874538 | 0.943418136 | 16 | 0 | KQK01424 | 0.869 | – | HORVU.MC |
| 0.95959892 | 0.997164358 | 16 | 0 | KQK03768 | 0.949 | – | genblast_C |
| 0.944432773 | 0.981428571 | 16 | 0 | KQK13706 | 0.972 | 0 | HORVU.MC |
| 0.954622583 | 0.994405594 | 16 | 0 | KQJ93298 | 0.972 | 0. | HORVU.MC |
| 0.949505419 | 0.998041264 | 16 | 0 | KQJ86942 | 0.905 | –1 | HORVU.MC |

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|---|---|---|---|
| 0.859659331 | 0.983072366 | 16 | 0 KQJ93289 0.789 −0genblast_C |
| 0.975312041 | 0.995249201 | 16 | 0 KQJ97890 0.977 0. HORVU.MC |
| 0.932085553 | 0.979959411 | 16 | 0 KQJ96053 0.957 0. HORVU.MC |
| 0.920755291 | 0.979800762 | 16 | 3 KQK05332 0.943 0 genblast_C |
| 0.960552171 | 0.984181568 | 16 | 0 KQK14061 0.965 0 HORVU.MC |
| 0.959880864 | 0.990595943 | 16 | 1 KQK01628 0.988 0 HORVU.MC |
| 0.920647618 | 0.976782696 | 16 | 1 KQK03419 0.936 0 HORVU.MC |
| 0.933781581 | 0.988101059 | 16 | 1 KQJ88926 0.938 0. HORVU.MC |
| 0.95746916 | 0.980570547 | 16 | 1 KQK00410 0.969 0 HORVU.MC |
| 0.945659456 | 0.987748851 | 16 | 0 KQK09961 0.952 0 HORVU.MC |
| 0.949502514 | 0.98791056 | 16 | 0 KQK16980 0.936 − HORVU.MC |
| 0.973865052 | 0.989565488 | 16 | 0 KQK02996 0.955 − HORVU.MC |
| 0.954593788 | 0.982471215 | 16 | 0 KQJ94354 0.939 −0HORVU.MC |
| 0.959266974 | 0.981473815 | 16 | 1 KQJ91282 0.956 −0HORVU.MC |
| 0.922556945 | 0.995460338 | 16 | 0 KQJ86808 0.848 −1HORVU.MC |
| 0.989363753 | 1.007455013 | 16 | 1 KQJ94779 0.981 −0HORVU.MC |
| 0.975866684 | 0.989034236 | 16 | 0 KQK18549 0.971 − HORVU.MC |
| 0.942088432 | 0.976041756 | 16 | 3 KQK00787 0.936 − HORVU.MC |
| 0.959907545 | 0.986302933 | 16 | 0 KQK07961 0.921 − HORVU.MC |
| 0.928258663 | 0.97743367 | 16 | 2 genblast_Os02t018 genblast_C |
| 0.97108259 | 0.994952207 | 16 | 0 KQJ97214 0.952 −1HORVU.MC |
| 0.948058482 | 0.971877174 | 16 | 0 KQK03120 0.921 − HORVU.MC |

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|---|---|---|---|---|
| 0.950058041 | 0.980793584 | 16 | 1 KQK13699 0.949 – | HORVU.MC |
| 0.978114532 | 1.001202439 | 16 | 0 KQJ84113 0.984 0. | genblast_C |
| 0.981327566 | 0.992028263 | 16 | 0 KQK02066 0.966 – | HORVU.MC |
| 0.942063131 | 0.986967489 | 16 | 2 KQJ94327 0.952 0. | HORVU.MC |
| 0.944811525 | 0.981408539 | 16 | 1 KQJ90116 0.934 –0 | HORVU.MC |
| 0.892259013 | 0.951930453 | 16 | 2 KQJ86452 0.912 0. | HORVU.MC |
| 0.98123815 | 0.991573625 | 16 | 0 KQK17109 0.986 0 | HORVU.MC |
| 0.979313423 | 0.9955973 | 16 | 0 KQJ83392 0.971 –0 | HORVU.MC |
| 0.972264438 | 0.991793313 | 16 | 0 KQK13080 0.964 – | HORVU.MC |
| 0.934968325 | 0.959030796 | 16 | 0 KQK18784 0.930 – | HORVU.MC |
| 0.885566891 | 0.985253884 | 16 | 4 genblast_Os08t033 | HORVU.MC |
| 0.925712673 | 0.965056011 | 16 | 1 KQJ84137 0.922 –0 | HORVU.MC |
| 0.913536849 | 0.952558556 | 16 | 2 KQJ90565 0.937 0. | HORVU.MC |
| 0.960952591 | 0.971529352 | 16 | 0 KQK10508 0.963 0 | HORVU.MC |
| 0.959635174 | 0.990407897 | 16 | 0 PNT71409 0.919 – | HORVU.MC |
| 0.979716057 | 0.992819843 | 16 | 0 KQJ91931 0.972 –0 | HORVU.MC |
| 0.949489087 | 0.984579408 | 16 | 2 KQK20427 0.960 0 | HORVU.MC |
| 0.987087268 | 1.00342227 | 16 | 0 KQK06998 0.986 – | HORVU.MC |
| 0.954412865 | 0.991194082 | 16 | 2 KQJ97459 0.951 –0 | HORVU.MC |
| 0.947186015 | 0.976955207 | 16 | 0 KQK21993 0.948 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.97004645 | 0.998315042 | 16 | 0 | KQK16854 | 0.972 | 0 | HORVU.MC |
| 0.938372763 | 0.981968547 | 16 | 1 | KQJ90499 | 0.968 | 0. | HORVU.MC |
| 0.976738764 | 0.995736365 | 16 | 0 | KQJ83295 | 0.972 | −0 | HORVU.MC |
| 0.968636508 | 0.991717107 | 16 | 0 | PNT69100 | 0.954 | − | HORVU.MC |
| 0.969069168 | 0.98766306 | 16 | 0 | KQK01782 | 0.970 | 0 | HORVU.MC |
| 0.957699878 | 0.98547577 | 16 | 0 | KQJ83702 | 0.972 | 0. | HORVU.MC |
| 0.977838029 | 1.005658376 | 16 | 0 | KQK22359 | 0.976 | − | HORVU.MC |
| 0.987801647 | 1.004076308 | 16 | 0 | KQJ91136 | 0.996 | 0. | HORVU.MC |
| 0.934917657 | 0.996686806 | 16 | 1 | KQK10284 | 0.963 | 0 | HORVU.MC |
| 0.941359736 | 0.978401905 | 16 | 0 | KQK24048 | 0.948 | 0 | HORVU.MC |
| 0.943321263 | 0.997787166 | 16 | 0 | KQK01074 | 0.881 | − | HORVU.MC |
| 0.916593009 | 1.013001825 | 16 | 0 | PNT65728 | 0.886 | − | HORVU.MC |
| 0.932064989 | 1.009512585 | 16 | 1 | KQK08848 | 0.921 | − | genblast_Z |
| 0.960617418 | 0.985923552 | 16 | 0 | KQK08987 | 0.937 | − | HORVU.MC |
| 0.981127797 | 1.004837734 | 16 | 0 | KQK22563 | 0.950 | − | HORVU.MC |
| 0.944848116 | 0.983311457 | 16 | 0 | KQK13663 | 0.938 | − | HORVU.MC |
| | | | | | | | |
| 0.93890382 | 0.985985794 | 16 | 0 | KQK02228 | 0.883 | − | HORVU.MC |
| 0.947685121 | 0.983884412 | 16 | 1 | KQK09160 | 0.968 | 0 | HORVU.MC |
| 0.923078098 | 0.987778049 | 16 | 0 | KQK06121 | 0.939 | 0 | HORVU.MC |
| 0.943184797 | 0.963302752 | 16 | 0 | KQJ88363 | 0.955 | 1. | HORVU.MC |
| 0.91165275 | 0.96574165 | 16 | 1 | KQJ85210 | 0.943 | 0. | genblast_C |
| 0.889799223 | 0.916062176 | 16 | 0 | KQK03343 | 0.870 | − | HORVU.MC |
| 0.969383628 | 0.990940466 | 16 | 0 | KQJ97212 | 0.972 | 0. | HORVU.MC |
| 0.96380916 | 0.985099874 | 16 | 2 | KQJ89004 | 0.973 | 0. | HORVU.MC |
| 0.934258596 | 0.981661891 | 16 | 0 | KQK00608 | 0.932 | − | HORVU.MC |
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| 0.960699649 | 0.995836586 | 16 | 0 | KQK17509 | 0.948 | − | HORVU.MC |
| 0.949337448 | 0.974620166 | 16 | 0 | KQK17670 | 0.950 | 0 | genblast_C |
| 0.965230144 | 1.002166065 | 16 | 1 | KQK12653 | 0.932 | − | HORVU.MC |
| 0.916419631 | 0.958366271 | 16 | 4 | KQK12767 | 0.917 | 0 | genblast_C |
| 0.956700648 | 0.982633546 | 16 | 0 | KQJ85353 | 0.956 | −0 | HORVU.MC |
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| 0.932757087 | 0.975594254 | 16 | 0 | KQJ95265 | 0.897 | −1 | HORVU.MC |
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| 0.94226811 | 0.961973583 | 16 | 0 | KQK00393 | 0.926 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.941145059 | 0.994799406 | 16 | 0 | KQJ98886 | 0.887 | -1 | HORVU.MC |
| 0.897784695 | 0.952490102 | 16 | 0 | KQK15743 | 0.870 | – | HORVU.MC |
| | | | | | | | |
| 0.956275136 | 0.990208078 | 16 | 0 | KQK08894 | 0.969 | 0 | HORVU.MC |
| 0.907726655 | 0.987249203 | 16 | 1 | KQJ84528 | 0.871 | -0 | genblast_C |
| 0.953622742 | 0.979146141 | 16 | 0 | KQJ83612 | 0.973 | 0. | HORVU.MC |
| 0.958899655 | 0.987957442 | 16 | 1 | KQK01929 | 0.951 | – | HORVU.MC |
| 0.980604279 | 0.994088923 | 16 | 0 | KQK09583 | 0.971 | – | HORVU.MC |
| 0.948245133 | 0.989580477 | 16 | 0 | KQK16272 | 0.894 | – | HORVU.MC |
| | | | | | | | |
| 0.954838069 | 0.981867464 | 16 | 0 | PNT72800 | 0.963 | 0. | HORVU.MC |
| 0.932253431 | 0.979093521 | 16 | 0 | KQK12901 | 0.926 | – | HORVU.MC |
| 0.966567026 | 0.98504547 | 16 | 0 | PNT69679 | 0.968 | 0. | HORVU.MC |
| 0.979455678 | 1.002703974 | 16 | 0 | KQK12382 | 0.973 | – | HORVU.MC |
| 0.902109186 | 0.951647411 | 16 | 0 | KQK05554 | 0.854 | – | HORVU.MC |
| 0.941973079 | 0.971634931 | 16 | 0 | PNT77967 | 0.924 | – | HORVU.MC |
| | | | | | | | |
| 0.950517319 | 1 | 16 | 0 | KQK21723 | 0.887 | – | HORVU.MC |
| | | | | | | | |
| 0.913721567 | 0.972367313 | 16 | 2 | KQK10165 | 0.921 | 0 | genblast_C |
| 0.972919102 | 0.997328435 | 16 | 0 | KQK12964 | 0.968 | – | HORVU.MC |
| | | | | | | | |
| 0.879805816 | 0.93715847 | 16 | 0 | KQK13896 | 0.900 | 0 | HORVU.MC |
| 0.974687456 | 0.996308678 | 16 | 0 | KQK22775 | 0.967 | – | HORVU.MC |
| 0.94829908 | 0.985461772 | 16 | 1 | KQK15211 | 0.909 | – | HORVU.MC |
| 0.900616032 | 0.959555001 | 16 | 0 | genblast_Os05t049 | | | HORVU.MC |
| 0.928092561 | 0.948961938 | 16 | 0 | KQK01553 | 0.935 | 0 | HORVU.MC |

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| 0.936072612 | 0.984135286 | 16 | 0 | KQJ90945 | 0.975 | 0. | HORVU.MC |
| 0.958755469 | 0.981349298 | 16 | 0 | PNT60802 | 0.934 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.922694324 | 0.954349167 | 16 | 0 | KQK00277 | 0.896 | – | HORVU.MC |
| 0.965827114 | 0.998507463 | 16 | 0 | KQK00863 | 0.945 | – | HORVU.MC |
| 0.962244986 | 0.993775934 | 16 | 0 | KQK06666 | 0.972 | 0 | HORVU.MC |
| 0.952443086 | 0.983397952 | 16 | 0 | KQK03697 | 0.950 | – | HORVU.MC |
| 0.890207095 | 0.948365527 | 16 | 0 | KQK18793 | 0.917 | 0 | HORVU.MC |
| 0.972664716 | 0.997615951 | 16 | 0 | KQK12669 | 0.941 | – | HORVU.MC |
| 0.961214226 | 0.993250667 | 16 | 1 | KQK13083 | 0.976 | 0 | HORVU.MC |
| 0.862265711 | 0.92216097 | 16 | 1 | KQJ86641 | 0.858 | –0 | HORVU.MC |
| 0.96633341 | 0.998386539 | 16 | 0 | KQK18106 | 0.967 | 0 | HORVU.MC |
| 0.931802628 | 0.970709006 | 16 | 0 | KQK22307 | 0.907 | – | HORVU.MC |
| 0.887762739 | 0.968917197 | 16 | 2 | KQK24194 | 0.869 | – | HORVU.MC |
| 0.920864248 | 0.959824128 | 16 | 2 | KQJ91394 | 0.879 | –1 | HORVU.MC |
| 0.953042883 | 0.976965224 | 16 | 0 | KQJ95607 | 0.957 | 0. | HORVU.MC |
| 0.917217052 | 0.965475833 | 16 | 0 | KQK11972 | 0.851 | – | HORVU.MC |
| 0.947468873 | 0.987418087 | 16 | 0 | KQJ90221 | 0.947 | –0 | HORVU.MC |
| 0.951994243 | 0.974154135 | 16 | 0 | KQJ86554 | 0.974 | 1. | HORVU.MC |
| 0.929584233 | 0.974777448 | 16 | 3 | KQK04619 | 0.942 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.967108089 | 0.996134574 | 16 | 2 | KQK15762 | 0.963 | – | HORVU.MC |
| 0.955174626 | 0.987441562 | 16 | 0 | KQK17002 | 0.934 | – | HORVU.MC |
| 0.971526427 | 1.021400778 | 16 | 0 | KQJ86622 | 1.004 | 0. | HORVU.MC |
| 0.959812262 | 0.987973013 | 16 | 0 | genblast_Os03t030 | | | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.945235123 | 0.971868498 | 16 | 0 | PNT66194 | 0.848 | – | genblast_C |
| 0.943491674 | 0.982917497 | 16 | 0 | KQK06119 | 0.948 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.957988513 | 1.001729249 | 16 | 0 | KQJ97943 | 0.960 | 0. | HORVU.MC |
| 0.943186971 | 0.978234583 | 16 | 0 | KQK13580 | 0.899 | – | HORVU.MC |
| 0.973539045 | 0.985519738 | 16 | 0 | KQK04108 | 0.971 | – | HORVU.MC |
| 0.968955171 | 0.986798447 | 16 | 0 | KQK05730 | 0.950 | – | HORVU.MC |
| 0.9172845 | 0.985896929 | 16 | 0 | KQJ98951 | 0.883 | –0 | HORVU.MC |
| 0.89178623 | 0.957369942 | 16 | 1 | KQK15981 | 0.899 | 0 | HORVU.MC |
| 0.950998793 | 0.985654914 | 16 | 2 | KQJ84340 | 0.950 | –0 | HORVU.MC |
| 0.95982502 | 0.988066506 | 16 | 2 | KQK06001 | 0.953 | – | HORVU.MC |
| 0.955431993 | 0.976390077 | 16 | 0 | KQK14316 | 0.949 | – | HORVU.MC |
| 0.957461529 | 0.981631288 | 16 | 0 | PNT77235 | 0.963 | 0. | HORVU.MC |
| 0.954333677 | 0.982487357 | 16 | 0 | KQK22099 | 0.967 | 0 | HORVU.MC |
| | | | | | | | |
| 0.911116309 | 0.937280254 | 16 | 2 | KQK18632 | 0.874 | – | HORVU.MC |
| 0.971286209 | 0.987163246 | 16 | 0 | KQJ90400 | 0.956 | –1 | HORVU.MC |
| | | | | | | | |
| 0.848485468 | 0.937510224 | 16 | 6 | PNT69243 | 0.851 | 0. | HORVU.MC |
| 0.963341346 | 0.983391608 | 16 | 0 | KQK21528 | 0.983 | 1 | HORVU.MC |
| | | | | | | | |
| 0.975312256 | 1.003903201 | 16 | 0 | KQJ82959 | 0.989 | 0. | HORVU.MC |
| 0.968963377 | 1.006207325 | 16 | 0 | PNT77603 | 0.979 | 0. | HORVU.MC |
| | | | | | | | |
| 0.95795675 | 0.98120915 | 16 | 0 | KQJ94595 | 0.952 | –0 | HORVU.MC |
| 0.925818746 | 0.979672501 | 16 | 0 | KQK09003 | 0.935 | 0 | genblast_C |
| 0.981601534 | 1.007487217 | 16 | 0 | KQJ94860 | 0.974 | –0 | HORVU.MC |
| 0.935144054 | 0.995684732 | 16 | 0 | KQK16914 | 0.935 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.975745249 | 0.991638955 | 16 | 0 | KQK04280 | 0.980 | 0 | HORVU.MC |
| 0.927336355 | 0.963051659 | 16 | 0 | KQK10227 | 0.890 | – | HORVU.MC |
| 0.965685217 | 0.996333046 | 16 | 0 | KQK12424 | 0.975 | 0 | HORVU.MC |
| 0.914848463 | 0.980054485 | 16 | 1 | KQK01010 | 0.912 | – | HORVU.MC |
| 0.914457791 | 0.970876392 | 16 | 0 | KQK04770 | 0.832 | – | HORVU.MC |
| 0.966398727 | 0.989554431 | 16 | 0 | KQK11060 | 0.977 | 0 | HORVU.MC |
| 0.935453869 | 0.959886128 | 16 | 0 | KQK17583 | 0.960 | 1 | HORVU.MC |

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| 0.934482074 | 0.989223542 | 16 | 1 | KQK12430 | 0.867 | – | HORVU.MC |
| 0.897402501 | 0.952664483 | 16 | 0 | KQK03274 | 0.883 | – | HORVU.MC |
| 0.886581263 | 0.943322981 | 16 | 0 | KQJ89791 | 0.775 | –2 | HORVU.MC |
| 0.972503948 | 0.983515941 | 16 | 0 | KQK00300 | 0.962 | – | HORVU.MC |
| 0.965356013 | 0.978101266 | 16 | 0 | KQK14755 | 0.970 | 0 | HORVU.MC |
| 0.950979225 | 0.985772963 | 16 | 1 | KQK21327 | 0.965 | 0 | HORVU.MC |
| 0.976179245 | 0.994339623 | 16 | 0 | KQJ89953 | 0.976 | 0. | HORVU.MC |
| 0.973363673 | 0.991299692 | 16 | 1 | KQK14112 | 0.977 | 0 | HORVU.MC |
| 0.960929748 | 0.992855725 | 16 | 0 | KQK19459 | 0.934 | – | HORVU.MC |
| 0.965474961 | 0.989502667 | 16 | 0 | KQK12127 | 0.937 | – | HORVU.MC |
| 0.97635975 | 0.994755033 | 16 | 1 | KQK23497 | 0.960 | – | HORVU.MC |
| 0.941623829 | 0.980283079 | 16 | 1 | KQJ96880 | 0.941 | –0 | HORVU.MC |
| 0.971699507 | 0.993474798 | 16 | 1 | KQJ97625 | 0.977 | 0. | HORVU.MC |
| 0.928539598 | 0.990832697 | 16 | 0 | KQJ91748 | 0.977 | 0. | genblast_C |
| 0.898178345 | 0.98061871 | 16 | 0 | KQJ92354 | 0.887 | –0 | HORVU.MC |
| 0.934445769 | 0.968414779 | 16 | 0 | KQK06453 | 0.942 | 0 | HORVU.MC |
| 0.969962006 | 0.984620061 | 16 | 0 | KQJ86176 | 0.968 | –0 | HORVU.MC |
| 0.987905032 | 1.004330297 | 16 | 0 | KQK07839 | 0.986 | – | HORVU.MC |
| 0.933107209 | 0.978537784 | 16 | 3 | KQK14481 | 0.949 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.919506746 | 0.987559138 | 16 | 0 | KQK24153 | 0.922 | 0 | HORVU.MC |
| 0.922540402 | 0.979253112 | 16 | 0 | KQK02852 | 0.900 | – | HORVU.MC |
| 0.926558281 | 0.95679568 | 16 | 0 | KQJ92550 | 0.937 | 0. | HORVU.MC |
| 0.939267756 | 0.969411272 | 16 | 0 | KQK19122 | 0.882 | – | HORVU.MC |
| 0.949150527 | 0.98080581 | 16 | 0 | KQK01250 | 0.963 | 0 | HORVU.MC |
| 0.943483596 | 0.97472099 | 16 | 0 | KQK09891 | 0.945 | 0 | HORVU.MC |
| 0.935020669 | 0.980419175 | 16 | 0 | KQJ99886 | 0.897 | –1 | HORVU.MC |
| 0.961555733 | 0.989392348 | 16 | 3 | KQJ93221 | 0.976 | 0. | HORVU.MC |
| 0.910343709 | 0.955901427 | 16 | 0 | genblast_Os03t035 | | | HORVU.MC |
| 0.940135668 | 0.966540894 | 16 | 3 | KQJ83516 | 0.967 | 0. | HORVU.MC |
| 0.96174088 | 0.982357489 | 16 | 0 | KQK22835 | 0.952 | – | HORVU.MC |
| 0.933128783 | 0.999615717 | 16 | 0 | KQK02506 | 0.927 | – | genblast_C |
| 0.94710607 | 0.975783016 | 16 | 0 | KQK15924 | 0.973 | 0 | HORVU.MC |
| 0.905990664 | 0.936277416 | 16 | 0 | KQK18343 | 0.890 | – | HORVU.MC |
| 0.940109622 | 0.964949029 | 16 | 1 | KQJ86943 | 0.897 | –2 | HORVU.MC |
| 0.898456307 | 0.958353394 | 16 | 1 | KQK13802 | 0.958 | 1 | HORVU.MC |
| 0.968899395 | 0.99071991 | 16 | 0 | KQK22674 | 0.963 | – | HORVU.MC |
| 0.911779184 | 0.987060478 | 16 | 1 | KQK01976 | 0.833 | – | HORVU.MC |
| 0.947357735 | 0.978380195 | 16 | 0 | KQK12175 | 0.957 | 0 | HORVU.MC |
| 0.95209998 | 0.971786525 | 16 | 0 | KQK01744 | 0.958 | 0 | HORVU.MC |
| 0.95423053 | 0.98061309 | 16 | 0 | KQJ84119 | 0.962 | 0. | genblast_C |
| 0.964635522 | 0.989469553 | 16 | 0 | KQK20514 | 0.967 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.913215925 | 0.976451806 | 16 | 0 | KQK10377 | 0.829 | – | HORVU.MC |
| 0.931324416 | 0.972321014 | 16 | 0 | KQK11448 | 0.924 | – | HORVU.MC |
| 0.919478308 | 0.963141026 | 16 | 1 | KQK18639 | 0.930 | 0 | HORVU.MC |
| 0.963730327 | 0.991006745 | 16 | 0 | KQK23458 | 0.941 | – | HORVU.MC |
| 0.89292814 | 0.954572228 | 16 | 2 | KQK04756 | 0.833 | – | genblast_C |
| 0.94059345 | 0.977837971 | 16 | 0 | KQK19795 | 0.909 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.947503236 | 0.990077653 | 16 | 0 | KQK23442 | 0.990 | 0 | genblast_C |
| 0.948574197 | 0.99158361 | 16 | 0 | KQJ83691 | 0.954 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.951952527 | 0.97002844 | 16 | 1 | PNT76107 | 0.958 | 0. | HORVU.MC |
| 0.87364083 | 0.957816594 | 16 | 4 | KQK11970 | 0.908 | 0 | HORVU.MC |
| 0.921035046 | 0.955746956 | 16 | 0 | KQK18382 | 0.918 | – | HORVU.MC |
| 0.96203553 | 0.984171531 | 16 | 0 | KQK23409 | 0.963 | 0 | HORVU.MC |
| 0.967164454 | 1.002212389 | 16 | 0 | KQK10863 | 0.969 | 0 | HORVU.MC |
| 0.952666728 | 0.975416819 | 16 | 0 | KQJ90318 | 0.954 | 0. | HORVU.MC |
| 0.956905562 | 0.979693916 | 16 | 1 | KQK18840 | 0.971 | 0 | HORVU.MC |

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| 0.937294514 | 0.972156581 | 16 | 0 | KQK22856 | 0.914 | – | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.923317963 | 0.964021301 | 16 | 0 | KQK15272 | 0.890 | – | HORVU.MC |
| 0.937944774 | 0.99851742 | 16 | 0 | KQK12567 | 0.882 | – | HORVU.MC |
| 0.95469856 | 0.988948218 | 16 | 0 | PNT65418 | 0.925 | –1 | HORVU.MC |
| 0.955502112 | 0.975504458 | 16 | 0 | KQK14771 | 0.952 | – | HORVU.MC |
| | | | | | | | |
| 0.964164856 | 0.992981283 | 16 | 1 | KQK16908 | 0.950 | – | HORVU.MC |
| 0.957547488 | 0.980870268 | 16 | 0 | PNT69583 | 0.981 | 0. | HORVU.MC |
| 0.981913347 | 0.998858758 | 16 | 1 | KQK23761 | 0.985 | 0 | HORVU.MC |
| 0.976705245 | 0.991953044 | 16 | 0 | KQJ81962 | 0.967 | –0 | HORVU.MC |
| | | | | | | | |
| 0.989993273 | 1.004036327 | 16 | 0 | PNT61709 | 0.981 | – | HORVU.MC |
| 0.966068656 | 0.986498346 | 16 | 0 | KQJ86858 | 0.961 | –0 | HORVU.MC |
| 0.960310587 | 0.992587818 | 16 | 0 | KQK15620 | 0.906 | – | HORVU.MC |
| 0.980240245 | 1.000493127 | 16 | 0 | KQK21938 | 0.925 | – | HORVU.MC |
| 0.974374234 | 0.986366587 | 16 | 0 | KQJ91016 | 0.970 | –0 | HORVU.MC |
| | | | | | | | |
| 0.928485577 | 0.987854251 | 16 | 0 | KQJ97191 | 0.904 | –0 | HORVU.MC |
| 0.950476367 | 0.97946053 | 16 | 0 | KQK19878 | 0.979 | 1 | HORVU.MC |
| | | | | | | | |
| 0.931147759 | 0.969412448 | 16 | 0 | KQK04633 | 0.850 | – | HORVU.MC |

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| 0.964483253 | 0.979021595 | 16 | 0 | KQJ89043 | 0.953 | –1 | HORVU.MC |
| 0.873184694 | 0.94315752 | 16 | 1 | KQK11199 | 0.813 | – | genblast_C |
| 0.883726685 | 0.9596164 | 16 | 3 | KQJ84462 | 0.843 | –0 | HORVU.MC |
| 0.974676187 | 0.983062106 | 16 | 0 | KQK17229 | 0.982 | 0. | HORVU.MC |
| 0.948781005 | 0.978051392 | 16 | 2 | KQJ92356 | 0.973 | 0. | genblast_C |
| 0.961732397 | 1.005222402 | 16 | 0 | KQK23958 | 0.927 | – | HORVU.MC |
| 0.948799988 | 0.975186702 | 16 | 2 | KQK03868 | 0.922 | – | HORVU.MC |
| 0.905260339 | 0.981929955 | 16 | 0 | KQK19651 | 0.879 | – | HORVU.MC |
| 0.936980413 | 0.994709661 | 16 | 1 | KQK23571 | 0.916 | – | HORVU.MC |
| 0.966424338 | 0.987872106 | 16 | 0 | KQK03648 | 0.978 | 0. | HORVU.MC |
| 0.98986048 | 1.007787151 | 16 | 0 | KQK22744 | 0.992 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.960182058 | 0.98232627 | 16 | 0 | KQJ96954 | 0.962 | 0. | HORVU.MC |
| 0.961679379 | 0.992115187 | 16 | 0 | KQK23802 | 0.960 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.919355089 | 0.961323912 | 16 | 9 | KQK01877 | 0.926 | 0. | HORVU.MC |
| 0.932938807 | 0.964975363 | 16 | 0 | KQJ92592 | 0.916 | −0 | HORVU.MC |
| 0.968353459 | 0.99263201 | 16 | 0 | KQJ90632 | 0.957 | −0 | HORVU.MC |
| 0.922157482 | 0.935308212 | 16 | 0 | KQJ83821 | 0.898 | −1 | HORVU.MC |
| 0.961002968 | 1.003840782 | 16 | 0 | KQK15017 | 0.980 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.936992207 | 0.970983253 | 16 | 0 | KQJ86763 | 0.896 | −1 | HORVU.MC |
| 0.947467852 | 0.993152973 | 16 | 0 | KQK05957 | 0.971 | 0. | HORVU.MC |
| 0.948372918 | 0.988032079 | 16 | 1 | genblast_Os11t026 | | | HORVU.MC |
| 0.918117637 | 1.005890506 | 16 | 0 | KQJ98338 | 0.952 | 0. | HORVU.MC |
| 0.956607298 | 0.992745212 | 16 | 0 | KQJ84118 | 0.939 | −0 | HORVU.MC |
| 0.959914049 | 0.984232365 | 16 | 0 | KQJ89852 | 0.950 | −0 | HORVU.MC |
| 0.975945816 | 0.98669373 | 16 | 0 | KQJ95552 | 0.983 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.970083873 | 0.985482029 | 16 | 1 | KQK07412 | 0.947 | – | HORVU.MC |
| 0.937244768 | 0.970137825 | 16 | 0 | KQJ90980 | 0.906 | −1 | HORVU.MC |
| 0.967553543 | 0.983957661 | 16 | 0 | KQK21509 | 0.955 | – | HORVU.MC |
| 0.973259645 | 0.980857017 | 16 | 0 | KQK06249 | 0.964 | – | HORVU.MC |
| 0.932607185 | 0.961589113 | 16 | 0 | KQK06830 | 0.922 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.980538695 | 0.996054628 | 16 | 0 | KQJ81451 | 0.968 | –1 | HORVU.MC |
| 0.957904848 | 0.989942366 | 16 | 0 | KQK11237 | 0.920 | – | HORVU.MC |
| 0.908084482 | 0.967330271 | 16 | 0 | KQK20318 | 0.917 | 0 | HORVU.MC |
| 0.972764381 | 0.988754325 | 16 | 0 | KQJ90408 | 0.984 | 0. | HORVU.MC |
| 0.94502242 | 0.983322845 | 16 | 1 | KQK03791 | 0.910 | – | HORVU.MC |
| 0.960139372 | 0.977577864 | 16 | 0 | KQK17357 | 0.944 | – | HORVU.MC |
| 0.98474299 | 0.997603013 | 16 | 0 | KQK13496 | 0.981 | – | HORVU.MC |
| 0.888290925 | 0.962074303 | 16 | 6 | KQK21182 | 0.742 | – | HORVU.MC |
| 0.965447529 | 0.988515436 | 16 | 1 | KQK00992 | 0.975 | 0 | HORVU.MC |
| 0.957877307 | 0.982735232 | 16 | 2 | KQK03011 | 0.975 | 0 | HORVU.MC |
| 0.987062553 | 0.99688297 | 16 | 0 | KQK01847 | 0.980 | – | HORVU.MC |
| 0.94833307 | 0.975588561 | 16 | 1 | KQJ91717 | 0.914 | –1 | HORVU.MC |
| 0.965439464 | 0.991956821 | 16 | 0 | KQJ93047 | 0.969 | 0. | HORVU.MC |
| 0.896066768 | 0.964399688 | 16 | 0 | KQK12076 | 0.846 | – | HORVU.MC |
| 0.947987684 | 0.975258412 | 16 | 0 | KQJ99842 | 0.942 | –0 | HORVU.MC |
| 0.980791038 | 1.002206694 | 16 | 0 | KQK05668 | 0.980 | – | HORVU.MC |
| 0.938996096 | 0.983648818 | 16 | 1 | KQK00153 | 0.904 | – | HORVU.MC |
| 0.972797397 | 0.992536634 | 16 | 0 | KQJ99001 | 0.959 | –0 | HORVU.MC |
| 0.915771771 | 0.972659384 | 16 | 1 | PNT65460 | 0.774 | – | HORVU.MC |
| 0.981708716 | 1.001834862 | 16 | 0 | KQK00962 | 0.988 | 0 | HORVU.MC |
| 0.951404715 | 0.976817289 | 16 | 0 | KQK05908 | 0.945 | – | HORVU.MC |
| 0.962419022 | 0.99057715 | 16 | 0 | KQK12905 | 0.970 | 0 | HORVU.MC |
| 0.974858597 | 1.004072398 | 16 | 0 | KQJ92277 | 0.931 | –1 | HORVU.MC |
| 0.969518468 | 0.995199373 | 16 | 0 | KQK10502 | 0.973 | 0 | HORVU.MC |
| 0.939825465 | 0.99679936 | 16 | 0 | KQK04898 | 0.907 | – | HORVU.MC |
| 0.974385799 | 0.997300216 | 16 | 0 | KQK17547 | 0.989 | 0 | HORVU.MC |
| 0.945339237 | 0.980093543 | 16 | 3 | KQK13458 | 0.952 | 0 | HORVU.MC |
| 0.908647218 | 0.975086164 | 16 | 1 | KQK16904 | 0.908 | – | HORVU.MC |
| 0.914641647 | 0.96636283 | 16 | 3 | KQK02565 | 0.915 | 0 | HORVU.MC |
| 0.937121009 | 0.985799816 | 16 | 1 | KQJ97349 | 0.920 | –0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.956532976 | 0.996235818 | 16 | 1 | genblast_Os03t078 | | | HORVU.MC |
| 0.947749029 | 0.981409545 | 16 | 0 | KQK21726 | 0.948 | 0. | HORVU.MC |
| 0.914861807 | 0.959915953 | 16 | 0 | KQJ96761 | 0.912 | −0 | HORVU.MC |
| 0.941015319 | 0.991501733 | 16 | 1 | KQJ96070 | 0.949 | 0. | HORVU.MC |
| 0.96547619 | 0.992753623 | 16 | 0 | KQK03267 | 0.953 | − | HORVU.MC |
| 0.966279127 | 1.000458175 | 16 | 0 | KQK11139 | 0.966 | − | HORVU.MC |
| 0.97167933 | 0.997803003 | 16 | 0 | KQJ82903 | 0.960 | −0 | HORVU.MC |
| 0.974242254 | 0.990121239 | 16 | 1 | KQK22561 | 0.981 | 0. | HORVU.MC |
| 0.977689445 | 1.002435724 | 16 | 0 | KQK21640 | 0.973 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.961795701 | 0.990223904 | 16 | 1 | KQK10177 | 0.960 | − | HORVU.MC |
| 0.887196049 | 0.992705167 | 16 | 2 | KQK19974 | 0.802 | − | HORVU.MC |
| 0.980431238 | 0.999818808 | 16 | 0 | KQJ95341 | 0.978 | −0 | HORVU.MC |
| 1.000589623 | 1.013140162 | 16 | 0 | KQK15071 | 0.990 | − | HORVU.MC |
| 0.977030159 | 0.9940483 | 16 | 0 | KQK19908 | 0.975 | − | HORVU.MC |
| 0.947900792 | 0.990704054 | 16 | 1 | KQK14555 | 0.911 | − | HORVU.MC |
| 0.983024957 | 1.000516351 | 16 | 0 | KQK00855 | 0.985 | 0. | HORVU.MC |
| 0.918174408 | 1.004294576 | 16 | 0 | KQK02637 | 0.887 | − | HORVU.MC |
| 0.948426495 | 0.991117491 | 16 | 2 | KQJ88302 | 0.951 | 0. | HORVU.MC |
| 0.937071918 | 1 | 16 | 0 | KQJ84874 | 0.868 | −1 | HORVU.MC |
| 0.958044886 | 0.991514069 | 16 | 0 | KQJ86457 | 0.931 | −1 | HORVU.MC |
| 0.951754805 | 0.975690467 | 16 | 0 | KQJ85689 | 0.929 | −1 | HORVU.MC |
| 0.921869449 | 0.981882771 | 16 | 2 | KQJ89917 | 0.935 | 0. | HORVU.MC |
| 0.914431545 | 0.987456632 | 16 | 1 | KQJ81642 | 0.928 | 0. | HORVU.MC |
| 0.957460139 | 0.98547636 | 16 | 1 | KQJ86078 | 0.948 | −0 | HORVU.MC |
| 0.962478156 | 1.007527894 | 16 | 0 | KQK21526 | 0.969 | 0. | HORVU.MC |
| 0.966682762 | 0.994688556 | 16 | 0 | KQK00140 | 0.980 | 0. | HORVU.MC |
| 0.957446809 | 0.987626377 | 16 | 1 | KQK06271 | 0.943 | − | HORVU.MC |
| 0.90982535 | 0.947814265 | 16 | 0 | PNT69486 | 0.878 | − | HORVU.MC |
| 0.872521246 | 0.917193288 | 16 | 0 | KQJ99889 | 0.882 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.937123151 | 0.98568516 | 16 | 1 | KQJ96510 | 0.935 | −0 | genblast_C |
| 0.941561845 | 0.988654581 | 16 | 1 | KQJ84268 | 0.928 | −0 | HORVU.MC |
| 0.916587205 | 0.966192788 | 16 | 2 | KQK12859 | 0.910 | − | HORVU.MC |
| 0.974653824 | 0.993557564 | 16 | 0 | KQJ93916 | 0.971 | −0 | HORVU.MC |
| 0.969037428 | 0.997118794 | 16 | 0 | KQK23291 | 0.975 | 0. | HORVU.MC |
| 0.933193481 | 0.971760529 | 16 | 1 | KQK17627 | 0.951 | 0. | HORVU.MC |
| 0.9391247 | 0.970647482 | 16 | 0 | KQK14504 | 0.909 | − | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.957860468 | 0.990459337 | 16 | 0 | KQJ84144 | 0.902 | -2 | HORVU.MC |
| 0.954250581 | 0.984336001 | 16 | 0 | KQK19474 | 0.966 | 0 | HORVU.MC |
| 0.934719793 | 0.968511808 | 16 | 0 | KQK22496 | 0.942 | 0 | HORVU.MC |
| 0.977263943 | 1.006294865 | 16 | 0 | KQK04367 | 0.976 | - | genblast_C |
| 0.964228359 | 0.984572452 | 16 | 1 | PNT68547 | 0.953 | - | HORVU.MC |
| 0.943423235 | 0.97764966 | 16 | 0 | KQK16886 | 0.964 | 0 | HORVU.MC |
| 0.959765953 | 0.9880308 | 16 | 0 | KQJ84053 | 0.972 | 0. | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.942333497 | 0.973767765 | 16 | 1 | KQJ82524 | 0.957 | 0. | HORVU.MC |
| 0.935109066 | 0.973142932 | 16 | 0 | KQJ85436 | 0.915 | -1 | HORVU.MC |
| 0.967577675 | 0.996164173 | 16 | 0 | KQK09854 | 0.975 | 0 | HORVU.MC |
| 0.975210781 | 0.993811104 | 16 | 0 | KQK20177 | 0.964 | - | HORVU.MC |
| 0.958446602 | 0.98776699 | 16 | 0 | KQK08295 | 0.955 | - | HORVU.MC |
| 0.949360665 | 0.993303198 | 16 | 0 | KQK21381 | 0.950 | 0 | HORVU.MC |
| 0.961931585 | 0.987125051 | 16 | 0 | KQJ89906 | 0.971 | 0. | HORVU.MC |
| 0.953921338 | 0.994536034 | 16 | 1 | KQK13321 | 0.951 | - | HORVU.MC |
| 0.955684422 | 0.986445208 | 16 | 0 | KQK21795 | 0.976 | 0 | HORVU.MC |

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|---|---|---|---|---|---|---|---|
| 0.94171891 | 0.979003405 | 16 | 1 | KQK14622 | 0.923 | – | HORVU.MC |
| 0.953540875 | 0.989353612 | 16 | 0 | KQK09587 | 0.968 | 0. | HORVU.MC |
| 0.898266944 | 0.942815249 | 16 | 0 | KQJ94105 | 0.900 | 0. | HORVU.MC |
| 0.946198735 | 0.998036649 | 16 | 0 | KQK14587 | 0.957 | 0. | HORVU.MC |
| 0.922284958 | 0.965265355 | 16 | 1 | KQJ98906 | 0.963 | 0. | HORVU.MC |
| 0.943108896 | 0.969432742 | 16 | 0 | KQJ85219 | 0.962 | 0. | HORVU.MC |
| 0.967196935 | 0.975499303 | 16 | 0 | PNT67855 | 0.971 | 0. | HORVU.MC |

group members: pep_id R deviation_in_R_SDs_from_mean number_of_

| Leersia_pe | Lolium_pe | Oryza_rufi | Oryza_sati | Secale_cer | Triticum_a | Echinochlo | Eragrostis_ |
|---|---|---|---|---|---|---|---|
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7A | scaffold16 | TVU04957 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3D | scaffold16 | TVU02737 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t025 | SECCE2Rv | TraesCS2A | scaffold15 | TVU13327 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t029 | SECCE4Rv | TraesCS7B | scaffold33 | TVU03309 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4D | scaffold11 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15594 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4B | scaffold35 | TVU45269 |
| LPERR02G | genblast_Z | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold19 | TVU29404 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1B | scaffold27 | TVU31991 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1D | scaffold45 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t016 | SECCE6Rv | TraesCS6A | scaffold1. | TVU32670 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t029 | SECCE6Rv | TraesCS6B | scaffold14 | TVU51631 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS7A | scaffold36 | TVT98473 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE7Rv | TraesCS7D | scaffold51 | TVT98467 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold53 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE5Rv | TraesCS5A | scaffold76 | TVU49630 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3B | scaffold47 | TVU22254 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t045 | SECCE6Rv | TraesCS7A | scaffold22 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7D | scaffold33 | TVU08694 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1D | scaffold80 | TVU20323 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08247 |
| LPERR02G | genblast_C | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6B | scaffold18 | TVU27916 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t039 | SECCE5Rv | TraesCS5B | scaffold27 | TVU09465 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold16 | TVU10135 |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7D | scaffold32 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold25 | TVU44014 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t032 | SECCE4Rv | TraesCS6A | scaffold44 | TVU32260 |
| LPERR12G | genblast_C | ORUFI11G | Os11t021 | SECCE3Rv | TraesCS4A | scaffold18 | TVU25865 |
| | | | | | | | |
| LPERR07G | cds.KYUSt_ | ORUFI12G | Os11t013 | SECCE4Rv | TraesCS4A | scaffold64 | TVU27102 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3A | scaffold14 | genblast_C |
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| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37408 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE7Rv | TraesCS7B | scaffold25 | TVU08242 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48281 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2B | scaffold58 | TVU38975 |
| LPERR06G | cds.KYUSt_ | ORUFI01G | Os01t053 | SECCE7Rv | TraesCS7B | scaffold60 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold11 | TVU09533 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t051 | SECCE4Rv | TraesCS7A | scaffold15 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS4A | genblast_C | genblast_C |
| LPERR03G | genblast_C | ORUFI03G | Os03t027 | SECCE5Rv | TraesCS4B | scaffold14 | TVU47578 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5A | scaffold11 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS2A | scaffold33 | TVU02817 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE7Rv | TraesCS7A | scaffold15 | TVU04591 |

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| LPERR04G | genblast_C | ORUFI04G | Os04t030 | SECCE2Rv | TraesCS2B | scaffold13 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49753 |
| LPERR03G | cds.KYUSt_ | genblast_C | genblast_C | SECCE7Rv | TraesCS4A | scaffold18 | TVU48383 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6D | scaffold25 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | genblast_C | TraesCS2A | scaffold16 | TVU16401 |
| LPERR05G | genblast_C | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE4Rv | TraesCS7D | scaffold30 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3B | scaffold4. | TVU22893 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t054 | SECCE1Rv | TraesCS1D | scaffold13 | TVU20429 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3A | scaffold14 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t057 | SECCE4Rv | TraesCS4D | scaffold17 | TVU29547 |
| genblast_C | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold25 | TVU07876 |
| LPERR02G | genblast_C | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6A | scaffold17 | TVU29425 |
| LPERR08G | genblast_C | ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7B | scaffold16 | TVU03917 |

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|---|---|---|---|---|---|---|---|
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t049 | SECCE3Rv | TraesCS6B | scaffold91 | TVT97664 |
| LPERR11G | genblast_C | ORUFI11G | Os11t019 | genblast_C | TraesCS4A | scaffold19 | TVU26224 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS5D | scaffold3. | TVU44077 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1D | scaffold20 | TVU31294 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t056 | SECCE3Rv | TraesCS3D | scaffold7. | TVU24888 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19602 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12297 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | genblast_C | TraesCS1D | scaffold18 | TVU20503 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t020 | SECCE6Rv | TraesCS6B | scaffold1. | TVU33003 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold48 | TVU32842 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1D | scaffold11 | TVU30418 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2D | scaffold81 | TVU14059 |
| LPERR03G | genblast_C | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5D | scaffold13 | TVU45955 |
| LPERR02G | genblast_C | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6D | scaffold27 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6A | genblast_C | TVU28522 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6A | scaffold19 | TVU27887 |
| LPERR01G | cds.KYUSt_ | ORUFI05G | Os01t021 | SECCE3Rv | TraesCS3B | scaffold84 | TVU16979 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE3Rv | TraesCS3D | scaffold50 | TVU33814 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1A | scaffold13 | TVU20253 |

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|---|---|---|---|---|---|---|---|
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t021 | SECCE4Rv | TraesCS4A | scaffold18 | TVU25832 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold31 | TVU36843 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3D | scaffold33 | TVU36464 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7D | scaffold48 | TVU04700 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6B | scaffold55 | TVU28620 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5D | scaffold21 | TVU09044 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold20 | TVU32353 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1A | scaffold85 | TVU31675 |
| LPERR03G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE4Rv | TraesCS4D | scaffold11 | TVU45535 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCE4Rv | TraesCS7A | scaffold37 | TVU11366 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1D | scaffold23 | TVU19468 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold23 | TVU38803 |
| LPERR03G | genblast_C | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44607 |
| LPERR04G | genblast_C | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2B | scaffold20 | TVU14847 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE2Rv1 | TraesCS2D | scaffold58 | TVU38609 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os08t043 | SECCE5Rv1 | TraesCS5B | scaffold11 | TVU09517 |
| | | | | | | | |
| LPERR09G | genblast_C | ORUFI09G | Os09t013 | SECCE5Rv1 | TraesCS5B | scaffold28 | TVU10907 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv1 | TraesCS5D | scaffold17 | TVU44466 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv1 | TraesCS5A | scaffold3. | TVU44823 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCE1Rv1 | TraesCS1B | scaffold20 | TVU30123 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE4Rv1 | TraesCS6D | scaffold17 | TVU28694 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv1 | TraesCS7A | scaffold14 | TVU04308 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv1 | TraesCS1B | scaffold13 | TVU00543 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t057 | genblast_C | TraesCS3A | scaffold46 | TVU34171 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv1 | TraesCS2A | scaffold2. | TVU01233 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t020 | genblast_C | TraesCS5A | scaffold62 | TVU02110 |
| LPERR02G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv1 | TraesCS6D | scaffold23 | genblast_Z |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t064 | SECCE5Rv1 | TraesCS7A | scaffold83 | TVU03791 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE4Rv1 | TraesCS4A | scaffold74 | TVU47078 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE6Rv1 | TraesCS3B | scaffold18 | TVU34702 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t027 | SECCE7Rv1 | TraesCS4B | scaffold22 | TVU47513 |
| | | | | | | | |
| LPERR04G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCE2Rv1 | TraesCS2B | scaffold53 | TVU13479 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv1 | TraesCS3B | scaffold59 | TVU21726 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t024 | SECCE3Rv1 | TraesCS3A | scaffold47 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE5Rv1 | TraesCS5D | scaffold11 | TVU32372 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t048 | SECCE2Rv1 | TraesCS2A | scaffold43 | TVU01048 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv1 | TraesCS3A | genblast_C | TVU36816 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv1 | TraesCS3B | scaffold14 | TVU36322 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv1 | TraesCS7D | scaffold38 | TVU05155 |
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| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t032 | SECCE1Rv1 | TraesCS1B | scaffold27 | TVU30732 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv1 | TraesCS1A | scaffold19 | TVU17807 |
| LPERR01G | genblast_C | ORUFI01G | Os01t059 | SECCE3Rv1 | TraesCS3A | scaffold13 | TVU34352 |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv1 | TraesCS5D | scaffold53 | TVU09770 |

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| LPERR07G | genblast_C | ORUFI07G | Os07t069 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37083 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t061 | SECCE6Rv | TraesCS6B | scaffold16 | TVU29255 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE2Rv | TraesCS3D | genblast_C | TVU34123 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t095 | SECCE6Rv | TraesCS3B | scaffold31 | TVU36841 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34526 |
| LPERR01G | genblast_C | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3A | scaffold89 | TVU35277 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE5Rv | TraesCS1A | scaffold12 | TVU19106 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7D | scaffold44 | TVU11885 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7B | scaffold25 | TVU32992 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12157 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3A | scaffold14 | TVU36312 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35964 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15706 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15543 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7B | scaffold26 | TVU43753 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t028 | SECCE6Rv | TraesCS6D | scaffold21 | TVU32511 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv1 | TraesCS4D | scaffold97 | TVU09662 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t054 | SECCE7Rv1 | TraesCS7D | scaffold18 | TVU07789 |
| LPERR04G | genblast_C | ORUFI04G | Os04t057 | SECCE2Rv1 | TraesCS2B | scaffold49 | TVT99706 |
| LPERR01G | cds.KYUSt_ | ORUFI12G | Os01t064 | SECCE3Rv1 | TraesCS3A | scaffold97 | TVU36686 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv1 | TraesCS2D | scaffold43 | TVU38408 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv1 | TraesCS5B | scaffold53 | TVU09778 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t028 | SECCE2Rv1 | TraesCS2D | scaffold95 | TVU18464 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv1 | TraesCS4D | scaffold55 | TVU45820 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | genblast_C | TraesCS1B | scaffold13 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv1 | TraesCS3A | scaffold84 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv1 | TraesCS1B | scaffold61 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t058 | SECCE7Rv1 | TraesCS7A | scaffold25 | TVU07979 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE7Rv1 | TraesCS7B | scaffold13 | TVU05080 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t056 | SECCE2Rv1 | TraesCS2A | scaffold18 | TVU46370 |

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| LPERR01G | cds.KYUSt_ | genblast_C | Os01t094 | SECCE6Rv1 | TraesCS3A | scaffold31 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE7Rv1 | TraesCS2B | scaffold14 | TVU06418 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t037 | SECCE5Rv1 | TraesCS5D | scaffold16 | TVU30855 |

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| LPERR01G | cds.KYUSt_ORUFI05G | Os01t022 | SECCE3Rv | TraesCS3A | scaffold36 | TVU29597 |
| genblast_C | genblast_C | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5D | scaffold23 | TVU39882 |

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|---|---|---|---|---|---|---|---|
| genblast_Z | cds.KYUSt_ | genblast_Z | Os02t058 | SECCE3Rv | TraesCS3A | scaffold38 | genblast_Z |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold65 | TVU44233 |

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| LPERR07G | genblast_C | ORUFI07G | Os07t013 | SECCE2Rv | TraesCS2D | scaffold12 | TVU41085 |
| genblast_C | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold39 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t047 | SECCE1Rv | TraesCS1A | scaffold16 | TVU02224 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1A | scaffold80 | TVU20460 |
| LPERR04G | genblast_C | ORUFI04G | Os04t069 | SECCE2Rv | TraesCS2D | scaffold42 | TVU16736 |
| LPERR09G | genblast_C | ORUFI09G | Os09t057 | SECCEUnv | TraesCS4D | scaffold12 | genblast_C |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | scaffold83 | TVU28375 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS4A | scaffold1. | TVU18640 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t056 | SECCE4Rv | TraesCS4D | scaffold10 | TVU10555 |
| LPERR12G | genblast_C | ORUFI04G | Os04t019 | SECCEUnv | TraesCS7D | scaffold61 | TVU46469 |
| LPERR09G | genblast_C | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5B | scaffold16 | TVU08803 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12296 |
| genblast_C | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold27 | TVU39067 |

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| LPERR11G | genblast_C | genblast_C | Os11t070 | SECCE4Rv | TraesCS4A | scaffold46 | TVU23277 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1A | scaffold19 | TVU20084 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6D | scaffold22 | TVU28681 |
| LPERR06G | genblast_C | ORUFI06G | genblast_C | genblast_C | TraesCS7B | scaffold30 | TVU01170 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3A | scaffold39 | TVU36165 |
| LPERR11G | cds.KYUSt_ | genblast_C | Os11t014 | SECCE5Rv | TraesCS5A | scaffold96 | TVU50807 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold12 | TVU16676 |
| LPERR07G | genblast_C | ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2B | scaffold96 | TVU38444 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os12t019 | SECCE2Rv | TraesCS2A | scaffold62 | TVU25831 |
| LPERR02G | genblast_C | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6D | scaffold26 | TVU28950 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCE4Rv | TraesCS4D | scaffold55 | TVU45824 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t051 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15281 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1B | genblast_C | TVU19276 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1A | scaffold30 | TVU35495 |
| genblast_C | genblast_C | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38673 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t013 | SECCE3Rv | TraesCS3B | scaffold59 | TVU22053 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4D | scaffold22 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t029 | genblast_C | genblast_C | scaffold21 | TVU32439 |
| genblast_C | cds.KYUSt_ORUFI11G | Os11t012 | SECCE6Rv | TraesCS6D | scaffold31 | TVU50649 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1A | scaffold19 | TVU20093 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45284 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2D | scaffold30 | TVT98346 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2B | scaffold13 | TVU01140 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold18 | TVU01800 |
| genblast_C | cds.KYUSt_ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold16 | TVT98589 |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE5Rv | TraesCS5B | scaffold71 | TVU32492 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold23 | TVU31793 |
| LPERR02G | cds.KYUSt_ORUFI09G | Os09t048 | SECCE3Rv | TraesCS3A | scaffold19 | TVU12989 |
| LPERR08G | genblast_C | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7B | scaffold20 | TVU43861 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t031 | SECCE1Rv | TraesCS1D | scaffold23 | TVU21208 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold89 | genblast_C |
| LPERR03G | genblast_C | ORUFI05G | Os05t022 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45598 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t021 | SECCE4Rv | TraesCSU0 | scaffold10 | TVU16959 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3A | scaffold11 | TVU35962 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold52 | TVU03131 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE5Rv | TraesCS5D | scaffold97 | TVU26989 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7B | scaffold25 | TVU07834 |
| LPERR05G | genblast_C | ORUFI05G | Os05t011 | genblast_C | TraesCS1D | scaffold19 | TVU18120 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE5Rv | TraesCS4D | scaffold25 | TVU51609 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7A | scaffold24 | TVT99148 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE6Rv | TraesCS6B | scaffold4. | TVU21119 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3A | scaffold18 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t014 | SECCE6Rv | TraesCS6A | scaffold48 | genblast_C |
| LPERR11G | genblast_Z | ORUFI01G | Os11t020 | SECCE5Rv | TraesCS5B | scaffold2. | TVT99756 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3A | scaffold48 | TVU37029 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t050 | SECCE5Rv | TraesCS5D | scaffold15 | TVU08820 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE7Rv | TraesCS7D | scaffold33 | TVU08754 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16539 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2B | scaffold77 | TVU38758 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE4Rv | TraesCS7A | scaffold2. | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7A | scaffold54 | TVU04668 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4D | scaffold8. | TVT97607 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5D | scaffold17 | TVU44327 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t024 | SECCE4Rv | TraesCS7A | scaffold84 | TVU51811 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | genblast_C | TraesCS3B | scaffold16 | TVU22960 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE6Rv | TraesCS6A | scaffold27 | TVT98448 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3A | scaffold88 | TVU21546 |
| LPERR05G | genblast_Z | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold13 | TVU17329 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t041 | SECCE6Rv | TraesCS6D | scaffold61 | TVU46443 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6B | scaffold17 | TVU28693 |
| LPERR02G | cds.KYUSt_ | genblast_C | genblast_C | SECCE6Rv | TraesCS6D | scaffold10 | TVU28820 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t029 | SECCE5Rv | TraesCS5A | scaffold41 | TVT97956 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t057 | SECCE2Rv | TraesCSU0 | scaffold12 | TVU10705 |
| LPERR03G | genblast_C | ORUFI03G | Os03t040 | SECCEUnv | TraesCSU0 | scaffold38 | TVU02937 |
| LPERR05G | genblast_C | ORUFI05G | Os05t017 | SECCE1Rv | TraesCS1B | scaffold13 | TVU17300 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1D | scaffold36 | TVU19107 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold15 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCEUnv | TraesCS6D | scaffold98 | TVU33520 |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS4A | scaffold10 | TVU12732 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold3. | TVU10971 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7B | scaffold22 | TVT97571 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3B | scaffold4. | TVU21504 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5A | scaffold32 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1D | scaffold13 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os11t012 | SECCE5Rv | TraesCS5B | scaffold48 | TVU50653 |
| LPERR04G | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2A | scaffold14 | TVU15311 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS5B | scaffold54 | TVU04712 |
| LPERR07G | genblast_C | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2B | scaffold2. | genblast_C |
| LPERR03G | genblast_C | ORUFI06G | Os06t073 | SECCE6Rv | TraesCS7B | scaffold60 | TVU04678 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3D | scaffold11 | TVU35566 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold3. | TVT97853 |
| LPERR11G | genblast_C | ORUFI11G | Os11t056 | genblast_C | TraesCS4B | scaffold17 | TVU24886 |
| LPERR03G | genblast_C | ORUFI03G | Os03t067 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45723 |
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| LPERR01G | genblast_C | ORUFI01G | Os01t073 | genblast_C | TraesCS3A | scaffold89 | TVU35180 |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold33 | TVU08453 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold38 | TVU05136 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6A | scaffold19 | TVU27865 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold4. | TVU22740 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5B | scaffold32 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE5Rv | TraesCS5D | scaffold11 | TVU05411 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1B | scaffold39 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t055 | SECCE5Rv | TraesCS5A | scaffold22 | TVU49848 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t083 | SECCE2Rv | TraesCS2B | scaffold20 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | scaffold19 | TVU30436 |
| LPERR02G | genblast_C | ORUFI08G | Os08t029 | SECCE6Rv | TraesCS6D | scaffold18 | TVU27893 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE7Rv | TraesCS4B | scaffold40 | TVU18042 |
| LPERR09G | genblast_C | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold23 | TVU09377 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold65 | TVU38127 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7D | scaffold22 | TVU07652 |

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| LPERR10G | cds.KYUSt_ | ORUFI04G | Os04t011 | SECCE3Rv | TraesCS7A | scaffold15 | TVT97656 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5D | scaffold65 | genblast_C |
| LPERR01G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE3Rv | TraesCS3B | scaffold25 | TVU22568 |
| LPERR04G | genblast_C | ORUFI09G | Os04t046 | SECCE2Rv | TraesCS2A | scaffold5. | TVU14166 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold32 | TVU31704 |
| LPERR11G | cds.KYUSt_ | genblast_C | Os11t013 | SECCE5Rv | TraesCS5A | scaffold41 | TVU27134 |
| LPERR03G | cds.KYUSt_ | genblast_Z | Os03t085 | SECCE7Rv | TraesCS5B | genblast_Z | TVU44213 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7A | scaffold22 | TVU43355 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3D | scaffold40 | TVU23042 |
| LPERR07G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS7B | scaffold11 | TVU47967 |

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| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1D | scaffold5. | TVU31656 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t043 | SECCE7Rv | TraesCS4A | scaffold34 | TVU39497 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t051 | SECCE1Rv | TraesCS1A | scaffold49 | TVU20586 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t043 | SECCE5Rv | TraesCS5A | scaffold31 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3A | scaffold15 | TVU22168 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS3B | scaffold46 | TVU28500 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold29 | TVU08861 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE4Rv | TraesCS4D | genblast_C | TVU03529 |
| LPERR04G | cds.KYUSt_ | ORUFI06G | Os06t027 | SECCE7Rv | TraesCS2A | scaffold19 | TVU07366 |
| LPERR09G | genblast_C | ORUFI09G | Os09t010 | SECCE5Rv | TraesCS5A | scaffold3. | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE2Rv | TraesCS2B | scaffold20 | TVU43767 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t048 | SECCE7Rv | TraesCS7A | scaffold24 | TVU05484 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold8. | TVU14261 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4B | scaffold11 | TVU45429 |

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| LPERR10G | cds.KYUSt_ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1D | scaffold19 | TVU30450 |
| genblast_C | cds.KYUSt_ORUFI04G | Os04t032 | SECCE2Rv | TraesCS2D | scaffold21 | TVU13682 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold84 | TVU36568 |
| genblast_C | cds.KYUSt_ORUFI03G | genblast_C | SECCE4Rv | TraesCS4B | genblast_C | genblast_C |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2B | scaffold12 | TVT97880 |
| LPERR09G | cds.KYUSt_ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold27 | genblast_Z |
| genblast_C | genblast_CORUFI12G | Os12t022 | SECCE5Rv | TraesCS5D | scaffold10 | TVU51424 |
| LPERR09G | cds.KYUSt_genblast_C | Os09t052 | SECCE5Rv | TraesCS5B | scaffold16 | genblast_C |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold97 | TVU47973 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t011 | SECCE5Rv | TraesCS4B | scaffold41 | TVU48628 |
| LPERR10G | cds.KYUSt_ORUFI02G | genblast_C | SECCE1Rv | TraesCS1A | scaffold11 | TVU30392 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48045 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold32 | TVU44812 |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold12 | TVU16269 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t036 | SECCEUnv | TraesCS5D | scaffold25 | TVU20867 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t051 | SECCE1Rv | TraesCS1A | scaffold12 | TVU20628 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t082 | SECCE1Rv | TraesCS2B | scaffold26 | TVU27598 |

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| LPERR09G | cds.KYUSt_ORUFI09G | Os09t011 | SECCE5Rv | TraesCS5D | scaffold20 | TVU10781 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6D | scaffold17 | genblast_C |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5B | scaffold76 | TVU49674 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6B | genblast_C | TVU33508 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49187 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os01t053 | SECCE1Rv | TraesCS2B | scaffold16 | TVU39087 |
| genblast_C | cds.KYUSt_ORUFI09G | Os09t057 | SECCE7Rv | TraesCS7D | scaffold3. | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t041 | genblast_C | genblast_C | scaffold5. | TVU46555 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2B | scaffold13 | TVU15470 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5D | scaffold65 | TVU44613 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3A | scaffold31 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2A | scaffold52 | TVU29904 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3A | scaffold22 | TVU45356 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4A | scaffold36 | TVU45437 |
| LPERR06G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold11 | TVU28626 |
| LPERR04G | genblast_C | ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2A | scaffold94 | TVU14867 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t029 | SECCE6Rv | TraesCS6A | scaffold21 | TVT99775 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t020 | genblast_C | genblast_C | scaffold28 | TVU41363 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t049 | SECCE1Rv | TraesCS1D | scaffold38 | TVU20735 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1D | scaffold80 | TVU20549 |
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t049 | SECCE4Rv | TraesCS7B | scaffold26 | TVU05358 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold13 | TVT98791 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t024 | SECCE3Rv | TraesCS3D | scaffold47 | TVU22378 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2A | scaffold43 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | genblast_C | TraesCS7D | scaffold16 | TVU07931 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20137 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7D | scaffold45 | genblast_C |
| LPERR10G | genblast_C | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1A | scaffold5. | TVU31508 |
| LPERR02G | cds.KYUSt_ | genblast_C | genblast_C | SECCE6Rv | TraesCS6A | scaffold1. | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t048 | genblast_C | TraesCS7D | scaffold24 | TVU05422 |
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| genblast_C | genblast_C | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1D | scaffold32 | TVU32199 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE1Rv | TraesCS1A | genblast_C | TVU37176 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6A | scaffold5. | TVU29703 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCEUnv | TraesCSU0 | genblast_C | TVU18530 |
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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t052 | SECCE7Rv | TraesCS7B | scaffold17 | TVU24576 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7D | scaffold17 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3D | scaffold36 | TVU22859 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold81 | TVU14646 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t019 | SECCE3Rv | TraesCS3A | scaffold25 | TVU22497 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5A | scaffold64 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t083 | SECCE6Rv | TraesCS1B | scaffold51 | TVT97706 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE2Rv | TraesCS2A | scaffold37 | TVU06022 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold49 | TVU15109 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t076 | genblast_C | TraesCS3A | scaffold22 | TVU35016 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold6. | TVU01977 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold12 | TVU16457 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t023 | genblast_C | TraesCS5D | scaffold10 | TVU51509 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t032 | SECCE6Rv | TraesCS6A | scaffold15 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30456 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t041 | SECCE7Rv | TraesCS7B | scaffold18 | TVU46779 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5A | scaffold57 | TVU00339 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t014 | SECCE2Rv | TraesCSU0 | scaffold11 | TVU17892 |
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| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7B | scaffold22 | TVU07682 |

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| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6B | scaffold48 | TVU33622 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold20 | TVU40275 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6A | scaffold48 | TVU33483 |
| LPERR08G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE7Rv | TraesCS4B | scaffold23 | TVU03005 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t011 | SECCE4Rv | TraesCS4B | scaffold31 | TVU51590 |
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t053 | SECCE4Rv | TraesCS7A | scaffold16 | TVU04930 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7A | scaffold14 | TVU28479 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7A | scaffold93 | TVU07927 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t045 | SECCE1Rv | TraesCS1D | scaffold19 | TVU30459 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t028 | SECCE5Rv | TraesCS5D | scaffold68 | TVU42355 |

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| LPERR04G | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2B | scaffold14 | TVU15871 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCSU0 | scaffold24 | TVU18252 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t019 | SECCE1Rv | TraesCS1D | scaffold13 | TVU17085 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5D | genblast_C | TVU02969 |
| LPERR08G | genblast_C | ORUFI08G | Os08t055 | SECCE4Rv | TraesCS7D | scaffold15 | TVU04544 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold45 | TVU31784 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold33 | TVU04012 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6A | scaffold6. | TVU32835 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5D | scaffold53 | TVU08789 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7B | scaffold26 | TVT99140 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_Z | SECCE7Rv | TraesCS7A | scaffold92 | TVU08217 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t057 | SECCE4Rv | TraesCS7A | scaffold61 | TVU46336 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE5Rv | TraesCS4D | scaffold28 | TVU05146 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t022 | SECCE4Rv | TraesCS4A | scaffold73 | TVU25848 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4D | scaffold55 | TVU13144 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os11t012 | SECCE4Rv1 | TraesCS4D | scaffold64 | TVU50678 |

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| LPERR08G | cds.KYUSt_ | ORUFI02G | Os02t029 | SECCE7Rv1 | TraesCS7B | scaffold21 | TVU42766 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv1 | TraesCS1A | scaffold19 | TVU17113 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t056 | SECCE4Rv1 | TraesCS4B | scaffold12 | TVU10563 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os12t013 | SECCE4Rv1 | TraesCS4A | scaffold97 | TVU50788 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t016 | SECCE3Rv1 | TraesCS3D | scaffold59 | TVU21684 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t037 | SECCE5Rv1 | TraesCS5B | scaffold87 | TVU09373 |
| LPERR07G | genblast_C | ORUFI07G | Os07t045 | SECCE7Rv1 | TraesCS7D | scaffold3. | TVU39415 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv1 | TraesCS7D | scaffold34 | TVU12285 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv1 | TraesCS2D | scaffold13 | TVU15486 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t010 | SECCE4Rv1 | TraesCS6D | scaffold19 | TVU33739 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE2Rv1 | TraesCS2D | scaffold5. | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t031 | SECCE7Rv1 | TraesCS4A | scaffold17 | genblast_C |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv1 | TraesCS7B | scaffold25 | TVU07836 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv1 | TraesCS1D | scaffold36 | genblast_C |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2A | scaffold43 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44340 |
| LPERR01G | genblast_C | ORUFI01G | Os01t068 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35479 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCEUnv | TraesCS5A | scaffold29 | TVU48827 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t017 | genblast_C | TraesCS4A | scaffold50 | TVU26636 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold59 | TVU21683 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4B | scaffold18 | TVU47092 |
| genblast_C | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1B | scaffold16 | TVT97889 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t018 | SECCE4Rv | TraesCS4A | scaffold12 | TVU31243 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t026 | SECCE4Rv | TraesCS4A | scaffold21 | TVU00333 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE3Rv | TraesCS6B | scaffold26 | genblast_C |
| LPERR05G | genblast_C | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1A | scaffold1. | TVU20300 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t021 | SECCE4Rv | TraesCS4D | scaffold49 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3A | scaffold36 | TVT97934 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3D | scaffold84 | TVU35201 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t018 | SECCE2Rv | TraesCS2B | scaffold83 | TVU51272 |

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| LPERR02G | cds.KYUSt_ | genblast_C | Os02t060 | SECCE6Rv | TraesCS6B | scaffold17 | TVU03512 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36106 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12403 |
| LPERR09G | genblast_C | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5A | scaffold16 | TVU10171 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t030 | SECCE5Rv | TraesCS5B | scaffold2. | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38721 |
| genblast_C | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold25 | TVU22628 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | genblast_C | TraesCS3A | scaffold31 | TVU02351 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7B | scaffold11 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3A | scaffold84 | TVU35209 |
| LPERR09G | cds.KYUSt_ | ORUFI07G | Os06t058 | SECCE4Rv | TraesCS4B | scaffold60 | TVU03770 |
| LPERR01G | genblast_C | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3D | scaffold20 | TVU35966 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold52 | TVU18932 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48111 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold36 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t013 | SECCE3Rv | TraesCSU0 | scaffold59 | TVU22045 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5D | scaffold64 | TVU09525 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5D | scaffold11 | TVU49034 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold14 | TVU47498 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold12 | genblast_C |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t038 | SECCE2Rv | TraesCS2A | scaffold10 | TVU14025 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold43 | TVU38381 |
| LPERR11G | cds.KYUSt_ | ORUFI08G | Os11t021 | SECCE6Rv | TraesCS5D | scaffold68 | TVU05794 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE5Rv | TraesCS5A | scaffold13 | TVU43157 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1D | scaffold13 | TVU17966 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold84 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7A | scaffold60 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3D | scaffold31 | TVU35988 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE4Rv | TraesCS6A | scaffold28 | TVU51576 |
| LPERR06G | cds.KYUSt_ | genblast_Z | Os02t029 | SECCE5Rv | TraesCS5D | scaffold24 | TVU11170 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7B | scaffold34 | TVU12488 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3D | scaffold36 | TVU21412 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold19 | TVU17819 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2D | scaffold34 | TVU37729 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1D | scaffold14 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI10G | Os10t017 | SECCE4Rv | TraesCS7A | scaffold20 | TVU40412 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t020 | SECCE4Rv | TraesCS4D | scaffold32 | TVU18104 |
| genblast_C | genblast_C | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2A | scaffold49 | TVU15133 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | genblast_C | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold31 | TVU02355 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3B | scaffold41 | TVU36741 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t066 | SECCE3Rv | TraesCS3A | genblast_C | TVT96964 |

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| LPERR01G | cds.KYUSt_ | genblast_C | Os01t013 | SECCE3Rv | TraesCS3D | scaffold88 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t056 | SECCE4Rv | TraesCS6B | scaffold5. | TVU29645 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t047 | SECCE2Rv | TraesCS2A | scaffold26 | TVU05516 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2D | scaffold14 | TVU16093 |
| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold15 | TVU35069 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7B | scaffold92 | TVU08443 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2D | scaffold20 | TVU16171 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3A | scaffold63 | TVU21653 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44791 |
| LPERR05G | genblast_C | ORUFI05G | Os05t056 | SECCE1Rv | genblast_C | scaffold1. | TVU20287 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold17 | TVU28857 |
| LPERR04G | genblast_C | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2A | scaffold99 | TVU14412 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | genblast_C | TraesCS5A | scaffold17 | TVU44432 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t028 | SECCE1Rv | TraesCS1A | scaffold10 | TVU17952 |
| genblast_C | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold9. | TVU08601 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t094 | SECCE6Rv | TraesCS3B | scaffold21 | TVU34713 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3B | genblast_C | TVU21491 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1D | scaffold40 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t042 | SECCE1Rv | TraesCS5A | genblast_C | TVU31088 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t035 | SECCE4Rv | TraesCS4D | scaffold18 | TVU46984 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37462 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5B | scaffold29 | TVU01482 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t030 | SECCE1Rv | TraesCS1D | scaffold50 | TVU21014 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t010 | SECCE3Rv | TraesCS3D | scaffold29 | TVU22359 |
| LPERR06G | genblast_Z | ORUFI06G | genblast_Z | SECCE4Rv | TraesCS7B | scaffold44 | TVU11882 |
| LPERR05G | genblast_C | ORUFI05G | Os05t029 | SECCE6Rv | TraesCS6D | scaffold16 | TVU18590 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28578 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os06t033 | SECCE3Rv | TraesCS3A | scaffold3. | TVU35690 |
| LPERR01G | cds.KYUSt_ | genblast_C | genblast_C | SECCE1Rv | TraesCS1B | scaffold47 | TVT96993 |
| LPERR10G | genblast_C | ORUFI10G | Os10t047 | SECCE1Rv | TraesCS1A | scaffold11 | genblast_C |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t073 | SECCE4Rv | TraesCS4A | scaffold3. | TVU45195 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5D | scaffold53 | TVU09784 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t045 | SECCE6Rv | TraesCS6A | scaffold12 | TVU39558 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold40 | TVU47397 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5B | scaffold29 | TVU08838 |
| LPERR03G | cds.KYUSt_ | ORUFI12G | Os12t043 | SECCE5Rv | TraesCS5A | scaffold10 | TVU00608 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE4Rv | TraesCS7D | scaffold68 | TVU11453 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t078 | SECCE5Rv | TraesCS5A | scaffold65 | TVU44707 |
| LPERR10G | genblast_C | ORUFI10G | Os10t045 | SECCE1Rv | genblast_C | genblast_C | TVU30465 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold22 | TVU21463 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5D | scaffold22 | TVU49974 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t046 | genblast_C | genblast_C | scaffold3. | TVU39395 |
| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2B | scaffold43 | TVU38866 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t012 | SECCE4Rv | TraesCSU0 | scaffold20 | TVU33613 |
| genblast_C | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold10 | TVU12057 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE4Rv | TraesCS7A | scaffold16 | TVU04938 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t024 | SECCE7Rv | TraesCS5D | scaffold31 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold60 | TVU07640 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5B | scaffold29 | TVU10105 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE5Rv | TraesCS5A | scaffold12 | TVU10545 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2A | scaffold66 | TVU04078 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6D | scaffold17 | TVU29227 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t040 | SECCE4Rv | TraesCS7A | scaffold16 | TVU13000 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold17 | genblast_C |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t038 | SECCE6Rv | genblast_C | scaffold18 | TVU46789 |
| genblast_C | genblast_C | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2B | scaffold32 | TVU16360 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCEUnv | TraesCS5B | scaffold29 | TVU49334 |
| LPERR11G | genblast_Z | ORUFI11G | genblast_Z | genblast_Z | TraesCS4B | scaffold18 | TVU26154 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1A | scaffold22 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | scaffold5. | TVU31504 |

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| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t024 | SECCE1Rv | TraesCS1A | scaffold68 | TVU42222 |
| LPERR08G | genblast_C | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold16 | TVU04958 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE2Rv | TraesCS2B | scaffold36 | TVU20091 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47524 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t054 | SECCE6Rv | TraesCS6A | scaffold12 | TVU18941 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6A | scaffold12 | TVU28091 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5B | genblast_Z | genblast_Z |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t065 | SECCE4Rv | TraesCS4D | scaffold55 | genblast_C |
|  |  |  |  |  |  |  |  |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS7D | scaffold49 | TVU12799 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t021 | SECCE4Rv | TraesCS7A | scaffold28 | TVU40005 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t034 | SECCE1Rv | TraesCS1A | scaffold10 | TVU30648 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2D | scaffold58 | TVU02450 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47468 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45454 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7B | scaffold38 | TVU04971 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE7Rv | TraesCS7B | scaffold9. | TVU22755 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os08t055 | SECCE4Rv | TraesCS4A | scaffold12 | TVU10564 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t091 | SECCE5Rv | TraesCS5D | scaffold21 | TVU36091 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5D | scaffold16 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1D | scaffold27 | TVU32035 |
|  |  |  |  |  |  |  |  |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t017 | SECCE2Rv | TraesCS2B | scaffold66 | TVU41834 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv | TraesCS3A | scaffold88 | TVU21748 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold17 | TVU44637 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1B | scaffold13 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold41 | TVU36657 |
|  |  |  |  |  |  |  |  |
| LPERR03G | genblast_C | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5D | scaffold13 | TVU46060 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t049 | SECCE2Rv | TraesCS2D | scaffold27 | TVU39047 |
|  |  |  |  |  |  |  |  |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2B | scaffold86 | TVU37168 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t010 | genblast_C | genblast_C | scaffold24 | TVT97661 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4A | scaffold9. | TVU47899 |
| LPERR04G | genblast_C | ORUFI04G | Os04t051 | SECCE2Rv | TraesCS2D | scaffold56 | TVU15284 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold44 | TVU11698 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3B | scaffold14 | TVU36167 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47495 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7B | scaffold16 | TVU04814 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16639 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold25 | TVU35816 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45285 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3A | scaffold54 | TVU22432 |
| LPERR02G | genblast_C | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold13 | TVU29292 |
| genblast_C | cds.KYUSt_ | genblast_C | Os04t067 | SECCE2Rv | TraesCS2B | scaffold12 | TVU16614 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3D | scaffold17 | TVU02356 |
| LPERR04G | genblast_C | ORUFI04G | Os04t059 | SECCE1Rv | TraesCS2A | scaffold49 | TVU15919 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t020 | SECCE4Rv | TraesCS4D | scaffold18 | genblast_C |
| LPERR04G | genblast_C | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2D | scaffold30 | TVU14151 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5B | scaffold27 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2D | scaffold32 | TVU16313 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12224 |

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| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE3Rv | TraesCS3A | scaffold14 | TVU36121 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t032 | SECCE4Rv | TraesCS7D | scaffold16 | TVU11401 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t031 | SECCE5Rv | TraesCS5D | genblast_C | TVU18797 |
| LPERR12G | genblast_C | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5B | scaffold76 | TVU49724 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold9. | TVU47950 |
| LPERR11G | genblast_C | ORUFI11G | Os11t064 | SECCE4Rv | TraesCS7B | scaffold30 | TVU23870 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1A | scaffold32 | TVU20537 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37767 |
| LPERR10G | cds.KYUSt_ | ORUFI06G | Os06t029 | SECCE4Rv | TraesCS7B | scaffold10 | TVU11492 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t038 | SECCE1Rv | TraesCS1B | scaffold12 | TVU46809 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE1Rv | TraesCS5A | scaffold65 | TVU44667 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t030 | SECCE3Rv | TraesCS3D | scaffold10 | TVU06650 |
| LPERR07G | genblast_C | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37987 |
| genblast_C | cds.KYUSt_ | genblast_C | Os06t021 | SECCE4Rv | TraesCS7D | scaffold14 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE7Rv | TraesCS7A | scaffold62 | TVU05157 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5A | scaffold29 | TVU49189 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold65 | TVU47602 |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t053 | SECCE1Rv | TraesCS1D | scaffold45 | TVU31891 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t037 | SECCE1Rv | TraesCS1A | scaffold25 | TVU20840 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28060 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold15 | TVT98944 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t015 | SECCE2Rv | TraesCS2D | scaffold32 | TVU31317 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4D | scaffold74 | TVU47304 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold19 | TVU16624 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t034 | SECCE7Rv | TraesCS7A | scaffold38 | TVU03136 |
| LPERR09G | genblast_C | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5A | scaffold53 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15343 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3D | scaffold17 | TVT97817 |
| LPERR05G | genblast_C | ORUFI05G | Os05t022 | SECCE7Rv | TraesCS5B | scaffold63 | TVU19224 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2A | scaffold2. | TVT97994 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7D | scaffold41 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09759 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2B | scaffold26 | TVU14270 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t050 | SECCE1Rv | TraesCS6A | scaffold14 | TVU25288 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3D | scaffold89 | genblast_C |
| genblast_C | genblast_C | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold59 | TVU21671 |
| genblast_C | genblast_C | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4B | scaffold55 | TVU45648 |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold35 | TVU44940 |
| LPERR06G | genblast_C | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7D | scaffold14 | TVU12131 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold55 | TVU45958 |
| LPERR02G | cds.KYUSt_ | ORUFI10G | Os02t065 | SECCE1Rv | TraesCS1D | scaffold85 | TVU31666 |
| LPERR05G | genblast_C | ORUFI05G | Os05t016 | SECCE1Rv | TraesCS1A | scaffold13 | TVU17289 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | genblast_C | TraesCS7B | scaffold25 | TVU08171 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6A | scaffold10 | TVU28024 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t064 | SECCE6Rv | TraesCS6A | scaffold26 | TVU02402 |
| LPERR01G | genblast_C | ORUFI01G | Os01t064 | SECCE3Rv | TraesCS3A | scaffold11 | TVU46392 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | genblast_C | TVU48005 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE7Rv | TraesCS4B | scaffold25 | TVU44240 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6A | scaffold17 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6B | scaffold10 | TVU28041 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t041 | SECCE4Rv | TraesCS4D | scaffold49 | TVU25665 |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold16 | genblast_C |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE3Rv | TraesCS3B | scaffold47 | TVU46329 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold97 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os06t064 | SECCEUnv | TraesCS7A | scaffold12 | TVU08281 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5D | scaffold24 | TVU09691 |
| LPERR02G | genblast_C | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28185 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t033 | SECCE3Rv | TraesCS3B | scaffold91 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t026 | SECCE7Rv | TraesCS7B | scaffold41 | TVU33352 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t032 | SECCE2Rv | TraesCS2D | scaffold10 | TVU13685 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5B | scaffold32 | TVU44779 |
| LPERR02G | genblast_C | ORUFI02G | Os02t052 | genblast_C | genblast_C | scaffold15 | TVU29902 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t040 | SECCE6Rv | TraesCS6B | genblast_C | TVU39119 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2B | scaffold13 | TVU01141 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE1Rv | TraesCS1B | scaffold4. | TVU20218 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5B | scaffold65 | TVU44438 |
| LPERR06G | cds.KYUSt_ | ORUFI02G | Os03t059 | SECCE7Rv | TraesCS7A | scaffold98 | TVU10662 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6B | scaffold13 | TVU29433 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t063 | SECCE7Rv | TraesCS7B | scaffold12 | TVU08222 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t022 | SECCE7Rv | TraesCS2A | scaffold32 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t013 | SECCE7Rv | TraesCS7D | scaffold18 | TVU43437 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t029 | SECCE4Rv | TraesCS4A | scaffold26 | TVT97629 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCEUnv | TraesCS7A | scaffold27 | TVU06537 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t042 | SECCE1Rv | TraesCS1B | scaffold28 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1A | scaffold39 | TVU20656 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE6Rv | TraesCS3B | scaffold31 | TVU36846 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2D | scaffold23 | TVU14918 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t051 | SECCE1Rv | TraesCS1B | scaffold32 | TVU20634 |
| LPERR02G | genblast_C | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6D | genblast_C | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold12 | TVU28214 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5A | scaffold36 | TVU51228 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1D | scaffold45 | TVU31904 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t050 | SECCE7Rv | TraesCS7A | scaffold11 | TVU03386 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold87 | TVU14814 |
| LPERR07G | cds.KYUSt_ | ORUFI09G | Os07t029 | SECCE5Rv | TraesCS5B | scaffold8. | TVU21803 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29322 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6D | scaffold51 | TVU33128 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold39 | TVU19997 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t043 | SECCE1Rv | TraesCS1D | scaffold69 | TVT99213 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold22 | TVU47401 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2B | scaffold10 | TVU13944 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t062 | SECCE4Rv | TraesCS4B | scaffold6. | TVU23965 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold27 | TVU08823 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7D | scaffold11 | TVU43608 |
| LPERR12G | genblast_C | ORUFI12G | Os12t018 | SECCE3Rv | TraesCS3B | scaffold10 | TVU51098 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7B | scaffold92 | TVU08373 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold16 | TVT98488 |
| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE1Rv | TraesCS1B | scaffold12 | TVU39435 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE5Rv | TraesCS4B | scaffold16 | TVU22278 |

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| LPERR05G | cds.KYUSt_ | ORUFI07G | Os05t012 | SECCE1Rv | TraesCS1A | scaffold13 | TVU18060 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2A | scaffold49 | TVU15124 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t026 | SECCE3Rv | TraesCS3B | scaffold25 | TVU22638 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | genblast_C | TVU27611 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t032 | SECCE4Rv | TraesCS7A | scaffold27 | genblast_C |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | genblast_C | TraesCS7D | scaffold36 | TVU01215 |
| LPERR12G | genblast_C | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5A | scaffold25 | TVU48938 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv | TraesCS3B | scaffold18 | TVU34679 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE1Rv | TraesCS1B | scaffold17 | TVU16600 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold27 | genblast_C |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t037 | SECCE1Rv | TraesCS1B | scaffold36 | TVU19163 |

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| LPERR05G | genblast_C | ORUFI05G | Os05t052 | genblast_C | genblast_C | scaffold32 | TVU20535 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t061 | SECCE2Rv | TraesCS2B | scaffold6. | TVU24196 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold17 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1D | scaffold52 | TVU20336 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3A | scaffold25 | TVU22633 |
| LPERR09G | genblast_C | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5D | scaffold64 | TVU09896 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t013 | SECCEUnv | TraesCS2A | scaffold13 | TVU07026 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3A | scaffold11 | TVU03676 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t024 | SECCE6Rv | TraesCS3D | scaffold31 | TVU39901 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t059 | SECCE4Rv | TraesCS4B | scaffold1. | TVU46237 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os07t013 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44764 |

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| LPERR03G | cds.KYUSt_ | genblast_C | Os03t023 | SECCE7Rv | TraesCS4B | scaffold97 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7B | scaffold21 | TVU02169 |
| LPERR11G | genblast_C | ORUFI11G | Os11t052 | SECCE4Rv | TraesCS4A | scaffold14 | TVU25220 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE7Rv | TraesCS4D | scaffold31 | TVU34583 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os05t055 | SECCE1Rv | TraesCS3A | scaffold33 | TVU35477 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t051 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15285 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t013 | SECCE7Rv | TraesCS7B | scaffold18 | TVU43489 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os09t056 | SECCE5Rv | TraesCS5D | scaffold27 | TVU10475 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t054 | genblast_C | TraesCS1B | scaffold13 | TVU20396 |
| genblast_C | genblast_C | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1B | scaffold45 | TVU31810 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t070 | SECCE4Rv | TraesCS4D | scaffold31 | TVU23314 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE7Rv | TraesCSU0 | scaffold12 | TVU43022 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCE5Rv | TraesCS5B | scaffold46 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t025 | SECCE6Rv | TraesCS6D | scaffold26 | TVU33287 |
| genblast_C | genblast_C | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1D | scaffold13 | TVU18183 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1D | scaffold23 | TVU19452 |
| LPERR03G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE7Rv | TraesCS4D | scaffold22 | TVU42997 |
| LPERR07G | genblast_C | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2A | scaffold2. | TVU00090 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5A | scaffold1. | TVU49046 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3B | scaffold25 | TVU22614 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t037 | SECCE6Rv | TraesCS6A | scaffold38 | TVU20837 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t048 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19930 |
| LPERR06G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS3A | scaffold30 | TVU16739 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold23 | TVU01619 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t060 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38000 |
| LPERR09G | genblast_C | ORUFI09G | Os09t030 | SECCE5Rv | TraesCS5D | scaffold16 | TVT98973 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2D | scaffold28 | TVU14990 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t031 | SECCE3Rv | TraesCS3A | scaffold34 | TVU21154 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1A | scaffold39 | genblast_C |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1A | scaffold11 | TVU17806 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os11t014 | genblast_C | TraesCS5B | scaffold97 | TVU27022 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS5A | scaffold10 | TVU48558 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19935 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t039 | SECCE3Rv | TraesCS3D | scaffold56 | TVU20757 |
| LPERR04G | genblast_C | ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2D | scaffold14 | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS5B | scaffold39 | TVU44218 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7B | scaffold21 | TVU08055 |
| LPERR10G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE7Rv | TraesCS7A | scaffold40 | TVU50159 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE2Rv | TraesCS2D | scaffold43 | TVU38677 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28011 |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold32 | TVU44967 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2B | scaffold12 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t018 | SECCE7Rv | TraesCS5B | scaffold70 | genblast_C |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t058 | SECCE7Rv | TraesCS7B | scaffold43 | TVU25075 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6B | scaffold1. | TVU03113 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold27 | TVU10218 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE2Rv | TraesCS2A | scaffold9. | TVU47931 |
| LPERR02G | genblast_C | genblast_C | Os02t061 | SECCE6Rv | TraesCS6D | scaffold19 | TVU29293 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE3Rv | TraesCS3B | scaffold26 | TVU02532 |
| LPERR01G | genblast_C | genblast_C | Os01t072 | SECCE3Rv | TraesCS3A | scaffold14 | TVU35234 |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold32 | TVU45038 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48100 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3A | scaffold18 | TVU21609 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2D | scaffold23 | TVU01405 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2D | scaffold30 | TVU16691 |

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| LPERR10G | genblast_C | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1A | scaffold37 | TVU32063 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3A | scaffold14 | TVU36449 |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6A | genblast_C | TVT97697 |
| LPERR10G | genblast_C | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1B | scaffold5. | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5B | scaffold3. | TVU43889 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4A | scaffold9. | TVU48108 |
| LPERR06G | genblast_C | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7D | scaffold60 | TVT97580 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE3Rv | TraesCS3D | scaffold28 | TVT99073 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5B | scaffold11 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5D | scaffold64 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7B | scaffold18 | TVU42784 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t024 | SECCE6Rv | TraesCS7B | scaffold20 | TVU42212 |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os02t020 | genblast_C | TraesCS6A | scaffold1. | TVU32984 |
| genblast_C | genblast_C | ORUFI03G | Os03t065 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45836 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6A | scaffold22 | TVU28743 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t045 | SECCE2Rv | TraesCS2B | scaffold12 | TVT99424 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48061 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t030 | SECCE7Rv | TraesCS7B | scaffold89 | TVU06651 |
| LPERR09G | genblast_C | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold27 | TVU08884 |
| LPERR05G | genblast_C | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1B | genblast_C | genblast_C |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t059 | SECCE3Rv | TraesCS3B | scaffold11 | TVU34320 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t044 | SECCE1Rv | TraesCS1B | scaffold57 | TVU30578 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCE5Rv | TraesCS4B | scaffold52 | TVU48680 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t019 | SECCE2Rv | TraesCS2D | scaffold2. | TVU43191 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold1. | TVU03500 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30414 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t038 | genblast_C | genblast_C | scaffold18 | TVU46791 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6D | scaffold28 | TVU28842 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3D | scaffold11 | TVU35908 |

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| LPERR03G | cds.KYUSt_ | genblast_C | Os03t030 | SECCE7Rv | TraesCS4B | scaffold74 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t026 | genblast_C | genblast_C | scaffold41 | TVU33374 |
| LPERR08G | genblast_C | ORUFI08G | Os08t042 | genblast_C | genblast_C | scaffold37 | TVU05834 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t013 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12743 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4B | scaffold9. | TVU47695 |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_C | SECCE7Rv | TraesCS4B | scaffold16 | TVU07901 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2A | scaffold12 | TVU06828 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold17 | TVU28684 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t016 | SECCE1Rv | TraesCS2B | scaffold13 | TVU07131 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t045 | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |

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| LPERR12G | cds.KYUSt_ORUFI11G | Os11t070 | genblast_Z | TraesCS4A | scaffold66 | TVU41869 |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | genblast_C | TraesCS2B | scaffold43 | TVU38354 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7D | scaffold10 | TVU12402 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t055 | SECCE4Rv | TraesCS7A | scaffold12 | TVU29748 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3A | scaffold11 | TVU35460 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48556 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6D | scaffold13 | TVU29408 |

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| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE7Rv | TraesCS4B | scaffold42 | TVU30111 |
| LPERR12G | cds.KYUSt_ORUFI04G | Os04t019 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16541 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7A | scaffold24 | TVU05178 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t036 | SECCE4Rv | TraesCSU0 | scaffold18 | genblast_C |
| LPERR11G | cds.KYUSt_genblast_C | Os11t024 | SECCE4Rv | TraesCS4D | scaffold73 | TVU25974 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t068 | SECCE3Rv | TraesCS3D | scaffold11 | TVU35506 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t069 | genblast_C | TraesCS2B | scaffold1. | TVU37098 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t028 | SECCEUnv | TraesCS7D | scaffold21 | TVU32421 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t041 | SECCE6Rv | TraesCS6B | scaffold37 | TVU06095 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19708 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t023 | SECCE5Rv | TraesCS5A | scaffold42 | TVU33184 |

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| LPERR09G | cds.KYUSt_ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5D | scaffold16 | genblast_C |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t036 | SECCE4Rv | TraesCS7B | scaffold10 | genblast_C |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | genblast_C |

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| LPERR07G | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE5Rv | TraesCS5A | scaffold71 | TVU37901 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t044 | SECCE7Rv | TraesCS7B | scaffold13 | TVU05700 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t028 | genblast_C | TraesCS4A | scaffold40 | TVU47515 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1D | scaffold13 | TVT97212 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE4Rv | TraesCS4D | scaffold70 | TVU27511 |

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| genblast_C | genblast_C | genblast_C | Os05t020 | SECCE7Rv | TraesCS5D | scaffold20 | TVU44004 |
| LPERR05G | genblast_Z | ORUFI05G | genblast_Z | SECCE6Rv | TraesCS7D | scaffold28 | TVU41348 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3B | scaffold36 | TVU22943 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28324 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t035 | SECCE5Rv | TraesCS5A | scaffold28 | TVU35823 |
| LPERR12G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCE5Rv | TraesCS5A | scaffold46 | TVU48675 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | genblast_C | TraesCS5A | scaffold3. | TVU45034 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold83 | TVU50924 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t042 | SECCE2Rv | TraesCS2D | scaffold31 | TVU14543 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t045 | SECCE7Rv | TraesCS7A | scaffold17 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | scaffold85 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCEUnv | TraesCS6A | scaffold98 | TVU33612 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold28 | TVU15373 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7D | scaffold54 | TVU04619 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold41 | TVU36728 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1D | scaffold23 | TVU02912 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold16 | TVU03357 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS7B | scaffold30 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold52 | TVU48391 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5B | scaffold16 | TVU09556 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | genblast_C | TVU44828 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7D | scaffold92 | TVU08345 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t057 | SECCE7Rv | TraesCS7B | scaffold25 | TVU07933 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t083 | SECCE2Rv | TraesCS2D | scaffold26 | TVU27585 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5A | scaffold17 | TVU44324 |

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| LPERR04G | genblast_C | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2D | scaffold99 | TVU14276 |
| LPERR06G | genblast_C | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold22 | TVU07752 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2A | scaffold30 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2A | scaffold40 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold17 | TVU28637 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6D | scaffold98 | TVU33535 |
| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2A | scaffold14 | TVU03181 |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t051 | SECCE1Rv | TraesCS1D | scaffold61 | TVU32032 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold81 | TVU15687 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold13 | TVT96751 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34474 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t056 | genblast_C | TraesCS2A | scaffold43 | TVU38378 |
| LPERR05G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE1Rv | TraesCS1B | scaffold18 | TVU18304 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t058 | SECCE5Rv | TraesCS5B | scaffold1. | TVU03863 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t061 | SECCE7Rv | TraesCS7D | scaffold25 | TVU08136 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5A | scaffold25 | TVU46044 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE4Rv | TraesCS4D | scaffold50 | TVU04194 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t057 | SECCEUnv | TraesCS4D | scaffold3. | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold49 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3D | scaffold33 | TVU36412 |
| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold84 | TVU35179 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold12 | TVU39490 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6A | scaffold15 | genblast_C |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t063 | SECCE6Rv | TraesCS6D | scaffold28 | TVU03706 |

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| genblast_C | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold75 | TVU20029 |

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| LPERR09G | cds.KYUSt_ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5A | scaffold18 | TVU00479 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t016 | SECCE1Rv | TraesCS1B | scaffold11 | TVU17375 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t025 | SECCE1Rv | TraesCS1B | scaffold10 | TVU51299 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t067 | SECCE4Rv | TraesCS4D | scaffold18 | TVU45733 |
| LPERR11G | cds.KYUSt_ORUFI08G | Os08t024 | SECCE4Rv | TraesCS4A | scaffold45 | TVU20862 |
| genblast_C | cds.KYUSt_genblast_C | Os01t088 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36296 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35577 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t011 | SECCEUnv | TraesCS7D | scaffold26 | TVU43602 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t013 | SECCE3Rv | TraesCS3A | scaffold88 | TVU22035 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold17 | TVU44645 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5B | scaffold76 | TVU49166 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t055 | SECCE2Rv | TraesCS2D | scaffold61 | TVU11259 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold11 | TVU28321 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1B | scaffold75 | genblast_C |
| LPERR07G | genblast_C | ORUFI07G | Os07t023 | genblast_C | TraesCS2B | scaffold23 | TVU39910 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t040 | genblast_C | genblast_C | scaffold37 | TVU06116 |
| LPERR01G | genblast_C | ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34970 |
| LPERR02G | genblast_C | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6B | scaffold13 | TVU29480 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7D | scaffold22 | TVU07508 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t020 | SECCE4Rv | TraesCS4A | scaffold62 | TVU25906 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7D | scaffold38 | TVU04896 |
| LPERR02G | genblast_C | ORUFI02G | Os02t014 | genblast_C | TraesCS6B | scaffold24 | TVU33470 |
| genblast_Z | cds.KYUSt_ | ORUFI06G | genblast_Z | SECCE7Rv | TraesCS7B | scaffold12 | TVU08253 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold15 | genblast_Z |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t029 | SECCE7Rv | TraesCS3B | scaffold15 | TVU21295 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t024 | SECCE6Rv | TraesCS3D | scaffold73 | TVU25980 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold11 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t057 | SECCE4Rv | TraesCS4A | scaffold78 | TVT96854 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3A | scaffold21 | genblast_C |

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| LPERR08G | cds.KYUSt_ | ORUFI07G | Os06t025 | SECCEUnv | TraesCS2D | scaffold38 | TVU42390 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold23 | genblast_C |
| LPERR11G | genblast_C | ORUFI11G | Os11t018 | SECCE5Rv | TraesCS5D | scaffold50 | TVU26188 |
| LPERR12G | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5D | scaffold15 | TVU48980 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t062 | SECCE2Rv | TraesCS2D | scaffold25 | TVU08194 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t018 | SECCE4Rv | TraesCS4B | scaffold50 | TVU26165 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE5Rv | TraesCS7A | scaffold34 | TVU12671 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3B | scaffold14 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | genblast_C | TraesCS7D | scaffold44 | TVU01212 |
| LPERR03G | genblast_C | ORUFI05G | Os05t030 | SECCE3Rv | TraesCS3D | scaffold93 | TVU13378 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5A | scaffold3. | TVU45482 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4D | scaffold97 | TVU47915 |
| LPERR01G | cds.KYUSt_ | ORUFI05G | Os01t080 | SECCE3Rv | TraesCS3A | scaffold12 | TVU20020 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3A | scaffold47 | TVU22265 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3D | scaffold48 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI12G | Os12t011 | SECCE3Rv | TraesCS3B | scaffold17 | TVU36592 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2B | scaffold12 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI06G | Os02t027 | SECCEUnv | TraesCS5D | scaffold81 | TVU32607 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t014 | SECCE2Rv | TraesCS2A | scaffold10 | TVU31350 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold12 | TVU20052 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7D | scaffold92 | TVU08349 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16461 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE3Rv | TraesCS3B | scaffold25 | genblast_ |
| LPERR07G | genblast_C | ORUFI07G | Os07t026 | genblast_C | TraesCS5D | scaffold28 | genblast_ |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3A | scaffold4. | TVU17051 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47769 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45572 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7A | scaffold10 | TVU12289 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold46 | TVU34865 |
| LPERR02G | cds.KYUSt_ | ORUFI07G | Os07t047 | SECCE6Rv | TraesCS6A | scaffold15 | TVU30164 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11956 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t028 | SECCE2Rv | TraesCS2A | scaffold14 | TVU13450 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t016 | SECCE5Rv | TraesCS5A | scaffold28 | TVU41527 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold20 | TVU19425 |
| LPERR02G | cds.KYUSt_ | ORUFI10G | Os10t012 | SECCE6Rv | TraesCS6D | scaffold3. | TVT98071 |
| LPERR06G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3B | scaffold45 | TVU35077 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5A | scaffold70 | TVU26881 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7A | scaffold23 | TVU43859 |
| LPERR01G | genblast_C | genblast_C | Os01t023 | SECCE3Rv | TraesCS3D | scaffold33 | TVU04007 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16696 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t069 | SECCE2Rv | TraesCS2B | scaffold1. | TVU03018 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold46 | genblast_C |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2A | scaffold96 | TVU38329 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold39 | TVU07432 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCEUnv | TraesCS6B | scaffold10 | TVU28597 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCE5Rv | TraesCS5D | scaffold29 | TVU48815 |
| LPERR08G | genblast_C | ORUFI08G | Os08t031 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08022 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36187 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE1Rv | TraesCS1D | scaffold66 | TVU41191 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold18 | TVU48360 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t033 | SECCE4Rv | TraesCS4B | scaffold14 | TVU51417 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37303 |
| LPERR04G | genblast_C | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2B | scaffold94 | TVU16059 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | genblast_C | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1A | scaffold5. | TVU31544 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold1. | TVU00565 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold17 | TVU47590 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5D | scaffold11 | genblast_C |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE1Rv | TraesCS1B | scaffold40 | TVU40048 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7A | genblast_C | TVU08388 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t061 | SECCE4Rv | TraesCS4B | scaffold61 | TVU46139 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1A | scaffold20 | TVU19479 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7A | scaffold9. | TVU08575 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5D | scaffold27 | TVU10258 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7D | scaffold33 | TVU08384 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t052 | SECCE1Rv | TraesCS1D | scaffold5. | TVU29897 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE3Rv | TraesCS3A | scaffold18 | TVU46780 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t043 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19497 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | genblast_C | TraesCS4B | scaffold12 | TVU26776 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t041 | genblast_C | TraesCS2B | scaffold38 | TVU46602 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t020 | SECCE6Rv | TraesCS6A | scaffold84 | TVU17004 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t016 | SECCE1Rv | TraesCS1A | scaffold19 | TVU17377 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3D | scaffold48 | TVU37038 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4A | scaffold17 | TVU48250 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1B | scaffold19 | TVU20083 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t018 | SECCE3Rv | TraesCS3A | scaffold4. | TVU21488 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2D | scaffold20 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t026 | SECCE6Rv | TraesCS6B | scaffold10 | TVU51749 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE4Rv | TraesCS4B | scaffold18 | TVU43048 |
| LPERR09G | genblast_C | ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5A | scaffold64 | TVU09912 |
| LPERR10G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE1Rv | TraesCS1A | scaffold5. | TVU31613 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os10t053 | SECCE5Rv | TraesCS4D | scaffold25 | TVU48531 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3A | scaffold36 | TVU22766 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1B | scaffold87 | TVU19135 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE7Rv | TraesCS7B | scaffold28 | TVU04589 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t013 | SECCE2Rv | TraesCS2B | scaffold23 | TVU41017 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t056 | genblast_C | TraesCS2B | scaffold49 | TVU14864 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7D | genblast_C | TVU08662 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | SECCE4Rv | TraesCS7A | scaffold42 | TVU12999 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2B | scaffold12 | TVU16265 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14439 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3D | scaffold17 | TVU34984 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t022 | SECCE6Rv | TraesCS4D | scaffold15 | TVU47827 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1B | scaffold39 | TVU01071 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6B | scaffold22 | genblast_ |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28398 |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_ | SECCE4Rv | TraesCS7A | scaffold49 | TVU12802 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold14 | TVU16005 |
| LPERR02G | genblast_ | ORUFI02G | Os02t024 | genblast_ | genblast_ | scaffold6. | TVU33241 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t043 | SECCE4Rv | TraesCS4A | scaffold13 | TVU05736 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48066 |
| genblast_ | cds.KYUSt_ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1D | scaffold12 | TVU20043 |
| LPERR01G | genblast_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3B | scaffold89 | TVU36054 |
| genblast_ | cds.KYUSt_ORUFI11G | genblast_ | genblast_ | TraesCS5A | scaffold66 | TVU41280 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_ | SECCE3Rv | TraesCS3D | scaffold11 | TVU34939 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3D | scaffold40 | genblast_ |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1D | scaffold45 | TVU31820 |
| genblast_ | cds.KYUSt_ORUFI11G | Os11t070 | SECCE4Rv | TraesCS4A | scaffold10 | TVU23431 |
| LPERR01G | genblast_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3A | scaffold17 | TVU35085 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t020 | SECCE7Rv | TraesCS2D | genblast_ | TVU00075 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_ | SECCE5Rv | genblast_ | scaffold25 | TVU46031 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t024 | SECCE5Rv | TraesCS5D | scaffold41 | TVU10922 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3B | scaffold31 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE3Rv | TraesCS3A | scaffold16 | TVU22245 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE3Rv | TraesCSU0 | scaffold59 | TVU34166 |

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|---|---|---|---|---|---|---|---|
| LPERR11G | genblast_C | ORUFI11G | Os11t022 | SECCE4Rv | TraesCS4D | scaffold21 | TVU25847 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t072 | SECCE4Rv | TraesCS4D | scaffold35 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1D | scaffold52 | TVU18939 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44452 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE1Rv | TraesCS1B | scaffold7. | TVU00895 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE2Rv | TraesCS2D | scaffold61 | TVU03860 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7B | scaffold14 | TVU12069 |
| LPERR11G | cds.KYUSt_ | ORUFI03G | Os11t061 | genblast_C | TraesCSU0 | scaffold11 | TVU24283 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6B | scaffold27 | TVU27717 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7A | scaffold24 | TVU05396 |
| LPERR07G | genblast_C | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2D | scaffold67 | TVU37798 |

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| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold27 | TVU28187 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | genblast_C | ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7A | scaffold28 | TVU12913 |
| LPERR06G | cds.KYUSt_ | ORUFI03G | Os03t043 | SECCE4Rv | TraesCS4D | scaffold7. | TVU46448 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t017 | SECCE5Rv | TraesCS4A | scaffold10 | TVU51217 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4A | scaffold1. | TVU50225 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4B | genblast_C | genblast_C |
| LPERR12G | genblast_C | ORUFI12G | Os12t023 | SECCE5Rv | TraesCS5D | scaffold10 | TVU51546 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t052 | SECCE4Rv | TraesCS7D | scaffold16 | TVU33865 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | genblast_C | TraesCS7D | scaffold22 | TVU07611 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2D | genblast_C | TVU37401 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2A | genblast_C | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE4Rv | TraesCS4A | scaffold83 | genblast_C |
| LPERR11G | genblast_C | ORUFI11G | genblast_C | SECCE6Rv | TraesCS6B | genblast_C | TVU50452 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35875 |
| LPERR04G | genblast_C | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16543 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4B | scaffold62 | TVU25846 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCEUnv | TraesCS6B | scaffold12 | TVU28112 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2B | scaffold8. | TVU14497 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3D | scaffold33 | TVT99387 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t029 | SECCE7Rv | TraesCS4A | scaffold12 | TVU18592 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4B | scaffold35 | TVU45355 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold35 | genblast_Z |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t047 | SECCE3Rv | TraesCS3D | scaffold60 | TVU25490 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3D | scaffold46 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7A | scaffold18 | TVU42896 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | genblast_C | scaffold87 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR12G | genblast_C | ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5A | scaffold17 | TVU49962 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t014 | SECCE2Rv | TraesCS2B | scaffold32 | TVU31325 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t058 | SECCE6Rv | TraesCS6D | scaffold17 | TVU29495 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7B | scaffold11 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold18 | TVU21574 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_Z | SECCEUnv | TraesCS7A | scaffold60 | TVU07559 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE7Rv | TraesCS2B | scaffold14 | TVU06844 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE1Rv | TraesCS1D | scaffold79 | TVU29721 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t028 | SECCE4Rv | TraesCS7B | genblast_C | TVU11601 |
| LPERR01G | genblast_C | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35184 |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE6Rv | TraesCS5D | scaffold38 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t013 | SECCE5Rv | TraesCS5A | scaffold12 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold11 | TVU45513 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t064 | SECCE3Rv | TraesCS3D | scaffold11 | TVU01162 |
| LPERR01G | genblast_C | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35183 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t031 | genblast_C | TraesCS7D | scaffold68 | TVU11454 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28358 |
| LPERR01G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE3Rv | TraesCS3A | scaffold24 | TVU21872 |
| LPERR01G | genblast_C | ORUFI01G | Os01t068 | genblast_C | TraesCS3B | scaffold33 | TVT99362 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE4Rv | TraesCS7D | scaffold19 | TVU30937 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t028 | SECCE4Rv | TraesCS7D | scaffold30 | TVU11616 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t049 | SECCE6Rv | TraesCS6A | genblast_C | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold35 | genblast_C |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold20 | TVU27619 |
| LPERR08G | genblast_C | genblast_C | Os09t049 | SECCE5Rv | TraesCS5B | scaffold16 | TVU05206 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15865 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t043 | SECCE6Rv | TraesCS3D | scaffold5. | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCS6A | scaffold48 | TVU33559 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2D | scaffold56 | TVU15295 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | SECCEUnv | TraesCS6D | scaffold12 | TVU28098 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t017 | genblast_C | genblast_C | scaffold10 | TVU41760 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_Z | SECCE4Rv | TraesCS7D | scaffold13 | TVU05659 |
| LPERR02G | genblast_Z | ORUFI02G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold51 | TVU33163 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold42 | TVU13403 |
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold12 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | genblast_C | TraesCSU0 | scaffold40 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold40 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3A | scaffold54 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2B | scaffold8. | TVU14440 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t046 | SECCE3Rv | TraesCS3B | scaffold26 | TVU05577 |
| LPERR03G | genblast_C | ORUFI03G | Os03t084 | SECCE7Rv | TraesCS4A | scaffold25 | TVT96979 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE5Rv | TraesCS5B | scaffold15 | TVU04581 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | genblast_C | TVT97133 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6A | scaffold35 | TVU28287 |
| LPERR07G | genblast_C | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold10 | TVU40104 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7A | scaffold92 | TVU08546 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t025 | SECCE5Rv | TraesCS5B | scaffold25 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t056 | SECCE6Rv | TraesCS6B | scaffold41 | TVU29611 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t034 | SECCE1Rv | TraesCS1A | scaffold52 | TVT99551 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t070 | SECCE4Rv | TraesCS7D | scaffold46 | TVU23267 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t026 | SECCE1Rv | TraesCS1A | scaffold6. | TVU33349 |
| LPERR09G | genblast_C | ORUFI09G | Os09t056 | SECCE5Rv | TraesCS5B | scaffold3. | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | genblast_C | TraesCS3D | scaffold18 | TVU22100 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44415 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold26 | TVU38177 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3D | scaffold11 | TVT99366 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t057 | SECCE3Rv | TraesCS3B | scaffold20 | TVU34208 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold15 | TVU47907 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t043 | SECCE4Rv | TraesCS5D | scaffold16 | TVU50440 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold94 | TVU06347 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2A | scaffold14 | TVU15636 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t042 | SECCE6Rv | TraesCS6D | scaffold45 | TVU46540 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv | TraesCS3A | scaffold18 | TVU34640 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1A | scaffold36 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t035 | SECCE4Rv | TraesCS4A | scaffold22 | TVU47049 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19944 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | genblast_C | TraesCSU0 | scaffold66 | TVU18216 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold2. | TVU38123 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3B | scaffold89 | TVU35297 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3D | scaffold20 | TVU39574 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2A | genblast_C | TVU13187 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | genblast_C | TraesCS6B | scaffold19 | TVU33689 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7A | scaffold13 | TVU05249 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5B | scaffold24 | TVU49651 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2D | scaffold14 | TVU29044 |
| LPERR06G | genblast_C | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7B | scaffold60 | TVU07539 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7D | scaffold25 | TVU07932 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | genblast_C | TraesCS1B | scaffold85 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6B | scaffold24 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold38 | TVU01176 |
| LPERR11G | genblast_C | ORUFI11G | genblast_C | SECCE7Rv | genblast_C | scaffold13 | TVU24930 |
| LPERR06G | cds.KYUSt_ | genblast_C | genblast_C | SECCE7Rv | TraesCS7A | scaffold22 | TVU07750 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6B | scaffold26 | genblast_C |
| LPERR03G | genblast_C | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44728 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t089 | SECCE3Rv | TraesCS3A | scaffold39 | TVU36183 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold75 | TVU19899 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold26 | TVU04972 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE5Rv | TraesCS5A | scaffold29 | TVU49547 |
| LPERR01G | genblast_C | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3D | scaffold47 | TVT98174 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCE5Rv | TraesCS5A | scaffold17 | TVU48801 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t012 | SECCE5Rv | TraesCS5A | scaffold3. | genblast_C |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3D | scaffold41 | TVU36662 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6D | scaffold11 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1B | scaffold23 | TVU19480 |
| genblast_C | genblast_C | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37555 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE7Rv | TraesCS7D | scaffold33 | TVU08466 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t062 | SECCE5Rv | TraesCS5A | scaffold13 | TVU05040 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1A | scaffold41 | TVU18953 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7D | scaffold34 | TVU12218 |
| LPERR01G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4D | scaffold55 | TVU03365 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t013 | SECCE5Rv | TraesCS5B | scaffold50 | TVT97963 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7B | scaffold24 | TVU05202 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t051 | genblast_C | TraesCS2B | scaffold20 | TVU15263 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2D | scaffold28 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7B | genblast_C | TVU12134 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t088 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36252 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t053 | SECCE4Rv | TraesCS4D | scaffold17 | TVU24646 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7B | scaffold26 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4A | scaffold97 | TVU47932 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE3Rv | TraesCS2B | scaffold43 | TVU04234 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t066 | SECCE3Rv | TraesCS3B | genblast_C | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48112 |
| LPERR01G | genblast_C | ORUFI01G | Os01t054 | SECCE5Rv | TraesCS5A | scaffold11 | TVU34044 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os02t051 | SECCE5Rv | TraesCS5D | scaffold12 | TVT99853 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t049 | SECCE2Rv | TraesCS2D | scaffold27 | TVU39064 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12156 |
| LPERR06G | genblast_C | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7A | scaffold24 | TVU07774 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2D | scaffold30 | TVU15621 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7B | scaffold41 | TVU08043 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os10t013 | SECCE4Rv | TraesCS7D | scaffold71 | TVU46649 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t043 | SECCE1Rv | TraesCS1A | scaffold33 | genblast_ |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os04t029 | SECCE2Rv | TraesCS2A | scaffold42 | TVU30130 |

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| LPERR04G | genblast_C | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14640 |
| LPERR06G | cds.KYUSt_ | ORUFI08G | Os06t071 | SECCE6Rv | TraesCS7A | scaffold60 | TVU07593 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE1Rv | TraesCS1D | scaffold75 | TVU04945 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5A | scaffold16 | TVU09559 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS5D | scaffold17 | TVU44301 |
| LPERR04G | genblast_C | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2B | scaffold8. | TVU14428 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7D | scaffold60 | TVU07730 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36512 |
| LPERR02G | genblast_C | ORUFI02G | Os02t032 | SECCE1Rv | TraesCS1B | scaffold67 | TVU32289 |
| LPERR01G | genblast_C | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3D | scaffold31 | TVU34595 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7B | scaffold54 | TVU08716 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7A | scaffold92 | genblast_C |
| LPERR10G | genblast_C | ORUFI10G | Os10t033 | SECCE7Rv | TraesCS4B | scaffold19 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold15 | TVU35164 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t018 | SECCE7Rv | TraesCS5B | scaffold10 | TVU51096 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold12 | TVU28189 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold3. | genblast_C |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37192 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | genblast_C | TVU19919 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36297 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3D | scaffold29 | TVU35336 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t065 | SECCE5Rv | TraesCS5B | scaffold20 | TVU45870 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE5Rv | TraesCS5B | scaffold14 | TVU31792 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3B | scaffold3. | TVU35738 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1D | scaffold1. | TVU20390 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold31 | TVU02410 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2A | scaffold20 | TVU40519 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | genblast_C |

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| LPERR12G | cds.KYUSt_ | ORUFI11G | Os12t012 | SECCE5Rv | TraesCS5B | scaffold64 | TVU27201 |

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| LPERR06G | genblast_C | genblast_C | Os06t016 | SECCE4Rv | TraesCS7D | scaffold34 | TVU12427 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1B | scaffold39 | TVU19464 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3B | scaffold63 | TVU21386 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE5Rv | TraesCS4D | scaffold32 | TVU32226 |
| LPERR02G | genblast_C | genblast_C | Os03t066 | SECCE4Rv | TraesCS4D | scaffold15 | TVU27525 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold3. | TVU44465 |

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| LPERR02G | genblast_C | ORUFI10G | Os10t013 | SECCE4Rv | TraesCS7D | scaffold10 | TVU31451 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t044 | SECCEUnv | TraesCS2A | scaffold3. | TVU00986 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t047 | SECCE3Rv | TraesCS3A | scaffold16 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold31 | TVU34597 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE4Rv | TraesCS7A | scaffold26 | TVU05134 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t017 | SECCE5Rv | TraesCS5B | scaffold70 | TVU51147 |
| LPERR06G | genblast_C | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7D | scaffold29 | TVU08666 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold41 | TVU36413 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3B | scaffold36 | TVU02941 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE4Rv | TraesCS4B | scaffold23 | genblast_C |

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| LPERR07G( | cds.KYUSt_ | ORUFI07G( | Os07t018⁴ | SECCE5Rv1 | TraesCS5A | scaffold66 | TVT97305 |

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| LPERR08G1 | cds.KYUSt_ | ORUFI08G1 | Os08t044: | SECCE6Rv1 | TraesCS6B | scaffold19 | TVU05703 |
| LPERR02G2 | cds.KYUSt_ | ORUFI02G1 | Os02t073( | SECCEUnv1 | TraesCS6A | scaffold83 | TVU28347 |
| LPERR08G1 | genblast_C | ORUFI08G1 | Os08t036⁴ | SECCE1Rv1 | TraesCS1B | scaffold11 | TVU06450 |
| LPERR01G1 | cds.KYUSt_ | ORUFI01G1 | Os01t029! | SECCE3Rv1 | TraesCS3A | scaffold54 | TVU21280 |
| LPERR02G2 | cds.KYUSt_ | genblast_C | Os02t0661 | SECCE6Rv1 | TraesCS6B | scaffold24 | TVU28936 |
| genblast_C | cds.KYUSt_ | ORUFI01G⁴ | Os01t096⁷ | SECCE6Rv1 | TraesCS3A | scaffold18 | TVU37007 |

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| LPERR01G1 | cds.KYUSt_ | ORUFI05G2 | Os05t045! | SECCE1Rv1 | TraesCS1B | scaffold12 | TVU19695 |
| LPERR05G1 | cds.KYUSt_ | ORUFI05G1 | genblast_C | SECCE1Rv1 | TraesCS1D | scaffold8.7 | genblast_C |
| LPERR05G( | cds.KYUSt_ | ORUFI05G( | genblast_C | SECCE1Rv1 | TraesCS1A | scaffold13 | TVU17237 |
| LPERR03G1 | cds.KYUSt_ | ORUFI03G1 | genblast_Z | SECCE5Rv1 | TraesCS5B | scaffold3.7 | TVU44504 |
| LPERR03G2 | cds.KYUSt_ | ORUFI03G1 | Os03t068{ | SECCE4Rv1 | TraesCS4B | scaffold55 | TVU45641 |
| LPERR01G( | genblast_C | ORUFI01G( | Os01t018⁴ | SECCE2Rv1 | TraesCS3A | scaffold12 | TVU21473 |
| LPERR03G2 | genblast_C | ORUFI03G2 | Os03t065( | genblast_C | TraesCS4D | scaffold11 | TVU45835 |
| LPERR11G1 | cds.KYUSt_ | ORUFI11G1 | Os11t044{ | SECCEUnv1 | TraesCS6B | scaffold68 | TVU00618 |
| LPERR04G1 | cds.KYUSt_ | ORUFI04G2 | Os04t056: | SECCE2Rv1 | TraesCS2A | scaffold49 | TVU14884 |
| LPERR07G1 | cds.KYUSt_ | ORUFI07G1 | Os07t054! | SECCE2Rv1 | TraesCS2B | scaffold43 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR07G( | cds.KYUSt_ | ORUFI07G( | Os07t016⁴ | SECCE2Rv1 | TraesCS2A | scaffold66 | TVU41504 |
| LPERR07G( | cds.KYUSt_ | ORUFI07G( | Os07t020! | SECCE2Rv1 | TraesCS2B | scaffold28 | TVU40053 |

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| LPERR08G1 | cds.KYUSt_ | ORUFI08G2 | Os08t049: | SECCE1Rv1 | TraesCS7B | scaffold26 | TVU05410 |
| genblast_C | cds.KYUSt_ | ORUFI09G1 | Os09t045⁴ | SECCE5Rv1 | TraesCS5D | scaffold27 | TVU09789 |

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| LPERR01G( | cds.KYUSt_ | ORUFI01G( | Os01t017] | SECCE3Rv] | TraesCS3D | scaffold88 | TVU21603 |
| genblast_C | cds.KYUSt_ | ORUFI06G] | Os06t027] | SECCE4Rv] | TraesCS7D | scaffold30 | genblast_C |
| LPERR11G] | cds.KYUSt_ | ORUFI11G] | Os11t0552 | SECCE3Rv] | TraesCS3D | scaffold43 | genblast_C |
| LPERR06G2 | cds.KYUSt_ | ORUFI07G( | Os07t0172 | SECCE6Rv] | TraesCS7A | scaffold60 | TVU07515 |
| LPERR01G2 | genblast_C | ORUFI01G2 | Os01t0687 | SECCE3Rv] | TraesCS3B | scaffold11 | TVU35485 |
| LPERR01G] | cds.KYUSt_ | ORUFI01G4 | Os01t0935 | SECCE3Rv] | TraesCS3B | scaffold21 | TVU34671 |

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| LPERR11G( | cds.KYUSt_ | ORUFI04G( | Os04t032( | SECCE1Rv] | TraesCS1A | scaffold32 | TVU04464 |
| LPERR03G2 | cds.KYUSt_ | ORUFI03G] | Os03t070] | SECCE4Rv] | TraesCS4D | scaffold11 | genblast_C |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t0187 | SECCE4Rv] | TraesCS7D | scaffold17 | genblast_C |
| LPERR01G] | genblast_C | ORUFI01G4 | Os01t0962 | SECCE6Rv] | TraesCS3B | scaffold15 | TVU36964 |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t0148 | SECCE7Rv] | TraesCS4D | scaffold29 | TVU48369 |

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| genblast_C | cds.KYUSt_ | ORUFI12G( | Os12t0122 | SECCE4Rv] | TraesCS4D | scaffold48 | TVU50658 |
| LPERR12G] | genblast_C | ORUFI12G] | Os12t054( | SECCE5Rv] | TraesCS5D | scaffold1.] | genblast_C |
| LPERR05G( | cds.KYUSt_ | ORUFI05G( | Os05t011( | SECCE6Rv] | TraesCS3D | scaffold46 | TVU18331 |
| LPERR04G2 | cds.KYUSt_ | genblast_C | Os04t0608 | SECCE2Rv] | TraesCS2D | scaffold14 | TVT98956 |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t0152 | SECCE1Rv] | TraesCS1D | scaffold46 | TVU48346 |
| LPERR01G] | cds.KYUSt_ | ORUFI01G2 | Os01t0558 | SECCE3Rv] | TraesCS3A | scaffold46 | TVU34115 |
| LPERR05G( | cds.KYUSt_ | ORUFI05G( | Os05t0132 | SECCE1Rv] | TraesCS1A | scaffold83 | TVU18410 |
| LPERR06G2 | cds.KYUSt_ | ORUFI06G2 | Os06t0698 | SECCE7Rv] | TraesCS7A | scaffold9.7 | TVU07748 |
| LPERR11G( | cds.KYUSt_ | ORUFI11G( | genblast_C | SECCE4Rv] | TraesCS4B | scaffold12 | TVU01382 |
| LPERR08G] | cds.KYUSt_ | ORUFI08G] | genblast_Z | SECCE6Rv] | TraesCS3B | scaffold24 | TVU05800 |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t0125 | SECCE5Rv] | TraesCS4B | scaffold25 | TVU48550 |
| LPERR07G( | cds.KYUSt_ | genblast_C | Os07t0104 | SECCE2Rv] | TraesCS2A | scaffold7.7 | TVU40208 |

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| LPERR10G( | cds.KYUSt_ | ORUFI10G( | Os10t0405 | SECCE5Rv] | TraesCS5D | scaffold19 | TVU30997 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t010 | SECCE6Rv | TraesCS7D | scaffold19 | TVU46859 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t032 | SECCE1Rv | TraesCS1B | scaffold23 | TVU32271 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t028 | SECCE1Rv | TraesCS1A | scaffold14 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | genblast_C | genblast_C | scaffold19 | TVT97206 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5D | scaffold17 | TVU02958 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7D | scaffold44 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3B | scaffold78 | TVU36897 |
| LPERR04G | genblast_C | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14326 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t032 | SECCE2Rv | TraesCS2A | genblast_C | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36463 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold2. | TVU37292 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t029 | SECCE5Rv | TraesCS5B | scaffold12 | TVU03180 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t019 | SECCE2Rv | TraesCS2B | scaffold66 | TVU41310 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold17 | TVU29164 |
| LPERR07G | genblast_C | ORUFI07G | Os07t041 | SECCE4Rv | TraesCS4B | scaffold20 | TVU03986 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t022 | SECCE4Rv | TraesCS7B | scaffold10 | TVU39979 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37261 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7D | scaffold44 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold13 | TVU04385 |
| genblast_Z | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE4Rv | TraesCS7D | scaffold92 | TVU30230 |
| LPERR07G | genblast_C | ORUFI07G | Os07t069 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37088 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5B | scaffold31 | TVU42357 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold84 | TVU28575 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t053 | genblast_C | TraesCS2A | scaffold20 | TVU15069 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7D | scaffold60 | TVU07745 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4A | scaffold55 | TVU45541 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3D | scaffold63 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold25 | TVU43918 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45341 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t019 | SECCE5Rv | genblast_C | scaffold10 | TVU51312 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold87 | TVU09363 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2A | scaffold14 | TVU15604 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5D | scaffold53 | TVU09882 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t064 | SECCE7Rv | TraesCS2A | scaffold47 | TVU04331 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1A | scaffold61 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE1Rv | TraesCS6D | scaffold13 | TVU29402 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t028 | genblast_C | genblast_C | scaffold14 | TVU18575 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os09t029 | SECCE3Rv | TraesCS3A | scaffold15 | TVT98942 |
| genblast_Z | genblast_Z | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7A | scaffold48 | TVU08565 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t014 | SECCE2Rv | TraesCS2A | scaffold12 | TVU41147 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t032 | SECCE5Rv | TraesCS5A | scaffold38 | TVU25631 |
| LPERR09G | cds.KYUSt_ | ORUFI04G | Os09t033 | SECCE5Rv | TraesCS5D | scaffold19 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t040 | SECCE7Rv | TraesCS7B | scaffold45 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7D | scaffold44 | genblast_C |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2A | scaffold30 | TVU14159 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5D | scaffold35 | TVT97459 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t053 | genblast_C | genblast_C | scaffold5. | TVU29815 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t029 | SECCE4Rv | TraesCS7B | scaffold11 | TVU31324 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t030 | SECCE3Rv | TraesCS3D | genblast_C | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7B | scaffold12 | TVU42916 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6B | scaffold17 | TVU03506 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3A | scaffold18 | TVU21952 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t024 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11828 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold31 | TVU14564 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS4A | scaffold3. | genblast_C |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7A | scaffold93 | TVU07930 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6D | scaffold10 | TVU02597 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE6Rv | TraesCS6B | scaffold60 | TVU20887 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | genblast_C | TraesCS4B | scaffold22 | TVU47299 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t058 | genblast_C | TraesCS3A | scaffold11 | TVU34286 |
| LPERR02G | genblast_C | ORUFI02G | Os02t057 | genblast_C | genblast_C | scaffold5. | TVU29549 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t043 | SECCE1Rv | TraesCS1B | scaffold18 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t064 | SECCE7Rv | TraesCS7D | scaffold8. | TVU23869 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t036 | SECCE2Rv | TraesCS2A | genblast_C | TVU30830 |
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| LPERR06G | genblast_C | ORUFI06G | Os06t068 | genblast_C | TraesCS7B | scaffold17 | TVU24564 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold27 | genblast_C |
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| LPERR02G | genblast_C | ORUFI02G | Os02t061 | genblast_C | TraesCS6A | scaffold16 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE4Rv | TraesCS5A | scaffold17 | TVU41244 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t013 | SECCE3Rv | TraesCS3A | scaffold88 | TVU22075 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2D | scaffold36 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCE5Rv | TraesCS5B | scaffold42 | genblast_C |
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| LPERR03G | cds.KYUSt_ | genblast_C | Os03t085 | SECCE7Rv | TraesCS5D | scaffold39 | TVU44182 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t028 | genblast_C | genblast_C | scaffold10 | TVU22729 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2A | scaffold96 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t064 | SECCE3Rv | TraesCS3A | scaffold76 | TVU49793 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3D | scaffold18 | TVU21897 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3B | scaffold15 | genblast_C |

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| genblast_C | cds.KYUSt_ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36773 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t053 | SECCE4Rv | TraesCS7A | scaffold54 | TVU04933 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t010 | SECCE1Rv | TraesCS1D | scaffold19 | TVU18434 |
| LPERR04G | cds.KYUSt_ORUFI01G | Os04t049 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15401 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2D | scaffold16 | TVU16362 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t014 | SECCE1Rv | TraesCS1A | scaffold19 | TVU17822 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3B | scaffold14 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t041 | genblast_C | genblast_C | scaffold28 | TVU06026 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2D | scaffold26 | TVU14350 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3A | scaffold25 | TVU22338 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1A | scaffold7. | TVU31899 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1D | scaffold24 | TVU18128 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t022 | SECCE4Rv | TraesCS4A | scaffold31 | TVU43308 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold13 | TVU02911 |

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| genblast_C | cds.KYUSt_ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2D | scaffold30 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5D | scaffold32 | TVU44752 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t060 | SECCE2Rv | TraesCS3A | scaffold26 | TVU03697 |
| LPERR03G | cds.KYUSt_genblast_C | Os03t073 | SECCE4Rv | TraesCS4D | scaffold35 | TVU45157 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold27 | TVU28146 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t010 | genblast_C | TraesCS3A | scaffold47 | TVU01865 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE3Rv | TraesCS3D | scaffold14 | TVU35271 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE7Rv | TraesCS7B | scaffold33 | TVU08749 |
| LPERR04G | genblast_C | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2B | scaffold94 | TVU15765 |
| LPERR01G | genblast_C | ORUFI03G | Os03t059 | SECCEUnv | TraesCSU0 | scaffold5. | TVU15191 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3D | scaffold41 | TVU36386 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os11t059 | SECCE5Rv | TraesCS5D | scaffold4. | TVT99841 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19827 |
| LPERR12G | genblast_C | ORUFI12G | Os12t047 | SECCE5Rv | TraesCS5A | scaffold58 | TVU50300 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCSU0 | scaffold22 | TVU07536 |
| LPERR05G | genblast_C | ORUFI05G | Os05t034 | SECCE1Rv | TraesCS1A | scaffold13 | TVU18242 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4B | scaffold14 | TVU47621 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t032 | SECCE3Rv | TraesCS3A | scaffold12 | TVU02876 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t046 | SECCE5Rv | TraesCS5D | scaffold16 | TVU50373 |
| genblast_C | genblast_C | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3B | scaffold17 | TVU35070 |
| genblast_C | genblast_C | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3B | scaffold45 | TVU36795 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS2B | scaffold13 | TVU21464 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1B | scaffold27 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36403 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3D | scaffold45 | genblast_C |

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|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t043 | SECCE1Rv | TraesCS1B | scaffold5. | TVU46420 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2A | scaffold49 | TVU13127 |

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|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold67 | TVU37611 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t083 | SECCE7Rv | TraesCS4A | scaffold32 | genblast_C |

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|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t021 | SECCE6Rv | TraesCS6D | scaffold6. | genblast_C |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1D | scaffold12 | TVU18936 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t055 | SECCE5Rv | TraesCS5A | scaffold12 | TVU29727 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | genblast_C | TVU36729 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t043 | SECCE4Rv | TraesCS7A | scaffold13 | TVU05745 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t064 | SECCE3Rv | TraesCS3D | scaffold11 | TVU35793 |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE4Rv | TraesCS6A | genblast_C | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5D | scaffold27 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2B | genblast_C | TVU32365 |
| LPERR10G | genblast_C | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1D | scaffold5. | TVU31657 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7D | scaffold60 | TVU08586 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t068 | genblast_Z | TraesCS3A | scaffold11 | TVT97169 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS4A | scaffold44 | TVT97012 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1A | scaffold40 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6A | scaffold37 | TVU28799 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE5Rv | TraesCS5B | scaffold48 | TVU37055 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37169 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28325 |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6B | scaffold17 | TVU28646 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCS6B | scaffold48 | TVU33580 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1D | scaffold20 | TVU19443 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold89 | TVU35150 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7A | scaffold33 | TVU08506 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t031 | SECCE5Rv | TraesCS5D | scaffold33 | TVU13616 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47665 |
| LPERR09G | genblast_C | ORUFI09G | Os09t054 | genblast_C | genblast_C | scaffold43 | TVU10263 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3D | scaffold18 | TVU36956 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCEUnv | TraesCS6D | scaffold24 | genblast_C |

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| LPERR01G | genblast_C | ORUFI01G | Os01t010 | SECCE1Rv | TraesCS1D | scaffold47 | TVU46976 |

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|---|---|---|---|---|---|---|---|
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1B | scaffold27 | TVU32180 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t028 | SECCE4Rv | TraesCS7B | scaffold34 | TVU11623 |
| LPERR07G | genblast_C | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2D | scaffold12 | TVU07455 |
| LPERR10G | cds.KYUSt_ | ORUFI11G | Os11t062 | SECCE3Rv | TraesCS3D | scaffold41 | TVU24114 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | genblast_C | TraesCS2D | scaffold2. | TVU37771 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38209 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t017 | SECCE1Rv | TraesCS1B | scaffold36 | TVU17202 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3A | scaffold17 | TVU36659 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t037 | SECCE2Rv | TraesCS2B | scaffold12 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1A | scaffold75 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3D | scaffold25 | TVU22271 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t065 | SECCE4Rv | TraesCS4D | scaffold13 | TVU23708 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37534 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t016 | SECCE5Rv | TraesCS5A | scaffold28 | TVU41561 |

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|---|---|---|---|---|---|---|---|
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t056 | SECCE5Rv | TraesCS5A | scaffold10 | TVU10543 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3A | genblast_C | TVU37042 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE3Rv | TraesCS3D | scaffold47 | TVU04323 |
| LPERR03G | genblast_C | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4A | scaffold55 | TVU45483 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4D | scaffold20 | genblast_C |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE5Rv | TraesCS6D | scaffold48 | TVU00517 |
| LPERR06G | genblast_C | ORUFI06G | Os06t048 | SECCE4Rv | TraesCS7D | scaffold19 | TVU11282 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4D | scaffold22 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1B | scaffold61 | TVU31986 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE2Rv | TraesCS2B | scaffold51 | TVU33333 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t059 | SECCE4Rv | TraesCS7D | scaffold78 | TVU25155 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5B | scaffold65 | TVU44443 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2D | scaffold34 | TVU37753 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1A | scaffold32 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE4Rv | TraesCS4D | scaffold22 | TVU47190 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37253 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44968 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7B | scaffold92 | TVU08446 |
| LPERR03G | genblast_C | ORUFI03G | Os03t042 | SECCE2Rv | TraesCS2A | scaffold5. | TVU46536 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE5Rv | TraesCS5A | scaffold12 | TVU26958 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4B | scaffold19 | TVU48127 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE5Rv | TraesCSU0 | scaffold52 | TVU48682 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4D | scaffold53 | TVU47922 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t035 | SECCE5Rv | TraesCS5B | scaffold14 | TVU09300 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold74 | TVU47062 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold10 | TVU28946 |
| LPERR06G | genblast_C | ORUFI08G | genblast_C | SECCEUnv | TraesCS7B | scaffold23 | TVU43837 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10042 |

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|---|---|---|---|---|---|---|---|
| LPERR11G | cds.KYUSt_ | ORUFI04G | Os11t010 | SECCE5Rv | TraesCS5B | scaffold70 | TVU00006 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t039 | SECCE2Rv | TraesCS2A | scaffold99 | TVU14755 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE7Rv | TraesCS7D | scaffold33 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t020 | SECCE7Rv | TraesCS7B | scaffold22 | TVU07713 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2A | scaffold8. | TVU14427 |
| LPERR08G | cds.KYUSt_ | ORUFI06G | Os08t044 | SECCE7Rv | TraesCS7A | scaffold13 | TVU05678 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os11t011 | SECCE5Rv | TraesCS5A | scaffold70 | TVU27341 |
| genblast_C | genblast_C | ORUFI09G | Os09t024 | SECCE1Rv | TraesCS1B | scaffold1. | TVU08556 |
| LPERR03G | genblast_C | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5A | scaffold17 | TVU44383 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold40 | TVU23034 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE4Rv | genblast_C | scaffold98 | TVU33588 |
| LPERR02G | genblast_Z | ORUFI02G | genblast_Z | genblast_Z | TraesCS6A | scaffold14 | TVU28502 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6D | scaffold5. | TVU29750 |
| LPERR02G | genblast_C | ORUFI02G | Os02t016 | SECCE6Rv | TraesCS6A | scaffold39 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os02t053 | SECCE6Rv | TraesCS6D | scaffold15 | TVU29850 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t011 | SECCE7Rv | TraesCS2B | scaffold63 | TVT96701 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7D | scaffold11 | TVU07894 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv | TraesCS3D | scaffold18 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv | TraesCS5D | scaffold57 | TVU49408 |
| genblast_C | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE6Rv | TraesCS6D | scaffold44 | TVU43288 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5A | scaffold17 | genblast_C |
| genblast_C | genblast_C | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7B | scaffold9. | TVU07671 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12436 |
| LPERR02G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE6Rv | TraesCS6B | scaffold1. | TVU27753 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t071 | SECCE6Rv | TraesCS7D | scaffold9. | TVU07588 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t066 | genblast_C | TraesCS2D | scaffold16 | TVT97987 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1B | scaffold13 | TVU17438 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold84 | TVU36572 |
| LPERR01G | cds.KYUSt_genblast_C | Os01t077 | SECCE3Rv | TraesCS3D | scaffold22 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | genblast_C | TVU44915 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | genblast_C | TraesCS4A | scaffold17 | TVU43950 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48131 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2A | scaffold58 | TVU38996 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_Z | SECCE4Rv | TraesCS4A | scaffold22 | TVU47040 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3A | scaffold21 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold39 | TVU36197 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold46 | TVU34091 |
| LPERR11G | genblast_Z | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4B | scaffold18 | TVU03657 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5A | scaffold35 | TVU44943 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold47 | TVU22305 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t016 | SECCE6Rv | TraesCS6A | scaffold35 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | genblast_C | genblast_C | scaffold39 | TVU36196 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t027 | SECCE1Rv | TraesCS5D | scaffold18 | TVU49888 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t057 | SECCE1Rv | TraesCS1D | scaffold5. | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | genblast_C | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37889 |
| LPERR05G | genblast_C | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1B | scaffold8. | TVU19368 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t058 | SECCE7Rv | TraesCS7A | scaffold19 | TVT96651 |
| LPERR04G | genblast_Z | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2B | scaffold32 | TVU16410 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | scaffold52 | TVU48439 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t050 | SECCE6Rv | TraesCS6D | scaffold25 | TVU25340 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47326 |
| LPERR05G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7B | scaffold38 | TVU00119 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE7Rv | TraesCS7A | scaffold27 | TVT98298 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE7Rv | TraesCS7D | scaffold83 | TVU06916 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold65 | TVU43957 |
| LPERR08G | genblast_C | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold26 | TVT99154 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1B | genblast_C | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1A | scaffold13 | TVU22581 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15877 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t020 | SECCE1Rv | TraesCS1B | scaffold10 | TVU41362 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t013 | SECCE5Rv | TraesCS5A | scaffold13 | TVU10892 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3D | scaffold89 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t043 | SECCE5Rv | TraesCS5B | scaffold19 | TVU05729 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE2Rv | TraesCS2A | genblast_C | TVU09973 |

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|---|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2A | scaffold94 | TVU14944 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold15 | TVT99047 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7B | scaffold41 | TVU08155 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14149 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t077 | genblast_C | TraesCS6B | scaffold11 | TVU28771 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t022 | SECCE2Rv | TraesCS2D | scaffold83 | TVU07420 |
| LPERR04G | cds.KYUSt_ | ORUFI07G | Os07t040 | SECCE6Rv | TraesCS6A | scaffold5. | TVU39425 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1B | scaffold11 | TVU47703 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4A | scaffold13 | TVU24920 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t062 | SECCE5Rv | TraesCS5A | scaffold15 | TVU48932 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37878 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3D | scaffold46 | TVU34856 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCEUnv | TraesCS4B | scaffold11 | TVU45788 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1D | scaffold24 | TVU35873 |

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| LPERR08G | genblast_C | ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7A | scaffold11 | TVU43580 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t019 | SECCE5Rv | TraesCSU0 | scaffold70 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3B | genblast_C | TVU22939 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t029 | SECCE3Rv | TraesCS3A | scaffold15 | TVU18584 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t027 | SECCE5Rv | TraesCS5D | scaffold22 | TVU32606 |

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| LPERR02G | cds.KYUSt_ | ORUFI03G | Os03t058 | SECCE3Rv | TraesCS3B | scaffold88 | TVU21348 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE7Rv | TraesCS7D | scaffold92 | TVU08461 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t031 | SECCE5Rv | TraesCS5B | scaffold45 | TVU21188 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5B | genblast_C | TVU11190 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t057 | SECCEUnv | TraesCS4B | scaffold10 | TVU25876 |
| LPERR08G | genblast_C | ORUFI08G | Os08t013 | SECCE7Rv | TraesCS7A | scaffold63 | TVU43490 |
| LPERR06G | genblast_C | ORUFI09G | Os09t032 | SECCE4Rv | TraesCS4A | scaffold74 | TVU04141 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6B | scaffold26 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCE4Rv | TraesCS7D | genblast_C | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3D | scaffold32 | TVU22991 |
| LPERR08G | genblast_C | ORUFI08G | Os08t043 | SECCE7Rv | TraesCS7D | scaffold13 | TVU05786 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold8. | TVU14314 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2D | scaffold26 | TVU14315 |
| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t052 | SECCE6Rv | TraesCS3D | scaffold12 | TVU24601 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold20 | TVU27724 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t038 | genblast_C | TraesCS6A | scaffold37 | TVU06307 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t047 | SECCE1Rv | TraesCS1A | scaffold14 | TVU50349 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t011 | SECCE5Rv | TraesCS5B | scaffold20 | TVU10817 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t052 | SECCE5Rv | TraesCS5D | scaffold22 | TVU50001 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6D | scaffold26 | TVU03002 |

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| LPERR01G | cds.KYUSt_ORUFI09G | Os09t011 | SECCE6Rv | TraesCS6D | scaffold95 | genblast_C |

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| genblast_C | cds.KYUSt_ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6D | scaffold83 | TVU28448 |

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|---|---|---|---|---|---|---|
| LPERR09G | cds.KYUSt_genblast_C | Os09t051 | SECCE5Rv | TraesCS5D | scaffold27 | TVU01435 |
| LPERR10G | cds.KYUSt_ORUFI02G | Os05t017 | SECCE6Rv | TraesCS6D | scaffold26 | TVU07732 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2A | scaffold26 | TVU38170 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7D | scaffold6. | TVU12158 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35003 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20471 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold18 | TVU35872 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5A | scaffold17 | TVU44563 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t058 | SECCE2Rv | TraesCS1A | scaffold15 | TVU39406 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold13 | TVU05152 |
|  |  |  |  |  |  |  |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28746 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t024 | SECCE7Rv | TraesCS7B | scaffold26 | TVU39665 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28320 |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | SECCE5Rv | TraesCS5D | scaffold31 | TVT98852 |
|  |  |  |  |  |  |  |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t053 | SECCE4Rv | TraesCS7A | scaffold54 | TVU04925 |
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| LPERR06G | genblast_CORUFI06G | Os06t048 | SECCE3Rv | TraesCS3B | scaffold47 | TVU11281 |
| LPERR07G | genblast_CORUFI07G | genblast_C | SECCE2Rv | TraesCS2B | scaffold43 | TVU38865 |
| LPERR12G | cds.KYUSt_ORUFI03G | Os03t059 | SECCE2Rv | TraesCS2D | scaffold45 | TVU46641 |
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| LPERR10G | cds.KYUSt_ORUFI10G | Os10t044 | SECCE1Rv | TraesCS1D | scaffold31 | TVU30537 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t013 | SECCE4Rv | TraesCS5B | scaffold36 | TVU19013 |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold13 | TVU14824 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE7Rv | TraesCS5A | scaffold15 | TVU36875 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2A | scaffold10 | TVU13949 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold85 | TVU31535 |
| genblast_Z | genblast_Z | genblast_Z | genblast_Z | SECCE4Rv | TraesCS4D | scaffold35 | TVU02497 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t056 | SECCE7Rv | TraesCS7D | scaffold15 | TVU50311 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE5Rv | TraesCS5B | scaffold31 | TVU27440 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE4Rv | TraesCS5D | scaffold38 | TVU04749 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold22 | TVU28878 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold12 | TVU16454 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16412 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3B | scaffold89 | TVU36108 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4B | scaffold23 | TVU47663 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold16 | TVU16487 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5A | scaffold20 | TVU45062 |
| LPERR01G | genblast_C | ORUFI01G | Os01t066 | SECCE3Rv | TraesCS3D | scaffold21 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE1Rv | TraesCS1A | scaffold15 | TVU29877 |

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| LPERR01G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold12 | TVU20016 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2D | scaffold43 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5B | scaffold16 | TVU09605 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t054 | SECCE7Rv | TraesCS7A | genblast_C | TVU01282 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t041 | SECCE1Rv | TraesCS1B | genblast_C | TVU31034 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold5. | TVT98350 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t040 | SECCE5Rv | TraesCS5A | scaffold64 | genblast_Z |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE7Rv | TraesCS7A | scaffold20 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE7Rv | TraesCS7B | scaffold28 | TVU17344 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t027 | SECCE2Rv | TraesCS2B | scaffold21 | TVU13300 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t014 | genblast_C | TraesCS2D | scaffold18 | TVU43384 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3D | scaffold21 | genblast_C |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49389 |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t049 | SECCE1Rv | TraesCS1D | scaffold32 | TVU32178 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t065 | SECCE3Rv | TraesCS3A | scaffold22 | TVU35722 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2B | genblast_C | TVU46093 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6D | scaffold26 | TVU27719 |
| LPERR01G | cds.KYUSt_ | genblast_Z | genblast_Z | genblast_Z | genblast_Z | scaffold11 | TVU35464 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold29 | TVU48389 |

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| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2D | scaffold1. | TVT96775 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold21 | TVU35987 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t016 | SECCE3Rv | TraesCS3A | scaffold14 | TVU19560 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6A | scaffold28 | TVU03705 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t083 | SECCE3Rv | TraesCS6D | scaffold20 | TVU27578 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7A | scaffold92 | TVU08389 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1D | scaffold27 | TVU32038 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2D | scaffold40 | TVU14967 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t018 | SECCE2Rv | TraesCS2B | scaffold66 | TVU41864 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6B | scaffold19 | TVU29419 |

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| LPERR09G | cds.KYUSt_ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5A | scaffold64 | genblast_ |

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| genblast_ | genblast_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38566 |
| LPERR01G | genblast_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3A | scaffold36 | TVU23067 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t058 | SECCE6Rv | TraesCS6D | scaffold17 | TVU29536 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t018 | SECCE1Rv | TraesCS6D | scaffold50 | TVU25690 |
| LPERR04G | cds.KYUSt_ | ORUFI02G | Os04t046 | SECCE2Rv | TraesCS2A | scaffold46 | TVU14181 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os12t020 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14251 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6D | scaffold26 | TVU27673 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE3Rv | TraesCS6D | scaffold22 | TVU07528 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6A | scaffold36 | genblast_ |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t012 | SECCE5Rv | TraesCS5D | scaffold48 | TVU50665 |
| LPERR04G | genblast_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2B | scaffold20 | TVU15169 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2D | scaffold20 | TVU32352 |
| LPERR03G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCE7Rv | TraesCS7D | scaffold65 | TVU05128 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28184 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCEUnv | TraesCS1B | scaffold47 | TVT97763 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t046 | SECCE4Rv | TraesCS7B | scaffold89 | TVU05597 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6D | scaffold42 | TVU33146 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3A | scaffold25 | TVU01323 |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4B | scaffold14 | TVU47613 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE2Rv | TraesCS1A | genblast_C | TVU35188 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6A | scaffold51 | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold24 | TVU09645 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t047 | SECCE2Rv | TraesCS2B | scaffold14 | TVU15617 |
| genblast_C | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS4A | scaffold13 | TVU13087 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t024 | SECCE4Rv | TraesCS4D | scaffold59 | TVU03608 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3D | scaffold17 | TVU35052 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t014 | SECCE6Rv | TraesCS6B | scaffold24 | TVU33452 |

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| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t014 | SECCE6Rv | TraesCS6D | scaffold12 | TVU41103 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7D | scaffold38 | TVU04963 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1B | scaffold36 | TVU18914 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t051 | SECCE7Rv | TraesCS6A | scaffold12 | TVU29912 |

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| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCEUnv | TraesCS4D | scaffold40 | TVU47418 |
| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t059 | SECCEUnv | TraesCS3B | scaffold13 | TVU03080 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3A | scaffold54 | TVU01321 |
| LPERR05G | cds.KYUSt_ | ORUFI11G | Os11t027 | SECCE1Rv | TraesCS1D | scaffold54 | TVU16654 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t019 | SECCE6Rv | TraesCS6D | scaffold10 | TVU41343 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold39 | TVU19725 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | scaffold96 | TVU38382 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t014 | SECCE1Rv | TraesCS1B | scaffold13 | TVU17861 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t028 | SECCE1Rv | TraesCS1A | scaffold26 | TVU39653 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7A | scaffold93 | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4D | scaffold22 | TVU47163 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47244 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold97 | TVU14948 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3A | scaffold16 | TVU22875 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7B | scaffold24 | TVU05320 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE7Rv | TraesCS7B | scaffold12 | TVU40537 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3B | scaffold88 | TVU21954 |
|  |  |  |  |  |  |  |  |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t050 | SECCE4Rv | TraesCS7D | scaffold47 | TVU29981 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold16 | TVU16580 |
| LPERR01G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE3Rv | TraesCS3B | scaffold33 | TVU36437 |
| LPERR01G | genblast_C | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3B | scaffold15 | TVT97920 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1D | scaffold1. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold22 | genblast_C |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t035 | SECCE5Rv | TraesCS4D | scaffold34 | TVU48702 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t066 | SECCE4Rv | TraesCS4D | scaffold13 | TVU23654 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold23 | TVU35881 |
| LPERR03G | genblast_C | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4D | scaffold74 | TVU47168 |

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| LPERR03G | cds.KYUSt_ORUFI03G | genblast_Z | SECCE4Rv | TraesCS4B | scaffold55 | TVU44685 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1A | scaffold36 | TVU34213 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7B | scaffold9. | TVU07558 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6A | scaffold6. | TVU32943 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5A | scaffold29 | TVU08900 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold19 | TVU09327 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t058 | SECCE6Rv | TraesCS6D | scaffold12 | TVU29508 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2D | scaffold1. | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold54 | TVU29166 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t075 | genblast_C | TraesCS3A | scaffold17 | TVU35088 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t039 | SECCE5Rv | TraesCS5A | scaffold87 | TVU09449 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t027 | SECCE4Rv | TraesCS7D | scaffold30 | TVU11654 |
| genblast_C | cds.KYUSt_ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2D | scaffold56 | TVU15407 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2D | scaffold2. | genblast_C |
| genblast_C | cds.KYUSt_ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28297 |
| LPERR12G | cds.KYUSt_ORUFI12G | genblast_C | SECCEUnv | TraesCS5D | scaffold22 | TVU49993 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t034 | SECCE1Rv | TraesCS1D | scaffold52 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6D | scaffold19 | TVU33696 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1B | scaffold24 | TVU18050 |

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| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE4Rv | TraesCS4B | scaffold11 | TVU45721 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3B | scaffold29 | TVU35384 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3A | scaffold46 | TVU36609 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold55 | TVU46150 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t016 | SECCE5Rv | TraesCS5B | scaffold22 | TVU07358 |
| genblast_C | cds.KYUSt_ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold17 | genblast_C |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold77 | TVU14475 |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | genblast_C | TVU16579 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t017 | SECCE4Rv | TraesCS6B | scaffold10 | TVU41711 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1A | scaffold11 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6A | scaffold41 | TVU29684 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3D | scaffold28 | TVU35078 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05357 |

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| LPERR01G | cds.KYUSt_genblast_C | Os01t065 | SECCE3Rv | TraesCS3A | scaffold42 | genblast_C |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t053 | SECCEUnv | TraesCS5B | scaffold22 | genblast_C |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold17 | TVU44538 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold12 | TVU28201 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold15 | TVU35547 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t051 | SECCE5Rv | TraesCS2A | scaffold16 | TVU08907 |
| genblast_C | cds.KYUSt_ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3D | scaffold18 | TVU36806 |

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|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6A | genblast_C | genblast_C |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2D | scaffold86 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t053 | SECCE3Rv | TraesCS3D | scaffold12 | genblast_C |

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|---|---|---|---|---|---|---|
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5A | scaffold53 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold11 | TVT98288 |

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|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ORUFI11G | Os02t062 | SECCE4Rv | TraesCS4A | scaffold10 | TVT97696 |
| LPERR09G | genblast_C | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold19 | TVT99810 |
| LPERR03G | genblast_C | ORUFI03G | Os03t036 | SECCE2Rv | TraesCS2B | genblast_C | TVU46920 |

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|---|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t056 | SECCE2Rv1 | TraesCS2D | scaffold14 | TVU16097 |
| LPERR07G | genblast_C | ORUFI07G | Os07t043 | SECCE3Rv1 | TraesCS3A | scaffold52 | TVU39510 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t040 | SECCE1Rv1 | TraesCS1B | scaffold57 | TVU30996 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t081 | SECCE3Rv1 | TraesCS3B | scaffold22 | TVU36567 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv1 | TraesCS2A | scaffold39 | TVU38086 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv1 | TraesCS3D | scaffold31 | TVU34634 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv1 | TraesCS3D | scaffold89 | TVU01571 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv1 | TraesCS2D | scaffold12 | TVU16641 |
| LPERR09G | genblast_C | ORUFI09G | Os09t030 | SECCE7Rv1 | TraesCS5A | scaffold16 | TVU09099 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_Z | SECCE1Rv1 | TraesCS1D | scaffold39 | TVU00936 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv1 | TraesCS1A | genblast_C | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE5Rv1 | TraesCS4D | scaffold85 | TVU31746 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv1 | TraesCS7A | scaffold39 | TVU12654 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t058 | SECCE7Rv1 | TraesCS7D | scaffold13 | TVU25115 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | genblast_C | TraesCS1A | scaffold85 | TVU31531 |

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| LPERR11G | genblast_C | ORUFI11G | Os11t063 | SECCE1Rv | TraesCS7A | scaffold6. | TVU24083 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t016 | SECCE6Rv | TraesCS6B | scaffold1. | TVU32714 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t040 | SECCE7Rv | TraesCS7A | scaffold37 | TVU05633 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2B | scaffold15 | TVU06863 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t023 | SECCE5Rv | TraesCS5D | scaffold10 | TVU51512 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2B | scaffold13 | TVU16123 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35874 |
| LPERR01G | genblast_C | ORUFI06G | Os06t027 | genblast_C | TraesCS5D | scaffold29 | TVU26696 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2D | scaffold2. | TVU32563 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCE3Rv | TraesCS3B | scaffold43 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6A | scaffold38 | TVU27830 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4A | scaffold42 | TVU48303 |
| LPERR01G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | genblast_C | scaffold11 | TVU28331 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6B | scaffold84 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1A | scaffold22 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5B | scaffold53 | TVU10021 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5A | scaffold16 | TVU08814 |
| LPERR09G | cds.KYUSt_ | ORUFI08G | Os08t036 | SECCE5Rv | TraesCS5B | scaffold87 | TVU45262 |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE7Rv | TraesCS5B | scaffold3. | TVU43936 |
| LPERR06G | genblast_C | genblast_C | genblast_C | SECCE4Rv | TraesCS7B | scaffold30 | TVU11647 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2D | scaffold23 | TVU38821 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE3Rv | TraesCS3D | scaffold10 | TVU48221 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2D | scaffold67 | TVU37706 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold14 | TVT99801 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35205 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2D | scaffold12 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t019 | SECCE2Rv | TraesCS2A | scaffold12 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t020 | SECCE5Rv | TraesCS5B | scaffold20 | TVU07263 |
| LPERR08G | genblast_C | ORUFI08G | Os08t036 | genblast_C | genblast_C | scaffold11 | TVU06441 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2D | scaffold23 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os12t013 | SECCE5Rv | TraesCS5D | scaffold36 | TVT99497 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2A | scaffold28 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold18 | TVU21611 |
| LPERR01G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE1Rv | TraesCS1B | scaffold36 | TVU34155 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE7Rv | TraesCS5B | scaffold65 | TVU44120 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7B | scaffold29 | TVU08564 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | genblast_C | TraesCS3D | scaffold15 | TVU35206 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38149 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1B | scaffold23 | TVU19599 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold79 | TVU13331 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3A | scaffold31 | TVU36812 |
| LPERR03G | genblast_C | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48566 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t022 | SECCE4Rv | TraesCS4A | scaffold4. | TVU42633 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1A | scaffold45 | TVU31781 |
| LPERR03G | genblast_Z | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold40 | TVU47496 |

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| LPERR01G | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold23 | TVU35850 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold99 | TVU14641 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3B | scaffold84 | TVU36649 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t026 | SECCE2Rv | TraesCS2A | scaffold5. | TVU25538 |
| LPERR08G | cds.KYUSt_ORUFI06G | Os08t050 | SECCE4Rv | TraesCS7D | scaffold24 | TVU05232 |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_C | SECCE7Rv | TraesCS7B | scaffold25 | TVU07887 |
| genblast_C | cds.KYUSt_ORUFI09G | Os09t053 | SECCE7Rv | TraesCS7D | scaffold16 | TVU10144 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3B | scaffold89 | TVU35171 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t021 | SECCE6Rv | TraesCS6B | scaffold6. | genblast_C |
| LPERR05G | genblast_C | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1B | scaffold12 | TVU19890 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold84 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5A | scaffold17 | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3B | scaffold33 | TVU36318 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21522 |
| LPERR03G | genblast_C | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold40 | TVU47464 |
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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2B | scaffold58 | TVU38512 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t065 | SECCE2Rv | TraesCS2B | scaffold11 | TVU15076 |
| LPERR03G | genblast_C | ORUFI03G | Os03t082 | SECCE5Rv | genblast_C | scaffold17 | genblast_C |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t073 | SECCE6Rv | TraesCS7A | scaffold45 | TVU07512 |
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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t025 | SECCE3Rv | TraesCS3B | scaffold51 | TVU33302 |
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| genblast_C | cds.KYUSt_ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2B | scaffold14 | TVU06812 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t011 | genblast_C | TraesCS1B | scaffold40 | TVU18224 |
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| LPERR04G | cds.KYUSt_ | genblast_C | Os04t044 | SECCE2Rv | TraesCS2B | scaffold77 | TVU00562 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16479 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t024 | SECCE5Rv | TraesCS5A | scaffold31 | TVU39837 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t090 | genblast_C | TraesCS3A | scaffold31 | TVU36105 |
| LPERR03G | genblast_C | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48288 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCE7Rv | TraesCS7B | genblast_C | genblast_C |

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| LPERR07G | genblast_C | ORUFI07G | Os07t025 | genblast_C | genblast_C | scaffold71 | TVU39787 |
| LPERR02G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE7Rv | TraesCS7D | scaffold92 | TVU29807 |
| LPERR02G | genblast_C | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold1. | TVU28557 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold35 | TVT97851 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCEUnv | TraesCS6B | scaffold42 | TVU30117 |
| LPERR07G | cds.KYUSt_ | genblast_C | genblast_C | SECCE7Rv | TraesCS2D | scaffold20 | TVU03461 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t020 | SECCE3Rv | TraesCS3D | scaffold32 | TVU07271 |
| LPERR07G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE2Rv | TraesCS2B | scaffold13 | TVU07029 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2A | scaffold2. | TVU38115 |
| LPERR07G | genblast_C | ORUFI07G | Os07t047 | SECCE6Rv | TraesCS7D | scaffold16 | TVU02796 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t035 | SECCE1Rv | TraesCS1D | scaffold14 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2D | scaffold58 | TVU38809 |
| LPERR04G | genblast_C | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15536 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold80 | TVT96749 |
| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold12 | TVU34183 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6B | scaffold1. | TVU33315 |
| LPERR03G | genblast_C | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48243 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t088 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36265 |

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| LPERR02G | genblast_C | genblast_C | Os02t074 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28452 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE4Rv | TraesCS4B | scaffold3. | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold24 | TVU09668 |
| LPERR04G | genblast_C | ORUFI04G | Os04t067 | SECCE7Rv | TraesCS7D | scaffold3. | TVU32498 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold16 | TVU10311 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE5Rv | TraesCS5A | scaffold28 | TVU04595 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3A | scaffold14 | TVU34477 |
| LPERR03G | genblast_C | genblast_C | genblast_C | SECCE5Rv | TraesCS5D | scaffold3. | TVT98417 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5A | scaffold33 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1B | scaffold36 | TVU19019 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t014 | SECCE2Rv | TraesCS2A | scaffold63 | TVU41172 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38067 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2A | scaffold56 | TVU15241 |
| LPERR09G | genblast_C | ORUFI09G | Os09t013 | SECCE3Rv | TraesCS3B | scaffold21 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1D | scaffold36 | TVU20116 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3A | scaffold26 | TVU34439 |

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| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t011 | SECCE4Rv | TraesCS4A | scaffold14 | TVU27250 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3B | scaffold17 | TVU34986 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44867 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t016 | SECCE5Rv | TraesCS5A | scaffold97 | TVU50966 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t012 | SECCE2Rv | TraesCS2B | scaffold19 | TVU41798 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t025 | SECCE2Rv | TraesCS2A | scaffold28 | genblast_C |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t057 | SECCE2Rv | TraesCS2D | scaffold17 | TVU29559 |
| LPERR03G | genblast_C | ORUFI03G | Os03t038 | SECCE4Rv | TraesCS4A | scaffold45 | TVU46784 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3A | scaffold47 | TVU22413 |
| LPERR12G | genblast_C | ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5D | scaffold76 | TVU49190 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE7Rv | TraesCS7A | scaffold33 | TVU08967 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE7Rv | TraesCS5A | scaffold19 | TVU44535 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t028 | SECCE5Rv | TraesCS5D | scaffold18 | TVU11120 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold21 | TVU34585 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t035 | SECCE2Rv | TraesCS2B | scaffold18 | TVU13808 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold15 | genblast_C |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6A | scaffold5. | TVT99115 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2B | scaffold30 | TVU14156 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6D | scaffold17 | TVU29399 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t037 | genblast_C | TraesCS5A | genblast_C | TVU09349 |

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| LPERR04G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1A | scaffold80 | TVU00547 |
| LPERR04G | genblast_C | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15038 |
| LPERR02G | genblast_C | ORUFI02G | Os02t030 | SECCE5Rv | TraesCS5A | scaffold11 | TVU32334 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t013 | SECCE7Rv | TraesCS7D | genblast_C | TVU31383 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2B | scaffold32 | TVU16407 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold53 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE6Rv | TraesCS6A | scaffold20 | TVU10868 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold16 | TVU07943 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold13 | TVU01620 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t025 | SECCE7Rv | TraesCS7A | scaffold42 | TVU33341 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4A | scaffold17 | TVU48202 |

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| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t059 | genblast_C | TraesCS6B | scaffold17 | TVU29484 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE2Rv | TraesCS2D | scaffold5. | genblast_C |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2A | scaffold28 | TVU10769 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7D | scaffold17 | TVT98089 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3B | scaffold14 | TVU35239 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4D | scaffold17 | TVU48164 |
| LPERR05G | genblast_C | genblast_C | Os05t035 | SECCE1Rv | TraesCS1A | scaffold12 | TVU18922 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t057 | SECCE7Rv | TraesCS7D | scaffold5. | TVU29574 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t047 | SECCE4Rv | TraesCS7B | scaffold51 | TVU11204 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3B | scaffold22 | TVU36632 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold37 | TVU32082 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold31 | TVU01882 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t047 | SECCE4Rv | TraesCS7B | scaffold35 | TVU30231 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold15 | TVU47730 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2B | scaffold8. | TVU14344 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4B | scaffold52 | TVU48419 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3D | scaffold84 | TVU36642 |
| LPERR02G | genblast_C | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6A | scaffold53 | TVU33628 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t019 | SECCE4Rv1 | TraesCS7D | scaffold10 | TVU12222 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t050 | SECCE5Rv1 | TraesCS5D | scaffold71 | TVU50068 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv1 | TraesCS5B | scaffold24 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv1 | TraesCS7B | scaffold32 | TVU08081 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv1 | TraesCS2A | scaffold2.1 | TVU37312 |
| LPERR12G | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv1 | TraesCS5D | scaffold14 | TVU49088 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t011 | SECCE5Rv1 | TraesCS5A | genblast_C | TVU16917 |
| LPERR08G | genblast_C | ORUFI08G | Os08t015 | SECCE7Rv1 | TraesCS7A | scaffold18 | TVT99818 |
| LPERR12G | genblast_Z | ORUFI12G | genblast_Z | SECCE5Rv1 | TraesCS5D | scaffold29 | TVU49712 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t031 | genblast_C | TraesCS2B | scaffold23 | TVU21187 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv1 | TraesCS6B | scaffold26 | TVU28963 |
| LPERR05G | genblast_C | ORUFI05G | Os05t044 | SECCE1Rv1 | TraesCS1B | scaffold39 | TVU19613 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE3Rv1 | TraesCS6D | scaffold26 | TVU28993 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv1 | TraesCS7B | scaffold22 | TVU07738 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv1 | TraesCS6D | scaffold2. | TVU28130 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv1 | TraesCS5A | scaffold3.1 | TVT97136 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv1 | TraesCS7A | scaffold16 | TVU04937 |
| LPERR11G | cds.KYUSt_ | genblast_C | Os11t064 | SECCE5Rv1 | TraesCS5A | scaffold8. | TVU23807 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE7Rv1 | TraesCS7B | scaffold28 | TVU17293 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv1 | TraesCS2B | scaffold16 | TVU37256 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv1 | TraesCS2B | scaffold19 | TVU16518 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | SECCE4Rv1 | TraesCS7A | scaffold4. | TVU12980 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t032 | SECCE5Rv1 | TraesCS5B | scaffold58 | TVU18790 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv1 | TraesCS5D | scaffold53 | TVU10001 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv1 | TraesCS4B | scaffold15 | TVU47669 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t050 | SECCE5Rv1 | TraesCS5D | scaffold31 | TVU08816 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE4Rv1 | TraesCS7A | scaffold38 | TVU04924 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv1 | TraesCS6D | scaffold10 | TVU29037 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv1 | TraesCS3B | scaffold89 | TVU36065 |
| LPERR12G | genblast_C | ORUFI12G | Os12t057 | SECCE5Rv1 | TraesCS5B | scaffold76 | genblast_C |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS2A | scaffold22 | TVU47380 |
| LPERR10G | genblast_C | ORUFI10G | Os10t046 | SECCE1Rv | TraesCS1D | scaffold11 | TVU30427 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold76 | TVU28210 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_Z | genblast_Z | TraesCS5B | scaffold24 | TVU49710 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE4Rv | TraesCS4D | scaffold45 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold42 | TVU47964 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35233 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47472 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1B | scaffold27 | TVU32236 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12151 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5A | scaffold11 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCEUnv | TraesCS5A | scaffold15 | TVU48763 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7D | scaffold22 | genblast_C |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6B | scaffold10 | TVU28923 |
| LPERR11G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE7Rv | TraesCS2A | scaffold14 | TVU04035 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv | TraesCS6B | scaffold26 | TVU02414 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7D | scaffold21 | TVU42699 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3B | scaffold41 | TVU36700 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS7A | scaffold27 | TVU12690 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1B | scaffold5. | TVU31523 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t059 | SECCE3Rv | TraesCS3D | scaffold29 | TVU34359 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47817 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2D | scaffold16 | TVU16361 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6D | scaffold10 | TVU27980 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | genblast_C | genblast_C | scaffold22 | TVU07627 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12575 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7D | scaffold21 | TVU08103 |
| LPERR03G | genblast_C | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48026 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09823 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t014 | SECCE1Rv | TraesCS1A | scaffold27 | TVU17900 |
| LPERR06G | cds.KYUSt_ | ORUFI03G | Os03t056 | SECCE1Rv | TraesCS1B | scaffold51 | TVU11206 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold29 | TVU48437 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | genblast_C | genblast_C | scaffold31 | TVU36425 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t030 | genblast_C | genblast_C | scaffold16 | TVT98969 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3B | scaffold11 | TVU34881 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE5Rv | TraesCS5D | scaffold11 | TVU00721 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t017 | SECCE4Rv | TraesCS4B | scaffold19 | TVU00917 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3D | genblast_C | TVU03283 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3A | scaffold36 | TVU22953 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t022 | SECCE2Rv | TraesCS2A | scaffold11 | TVU13330 |
| LPERR10G | genblast_Z | ORUFI10G | genblast_Z | SECCE7Rv | TraesCS4D | scaffold10 | TVU07651 |
| LPERR07G | genblast_C | ORUFI07G | Os07t027 | SECCE1Rv | TraesCS1A | scaffold14 | TVU39675 |
| LPERR05G | genblast_C | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1D | scaffold32 | TVU20489 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t029 | SECCE4Rv | TraesCS7D | scaffold15 | TVU21320 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t065 | SECCE5Rv | TraesCS5A | scaffold55 | TVU45857 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48144 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t033 | SECCE2Rv | TraesCS7B | scaffold4. | TVU21042 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4B | scaffold3. | TVU45255 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5D | scaffold25 | TVU46020 |
| LPERR03G | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE5Rv | TraesCS5D | scaffold5. | TVU29848 |

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| LPERR08G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE6Rv | TraesCS6B | genblast_C | TVU27789 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2B | scaffold96 | TVU38445 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37929 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t032 | SECCE2Rv | TraesCS2D | scaffold13 | TVU30244 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t022 | SECCE4Rv | TraesCS4D | scaffold45 | TVU02206 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2A | scaffold2. | TVU38172 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38368 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45231 |
| genblast_C | genblast_C | ORUFI04G | Os09t040 | SECCE2Rv | TraesCS2A | scaffold21 | TVU13867 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold10 | TVU48679 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t043 | SECCE6Rv | TraesCS1D | scaffold57 | TVU30594 |
| LPERR02G | genblast_C | ORUFI02G | Os02t053 | SECCE6Rv | TraesCS6D | scaffold5. | TVU29808 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE4Rv | TraesCS4D | scaffold14 | TVU26764 |
| LPERR02G | genblast_C | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28097 |
| LPERR07G | genblast_C | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37450 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7B | scaffold60 | TVU07694 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t062 | SECCE7Rv | TraesCS7D | scaffold25 | TVU08205 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2A | scaffold56 | TVU15323 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t024 | SECCE3Rv | TraesCS3B | scaffold34 | TVU23171 |
| LPERR09G | genblast_C | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold19 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1A | scaffold75 | TVU19879 |
| LPERR04G | genblast_C | ORUFI04G | Os04t037 | SECCE2Rv | TraesCS2D | scaffold81 | TVU13899 |
| LPERR01G | genblast_C | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3D | scaffold14 | TVU35237 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t057 | SECCE5Rv | TraesCS5B | scaffold5. | TVU29584 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t025 | SECCE1Rv | TraesCS3B | scaffold21 | TVU00417 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7B | scaffold29 | TVU08590 |
| LPERR12G | genblast_Z | ORUFI12G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold56 | TVU15530 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2D | scaffold36 | TVU40214 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3A | scaffold15 | TVU01678 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t033 | SECCE1Rv | TraesCS1D | scaffold34 | TVU30246 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv | TraesCS3D | scaffold18 | TVU34681 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t011 | genblast_C | TraesCS5B | scaffold47 | TVU27307 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold14 | TVU47509 |
| LPERR01G | genblast_C | ORUFI01G | Os01t063 | SECCE4Rv | TraesCS6A | scaffold25 | TVU02560 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1B | scaffold80 | TVU20329 |
| LPERR01G | genblast_C | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3D | scaffold4. | TVU21496 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4D | scaffold22 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t083 | SECCE3Rv | TraesCS6A | scaffold12 | TVU19450 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3A | scaffold31 | TVU36814 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1D | scaffold40 | TVU40996 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t024 | SECCE4Rv | TraesCS4A | scaffold62 | TVU03614 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCEUnv | TraesCS6A | scaffold24 | TVU27938 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1D | scaffold40 | genblast_C |
| LPERR08G | genblast_C | ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7B | scaffold26 | TVU43569 |
| LPERR05G | genblast_C | ORUFI05G | Os05t050 | genblast_C | TraesCS1D | scaffold12 | TVU20650 |
| LPERR12G | genblast_C | ORUFI12G | Os12t054 | genblast_C | TraesCS5D | scaffold1. | TVU49892 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7A | scaffold12 | TVU42894 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5D | scaffold29 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| genblast_C | genblast_C | ORUFI10G | Os10t041 | SECCE1Rv | TraesCS1A | scaffold57 | TVU31050 |

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| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold17 | TVU48273 |
| LPERR06G | genblast_C | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS4A | scaffold11 | TVU12831 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44984 |
| LPERR02G | genblast_C | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6A | scaffold17 | TVU29256 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t069 | genblast_C | genblast_C | scaffold15 | TVT99364 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t014 | SECCE1Rv | TraesCS1D | scaffold13 | TVU17916 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os05t053 | SECCE2Rv | TraesCS2A | scaffold7. | TVU44580 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3A | scaffold4. | TVU22778 |
| LPERR01G | genblast_C | ORUFI01G | Os01t081 | SECCE3Rv | genblast_C | scaffold84 | TVU36617 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t023 | SECCE6Rv | TraesCS6D | scaffold51 | TVU33159 |
| LPERR11G | genblast_C | ORUFI11G | Os11t049 | SECCE2Rv | TraesCS2A | scaffold91 | TVU25385 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold80 | TVU00570 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5D | scaffold20 | TVU45063 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7B | scaffold68 | TVU42314 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1B | scaffold7. | TVU31885 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5D | scaffold53 | TVU10118 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold29 | TVU48447 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t041 | SECCE1Rv | TraesCS1D | scaffold27 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5B | scaffold16 | TVU05695 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold94 | TVU15885 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCE3Rv | TraesCS3B | scaffold42 | TVU30147 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | genblast_C | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4D | scaffold55 | TVU45466 |
| LPERR06G | genblast_C | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7B | scaffold25 | TVU08427 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2A | scaffold13 | TVU14823 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1A | scaffold18 | TVU20461 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE3Rv | TraesCS3B | scaffold80 | TVU20459 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv | TraesCS5D | scaffold76 | TVU49394 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7D | scaffold23 | TVU43856 |
| LPERR06G | genblast_C | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7B | scaffold22 | TVU07657 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t024 | SECCE6Rv | TraesCS6A | scaffold42 | TVU33226 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5B | scaffold97 | TVU50950 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7D | scaffold38 | TVU05052 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t045 | SECCE5Rv | TraesCS5A | scaffold64 | TVU09801 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t049 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10066 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7D | scaffold44 | TVU11977 |

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| LPERR02G( | genblast_C | ORUFI02G( | Os02t013{ | SECCE6Rv] | TraesCS6B | scaffold24 | TVU33489 |
| LPERR02G( | cds.KYUSt_ | ORUFI10G( | genblast_Z | SECCE6Rv] | TraesCS6A | scaffold72 | TVU30808 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t058( | SECCE2Rv] | TraesCS2A | scaffold14 | TVU15992 |

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| LPERR05G: | cds.KYUSt_ | ORUFI05G: | genblast_C | SECCE1Rv] | TraesCS1D | scaffold30 | TVU19259 |
| LPERR10G: | cds.KYUSt_ | ORUFI10G: | Os10t048! | SECCE1Rv] | TraesCS1A | scaffold11 | TVU30309 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t055; | SECCE2Rv] | TraesCS2B | scaffold94 | TVU14939 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | genblast_Z | SECCE6Rv] | TraesCS6D | scaffold27 | TVU27807 |
| LPERR03G: | cds.KYUSt_ | genblast_C | Os03t078! | SECCE5Rv] | TraesCS5D | scaffold3.{ | TVU44693 |
| LPERR04G( | cds.KYUSt_ | ORUFI04G: | Os04t038( | SECCE2Rv] | TraesCS2D | scaffold81 | TVU13908 |

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| LPERR07G: | cds.KYUSt_ | ORUFI07G: | Os07t058: | SECCE2Rv] | TraesCS2B | scaffold2.( | TVU03949 |
| LPERR05G: | genblast_C | ORUFI05G: | Os05t056( | SECCE1Rv] | TraesCS1A | scaffold13 | TVU20293 |
| LPERR06G( | genblast_C | ORUFI06G( | Os06t024: | SECCE4Rv] | TraesCS1B | scaffold44 | genblast_C |
| LPERR11G: | cds.KYUSt_ | ORUFI11G: | Os11t065: | SECCE7Rv] | TraesCS7A | scaffold61 | genblast_C |
| LPERR07G: | cds.KYUSt_ | ORUFI07G: | Os07t048] | SECCE5Rv] | TraesCS5A | scaffold16 | TVU39197 |
| LPERR04G( | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE2Rv] | TraesCS2B | scaffold52 | TVU14751 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G: | Os01t069{ | SECCE3Rv] | TraesCS3A | scaffold33 | TVT98900 |

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| LPERR01G: | cds.KYUSt_ | ORUFI01G: | Os01t082] | SECCE3Rv] | TraesCS3B | scaffold89 | TVU36629 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | genblast_C | SECCE5Rv] | TraesCS5B | scaffold20 | TVU45060 |
| LPERR02G( | cds.KYUSt_ | ORUFI02G( | Os02t014{ | SECCE6Rv] | TraesCS6B | scaffold31 | TVU33466 |
| LPERR12G: | genblast_C | ORUFI12G: | genblast_C | SECCEUnv] | TraesCS5D | scaffold29 | TVU49364 |
| LPERR01G: | genblast_C | ORUFI01G: | Os01t066: | SECCE3Rv] | TraesCS3B | scaffold21 | TVU35638 |
| LPERR11G( | cds.KYUSt_ | ORUFI11G: | Os11t042: | SECCEUnv] | TraesCS5A | scaffold45 | TVU25643 |
| LPERR07G( | cds.KYUSt_ | ORUFI07G( | Os07t017( | SECCE4Rv] | TraesCS4D | scaffold10 | TVU41709 |
| LPERR03G( | genblast_C | ORUFI03G( | Os03t018: | SECCE7Rv] | TraesCS4D | scaffold15 | TVU48172 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t017! | SECCE3Rv] | TraesCS3D | scaffold36 | TVU21512 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G: | Os01t087! | SECCE3Rv] | TraesCS3D | scaffold31 | TVU36323 |

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| LPERR05G( | cds.KYUSt_ | ORUFI05G( | Os05t015: | genblast_C | TraesCS1B | scaffold11 | TVU17536 |
| LPERR08G: | cds.KYUSt_ | ORUFI08G: | Os08t035( | SECCE6Rv] | TraesCS3A | scaffold20 | TVU06479 |
| LPERR07G( | cds.KYUSt_ | ORUFI07G: | Os07t041! | SECCE1Rv] | TraesCS1D | genblast_C | TVU39471 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | genblast_Z | SECCE6Rv] | TraesCS6D | scaffold27 | TVU27709 |
| LPERR01G( | genblast_C | ORUFI01G: | Os01t026] | SECCE3Rv] | TraesCS3B | scaffold10 | TVU22489 |
| LPERR12G( | cds.KYUSt_ | ORUFI12G( | Os12t015! | SECCE6Rv] | TraesCS6A | scaffold83 | TVU50964 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold27 | TVU27652 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t067 | SECCE3Rv | TraesCS4D | scaffold51 | TVU23583 |
| LPERR02G | genblast_C | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | genblast_C | TVU28417 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS5D | scaffold29 | TVU08629 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold17 | TVU47582 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | genblast_C | TraesCS2D | scaffold1. | TVU37205 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t043 | SECCE7Rv | TraesCS7D | scaffold71 | TVU50422 |
| LPERR06G | cds.KYUSt_ | ORUFI07G | Os07t041 | SECCE4Rv | TraesCS7A | scaffold18 | TVU27910 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCEUnv | TraesCS5D | scaffold29 | genblast_C |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36467 |
| LPERR01G | genblast_C | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35543 |

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|---|---|---|---|---|---|---|---|
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t056 | SECCE1Rv | TraesCS1A | scaffold32 | genblast_C |
| genblast_C | genblast_C | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2B | scaffold8. | TVU14468 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47710 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1D | genblast_C | TVU19907 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t065 | SECCE3Rv | TraesCS3A | scaffold22 | TVU35764 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold40 | TVU23064 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t047 | SECCEUnv | TraesCS4B | scaffold23 | TVU31132 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | genblast_C | TVU19380 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2B | scaffold99 | TVU14666 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t057 | genblast_C | TraesCS5A | scaffold1. | TVU46222 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | genblast_C | genblast_C | scaffold6. | TVU12148 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCEUnv | TraesCS7B | scaffold25 | TVU08322 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t019 | SECCE3Rv | TraesCS3D | scaffold3. | TVU45215 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36460 |
| LPERR01G | genblast_C | genblast_C | Os01t054 | SECCE4Rv | TraesCS1B | scaffold46 | TVU45595 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t020 | SECCE1Rv | TraesCS1D | scaffold10 | TVU17031 |
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold12 | TVU20632 |
| LPERR03G | genblast_C | ORUFI03G | Os03t070 | SECCE7Rv | TraesCS7B | scaffold12 | TVU21594 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1A | scaffold30 | TVU19263 |
| LPERR03G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE4Rv | TraesCS4D | scaffold71 | TVU46700 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold48 | TVU33411 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1A | scaffold85 | TVU31743 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3D | scaffold33 | TVU36468 |
| LPERR12G | genblast_Z | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold1. | TVU49980 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t060 | SECCE4Rv | TraesCS4B | scaffold6. | TVU24373 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold10 | TVU10586 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t058 | SECCE7Rv | TraesCS7D | scaffold43 | TVU07995 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold36 | TVU19108 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3B | scaffold36 | TVU21384 |
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold1. | TVU20299 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold16 | TVU29209 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2B | scaffold12 | TVU16282 |
| LPERR02G | genblast_C | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold12 | TVU28177 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold9. | genblast_C |
| LPERR03G | genblast_C | ORUFI03G | Os03t037 | SECCE4Rv | TraesCS7A | scaffold74 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold9. | TVU48053 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2A | scaffold13 | TVU14831 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | scaffold29 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold15 | TVU48146 |
| LPERR01G | genblast_C | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3B | scaffold25 | TVU22284 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6A | scaffold15 | TVU42250 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold10 | TVU27977 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold32 | TVT97135 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2B | scaffold14 | TVU15991 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCEUnv | TraesCS7A | scaffold25 | TVU08406 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5A | scaffold20 | TVU45105 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5A | scaffold35 | TVU45106 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6D | scaffold26 | TVU28987 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1A | scaffold40 | TVU18199 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4A | scaffold17 | TVU47580 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6B | scaffold18 | TVU32803 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20267 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t027 | SECCE5Rv | TraesCS5A | scaffold25 | TVU11093 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold17 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36038 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2B | scaffold7. | TVU40230 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5A | scaffold64 | genblast_C |

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| LPERR07G | genblast_C | ORUFI07G | genblast_C | SECCEUnv | TraesCS6A | scaffold38 | TVU04771 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t069 | SECCE2Rv | TraesCS2A | scaffold1. | TVU37082 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4B | scaffold18 | genblast_C |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1D | scaffold20 | TVU19363 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold17 | TVU27872 |
| LPERR09G | genblast_C | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5B | scaffold18 | TVU09055 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6D | scaffold6. | TVU33111 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE2Rv | TraesCS2D | scaffold22 | TVU47100 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t016 | SECCE6Rv | TraesCS6B | scaffold18 | TVU42958 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6A | scaffold48 | TVU33509 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1D | scaffold23 | TVU19376 |
| LPERR01G | genblast_C | ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3A | scaffold33 | TVU35438 |
| LPERR09G | genblast_C | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5D | scaffold53 | TVU08793 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold49 | TVU16056 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold15 | TVU47870 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t030 | SECCE5Rv | TraesCS5A | scaffold16 | TVU09066 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold41 | TVU48659 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold32 | TVU16372 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7B | scaffold23 | TVU43840 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t030 | SECCE2Rv | TraesCS2B | scaffold4. | TVU21233 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3A | scaffold13 | TVU34498 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3A | scaffold31 | TVU02357 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5A | scaffold29 | TVU10083 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold46 | TVU48670 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t064 | SECCE3Rv | TraesCS3A | scaffold11 | TVU35791 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold34 | TVU37617 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t035 | SECCE5Rv | TraesCS5A | scaffold74 | TVU47020 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t029 | SECCE1Rv | TraesCS1B | scaffold14 | TVU18645 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15031 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold32 | TVU44822 |

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|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6A | scaffold52 | TVU02901 |
| genblast_C | cds.KYUSt_genblast_C | genblast_C | SECCE5Rv | TraesCS5A | scaffold98 | TVU09344 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6A | scaffold17 | TVU03505 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2D | scaffold2. | TVU01253 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16359 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5B | scaffold20 | genblast_C |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t057 | SECCE3Rv | TraesCS3B | scaffold20 | TVU34202 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold13 | TVT97190 |
| LPERR05G | genblast_C | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1A | scaffold24 | TVU18033 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE7Rv | TraesCS5B | scaffold65 | TVU44160 |
| LPERR09G | genblast_C | genblast_C | Os09t052 | SECCE5Rv | TraesCS5A | scaffold29 | TVU08854 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t024 | SECCE6Rv | TraesCS6D | scaffold6. | TVU33242 |
| LPERR05G | genblast_CORUFI05G | Os05t058 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20141 |
| LPERR05G | cds.KYUSt_genblast_Z | Os05t015 | SECCE1Rv | TraesCS1A | scaffold19 | TVU17436 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3D | scaffold11 | TVU35949 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3A | scaffold59 | TVU21971 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t015 | SECCE4Rv | TraesCS4B | scaffold12 | TVU26792 |
| LPERR07G | genblast_C | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2A | scaffold43 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t045 | SECCE4Rv | TraesCS7A | scaffold69 | TVU30166 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t056 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10483 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37276 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2D | scaffold28 | TVU15406 |
| LPERR06G | cds.KYUSt_ | genblast_C | genblast_C | SECCE4Rv | TraesCS7D | scaffold3. | TVU12471 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2B | scaffold14 | TVU06840 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3B | scaffold14 | TVU36128 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2A | scaffold77 | TVU01745 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t066 | SECCE3Rv | TraesCS3A | scaffold21 | TVU35627 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37728 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1D | scaffold36 | TVU17127 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4A | scaffold10 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS5A | scaffold52 | TVU48575 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3D | scaffold84 | TVU35147 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1B | genblast_C | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold15 | TVU47837 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6B | scaffold24 | TVU33500 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4D | scaffold50 | TVU26784 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE7Rv | TraesCS7A | scaffold93 | TVU08942 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t039 | SECCE5Rv | TraesCS5D | scaffold64 | TVU09448 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t052 | SECCE2Rv | TraesCS2D | scaffold15 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold31 | TVU14568 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE3Rv | TraesCS6D | scaffold20 | TVU27603 |
| LPERR04G | cds.KYUSt_ | ORUFI08G | Os04t015 | SECCE2Rv | TraesCS2B | scaffold10 | TVU07046 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t056 | SECCE3Rv | TraesCS3D | scaffold46 | TVU34151 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t020 | SECCE4Rv | TraesCS6B | scaffold51 | TVU33001 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6D | scaffold27 | TVU27773 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t049 | SECCE1Rv | TraesCS1D | genblast_C | TVU20044 |

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| genblast_C | genblast_C | genblast_C | Os08t015 | SECCE7Rv | TraesCS7D | scaffold18 | TVU42760 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12494 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold41 | TVU02346 |
| LPERR11G | genblast_C | ORUFI11G | Os11t063 | SECCE4Rv | TraesCS4B | scaffold19 | TVT98990 |
| LPERR06G | genblast_C | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold12 | TVT98740 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold94 | TVT99684 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1A | scaffold16 | TVU18969 |
| LPERR08G | genblast_C | ORUFI08G | Os08t018 | SECCE7Rv | TraesCS7A | scaffold12 | TVU43121 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t061 | SECCE7Rv | TraesCS7D | scaffold25 | TVU08196 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCSU0 | genblast_C | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold59 | TVU21643 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5D | scaffold64 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3D | scaffold89 | TVU36034 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7B | scaffold22 | TVU07645 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7B | scaffold25 | TVU08097 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5A | scaffold16 | TVU08821 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t015 | SECCE1Rv | TraesCS1D | scaffold19 | TVU17640 |
| genblast_C | genblast_C | ORUFI08G | Os08t056 | SECCE7Rv | TraesCS7B | scaffold28 | TVU50310 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold27 | TVU10244 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t028 | SECCE4Rv | TraesCS7D | scaffold9. | TVU11637 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5A | scaffold11 | genblast_C |
| LPERR08G | genblast_C | ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7A | scaffold16 | TVU04889 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48554 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t012 | SECCE2Rv | TraesCS2A | scaffold12 | TVU40828 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3B | scaffold20 | TVU35953 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t012 | SECCE2Rv | TraesCS2B | scaffold14 | TVU40896 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold96 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold35 | TVU45298 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t016 | SECCE5Rv | TraesCS5B | scaffold70 | genblast_C |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t016 | SECCE6Rv | TraesCS6B | scaffold48 | TVU32674 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37486 |

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| LPERR04G | cds.KYUSt_ | ORUFI06G | Os04t063 | SECCE2Rv | TraesCS2D | scaffold20 | TVU16215 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS7A | scaffold13 | TVT97011 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3A | scaffold18 | TVU36817 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE5Rv | TraesCS5D | scaffold12 | TVU26948 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6D | scaffold37 | TVU27950 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2A | scaffold99 | TVU01761 |
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t051 | SECCE4Rv | TraesCS7B | scaffold13 | TVU05154 |
| LPERR03G | genblast_C | ORUFI03G | Os03t085 | SECCEUnv | TraesCS5B | scaffold39 | TVU44235 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t022 | SECCE7Rv | TraesCS7A | scaffold4. | TVU43320 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1D | scaffold75 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold27 | TVU28228 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold23 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08787 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38151 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_Z | SECCE4Rv | TraesCS7D | scaffold24 | TVU05273 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15405 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE5Rv | TraesCS5B | scaffold24 | TVU49590 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | genblast_C | TraesCS6A | scaffold37 | TVU28931 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35548 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t010 | SECCE1Rv | TraesCS1D | scaffold13 | TVU18448 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3B | scaffold14 | TVU35243 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4D | scaffold10 | TVU48263 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE1Rv | TraesCS1B | scaffold2. | TVU38130 |

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| genblast_C | genblast_C | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3B | scaffold10 | TVU22466 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7A | scaffold14 | TVU11701 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37740 |
| LPERR03G | genblast_C | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5A | scaffold65 | TVU44351 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t030 | SECCE2Rv | TraesCS2A | scaffold54 | TVU21254 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6D | scaffold48 | TVU33433 |
| LPERR03G | genblast_C | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4D | scaffold22 | TVU47151 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS6A | scaffold28 | TVU41870 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6B | scaffold1. | TVU32901 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47642 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | genblast_C | genblast_C | scaffold27 | TVU02385 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold34 | TVU37723 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCE6Rv | TraesCS7A | scaffold25 | genblast_C |

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| LPERR11G | cds.KYUSt_ | genblast_C | Os11t049 | SECCE5Rv | TraesCS5D | scaffold24 | TVU25363 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6D | scaffold12 | TVU28198 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6D | scaffold10 | TVU27925 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t083 | SECCE7Rv | TraesCS4A | scaffold3. | TVU20694 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21503 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold23 | TVU47770 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t019 | SECCE4Rv | TraesCS4A | scaffold19 | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t024 | SECCE7Rv1 | TraesCS5B | scaffold65 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv1 | TraesCS6A | scaffold10 | TVU02404 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv1 | TraesCS4A | scaffold17 | TVU48178 |
| LPERR03G | genblast_Z | ORUFI03G | genblast_Z | SECCE6Rv1 | TraesCS6A | scaffold14 | TVU47490 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t046 | SECCE1Rv1 | TraesCS1A | genblast_C | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t047 | SECCE1Rv1 | TraesCS1A | genblast_C | genblast_C |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv1 | TraesCS7B | scaffold9. | TVU08676 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t059 | SECCE5Rv1 | TraesCS5B | scaffold29 | TVT99076 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t039 | SECCE1Rv1 | TraesCS1B | scaffold81 | TVU15723 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv1 | TraesCS2A | scaffold12 | TVU16652 |
| LPERR04G | genblast_C | ORUFI04G | Os04t037 | SECCE2Rv1 | TraesCS2B | scaffold21 | TVU13862 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t055 | SECCE2Rv1 | TraesCS2A | scaffold58 | TVU38503 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t016 | SECCE6Rv1 | TraesCS6D | scaffold39 | genblast_C |
| LPERR04G | genblast_C | ORUFI04G | Os04t062 | genblast_C | TraesCS2A | scaffold36 | TVU16205 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t054 | SECCE4Rv1 | TraesCS4A | scaffold17 | TVU24703 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv1 | TraesCS7A | scaffold21 | TVU07843 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv1 | TraesCS6D | scaffold26 | TVU27730 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv1 | TraesCS5A | scaffold16 | genblast_C |
| genblast_C | genblast_C | ORUFI02G | Os02t081 | SECCE6Rv1 | TraesCS6B | scaffold26 | genblast_C |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold96 | TVU38416 |
| LPERR07G | cds.KYUSt_genblast_C | genblast_C | SECCE4Rv | TraesCS7A | scaffold34 | TVU39469 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7A | scaffold13 | TVU05118 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t011 | SECCE3Rv | TraesCS3D | scaffold15 | TVU22199 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t020 | SECCE4Rv | TraesCS4D | scaffold14 | TVU11982 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold26 | TVU27669 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3B | scaffold33 | TVU22984 |
| genblast_C | genblast_CORUFI03G | Os03t017 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48219 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10240 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t061 | SECCE4Rv | TraesCS4A | scaffold6. | TVU24155 |
| genblast_Z | cds.KYUSt_ORUFI03G | genblast_Z | SECCE3Rv | TraesCS4D | scaffold13 | genblast_Z |
| genblast_C | cds.KYUSt_ORUFI07G | Os07t046 | SECCE2Rv | TraesCS2B | scaffold16 | TVU39372 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1B | scaffold40 | TVU18244 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold20 | TVU19442 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t025 | SECCE3Rv | TraesCS3B | scaffold42 | TVU33285 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t056 | SECCE4Rv | TraesCS4D | scaffold10 | TVU10560 |

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| LPERR08G | cds.KYUSt_genblast_C | genblast_C | SECCE5Rv | TraesCS5A | scaffold68 | TVU42260 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7D | scaffold38 | TVU04885 |
| LPERR06G | genblast_CORUFI06G | Os06t053 | SECCE7Rv | TraesCS7D | scaffold33 | TVU08704 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10288 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t021 | SECCE4Rv | TraesCS4B | scaffold18 | TVU25867 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold26 | TVU28955 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45694 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2A | scaffold23 | TVU39000 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2D | scaffold67 | TVU38168 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2A | scaffold49 | TVU15804 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t020 | SECCE6Rv | TraesCS6D | scaffold51 | TVU33000 |
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| LPERR04G | genblast_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2D | scaffold30 | TVU16695 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6A | scaffold13 | TVU29432 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1D | scaffold12 | TVU00701 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t020 | SECCE1Rv | TraesCS1A | scaffold84 | TVU16986 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15953 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t094 | SECCE6Rv | TraesCS3D | scaffold18 | TVU36863 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t016 | SECCE7Rv | TraesCS2A | scaffold13 | TVU07112 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t062 | SECCE5Rv | TraesCS5B | scaffold29 | TVU48914 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t064 | SECCE3Rv | TraesCS3A | scaffold26 | TVU46391 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t054 | SECCE7Rv | TraesCS7B | scaffold24 | TVU07798 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7B | scaffold17 | genblast_ |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3D | scaffold32 | TVU22983 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold40 | TVU04020 |
| LPERR01G | genblast_ | ORUFI01G | Os01t024 | SECCE7Rv | TraesCS2B | scaffold27 | genblast_ |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15994 |
| genblast_ | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7B | scaffold24 | TVU07772 |
| LPERR02G | genblast_Z | ORUFI02G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold6. | TVU33162 |
| LPERR01G | genblast_ | ORUFI01G | Os01t026 | SECCE3Rv | TraesCS3B | scaffold25 | TVU22493 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48052 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_ | genblast_ | TraesCS4B | scaffold36 | TVU45449 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t079 | SECCE3Rv | TraesCS3B | scaffold46 | TVU34835 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_ | SECCE2Rv | TraesCS2A | scaffold2. | TVU38162 |
| LPERR09G | genblast_ | ORUFI12G | Os12t023 | SECCE3Rv | TraesCS3A | scaffold12 | TVU36332 |
| LPERR04G | genblast_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2A | scaffold49 | TVU16101 |
| genblast_ | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE3Rv | TraesCS3B | scaffold11 | TVU28762 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE7Rv | TraesCS4A | scaffold37 | TVU06062 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold9. | TVU48101 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36408 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2D | scaffold30 | TVU37932 |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold2. | TVU37163 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t027 | SECCE4Rv | TraesCS7D | scaffold22 | TVU11656 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold3. | TVU44302 |
| LPERR08G | cds.KYUSt_ORUFI08G | genblast_Z | SECCE7Rv | TraesCS7D | scaffold15 | TVU04557 |
| genblast_C | cds.KYUSt_genblast_C | Os03t020 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48003 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t064 | SECCEUnv | TraesCS7D | scaffold92 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t028 | SECCE5Rv | TraesCS5B | scaffold10 | TVU21330 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t015 | SECCE5Rv | TraesCS5D | scaffold20 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t011 | SECCE5Rv | TraesCS4B | scaffold34 | TVU48600 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold40 | genblast_Z |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37531 |
| LPERR02G | genblast_CORUFI06G | Os02t024 | SECCE7Rv | TraesCS7D | scaffold42 | TVU33277 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold40 | TVU18028 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold14 | genblast_C |
| LPERR01G | genblast_CORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold15 | TVU35529 |

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| LPERR01G | genblast_CORUFI01G | Os01t091 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36069 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | scaffold52 | TVU48503 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7B | scaffold9. | TVU08517 |
| genblast_C | cds.KYUSt_ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold12 | TVU41046 |
| LPERR08G | cds.KYUSt_ORUFI07G | Os07t027 | SECCE3Rv | TraesCS6A | scaffold7. | TVU10482 |
| LPERR10G | genblast_CORUFI10G | genblast_C | SECCE2Rv | TraesCS1D | scaffold57 | TVU30584 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28026 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2A | scaffold23 | TVU38806 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold12 | TVU28138 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t030 | SECCE5Rv | TraesCS5B | scaffold16 | TVU09057 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5A | scaffold18 | genblast_ |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t051 | SECCE2Rv | TraesCS2D | scaffold56 | TVU15291 |
| LPERR02G | genblast_C | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6B | scaffold17 | TVU51692 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6A | scaffold48 | genblast_ |
| LPERR04G | genblast_C | ORUFI04G | Os04t042 | SECCE4Rv | TraesCS4A | scaffold13 | TVU19545 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_ | SECCE7Rv | TraesCS7A | scaffold23 | TVU08051 |
| LPERR06G | genblast_C | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7A | scaffold23 | TVU08044 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCEUnv | TraesCS4D | scaffold20 | TVU45780 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7D | scaffold9. | TVU07581 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_ | SECCEUnv | TraesCS5A | scaffold14 | TVU50281 |
| LPERR04G | genblast_C | ORUFI04G | Os04t018 | SECCE7Rv | TraesCS2B | scaffold34 | TVU28359 |
| LPERR04G | genblast_C | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2A | scaffold49 | TVU15032 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16465 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t018 | SECCE2Rv | TraesCS2B | scaffold10 | genblast_ |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2B | scaffold49 | TVT98958 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCEUnv | TraesCS4B | scaffold9. | TVU47848 |
| LPERR06G | genblast_C | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7B | scaffold51 | TVU08703 |
| LPERR05G | genblast_C | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1B | scaffold75 | TVU19929 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold1. | TVU00541 |
| LPERR01G | genblast_C | ORUFI01G | Os01t093 | SECCE6Rv | TraesCS3A | scaffold31 | TVU34708 |
| genblast_C | cds.KYUSt_ | genblast_C | Os06t029 | SECCE4Rv | TraesCS7B | scaffold33 | TVU11580 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3A | scaffold17 | TVU35110 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09902 |
| LPERR09G | cds.KYUSt_genblast_C | Os09t047 | SECCE5Rv | TraesCS5B | scaffold33 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold84 | TVU36616 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28630 |
| LPERR03G | cds.KYUSt_genblast_C | Os03t076 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44846 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2B | scaffold29 | TVU13974 |
| genblast_C | cds.KYUSt_ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21408 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t064 | SECCE6Rv | TraesCS6B | scaffold26 | TVU29014 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t068 | SECCE6Rv | genblast_C | scaffold46 | TVT99737 |
| LPERR07G | genblast_C | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | scaffold43 | TVU38376 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t061 | SECCE4Rv | TraesCS4A | scaffold11 | TVU24159 |
| LPERR12G | cds.KYUSt_genblast_C | Os11t012 | SECCE4Rv | TraesCS4B | scaffold70 | TVU50632 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5B | scaffold97 | TVU50948 |
| LPERR07G | cds.KYUSt_ORUFI03G | Os03t037 | SECCE4Rv | TraesCS4B | scaffold28 | TVU37613 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6A | scaffold11 | TVU33711 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold87 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3A | scaffold4. | TVU22779 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t013 | SECCE1Rv | TraesCS1A | scaffold29 | TVU48467 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold15 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold31 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7D | scaffold26 | TVU43582 |
| LPERR10G | cds.KYUSt_ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold16 | genblast_Z |
| LPERR06G | genblast_C | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold9. | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t035 | SECCE4Rv | TraesCS6A | scaffold22 | TVU47031 |
| LPERR02G | cds.KYUSt_genblast_C | Os02t076 | SECCE6Rv | TraesCS6A | scaffold17 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t037 | genblast_C | TraesCS2D | scaffold37 | TVU06387 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t032 | SECCE4Rv | TraesCS7A | scaffold10 | TVU32263 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3A | scaffold41 | TVU36457 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2D | scaffold65 | TVU38147 |
| LPERR11G | cds.KYUSt_ORUFI11G | genblast_C | SECCE5Rv | TraesCS5D | scaffold6. | TVU03416 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3D | scaffold89 | TVU35217 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t030 | SECCE4Rv | TraesCS7D | scaffold68 | TVU11555 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6D | scaffold17 | TVU01182 |

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| LPERR11G | cds.KYUSt_ORUFI11G | genblast_C | SECCE4Rv | TraesCS4D | scaffold18 | TVU26270 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold17 | TVU35012 |
| genblast_C | cds.KYUSt_ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3B | scaffold36 | TVU21398 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1B | scaffold13 | TVU17181 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6A | scaffold27 | TVU28160 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3B | scaffold15 | TVT99365 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t037 | SECCE7Rv | TraesCS7D | scaffold11 | TVU06394 |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold14 | TVU14887 |
| LPERR06G | genblast_C | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7A | scaffold93 | TVU08724 |
| LPERR08G | cds.KYUSt_ORUFI08G | genblast_Z | SECCE4Rv | TraesCS7A | scaffold26 | TVT99153 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t034 | SECCE5Rv | TraesCS5A | scaffold19 | TVU09236 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3D | scaffold4. | TVU03275 |

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|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21526 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3B | scaffold15 | TVU37027 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t053 | SECCE2Rv | TraesCS2D | scaffold58 | TVU38685 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48570 |
| LPERR12G | cds.KYUSt_ORUFI12G | genblast_C | SECCE5Rv | TraesCS5D | scaffold57 | TVU49343 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t019 | SECCE1Rv | TraesCS1A | scaffold20 | TVU31266 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7D | scaffold54 | TVU04779 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t059 | SECCE5Rv | TraesCS5B | scaffold29 | TVU49322 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold17 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE3Rv | TraesCS3D | scaffold15 | TVU22197 |
| LPERR10G | genblast_C | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1A | scaffold85 | TVU31661 |
| LPERR06G | genblast_C | ORUFI06G | Os06t017 | SECCE4Rv | TraesCS7B | scaffold34 | TVU29931 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1D | scaffold36 | TVU17177 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t051 | SECCE1Rv | TraesCS1D | scaffold32 | TVU20655 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE6Rv | TraesCS6B | scaffold19 | TVU29112 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | genblast_C | TraesCS2B | scaffold58 | TVU38618 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5B | scaffold29 | TVU08868 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t032 | SECCE4Rv | TraesCS4D | scaffold18 | TVU47203 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7D | scaffold34 | TVU12299 |
| LPERR12G | genblast_C | ORUFI12G | Os12t018 | SECCE3Rv | TraesCS3B | scaffold46 | TVU36550 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold17 | TVU28677 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4D | scaffold11 | TVU45509 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6B | scaffold24 | TVU33495 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold23 | TVU35859 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1A | scaffold20 | TVU19346 |
| LPERR06G | genblast_C | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7B | scaffold36 | TVU12409 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2D | scaffold30 | TVU14131 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold3. | TVU45328 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE6Rv | TraesCS6A | scaffold37 | TVU06341 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48591 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5B | scaffold64 | TVU09814 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold36 | TVU19025 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t027 | genblast_C | TraesCS1A | scaffold68 | TVU42353 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5A | scaffold17 | TVU44411 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold9. | TVU29803 |
| LPERR01G | genblast_C | ORUFI01G | Os01t088 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36247 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t026 | SECCE6Rv | TraesCS6B | scaffold39 | TVU32801 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1A | scaffold32 | genblast_C |
| genblast_Z | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE4Rv | TraesCS7D | genblast_Z | TVU33577 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6B | scaffold22 | TVU28751 |
| genblast_Z | genblast_Z | genblast_Z | genblast_Z | SECCE4Rv | TraesCS7A | scaffold10 | TVU12600 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3D | scaffold33 | TVU36320 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold36 | TVU22863 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t011 | SECCE3Rv | TraesCS3A | scaffold15 | TVU22183 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv | TraesCS3B | scaffold31 | TVU34668 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28322 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45416 |
| LPERR02G | genblast_C | ORUFI02G | Os02t050 | SECCE2Rv | TraesCS2B | scaffold38 | TVU29971 |
| genblast_C | genblast_C | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold54 | TVU50184 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2A | scaffold40 | TVU15002 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t016 | SECCE6Rv | TraesCS6A | scaffold1. | TVU00167 |
| LPERR06G | genblast_C | ORUFI06G | Os06t048 | SECCE4Rv | TraesCS7D | scaffold30 | TVU11240 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold40 | TVU23065 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold18 | TVU48377 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS4A | scaffold34 | TVU12589 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44857 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t030 | SECCE4Rv | TraesCS4D | scaffold16 | TVU25020 |
| LPERR01G | genblast_Z | ORUFI01G | genblast_Z | SECCE4Rv | TraesCS6D | scaffold13 | TVU34332 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6A | scaffold17 | TVU01181 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5B | scaffold17 | TVU44444 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2B | scaffold20 | TVU16107 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4A | scaffold35 | TVU45194 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7D | scaffold24 | TVU01086 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1A | scaffold8. | TVU19051 |
| LPERR05G | genblast_C | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1D | scaffold18 | TVU20512 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold2. | TVU38181 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t011 | SECCE7Rv | TraesCS2B | scaffold15 | TVT96693 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold94 | TVU16025 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold42 | TVU47995 |

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| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t010 | SECCE4Rv | TraesCS4D | scaffold50 | TVU01331 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5B | scaffold1. | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t031 | genblast_C | TraesCS2B | scaffold49 | TVT99942 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6B | scaffold27 | TVU28268 |

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| genblast_C | cds.KYUSt_ | genblast_C | Os07t068 | SECCEUnv | TraesCS2D | scaffold86 | TVU37204 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1D | genblast_C | TVU20105 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold10 | TVU27953 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4D | scaffold11 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t019 | SECCE1Rv | TraesCS1A | scaffold72 | TVU31269 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE6Rv | TraesCS3A | scaffold31 | TVU34696 |
| genblast_C | genblast_C | ORUFI04G | Os04t042 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14527 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold40 | genblast_C |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t069 | SECCE2Rv1 | TraesCS2B | scaffold30 | TVU16709 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv1 | TraesCS2A | scaffold43 | TVU38710 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t024 | SECCE2Rv1 | TraesCS2A | scaffold21 | TVU13404 |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t045 | SECCE1Rv1 | TraesCS1A | scaffold11 | TVU30473 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv1 | TraesCS3D | scaffold31 | TVU34609 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv1 | TraesCS2D | scaffold36 | TVU13201 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCE4Rv1 | TraesCS4D | scaffold11 | TVU45825 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv1 | TraesCS2D | scaffold8. | TVU14324 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv1 | TraesCS6A | scaffold1. | TVU01999 |
| LPERR01G | genblast_C | ORUFI01G | Os01t092 | SECCE3Rv1 | TraesCS3B | scaffold21 | TVU34610 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t015 | SECCE3Rv1 | TraesCS3A | scaffold59 | TVU21719 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE5Rv1 | TraesCS5A | scaffold23 | TVU02533 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE5Rv1 | TraesCS5B | genblast_C | TVU20045 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv1 | TraesCS6D | scaffold2. | TVU28025 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv1 | TraesCS4D | scaffold23 | TVU47681 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE7Rv1 | TraesCS7A | scaffold67 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t055 | SECCE5Rv1 | TraesCS5A | scaffold1. | TVU49859 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv1 | TraesCS5A | scaffold55 | TVU45907 |
| LPERR10G | genblast_C | ORUFI10G | Os10t048 | genblast_C | TraesCS1B | scaffold11 | TVU30296 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE5Rv1 | TraesCS5D | scaffold50 | TVU27073 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t029 | SECCE4Rv1 | TraesCS4B | scaffold19 | TVU32378 |

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| LPERR07G | genblast_C | ORUFI07G | Os07t047 | SECCE6Rv1 | TraesCS6D | scaffold27 | TVU39365 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t017 | SECCE1Rv1 | TraesCS1A | scaffold13 | TVU17212 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv1 | TraesCS3D | scaffold41 | TVU35748 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE5Rv1 | TraesCS5D | scaffold18 | TVU46655 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv1 | TraesCS6A | scaffold2. | TVU28329 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv1 | TraesCS6A | scaffold34 | TVU33587 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv1 | TraesCS6B | scaffold12 | TVU28176 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2D | scaffold58 | TVU38506 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_C | SECCE7Rv | TraesCS2B | scaffold30 | TVU23843 |

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| genblast_C | cds.KYUSt_ORUFI07G | Os07t024 | SECCE5Rv | TraesCS5B | scaffold31 | TVU39836 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4B | scaffold23 | TVU47645 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t062 | SECCE4Rv | TraesCS4A | scaffold41 | TVU24131 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t071 | SECCE6Rv | TraesCS7A | scaffold9. | TVU07577 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5D | scaffold65 | TVU44586 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t032 | SECCE4Rv | TraesCS7D | scaffold27 | TVU11392 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48492 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold35 | TVU45325 |
| LPERR09G | cds.KYUSt_ORUFI03G | Os03t057 | SECCE6Rv | TraesCS6B | scaffold25 | TVU44871 |
| LPERR04G | genblast_C | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold99 | TVU14606 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6A | genblast_C | TVU17885 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6A | scaffold16 | TVU29079 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t041 | SECCE2Rv | genblast_C | scaffold35 | TVU06009 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3B | scaffold89 | TVU36018 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold20 | TVU27678 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t011 | SECCE5Rv | TraesCS5B | scaffold37 | TVU10766 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t064 | SECCE5Rv | TraesCS5B | scaffold20 | TVU23847 |
| genblast_C | genblast_C | genblast_C | Os04t060 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15886 |
| genblast_C | cds.KYUSt_ORUFI02G | Os02t056 | SECCE2Rv | TraesCS2A | scaffold17 | genblast_C |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold65 | TVU38159 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7B | scaffold26 | TVU43559 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2B | scaffold49 | TVU13122 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1D | scaffold85 | genblast_ |
| | | | | | | | |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5B | scaffold29 | TVU08921 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12203 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1B | scaffold13 | TVT98780 |
| LPERR07G | genblast_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2A | scaffold2. | TVT96769 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2D | scaffold23 | TVU38808 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t086 | SECCE7Rv | TraesCS5B | scaffold39 | TVU44266 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE2Rv | TraesCS2A | scaffold58 | TVU38632 |
| LPERR03G | genblast_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU09383 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2B | scaffold20 | TVU14767 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold20 | TVU27630 |
| LPERR09G | genblast_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5B | scaffold64 | TVU09794 |
| LPERR03G | genblast_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48143 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7A | scaffold24 | TVU01083 |
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| LPERR09G | genblast_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5D | scaffold43 | TVU10293 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCEUnv | TraesCSU0 | scaffold78 | TVU36923 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_ | SECCE7Rv | TraesCS7A | scaffold33 | TVU08482 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS5D | scaffold25 | TVU44244 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCEUnv | TraesCS6D | scaffold10 | TVU28077 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_ | SECCE2Rv | TraesCS2A | scaffold27 | TVU39055 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6A | scaffold31 | TVU12118 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold35 | TVU44845 |
| genblast_ | cds.KYUSt_ | ORUFI03G | Os03t083 | genblast_ | TraesCS5B | scaffold3. | TVU43928 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7A | scaffold38 | TVU05111 |
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| genblast_ | cds.KYUSt_ | ORUFI11G | Os11t062 | SECCE4Rv | TraesCSU0 | scaffold19 | TVU03417 |
| LPERR03G | genblast_ | ORUFI03G | Os03t066 | SECCE4Rv | TraesCS4A | scaffold20 | TVT98533 |
| LPERR11G | genblast_ | ORUFI11G | genblast_ | SECCE4Rv | TraesCS4B | scaffold13 | TVU23492 |
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| LPERR11G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE6Rv | TraesCS7D | scaffold43 | TVU02162 |
| LPERR03G | genblast_ | ORUFI03G | genblast_ | SECCE7Rv | TraesCS4B | scaffold9. | genblast_ |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2A | scaffold1. | TVU37428 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t039 | SECCE6Rv | TraesCS6B | scaffold17 | TVT97843 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | genblast_C | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2B | scaffold2. | genblast_C |
| genblast_C | cds.KYUSt_ORUFI01G | | Os01t097 | SECCE2Rv | TraesCS3B | scaffold2. | TVU49011 |
| LPERR11G | cds.KYUSt_ORUFI11G | | genblast_C | SECCE6Rv | TraesCS6A | scaffold13 | TVU24977 |
| LPERR02G | cds.KYUSt_ORUFI02G | | Os02t063 | SECCE6Rv | TraesCS6D | scaffold10 | TVU29064 |
| LPERR09G | cds.KYUSt_ORUFI09G | | Os09t050 | SECCE5Rv | TraesCS5D | scaffold29 | TVU08796 |
| LPERR01G | cds.KYUSt_ORUFI01G | | Os01t076 | SECCE3Rv | TraesCS3B | scaffold15 | TVU35020 |

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| LPERR05G | cds.KYUSt_ORUFI05G | | Os05t045 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19652 |
| LPERR03G | cds.KYUSt_ORUFI03G | | Os03t081 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44423 |
| LPERR01G | cds.KYUSt_ORUFI01G | | Os01t011 | SECCE3Rv | TraesCS3A | scaffold16 | TVU22238 |

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| genblast_C | cds.KYUSt_ORUFI01G | | Os01t078 | SECCE3Rv | TraesCS3D | scaffold48 | TVU34896 |
| LPERR06G | cds.KYUSt_ORUFI06G | | Os06t065 | SECCEUnv | TraesCS7B | scaffold25 | TVU08402 |
| LPERR03G | cds.KYUSt_ORUFI03G | | Os03t016 | SECCE7Rv | TraesCS4B | scaffold42 | TVU48295 |
| LPERR05G | cds.KYUSt_ORUFI05G | | Os05t055 | SECCE1Rv | TraesCS1A | scaffold1. | TVU20357 |
| LPERR02G | cds.KYUSt_ORUFI02G | | Os02t070 | SECCE6Rv | TraesCS6B | scaffold27 | TVU28123 |
| LPERR12G | cds.KYUSt_ORUFI12G | | Os12t016 | SECCE5Rv | TraesCS5A | scaffold83 | TVU50976 |

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| LPERR04G | genblast_Z | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2B | scaffold77 | TVU15628 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3A | scaffold63 | TVU21645 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t038 | SECCE4Rv | TraesCS4D | scaffold18 | TVU46799 |
| LPERR11G | genblast_C | ORUFI11G | Os11t060 | SECCE1Rv | TraesCS1A | scaffold78 | TVU23141 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7A | scaffold38 | TVU04727 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t089 | SECCE3Rv | genblast_C | scaffold31 | TVU46506 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5B | scaffold83 | TVU50897 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09996 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold20 | TVU27641 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold37 | TVU34189 |
| genblast_C | genblast_C | ORUFI08G | Os08t046 | SECCE5Rv | TraesCS5B | scaffold11 | TVU06384 |
| LPERR09G | genblast_C | genblast_C | Os09t036 | SECCE5Rv | TraesCS5B | scaffold14 | TVU09308 |

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| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2A | scaffold56 | TVU15404 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7A | scaffold30 | TVU01667 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold97 | TVU47898 |
| genblast_C | cds.KYUSt_ | genblast_C | Os03t017 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48207 |

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| LPERR10G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCE1Rv | TraesCS1B | scaffold18 | TVU49762 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3A | scaffold36 | TVU23062 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48532 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t029 | SECCE6Rv | TraesCS6B | scaffold16 | TVU25782 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold88 | TVU21633 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5B | scaffold29 | TVU10132 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1A | scaffold22 | TVU19245 |
| LPERR08G | genblast_C | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7D | scaffold20 | TVU43743 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t042 | SECCE1Rv | TraesCS1D | scaffold64 | TVU06406 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t032 | SECCE5Rv | TraesCS5A | scaffold14 | genblast_C |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05028 |
| genblast_Z | genblast_Z | ORUFI06G | genblast_Z | SECCE4Rv | TraesCS7D | scaffold30 | TVU11600 |
| LPERR04G | genblast_C | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold14 | TVU15894 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3B | scaffold29 | TVU35318 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6B | scaffold46 | TVU28061 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold84 | TVU28524 |

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| LPERR03G | cds.KYUSt_ | genblast_Z | Os03t076 | SECCE5Rv | TraesCS5B | genblast_Z | TVU44853 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6B | scaffold85 | TVU28470 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t020 | SECCE4Rv | TraesCS6B | scaffold10 | TVU17030 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5A | scaffold16 | TVU01432 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7D | scaffold34 | TVU12486 |
| LPERR01G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE6Rv | TraesCS3D | scaffold31 | TVU02656 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1D | scaffold82 | TVU30918 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3D | scaffold17 | TVU35081 |

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| LPERR05G | cds.KYUSt_ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1A | scaffold14 | TVU04257 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t047 | SECCE2Rv | TraesCS2A | scaffold16 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7B | scaffold38 | TVU04948 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t043 | SECCE2Rv | TraesCS2A | scaffold19 | TVU05713 |
| LPERR10G | genblast_C | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1A | scaffold27 | TVU32149 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t028 | genblast_C | TraesCS4D | scaffold74 | TVU47459 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold36 | TVU22958 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7A | scaffold44 | TVU12083 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t010 | SECCE4Rv | TraesCS7D | scaffold44 | TVU12977 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3B | scaffold17 | TVU34957 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2A | scaffold14 | TVU14877 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2B | scaffold39 | TVU37951 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t028 | SECCE3Rv | TraesCS3B | scaffold15 | TVU21360 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold17 | TVU48041 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1D | scaffold45 | TVU31915 |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold23 | TVU07994 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t055 | SECCE5Rv | TraesCS5D | scaffold41 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7D | scaffold11 | TVU43591 |
| LPERR03G | genblast_CORUFI03G | Os03t032 | SECCE6Rv | TraesCS6A | scaffold32 | TVU47219 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1B | scaffold32 | genblast_C |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7A | scaffold60 | genblast_C |
| LPERR12G | genblast_CORUFI12G | Os12t020 | genblast_C | genblast_C | scaffold10 | TVU51388 |

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| genblast_C | genblast_C | genblast_C | Os06t070 | SECCE7Rv | TraesCS7A | scaffold9. | TVU07709 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t065 | SECCE6Rv | TraesCS7A | scaffold33 | TVU08338 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t050 | SECCE3Rv | TraesCS2D | scaffold27 | TVU39044 |
| genblast_C | genblast_CORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold34 | TVU37727 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t037 | SECCE5Rv | TraesCS5A | scaffold14 | genblast_C |
| LPERR05G | genblast_CORUFI05G | Os05t042 | SECCE1Rv | TraesCS1B | scaffold20 | TVU19449 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t057 | SECCE6Rv | TraesCS6B | scaffold18 | TVU46356 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6D | scaffold10 | TVU28929 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv1 | TraesCS3B | scaffold32 | TVU02946 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t010 | SECCE7Rv1 | TraesCS2D | scaffold14 | TVU06838 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t056 | SECCE7Rv1 | TraesCS7B | scaffold53 | TVU04456 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE4Rv1 | TraesCS7D | scaffold28 | TVU20966 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv1 | TraesCS5A | scaffold25 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE1Rv1 | TraesCS1B | scaffold16 | TVU30314 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv1 | TraesCS3B | scaffold11 | TVU23063 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t013 | SECCE5Rv1 | TraesCS4D | scaffold29 | TVU48472 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE3Rv1 | TraesCS2D | scaffold86 | TVT99572 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv1 | TraesCS2B | scaffold67 | TVU37808 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv1 | TraesCS2B | scaffold10 | TVU40219 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv1 | TraesCS3B | scaffold11 | TVU34760 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE4Rv1 | TraesCS4A | scaffold42 | genblast_Z |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv1 | TraesCS2A | scaffold67 | TVU37805 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE3Rv1 | TraesCS3D | scaffold37 | TVT99676 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCEUnv1 | TraesCS5A | scaffold15 | TVU48779 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv1 | TraesCS5B | scaffold65 | TVU44703 |
| genblast_C | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv1 | TraesCS5A | scaffold76 | TVU49080 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | SECCE4Rv1 | TraesCS7A | scaffold36 | TVT99330 |
| LPERR01G | genblast_C | ORUFI01G | Os01t020 | SECCE3Rv1 | TraesCS3A | genblast_C | TVU22780 |
| LPERR08G | genblast_Z | ORUFI08G | genblast_Z | SECCE7Rv1 | TraesCS7B | scaffold15 | TVU42261 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv1 | TraesCSU0 | scaffold41 | TVU48662 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv1 | TraesCS1A | scaffold24 | genblast_C |
| LPERR11G | genblast_C | ORUFI11G | Os11t021 | SECCE4Rv1 | TraesCS4B | scaffold24 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE4Rv1 | TraesCS4D | scaffold11 | TVU00824 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv1 | TraesCS2B | scaffold94 | TVU00458 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv1 | TraesCS2D | scaffold94 | TVU15913 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv1 | TraesCS2A | scaffold58 | TVU38578 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1D | scaffold1. | TVU20263 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE3Rv | TraesCS3D | scaffold67 | TVT97732 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t050 | SECCE5Rv | TraesCS5A | scaffold30 | TVU33766 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | scaffold9. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4A | scaffold9. | TVU48015 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4A | scaffold10 | TVU48275 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3B | scaffold46 | TVU34853 |
| genblast_C | cds.KYUSt_ | genblast_C | Os10t057 | SECCE1Rv | TraesCS1A | scaffold5. | TVU31545 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE6Rv | TraesCS6D | scaffold18 | TVU32781 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t048 | genblast_C | TraesCS7A | scaffold10 | TVU11288 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7B | scaffold25 | TVU08095 |
| LPERR03G | genblast_C | ORUFI03G | Os03t044 | SECCE4Rv | TraesCS4B | scaffold45 | TVU46473 |
| LPERR05G | genblast_C | ORUFI05G | Os05t027 | genblast_C | TraesCS1B | scaffold14 | TVU18495 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5B | scaffold27 | TVU10154 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t060 | SECCE4Rv | TraesCS4D | scaffold1. | TVU46198 |
| LPERR03G | genblast_C | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4B | scaffold55 | TVU45655 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t047 | SECCE2Rv | TraesCS2D | scaffold77 | TVU15641 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t045 | SECCE4Rv | TraesCS7D | scaffold63 | TVU33794 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold42 | TVU48022 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6D | scaffold11 | TVU01703 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15566 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44852 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5B | scaffold3. | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1B | scaffold25 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2B | scaffold30 | TVU14163 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10276 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37900 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os10t018 | SECCE7Rv | TraesCS7A | scaffold14 | TVU46128 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2D | scaffold77 | TVU15627 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCEUnv | TraesCS6D | scaffold11 | TVU28366 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold31 | TVU34598 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS7D | scaffold44 | TVU13066 |
| LPERR08G | genblast_C | ORUFI08G | Os08t043 | SECCE1Rv | TraesCS1B | scaffold13 | TVU05789 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCE6Rv | TraesCS7B | scaffold92 | TVU08335 |
| genblast_C | genblast_C | ORUFI10G | Os09t056 | SECCE5Rv | TraesCS5A | scaffold27 | TVT98808 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold1. | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3D | scaffold22 | TVU47018 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48098 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t052 | SECCE5Rv | TraesCS5B | scaffold27 | TVU10129 |
| LPERR10G | genblast_C | ORUFI10G | genblast_C | SECCE5Rv | TraesCS5B | scaffold16 | TVU30846 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1A | scaffold8. | TVU19285 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_ | SECCE5Rv | TraesCS5A | scaffold3. | TVU44755 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48033 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3B | scaffold89 | TVU35978 |
| genblast_ | genblast_ | ORUFI11G | Os11t029 | SECCE6Rv | TraesCS6A | scaffold27 | TVU27665 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44585 |
| LPERR09G | genblast_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5B | scaffold27 | TVU08926 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2B | scaffold43 | genblast_ |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4D | scaffold11 | TVU45542 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5A | scaffold53 | TVU09800 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_ | SECCE7Rv | TraesCS4A | scaffold22 | TVU47396 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1A | scaffold36 | TVU17168 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_ | SECCE6Rv | TraesCS6A | scaffold48 | TVU33557 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold16 | TVU10143 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t016 | SECCE7Rv | TraesCS7D | scaffold17 | TVU42928 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3D | scaffold18 | TVU34617 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold13 | TVU00533 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t038 | SECCE5Rv | TraesCS5B | scaffold27 | genblast_ |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t045 | SECCE1Rv | TraesCS1A | genblast_ | genblast_ |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_ | SECCE1Rv | TraesCS1B | scaffold12 | TVU19173 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold22 | TVU07629 |
| LPERR03G | genblast_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45294 |

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|---|---|---|---|---|---|---|---|
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t017 | SECCE4Rv1 | TraesCS4D | scaffold19 | genblast_ |
| LPERR01G | cds.KYUSt_ | genblast_ | Os01t077 | SECCE3Rv1 | TraesCS3A | scaffold22 | TVU34907 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv1 | TraesCS3B | scaffold89 | TVU36010 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv1 | TraesCS3D | scaffold31 | TVU36423 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv1 | TraesCS3A | scaffold4. | TVU22897 |
| LPERR01G | cds.KYUSt_ | genblast_ | Os01t057 | SECCE3Rv1 | TraesCS3D | scaffold11 | TVU34211 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_ | SECCE7Rv1 | TraesCS4A | scaffold15 | TVU48170 |
| genblast_ | genblast_ | genblast_ | Os09t045 | SECCE5Rv1 | TraesCS5A | scaffold53 | TVT98642 |
| LPERR01G | genblast_ | ORUFI01G | Os01t069 | SECCE3Rv1 | TraesCS3A | scaffold15 | TVU35428 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv1 | TraesCS3B | scaffold17 | TVU02361 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE3Rv1 | TraesCS3B | scaffold11 | TVU02529 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t021 | SECCE1Rv1 | TraesCS1A | scaffold10 | TVU16988 |
| LPERR06G | cds.KYUSt_ | genblast_ | Os06t011 | SECCE4Rv1 | TraesCS4A | scaffold44 | TVT97016 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t051 | SECCE1Rv1 | TraesCS1B | scaffold39 | TVU20573 |
| LPERR01G | genblast_ | ORUFI01G | Os01t097 | SECCEUnv1 | TraesCS4A | scaffold97 | TVU50797 |
| genblast_ | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv1 | TraesCS4A | scaffold97 | TVU47846 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv1 | TraesCS5B | scaffold29 | TVU03823 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv1 | TraesCS2B | scaffold94 | genblast_ |
| LPERR03G | genblast_Z | ORUFI03G | genblast_Z | SECCEUnv1 | TraesCS5B | scaffold65 | TVU44269 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv1 | TraesCS4B | scaffold9. | TVU48102 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t037 | SECCE5Rv1 | TraesCS5D | scaffold18 | TVU46865 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_ | SECCE1Rv1 | TraesCS1D | scaffold13 | TVU20294 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t065 | SECCE3Rv1 | TraesCS3B | scaffold3. | TVU35732 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv1 | TraesCS4A | scaffold74 | TVU47451 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t056 | SECCE7Rv1 | TraesCS7B | scaffold32 | TVU04462 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCEUnv1 | TraesCS3B | scaffold15 | TVU36886 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv1 | TraesCS2A | scaffold77 | TVU14476 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv1 | TraesCS4A | scaffold39 | TVU12816 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE7Rv1 | TraesCS7A | scaffold16 | TVU03928 |
| LPERR01G | genblast_C | ORUFI01G | Os01t076 | SECCE3Rv1 | TraesCS3A | scaffold11 | TVU34989 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE5Rv1 | TraesCS4B | scaffold10 | TVU48431 |
| LPERR02G | genblast_C | ORUFI02G | Os02t048 | SECCE4Rv1 | TraesCS6B | scaffold80 | TVU30061 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE1Rv1 | TraesCS1B | scaffold13 | TVU20452 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE1Rv1 | TraesCS1B | scaffold19 | TVU33769 |
| LPERR08G | genblast_C | ORUFI08G | Os08t011 | SECCE7Rv1 | TraesCS7D | scaffold20 | TVU43664 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv1 | TraesCS4A | scaffold3. | TVU43934 |
| LPERR01G | genblast_C | ORUFI01G | Os01t025 | SECCE3Rv1 | TraesCS5D | scaffold47 | TVU22429 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t012 | SECCE2Rv1 | TraesCS2D | scaffold11 | TVU00355 |
| LPERR03G | genblast_C | ORUFI03G | Os03t071 | SECCE4Rv1 | TraesCS4D | scaffold35 | TVU45375 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t013 | SECCE6Rv1 | TraesCS6B | scaffold24 | TVU33504 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19881 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3B | scaffold41 | TVU36782 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1D | scaffold19 | TVU17434 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44751 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10419 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5B | scaffold16 | TVU08785 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t031 | SECCE4Rv | TraesCS7B | scaffold33 | TVU50239 |

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| genblast_C | cds.KYUSt_ | genblast_C | Os03t064 | SECCE5Rv | TraesCS5B | scaffold20 | TVU45914 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE3Rv | TraesCS3A | scaffold25 | TVU02549 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12858 |
| LPERR01G | genblast_C | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3B | scaffold48 | TVU34806 |
| genblast_C | genblast_C | ORUFI08G | genblast_C | SECCE3Rv | TraesCS3D | scaffold28 | TVU42416 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2A | scaffold23 | TVU38933 |

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| LPERR04G | cds.KYUSt_ | genblast_C | Os04t045 | SECCE2Rv | TraesCS2D | scaffold46 | TVU14347 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS4D | genblast_Z | TVU48474 |
| LPERR01G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE3Rv | TraesCS3A | scaffold14 | TVU35279 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11815 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1D | scaffold24 | TVU17973 |
| LPERR03G | genblast_C | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4D | scaffold23 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2B | scaffold28 | TVU41421 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | scaffold23 | TVU47777 |
| LPERR02G | genblast_C | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6A | scaffold46 | TVU28084 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold25 | TVU32892 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4A | scaffold18 | TVU47264 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t017 | SECCE4Rv | TraesCS7A | scaffold18 | TVU21552 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7D | scaffold14 | TVU11953 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold16 | TVU29286 |
| LPERR12G | genblast_C | ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5A | scaffold17 | TVU45596 |

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| LPERR08G | genblast_C | ORUFI08G | Os08t011 | SECCE6Rv | TraesCS3A | scaffold26 | TVU43736 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2A | scaffold30 | TVU15036 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4B | scaffold23 | genblast_C |

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| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold27 | TVU28132 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold14 | TVU16004 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t016 | SECCE7Rv | TraesCS2D | scaffold10 | TVU04293 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7D | scaffold13 | TVU01084 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold9. | TVU08535 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE7Rv | TraesCS7B | scaffold17 | TVU29095 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2D | scaffold20 | TVU15119 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19114 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE4Rv | TraesCS7B | scaffold38 | TVU04922 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44467 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47745 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t010 | SECCE3Rv | TraesCS3D | scaffold47 | TVT98172 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45424 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t030 | SECCE6Rv | TraesCS4D | scaffold16 | TVU26088 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1B | scaffold36 | TVU31525 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1D | scaffold13 | TVT98110 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold28 | TVU28892 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38135 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7A | scaffold23 | TVU06637 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | scaffold23 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38012 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t033 | SECCE5Rv | TraesCS5A | scaffold35 | TVU01605 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t032 | SECCE5Rv | TraesCS5B | scaffold26 | TVU06645 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE4Rv | TraesCS7B | scaffold38 | TVU01559 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t042 | SECCE2Rv | TraesCS2A | scaffold13 | TVU05784 |
| LPERR01G | genblast_C | ORUFI05G | genblast_C | SECCE3Rv | TraesCS3B | scaffold14 | TVU36281 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7B | scaffold92 | TVU08537 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t056 | SECCE5Rv | TraesCS5A | scaffold18 | TVT96938 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3D | scaffold36 | TVU04010 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t062 | SECCE5Rv | TraesCS5A | scaffold1. | TVU48916 |
| LPERR11G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCE3Rv | TraesCS3A | scaffold11 | TVU18473 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5B | scaffold24 | TVU09729 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10003 |
| LPERR03G | cds.KYUSt_ | genblast_C | genblast_C | SECCE5Rv | TraesCS5B | scaffold3. | TVU44991 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t012 | SECCE5Rv | TraesCS5B | scaffold20 | TVU10822 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t064 | genblast_C | TraesCS3A | scaffold11 | TVU35796 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7D | scaffold10 | TVU12170 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1D | scaffold24 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6D | scaffold17 | TVU27799 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6B | scaffold31 | TVU33670 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6A | scaffold10 | genblast_C |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t010 | SECCE5Rv | TraesCS2B | scaffold7. | TVU40201 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold12 | TVU28148 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold2. | TVU38167 |
| LPERR06G | genblast_C | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7D | scaffold33 | TVU08433 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t057 | SECCE5Rv | TraesCS5B | scaffold27 | TVU10239 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t058 | SECCE3Rv | TraesCS3A | scaffold20 | TVU34264 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE7Rv | TraesCS2A | scaffold13 | TVU07308 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3D | scaffold13 | TVT99781 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold8. | TVU14333 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t044 | SECCE4Rv | TraesCS7A | scaffold98 | TVU33595 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold14 | TVU09286 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6B | scaffold19 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold42 | TVU33130 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE2Rv | TraesCS2A | scaffold35 | TVU00324 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3B | scaffold18 | TVU37024 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2A | scaffold21 | TVU14054 |
| LPERR01G | genblast_C | ORUFI01G | Os01t061 | SECCE3Rv | genblast_C | scaffold25 | TVU35907 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2D | scaffold5. | TVU14145 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5A | scaffold27 | TVU09782 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t019 | SECCE1Rv | TraesCS1B | scaffold36 | TVU17058 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5D | scaffold14 | TVU09325 |
| LPERR07G | genblast_C | ORUFI07G | Os07t040 | SECCE7Rv | TraesCS7A | scaffold15 | TVU02916 |
| genblast_Z | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS5D | scaffold25 | TVU44056 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | genblast_Z | TraesCS6D | scaffold83 | TVU28449 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35367 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6A | scaffold27 | TVU03829 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2A | scaffold2. | TVU38009 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold6. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5B | scaffold3. | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1A | scaffold40 | TVU18117 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7B | scaffold60 | TVU08536 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34129 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7A | scaffold32 | TVU01913 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7A | scaffold26 | TVU05207 |
| LPERR03G | genblast_C | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4D | scaffold55 | TVU45658 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2D | scaffold81 | TVU14673 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34978 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3A | scaffold17 | TVU35080 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48008 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t051 | SECCEUnv | TraesCS5D | scaffold1. | TVU50019 |
| LPERR02G | cds.KYUSt_ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold38 | TVU29505 |
| LPERR11G | cds.KYUSt_ORUFI12G | Os11t015 | SECCE4Rv | TraesCS4A | scaffold14 | TVU26906 |
| genblast_C | cds.KYUSt_ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2A | scaffold24 | TVU11010 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4B | scaffold23 | TVU47758 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t047 | SECCE5Rv | TraesCS5B | scaffold26 | TVU05548 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold3. | TVU45085 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold36 | TVU07100 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t055 | SECCE3Rv | TraesCS3A | scaffold17 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3D | scaffold88 | TVU21626 |
| LPERR09G | cds.KYUSt_ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold53 | TVU10019 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t032 | genblast_C | TraesCS4D | scaffold22 | TVU47225 |
| genblast_C | cds.KYUSt_ORUFI11G | Os11t018 | SECCE4Rv | TraesCS4D | scaffold50 | TVU26176 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t028 | SECCE2Rv | TraesCS2A | scaffold14 | TVU13400 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t064 | SECCE6Rv | TraesCS6A | scaffold26 | TVU29030 |
| genblast_Z | genblast_ZORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold31 | TVU02366 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t061 | SECCEUnv | TraesCS4B | scaffold20 | TVU35950 |
| LPERR11G | cds.KYUSt_ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4A | scaffold13 | TVU24982 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4D | scaffold40 | TVU47597 |
| genblast_C | genblast_Cgenblast_C | Os01t010 | SECCE3Rv | TraesCS3D | scaffold76 | TVU49637 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3B | scaffold4. | TVU22832 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37807 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold22 | TVU19726 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold1. | TVU00557 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS4A | scaffold31 | TVU45832 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7D | scaffold63 | TVU43538 |

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| LPERR01G | cds.KYUSt_ | genblast_C | Os01t073 | SECCE5Rv | TraesCS5B | genblast_C | TVU34749 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1B | scaffold27 | TVU32070 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv | TraesCS3B | scaffold88 | TVU21888 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2B | scaffold34 | TVU02440 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2B | scaffold49 | TVU14871 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t049 | SECCE4Rv | TraesCS4D | scaffold1. | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold10 | TVU12316 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE7Rv | TraesCS7A | scaffold46 | TVU34071 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2B | scaffold56 | TVU15567 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t034 | SECCE7Rv | TraesCS7A | scaffold18 | TVU09028 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCEUnv | TraesCS7D | scaffold22 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE3Rv | TraesCS3D | scaffold25 | TVU02547 |
| LPERR08G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS7B | scaffold11 | TVU06413 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold22 | TVU28876 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold18 | TVU21867 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE3Rv | TraesCS6A | scaffold26 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6A | scaffold98 | TVU33542 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t049 | SECCE5Rv | TraesCS5D | scaffold16 | TVU50219 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2A | scaffold43 | TVU38950 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5D | scaffold87 | TVU09694 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_Z | SECCE1Rv | TraesCS1D | scaffold11 | TVU49006 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold14 | TVU15924 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48701 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t054 | SECCE7Rv | TraesCS7D | scaffold86 | TVU34107 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t018 | SECCE4Rv | TraesCS7A | scaffold17 | TVU12291 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t032 | SECCE4Rv | TraesCS6B | scaffold12 | TVU24213 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | genblast_C | TraesCS3A | scaffold25 | TVU01327 |
| LPERR04G | genblast_C | ORUFI04G | Os04t051 | genblast_C | TraesCS2A | scaffold56 | TVU15275 |
| LPERR05G | genblast_C | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1D | scaffold13 | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold15 | TVU35513 |
| LPERR11G | cds.KYUSt_ | genblast_C | Os11t019 | SECCE4Rv | TraesCS4A | scaffold18 | TVU26293 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t058 | SECCE5Rv | TraesCS5B | scaffold55 | TVU46305 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t026 | SECCE7Rv | TraesCS7D | scaffold14 | TVU51775 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t014 | SECCE4Rv | TraesCS4B | scaffold12 | TVU50894 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3B | scaffold14 | TVU36215 |
| LPERR02G | genblast_C | ORUFI02G | Os02t051 | SECCE7Rv | TraesCS4D | scaffold12 | TVU29924 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t050 | SECCE2Rv | TraesCS7D | scaffold47 | TVU29977 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45591 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1A | scaffold13 | genblast_C |
| LPERR08G | genblast_C | ORUFI08G | Os08t054 | SECCE4Rv | TraesCS7B | genblast_C | TVU04732 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE2Rv | TraesCS2D | scaffold58 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t015 | SECCE4Rv | TraesCS4B | scaffold12 | TVU26851 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47485 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t025 | SECCE2Rv | TraesCS2A | scaffold14 | TVU16071 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47212 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7D | scaffold17 | TVT97262 |
| genblast_C | cds.KYUSt_ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1D | scaffold8. | TVU19192 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t023 | SECCE3Rv | TraesCS3A | scaffold36 | TVU21369 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t011 | SECCE5Rv | TraesCS4B | scaffold10 | TVU48594 |
| LPERR05G | cds.KYUSt_genblast_C | Os05t049 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19921 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48484 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1D | scaffold11 | TVU01965 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_ | SECCE6Rv | TraesCS6B | scaffold26 | TVU28967 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os04t021 | SECCE6Rv | TraesCS7A | scaffold19 | TVU18669 |
| genblast_ | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47338 |
| LPERR09G | genblast_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold87 | TVU09624 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6A | scaffold6. | TVU01991 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold96 | TVU38383 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t045 | SECCE1Rv | TraesCS1B | scaffold39 | TVU19675 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47928 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15901 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCEUnv | TraesCS4A | scaffold25 | TVU44210 |

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| genblast_ | cds.KYUSt_ | ORUFI09G | Os09t036 | SECCE5Rv | TraesCS5B | scaffold36 | TVU09316 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold52 | TVU48394 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_ | SECCE5Rv | TraesCS5B | scaffold28 | TVU18585 |

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| LPERR06G | genblast_ | ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7D | scaffold17 | genblast_ |

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| LPERR02G( | cds.KYUSt_ORUFI02G( | genblast_C | SECCE6Rv] | TraesCS6D | scaffold34 | TVU33578 | |
| LPERR01G( | genblast_C | ORUFI01G( | Os01t014 | SECCE3Rv] | TraesCS3B | scaffold88 | TVU21957 |
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| LPERR05G( | genblast_C | ORUFI05G( | Os05t019( | SECCE1Rv] | TraesCS1B | scaffold22 | TVU27786 |
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| genblast_C | cds.KYUSt_ORUFI03G: | Os03t077: | SECCE5Rv] | TraesCS5A | scaffold32 | TVU44792 | |
| LPERR10G: | cds.KYUSt_ORUFI10G: | Os10t048 | SECCE1Rv] | TraesCS1B | scaffold16 | TVU30322 | |
| genblast_C | cds.KYUSt_ORUFI11G( | Os11t016( | SECCE4Rv] | TraesCS4B | scaffold70 | genblast_C | |
| genblast_C | cds.KYUSt_ORUFI01G: | Os01t076 | SECCE3Rv] | TraesCS3B | scaffold22 | TVU35000 | |
| LPERR04G: | cds.KYUSt_ORUFI04G: | Os04t049 | SECCE2Rv] | TraesCS2A | scaffold13 | TVU15402 | |
| LPERR09G( | cds.KYUSt_ORUFI09G( | genblast_Z | SECCE5Rv] | TraesCS5A | scaffold35 | TVU10844 | |
| LPERR01G( | cds.KYUSt_ORUFI01G( | Os01t023: | SECCE3Rv] | TraesCS3D | scaffold33 | TVU23051 | |
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| LPERR02G( | cds.KYUSt_ORUFI02G( | Os02t020( | SECCE6Rv] | TraesCS6B | scaffold6.] | TVU32959 | |
| LPERR06G( | cds.KYUSt_ORUFI06G( | Os06t016 | SECCE4Rv] | TraesCS7A | scaffold34 | TVU12391 | |
| LPERR03G( | cds.KYUSt_ORUFI03G( | genblast_Z | SECCE7Rv] | TraesCS4A | scaffold97 | TVU47809 | |
| LPERR03G( | genblast_C | ORUFI03G: | Os03t023 | SECCE7Rv] | TraesCS4D | scaffold15 | TVU47788 |
| LPERR08G( | cds.KYUSt_ORUFI08G( | Os08t019( | SECCE7Rv] | TraesCS7B | scaffold2.] | TVU43140 | |
| genblast_C | cds.KYUSt_ORUFI09G: | Os09t045 | SECCE5Rv] | TraesCS5B | scaffold64 | TVU09807 | |
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| genblast_Z | genblast_Z | ORUFI11G( | genblast_Z | SECCE4Rv] | TraesCS4A | scaffold11 | TVU49290 |
| LPERR01G( | cds.KYUSt_ | genblast_C | genblast_C | SECCE3Rv] | TraesCS3B | scaffold16 | TVU22260 |
| LPERR02G: | cds.KYUSt_ORUFI02G2 | Os02t061( | SECCE6Rv] | TraesCS6B | scaffold17 | genblast_C | |
| LPERR05G: | cds.KYUSt_ORUFI05G2 | Os05t049 | SECCE1Rv] | TraesCS1D | scaffold75 | TVU20037 | |
| LPERR01G: | cds.KYUSt_ORUFI01G: | Os01t037 | SECCE3Rv] | TraesCS3A | genblast_C | TVU41782 | |
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| LPERR04G( | cds.KYUSt_ORUFI04G( | Os04t020( | SECCE7Rv] | TraesCS2A | scaffold32 | TVU07275 | |
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| LPERR10G: | cds.KYUSt_ | genblast_C | Os10t057 | SECCE1Rv] | TraesCS1A | scaffold85 | TVU31537 |
| genblast_C | cds.KYUSt_ | genblast_C | Os03t027] | SECCE7Rv] | TraesCS4D | scaffold14 | TVU47600 |
| LPERR03G2 | genblast_C | ORUFI03G2 | Os03t059 | SECCE3Rv] | TraesCS3B | scaffold61 | TVU46234 |
| LPERR08G( | cds.KYUSt_ORUFI08G( | Os08t012 | SECCE7Rv] | TraesCS7B | scaffold63 | TVU43513 | |
| LPERR07G: | cds.KYUSt_ORUFI07G2 | Os07t056 | genblast_C | TraesCS2D | scaffold2.7 | TVU38365 | |
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| LPERR01G: | cds.KYUSt_ORUFI01G4 | Os01t095( | SECCE6Rv] | TraesCS3D | scaffold15 | TVU01875 | |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE1Rv | TraesCS1D | scaffold13 | TVU18225 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t079 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34834 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5B | scaffold25 | TVU45935 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | genblast_C | TraesCS4B | scaffold17 | TVU48213 |
| LPERR08G | genblast_C | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7A | scaffold23 | TVU43757 |
| LPERR09G | genblast_C | ORUFI09G | Os09t032 | SECCEUnv | TraesCS6D | scaffold19 | TVU00847 |
| genblast_C | genblast_C | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3A | scaffold16 | TVU37046 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7D | scaffold9. | TVU08665 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19622 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t048 | SECCE6Rv | TraesCS6D | scaffold27 | TVU39208 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | scaffold5. | TVU31707 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7D | scaffold60 | TVU01112 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold13 | TVU31796 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCE4Rv | TraesCS7D | scaffold16 | TVU03369 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold8. | TVU19293 |
| LPERR06G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS7B | scaffold17 | TVU12240 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t029 | SECCE4Rv | TraesCS7B | scaffold5. | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2A | scaffold21 | TVU14014 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold74 | TVU00571 |
| LPERR03G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2D | scaffold10 | TVU13244 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3B | scaffold11 | TVT98943 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3A | scaffold29 | TVU35363 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE2Rv | TraesCS6D | scaffold53 | TVU33614 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t086 | genblast_C | TraesCS5D | scaffold65 | genblast_C |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold94 | TVU15911 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4A | scaffold18 | TVU47111 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6D | scaffold19 | TVU03508 |
| LPERR12G | genblast_C | ORUFI12G | Os12t012 | SECCE4Rv | TraesCS4B | scaffold14 | TVU27165 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5A | scaffold3. | TVU02975 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2B | scaffold12 | TVU16612 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE6Rv | TraesCS7D | scaffold60 | TVU07594 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3A | scaffold59 | TVU22096 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t015 | SECCE7Rv | TraesCS4B | scaffold18 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold53 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold60 | TVU08633 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE3Rv | TraesCS6B | scaffold20 | TVU27599 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t063 | SECCE6Rv | TraesCS6D | scaffold10 | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4A | scaffold17 | TVU48186 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5B | scaffold24 | TVU09774 |

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| LPERR04G | genblast_C | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2B | scaffold32 | TVU16363 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv | TraesCS5A | scaffold34 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38136 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7A | scaffold92 | TVU08538 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold2. | TVU01167 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold24 | TVU33514 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold48 | TVU33422 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE4Rv | TraesCS1B | scaffold12 | TVU29943 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7D | scaffold41 | TVU08039 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t027 | SECCE7Rv | TraesCS4A | scaffold65 | TVU47601 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE1Rv | TraesCS1D | scaffold45 | TVU46666 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS5B | scaffold65 | TVU12823 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE3Rv | TraesCS6D | scaffold27 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21395 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold18 | TVU48368 |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | genblast_C | genblast_C | scaffold10 | TVU48357 |
| LPERR12G | genblast_Z | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold17 | TVU49938 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7B | scaffold14 | TVU12085 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold35 | TVU45346 |
| LPERR02G | genblast_C | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28147 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36452 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48491 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21564 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5A | scaffold28 | TVT97512 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold27 | TVU08860 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1B | scaffold19 | TVU20117 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3D | scaffold23 | TVU35877 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold39 | TVU44216 |
| LPERR02G | cds.KYUSt_ | ORUFI05G | Os02t017 | SECCE6Rv | TraesCS6B | scaffold18 | TVU32795 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4B | scaffold20 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold3. | TVU44516 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2A | scaffold32 | TVU16364 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold13 | TVU15317 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t044 | SECCE1Rv | TraesCS1D | scaffold57 | TVU30572 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t027 | SECCE7Rv | TraesCS4A | scaffold14 | TVU47529 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t038 | SECCE5Rv | TraesCS5A | scaffold14 | TVU09399 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t034 | SECCE5Rv | TraesCS5A | scaffold19 | TVU09245 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3D | scaffold4. | TVU21406 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6A | scaffold11 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold59 | TVU21655 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t017 | SECCE1Rv | TraesCS1A | scaffold19 | TVU17253 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12912 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t019 | SECCE5Rv | TraesCS5A | scaffold70 | TVU51317 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47449 |

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| LPERR05G | cds.KYUSt_ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47306 |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold48 | TVU33511 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6A | scaffold19 | TVU29226 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4D | scaffold97 | TVU47861 |
| LPERR01G | genblast_C | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3D | scaffold10 | TVU22470 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t049 | genblast_C | TraesCS2D | scaffold56 | TVU15367 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4A | scaffold3. | TVU45198 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35396 |
| genblast_C | cds.KYUSt_ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1B | scaffold80 | TVU20406 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6D | scaffold12 | TVU28174 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7D | scaffold54 | TVU04874 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4B | scaffold3. | TVU45259 |
| LPERR02G | genblast_C | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28208 |
| genblast_C | cds.KYUSt_ | genblast_C | Os02t073 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28463 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16371 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7B | scaffold17 | TVU47033 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold10 | TVU28016 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7B | scaffold34 | TVU12260 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE6Rv | TraesCS6A | scaffold83 | TVU51498 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold74 | TVU47347 |
| LPERR03G | genblast_C | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4D | scaffold74 | TVU47262 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t069 | genblast_C | TraesCS3A | scaffold15 | TVU03684 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold9. | TVU48046 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2A | scaffold23 | TVU38839 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t018 | genblast_C | TraesCS4A | scaffold39 | genblast_C |
| LPERR04G | genblast_C | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2A | scaffold36 | TVU16172 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t021 | SECCE7Rv | TraesCS4B | scaffold97 | genblast_C |
| LPERR06G | genblast_C | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7D | scaffold16 | TVU12207 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE4Rv | TraesCS6B | scaffold16 | TVU29108 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4A | scaffold22 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | SECCEUnv | TraesCS7B | scaffold33 | TVU08396 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t024 | SECCE4Rv | TraesCS7A | scaffold30 | TVU01671 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold84 | TVU35169 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold84 | TVU34422 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4D | scaffold22 | TVU47095 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t033 | SECCE7Rv | TraesCS7D | scaffold30 | TVU08994 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7D | scaffold9. | TVU08670 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold47 | TVU22236 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t022 | SECCE2Rv | TraesCS2B | scaffold83 | TVU51425 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE1Rv | TraesCS1B | scaffold73 | TVU45998 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t061 | SECCE2Rv | TraesCS2B | scaffold13 | TVU15784 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t026 | SECCE5Rv | TraesCS5A | scaffold4. | TVU43258 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6B | scaffold42 | TVU12928 |
| genblast_C | genblast_C | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6A | scaffold10 | TVU29062 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2D | genblast_C | TVU15005 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold28 | TVU28891 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15163 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold85 | TVU31737 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2D | scaffold67 | TVU37939 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5D | scaffold43 | TVU10201 |
| LPERR07G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE2Rv | TraesCS2A | scaffold43 | TVU38852 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t040 | SECCE4Rv | TraesCS7B | scaffold12 | TVU30974 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold31 | TVT98571 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6A | scaffold48 | TVU32841 |

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| LPERR12G | genblast_C | ORUFI12G | Os12t022 | SECCE7Rv | TraesCS7B | scaffold83 | TVU51411 |
| LPERR03G | genblast_Z | ORUFI03G | genblast_Z | SECCE4Rv | TraesCS4B | scaffold20 | TVU45138 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7A | scaffold20 | TVU43714 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv | TraesCS6A | scaffold17 | TVU02419 |
| LPERR02G | genblast_C | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6D | scaffold27 | TVU27796 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15351 |
| genblast_C | genblast_C | ORUFI04G | Os04t060 | SECCE5Rv | TraesCS5D | scaffold94 | TVU15837 |
| genblast_Z | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold14 | TVU36288 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44389 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2A | scaffold28 | TVU14654 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCEUnv | TraesCS6B | scaffold2. | TVU28303 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t051 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15289 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2D | scaffold31 | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold10 | TVU48318 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47746 |
| LPERR03G | genblast_C | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5D | scaffold17 | TVU44571 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3B | scaffold41 | TVU02359 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t038 | SECCE2Rv | TraesCS7A | scaffold46 | TVU03472 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold39 | TVU20036 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold2. | TVU28511 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t032 | SECCE4Rv | TraesCS7A | scaffold16 | TVU11402 |
| LPERR02G | genblast_C | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold46 | TVU27993 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold65 | TVU43933 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t033 | SECCE1Rv | TraesCS1B | scaffold12 | TVU18848 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold94 | TVU16011 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold87 | TVU09521 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1A | scaffold1. | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE7Rv | TraesCS2A | genblast_Z | TVU07022 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37853 |
| LPERR08G | cds.KYUSt_ | ORUFI05G | Os05t014 | SECCE1Rv | TraesCS1A | scaffold19 | TVU17864 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3B | scaffold14 | TVU36122 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold10 | TVU22558 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48218 |
| LPERR06G | genblast_C | ORUFI06G | Os06t053 | SECCE6Rv | TraesCS6A | genblast_C | TVU03161 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | scaffold85 | TVU31669 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold16 | TVU08855 |
| LPERR06G | genblast_C | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold16 | TVU07951 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t037 | SECCE4Rv | TraesCS7B | scaffold37 | TVU06395 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t013 | SECCE2Rv | TraesCS2B | scaffold12 | TVU41013 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6D | scaffold14 | genblast_C |
| LPERR12G | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5A | scaffold14 | TVU49116 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1B | scaffold11 | TVU30318 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t046 | SECCE5Rv | TraesCS5A | scaffold11 | TVU21148 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48216 |

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| LPERR12G | genblast_C | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5B | scaffold29 | TVU49696 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2D | scaffold67 | TVU03941 |
| genblast_C | genblast_C | genblast_C | Os10t057 | SECCE1Rv | TraesCS1A | scaffold5. | TVU31570 |
| genblast_C | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold46 | TVU34783 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t067 | SECCE4Rv | TraesCS4B | scaffold11 | TVU01548 |
| LPERR10G | genblast_C | ORUFI10G | Os10t018 | SECCE1Rv | TraesCS1A | scaffold82 | TVU31246 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t037 | SECCE5Rv | TraesCS5A | genblast_C | TVT99805 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5B | scaffold16 | TVU10186 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold14 | TVU15598 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47213 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE5Rv | TraesCS5B | scaffold53 | TVU09869 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t010 | genblast_C | TraesCS5A | scaffold31 | TVU27529 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1A | scaffold27 | TVU32177 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold10 | TVU28001 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4B | scaffold35 | genblast_C |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08780 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4A | genblast_C | genblast_C |
| LPERR03G | genblast_C | ORUFI03G | Os03t065 | genblast_C | TraesCS4D | scaffold20 | TVU45859 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t052 | SECCE6Rv | TraesCS6A | genblast_C | TVT99483 |
| LPERR02G | genblast_C | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6A | scaffold13 | TVU29363 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold17 | TVU16659 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35240 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6A | scaffold2. | TVU28493 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1B | scaffold52 | TVU31698 |
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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t016 | SECCE5Rv | TraesCS5D | scaffold29 | genblast_C |
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| LPERR02G | genblast_C | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6D | scaffold45 | TVU01698 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold14 | TVU47581 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3A | scaffold59 | TVU22119 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t021 | SECCE6Rv | TraesCS6A | scaffold6. | TVU33095 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t024 | SECCE7Rv | TraesCS4A | scaffold23 | TVU47741 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4D | scaffold11 | TVU45411 |
| LPERR07G | genblast_C | ORUFI07G | genblast_C | SECCE6Rv | TraesCS5B | scaffold12 | TVU41062 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold49 | TVU42473 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t052 | SECCE3Rv | TraesCS3B | scaffold14 | TVU25232 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4A | scaffold10 | genblast_C |
| genblast_Z | genblast_Z | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold89 | TVU36028 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2B | scaffold1. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI01G | Os03t039 | SECCE1Rv | TraesCS1A | scaffold45 | TVU46670 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t054 | SECCEUnv | TraesCS5D | scaffold22 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6A | scaffold98 | TVU33579 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t051 | SECCE1Rv | TraesCS1B | scaffold49 | TVU20602 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold19 | TVU21489 |
| LPERR01G | genblast_C | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3A | scaffold21 | TVU35598 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5D | scaffold27 | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t077 | genblast_C | TraesCS3D | scaffold48 | TVU34906 |
| LPERR02G | genblast_C | ORUFI02G | Os02t073 | SECCEUnv | TraesCS6B | scaffold2. | TVU28360 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold12 | TVU20032 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5D | scaffold16 | TVU10421 |
| LPERR06G | cds.KYUSt_ | ORUFI11G | Os06t010 | SECCE6Rv | TraesCS7D | scaffold42 | TVU12947 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv | TraesCS5A | scaffold34 | TVU48624 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold26 | TVU05079 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS4A | scaffold44 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold3. | TVU10457 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t038 | SECCE6Rv | TraesCS6A | scaffold33 | TVU20774 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1B | scaffold10 | TVU32181 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t051 | SECCE5Rv | TraesCS5D | scaffold12 | TVT99857 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1D | scaffold13 | TVU20265 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2D | scaffold14 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold55 | TVU45549 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6A | scaffold1. | TVU32919 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE4Rv | TraesCS7B | scaffold24 | TVU11810 |
| LPERR01G | genblast_C | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3A | scaffold41 | TVU02374 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2B | scaffold58 | genblast_C |
| LPERR07G | genblast_C | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2A | scaffold67 | TVU37525 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | genblast_C | TraesCS4A | scaffold9. | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | scaffold11 | TVU32146 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6D | scaffold17 | TVU03004 |
| genblast_Z | genblast_Z | genblast_Z | genblast_Z | SECCE2Rv | TraesCS2B | scaffold30 | TVU14111 |
| LPERR07G | genblast_C | ORUFI07G | Os07t044 | SECCE1Rv | TraesCS1B | scaffold3. | TVU39529 |
| LPERR10G | genblast_C | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47998 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t057 | SECCE7Rv | TraesCS7A | scaffold25 | genblast_C |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3A | scaffold18 | TVU21627 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold16 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38006 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1B | scaffold14 | TVU19353 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t010 | SECCE5Rv | TraesCS5A | scaffold12 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15966 |
| LPERR04G | genblast_C | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14426 |

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| LPERR05G | genblast_C | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1D | scaffold8. | TVU19329 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE7Rv | TraesCS5D | scaffold3. | TVT96981 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold24 | TVU09656 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30298 |
| LPERR05G | genblast_C | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1B | scaffold23 | TVU19392 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1B | scaffold68 | TVU21439 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t070 | SECCE4Rv | TraesCS4B | scaffold36 | TVU45444 |
| LPERR05G | genblast_C | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19823 |
| LPERR04G | genblast_C | ORUFI04G | Os04t058 | SECCEUnv | TraesCS2B | scaffold49 | TVU15968 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6A | scaffold2. | TVU28460 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE5Rv | TraesCS5A | scaffold17 | TVU42986 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os12t019 | SECCE5Rv | TraesCS5A | scaffold83 | TVU51363 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t022 | SECCE6Rv | TraesCS7B | scaffold10 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t093 | SECCE6Rv | TraesCS3A | scaffold18 | TVU11355 |

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| LPERR02G | cds.KYUSt_ | genblast_C | Os02t017 | SECCE6Rv | TraesCS6A | scaffold39 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCSU0 | scaffold25 | TVU45971 |
| LPERR02G | genblast_C | ORUFI02G | Os02t025 | SECCE7Rv | TraesCS7D | scaffold50 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t068 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35475 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE2Rv | TraesCS5D | scaffold31 | TVU01187 |
| LPERR01G | genblast_C | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3A | scaffold78 | TVU37009 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t068 | SECCE4Rv | TraesCS4D | scaffold29 | TVU23477 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t062 | SECCE5Rv | TraesCS5D | scaffold1. | TVU48911 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCE1Rv | TraesCS1D | scaffold27 | TVU32206 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCEUnv | TraesCS4D | scaffold44 | TVU06006 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t030 | SECCE5Rv | TraesCS5B | scaffold20 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3D | scaffold15 | TVU37001 |
| LPERR08G | cds.KYUSt_ | ORUFI06G | Os08t044 | SECCE4Rv | TraesCS7D | scaffold13 | TVU05675 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3B | scaffold11 | TVU34857 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t056 | SECCE6Rv | TraesCS3B | scaffold11 | TVU34148 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t017 | SECCE5Rv | TraesCS5A | scaffold10 | TVU41666 |
| LPERR03G | cds.KYUSt_genblast_C | Os03t083 | SECCE7Rv | TraesCS4A | scaffold65 | TVU44012 |
| LPERR08G | cds.KYUSt_ORUFI08G | genblast_C | SECCE7Rv | TraesCS7A | scaffold25 | TVU43467 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t020 | SECCE3Rv | TraesCS3B | scaffold84 | TVU16987 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1D | scaffold13 | TVU17153 |
| LPERR12G | cds.KYUSt_ORUFI12G | genblast_C | SECCE5Rv | TraesCS5B | scaffold76 | TVU49246 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t015 | genblast_C | TraesCS4A | scaffold11 | TVT97883 |
|  |  |  |  |  |  |  |
| LPERR05G | genblast_CORUFI10G | Os10t035 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19723 |
| LPERR02G | cds.KYUSt_genblast_C | Os02t080 | SECCE5Rv | TraesCS4D | scaffold2. | TVU27884 |
|  |  |  |  |  |  |  |
| LPERR06G | genblast_CORUFI06G | Os06t013 | SECCE4Rv | TraesCS4A | scaffold16 | TVU12832 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t064 | SECCE6Rv | TraesCS7D | scaffold92 | TVU08292 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold46 | TVU36585 |
|  |  |  |  |  |  |  |
| genblast_C | cds.KYUSt_ORUFI04G | Os04t047 | SECCE6Rv | TraesCS2D | scaffold14 | TVU15597 |
| LPERR04G | cds.KYUSt_ORUFI10G | Os10t035 | SECCE7Rv | TraesCS2D | scaffold94 | TVU16051 |
| LPERR08G | cds.KYUSt_ORUFI08G | genblast_C | SECCE7Rv | TraesCS7B | scaffold30 | TVU06295 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6B | scaffold24 | TVU27945 |
| genblast_C | genblast_CORUFI10G | Os10t050 | SECCE1Rv | TraesCS1B | scaffold37 | TVU32051 |
|  |  |  |  |  |  |  |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5A | scaffold1. | TVU49983 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6A | scaffold98 | TVU33672 |
|  |  |  |  |  |  |  |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47702 |
| genblast_C | cds.KYUSt_ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1B | scaffold13 | TVU18087 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t021 | SECCE5Rv | TraesCS5D | scaffold40 | TVU16990 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold13 | genblast_C |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3B | scaffold4. | TVU22745 |
|  |  |  |  |  |  |  |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7A | scaffold44 | TVU11992 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5A | scaffold17 | TVU29833 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t053 | SECCEUnv | TraesCS2D | scaffold49 | TVT98053 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold26 | TVU35821 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t058 | SECCE1Rv | TraesCS3B | scaffold11 | TVU34322 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5B | scaffold11 | TVU45897 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3D | scaffold89 | TVU01675 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5A | scaffold20 | TVU45913 |
| LPERR07G | genblast_C | ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2D | scaffold63 | TVU41371 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | genblast_C | TraesCS3A | scaffold13 | TVU34525 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3B | scaffold36 | TVU21445 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4D | scaffold3. | TVU45225 |
| LPERR01G | genblast_C | ORUFI08G | Os08t023 | SECCE5Rv | TraesCS5A | scaffold28 | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t049 | genblast_C | TraesCS5D | scaffold16 | TVU10102 |
| LPERR03G | genblast_C | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4B | scaffold22 | TVU47133 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE6Rv | TraesCS6D | scaffold7. | TVU47064 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t041 | genblast_C | TraesCS5D | scaffold11 | TVU09507 |
| LPERR10G | genblast_C | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1D | scaffold32 | TVU31533 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6B | scaffold26 | TVU28995 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t035 | SECCE7Rv | TraesCS7A | scaffold33 | TVU10707 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19323 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t040 | SECCE6Rv | TraesCS3D | scaffold45 | TVU46610 |

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|---|---|---|---|---|---|---|---|
| LPERR10G | genblast_C | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30346 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7D | scaffold34 | TVU12569 |
| LPERR12G | genblast_C | ORUFI12G | genblast_C | SECCE2Rv | TraesCS2A | scaffold63 | TVU50236 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t027 | SECCE5Rv | TraesCS5B | scaffold74 | TVU45107 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold45 | TVU02323 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold11 | TVU28635 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t035 | SECCE7Rv | TraesCS7D | scaffold82 | genblast_C |
| LPERR04G | genblast_C | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold49 | TVU16018 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCE5Rv | TraesCS4D | scaffold12 | TVU48669 |
| LPERR01G | cds.KYUSt_ | genblast_C | genblast_C | SECCE3Rv | TraesCS3D | scaffold33 | TVU36295 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t038 | SECCE6Rv | TraesCS7D | scaffold82 | TVU30893 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t054 | SECCE4Rv | TraesCS4B | scaffold37 | TVU24704 |
| LPERR06G | cds.KYUSt_ | genblast_ | Os06t060 | SECCE7Rv | TraesCS7B | scaffold32 | TVU08084 |
| LPERR03G | genblast_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold17 | genblast_ |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7A | scaffold60 | TVU08636 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1D | scaffold45 | TVU31894 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t023 | SECCE6Rv | TraesCS6D | scaffold42 | TVU33193 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE6Rv | TraesCS7B | scaffold12 | TVU08263 |
| LPERR11G | cds.KYUSt_ | ORUFI06G | Os06t052 | SECCE4Rv | TraesCS7B | scaffold18 | TVU39085 |
| genblast_ | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1B | scaffold13 | TVT99003 |
| LPERR03G | genblast_ | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4A | scaffold74 | TVU47231 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t035 | SECCE7Rv | TraesCS7D | scaffold22 | TVU37424 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t034 | SECCE2Rv | TraesCS2D | scaffold74 | TVU47047 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3A | scaffold4. | TVU21385 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t058 | SECCE3Rv | TraesCS3B | scaffold29 | TVU34326 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2D | scaffold67 | TVU38068 |
| genblast_ | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35398 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold2. | genblast_ |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold15 | TVU47845 |
| LPERR01G | genblast_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS5A | scaffold15 | TVU35411 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | genblast_ | genblast_ | scaffold14 | TVU26741 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold22 | TVU07615 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t037 | SECCE5Rv | TraesCS5D | scaffold98 | TVU09342 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold75 | TVU20031 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE2Rv | TraesCS2B | scaffold17 | genblast_ |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t020 | genblast_ | TraesCS6A | scaffold11 | TVU34584 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2A | scaffold30 | TVU37869 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6B | scaffold24 | TVU27967 |

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| LPERR03G | cds.KYUSt_ | genblast_C | Os03t079 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44576 |
| LPERR07G | genblast_C | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2D | scaffold67 | TVU37928 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1B | scaffold1. | TVU32034 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os11t012 | SECCE5Rv | TraesCS5D | scaffold96 | TVU50659 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1A | scaffold80 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t020 | SECCE4Rv | TraesCS4D | scaffold59 | TVU51268 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold25 | TVU03221 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t022 | SECCE1Rv | TraesCS1A | scaffold40 | TVU16920 |
| LPERR05G | genblast_C | ORUFI05G | Os05t021 | genblast_C | genblast_C | scaffold40 | TVU20264 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t010 | SECCE1Rv | TraesCS1A | scaffold13 | TVU18437 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t036 | SECCE3Rv | TraesCS3B | scaffold28 | TVU07079 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t031 | SECCE1Rv | TraesCS1B | scaffold10 | TVU18705 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold63 | TVU21599 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5D | scaffold43 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6D | scaffold1. | TVU32895 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE7Rv | genblast_C | scaffold22 | TVU14142 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold31 | TVU50641 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t016 | SECCE1Rv | TraesCS1B | scaffold36 | TVU17332 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2D | scaffold40 | TVU15001 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1A | scaffold1. | TVU32004 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t015 | SECCE5Rv | TraesCS5A | scaffold70 | TVU04432 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1B | scaffold36 | TVU19169 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t055 | SECCE2Rv | TraesCS2A | scaffold96 | TVU38504 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | TraesCS7B | scaffold17 | TVU12274 |
| LPERR04G | cds.KYUSt_ | ORUFI10G | Os10t012 | SECCE2Rv | TraesCSU0 | scaffold19 | TVU39814 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t073 | SECCE3Rv | TraesCS3D | genblast_C | TVU35196 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS3D | scaffold11 | TVU23215 |

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| LPERR02G | cds.KYUSt_ | genblast_C | Os06t068 | SECCE6Rv | TraesCS6D | scaffold48 | TVU32686 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t024 | genblast_C | genblast_C | scaffold6. | TVU33232 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1D | scaffold11 | TVU17791 |
| LPERR07G | genblast_C | ORUFI07G | Os07t050 | SECCE6Rv | TraesCS2A | scaffold27 | TVU39021 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t012 | SECCE2Rv | TraesCS2D | scaffold12 | TVU40866 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2A | scaffold87 | TVU14812 |
| LPERR01G | genblast_C | ORUFI01G | Os01t059 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34355 |

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| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold1. | TVU20149 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1A | scaffold13 | TVU20342 |

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| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2A | scaffold10 | TVU13939 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19836 |
| LPERR02G | genblast_C | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold1. | TVU32661 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5A | scaffold17 | genblast_C |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold22 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE1Rv | TraesCS4D | scaffold61 | TVU46141 |
| LPERR05G | genblast_C | ORUFI05G | Os05t013 | genblast_C | TraesCS5D | scaffold13 | TVU18027 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1D | scaffold1. | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | genblast_C | TVU33430 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29295 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t048 | SECCE4Rv | TraesCS7B | scaffold16 | TVU39081 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1D | scaffold5. | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t012 | SECCE5Rv | TraesCS5B | scaffold14 | TVU10833 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold53 | TVU09761 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4B | scaffold74 | TVU47415 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3B | scaffold11 | TVU35947 |
| LPERR12G | genblast_C | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5D | scaffold24 | TVU49752 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1B | scaffold1. | TVU00546 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1D | scaffold1. | genblast_C |
| genblast_C | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold19 | TVU17799 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37340 |
| LPERR03G | genblast_C | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44381 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t026 | SECCE2Rv | TraesCS2B | scaffold20 | TVU42238 |
| LPERR03G | cds.KYUSt_ | ORUFI10G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold22 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4A | scaffold97 | TVU47841 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48470 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34905 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t062 | SECCE7Rv | TraesCS7D | scaffold19 | TVU23962 |
| LPERR07G | genblast_C | ORUFI07G | Os07t022 | SECCE2Rv | TraesCS2D | scaffold23 | TVU39993 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5A | scaffold27 | TVT98641 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09860 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2A | scaffold16 | TVU37349 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold2. | TVU27955 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t090 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36103 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5A | scaffold53 | TVU09802 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold40 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6D | scaffold48 | TVU32844 |
| LPERR04G | genblast_C | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16295 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3B | scaffold84 | TVU35140 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t041 | SECCE5Rv | TraesCS5D | scaffold87 | TVU09518 |
| LPERR06G | cds.KYUSt_ORUFI02G | Os06t017 | SECCE5Rv | TraesCS5D | scaffold45 | TVU02335 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t066 | SECCE7Rv | TraesCS7A | scaffold33 | TVU08441 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_ | SECCE7Rv | TraesCS4D | scaffold9. | TVU47765 |
| genblast_C | cds.KYUSt_ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1B | scaffold1. | TVU00556 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t032 | SECCE7Rv | TraesCS7D | scaffold14 | TVU30721 |
| LPERR12G | cds.KYUSt_ORUFI12G | genblast_ | SECCE5Rv | TraesCS5A | scaffold29 | TVU49266 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6A | scaffold17 | TVU29080 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_ | SECCE1Rv | TraesCS1D | scaffold36 | TVU18925 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t054 | SECCE5Rv | TraesCS5A | scaffold22 | TVU49884 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t050 | SECCE5Rv | TraesCS5B | scaffold40 | TVU50130 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t024 | SECCE6Rv | TraesCS6D | scaffold51 | TVU33240 |
| LPERR02G | genblast_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6A | scaffold12 | TVU28152 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold60 | TVU07623 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3B | scaffold22 | TVU34995 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2D | scaffold94 | TVU14981 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3A | scaffold13 | TVU03696 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv | TraesCS3D | scaffold88 | TVU21733 |
| LPERR12G | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5D | scaffold41 | TVU49064 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48115 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28293 |
| LPERR03G | genblast_C | ORUFI03G | Os03t065 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45822 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t046 | SECCE7Rv | TraesCS5D | scaffold41 | TVU50386 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1B | scaffold23 | TVU19451 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7A | scaffold9. | TVU07551 |

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| genblast_C | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2D | scaffold9. | TVT97793 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t024 | SECCEUnv | TraesCS2B | scaffold20 | TVU42129 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36663 |
| LPERR02G | cds.KYUSt_ | genblast_C | genblast_C | SECCE6Rv | TraesCS6B | scaffold26 | TVU28948 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE1Rv | TraesCS1D | scaffold1. | TVU32132 |
| LPERR02G | genblast_C | genblast_C | Os02t076 | SECCE6Rv | TraesCS6D | scaffold22 | TVU28690 |
| LPERR11G | genblast_C | genblast_C | Os11t029 | SECCE4Rv | TraesCS4B | scaffold16 | TVU25785 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6B | scaffold11 | TVU33648 |
| LPERR02G | genblast_C | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29183 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t030 | SECCE4Rv | TraesCS7B | scaffold30 | TVU11460 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os06t070 | SECCE6Rv | TraesCS6D | scaffold48 | TVU33482 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1D | scaffold20 | TVU19356 |
| LPERR02G | genblast_C | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6D | scaffold19 | TVU29190 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4A | scaffold40 | TVU47659 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t011 | SECCE7Rv | TraesCS4B | scaffold26 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE5Rv | TraesCS5A | scaffold52 | TVU48448 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49123 |
| genblast_C | genblast_C | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold38 | TVT99557 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6A | scaffold2. | TVT99951 |
| genblast_Z | genblast_Z | genblast_Z | genblast_Z | SECCE3Rv | TraesCS3B | scaffold63 | TVU21365 |
| LPERR09G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCEUnv | TraesCS4B | scaffold5. | TVU11842 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE1Rv | TraesCS1B | scaffold14 | TVU26759 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3D | scaffold18 | TVU34605 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t018 | SECCE4Rv | genblast_C | scaffold17 | TVU12292 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5B | scaffold29 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t023 | SECCE1Rv | TraesCS1D | scaffold86 | TVU42054 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5A | scaffold24 | TVU49755 |
| genblast_Z | cds.KYUSt_ | ORUFI10G | genblast_Z | SECCE1Rv | TraesCS1A | scaffold85 | TVU31639 |
| LPERR10G | genblast_C | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1B | scaffold16 | TVU30448 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE4Rv | TraesCS4D | scaffold50 | TVU50852 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE5Rv | TraesCS5D | scaffold24 | TVU49598 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5D | scaffold53 | TVU09834 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold10 | TVU28973 |

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| LPERR06G | genblast_C | ORUFI06G | genblast_C | genblast_C | TraesCS7A | scaffold22 | TVU07660 |
| LPERR07G | genblast_C | ORUFI07G | Os07t058 | SECCE2Rv1 | TraesCS2B | scaffold67 | TVU03940 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv1 | TraesCS4B | scaffold15 | TVU48069 |
| LPERR08G | genblast_C | ORUFI08G | Os08t036 | SECCE6Rv1 | TraesCS6B | scaffold20 | TVU06459 |
| LPERR02G | genblast_C | ORUFI02G | Os02t081 | SECCE6Rv1 | TraesCS6B | scaffold20 | TVU27706 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv1 | TraesCS4D | scaffold23 | TVU47756 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv1 | TraesCS6B | scaffold22 | TVU36958 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv1 | TraesCS7D | scaffold10 | TVU12079 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv1 | TraesCS3D | scaffold15 | TVU35292 |
| LPERR02G | genblast_C | ORUFI02G | Os02t056 | SECCE1Rv1 | TraesCS1B | scaffold17 | TVU29612 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os11t049 | SECCE2Rv1 | TraesCS2A | scaffold88 | TVU34675 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv1 | TraesCS7A | scaffold27 | TVU11363 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv1 | TraesCS2D | scaffold13 | TVU15756 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv1 | TraesCS3A | scaffold10 | TVU22492 |
| LPERR09G | genblast_C | ORUFI09G | Os09t049 | SECCE5Rv1 | TraesCS5A | scaffold53 | TVU10088 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv1 | TraesCS2D | scaffold49 | TVU02403 |
| LPERR04G | genblast_C | ORUFI04G | Os04t037 | SECCE2Rv1 | TraesCS2A | scaffold18 | TVU13889 |
| LPERR05G | genblast_C | ORUFI05G | Os05t051 | SECCE1Rv1 | TraesCS1A | scaffold32 | TVU20642 |

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| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2D | scaffold14 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4D | scaffold52 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t058 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29512 |
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| LPERR04G | genblast_C | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15775 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1D | scaffold11 | TVU32215 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_Z | SECCE7Rv | TraesCS7A | scaffold9. | TVU07722 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t011 | SECCE4Rv | TraesCS4D | scaffold50 | TVU31824 |
| genblast_Z | cds.KYUSt_ | ORUFI05G | genblast_Z | genblast_Z | TraesCS1B | scaffold40 | TVU16993 |
| LPERR05G | cds.KYUSt_ | ORUFI11G | Os11t027 | SECCEUnv | TraesCS6D | scaffold38 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6B | scaffold45 | TVU28270 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3B | scaffold36 | TVU22868 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t021 | SECCE6Rv | TraesCS6D | scaffold51 | TVU33107 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7A | scaffold33 | TVU43694 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t057 | SECCE2Rv | TraesCS2D | scaffold5. | TVU29545 |
| LPERR10G | genblast_C | ORUFI10G | Os10t043 | SECCE1Rv | TraesCS1B | scaffold57 | TVU01129 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16463 |
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| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16325 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t035 | SECCE3Rv | TraesCS3A | scaffold4. | TVU20952 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t015 | SECCE5Rv | TraesCS5A | scaffold14 | TVT98100 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5D | scaffold17 | TVU44528 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6A | scaffold22 | genblast_C |
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| LPERR05G | genblast_C | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1B | scaffold58 | TVU19936 |
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| LPERR10G | cds.KYUSt_ | genblast_C | Os10t049 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11212 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold8. | TVU14228 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold2. | TVU28245 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4A | scaffold15 | TVU48194 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold49 | TVU47332 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t016 | SECCEUnv | TraesCS7B | scaffold83 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold14 | TVU13764 |
| LPERR03G | genblast_C | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44841 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t031 | SECCE5Rv | TraesCS5D | scaffold16 | TVU09112 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4A | scaffold50 | TVU26684 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCEUnv | TraesCS5B | scaffold29 | TVU49346 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t043 | SECCE1Rv | TraesCS1A | scaffold38 | TVU09038 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCSU0 | scaffold20 | TVU33610 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15003 |
| LPERR01G | genblast_C | ORUFI01G | Os01t030 | SECCE1Rv | TraesCS1D | scaffold39 | TVU20570 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6A | scaffold17 | genblast_C |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t096 | SECCE6Rv | TraesCS3B | scaffold15 | TVU36991 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6D | scaffold98 | TVU33652 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5D | scaffold35 | TVU45123 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t012 | SECCE5Rv | TraesCS4B | scaffold25 | TVU48589 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16599 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7A | scaffold26 | TVU43655 |
| genblast_Z | cds.KYUSt_genblast_Z | genblast_Z | SECCE5Rv | TraesCS5D | scaffold70 | TVU03530 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t038 | SECCE4Rv | TraesCS4B | scaffold18 | TVU46792 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37453 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold29 | TVU48465 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t043 | SECCE1Rv | TraesCS1D | scaffold20 | genblast_ |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28203 |
| LPERR02G | genblast_CORUFI02G | Os02t066 | SECCE6Rv | TraesCS6A | scaffold24 | TVU28927 |

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| LPERR05G | cds.KYUSt_ORUFI05G | Os05t047 | SECCE1Rv | TraesCS1B | scaffold75 | TVU19832 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7D | scaffold10 | TVU12208 |
| genblast_C | cds.KYUSt_genblast_C | Os02t077 | SECCE6Rv | TraesCS6A | scaffold17 | TVU28701 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold15 | TVU47825 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4D | scaffold97 | TVU47830 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t056 | SECCE5Rv | TraesCS5D | scaffold3. | TVU10508 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3A | scaffold46 | TVU34851 |

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| LPERR04G | cds.KYUSt_ | genblast_C | Os04t046 | genblast_C | TraesCS2A | scaffold77 | TVU14109 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7D | scaffold30 | TVU11848 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold14 | TVU36144 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold9. | TVU47789 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t041 | SECCE1Rv | TraesCS1A | scaffold19 | TVT99184 |
| LPERR06G | genblast_Z | ORUFI06G | genblast_Z | SECCE4Rv | TraesCS7B | scaffold45 | TVU12361 |
| LPERR05G | genblast_C | ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | scaffold13 | TVU31801 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE3Rv | TraesCS3D | scaffold24 | TVU33821 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold27 | TVU08843 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE6Rv | TraesCS3D | scaffold31 | TVU34695 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t056 | SECCEUnv | TraesCS1D | scaffold3. | TVT97466 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold33 | TVU09978 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37538 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold75 | TVU19904 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t049 | SECCEUnv | TraesCS4B | scaffold34 | TVU25386 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47483 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t056 | SECCE1Rv | TraesCS1D | scaffold41 | TVU29619 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4D | scaffold53 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2D | scaffold8. | TVU00299 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE4Rv | TraesCS4D | scaffold45 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3D | scaffold14 | TVU35253 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE5Rv | TraesCS4B | scaffold10 | TVU48446 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1A | scaffold75 | TVU20039 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2B | scaffold30 | TVU15090 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2B | scaffold52 | TVU14671 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t017 | SECCE5Rv | TraesCS5B | scaffold83 | TVU51188 |
| LPERR03G | genblast_C | ORUFI03G | Os03t068 | SECCE4Rv | TraesCS4D | scaffold55 | TVU45653 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t052 | SECCE5Rv | TraesCS5A | scaffold17 | TVU50000 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t062 | SECCE5Rv | TraesCS5D | scaffold15 | TVU48967 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t010 | SECCEUnv | TraesCS7D | scaffold42 | TVT99321 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16573 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t018 | SECCE3Rv | TraesCS3A | scaffold36 | TVU21505 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6D | scaffold20 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t081 | SECCE3Rv | genblast_C | scaffold46 | TVU36584 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3D | scaffold88 | TVU21959 |

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| LPERR12G | genblast_C | ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5A | scaffold22 | TVU49975 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t049 | SECCE5Rv | TraesCS5B | scaffold16 | TVU50194 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t048 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15499 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6D | scaffold20 | TVU27767 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7A | scaffold54 | TVU04729 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29475 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold29 | TVU08947 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t011 | SECCE1Rv | TraesCS1D | scaffold65 | TVU44545 |
| genblast_Z | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1D | genblast_Z | TVU17898 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os02t051 | SECCE2Rv | TraesCS2A | scaffold21 | TVU29975 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09859 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold84 | TVU28571 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3B | scaffold17 | TVU35093 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t026 | SECCE1Rv | TraesCS1A | scaffold20 | TVU42259 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold16 | TVU10228 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3A | genblast_C | TVU36391 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2A | scaffold16 | TVU16512 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | TVU41326 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t016 | SECCE1Rv | TraesCS1A | scaffold13 | TVU17398 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | genblast_C | TVU21631 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t013 | SECCE7Rv | TraesCS7D | scaffold25 | TVU43429 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold15 | TVU35605 |
| genblast_C | genblast_C | ORUFI03G | Os03t032 | genblast_C | TraesCS4B | scaffold18 | TVU47227 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold27 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6B | scaffold45 | TVU28259 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS7D | scaffold28 | TVU41724 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t013 | SECCEUnv | TraesCS6B | scaffold48 | TVU33540 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3A | scaffold39 | TVU36142 |
| LPERR04G | genblast_C | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16490 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1B | scaffold11 | TVU30321 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3B | scaffold15 | TVU22176 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1A | scaffold85 | TVU31740 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44992 |
| LPERR04G | genblast_C | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2A | scaffold56 | TVU15485 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1B | genblast_C | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4B | scaffold74 | TVU47096 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t022 | genblast_C | TraesCS4D | scaffold9. | TVU47857 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1D | scaffold75 | TVU19747 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t051 | SECCE2Rv | TraesCS2A | scaffold20 | TVU15226 |
| LPERR07G | genblast_C | ORUFI07G | Os07t069 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37108 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv | TraesCS7B | scaffold33 | TVU43698 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4A | scaffold18 | TVU47284 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4B | scaffold16 | TVU46651 |
| LPERR08G | genblast_C | ORUFI08G | Os08t026 | SECCE4Rv | TraesCS7A | scaffold23 | TVU42244 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t018 | SECCE4Rv | TraesCS4A | scaffold39 | TVU02650 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3B | scaffold18 | TVU21593 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE7Rv | TraesCS4A | scaffold25 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t026 | SECCE5Rv | TraesCS5B | scaffold12 | TVU39704 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5A | scaffold11 | TVU09675 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold10 | TVU28588 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold55 | TVU28621 |
| genblast_C | cds.KYUSt_ | genblast_C | Os06t063 | SECCE7Rv | TraesCS7B | scaffold12 | TVU08244 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold89 | TVU36007 |
| LPERR09G | genblast_C | ORUFI09G | Os09t037 | SECCE5Rv | TraesCS5A | scaffold14 | TVU09345 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold77 | TVU14496 |
| LPERR01G | genblast_C | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3D | genblast_C | TVU35084 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2D | scaffold49 | TVU15150 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4B | scaffold10 | TVU48212 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5A | scaffold11 | TVU09743 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os06t011 | SECCE4Rv | TraesCS7D | scaffold10 | TVT98608 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1B | scaffold45 | TVU31799 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold70 | TVU50998 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE6Rv | TraesCS6A | scaffold13 | TVU20142 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1D | scaffold7. | TVU31895 |
| LPERR10G | genblast_C | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1B | scaffold16 | TVU30315 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold43 | TVU38384 |
| LPERR01G | cds.KYUSt_ | genblast_C | genblast_C | genblast_C | TraesCS1D | scaffold16 | TVU13443 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold27 | TVU27668 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5B | scaffold70 | TVU50996 |
| LPERR01G | genblast_C | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3D | scaffold18 | TVU18714 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t013 | SECCE3Rv | TraesCS3D | scaffold59 | TVU22062 |

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| LPERR02G( | genblast_C | ORUFI02G: | Os02t024! | SECCE6Rv1 | TraesCS6D | scaffold42 | TVU33243 |
| LPERR08G( | cds.KYUSt_ | ORUFI08G: | Os08t029( | SECCE1Rv1 | TraesCS1D | genblast_C | TVU46549 |
| LPERR09G: | cds.KYUSt_ | genblast_C | Os09t050⁴ | SECCE5Rv1 | TraesCS5B | scaffold16 | TVU08826 |
| LPERR06G: | cds.KYUSt_ | genblast_C | Os06t065: | SECCE6Rv1 | TraesCS7A | scaffold92 | TVU08350 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t059⁴ | SECCE2Rv1 | TraesCS2D | scaffold94 | TVU15915 |
| LPERR12G: | cds.KYUSt_ | ORUFI12G: | genblast_C | SECCEUnv1 | TraesCS5B | scaffold29 | TVU49409 |
| LPERR02G( | cds.KYUSt_ | ORUFI02G( | Os02t010: | SECCE4Rv1 | TraesCS6B | scaffold19 | TVU33721 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t070: | SECCE4Rv1 | TraesCS4B | scaffold20 | TVU45512 |
| LPERR08G: | cds.KYUSt_ | ORUFI08G: | genblast_Z | SECCE7Rv1 | TraesCS7A | scaffold15 | TVU04664 |
| LPERR03G: | genblast_C | ORUFI03G: | genblast_C | SECCE4Rv1 | TraesCS4D | scaffold3.: | TVU45337 |
| LPERR05G( | cds.KYUSt_ | ORUFI06G: | Os06t030{ | SECCE1Rv1 | TraesCS1B | scaffold14 | TVU18485 |
| LPERR06G: | cds.KYUSt_ | ORUFI06G: | Os06t029: | SECCE4Rv1 | TraesCS7D | scaffold68 | TVU11577 |
| LPERR07G: | cds.KYUSt_ | ORUFI07G: | Os07t056: | SECCE2Rv1 | TraesCS2B | scaffold2.: | TVU38386 |
| LPERR05G: | cds.KYUSt_ | ORUFI05G: | Os05t051! | SECCE1Rv1 | TraesCS1B | scaffold32 | TVU20617 |
| LPERR06G: | cds.KYUSt_ | ORUFI06G: | Os06t070( | SECCE7Rv1 | TraesCS7B | scaffold22 | TVU07743 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t064! | SECCE2Rv1 | TraesCS2B | scaffold32 | TVU16370 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G: | Os01t082! | SECCE3Rv1 | TraesCS3B | scaffold31 | TVU36658 |
| LPERR11G( | cds.KYUSt_ | ORUFI11G( | Os11t016: | SECCE4Rv1 | TraesCS4B | scaffold12 | TVU26716 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G: | genblast_Z | SECCE3Rv1 | TraesCS3A | scaffold86 | TVU34108 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G⁴ | genblast_Z | SECCE3Rv1 | TraesCS3B | scaffold39 | TVU36169 |
| genblast_C | cds.KYUSt_ | ORUFI02G: | Os02t033: | SECCE6Rv1 | TraesCS6B | scaffold55 | TVU30247 |
| genblast_C | cds.KYUSt_ | ORUFI02G: | Os02t079{ | SECCE6Rv1 | TraesCS6A | scaffold38 | TVU27880 |
| genblast_C | cds.KYUSt_ | ORUFI03G( | Os03t011( | SECCE6Rv1 | TraesCS6B | scaffold25 | TVU48617 |
| LPERR02G( | cds.KYUSt_ | ORUFI02G( | Os02t013: | SECCE6Rv1 | TraesCS6D | scaffold98 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI07G: | Os07t047: | SECCE5Rv1 | TraesCS5D | scaffold27 | TVU21375 |
| LPERR02G: | cds.KYUSt_ | genblast_C | Os02t076: | SECCE6Rv1 | TraesCS6D | scaffold22 | TVU28623 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4D | scaffold10 | TVU48240 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os11t029 | SECCE7Rv | TraesCS4B | scaffold10 | TVU51497 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t014 | SECCE1Rv | TraesCS1D | scaffold25 | TVU43415 |
| LPERR05G | cds.KYUSt_genblast_C | Os05t042 | SECCE1Rv | TraesCS1B | scaffold20 | TVT98324 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5A | scaffold53 | genblast_ |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38388 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCE6Rv | TraesCS3A | scaffold18 | TVU37000 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t070 | SECCE6Rv | TraesCS6D | genblast_C | TVT98946 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2B | scaffold94 | TVU14993 |

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| LPERR01G | cds.KYUSt_ | ORUFI09G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36757 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE5Rv | TraesCS4D | scaffold52 | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t019 | SECCE4Rv | TraesCS4D | scaffold18 | TVU26269 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5D | scaffold10 | TVU23479 |
| LPERR04G | genblast_C | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2B | scaffold14 | TVU16063 |
| LPERR09G | cds.KYUSt_ | genblast_C | genblast_C | SECCE5Rv | TraesCS5A | scaffold29 | TVU08815 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2D | scaffold99 | TVU01765 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os11t060 | SECCE6Rv | TraesCS7D | scaffold22 | TVU07531 |
| LPERR02G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE6Rv | TraesCS6D | scaffold39 | TVU32796 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05314 |
| LPERR02G | genblast_C | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold26 | TVU27637 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2D | scaffold43 | TVU38698 |
| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t051 | SECCE3Rv | TraesCS3A | scaffold7. | TVU25258 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold4. | TVU21490 |
| LPERR01G | genblast_Z | genblast_Z | genblast_Z | SECCE3Rv | TraesCS3B | scaffold14 | TVU36350 |

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| LPERR01G | cds.KYUSt_ | genblast_C | Os01t032 | SECCE3Rv | TraesCS3D | scaffold36 | TVU21107 |
| LPERR03G | genblast_C | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47739 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t049 | SECCE2Rv | TraesCS2A | scaffold16 | TVU39074 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | genblast_C | TraesCS3B | scaffold11 | TVU05187 |
| LPERR08G | genblast_C | ORUFI08G | Os08t011 | SECCEUnv | TraesCS7D | scaffold26 | TVU00727 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1A | scaffold80 | TVU00555 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1D | scaffold23 | TVT98329 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE4Rv | TraesCS7D | scaffold13 | TVU05163 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t030 | SECCE4Rv | TraesCS7D | scaffold68 | TVU11524 |
| LPERR04G | genblast_C | ORUFI04G | Os04t037 | SECCE2Rv | TraesCS2D | scaffold21 | TVU13859 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7D | scaffold9. | TVU10659 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28636 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7D | scaffold24 | TVU05359 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3A | scaffold80 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47441 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15818 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold24 | TVU33491 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold27 | TVU10282 |
| LPERR06G | genblast_C | ORUFI06G | Os06t061 | SECCE7Rv | TraesCS7D | scaffold12 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t062 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08213 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4D | scaffold97 | TVU47951 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t059 | SECCE5Rv | TraesCS5B | scaffold29 | TVU49301 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold3. | TVU43940 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5B | scaffold53 | TVU09851 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2A | scaffold58 | TVU38985 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t058 | SECCE2Rv | TraesCS2B | scaffold67 | TVU38166 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5A | scaffold27 | genblast_C |

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| LPERR04G | genblast_C | ORUFI04G | Os04t039 | SECCE1Rv | TraesCS1A | scaffold10 | TVU15726 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35561 |
| LPERR07G | genblast_C | ORUFI07G | Os07t045 | SECCE2Rv | TraesCS2A | scaffold3. | TVU39417 |
| LPERR10G | genblast_Z | ORUFI10G | genblast_Z | SECCE1Rv | TraesCS1A | scaffold5. | TVU31553 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2B | scaffold14 | TVT99711 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold24 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6B | scaffold41 | TVU29698 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t044 | SECCE4Rv | TraesCS4D | scaffold13 | TVU25585 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold48 | TVU32662 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t028 | SECCE1Rv | TraesCS7D | scaffold21 | TVU13452 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t065 | SECCE4Rv | TraesCS4B | scaffold11 | TVU45831 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44814 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold16 | TVU29206 |
| LPERR07G | genblast_Z | ORUFI07G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold9. | TVU48632 |
| LPERR11G | genblast_C | ORUFI03G | Os11t061 | SECCE7Rv | TraesCS7D | scaffold11 | TVU30336 |
| LPERR09G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE5Rv | TraesCS5B | scaffold16 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE5Rv | TraesCS5D | scaffold19 | TVU48297 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold29 | TVU00508 |
| LPERR06G | genblast_C | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12217 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35313 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5D | scaffold16 | TVU01433 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5A | scaffold11 | genblast_C |
| genblast_C | genblast_C | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5A | scaffold24 | TVU09772 |

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| LPERR02G | genblast_Z | ORUFI10G | Os10t013 | SECCE3Rv | TraesCS3D | scaffold32 | TVU39880 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6B | scaffold10 | TVU29071 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4B | scaffold15 | TVU47716 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6A | scaffold20 | TVU27720 |
| LPERR01G | genblast_C | ORUFI01G | Os01t024 | SECCE3Rv | TraesCS3B | scaffold40 | TVU23089 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t028 | SECCE4Rv | TraesCS7A | scaffold36 | TVU32500 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7A | scaffold38 | TVU04774 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE4Rv | TraesCS4B | scaffold19 | TVU04188 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2B | scaffold1. | genblast_C |
| LPERR05G | genblast_C | ORUFI12G | Os12t043 | SECCE5Rv | TraesCS1B | scaffold46 | TVU18338 |
| LPERR04G | genblast_C | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2B | scaffold39 | TVU15108 |
| LPERR09G | genblast_C | ORUFI09G | Os09t012 | SECCE5Rv | TraesCS5D | scaffold20 | TVU10835 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6D | scaffold20 | TVU27759 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45775 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2D | scaffold32 | TVU16406 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t020 | genblast_C | TraesCS5B | scaffold70 | TVU01355 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | genblast_C | TraesCS3B | scaffold18 | TVU21533 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold40 | TVU47458 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3B | scaffold4. | TVU21532 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE4Rv | TraesCS4D | scaffold20 | TVU45557 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2B | scaffold14 | TVU15995 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold11 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCE1Rv | TraesCS1A | scaffold14 | TVU18465 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t049 | SECCE2Rv | genblast_C | scaffold16 | TVU28133 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold29 | TVU08852 |
| LPERR09G | genblast_C | ORUFI09G | Os09t057 | SECCEUnv | TraesCS4D | scaffold10 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE7Rv | TraesCS7A | scaffold74 | TVU47105 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t067 | SECCE3Rv | TraesCS3B | scaffold8. | TVU23448 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE2Rv | TraesCS2D | scaffold26 | TVU35862 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36715 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE2Rv | TraesCS2D | scaffold14 | TVU03182 |
| LPERR08G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE5Rv | TraesCS5A | genblast_C | TVU46467 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2D | scaffold12 | TVU40511 |
| LPERR03G | genblast_C | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5B | scaffold65 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49134 |

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| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3D | scaffold22 | TVU35009 |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t038 | SECCE3Rv | TraesCS3B | scaffold18 | TVU46782 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44780 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t078 | SECCE1Rv | TraesCS1B | scaffold85 | TVU31516 |
| LPERR01G | genblast_C | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3A | scaffold14 | TVU36203 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7B | scaffold26 | TVU05290 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2B | scaffold2. | TVU38411 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36352 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t028 | SECCE2Rv | TraesCS2D | scaffold68 | TVU42371 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2B | scaffold46 | TVU14210 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3A | scaffold29 | TVU35316 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47783 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2B | scaffold1. | TVU37560 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold20 | genblast_Z |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE5Rv | TraesCS5D | scaffold32 | TVU44998 |
| genblast_C | genblast_C | genblast_C | Os05t016 | SECCE1Rv | TraesCS1D | scaffold19 | TVU25145 |
| LPERR03G | genblast_C | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45264 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | scaffold85 | TVU31662 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t036 | SECCE6Rv | TraesCS3D | scaffold28 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI03G | genblast_C | SECCEUnv | TraesCS5A | scaffold34 | TVU48714 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t018 | genblast_C | TraesCS2D | scaffold10 | TVU41971 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t051 | SECCE3Rv | TraesCS3B | scaffold12 | TVU29937 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3A | scaffold22 | TVU35062 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4A | scaffold9. | TVU47949 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6B | scaffold18 | TVU27894 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE5Rv | TraesCS5B | scaffold12 | TVU50815 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t015 | SECCE2Rv | TraesCS2D | scaffold66 | TVU41431 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCE5Rv | TraesCS5A | scaffold52 | TVU48674 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t012 | SECCE7Rv | TraesCS2B | scaffold15 | TVU07023 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4D | scaffold22 | TVU47199 |
| LPERR06G | genblast_C | ORUFI06G | Os06t030 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11551 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold70 | TVU01001 |
| LPERR01G | genblast_C | ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35123 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1A | scaffold13 | TVT98998 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE4Rv | TraesCS6D | scaffold14 | TVU28517 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3B | scaffold46 | TVU34747 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t044 | SECCE4Rv | TraesCS4B | scaffold33 | TVU25593 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2D | scaffold13 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold7. | TVU40135 |
| LPERR08G | genblast_C | ORUFI08G | Os08t012 | SECCE7Rv | TraesCS7B | scaffold21 | TVU43543 |
| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold33 | TVU23059 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t010 | SECCE5Rv | TraesCS5A | scaffold32 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t055 | SECCE2Rv | TraesCS2A | scaffold94 | TVU01423 |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t048 | SECCE1Rv | TraesCS1D | scaffold16 | TVU30307 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE5Rv | TraesCS5A | scaffold37 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold45 | TVU31826 |

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| LPERR08G | genblast_C | ORUFI08G | Os08t055 | SECCE7Rv | TraesCS7B | scaffold28 | TVU50294 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t059 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08028 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t049 | SECCE6Rv | TraesCS3D | scaffold91 | TVT97662 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t055 | SECCE7Rv | TraesCS7D | scaffold15 | TVU04554 |
| LPERR01G | genblast_C | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3A | scaffold15 | TVT98930 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5D | scaffold53 | TVU10034 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5A | scaffold20 | TVU45886 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t037 | SECCE7Rv | TraesCS7B | scaffold37 | TVU06388 |
| LPERR02G | genblast_C | ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6A | scaffold98 | TVU33506 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t047 | SECCE1Rv | TraesCS1A | scaffold11 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2B | scaffold43 | TVU38993 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2D | scaffold56 | TVT98580 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t026 | SECCE4Rv | TraesCS7D | scaffold22 | TVU11733 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t070 | SECCE4Rv | TraesCS4B | scaffold10 | TVU23275 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t061 | SECCE7Rv | TraesCS7B | scaffold41 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2A | scaffold81 | TVU14649 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7B | scaffold38 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold39 | genblast_C |
| LPERR05G | genblast_C | ORUFI05G | Os05t030 | SECCE1Rv | TraesCS1A | scaffold10 | TVU18643 |
| LPERR09G | genblast_C | ORUFI09G | Os09t035 | SECCE5Rv | TraesCS5D | scaffold14 | TVU09250 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t038 | SECCE3Rv | TraesCS3B | scaffold18 | TVU46810 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7A | scaffold23 | TVU43854 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5A | scaffold29 | TVU49091 |
| LPERR06G | genblast_C | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7D | scaffold44 | TVT99277 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28457 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv | TraesCS5B | scaffold57 | TVU49393 |
| LPERR02G | cds.KYUSt_ | ORUFI06G | Os06t049 | SECCE5Rv | TraesCS5A | scaffold45 | TVU46545 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t085 | SECCE7Rv | TraesCS5B | scaffold39 | TVU44251 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | scaffold5. | TVU31671 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold94 | TVU03896 |
| genblast_C | cds.KYUSt_ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6B | scaffold84 | TVU28506 |
| genblast_C | cds.KYUSt_ORUFI12G | Os12t049 | SECCE5Rv | TraesCS5A | scaffold1. | genblast_C |
| LPERR08G | genblast_C | genblast_C | Os08t026 | SECCE7Rv | TraesCS7D | genblast_C | TVU17072 |
| LPERR07G | genblast_C | ORUFI07G | Os07t047 | SECCE2Rv | TraesCS2D | scaffold16 | TVU03972 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47474 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5B | scaffold17 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold40 | TVU47533 |

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| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE4Rv | TraesCS7A | scaffold26 | TVU05243 |
| LPERR01G | genblast_C | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3D | scaffold48 | TVU34775 |
| genblast_Z | cds.KYUSt_ORUFI05G | | Os05t052 | SECCE1Rv | TraesCS1A | scaffold32 | TVU20556 |
| LPERR02G | cds.KYUSt_ORUFI02G | | Os02t081 | SECCE6Rv | TraesCS6B | scaffold27 | TVU27742 |

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| LPERR01G | cds.KYUSt_ORUFI01G | | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36490 |
| LPERR12G | cds.KYUSt_ORUFI12G | | Os12t059 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49342 |
| LPERR04G | cds.KYUSt_ORUFI04G | | genblast_C | genblast_C | TraesCS2B | scaffold18 | TVU13793 |
| LPERR01G | cds.KYUSt_ORUFI01G | | Os01t078 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34861 |
| genblast_C | cds.KYUSt_ORUFI03G | | Os03t083 | SECCE7Rv | TraesCS5B | scaffold65 | TVU44279 |
| LPERR02G | genblast_C | ORUFI02G | Os02t029 | SECCE5Rv | TraesCS5D | scaffold36 | TVU02727 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t061 | SECCE2Rv | TraesCS2D | scaffold26 | TVU03320 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1B | scaffold10 | TVU31943 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t026 | SECCE4Rv | TraesCS4B | scaffold28 | TVU03660 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2D | scaffold13 | TVU15464 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48627 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE7Rv | TraesCS4D | scaffold5. | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2D | scaffold1. | TVU37527 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34537 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1A | scaffold85 | TVU31702 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7A | scaffold22 | TVU07647 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t056 | SECCE2Rv | TraesCS2D | scaffold94 | TVU14874 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7A | scaffold17 | TVU12262 |
| LPERR03G | cds.KYUSt_ | ORUFI04G | Os04t027 | SECCE7Rv | TraesCS4A | scaffold25 | TVU44070 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold28 | TVU41970 |
| genblast_Z | cds.KYUSt_ | ORUFI09G | genblast_Z | SECCE7Rv | TraesCS4D | scaffold53 | TVU09913 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t058 | SECCE6Rv | TraesCS7D | scaffold26 | TVU34221 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os07t016 | SECCE4Rv | TraesCS7A | scaffold71 | TVU41562 |
| LPERR03G | genblast_C | ORUFI03G | Os03t062 | SECCE4Rv | TraesCS4B | scaffold55 | TVT98868 |
| LPERR10G | cds.KYUSt_ | ORUFI03G | Os03t045 | genblast_C | TraesCS4D | scaffold18 | TVU46437 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t037 | SECCE7Rv | TraesCS7A | scaffold28 | TVT98479 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t030 | SECCE3Rv | TraesCS3D | scaffold4. | TVU21221 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold16 | TVU16449 |
| LPERR05G | genblast_C | ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20431 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14161 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t052 | SECCE1Rv | TraesCS1A | scaffold18 | TVU20516 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS7D | scaffold56 | TVT97005 |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t079 | genblast_C | TraesCS5D | scaffold17 | TVU44633 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4B | scaffold22 | TVU47148 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold75 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t049 | SECCE6Rv | TraesCS6B | scaffold34 | TVU30009 |
| LPERR12G | genblast_C | ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5A | scaffold70 | TVU50962 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS5A | scaffold10 | TVU48563 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1A | scaffold8. | TVU19219 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3B | scaffold22 | TVU35025 |
| LPERR03G | genblast_C | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS6D | scaffold65 | TVU44531 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1B | scaffold80 | TVU20427 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t061 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15755 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold94 | TVU15984 |
| LPERR12G | genblast_C | ORUFI12G | Os12t061 | SECCE5Rv | TraesCS5D | scaffold76 | TVU49122 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t052 | SECCE3Rv | TraesCS3A | scaffold90 | TVU33955 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19605 |
| LPERR07G | cds.KYUSt_ | ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5B | scaffold76 | TVU49216 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | genblast_C | TraesCS2B | scaffold12 | TVU16475 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3B | scaffold89 | TVU36075 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t063 | SECCE6Rv | TraesCS7A | scaffold74 | TVU02572 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t016 | SECCE7Rv | TraesCS3A | scaffold11 | TVU30771 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t018 | SECCE7Rv | TraesCS7B | scaffold68 | TVU31245 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t065 | SECCE5Rv | TraesCS5D | scaffold55 | TVU45866 |
| genblast_C | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold12 | TVU19140 |
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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2D | scaffold67 | TVU38200 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold60 | TVU08635 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | genblast_C | genblast_C | scaffold34 | TVU00988 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t049 | SECCE2Rv | TraesCS2D | scaffold27 | TVU39076 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t061 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08190 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2B | scaffold27 | TVU39070 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t015 | SECCE7Rv | TraesCS4A | scaffold46 | TVU48326 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2D | scaffold94 | TVU15867 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2B | scaffold94 | TVU14919 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t079 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44635 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t063 | SECCE6Rv | TraesCS6A | scaffold10 | TVU29086 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold1. | TVU33108 |
| LPERR06G | cds.KYUSt_ | ORUFI10G | Os01t054 | SECCE3Rv | TraesCS4B | genblast_C | TVU26272 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold77 | TVU14631 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t013 | SECCE5Rv | TraesCS5B | scaffold97 | TVU50806 |
| LPERR01G | genblast_C | ORUFI01G | Os01t079 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34804 |
| LPERR06G | genblast_Z | ORUFI06G | genblast_Z | SECCE6Rv | TraesCS7B | scaffold45 | TVU07513 |
| LPERR09G | genblast_C | ORUFI09G | Os09t055 | genblast_C | genblast_C | scaffold16 | TVU10354 |
| LPERR03G | genblast_C | ORUFI03G | Os03t012 | SECCE5Rv | TraesCS5A | scaffold52 | TVU48573 |
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| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold80 | TVU20315 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7D | scaffold14 | TVU12046 |
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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t059 | SECCE4Rv | TraesCS4B | scaffold78 | TVU03064 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5D | scaffold87 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4D | scaffold14 | TVU47608 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | genblast_C | TVU18094 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t032 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47256 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t045 | SECCE1Rv | TraesCS1D | scaffold16 | TVU30485 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4A | scaffold9. | TVU48090 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5D | scaffold76 | TVU49698 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t051 | SECCE4Rv | TraesCS7D | scaffold38 | TVU29947 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4B | scaffold9. | TVU48013 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t052 | SECCE7Rv | TraesCS7B | scaffold12 | genblast_C |
| LPERR08G | genblast_C | ORUFI08G | Os08t036 | SECCE6Rv | TraesCS7B | scaffold11 | TVU06455 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t060 | SECCE3Rv | TraesCS3B | scaffold11 | TVU34505 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold9. | TVU48037 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t034 | SECCE2Rv | TraesCS2B | scaffold14 | TVU13773 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1A | genblast_C | TVU18108 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5D | scaffold32 | TVT97852 |
| LPERR08G | genblast_C | ORUFI08G | Os08t024 | SECCE4Rv | TraesCS7D | scaffold34 | TVU42091 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCEUnv | TraesCS5A | scaffold29 | TVU27608 |
| LPERR07G | genblast_C | ORUFI07G | Os07t012 | SECCE2Rv | TraesCS2A | scaffold63 | TVU40946 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t053 | SECCE7Rv | TraesCS7A | scaffold16 | TVU04902 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1B | scaffold11 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2A | scaffold14 | TVU15864 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold24 | TVU11747 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6A | scaffold51 | TVU33120 |

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| LPERR11G | cds.KYUSt_ | genblast_C | Os11t052 | SECCE4Rv | TraesCS4B | scaffold7. | TVU25237 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36050 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t012 | SECCE4Rv | TraesCS4B | scaffold14 | TVU27224 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t032 | SECCE6Rv | TraesCS7B | scaffold19 | TVU07542 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4B | scaffold35 | TVU45345 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28496 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2A | scaffold30 | TVT98349 |
| LPERR08G | genblast_C | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7D | scaffold24 | TVU05305 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold1. | TVU24232 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38999 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16660 |
| LPERR03G | genblast_C | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold15 | TVU47687 |
| LPERR05G | genblast_C | genblast_C | Os05t025 | SECCE3Rv | TraesCS3D | scaffold32 | TVU20809 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2D | scaffold40 | TVU15026 |
| LPERR03G | genblast_C | ORUFI03G | Os03t016 | SECCE2Rv | TraesCS2A | scaffold30 | TVU16708 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t051 | SECCE5Rv | TraesCS5B | scaffold1. | TVU50048 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | genblast_C | TraesCS3D | scaffold10 | TVU22570 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4D | scaffold15 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45472 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE1Rv | TraesCS5D | scaffold6. | TVU38732 |

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| LPERR10G | cds.KYUSt_ORUFI10G | genblast_ | SECCE1Rv | TraesCS1B | scaffold37 | TVU32050 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t059 | SECCE5Rv | TraesCS5D | scaffold61 | TVU43548 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7A | scaffold60 | TVU08599 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2B | scaffold12 | TVU06843 |

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| LPERR09G | cds.KYUSt_ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold11 | TVU09665 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2D | scaffold42 | TVU16707 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold84 | TVU28582 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t018 | SECCE5Rv | TraesCS5D | scaffold10 | TVU51141 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold52 | TVU48464 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t086 | SECCEUnv | TraesCS5B | scaffold25 | TVU44267 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t015 | SECCE4Rv | TraesCS7D | scaffold10 | TVU12576 |

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| LPERR01G | genblast_ | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3A | scaffold84 | TVU36576 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3A | scaffold15 | TVU35014 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold9. | TVU47787 |
| LPERR06G | genblast_C | ORUFI06G | Os06t017 | SECCE4Rv | TraesCS7A | scaffold45 | TVU12368 |
| LPERR06G | genblast_C | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold68 | TVU11521 |
| LPERR01G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE3Rv | TraesCS3D | scaffold22 | TVU35727 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t030 | SECCE1Rv | TraesCS1B | scaffold21 | TVU18650 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | genblast_C | TraesCS5A | scaffold65 | TVU44511 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCEUnv | TraesCS5A | scaffold46 | TVU27632 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4B | scaffold3. | TVU45222 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2B | scaffold13 | TVU15300 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold22 | TVU28668 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t035 | SECCE5Rv | TraesCSU0 | scaffold82 | TVU30762 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE7Rv | TraesCS5D | scaffold65 | TVU43886 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t044 | SECCE5Rv | TraesCS5A | scaffold24 | TVU09744 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47719 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold9. | TVU07616 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold44 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os03t080 | SECCE5Rv | TraesCS5D | scaffold65 | TVU44496 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCSU0 | scaffold48 | TVU33561 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t032 | SECCE1Rv | TraesCS1D | scaffold12 | TVU21078 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t023 | SECCE3Rv | TraesCS3D | scaffold36 | TVU04006 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t041 | SECCE2Rv | TraesCS2D | scaffold2. | TVU37606 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2D | scaffold30 | TVU37791 |
| LPERR05G | genblast_C | ORUFI05G | Os05t045 | SECCE1Rv | TraesCS1A | scaffold39 | TVT96666 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t017 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12362 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t056 | SECCE3Rv | TraesCS3D | scaffold5. | TVU29598 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3B | scaffold16 | TVU22843 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4D | scaffold20 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCE6Rv | TraesCS7A | scaffold92 | TVU08290 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3B | scaffold31 | TVU02377 |
| LPERR11G | genblast_C | ORUFI11G | Os11t022 | SECCE4Rv | TraesCS4A | scaffold62 | TVU25874 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1B | scaffold13 | TVU20368 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t060 | SECCE4Rv | TraesCS4B | scaffold61 | genblast_C |

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| LPERR10G | cds.KYUSt_ORUFI10G | Os10t047 | SECCE1Rv | TraesCS1D | scaffold15 | TVU30401 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t025 | SECCE7Rv | TraesCS7A | scaffold20 | TVU42168 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48051 |
| genblast_Z | cds.KYUSt_genblast_Z | genblast_Z | SECCE3Rv | TraesCS3A | scaffold36 | TVU15761 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold27 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t016 | SECCE6Rv | TraesCS6D | genblast_C | genblast_C |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t041 | SECCE6Rv | TraesCS6D | scaffold57 | TVU31127 |
| LPERR03G | cds.KYUSt_genblast_C | Os03t038 | SECCE5Rv | TraesCS5D | scaffold18 | TVU46770 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t056 | SECCE5Rv | TraesCS4D | scaffold10 | TVU10557 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t015 | genblast_C | TraesCS4B | scaffold18 | TVU48323 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t024 | SECCE4Rv | TraesCS7D | scaffold10 | TVU18560 |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | genblast_C | TVU15101 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29125 |
| LPERR09G | genblast_C | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08833 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t014 | SECCE5Rv | TraesCS5A | scaffold96 | TVU26968 |
| LPERR04G | cds.KYUSt_genblast_C | Os04t055 | SECCE3Rv | TraesCS3A | scaffold25 | TVU13814 |
| LPERR04G | genblast_C | ORUFI10G | Os10t010 | SECCE2Rv | TraesCS2A | scaffold99 | TVU37084 |
| genblast_C | cds.KYUSt_genblast_C | Os12t063 | SECCE5Rv | TraesCS5B | scaffold17 | TVU48786 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t037 | SECCEUnv | TraesCS7D | scaffold18 | genblast_C |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t037 | SECCE4Rv | TraesCSU0 | genblast_C | TVU06407 |
| LPERR01G | cds.KYUSt_genblast_C | Os01t077 | SECCE3Rv | TraesCS3D | scaffold17 | genblast_C |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t055 | SECCE1Rv | TraesCS1D | scaffold1. | TVU00535 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5A | genblast_C | TVU45072 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold53 | TVU10005 |

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| LPERR08G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold11 | TVU19588 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12705 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t060 | SECCE4Rv | TraesCS4B | scaffold1. | TVU46203 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold13 | TVU31297 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1B | scaffold20 | TVU19342 |
| LPERR07G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv | TraesCS1D | scaffold10 | TVT97430 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1D | scaffold1. | TVU32065 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE4Rv | TraesCS1B | genblast_C | TVU39011 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3D | scaffold85 | TVU14389 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12376 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os02t014 | SECCE6Rv | TraesCS6D | scaffold31 | TVU33461 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t017 | SECCE4Rv | TraesCS4B | scaffold50 | TVU26145 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t010 | genblast_C | TraesCS3B | scaffold16 | TVU22268 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12780 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28403 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5A | scaffold16 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI02G | Os02t052 | SECCE5Rv | TraesCS5D | scaffold57 | TVU49314 |
| LPERR06G | genblast_C | ORUFI06G | Os06t025 | SECCE1Rv | TraesCS6D | scaffold44 | genblast_C |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t045 | SECCE1Rv | TraesCS1D | scaffold75 | TVT96670 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t035 | SECCE3Rv | TraesCS3B | scaffold28 | TVU20930 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t024 | SECCE7Rv | TraesCS7A | scaffold34 | TVU42080 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t067 | SECCE1Rv | TraesCS3B | scaffold15 | TVU35601 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE6Rv | TraesCS3B | scaffold31 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3D | scaffold16 | TVU22830 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7D | genblast_C | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3A | scaffold20 | TVU36648 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7A | scaffold22 | TVU07546 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6A | scaffold19 | TVU33722 |
| genblast_Z | genblast_Z | genblast_Z | genblast_Z | SECCE1Rv | TraesCS1B | scaffold12 | TVU42974 |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold46 | TVU27974 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7B | scaffold60 | TVU09706 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6D | scaffold10 | TVU28920 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t043 | SECCE1Rv | TraesCS1D | scaffold23 | TVU19492 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6D | scaffold13 | TVU29467 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t037 | SECCE6Rv | TraesCS6A | scaffold18 | TVU17000 |
| LPERR07G | genblast_C | ORUFI07G | Os07t046 | SECCE2Rv | TraesCS2A | scaffold12 | TVU39401 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold18 | TVU02398 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t024 | SECCE5Rv | TraesCS5A | scaffold12 | TVU10939 |
| LPERR04G | genblast_C | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15555 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t026 | SECCE5Rv | TraesCS5D | scaffold20 | TVU42266 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6A | scaffold19 | TVU29396 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE4Rv | TraesCS6A | scaffold1. | genblast_C |

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|---|---|---|---|---|---|---|---|
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t020 | SECCE5Rv | TraesCS5B | scaffold10 | TVU01354 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44477 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6B | scaffold2. | TVU27976 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_ | SECCE2Rv | TraesCS2B | scaffold21 | TVU32530 |
| LPERR01G | genblast_ | ORUFI01G | Os01t058 | SECCE3Rv | TraesCS3A | scaffold26 | TVU34228 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7B | scaffold28 | TVU04662 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os02t052 | SECCE2Rv | TraesCS2B | scaffold81 | TVU14658 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16588 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2A | scaffold16 | TVU16396 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_ | SECCE5Rv | TraesCS5D | scaffold10 | TVU10714 |
| LPERR02G | cds.KYUSt_ | genblast_ | Os02t073 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28388 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2B | scaffold2. | TVU01169 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t025 | SECCE6Rv | TraesCS6A | scaffold41 | TVU33319 |
| genblast_ | cds.KYUSt_ | ORUFI01G | Os01t068 | SECCE3Rv | TraesCS3D | scaffold15 | TVT98886 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold99 | TVU01784 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE6Rv | TraesCS6B | scaffold14 | TVU15873 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10255 |
| LPERR01G | cds.KYUSt_ | genblast_ | Os01t070 | SECCE3Rv | TraesCS3B | scaffold39 | TVU20401 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t052 | SECCE5Rv | TraesCS5D | scaffold22 | TVU50004 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1D | scaffold75 | genblast_ |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE2Rv | TraesCS2D | scaffold65 | TVU44247 |
| genblast_Z | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16440 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5D | scaffold35 | TVU44979 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t058 | SECCE1Rv | TraesCS1D | scaffold85 | TVU31502 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38579 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE7Rv | TraesCS5D | scaffold25 | TVU44074 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t066 | SECCE3Rv | TraesCS3A | scaffold21 | TVU02469 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCEUnv | TraesCS5D | scaffold24 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3A | scaffold31 | TVU34592 |

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|---|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t030 | SECCE2Rv | TraesCS2A | scaffold13 | TVU13491 |
| LPERR09G | genblast_C | ORUFI09G | Os09t053 | SECCE5Rv | TraesCS5A | scaffold27 | TVU10163 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3D | scaffold22 | TVU36645 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t018 | SECCE2Rv | TraesCS2A | scaffold10 | TVT99521 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE3Rv | TraesCS3A | scaffold46 | TVT99575 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold77 | TVU14334 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | scaffold52 | TVU48500 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1A | scaffold8. | TVU19144 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t055 | SECCE1Rv | TraesCS1B | scaffold32 | TVU22993 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t053 | SECCE1Rv | TraesCS1B | scaffold45 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3B | scaffold21 | TVU34606 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE7Rv | TraesCS4A | scaffold45 | TVU46684 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3D | scaffold4. | TVU22760 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold40 | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t028 | SECCE5Rv | TraesCS5D | scaffold18 | TVU11137 |
| LPERR01G | genblast_C | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3D | scaffold63 | TVU21677 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE1Rv | TraesCS1A | scaffold54 | TVU22582 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCEUnv | TraesCS5D | scaffold15 | TVU48743 |
| LPERR04G | genblast_C | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14469 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12242 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2B | scaffold16 | TVU16507 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t027 | SECCE4Rv | TraesCS4B | scaffold41 | TVU49044 |
| LPERR06G | genblast_C | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS7A | scaffold50 | TVU12742 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t054 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34103 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5D | scaffold28 | TVU46061 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2D | genblast_C | TVU44078 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCEUnv | TraesCS6D | scaffold12 | TVU28106 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2D | scaffold7. | TVU40203 |
| LPERR01G | genblast_C | ORUFI01G | Os01t024 | SECCE3Rv | TraesCS3D | scaffold40 | TVU23187 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | genblast_C | genblast_C | scaffold22 | TVU07618 |
| LPERR09G | genblast_C | ORUFI09G | Os09t051 | genblast_C | TraesCS5A | scaffold29 | TVU08960 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCSU0 | scaffold34 | TVU33560 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t038 | SECCE5Rv | TraesCS5A | scaffold87 | TVU09434 |
| LPERR07G | genblast_C | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold43 | TVU38406 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t070 | SECCE3Rv | TraesCS3B | scaffold29 | TVU03677 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3D | scaffold29 | TVU22471 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t051 | SECCE1Rv | TraesCS1B | scaffold39 | TVU20560 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4D | scaffold35 | TVU45144 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t019 | SECCE4Rv | TraesCS4D | scaffold39 | TVU26227 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | genblast_C | TVU34190 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold50 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE2Rv | TraesCS2B | scaffold1. | TVU46269 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5B | scaffold35 | TVT98021 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2B | scaffold2. | TVU01234 |
| LPERR07G | genblast_C | ORUFI07G | Os07t066 | SECCE1Rv | TraesCS2A | scaffold2. | TVT98018 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t045 | genblast_C | TraesCS6A | scaffold29 | TVU50412 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t031 | SECCE1Rv | TraesCS1A | scaffold23 | TVU21153 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5A | scaffold86 | TVU10146 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE7Rv | TraesCS5D | scaffold3. | TVU44310 |
| LPERR04G | genblast_C | ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16381 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t048 | SECCE3Rv | TraesCS3A | scaffold26 | TVU05475 |
| LPERR02G | genblast_C | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28352 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold27 | TVU02766 |

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| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08897 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5A | scaffold22 | TVU49868 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t060 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29428 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5D | scaffold64 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os10t047 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30390 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6A | scaffold11 | TVU28579 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t020 | SECCE6Rv | TraesCS6B | scaffold28 | TVU41366 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold50 | TVU09995 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6D | scaffold10 | TVU03003 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t057 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34181 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t042 | SECCE4Rv | TraesCS6A | scaffold11 | TVU33730 |
| LPERR11G | genblast_C | ORUFI11G | Os11t065 | SECCE4Rv | TraesCS4A | scaffold8. | TVU23784 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCEUnv | TraesCS5A | scaffold76 | TVU49728 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | genblast_C | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE5Rv | TraesCS5D | scaffold3. | TVU45137 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold14 | TVU15897 |
| LPERR02G | genblast_C | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6A | scaffold6. | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t094 | SECCE6Rv | TraesCS3B | scaffold31 | TVU36865 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t043 | SECCE5Rv | TraesCS5D | scaffold11 | TVU09630 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE1Rv | TraesCS1A | genblast_C | TVU39012 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold96 | TVU38397 |
| LPERR11G | genblast_C | ORUFI11G | genblast_C | SECCE7Rv | TraesCS7A | scaffold78 | TVU25061 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t034 | SECCE1Rv | TraesCS1B | scaffold34 | TVU18875 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold29 | TVU08660 |
| LPERR05G | genblast_C | ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19273 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36326 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCE6Rv | TraesCS6B | scaffold98 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE1Rv | TraesCS1D | scaffold15 | TVU42277 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t048 | SECCE3Rv | TraesCS3B | scaffold26 | TVU05430 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7A | scaffold9. | TVU08544 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5B | scaffold87 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS5D | scaffold3. | TVU44005 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t051 | SECCE1Rv | TraesCS1A | scaffold61 | TVU32010 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold53 | TVU47918 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os12t014 | SECCE5Rv | TraesCS5A | scaffold70 | TVU50833 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7B | scaffold25 | TVU08058 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold39 | TVU19471 |
| LPERR03G | genblast_C | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4D | scaffold22 | genblast_C |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t028 | SECCE2Rv | TraesCS2A | scaffold16 | TVU25808 |
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| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2B | scaffold3. | TVU10780 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6D | scaffold12 | TVU28216 |
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t032 | SECCE5Rv | TraesCS5B | scaffold26 | TVU06630 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t038 | SECCE4Rv | TraesCS4D | scaffold32 | TVU20777 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold15 | TVU16288 |
| LPERR04G | genblast_C | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16547 |
| LPERR02G | genblast_C | ORUFI02G | Os02t069 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28119 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t010 | SECCE1Rv | TraesCS5B | scaffold13 | TVU18438 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t095 | SECCE6Rv | TraesCS3A | scaffold15 | TVU36888 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold94 | TVU42475 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t059 | SECCE5Rv | TraesCS5A | scaffold29 | TVU49378 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1A | scaffold8. | TVU19269 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34893 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE5Rv | TraesCS5A | scaffold2. | TVU38261 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4D | scaffold18 | TVU47057 |
| LPERR01G | genblast_C | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36315 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4A | scaffold55 | TVU45814 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | genblast_C | TraesCS3D | scaffold15 | TVU22179 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold23 | TVU47764 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6B | scaffold2. | genblast_C |
| | | | | | | | |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4D | scaffold97 | TVU47871 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2A | scaffold20 | TVU15127 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3B | scaffold47 | TVU22410 |
| LPERR11G | cds.KYUSt_ | genblast_C | Os11t046 | SECCEUnv | TraesCS3A | scaffold28 | TVU14580 |

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|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold16 | TVU16310 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t037 | SECCE1Rv | TraesCS1B | scaffold16 | TVU30845 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold15 | TVU47660 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t043 | SECCE1Rv | TraesCS1B | scaffold49 | genblast_C |

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| LPERR04G | genblast_C | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15378 |
| LPERR01G | cds.KYUSt_ORUFI12G | Os01t028 | genblast_C | TraesCS3D | scaffold15 | TVU03208 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7D | scaffold17 | TVU42757 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4D | scaffold74 | TVU47084 |
| genblast_Z | cds.KYUSt_ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold87 | TVU09432 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2A | scaffold16 | TVT98013 |

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|---|---|---|---|---|---|---|
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t056 | SECCE1Rv | TraesCS1B | scaffold32 | TVU50322 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1B | scaffold75 | TVU19875 |
| LPERR11G | cds.KYUSt_ORUFI07G | Os07t028 | SECCE4Rv | TraesCS4D | scaffold30 | TVU25676 |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold66 | TVU41524 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48004 |
| LPERR04G | genblast_C | ORUFI04G | Os04t011 | SECCE2Rv | TraesCS2D | scaffold30 | TVU11548 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold31 | TVU36097 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t033 | SECCE4Rv | TraesCS7D | scaffold20 | TVU12093 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t021 | SECCE3Rv | TraesCS5A | scaffold10 | TVU16973 |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold2. | TVU28102 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t050 | SECCE4Rv | TraesCS3A | scaffold11 | TVU33775 |
| LPERR07G | genblast_C | ORUFI07G | genblast_C | SECCEUnv | TraesCS2B | scaffold12 | TVU39907 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5D | scaffold32 | TVU44756 |
| genblast_C | cds.KYUSt_genblast_C | Os04t049 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15426 |
| LPERR04G | genblast_C | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold94 | TVU16030 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t013 | SECCE6Rv | TraesCS6A | scaffold48 | genblast_C |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCEUnv | TraesCS7B | scaffold32 | TVU08083 |
| LPERR05G | genblast_C | ORUFI05G | Os05t019 | SECCE1Rv | TraesCS1D | scaffold19 | TVU17064 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3A | scaffold36 | TVU22885 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1D | scaffold40 | TVU20236 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5A | scaffold65 | TVU44430 |
| LPERR03G | cds.KYUSt_ | ORUFI09G | Os09t011 | SECCE6Rv | TraesCS6B | scaffold14 | TVU19278 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16521 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5D | scaffold18 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1A | scaffold7. | TVU31833 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t011 | genblast_C | TraesCS7B | scaffold36 | TVU13049 |
| genblast_C | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold49 | TVU16106 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t054 | SECCE3Rv | TraesCS3D | scaffold46 | TVU34099 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2D | scaffold56 | TVU15465 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t053 | SECCE2Rv | TraesCS2A | scaffold58 | TVU39461 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47450 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE6Rv | TraesCS7D | scaffold25 | TVU08256 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCEUnv | TraesCS5A | scaffold29 | TVU49427 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2B | scaffold49 | TVT99724 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6B | scaffold2. | TVU03830 |
| LPERR12G | genblast_C | ORUFI12G | Os12t050 | SECCEUnv | TraesCS5B | genblast_C | genblast_C |
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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t041 | SECCE1Rv | TraesCS1A | scaffold62 | TVU26034 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1B | scaffold12 | TVU19621 |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t028 | SECCE5Rv | TraesCS5D | scaffold18 | TVU11148 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6A | scaffold6. | TVU01982 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6B | scaffold16 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold29 | TVU08615 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t011 | SECCE3Rv | TraesCS3B | scaffold49 | TVT96695 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t070 | SECCE3Rv | TraesCS3A | scaffold15 | TVT97918 |
| LPERR03G | genblast_C | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold97 | TVU47958 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1D | scaffold75 | TVU19815 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t036 | SECCE6Rv | TraesCS6B | scaffold28 | TVU20292 |
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| LPERR09G | genblast_C | ORUFI09G | Os09t055 | SECCE4Rv | TraesCS7D | scaffold16 | TVU10305 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4D | scaffold97 | TVU47878 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold40 | TVU47657 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t014 | SECCE1Rv | TraesCS1D | scaffold97 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold43 | TVU38676 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold22 | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5D | scaffold43 | TVU10412 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5B | scaffold32 | TVU44804 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t040 | SECCE5Rv | TraesCS5A | scaffold27 | TVU30999 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4A | scaffold14 | TVU47622 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1D | scaffold8. | TVU04253 |
| LPERR01G | genblast_C | ORUFI01G | Os01t058 | SECCE3Rv | TraesCS3D | scaffold26 | TVT97593 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold26 | TVU27682 |
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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t013 | SECCE7Rv | TraesCS7D | scaffold25 | TVU43420 |
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| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE5Rv | TraesCS5D | scaffold41 | TVU29708 |
| LPERR10G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE2Rv | TraesCS2A | scaffold15 | TVU13335 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t058 | SECCE7Rv | TraesCS7D | scaffold43 | TVT96654 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t064 | SECCE3Rv | TraesCS3D | scaffold37 | TVU23919 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05230 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE3Rv | TraesCS3B | scaffold64 | TVU50203 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2B | scaffold49 | TVU15051 |

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| LPERR01G | cds.KYUSt_ | genblast_C | Os01t092 | SECCE3Rv | TraesCS3D | scaffold21 | TVU05839 |
| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t046 | SECCE1Rv | TraesCS1B | scaffold39 | genblast_C |

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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5A | scaffold35 | TVT97469 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36020 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t034 | SECCE7Rv | TraesCS7D | scaffold93 | TVU10719 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS4A | scaffold39 | TVU12707 |
| LPERR06G | genblast_C | ORUFI06G | Os06t073 | SECCE3Rv | TraesCS3D | scaffold22 | TVU07497 |
| LPERR03G | genblast_C | ORUFI03G | Os03t015 | SECCE7Rv | TraesCS4D | scaffold18 | TVU48325 |
| LPERR08G | genblast_C | ORUFI08G | genblast_C | SECCE5Rv | TraesCS5A | scaffold35 | TVU05715 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1A | scaffold7. | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t067 | SECCE3Rv | TraesCS3B | scaffold15 | TVU35579 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold12 | TVU14569 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold29 | TVU08902 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28432 |

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| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold16 | TVU16535 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7D | scaffold26 | TVU01076 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t010 | SECCE1Rv | TraesCS1A | scaffold46 | TVU18373 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE4Rv | TraesCS7A | scaffold44 | TVU22366 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold33 | TVU35430 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os11t015 | SECCE4Rv | TraesCS4D | scaffold70 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28461 |

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| LPERR07G | genblast_C | ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2B | scaffold96 | TVU38198 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold17 | TVU44384 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold64 | TVU09445 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48279 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48475 |
| LPERR07G | genblast_C | ORUFI07G | Os07t055 | SECCE2Rv | TraesCS2D | scaffold96 | TVU38435 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19959 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | genblast_C | TraesCS1D | scaffold8. | TVU19188 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3A | scaffold45 | TVU36484 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_Z | SECCE5Rv | TraesCS5A | scaffold1. | TVU48975 |
| LPERR02G | genblast_C | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6A | scaffold20 | TVU30252 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t089 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36206 |
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| LPERR08G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE7Rv | TraesCS7A | scaffold54 | TVU04658 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47362 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE1Rv | TraesCS1A | scaffold19 | TVU17833 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCE6Rv | TraesCS7A | scaffold92 | TVU46212 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t013 | SECCE2Rv | TraesCS2D | scaffold63 | TVU41028 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE7Rv | TraesCS7A | scaffold25 | TVU08241 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold15 | TVU47751 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1D | scaffold75 | TVU19880 |
| LPERR07G | cds.KYUSt_ | genblast_Z | Os07t024 | SECCE4Rv | TraesCS4B | scaffold31 | TVU39931 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE2Rv | TraesCS2B | scaffold77 | TVU14484 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5D | scaffold3. | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE4Rv | TraesCS2A | scaffold41 | TVU36668 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCEUnv | TraesCS5D | scaffold76 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t043 | SECCE1Rv | TraesCS1D | scaffold57 | TVU01126 |
| LPERR01G | genblast_C | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3A | scaffold33 | TVU36304 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE6Rv | TraesCS3A | scaffold21 | TVU00627 |
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| LPERR03G | genblast_C | ORUFI03G | Os03t034 | SECCE4Rv | TraesCS4B | scaffold74 | TVU47088 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2A | scaffold94 | TVU15875 |
| LPERR06G | genblast_C | ORUFI06G | Os06t070 | SECCE7Rv | TraesCS7A | scaffold22 | TVU07638 |
| genblast_C | genblast_C | genblast_C | Os04t041 | SECCE2Rv | TraesCS2A | scaffold77 | TVU01768 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t043 | SECCE2Rv | TraesCS2D | scaffold45 | TVU46484 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37677 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4D | scaffold22 | TVU47180 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t023 | SECCE5Rv | TraesCS5A | scaffold40 | TVU16895 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t093 | SECCE3Rv | TraesCS3B | scaffold18 | TVU34670 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t038 | SECCE5Rv | TraesCS5A | scaffold27 | TVU09416 |
| LPERR12G | genblast_C | ORUFI12G | Os12t016 | SECCE5Rv | TraesCS5B | scaffold97 | TVU26720 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold2. | TVU38423 |
| LPERR06G | genblast_C | ORUFI06G | Os06t011 | SECCE4Rv | TraesCS7A | scaffold44 | TVU13033 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE4Rv | TraesCS7A | scaffold44 | TVU11791 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3A | scaffold23 | TVU35836 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold77 | TVU00285 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | genblast_C | TraesCS6D | scaffold12 | TVU03374 |
| genblast_Z | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold48 | TVU00166 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold2. | genblast_Z |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCEUnv | TraesCS5B | scaffold29 | TVU10133 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t018 | SECCE7Rv | TraesCS7D | scaffold10 | TVU43058 |
| LPERR05G | cds.KYUSt_ | ORUFI06G | Os05t043 | SECCE1Rv | TraesCS1A | scaffold63 | genblast_C |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t065 | SECCEUnv | TraesCS2A | scaffold12 | TVU16387 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t022 | genblast_C | TraesCS2D | scaffold16 | TVU07413 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE6Rv | TraesCS7A | scaffold9. | TVU07589 |
| LPERR08G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE5Rv | TraesCS5A | scaffold17 | TVU05658 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6B | scaffold22 | TVU28687 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t053 | SECCE6Rv | TraesCS6B | scaffold12 | TVU29818 |
| LPERR10G | genblast_C | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1A | scaffold7. | TVU31922 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t049 | SECCE4Rv | TraesCS4A | scaffold65 | TVU20738 |
| LPERR07G | genblast_C | ORUFI07G | Os07t053 | SECCE7Rv | TraesCS7B | scaffold43 | TVU38711 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2A | scaffold5. | TVU15675 |

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|---|---|---|---|---|---|---|---|
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold84 | TVU28591 |
| LPERR03G | genblast_C | ORUFI03G | Os03t011 | SECCE4Rv | TraesCS4B | scaffold34 | genblast_C |
| LPERR07G | genblast_C | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2A | scaffold16 | TVU37245 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE6Rv | TraesCS6A | scaffold24 | TVU05405 |

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| LPERR08G | genblast_C | genblast_C | Os08t055 | SECCE7Rv | TraesCS7B | scaffold28 | TVU04588 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE4Rv | TraesCS6D | scaffold97 | genblast_C |
| LPERR09G | genblast_C | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5D | scaffold29 | TVU10108 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold16 | TVU10002 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t026 | SECCE4Rv | TraesCS4B | scaffold11 | TVU03658 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1A | scaffold1. | TVU20214 |
| LPERR07G | cds.KYUSt_ | ORUFI01G | Os01t090 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36116 |

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| LPERR05G | cds.KYUSt_ | ORUFI12G | Os12t044 | SECCE6Rv | TraesCS1D | scaffold32 | TVU20591 |
| LPERR08G | genblast_C | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7D | scaffold15 | TVU04603 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2A | scaffold96 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t035 | SECCE1Rv | TraesCS1B | scaffold12 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t016 | SECCE2Rv | TraesCS2B | scaffold28 | TVU41550 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | genblast_C | TraesCS1B | scaffold11 | TVU17619 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCE5Rv | TraesCS5B | scaffold57 | TVU49575 |
| LPERR03G | cds.KYUSt_ | ORUFI09G | Os09t038 | SECCE1Rv | TraesCS1D | scaffold45 | TVU46505 |
| LPERR03G | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE7Rv | TraesCS4B | scaffold18 | genblast_C |
| LPERR07G | genblast_C | ORUFI07G | Os07t047 | SECCE3Rv | TraesCS3A | scaffold27 | TVU39300 |

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| LPERR03G | genblast_C | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4D | scaffold10 | TVU48305 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold22 | TVU36591 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold87 | TVU09690 |
| LPERR08G | genblast_C | ORUFI08G | Os08t025 | SECCE4Rv | TraesCS7D | scaffold68 | TVU42224 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6A | scaffold27 | genblast_C |
| LPERR10G | genblast_C | ORUFI10G | Os10t038 | SECCE6Rv | TraesCS6D | genblast_C | TVU30774 |
| LPERR09G | genblast_C | ORUFI09G | Os09t037 | SECCE5Rv | TraesCS5A | scaffold14 | TVU09371 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold25 | TVU32905 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2D | scaffold17 | TVU16622 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t047 | SECCE2Rv | TraesCS2D | scaffold77 | TVU15630 |
| LPERR07G | genblast_Z | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold58 | TVU38899 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | genblast_C | TraesCS5A | scaffold52 | TVU48623 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_Z | genblast_Z | TraesCS7D | scaffold11 | genblast_Z |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7B | scaffold9. | TVU08568 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7A | scaffold17 | TVU05669 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t032 | SECCE7Rv | TraesCS4B | scaffold74 | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t069 | SECCE3Rv | TraesCS3B | scaffold22 | genblast_C |
| LPERR07G | genblast_Z | genblast_Z | genblast_Z | SECCE2Rv | TraesCS2D | scaffold67 | TVU37496 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t024 | SECCE3Rv | TraesCS3A | scaffold40 | TVU23170 |
| LPERR06G | genblast_C | genblast_C | genblast_C | SECCE6Rv | TraesCS7D | scaffold22 | TVU07494 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28391 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2B | scaffold13 | TVU15420 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47471 |
| LPERR01G | genblast_C | ORUFI01G | Os01t087 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36327 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t038 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19240 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold63 | TVU21693 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | TraesCS2B | scaffold19 | TVU16578 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t027 | SECCE3Rv | TraesCS3A | scaffold68 | TVU42320 |
| LPERR01G | genblast_C | ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3B | scaffold46 | TVU36558 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold22 | TVU28854 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t056 | SECCE7Rv | TraesCS7B | scaffold11 | TVU07893 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t047 | SECCE3Rv | TraesCS3A | scaffold34 | TVU09531 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold22 | TVU47522 |
| genblast_C | genblast_C | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5B | scaffold50 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7D | scaffold44 | TVU11900 |

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| LPERR02G | cds.KYUSt_ | genblast_C | Os02t080 | SECCE6Rv | TraesCS6D | scaffold20 | TVU27764 |
| LPERR09G | genblast_C | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5D | scaffold16 | TVU08941 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS5B | scaffold65 | TVU12814 |
| LPERR09G | genblast_C | ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5D | scaffold53 | TVU03723 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6B | scaffold10 | TVT99734 |
| genblast_C | genblast_C | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1B | scaffold40 | TVU20302 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1B | scaffold12 | TVU20017 |
| LPERR02G | genblast_C | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6A | scaffold28 | TVU28907 |
| LPERR02G | genblast_C | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6B | scaffold26 | TVU07485 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold38 | TVU27891 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6D | scaffold19 | TVU27784 |
| LPERR02G | genblast_C | ORUFI02G | Os02t059 | genblast_C | TraesCS2B | scaffold13 | TVU29427 |
| LPERR03G | genblast_C | ORUFI03G | Os03t036 | SECCE4Rv | TraesCS4D | scaffold74 | genblast_C |
| LPERR04G | genblast_C | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2D | scaffold14 | TVU15293 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3B | scaffold29 | TVU22437 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t026 | SECCE4Rv | TraesCS3B | scaffold11 | TVU18558 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE6Rv | TraesCS7B | scaffold12 | TVU08252 |

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| genblast_ | cds.KYUSt_ | ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3A | scaffold41 | TVU36716 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5B | scaffold35 | TVU45059 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t045 | SECCE1Rv | TraesCS1B | scaffold75 | TVU19699 |
| LPERR09G | genblast_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5A | scaffold29 | genblast_ |
| LPERR09G | cds.KYUSt_ | genblast_ | Os09t053 | SECCE5Rv | TraesCS5D | scaffold16 | TVU10199 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold12 | TVU40909 |

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| LPERR02G | genblast_ | ORUFI02G | Os02t029 | SECCEUnv | TraesCS5D | scaffold15 | TVU32451 |
| LPERR04G | genblast_ | genblast_ | Os04t019 | SECCE7Rv | TraesCS2D | scaffold19 | TVU07325 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold75 | TVU20050 |
| LPERR12G | genblast_Z | ORUFI10G | genblast_Z | genblast_Z | TraesCS6B | scaffold16 | TVU50338 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t064 | SECCE2Rv | TraesCS2D | scaffold12 | TVU16312 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3A | scaffold31 | TVU12713 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t058 | SECCE7Rv | TraesCS7A | scaffold43 | TVU13123 |
| LPERR03G | genblast_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS5A | scaffold52 | TVU48499 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t053 | SECCE4Rv | TraesCS4A | scaffold32 | TVU24658 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | SECCE3Rv | TraesCS3D | scaffold88 | TVU21788 |
| LPERR03G | cds.KYUSt_ | genblast_ | Os03t072 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45280 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t073 | SECCE4Rv | TraesCS4B | scaffold3. | TVU45205 |
| LPERR04G | genblast_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold16 | TVU16436 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19913 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCE4Rv | TraesCS4A | scaffold55 | TVU45778 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15017 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4B | scaffold15 | genblast_ |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_ | SECCE5Rv | TraesCS5D | scaffold64 | TVU09490 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5D | scaffold32 | TVU44748 |
| LPERR02G | cds.KYUSt_ | genblast_ | Os02t064 | SECCE6Rv | TraesCS6B | scaffold17 | TVU29018 |

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| LPERR06G | cds.KYUSt_ | ORUFI02G | Os06t022 | SECCE4Rv | TraesCS7A | scaffold14 | TVU11968 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t014 | SECCE6Rv | TraesCS6D | scaffold48 | TVU33469 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold96 | TVU38179 |
| LPERR02G | cds.KYUSt_ | genblast_C | Os01t011 | SECCE3Rv | TraesCS3B | scaffold15 | TVU22200 |
| LPERR07G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE2Rv | TraesCS2A | scaffold2. | TVU38092 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6B | scaffold19 | TVU03515 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE2Rv | TraesCS2A | scaffold9. | TVU48076 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t040 | SECCE1Rv | TraesCS1B | scaffold12 | TVU30973 |
| LPERR11G | genblast_C | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4A | scaffold30 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t051 | SECCE2Rv | TraesCS2A | scaffold58 | TVU38868 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t088 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36223 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t056 | SECCE2Rv | TraesCS2A | scaffold49 | TVU14883 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t021 | SECCE3Rv | TraesCS3A | scaffold40 | TVU16969 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3B | scaffold17 | TVU35122 |

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| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2A | scaffold1. | TVU37442 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28581 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5B | scaffold35 | TVU45040 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7B | scaffold44 | TVU11912 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t029 | SECCE7Rv | TraesCS7A | scaffold64 | TVU06687 |
| LPERR09G | cds.KYUSt_ | ORUFI08G | Os08t017 | SECCE2Rv | TraesCS2D | scaffold31 | TVU08258 |

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| genblast_C | cds.KYUSt_ | ORUFI05G | Os05t030 | SECCE1Rv | TraesCS4A | scaffold20 | TVU49562 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold3. | TVU45283 |

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| LPERR09G | genblast_C | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold11 | TVU09641 |
| LPERR02G | genblast_C | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6B | scaffold17 | TVU28841 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold25 | TVU44223 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t016 | SECCE4Rv | TraesCS4D | scaffold50 | TVU26653 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2D | scaffold23 | TVU38976 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t032 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12857 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t047 | SECCE2Rv | TraesCS2D | scaffold30 | TVU15596 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t065 | SECCE6Rv | TraesCS6B | scaffold8. | TVU23747 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t082 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36672 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os06t061 | SECCE6Rv | TraesCS6A | scaffold1. | TVU32934 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t065 | SECCE2Rv | TraesCS2A | scaffold1. | TVU37407 |
| genblast_C | genblast_C | ORUFI10G | Os10t058 | SECCE1Rv | TraesCS1D | scaffold32 | TVU31477 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4B | scaffold3. | TVU45344 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7B | scaffold33 | TVU08378 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t053 | SECCE6Rv | TraesCS6A | scaffold17 | TVT97255 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t066 | SECCE2Rv | TraesCS2D | scaffold12 | TVU16438 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold3. | TVU44893 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5A | scaffold43 | TVU10369 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCEUnv | TraesCS5B | scaffold15 | TVU48824 |
| LPERR01G | genblast_C | ORUFI01G | Os01t078 | SECCE3Rv | TraesCS3A | scaffold46 | TVU34880 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4D | scaffold29 | TVU48468 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2D | scaffold1. | TVU37178 |
| LPERR12G | genblast_C | ORUFI12G | Os12t015 | SECCE4Rv | TraesCS4B | scaffold97 | TVU50908 |
| genblast_C | genblast_C | ORUFI07G | Os07t029 | SECCEUnv | TraesCS6B | scaffold12 | TVT97620 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold21 | TVU44237 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t040 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19315 |
| LPERR01G | cds.KYUSt_ | ORUFI05G | Os05t039 | SECCE2Rv | TraesCS2B | scaffold12 | TVU34573 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t022 | SECCE1Rv | TraesCS1D | scaffold40 | TVU07152 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t010 | SECCE1Rv | TraesCS1B | scaffold36 | TVU18435 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t033 | SECCE2Rv | TraesCS2D | scaffold23 | TVU08231 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t054 | SECCE7Rv | TraesCS7B | scaffold33 | TVT98318 |
| LPERR07G | genblast_C | ORUFI07G | Os07t029 | SECCE4Rv | TraesCS4A | scaffold5. | TVU43546 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t060 | SECCE5Rv | TraesCS5B | scaffold76 | TVU01483 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE4Rv | TraesCS6D | scaffold11 | TVU33664 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE3Rv | TraesCS4A | scaffold20 | TVT99624 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t022 | SECCE1Rv | TraesCS1D | scaffold13 | TVU07230 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5A | scaffold53 | TVU09178 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t024 | SECCE6Rv | TraesCS3A | scaffold10 | TVU22564 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1D | scaffold32 | TVU31594 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t011 | SECCE2Rv | TraesCS2A | scaffold10 | TVU01911 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t096 | SECCE5Rv | TraesCS5D | scaffold78 | TVU37008 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7B | scaffold26 | TVU43762 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_Z | SECCE1Rv | TraesCS1D | genblast_Z | TVU20432 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold17 | TVU48271 |
| genblast_C | genblast_C | ORUFI03G | Os03t015 | SECCE7Rv | TraesCS4B | scaffold46 | TVU48335 |
| genblast_C | genblast_C | ORUFI06G | Os06t071 | SECCE5Rv | TraesCS5A | scaffold96 | TVU27155 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t062 | SECCE4Rv | TraesCS4B | scaffold28 | TVU46079 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | SECCEUnv | TraesCS5B | scaffold71 | TVU50517 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2D | scaffold12 | TVU16523 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t027 | SECCE5Rv | TraesCS5A | scaffold10 | TVU51740 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t058 | SECCE6Rv | TraesCS6A | scaffold78 | TVU25015 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCE4Rv | TraesCS6B | scaffold53 | TVU33651 |
| LPERR09G | cds.KYUSt_ | ORUFI10G | Os09t056 | SECCE5Rv | TraesCS5D | scaffold43 | TVU10502 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t010 | SECCE4Rv | TraesCS7D | scaffold44 | TVU12993 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4B | scaffold9. | TVU48024 |
| LPERR12G | cds.KYUSt_ | ORUFI11G | Os11t013 | SECCE5Rv | TraesCS5A | scaffold14 | TVU50690 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2B | scaffold2. | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE6Rv | TraesCS7A | scaffold9. | TVU07579 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2B | scaffold99 | TVU14620 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t010 | SECCE5Rv | TraesCS5D | scaffold70 | TVU51570 |
| LPERR11G | cds.KYUSt_ | ORUFI12G | Os12t012 | SECCE4Rv | TraesCS4B | scaffold31 | TVU27214 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2B | scaffold13 | TVU14837 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE5Rv | TraesCS5A | scaffold29 | TVU48442 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t027 | SECCE3Rv | TraesCS3A | scaffold54 | TVU04166 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6A | scaffold27 | TVU27715 |

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| LPERR01G | genblast_C | ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3D | scaffold84 | TVU35148 |
| LPERR03G | genblast_C | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold49 | TVU47317 |
| LPERR02G | genblast_C | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold10 | TVU28976 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t021 | SECCE4Rv | TraesCS7B | scaffold14 | TVU12053 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t064 | SECCEUnv | TraesCS7D | scaffold25 | TVU08287 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1A | scaffold36 | genblast_C |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7D | scaffold92 | TVU08311 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2B | scaffold13 | TVU15501 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t010 | SECCE5Rv | TraesCS5D | scaffold32 | TVU31466 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5B | scaffold27 | TVU09879 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold2. | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE3Rv | TraesCS3B | scaffold13 | TVU25000 |
| LPERR02G | cds.KYUSt_ | ORUFI03G | Os02t058 | SECCE5Rv | TraesCS7B | scaffold43 | TVU45502 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4A | scaffold17 | TVU48148 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7A | scaffold51 | TVU08709 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6A | scaffold26 | genblast_C |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15004 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | genblast_C | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7D | scaffold60 | TVU07641 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold18 | TVU20485 |
| LPERR02G | genblast_C | ORUFI02G | Os02t028 | SECCE3Rv | TraesCS3D | scaffold10 | TVU32484 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t035 | SECCE5Rv | TraesCS5B | scaffold98 | TVU09299 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7A | scaffold11 | TVU07841 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2A | scaffold34 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t048 | SECCE2Rv | TraesCS2B | scaffold28 | TVU15483 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2D | scaffold60 | TVU46608 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold11 | TVU34239 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t032 | SECCE5Rv | TraesCS5A | scaffold14 | TVU09188 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3D | scaffold46 | TVU34744 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t081 | SECCE6Rv | TraesCS6A | scaffold26 | genblast_C |
| LPERR05G | genblast_C | ORUFI05G | Os05t053 | SECCE1Rv | TraesCS1D | scaffold40 | TVU20476 |
| genblast_C | genblast_C | ORUFI12G | Os12t018 | SECCEUnv | TraesCS5A | scaffold13 | TVU51106 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t012 | SECCEUnv | TraesCS6B | scaffold48 | TVU33567 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2A | scaffold2. | TVU38270 |

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| LPERR10G | genblast_C | ORUFI10G | Os10t056 | SECCE1Rv | genblast_C | scaffold5. | TVU31673 |
| LPERR11G | genblast_C | ORUFI11G | Os11t018 | genblast_C | TraesCS4D | scaffold19 | TVU26185 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE4Rv | TraesCS7D | scaffold24 | TVU18106 |
| LPERR05G | genblast_C | ORUFI05G | Os05t059 | SECCE1Rv | TraesCS1A | scaffold36 | TVT99013 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6D | scaffold5. | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4D | scaffold17 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14274 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2D | scaffold19 | TVU16642 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t043 | SECCE2Rv | TraesCS2A | scaffold99 | TVU14435 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4B | scaffold11 | TVU45515 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6D | scaffold48 | TVU32753 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t056 | SECCE1Rv | TraesCS1B | genblast_C | TVU31659 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4B | scaffold74 | TVU47403 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2A | scaffold31 | TVU01767 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4A | scaffold10 | TVU48375 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2B | scaffold77 | TVT98243 |
| LPERR04G | cds.KYUSt_ | ORUFI07G | Os07t048 | SECCE2Rv | TraesCS2D | scaffold43 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t030 | SECCE2Rv | TraesCS2D | scaffold75 | TVU00351 |

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| LPERR01G | genblast_ | ORUFI01G | Os01t078 | genblast_ | TraesCS3D | scaffold11 | TVU34866 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2A | scaffold2. | genblast_ |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44879 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE7Rv | TraesCS2A | scaffold23 | TVU07435 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6A | scaffold17 | genblast_ |
| LPERR03G | genblast_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold17 | TVU44578 |
| LPERR03G | genblast_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4B | scaffold9. | TVU09735 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t037 | SECCE2Rv | TraesCS2A | scaffold81 | TVU13901 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_ | SECCE2Rv | TraesCS7D | scaffold33 | TVU08425 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7D | scaffold10 | TVU12239 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1B | scaffold16 | TVU19024 |
| LPERR01G | genblast_ | ORUFI01G | Os01t050 | SECCE2Rv | TraesCS2B | scaffold32 | TVU33745 |
| LPERR11G | cds.KYUSt_ | ORUFI03G | Os03t059 | SECCE5Rv | TraesCS5A | scaffold61 | genblast_ |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t028 | SECCE5Rv | TraesCS4B | scaffold5. | genblast_ |
| LPERR01G | genblast_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3B | scaffold48 | TVU34877 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t020 | genblast_ | TraesCS2D | scaffold16 | TVU07289 |
| genblast_ | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19616 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_ | SECCE2Rv | TraesCS2A | scaffold46 | TVU14361 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1D | scaffold5. | TVU31549 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t015 | SECCE6Rv | TraesCS6A | scaffold34 | TVU33412 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5B | scaffold65 | TVU44534 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE4Rv | TraesCS7A | scaffold22 | TVU11694 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE7Rv | TraesCS4A | scaffold42 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t079 | SECCE3Rv | TraesCS3D | scaffold11 | TVU34839 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t048 | SECCE3Rv | TraesCS3B | scaffold13 | TVU03805 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t054 | SECCE2Rv | TraesCS2B | scaffold40 | TVU15033 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05378 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold86 | TVT96766 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2D | scaffold36 | TVU16261 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold55 | TVU46065 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE3Rv | TraesCS3D | scaffold41 | TVU36767 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2A | scaffold2. | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold2. | TVU28179 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t055 | SECCE5Rv | TraesCS5A | genblast_C | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | scaffold29 | genblast_Z |
| LPERR10G | cds.KYUSt_ | genblast_C | Os10t054 | SECCE1Rv | TraesCS1A | scaffold13 | TVU31786 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7B | genblast_C | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold31 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t056 | SECCE1Rv | TraesCS1A | scaffold32 | TVU04460 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5D | genblast_C | genblast_C |
| LPERR08G | cds.KYUSt_ | genblast_C | Os08t047 | SECCE6Rv | TraesCS6A | scaffold26 | TVU01452 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t020 | SECCE2Rv | TraesCS1D | scaffold13 | TVT99340 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36009 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv | TraesCS6A | scaffold12 | TVU39536 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE1Rv | TraesCS1D | scaffold49 | TVU42225 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t016 | SECCE3Rv | TraesCS3B | scaffold63 | TVU21625 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t018 | genblast_C | TraesCS6B | scaffold28 | TVU41269 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48290 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t019 | SECCE7Rv | TraesCS4B | scaffold15 | TVU48075 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1D | scaffold5. | TVU31514 |
| LPERR07G | cds.KYUSt_ | genblast_C | Os01t095 | SECCE6Rv | TraesCS3A | scaffold78 | TVU36889 |

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| LPERR04G | cds.KYUSt_ | genblast_C | Os04t069 | SECCE2Rv | TraesCS2A | scaffold42 | TVU16728 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t050 | SECCE5Rv | TraesCS5A | genblast_C | TVU20741 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2B | genblast_C | TVU14438 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os11t011 | SECCE4Rv | TraesCS4D | scaffold48 | TVU27149 |
| LPERR04G | genblast_C | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2A | scaffold12 | TVU16620 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t025 | SECCE4Rv | TraesCS7D | scaffold44 | TVU03194 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t018 | SECCE6Rv | TraesCS6D | scaffold52 | TVU32845 |
| LPERR05G | cds.KYUSt_ORUFI01G | Os05t044 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36410 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os11t012 | SECCE4Rv | TraesCS4A | scaffold50 | TVU27204 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold2. | TVU27952 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3D | scaffold84 | TVU35135 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t058 | SECCE2Rv | TraesCS2A | genblast_ | TVU38146 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t084 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36770 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_ | SECCE6Rv | TraesCS3B | scaffold16 | TVU37043 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t045 | SECCE4Rv | TraesCS7A | scaffold71 | TVU50392 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1D | scaffold37 | TVU32075 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t086 | SECCE3Rv | TraesCS3A | scaffold41 | TVU36378 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5B | scaffold11 | TVU09569 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t027 | SECCE2Rv | TraesCS2B | scaffold96 | TVU13362 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1A | scaffold1. | TVU20326 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t062 | SECCE3Rv | TraesCS3B | scaffold25 | TVU35868 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t030 | SECCE5Rv | TraesCS4D | scaffold15 | TVU21223 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t029 | SECCE1Rv | TraesCS1A | scaffold38 | TVU51610 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t039 | SECCE2Rv | TraesCS2A | scaffold19 | TVU14750 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t018 | SECCE7Rv | TraesCS2D | scaffold23 | TVT98368 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6D | scaffold16 | TVU02598 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold40 | genblast_C |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold13 | TVU20443 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | scaffold18 | TVU22068 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5D | scaffold18 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t079 | SECCE4Rv | TraesCS4D | scaffold12 | TVU01381 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t044 | SECCE5Rv | TraesCS5B | scaffold87 | TVU09708 |
| LPERR04G | genblast_C | ORUFI04G | Os04t020 | SECCE7Rv | TraesCS2D | scaffold32 | TVU07241 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3A | scaffold45 | TVU36486 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold24 | TVU09725 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t046 | SECCE5Rv | TraesCS5A | scaffold53 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6A | scaffold42 | TVU33157 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE7Rv | TraesCS7A | scaffold43 | TVU10392 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t027 | SECCE4Rv1 | TraesCS7B | scaffold22 | TVU11660 |  |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE6Rv1 | TraesCS6D | scaffold83 | TVU28339 |  |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE6Rv1 | TraesCS6A | scaffold46 | TVU28462 |  |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t052 | SECCE4Rv1 | TraesCS7D | scaffold38 | TVU05115 |  |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_Z | SECCE2Rv1 | TraesCS2B | scaffold14 | TVU15975 |  |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | SECCE1Rv1 | TraesCS1D | scaffold66 | TVU16678 |  |
| genblast_C | cds.KYUSt_ORUFI02G | Os02t011 | SECCE4Rv1 | TraesCS6B | scaffold48 | TVU33643 |  |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t012 | SECCE1Rv1 | TraesCS1A | scaffold24 | TVU18086 |  |
| LPERR01G | cds.KYUSt_genblast_C | Os01t092 | SECCE3Rv1 | TraesCS3B | scaffold21 | TVU34607 |  |
| LPERR03G | genblast_C | ORUFI03G | genblast_C | SECCE5Rv1 | TraesCS5D | scaffold35 | TVU44896 |
| LPERR01G | cds.KYUSt_genblast_C | genblast_C | SECCE7Rv1 | TraesCS7A | scaffold10 | genblast_C |  |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t018 | SECCE3Rv1 | TraesCS3A | scaffold4. | TVU21460 |  |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t044 | SECCE4Rv1 | TraesCS7A | scaffold19 | TVU05684 |  |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4A | scaffold23 | TVU47677 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7D | scaffold20 | TVU43770 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7B | scaffold60 | TVU08570 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t029 | SECCE4Rv | TraesCS4D | scaffold16 | TVU25763 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t049 | SECCEUnv | TraesCS5B | scaffold10 | TVU33532 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t011 | SECCEUnv | TraesCS6B | scaffold19 | TVU33692 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t061 | SECCE3Rv | TraesCS3B | scaffold20 | TVU35955 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t050 | SECCE2Rv | TraesCS2A | genblast_C | TVU15187 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold16 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3A | scaffold10 | TVU22391 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47377 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t026 | SECCE5Rv | TraesCS5A | scaffold24 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7A | scaffold48 | TVT97568 |
| LPERR06G | genblast_C | ORUFI06G | Os06t019 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12243 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE2Rv | TraesCS2A | scaffold7. | TVU46653 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4A | scaffold42 | TVU48009 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1D | scaffold24 | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | genblast_C | genblast_C | TraesCS5B | scaffold1. | TVU50073 |
| LPERR03G | genblast_C | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47408 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28529 |
| LPERR06G | genblast_C | genblast_C | Os06t012 | SECCE4Rv | TraesCSU0 | scaffold13 | TVU12914 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t033 | SECCE7Rv | TraesCS7A | scaffold38 | TVT99556 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t054 | SECCE2Rv | TraesCS2B | scaffold58 | genblast_C |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_C | SECCE7Rv | TraesCS7B | scaffold37 | TVU06008 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold15 | TVU48042 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t069 | SECCE2Rv1 | TraesCS2A | scaffold2.1 | TVU37095 |
| LPERR03G | genblast_C | ORUFI03G | Os03t015 | SECCE7Rv1 | TraesCS4A | scaffold46 | TVU48321 |
| genblast_C | genblast_C | ORUFI05G | Os05t014 | SECCE6Rv1 | TraesCS6B | scaffold13 | TVU32266 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t058 | SECCE5Rv1 | TraesCS5A | scaffold57 | TVU49426 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t031 | SECCE5Rv1 | TraesCS5B | scaffold16 | TVU09116 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv1 | TraesCS3B | scaffold84 | TVU36614 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t055 | SECCE2Rv1 | TraesCS2A | scaffold43 | TVU38431 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv1 | TraesCS2B | scaffold2. | TVU37686 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t019 | SECCE3Rv1 | TraesCS3B | scaffold25 | TVU31268 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t065 | SECCE6Rv1 | TraesCS6B | scaffold26 | TVU29000 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv1 | TraesCS4A | scaffold74 | TVU47430 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCEUnv1 | TraesCS5D | scaffold29 | TVU49727 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE7Rv1 | TraesCS7D | scaffold5. | TVU39629 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t051 | SECCE3Rv1 | TraesCS3D | genblast_C | TVU15253 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t018 | SECCE1Rv1 | TraesCS1D | scaffold19 | TVU17108 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_Z | SECCE7Rv1 | TraesCS7A | scaffold19 | TVU05787 |

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|---|---|---|---|---|---|---|---|
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t059 | SECCE1Rv1 | TraesCS1B | scaffold19 | TVT99017 |
| LPERR02G | cds.KYUSt_ | ORUFI08G | Os02t081 | SECCE6Rv1 | TraesCS5D | scaffold70 | TVU45467 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv1 | TraesCS7D | scaffold34 | TVU12689 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv1 | TraesCS4B | scaffold15 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t084 | SECCE7Rv1 | TraesCS5D | scaffold65 | TVU44165 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t075 | SECCE3Rv1 | TraesCS3D | scaffold22 | TVT97089 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE1Rv1 | TraesCS1D | scaffold18 | TVU47007 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv1 | TraesCS5B | scaffold64 | genblast_C |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv1 | TraesCS7D | scaffold48 | TVU04697 |
| LPERR01G | cds.KYUSt_ | genblast_C | Os01t079 | SECCE3Rv1 | TraesCS3D | scaffold11 | TVU34814 |

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|---|---|---|---|---|---|---|---|
| LPERR06G | genblast_C | ORUFI06G | Os06t020 | SECCE4Rv | TraesCS7D | scaffold44 | TVU12130 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t063 | SECCE5Rv | TraesCS5B | scaffold13 | TVT97147 |
| LPERR08G | genblast_C | ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7B | scaffold24 | TVU05251 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t064 | SECCE5Rv | TraesCS5D | scaffold20 | TVU45928 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6D | scaffold24 | TVU28935 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold10 | TVU40210 |
| LPERR02G | genblast_C | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6A | scaffold11 | TVU28465 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5A | scaffold12 | TVU10539 |
| LPERR04G | genblast_C | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2D | scaffold22 | TVU15906 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19587 |
| LPERR01G | genblast_C | ORUFI01G | Os01t075 | SECCE3Rv | TraesCS3A | scaffold17 | TVT99347 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5D | scaffold3. | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE1Rv | TraesCS1B | scaffold16 | TVU02601 |
| LPERR07G | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2A | scaffold10 | TVU41335 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t056 | SECCE7Rv | TraesCS7B | scaffold28 | TVU04463 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6B | scaffold26 | TVU27655 |
| LPERR06G | genblast_C | ORUFI06G | Os06t024 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11861 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5D | scaffold76 | TVU50002 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE4Rv | TraesCS4D | scaffold36 | TVU45403 |
| LPERR02G | genblast_C | ORUFI02G | Os02t077 | SECCE6Rv | TraesCS6A | scaffold17 | TVU28741 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t060 | genblast_C | TraesCS2A | scaffold61 | TVU17116 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS2B | scaffold52 | TVU14691 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t022 | SECCE3Rv | TraesCS3B | scaffold16 | TVU22940 |
| LPERR06G | genblast_C | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7B | scaffold92 | TVU08545 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3B | scaffold36 | TVU22864 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44826 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE5Rv | TraesCS5D | scaffold86 | TVU34073 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE2Rv | TraesCS2A | scaffold33 | TVU07780 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t016 | SECCE7Rv | TraesCS4B | scaffold46 | TVU48310 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4D | scaffold32 | TVU24080 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7B | scaffold16 | TVU04761 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t032 | SECCE3Rv | TraesCS3A | scaffold23 | TVU21121 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t031 | SECCE4Rv | TraesCS4A | scaffold16 | TVU25703 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t039 | SECCE1Rv | TraesCS1D | scaffold30 | genblast_C |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t023 | SECCE1Rv | TraesCS1D | scaffold10 | TVU16902 |
| LPERR04G | genblast_C | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2B | scaffold26 | TVU14321 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t021 | SECCE4Rv | TraesCS7B | scaffold10 | TVU12098 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t050 | SECCE5Rv | TraesCS5A | scaffold16 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t027 | SECCE5Rv | TraesCS5A | scaffold79 | TVU11134 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE2Rv | TraesCS2D | scaffold40 | TVU14820 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t040 | SECCE2Rv | TraesCS3B | scaffold10 | TVT98086 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t057 | SECCEUnv | TraesCS4A | scaffold10 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t072 | SECCE3Rv | TraesCS3B | scaffold15 | genblast_C |
| genblast_C | cds.KYUSt_ | genblast_C | Os07t061 | SECCE2Rv | TraesCS2B | scaffold2. | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1D | scaffold5. | TVU31745 |
| LPERR10G | genblast_C | ORUFI10G | Os10t044 | SECCE1Rv | TraesCS1A | scaffold11 | TVU30519 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7A | scaffold9. | TVU08566 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t017 | SECCE4Rv | genblast_C | scaffold13 | TVU31242 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t015 | genblast_C | genblast_C | scaffold18 | TVU21814 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t017 | SECCE5Rv | TraesCS5A | scaffold47 | TVU22401 |

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| LPERR12G0 | cds.KYUSt_ | ORUFI12G0 | Os12t0197 | SECCE5Rv1 | TraesCS5B | scaffold70 | TVU51337 |
| LPERR02G0 | cds.KYUSt_ | ORUFI02G0 | genblast_C | SECCE6Rv1 | TraesCS6D | scaffold48 | genblast_C |
| LPERR12G0 | cds.KYUSt_ | ORUFI12G0 | Os12t0230 | SECCE5Rv1 | TraesCS5A | scaffold70 | TVU51455 |
| LPERR01G0 | cds.KYUSt_ | ORUFI01G1 | Os01t0248 | SECCE3Rv1 | TraesCS3B | scaffold29 | TVU04329 |
| LPERR02G1 | cds.KYUSt_ | ORUFI02G2 | Os02t0534 | SECCE5Rv1 | TraesCS5A | scaffold12 | TVU29873 |
| LPERR02G2 | cds.KYUSt_ | ORUFI02G2 | genblast_C | SECCE6Rv1 | TraesCS6A | scaffold26 | TVU29010 |
| LPERR03G1 | genblast_C | ORUFI03G1 | Os03t0378 | SECCE6Rv1 | TraesCS6B | scaffold18 | TVU46828 |
| LPERR01G2 | cds.KYUSt_ | ORUFI01G2 | Os01t0680 | SECCE3Rv1 | TraesCS3D | scaffold15 | TVU35507 |
| LPERR01G1 | cds.KYUSt_ | ORUFI01G1 | genblast_C | SECCE3Rv1 | TraesCS3A | scaffold2.1 | TVU22630 |
| genblast_C | cds.KYUSt_ | ORUFI02G0 | genblast_C | SECCE6Rv1 | TraesCS6B | scaffold1.7 | TVU00042 |
| LPERR07G0 | genblast_C | ORUFI07G0 | Os07t0211 | SECCE2Rv1 | TraesCS2B | scaffold28 | TVU40012 |
| LPERR01G0 | genblast_C | ORUFI01G0 | Os01t0111 | SECCE3Rv1 | TraesCS3B | scaffold25 | TVU22233 |
| LPERR11G1 | cds.KYUSt_ | ORUFI11G2 | genblast_C | SECCE4Rv1 | TraesCS4D | scaffold13 | TVU23599 |
| LPERR10G0 | cds.KYUSt_ | ORUFI10G1 | Os10t0437 | SECCE1Rv1 | TraesCS1D | scaffold33 | TVU30614 |
| LPERR07G1 | cds.KYUSt_ | ORUFI11G0 | Os11t0256 | SECCE4Rv1 | TraesCS4A | scaffold59 | TVU03035 |
| LPERR04G2 | cds.KYUSt_ | ORUFI04G2 | Os04t0641 | SECCE2Rv1 | TraesCS2B | scaffold12 | TVU16300 |
| LPERR05G0 | cds.KYUSt_ | ORUFI05G0 | Os05t0179 | SECCE1Rv1 | TraesCS1B | scaffold55 | TVU17236 |
| LPERR06G1 | genblast_C | ORUFI06G2 | Os06t0621 | SECCE7Rv1 | TraesCS7D | scaffold31 | TVU08193 |
| LPERR02G1 | cds.KYUSt_ | ORUFI02G2 | Os02t0551 | genblast_C | TraesCS6A | scaffold12 | TVU29736 |

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|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36461 |
| LPERR06G | genblast_C | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7D | scaffold21 | TVU07857 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2A | scaffold8. | TVU14244 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t017 | SECCE2Rv | TraesCS2B | scaffold28 | TVU41722 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE7Rv | TraesCS4B | scaffold17 | TVU48283 |
| LPERR06G | genblast_CORUFI06G | Os06t021 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12071 |

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|---|---|---|---|---|---|---|
| LPERR09G | genblast_CORUFI04G | Os04t035 | SECCE1Rv | TraesCS2B | genblast_C | TVT97382 |
| LPERR07G | cds.KYUSt_genblast_C | Os07t065 | SECCE2Rv | TraesCS2B | scaffold6. | TVU37444 |
| LPERR06G | genblast_CORUFI06G | Os06t022 | SECCE4Rv | TraesCS7B | scaffold14 | TVU11969 |

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|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t029 | SECCE7Rv | TraesCS7D | scaffold22 | TVU13360 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t016 | SECCE2Rv | TraesCS2D | scaffold61 | TVU31193 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_Z | genblast_Z | TraesCS5B | scaffold65 | TVU44152 |
| LPERR03G | cds.KYUSt_ORUFI03G | genblast_C | SECCE6Rv | TraesCS7A | scaffold18 | TVU13291 |

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|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t021 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47920 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1D | scaffold1. | TVU20279 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5A | genblast_C | TVU44821 |
| LPERR11G | cds.KYUSt_ORUFI11G | Os11t026 | SECCE4Rv | TraesCS4B | scaffold26 | TVU03654 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold41 | TVU02363 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3D | scaffold88 | TVU22094 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | scaffold2. | genblast_C |
| LPERR10G | genblast_CORUFI10G | genblast_C | SECCE1Rv | TraesCS1B | scaffold17 | TVU30951 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2D | scaffold2. | TVT98006 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t052 | SECCE2Rv | TraesCS2B | scaffold16 | TVU33862 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4A | scaffold15 | TVU47767 |

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|---|---|---|---|---|---|---|---|
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE1Rv | TraesCS1B | scaffold33 | TVU30655 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | scaffold43 | TVU38369 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14209 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t050 | SECCE7Rv | TraesCS7D | scaffold71 | TVT98741 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6D | scaffold17 | TVU29413 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2A | scaffold94 | TVT99726 |
| genblast_Z | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold89 | TVU36110 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t029 | SECCE1Rv | TraesCS1B | scaffold10 | TVU18580 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t048 | SECCE5Rv | TraesCS5D | scaffold33 | TVU09970 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS4A | scaffold49 | TVU12798 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI05G | Os01t088 | SECCE3Rv | TraesCS3A | scaffold31 | TVU36277 |
| LPERR08G | genblast_C | ORUFI08G | Os08t015 | SECCE4Rv | TraesCS6A | scaffold12 | TVU42921 |
| LPERR03G | genblast_C | ORUFI07G | Os07t016 | SECCE4Rv | TraesCS4B | scaffold18 | TVU47196 |
| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold54 | TVU22587 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold13 | TVU18270 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4A | scaffold21 | TVU25975 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3B | scaffold84 | TVU35200 |
| LPERR08G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE7Rv | TraesCS7D | scaffold38 | TVU48109 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t015 | SECCE7Rv | TraesCS4D | scaffold10 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t079 | SECCE6Rv | TraesCS6B | scaffold28 | TVU27934 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t043 | SECCE2Rv | TraesCS2A | scaffold99 | TVU14433 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t061 | SECCE4Rv | TraesCS4D | scaffold28 | TVT97809 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t046 | genblast_C | TraesCS2B | scaffold5. | TVU14176 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold41 | TVU36469 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t010 | SECCE7Rv | TraesCS2B | scaffold12 | TVU06885 |
| LPERR12G | genblast_C | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5D | scaffold29 | TVU49748 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1A | scaffold40 | TVU20132 |
| LPERR01G | genblast_C | ORUFI01G | Os01t071 | SECCE3Rv | TraesCS3D | scaffold92 | TVU06433 |
| LPERR04G | genblast_C | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2A | scaffold13 | TVU15336 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t016 | SECCE1Rv | TraesCS1D | scaffold36 | TVU17288 |
| genblast_C | cds.KYUSt_ | genblast_C | Os12t059 | SECCE5Rv | TraesCS5D | genblast_C | TVU49335 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t040 | SECCE2Rv | TraesCS2A | scaffold71 | TVU37963 |
| LPERR04G | genblast_C | ORUFI04G | genblast_C | SECCEUnv | TraesCS2B | scaffold30 | TVU15068 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t063 | SECCE6Rv | TraesCS6B | scaffold16 | TVU25334 |
| LPERR09G | genblast_C | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5A | scaffold43 | genblast_C |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7D | scaffold26 | TVU05174 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t049 | SECCE4Rv | TraesCS7B | scaffold26 | TVU05335 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t014 | SECCE2Rv | TraesCS2A | scaffold12 | TVU41162 |
| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t015 | SECCE5Rv | TraesCS5D | scaffold50 | TVU26894 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28494 |
| LPERR01G | genblast_C | ORUFI01G | Os01t074 | SECCE3Rv | TraesCS3A | scaffold17 | TVU35113 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t042 | SECCE5Rv | TraesCS5A | scaffold64 | TVU09552 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t066 | SECCEUnv | TraesCS4D | scaffold55 | genblast_C |
| LPERR07G | cds.KYUSt_ | ORUFI09G | Os09t049 | SECCE5Rv | TraesCS5B | scaffold53 | TVU10109 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t055 | SECCE7Rv | TraesCS7A | scaffold21 | TVU07853 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t023 | SECCE4Rv | TraesCS4D | scaffold73 | TVU25932 |
| LPERR09G | genblast_Z | ORUFI09G | genblast_Z | SECCE5Rv | TraesCS5B | scaffold23 | TVU11034 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44348 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1D | scaffold1. | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE2Rv | TraesCS2D | scaffold13 | TVU16181 |
| LPERR05G | genblast_C | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1B | scaffold1. | genblast_C |
| LPERR01G | genblast_C | ORUFI01G | Os01t058 | SECCE3Rv | TraesCS3A | scaffold20 | TVU34244 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t012 | SECCE3Rv | TraesCS3D | scaffold59 | TVU22122 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t056 | SECCE4Rv | TraesCS7B | scaffold1. | TVT96939 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4B | scaffold74 | TVU47426 |
| LPERR09G | genblast_C | ORUFI09G | Os09t039 | SECCE5Rv | TraesCS5A | scaffold64 | TVU09462 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1A | scaffold32 | TVU31757 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t082 | SECCE5Rv | TraesCS5A | scaffold17 | TVU44368 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t034 | SECCE2Rv | TraesCS2A | scaffold18 | TVU13780 |
| LPERR06G | genblast_C | ORUFI09G | Os06t055 | SECCE7Rv | TraesCS7B | scaffold25 | TVU07867 |
| LPERR03G | genblast_Z | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4D | scaffold15 | TVU47890 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE7Rv1 | TraesCS7B | scaffold20 | TVU43723 |
| LPERR06G | cds.KYUSt_ | ORUFI02G | Os02t048 | SECCE5Rv1 | TraesCS5A | scaffold44 | TVU30217 |
| genblast_C | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv1 | TraesCS1A | scaffold45 | TVU31969 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv1 | TraesCS1A | scaffold36 | TVU20094 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t041 | SECCE1Rv1 | TraesCS1A | scaffold39 | TVU19369 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv1 | TraesCS1A | scaffold12 | TVU19252 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv1 | TraesCS2D | scaffold14 | TVU15321 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t042 | SECCE5Rv1 | TraesCS5A | genblast_C | TVU46534 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv1 | TraesCS5B | scaffold16 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv1 | TraesCS5B | scaffold65 | TVT98415 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t020 | SECCE2Rv1 | TraesCS2D | scaffold10 | TVU17927 |
| LPERR04G | genblast_C | ORUFI04G | Os04t061 | SECCE2Rv1 | TraesCS2B | scaffold13 | TVU15746 |
| LPERR02G | genblast_C | ORUFI02G | Os02t079 | SECCE6Rv1 | TraesCS6D | scaffold28 | TVU27930 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE3Rv1 | TraesCS3B | scaffold11 | TVU34104 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv1 | TraesCS2D | scaffold28 | TVU39947 |
| LPERR01G | genblast_C | ORUFI01G | Os01t077 | SECCE3Rv1 | TraesCS3D | scaffold48 | TVU34909 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv1 | TraesCS7D | scaffold22 | TVU07777 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t052 | SECCE5Rv1 | TraesCS5A | scaffold22 | TVU49996 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv1 | TraesCS6B | scaffold2.1 | TVU28254 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv1 | TraesCS2A | scaffold87 | TVU14832 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv1 | TraesCS6A | scaffold35 | TVU32675 |
| LPERR04G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE7Rv1 | TraesCS2A | scaffold16 | TVU07269 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv1 | TraesCS6B | scaffold10 | TVU29047 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv1 | TraesCS6D | scaffold24 | TVU28925 |
| LPERR03G | genblast_C | ORUFI03G | Os03t076 | SECCE5Rv1 | TraesCS5D | scaffold32 | TVU44837 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t019 | SECCE6Rv1 | TraesCS3A | scaffold2.1 | TVU43156 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t087 | SECCE3Rv1 | TraesCS3D | scaffold14 | TVU36351 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t056 | SECCE6Rv1 | TraesCS6A | scaffold41 | TVU29635 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t022 | SECCE4Rv1 | TraesCS7B | scaffold23 | TVU39978 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv1 | TraesCS2A | scaffold45 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv1 | TraesCS5B | scaffold11 | TVU09681 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t076 | SECCE3Rv | TraesCS3B | scaffold22 | TVU34996 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2D | scaffold10 | TVU40284 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t060 | SECCE2Rv | TraesCS2A | scaffold2. | TVU00084 |
| LPERR01G | cds.KYUSt_ORUFI03G | Os01t094 | SECCE4Rv | TraesCS7A | scaffold31 | TVU09864 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t037 | SECCE1Rv | TraesCS1A | scaffold11 | TVU06374 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t021 | SECCE2Rv | TraesCS7D | scaffold15 | TVU30746 |

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| LPERR12G | cds.KYUSt_ORUFI12G | Os11t012 | SECCE5Rv | TraesCS5B | scaffold48 | TVU27225 |
| LPERR07G | cds.KYUSt_ORUFI09G | genblast_ | SECCE2Rv | TraesCS2A | scaffold5. | TVT97619 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t092 | SECCE3Rv | TraesCS3A | scaffold31 | TVU34596 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t017 | SECCE5Rv | TraesCS5B | scaffold96 | TVU33558 |
| LPERR05G | genblast_ | ORUFI05G | Os05t036 | SECCE1Rv | TraesCS1B | scaffold24 | TVU19033 |
| LPERR11G | cds.KYUSt_ORUFI11G | genblast_ | SECCE4Rv | TraesCS4D | scaffold21 | TVU26025 |
| LPERR02G | genblast_ | ORUFI02G | genblast_ | SECCE5Rv | TraesCS5A | scaffold66 | TVU21673 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t063 | SECCEUnv | TraesCS5D | scaffold36 | genblast_ |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_ | SECCE4Rv | TraesCS7D | scaffold31 | TVU11639 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t044 | SECCE4Rv | TraesCS7A | scaffold13 | TVU05702 |
| LPERR12G | cds.KYUSt_ORUFI12G | Os12t048 | SECCE3Rv | TraesCS3A | scaffold16 | TVU50244 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t017 | SECCE5Rv | TraesCS5D | scaffold28 | TVU41585 |

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| LPERR10G | cds.KYUSt_ORUFI10G | genblast_ | SECCE6Rv | TraesCS6A | scaffold33 | TVU30625 |
| genblast_ | cds.KYUSt_ORUFI04G | Os04t065 | SECCE2Rv | TraesCS2A | scaffold19 | TVU16422 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1B | scaffold45 | TVU31923 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t034 | SECCE6Rv | TraesCS6A | scaffold10 | TVU18865 |

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| genblast_ | genblast_ | genblast_ | Os03t065 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45842 |

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| genblast_C | cds.KYUSt_ | ORUFI11G | Os11t012 | SECCE5Rv | TraesCS4B | scaffold50 | TVU03627 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t021 | SECCE7Rv | TraesCS7A | scaffold70 | TVU43590 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold39 | genblast_C |
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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t064 | SECCE2Rv | TraesCS2D | scaffold1. | TVU37535 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_Z | SECCE1Rv | TraesCS1B | scaffold45 | TVU31811 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t068 | SECCE3Rv | TraesCS3D | scaffold15 | TVT99359 |
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| LPERR06G | genblast_C | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold34 | TVU12392 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2B | scaffold27 | TVU39327 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE3Rv | TraesCS3A | scaffold25 | TVU22583 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3A | scaffold36 | TVU21393 |
| LPERR01G | genblast_C | ORUFI01G | Os01t097 | SECCE6Rv | TraesCS3D | scaffold16 | TVU37071 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2D | genblast_C | TVU37601 |
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| LPERR06G | cds.KYUSt_ | genblast_C | Os06t048 | SECCE4Rv | TraesCS7B | scaffold2. | TVU02950 |
| genblast_C | cds.KYUSt_ | genblast_C | Os01t077 | SECCE3Rv | TraesCS3A | scaffold22 | TVU34973 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t039 | SECCE2Rv | TraesCS2B | scaffold81 | TVU14050 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold14 | TVU16046 |
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| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44391 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5A | scaffold65 | TVU44698 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t060 | SECCEUnv | TraesCS5B | scaffold76 | TVU06258 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t029 | SECCE5Rv | TraesCS5A | scaffold79 | TVU11192 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t010 | SECCEUnv | TraesCS5A | scaffold52 | TVU48671 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | genblast_Z | SECCEUnv | TraesCS7B | scaffold26 | TVU00811 |
| LPERR03G | genblast_C | ORUFI03G | Os03t074 | genblast_C | TraesCS5D | scaffold3. | TVU45065 |

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| LPERR05G | cds.KYUSt_ORUFI05G | Os05t054 | SECCE1Rv | TraesCS1A | scaffold40 | TVU04382 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t020 | SECCE3Rv | TraesCS3B | scaffold16 | TVU22805 |
| LPERR03G | genblast_C | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47754 |
| LPERR01G | genblast_C | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold88 | TVU21565 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44737 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2A | scaffold13 | TVU16219 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t049 | SECCEUnv | TraesCS5D | scaffold13 | TVU11362 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5D | scaffold27 | TVU10260 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7A | scaffold22 | genblast_C |

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| LPERR01G | genblast_C | ORUFI01G | Os01t088 | SECCE3Rv | TraesCS3D | scaffold14 | TVU36306 |
| LPERR10G | cds.KYUSt_ORUFI10G | Os10t048 | SECCE5Rv | TraesCS5D | scaffold27 | TVU30268 |

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| LPERR11G | cds.KYUSt_ORUFI11G | Os11t018 | SECCE4Rv | TraesCS4A | scaffold46 | TVU02653 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t014 | SECCE5Rv | TraesCS4D | scaffold10 | TVU48429 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t045 | SECCE7Rv | TraesCS7B | scaffold19 | TVU05629 |

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| LPERR02G | genblast_C | ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6D | scaffold83 | TVU28312 |

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| LPERR04G | cds.KYUSt_ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2A | scaffold94 | TVU15982 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3D | scaffold21 | TVU36068 |
| LPERR11G | cds.KYUSt_ORUFI11G | genblast_ | SECCE4Rv | TraesCS1A | scaffold7. | TVU24716 |
| genblast_C | cds.KYUSt_ORUFI10G | Os10t054 | SECCE1Rv | TraesCS1D | scaffold7. | TVU49919 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t055 | SECCE1Rv | TraesCS1D | scaffold15 | TVU04584 |

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|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ORUFI11G | Os11t058 | SECCE7Rv | TraesCS7A | scaffold10 | TVU14762 |
| genblast_C | genblast_CORUFI01G | Os01t093 | SECCE3Rv | TraesCS3D | scaffold31 | TVU34653 |
| genblast_C | cds.KYUSt_ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5B | scaffold27 | TVU08892 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4B | scaffold14 | TVU47635 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold14 | TVU15969 |
| LPERR11G | genblast_CORUFI11G | Os11t011 | SECCE4Rv | TraesCS4A | scaffold14 | TVU27362 |

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| genblast_C | cds.KYUSt_ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2B | scaffold94 | TVU15853 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t032 | SECCE5Rv | TraesCS5D | scaffold11 | TVU06619 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47694 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t049 | SECCE6Rv | TraesCS6B | scaffold34 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t017 | SECCE6Rv | TraesCS6D | scaffold48 | TVU02392 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t014 | SECCE6Rv | TraesCS6B | scaffold24 | TVU33454 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4D | scaffold20 | TVU45451 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t083 | SECCE3Rv | TraesCS3D | scaffold17 | TVU36731 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t065 | SECCE3Rv | TraesCS3B | scaffold42 | TVU35678 |

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| LPERR07G | cds.KYUSt_genblast_C | Os07t055 | SECCE2Rv | TraesCS2D | scaffold58 | TVU38489 |

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| LPERR11G( | cds.KYUSt_ | ORUFI11G( | Os11t0234 | SECCE4Rv] | TraesCS4D | scaffold62 | TVU25939 |

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|---|---|---|---|---|---|---|---|
| LPERR10G: | cds.KYUSt_ | ORUFI10G: | Os10t048: | genblast_C | TraesCS1D | scaffold27 | TVT99422 |
| LPERR11G( | cds.KYUSt_ | ORUFI11G( | Os11t0152 | SECCE4Rv] | TraesCS4D | scaffold14 | TVU26882 |
| LPERR05G: | cds.KYUSt_ | ORUFI05G: | Os05t0449 | SECCE1Rv] | TraesCS1B | scaffold75 | TVU19633 |
| LPERR05G( | cds.KYUSt_ | ORUFI05G( | Os05t0109 | SECCE1Rv] | TraesCS1A | scaffold40 | TVU18327 |
| LPERR08G( | cds.KYUSt_ | ORUFI08G( | Os08t0112 | SECCE7Rv] | TraesCS7D | genblast_C | TVU43699 |
| LPERR05G2 | cds.KYUSt_ | ORUFI05G2 | Os05t0567 | SECCE1Rv] | TraesCS1A | scaffold40 | TVU20276 |
| LPERR01G: | cds.KYUSt_ | genblast_C | Os01t0914 | SECCE3Rv] | TraesCS3D | scaffold21 | TVU36072 |

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| LPERR12G: | cds.KYUSt_ | ORUFI12G2 | Os12t061: | SECCE5Rv] | TraesCS5B | scaffold41 | TVU49060 |
| LPERR02G2 | cds.KYUSt_ | ORUFI02G: | Os02t077( | genblast_C | TraesCS6D | scaffold17 | TVU01723 |
| LPERR08G: | cds.KYUSt_ | ORUFI08G2 | Os08t0542 | SECCE7Rv] | TraesCS7A | scaffold16 | TVU04747 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t0236 | SECCE4Rv] | TraesCS7B | scaffold14 | TVU11895 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t0265 | SECCE7Rv] | TraesCS4B | scaffold40 | TVU47640 |
| LPERR08G( | cds.KYUSt_ | ORUFI08G( | Os08t016] | SECCE7Rv] | TraesCS7B | scaffold17 | TVU42940 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t0212 | SECCE4Rv] | TraesCS7D | scaffold14 | TVU12087 |
| LPERR07G( | cds.KYUSt_ | ORUFI07G: | Os07t0408 | SECCE2Rv] | TraesCS2D | scaffold12 | TVU39437 |
| LPERR01G2 | cds.KYUSt_ | ORUFI01G2 | Os01t066( | SECCE3Rv] | TraesCS3D | scaffold21 | TVT96956 |
| LPERR07G( | cds.KYUSt_ | ORUFI07G( | Os07t0102 | SECCE2Rv] | TraesCS2B | scaffold7.7 | TVU40112 |
| genblast_C | cds.KYUSt_ | ORUFI06G2 | Os06t0695 | SECCE7Rv] | TraesCS7D | scaffold9.7 | TVU08659 |
| LPERR03G2 | cds.KYUSt_ | ORUFI03G: | Os03t0742 | SECCE5Rv] | TraesCS5D | scaffold3.] | TVU45099 |
| LPERR03G( | genblast_C | ORUFI03G( | Os03t0125 | SECCE5Rv] | TraesCS4D | scaffold52 | TVU48539 |
| LPERR09G( | genblast_C | genblast_C | Os09t0394 | SECCE5Rv] | TraesCS5B | scaffold87 | TVU09453 |
| LPERR06G: | cds.KYUSt_ | ORUFI06G: | genblast_Z | SECCE4Rv] | TraesCS7B | scaffold22 | TVU00201 |

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| LPERR12G: | genblast_C | ORUFI12G: | Os12t0502 | SECCE6Rv] | TraesCSU0 | scaffold8.2 | TVU50147 |
| LPERR01G( | cds.KYUSt_ | ORUFI01G: | Os01t0248 | SECCE3Rv] | TraesCS3B | scaffold32 | TVU23173 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t0336 | SECCE4Rv] | TraesCS4A | scaffold22 | TVU47145 |
| LPERR11G2 | cds.KYUSt_ | ORUFI11G2 | Os11t0705 | SECCE4Rv] | TraesCS4D | scaffold46 | TVU23269 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t0299 | genblast_C | TraesCS4D | scaffold22 | TVU47374 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t0109 | SECCE4Rv] | TraesCS4A | scaffold44 | TVU13005 |

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| LPERR01G: | cds.KYUSt_ | ORUFI01G2 | Os01t0588 | SECCE3Rv] | TraesCS3A | scaffold29 | TVU34292 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t037 | SECCE6Rv | TraesCS6A | scaffold10 | TVU30844 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t039 | SECCE2Rv | TraesCS2D | scaffold19 | TVU30967 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t038 | SECCE2Rv | TraesCS2B | scaffold10 | TVU13971 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4B | scaffold74 | TVU47437 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2B | scaffold43 | TVU38295 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t048 | SECCE2Rv | TraesCS7A | scaffold14 | genblast_ |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS7D | scaffold17 | genblast_ |
| LPERR01G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCE3Rv | TraesCS3B | scaffold11 | TVU34366 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold65 | genblast_ |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t047 | genblast_C | genblast_C | scaffold24 | TVU05497 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1B | scaffold45 | TVU31973 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t019 | SECCE7Rv | TraesCS7A | scaffold23 | TVU43860 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t019 | SECCE6Rv | TraesCS6D | scaffold6. | TVU32894 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t047 | SECCE1Rv | TraesCS1A | scaffold11 | TVU30347 |
| LPERR04G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE2Rv | genblast_Z | scaffold14 | TVU15601 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE1Rv | TraesCS1B | scaffold47 | TVT97218 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t028 | SECCE3Rv | genblast_C | scaffold10 | TVU22711 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28212 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold66 | TVU41411 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t062 | SECCE2Rv | TraesCS2B | scaffold34 | TVU02437 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4D | scaffold50 | TVU26770 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47285 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5B | scaffold18 | TVU46918 |
| LPERR06G | genblast_C | ORUFI06G | Os06t032 | SECCE4Rv | TraesCS7B | scaffold22 | TVU11424 |
| LPERR09G | genblast_C | genblast_C | Os09t045 | SECCE5Rv | TraesCS5D | scaffold53 | TVU09799 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10220 |
| LPERR09G | genblast_C | ORUFI09G | Os09t044 | SECCE5Rv | TraesCS5B | scaffold87 | TVU09736 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t010 | SECCE4Rv | TraesCS6D | scaffold19 | TVU33708 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t026 | SECCE7Rv | TraesCS4A | scaffold14 | genblast_ |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t043 | SECCE2Rv | TraesCS2D | scaffold35 | TVU05752 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t044 | SECCE2Rv | TraesCS2D | scaffold77 | TVU14299 |
| LPERR10G | genblast_C | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1A | scaffold27 | TVU32117 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t017 | SECCE5Rv | TraesCS5B | scaffold83 | TVT98693 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t030 | SECCE1Rv | TraesCS1D | scaffold3. | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI08G | Os08t041 | SECCE4Rv | TraesCS6A | scaffold35 | TVT97222 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7B | scaffold21 | TVU08129 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE4Rv | TraesCSU0 | scaffold15 | TVT98476 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t072 | SECCE6Rv | TraesCS7A | scaffold22 | TVU07572 |
| LPERR10G | cds.KYUSt_ | ORUFI07G | Os07t017 | SECCE1Rv | TraesCS1B | scaffold16 | TVU30464 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE6Rv | TraesCS6A | scaffold39 | TVU32384 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCEUnv | TraesCSU0 | genblast_C | TVU48772 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t040 | SECCE7Rv | TraesCS7D | scaffold37 | TVU06133 |
| LPERR10G | genblast_C | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1B | scaffold27 | TVU01853 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t052 | SECCE1Rv | TraesCS1D | scaffold7. | TVU31926 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t085 | SECCE3Rv | TraesCS3B | scaffold31 | TVU36458 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t067 | SECCE6Rv | TraesCS6A | scaffold46 | genblast_C |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t039 | SECCE1Rv | TraesCS1D | scaffold19 | TVU30938 |
| LPERR07G | genblast_C | ORUFI07G | Os07t050 | SECCE2Rv | TraesCS2A | scaffold23 | genblast_C |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t080 | SECCE6Rv | TraesCS6D | scaffold19 | TVU27795 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_Z | SECCE4Rv | TraesCS7A | scaffold30 | TVU11459 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t014 | SECCE7Rv | TraesCS4D | scaffold10 | TVU48381 |
| LPERR01G | genblast_C | ORUFI01G | Os01t089 | genblast_C | TraesCS3D | scaffold14 | TVU36219 |
| LPERR09G | cds.KYUSt_ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5B | scaffold43 | TVU10224 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2D | scaffold28 | TVU14643 |
| genblast_C | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold29 | TVU35400 |

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| LPERR05G | cds.KYUSt_ORUFI05G | Os05t030 | SECCE2Rv | TraesCS2D | scaffold33 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4A | scaffold74 | TVT98667 |
| LPERR08G | cds.KYUSt_ORUFI08G | Os08t036 | SECCE3Rv | TraesCS3B | scaffold24 | TVU25338 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t026 | SECCE4Rv | TraesCS7A | scaffold30 | TVU11706 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t081 | SECCE3Rv | TraesCS3D | scaffold22 | TVU36586 |
| LPERR04G | cds.KYUSt_ORUFI04G | Os04t046 | SECCE2Rv | TraesCS2B | scaffold77 | TVU14172 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t051 | SECCE6Rv | TraesCS3D | scaffold43 | TVU29922 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4D | scaffold11 | TVU45443 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t059 | SECCE6Rv | TraesCS6A | scaffold23 | TVU08021 |
| LPERR01G | cds.KYUSt_ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold25 | TVU22501 |

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| LPERR02G | cds.KYUSt_ORUFI02G | Os02t032 | SECCE2Rv | TraesCS2A | scaffold54 | TVU32265 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t022 | SECCE7Rv | TraesCS4A | scaffold9. | TVU47832 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t084 | SECCE7Rv | TraesCS5B | scaffold25 | TVU44034 |
| LPERR06G | cds.KYUSt_ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold12 | TVU08203 |

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| LPERR06G | genblast_C | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold36 | TVU12424 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3B | scaffold34 | TVU22877 |

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| LPERR04G | genblast_C | ORUFI06G | Os04t063 | SECCE2Rv | TraesCS2D | scaffold20 | TVU16226 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t074 | SECCE5Rv | TraesCS5A | scaffold20 | TVU45119 |

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| LPERR06G | cds.KYUSt_ORUFI06G | Os06t014 | SECCE4Rv | TraesCS7D | scaffold34 | TVT97524 |
| genblast_C | cds.KYUSt_ORUFI03G | Os03t028 | SECCE7Rv | TraesCS4A | scaffold22 | TVU47480 |
| genblast_C | cds.KYUSt_ORUFI07G | Os07t040 | SECCE2Rv | TraesCS2A | scaffold65 | TVU51607 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t012 | SECCE4Rv | TraesCS7D | scaffold13 | TVT98097 |
| LPERR02G | cds.KYUSt_ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold1. | TVU32900 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | SECCE2Rv | TraesCS7B | scaffold25 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5A | scaffold27 | TVT98817 |
| LPERR03G | genblast_C | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4A | scaffold74 | TVU47421 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t059 | SECCE2Rv | TraesCS2A | scaffold2. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4A | scaffold11 | TVU45476 |
| LPERR08G | genblast_C | ORUFI08G | Os08t017 | SECCE4Rv | genblast_C | scaffold32 | TVU04472 |

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| LPERR05G | cds.KYUSt_ | genblast_C | Os05t049 | SECCE1Rv | TraesCS1D | scaffold39 | TVU20018 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t029 | SECCE4Rv | TraesCS7A | scaffold48 | TVU42448 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6B | scaffold11 | TVU28601 |
| LPERR09G | cds.KYUSt_ | genblast_C | Os09t052 | SECCE5Rv | TraesCS5A | scaffold29 | TVU08853 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1B | scaffold24 | TVU18098 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t060 | SECCE7Rv | TraesCS7B | scaffold21 | TVU08082 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3A | scaffold11 | TVU34777 |
| LPERR12G | genblast_C | ORUFI12G | Os12t023 | genblast_C | genblast_C | scaffold70 | TVU51465 |
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t043 | SECCE1Rv | TraesCS1D | scaffold47 | TVU39494 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE7Rv | TraesCS7D | scaffold12 | TVU08251 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t064 | SECCE6Rv | TraesCS6B | scaffold26 | TVU29017 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t061 | SECCE4Rv | TraesCS4D | scaffold55 | TVU46130 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | scaffold83 | TVT98445 |

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| LPERR07G | genblast_C | ORUFI07G | Os07t063 | SECCE2Rv | TraesCS2B | scaffold2. | TVU37730 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS5A | scaffold78 | TVU17489 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5D | scaffold49 | TVU47323 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE2Rv | TraesCS6D | scaffold46 | TVU33960 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t042 | SECCE5Rv | TraesCS4B | scaffold19 | TVU31110 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t054 | SECCE2Rv | TraesCS2A | scaffold28 | TVU15018 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t056 | SECCE5Rv | TraesCS5A | scaffold29 | TVU49718 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold2. | TVU01164 |
| genblast_C | cds.KYUSt_ | ORUFI06G | Os06t022 | SECCE4Rv | TraesCS7A | scaffold30 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t028 | SECCE3Rv | TraesCS3D | scaffold15 | TVU03203 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t041 | SECCE4Rv | TraesCS6A | scaffold38 | TVU46596 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t017 | SECCE7Rv | TraesCS4D | scaffold15 | genblast_C |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t062 | SECCE2Rv | TraesCS2A | scaffold20 | TVU16151 |
| LPERR09G | genblast_C | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold27 | TVU09444 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1D | scaffold13 | genblast_C |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t017 | SECCE7Rv | TraesCS4A | scaffold10 | genblast_C |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t051 | SECCE5Rv | TraesCS5A | scaffold16 | TVU11155 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6B | scaffold46 | TVT99738 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45398 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2D | scaffold1. | TVT96765 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t032 | SECCE5Rv | TraesCS5B | scaffold39 | TVU00858 |
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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44618 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t038 | SECCE1Rv | TraesCS1D | scaffold8. | genblast_C |
| LPERR11G | cds.KYUSt_ | ORUFI02G | Os02t046 | SECCE4Rv | TraesCS4D | scaffold64 | TVU02617 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os02t078 | SECCE3Rv | TraesCS6B | scaffold28 | TVU28889 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44627 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t066 | SECCE6Rv | TraesCS6B | scaffold24 | TVU27963 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2B | scaffold13 | TVU15342 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t029 | SECCE1Rv | TraesCS1B | scaffold21 | TVU32435 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCE5Rv | TraesCS5A | scaffold75 | TVU48762 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t083 | SECCE7Rv | TraesCS4A | scaffold25 | TVU43931 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold2. | TVU37615 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold14 | TVU47521 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t082 | SECCE6Rv | TraesCS6D | scaffold27 | TVU27662 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE3Rv | TraesCS3A | scaffold54 | TVU22556 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45594 |
| LPERR02G | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE6Rv | TraesCS6B | scaffold31 | TVU33465 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t013 | SECCE5Rv | TraesCS5B | scaffold14 | TVU01496 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t014 | SECCE6Rv | TraesCS6A | scaffold48 | TVU07201 |
| LPERR10G | genblast_C | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1A | scaffold92 | TVU08451 |
| LPERR08G | genblast_C | ORUFI08G | Os08t032 | SECCE7Rv | TraesCS7A | scaffold26 | TVU06627 |
| LPERR05G | genblast_C | ORUFI05G | Os05t052 | genblast_C | genblast_C | scaffold32 | TVU20532 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_C | SECCE5Rv | TraesCS5B | scaffold55 | TVU04149 |
| LPERR02G | genblast_C | genblast_C | Os02t077 | SECCE6Rv | TraesCS6D | scaffold28 | TVU28775 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE3Rv | TraesCS3D | scaffold33 | TVU22994 |
| LPERR02G | genblast_C | ORUFI11G | genblast_C | SECCE4Rv | TraesCS4B | scaffold76 | TVU46010 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6A | scaffold16 | TVU29162 |
| LPERR01G | genblast_C | ORUFI01G | Os01t077 | SECCE3Rv | TraesCS3A | scaffold17 | TVU34974 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE2Rv | TraesCS7D | scaffold25 | TVU08447 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3A | scaffold36 | TVU21534 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t027 | SECCE6Rv | TraesCS6D | scaffold15 | TVU32613 |
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| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t054 | SECCE5Rv | TraesCS5A | scaffold27 | genblast_C |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t025 | SECCE2Rv | TraesCS2B | scaffold19 | TVU16482 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t010 | SECCE7Rv | TraesCS7B | scaffold36 | TVU43836 |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t029 | SECCE4Rv | TraesCS7A | scaffold68 | TVU03305 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE6Rv | TraesCS6D | scaffold46 | TVU28009 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t013 | SECCE1Rv | TraesCS1A | scaffold24 | TVU18026 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t018 | SECCE6Rv | TraesCS2B | scaffold1. | TVU00046 |
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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1A | scaffold16 | TVU30262 |
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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t019 | SECCE3Rv | TraesCS3D | scaffold63 | TVU01696 |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4D | scaffold20 | genblast_ |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2B | scaffold49 | TVU16094 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold28 | TVU28871 |
| LPERR02G | genblast_Z | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold41 | TVU33398 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5B | scaffold27 | TVU09421 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os12t054 | SECCE5Rv | TraesCS5B | scaffold1. | TVU49943 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t067 | SECCE7Rv | TraesCS7D | scaffold16 | TVU08551 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t050 | SECCE2Rv | TraesCS2B | scaffold56 | TVU15352 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t076 | SECCE5Rv | TraesCS5D | scaffold32 | TVU44882 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7A | scaffold44 | TVT99288 |
| LPERR03G | cds.KYUSt_ | ORUFI08G | Os10t036 | SECCEUnv | TraesCS5D | scaffold46 | TVU22417 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t034 | SECCE2Rv | TraesCS2A | scaffold94 | TVT99713 |
| genblast_C | genblast_C | ORUFI09G | Os09t046 | SECCE5Rv | TraesCS5A | scaffold27 | genblast_ |
| LPERR01G | cds.KYUSt_ | ORUFI09G | Os01t084 | SECCE3Rv | TraesCS3D | scaffold31 | TVU36755 |
| LPERR05G | genblast_C | ORUFI05G | Os05t037 | SECCE1Rv | TraesCS1A | scaffold36 | TVU19142 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t020 | SECCE1Rv | TraesCS1A | scaffold20 | TVU42093 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_C | SECCE2Rv | TraesCS2A | scaffold10 | TVU41359 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t022 | SECCE1Rv | TraesCS1A | scaffold84 | TVU07147 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE1Rv | TraesCS1D | scaffold1. | TVU31989 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4A | scaffold49 | TVU47315 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE6Rv | TraesCS7A | scaffold92 | TVU08366 |
| genblast_C | genblast_C | ORUFI09G | Os09t045 | SECCE5Rv | TraesCS5D | scaffold27 | TVU09790 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t049 | SECCE2Rv | TraesCS2A | scaffold56 | TVU15454 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold54 | TVU29148 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6B | scaffold22 | TVU28614 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t052 | SECCE2Rv | TraesCS2B | scaffold20 | TVU15126 |
| LPERR03G | genblast_C | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4B | scaffold14 | TVU47596 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t052 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08848 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3D | genblast_C | TVU36598 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv | TraesCS4B | scaffold52 | genblast_C |
| LPERR02G | genblast_C | ORUFI02G | Os02t078 | SECCE6Rv | TraesCS6D | scaffold17 | TVU28860 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE4Rv | TraesCS6D | scaffold11 | TVU32080 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCEUnv | TraesCS6B | scaffold23 | TVU35838 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t065 | SECCE3Rv | TraesCS3A | scaffold3. | TVU35740 |
| genblast_C | genblast_C | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4B | scaffold15 | TVU47737 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t069 | SECCE4Rv | TraesCS4D | scaffold55 | TVU45532 |

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| LPERR01G | genblast_C | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold59 | TVU21727 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3B | scaffold11 | TVU35563 |
| genblast_C | cds.KYUSt_ | genblast_C | Os05t042 | SECCE1Rv | TraesCS1A | scaffold20 | TVU19473 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t052 | SECCE5Rv | TraesCS5B | scaffold18 | TVU24604 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_C | SECCE2Rv | genblast_C | scaffold16 | TVU16513 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t021 | SECCE1Rv | TraesCS1A | scaffold10 | TVU16964 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t048 | SECCE1Rv | TraesCS1D | scaffold16 | TVU30285 |
| LPERR11G | genblast_Z | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4D | scaffold62 | TVU25888 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t041 | SECCE2Rv | TraesCS2B | scaffold45 | TVU46594 |

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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t071 | SECCE7Rv | TraesCS7B | scaffold9. | TVU07637 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t061 | SECCE7Rv | TraesCS7B | scaffold31 | TVU08168 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t080 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44540 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t079 | genblast_C | TraesCS5A | scaffold3. | TVU44636 |
| LPERR04G | genblast_C | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2D | scaffold26 | TVU16637 |

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| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t016 | SECCE4Rv | TraesCS7A | scaffold12 | TVU42952 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t062 | SECCE6Rv | TraesCS6A | scaffold16 | TVU29180 |

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| LPERR08G | cds.KYUSt_ORUFI08G | Os08t050 | SECCE4Rv | TraesCS7B | scaffold13 | TVU05245 |
| LPERR07G | cds.KYUSt_ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | genblast_C | TVU39006 |

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| LPERR01G | cds.KYUSt_ORUFI01G | Os01t063 | SECCE3Rv | TraesCS3B | scaffold92 | TVU02528 |
| LPERR06G | cds.KYUSt_ORUFI06G | Os06t064 | SECCEUnv | TraesCS6B | scaffold92 | genblast_C |
| LPERR04G | cds.KYUSt_ORUFI04G | genblast_C | SECCE2Rv | TraesCS2D | scaffold49 | TVU15222 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t074 | SECCE6Rv | TraesCS6D | scaffold11 | TVU28521 |
| LPERR01G | cds.KYUSt_ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3D | scaffold89 | TVU01589 |
| LPERR09G | genblast_C | ORUFI09G | Os09t010 | SECCE7Rv | TraesCS7D | scaffold3. | TVU10723 |

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| LPERR01G | cds.KYUSt_genblast_C | Os01t073 | SECCE3Rv | TraesCS3D | scaffold15 | TVU35175 |
| LPERR03G | genblast_CORUFI03G | Os03t078 | SECCE5Rv | TraesCS5A | scaffold3. | TVU44730 |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t073 | SECCE6Rv | TraesCS6B | scaffold11 | genblast_C |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold41 | TVU44325 |
| LPERR05G | cds.KYUSt_ORUFI05G | Os05t050 | SECCE1Rv | TraesCS1D | scaffold39 | TVU20048 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t020 | SECCE7Rv | TraesCS4D | scaffold9. | TVU48038 |

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| LPERR07G | cds.KYUSt_ORUFI07G | Os07t067 | SECCE2Rv | TraesCS2D | scaffold1. | TVU37287 |

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| LPERR01G | genblast_CORUFI01G | Os01t079 | SECCE3Rv | TraesCS3B | scaffold46 | TVU34818 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t077 | SECCE5Rv | TraesCS5B | scaffold3. | TVU44776 |

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| LPERR03G | cds.KYUSt_ORUFI03G | Os03t065 | SECCE4Rv | TraesCS4D | scaffold11 | TVU45827 |
| LPERR03G | cds.KYUSt_ORUFI03G | Os03t023 | SECCE7Rv | TraesCS4B | scaffold9. | genblast_C |
| LPERR07G | cds.KYUSt_ORUFI07G | genblast_C | SECCE2Rv | TraesCS2D | scaffold30 | TVU37819 |
| LPERR05G | cds.KYUSt_ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold12 | genblast_C |
| LPERR02G | cds.KYUSt_ORUFI02G | Os02t072 | SECCE6Rv | TraesCS6B | scaffold45 | TVU01702 |

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| LPERR09G | cds.KYUSt_ | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold29 | TVU08797 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t028 | SECCE2Rv | TraesCS2A | scaffold99 | TVU13401 |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2A | scaffold49 | TVU15942 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t069 | SECCEUnv | TraesCS6B | scaffold12 | TVU28094 |
| LPERR05G | cds.KYUSt_ | genblast_C | Os05t036 | SECCE1Rv | TraesCS1D | scaffold24 | TVU19031 |
| LPERR01G | genblast_C | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3A | scaffold10 | TVU22467 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t023 | SECCE4Rv | TraesCS7B | scaffold30 | TVU28453 |
| genblast_C | genblast_C | ORUFI03G | Os03t079 | SECCE5Rv | TraesCS5B | scaffold65 | TVU44561 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t075 | SECCE5Rv | TraesCS5A | genblast_C | genblast_C |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t050 | SECCE3Rv | TraesCS3A | scaffold40 | TVU50154 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | genblast_C | SECCE7Rv | TraesCS7D | scaffold18 | TVU08707 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t027 | SECCE7Rv | TraesCS4D | scaffold40 | TVU47512 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCEUnv | TraesCSU0 | scaffold46 | genblast_Z |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t055 | SECCE5Rv | TraesCS5A | scaffold27 | TVU10367 |
| LPERR08G | cds.KYUSt_ | ORUFI01G | Os01t030 | SECCE5Rv | TraesCS5D | scaffold11 | TVU06635 |
| genblast_Z | cds.KYUSt_ | genblast_Z | Os05t018 | SECCE1Rv | TraesCS1A | scaffold10 | TVU07105 |
| LPERR09G | genblast_C | ORUFI09G | genblast_C | SECCE5Rv | TraesCS5A | scaffold64 | TVU09515 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t051 | SECCEUnv | TraesCS5B | scaffold10 | TVU50014 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t058 | SECCE1Rv | TraesCS1D | scaffold15 | TVT97204 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t056 | SECCE2Rv | TraesCS2A | scaffold2. | TVU38415 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t066 | genblast_C | TraesCS7D | scaffold92 | TVU08462 |
| LPERR12G | genblast_C | ORUFI12G | Os12t050 | SECCE5Rv | TraesCS5B | scaffold8. | TVU50079 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t030 | SECCE7Rv | TraesCS4B | scaffold22 | TVU47297 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS6A | scaffold6. | TVU33117 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t042 | SECCE1Rv | TraesCS1D | scaffold39 | TVU19482 |

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| genblast_C | genblast_C | ORUFI10G | Os10t057 | SECCE1Rv | TraesCS1A | scaffold85 | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t070 | SECCE4Rv | TraesCS4B | scaffold20 | TVU45455 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_Z | SECCE7Rv | TraesCS2D | scaffold4. | TVU21215 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t048 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19969 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t051 | SECCE4Rv | TraesCS7D | scaffold24 | TVT99156 |
| LPERR07G | cds.KYUSt_ | genblast_C | genblast_C | SECCE2Rv | TraesCS2A | scaffold43 | TVU38863 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t059 | SECCE2Rv | TraesCS2B | scaffold37 | TVU15903 |
| LPERR05G | genblast_C | ORUFI05G | Os05t044 | SECCE1Rv | TraesCS1A | scaffold75 | TVU19606 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t058 | SECCE7Rv | TraesCS7B | scaffold18 | TVU46311 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2B | scaffold36 | TVU40113 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t029 | SECCE7Rv | TraesCS4D | scaffold40 | TVU47409 |
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| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t027 | SECCE4Rv | TraesCS7B | scaffold38 | TVU11684 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t043 | SECCE5Rv | TraesCS5B | scaffold24 | TVU09711 |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t068 | SECCE2Rv | TraesCS6A | scaffold46 | TVU28028 |
| LPERR03G | genblast_C | ORUFI03G | Os03t037 | SECCE6Rv | TraesCS6B | scaffold18 | TVU46847 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t045 | SECCE2Rv | TraesCS2A | scaffold77 | TVU14183 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4A | scaffold40 | genblast_Z |
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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t030 | SECCE1Rv | TraesCS1A | scaffold14 | TVU11138 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t065 | SECCE3Rv | TraesCS3A | scaffold42 | TVU35725 |
| genblast_C | cds.KYUSt_ | ORUFI09G | Os09t040 | SECCE4Rv | TraesCS4A | scaffold36 | TVU13002 |
| genblast_Z | cds.KYUSt_ | genblast_Z | genblast_Z | SECCE2Rv | TraesCS7B | genblast_Z | TVU08412 |

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| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t036 | SECCE3Rv | TraesCS3B | scaffold28 | TVU20921 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t080 | SECCE3Rv | TraesCS3A | scaffold46 | TVU34728 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold17 | TVU02953 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t071 | SECCE6Rv | TraesCS6A | scaffold27 | TVU28224 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t057 | SECCE1Rv | TraesCS1B | scaffold40 | genblast_ |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_ | SECCE3Rv | TraesCS3D | scaffold31 | TVU36154 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t063 | SECCE7Rv | TraesCS7D | scaffold25 | genblast_ |

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| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t082 | SECCE5Rv | TraesCS5B | scaffold3. | TVU02956 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE2Rv | TraesCS2A | scaffold4. | TVU02749 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t030 | SECCE5Rv | TraesCS5D | scaffold72 | TVU09095 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t061 | SECCE6Rv | TraesCS6A | scaffold17 | TVU29284 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2B | scaffold1. | TVT97985 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | genblast_ | SECCE5Rv | TraesCS5D | scaffold38 | TVU46604 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t013 | SECCE5Rv | TraesCS5A | scaffold70 | TVU10893 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t062 | SECCE4Rv | TraesCS4D | genblast_ | TVU46075 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7A | scaffold10 | TVU12399 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t085 | SECCE7Rv | TraesCS4A | scaffold65 | TVU44166 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_ | SECCE5Rv | TraesCS5B | scaffold32 | TVU07913 |
| genblast_ | genblast_ | ORUFI10G | Os10t044 | SECCE1Rv | TraesCS1D | scaffold27 | TVU30568 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1B | genblast_ | genblast_ |
| genblast_ | genblast_ | ORUFI12G | Os12t024 | SECCE5Rv | TraesCS5A | scaffold83 | genblast_ |
| LPERR12G | genblast_ | ORUFI12G | Os11t014 | SECCE5Rv | TraesCS5A | scaffold70 | TVU50824 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t053 | SECCE7Rv | TraesCS7A | scaffold18 | TVU07790 |
| genblast_ | cds.KYUSt_ | ORUFI12G | Os12t057 | SECCE5Rv | TraesCS5B | scaffold29 | TVU49568 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t012 | SECCE1Rv | TraesCS1A | scaffold40 | TVT98111 |
| LPERR07G | cds.KYUSt_ | genblast_ | Os07t069 | SECCE2Rv | TraesCS2D | scaffold1. | TVU37101 |

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| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t010] | SECCE5Rv] | TraesCS4D | scaffold46 | TVU48697 |
| LPERR01G( | cds.KYUSt_ | ORUFI01G( | Os01t016( | SECCE3Rv] | TraesCS3B | scaffold88 | TVU21662 |
| LPERR12G( | cds.KYUSt_ | ORUFI12G( | Os12t011! | SECCE5Rv] | TraesCS5B | scaffold47 | TVU27299 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t020: | SECCE4Rv] | TraesCS7D | scaffold10 | TVU12167 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | Os02t080( | SECCE6Rv] | TraesCS6B | scaffold17 | TVU27806 |
| LPERR08G( | genblast_C | ORUFI01G: | Os08t017: | SECCE3Rv] | TraesCS3B | scaffold17 | TVU35019 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | Os02t055( | SECCEUnv] | TraesCS5A | scaffold41 | TVU29697 |
| LPERR02G( | genblast_C | ORUFI02G( | genblast_C | SECCE6Rv] | TraesCS6A | scaffold98 | TVU33503 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t035( | SECCE1Rv] | TraesCS1B | scaffold81 | TVU14723 |
| genblast_C | cds.KYUSt_ | ORUFI04G: | Os04t051( | SECCE2Rv] | TraesCS2B | scaffold13 | TVU20233 |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t022: | SECCE7Rv] | TraesCS4D | scaffold97 | TVU47880 |
| LPERR01G( | cds.KYUSt_ | ORUFI01G( | Os01t012; | SECCE3Rv] | TraesCS3D | scaffold88 | TVU22083 |
| LPERR07G: | cds.KYUSt_ | ORUFI07G: | Os07t053( | SECCE2Rv] | TraesCS2A | scaffold43 | TVU38607 |
| LPERR06G: | cds.KYUSt_ | ORUFI06G: | Os06t036; | SECCE7Rv] | TraesCS7A | scaffold56 | TVU10680 |
| LPERR09G( | cds.KYUSt_ | ORUFI09G( | Os09t013: | SECCE5Rv] | TraesCS5A | scaffold83 | TVU10878 |
| LPERR03G: | cds.KYUSt_ | ORUFI03G: | Os03t067( | SECCE4Rv] | TraesCS4D | scaffold11 | TVU45720 |
| genblast_C | genblast_C | ORUFI03G( | Os03t023; | SECCE7Rv] | TraesCS4A | scaffold15 | TVU47801 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | Os02t074] | SECCE6Rv] | TraesCS6A | scaffold2.] | genblast_C |
| LPERR05G( | cds.KYUSt_ | ORUFI05G( | Os05t011! | SECCE7Rv] | TraesCS4A | scaffold3.4 | TVU44083 |
| LPERR02G: | cds.KYUSt_ | ORUFI02G: | Os02t076; | SECCE6Rv] | TraesCS6D | scaffold22 | TVU28640 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t057] | SECCE2Rv] | TraesCS2D | scaffold94 | genblast_C |
| genblast_C | cds.KYUSt_ | ORUFI07G( | Os07t018; | SECCE1Rv] | TraesCS1A | scaffold10 | TVU41223 |
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| LPERR01G: | cds.KYUSt_ | ORUFI01G: | Os01t082! | SECCE3Rv] | TraesCS3D | scaffold31 | TVU36654 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G4 | genblast_Z | SECCE6Rv] | TraesCS3B | scaffold21 | TVU34700 |
| LPERR06G( | genblast_C | ORUFI06G: | genblast_C | SECCE4Rv] | TraesCS7B | scaffold22 | TVU11699 |
| LPERR10G( | cds.KYUSt_ | ORUFI03G( | Os03t016; | SECCE7Rv] | TraesCS4A | scaffold17 | TVU48274 |
| LPERR05G: | cds.KYUSt_ | ORUFI05G: | genblast_C | SECCE1Rv] | TraesCS1D | scaffold13 | TVU35743 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t0114 | SECCE4Rv] | TraesCS7A | scaffold44 | TVT98461 |
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| LPERR10G( | genblast_C | ORUFI03G( | Os03t016{ | SECCE7Rv] | TraesCS4D | genblast_C | TVU48260 |
| LPERR04G: | cds.KYUSt_ | ORUFI04G: | Os04t052; | SECCE2Rv] | TraesCS2D | scaffold20 | TVU15120 |
|  |  |  |  |  |  |  |  |
| LPERR06G( | cds.KYUSt_ | ORUFI06G: | Os06t0254 | SECCE4Rv] | TraesCS7A | scaffold30 | TVU11811 |
| LPERR03G: | cds.KYUSt_ | genblast_C | Os03t085( | SECCE1Rv] | TraesCS1A | scaffold39 | TVU44255 |
| LPERR06G: | cds.KYUSt_ | ORUFI06G: | Os06t0484 | SECCE4Rv] | TraesCS7A | scaffold10 | TVU11272 |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t017( | SECCE7Rv] | TraesCS4B | scaffold17 | TVU48255 |
| LPERR01G: | cds.KYUSt_ | ORUFI01G4 | Os01t087( | SECCE3Rv] | TraesCS3D | scaffold31 | TVU36325 |
| LPERR09G( | cds.KYUSt_ | ORUFI09G: | Os09t042{ | SECCE5Rv] | TraesCS5A | scaffold87 | TVU09625 |
| LPERR06G( | cds.KYUSt_ | ORUFI06G( | Os06t023] | SECCE4Rv] | TraesCS7A | scaffold30 | TVU11926 |
|  |  |  |  |  |  |  |  |
| LPERR03G( | cds.KYUSt_ | ORUFI03G( | Os03t021( | SECCE7Rv] | TraesCS4B | scaffold53 | TVU47906 |

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| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t061 | SECCE2Rv | TraesCS2D | scaffold30 | TVU37941 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t081 | SECCE5Rv | TraesCS5D | genblast_C | TVU44453 |
| LPERR12G | genblast_C | ORUFI12G | Os12t015 | SECCE5Rv | TraesCS5D | scaffold97 | TVU50923 |
| LPERR07G | genblast_C | ORUFI07G | Os07t066 | SECCE2Rv | TraesCS2A | scaffold2. | TVU37347 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t027 | SECCEUnv | TraesCS7D | scaffold92 | TVU08398 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t076 | SECCE6Rv | TraesCS6A | scaffold55 | TVU28615 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS4B | genblast_C | TVU48458 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t052 | SECCE2Rv | TraesCS2B | scaffold43 | genblast_C |

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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold49 | TVU16029 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t040 | SECCE5Rv | TraesCS5D | scaffold23 | TVU46731 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t057 | SECCE2Rv | TraesCS2B | scaffold96 | TVT97553 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t031 | SECCE7Rv | TraesCS4B | scaffold18 | TVU47275 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold16 | TVU08937 |

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| LPERR01G | cds.KYUSt_ | ORUFI03G | Os03t036 | SECCE5Rv | TraesCS5D | scaffold18 | TVU33829 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t014 | SECCE4Rv | TraesCS4A | scaffold34 | TVU12646 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1D | scaffold36 | TVT97174 |

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| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t019 | SECCE4Rv | TraesCS4B | scaffold9. | TVU26294 |
| LPERR06G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1A | scaffold32 | TVU27831 |
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| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t060 | SECCE2Rv | TraesCS2B | scaffold94 | TVU15838 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t068 | SECCE7Rv | TraesCS7D | scaffold60 | TVU08588 |
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| LPERR11G | cds.KYUSt_ | genblast_C | Os11t014 | SECCE5Rv | TraesCS5B | scaffold14 | TVU27039 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t011 | SECCE5Rv | TraesCS5A | scaffold34 | TVU48597 |
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| LPERR01G | genblast_C | ORUFI01G | Os01t027 | SECCE5Rv | TraesCS5A | scaffold54 | TVU22631 |
| LPERR06G | genblast_C | genblast_C | Os06t012 | SECCE4Rv | TraesCS4A | scaffold23 | TVT98093 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t010 | SECCE3Rv | TraesCS3D | scaffold47 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t025 | SECCE3Rv | TraesCS3B | scaffold10 | TVU22434 |
| LPERR03G | genblast_Z | ORUFI03G | genblast_Z | SECCE7Rv | TraesCS4A | scaffold97 | TVU47843 |

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| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t045 | SECCE1Rv | TraesCS1B | scaffold16 | genblast_ |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t013 | SECCE5Rv | TraesCS5A | scaffold10 | TVU48483 |

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| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold84 | TVU28544 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os12t011 | SECCE5Rv | TraesCS5A | scaffold14 | TVU51577 |
| genblast_ | cds.KYUSt_ | ORUFI09G | Os09t047 | SECCE5Rv | TraesCS5B | scaffold33 | TVU09925 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t053 | SECCE2Rv | TraesCS2D | scaffold28 | TVU15043 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_ | SECCE2Rv | TraesCS2B | genblast_ | TVU37655 |

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| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t047 | SECCE6Rv | TraesCS6B | scaffold58 | TVU50334 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_ | genblast_ | TraesCS1B | scaffold75 | TVT96676 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t026 | SECCE4Rv | TraesCS4D | genblast_ | TVU16870 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t042 | SECCE2Rv | TraesCS2A | scaffold38 | TVU05801 |
| LPERR04G | genblast_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2A | scaffold14 | TVU16103 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t032 | SECCE5Rv | TraesCS5A | scaffold14 | TVU09193 |
| LPERR10G | genblast_ | ORUFI10G | Os10t014 | SECCE5Rv | TraesCS5B | scaffold10 | TVU31342 |

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| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t015 | SECCE1Rv | TraesCS1A | scaffold11 | TVU17538 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t051 | SECCE5Rv | TraesCS5D | scaffold53 | TVU08782 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t037 | SECCE4Rv | TraesCS4A | scaffold15 | TVU46823 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t041 | SECCE1Rv | TraesCS1B | scaffold39 | TVU19385 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_ | SECCE3Rv | TraesCS3D | scaffold6. | TVU18611 |

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| LPERR04G | genblast_C | ORUFI04G | Os04t018 | SECCE7Rv | TraesCS2A | scaffold23 | TVT96888 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold21 | TVU36013 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t022 | SECCE4Rv | TraesCS6D | scaffold23 | TVU01525 |
| LPERR09G | genblast_C | ORUFI09G | Os09t057 | SECCE5Rv | TraesCS5B | scaffold3. | TVU10786 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t026 | SECCE3Rv | TraesCS3A | scaffold10 | TVU22585 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t069 | SECCE7Rv | TraesCS7B | scaffold9. | genblast_C |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t071 | SECCE4Rv | TraesCS4D | scaffold3. | TVU45343 |
| LPERR07G | genblast_C | ORUFI07G | Os07t010 | SECCE2Rv | TraesCS2A | scaffold7. | TVU13193 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCE6Rv | TraesCS6A | scaffold27 | TVU28202 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t017 | SECCE3Rv | TraesCS3D | scaffold36 | TVU21519 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t075 | SECCE6Rv | TraesCS6D | scaffold2. | TVU28558 |
| LPERR12G | genblast_C | ORUFI12G | Os12t025 | SECCE1Rv | TraesCS1A | scaffold14 | TVU03551 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | genblast_Z | SECCEUnv | TraesCS6B | scaffold48 | genblast_Z |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t011 | SECCE7Rv | TraesCS5B | scaffold39 | TVU44180 |
| genblast_C | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE6Rv | TraesCS6A | scaffold12 | TVU29740 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t049 | SECCE1Rv | TraesCS1A | scaffold12 | TVU19926 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os04t047 | SECCE6Rv | TraesCS6B | scaffold19 | TVU29437 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t052 | SECCE4Rv | TraesCS7A | scaffold26 | TVU01498 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t014 | SECCE5Rv | TraesCS5B | scaffold97 | TVU26949 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t070 | SECCE6Rv | TraesCS6B | scaffold12 | TVU28195 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | Os05t045 | SECCE1Rv | TraesCS1D | scaffold12 | TVU19690 |
| genblast_C | genblast_C | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5D | scaffold65 | TVU44740 |
| LPERR11G | cds.KYUSt_ | ORUFI11G | Os11t015 | SECCE5Rv | TraesCS5A | scaffold97 | TVU26905 |
| LPERR01G | cds.KYUSt_ | ORUFI09G | Os01t083 | SECCE3Rv | TraesCS3A | scaffold41 | TVT98567 |
| genblast_C | genblast_C | ORUFI05G | Os05t056 | SECCE1Rv | TraesCS1D | scaffold13 | TVU20317 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t071 | SECCE7Rv | TraesCS7D | scaffold22 | TVU07592 |
| genblast_C | cds.KYUSt_ | ORUFI03G | Os03t072 | SECCE4Rv | TraesCS4A | scaffold20 | TVU45301 |
| LPERR06G | cds.KYUSt_ | genblast_C | Os06t065 | SECCEUnv | TraesCS7A | scaffold25 | TVU08399 |
| genblast_C | cds.KYUSt_ | ORUFI01G | genblast_C | SECCE3Rv | TraesCS3A | scaffold59 | TVU22052 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | Os10t050 | SECCE1Rv | TraesCS1B | scaffold37 | TVU32094 |

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|---|---|---|---|---|---|---|---|
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5D | scaffold3. | TVU44735 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t034 | SECCE7Rv | TraesCS7D | scaffold18 | TVU47080 |
| LPERR10G | cds.KYUSt_ | ORUFI10G | genblast_C | SECCE3Rv | TraesCS3B | scaffold19 | TVU31108 |
| LPERR10G | genblast_C | ORUFI10G | Os10t016 | SECCE1Rv | TraesCS1B | scaffold26 | TVU31176 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t021 | SECCE3Rv | TraesCS3D | scaffold4. | TVU02752 |
| genblast_C | cds.KYUSt_ | ORUFI01G | Os01t091 | SECCE3Rv | TraesCS3A | scaffold21 | TVU36096 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t045 | genblast_C | TraesCS2B | scaffold8. | TVU14346 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t024 | SECCE7Rv | TraesCS4D | scaffold23 | TVU47734 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t035 | SECCE7Rv | TraesCS4A | scaffold74 | TVT99270 |

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|---|---|---|---|---|---|---|---|
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t079 | SECCE3Rv | TraesCS3B | scaffold46 | TVU34805 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t013 | SECCE4Rv | TraesCS4A | scaffold34 | TVU12767 |
| genblast_C | genblast_C | ORUFI08G | Os08t015 | SECCE7Rv | TraesCS7D | scaffold21 | TVU42844 |
| genblast_C | cds.KYUSt_ | ORUFI08G | Os08t011 | SECCE2Rv | TraesCS2B | scaffold67 | TVU37734 |
| LPERR06G | genblast_Z | ORUFI06G | genblast_Z | SECCE4Rv | TraesCS4A | scaffold10 | TVU12687 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold1. | TVU37172 |
| LPERR02G | genblast_C | ORUFI02G | genblast_C | SECCE6Rv | TraesCS6D | scaffold10 | TVU28089 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t014 | SECCE3Rv | TraesCS3D | scaffold59 | TVU21993 |
| genblast_Z | cds.KYUSt_ | ORUFI11G | genblast_Z | SECCE4Rv | TraesCS4B | scaffold17 | TVU24700 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t063 | SECCE2Rv | TraesCS2B | scaffold16 | TVU16279 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t053 | SECCE5Rv | TraesCS5D | scaffold22 | TVU49955 |
| LPERR12G | cds.KYUSt_ | ORUFI12G | Os12t063 | SECCEUnv | TraesCS5D | scaffold15 | TVU48845 |
| LPERR09G | genblast_C | ORUFI09G | Os09t034 | SECCE5Rv | TraesCS5B | scaffold14 | TVU09248 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | genblast_Z | SECCE7Rv | TraesCS2D | scaffold35 | TVU06939 |
| genblast_C | cds.KYUSt_ | ORUFI12G | Os03t024 | SECCE5Rv | TraesCS5B | scaffold29 | TVU49406 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t037 | SECCE5Rv | TraesCS4B | scaffold18 | TVU46853 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t059 | SECCE6Rv | TraesCS6B | scaffold13 | TVU29435 |
| LPERR05G | cds.KYUSt_ | ORUFI05G | genblast_C | SECCE1Rv | TraesCS1A | scaffold8. | TVU19352 |
| LPERR02G | genblast_C | ORUFI02G | Os02t072 | SECCE1Rv | TraesCS1A | scaffold83 | TVU28317 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t055 | SECCE1Rv | TraesCS1A | scaffold5. | TVU29704 |

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|---|---|---|---|---|---|---|---|
| LPERR10G | genblast_C | ORUFI10G | Os10t037 | genblast_C | genblast_C | scaffold17 | TVU30847 |
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t058 | SECCE2Rv | TraesCS2D | scaffold94 | TVU16002 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t078 | SECCE5Rv | TraesCS5A | scaffold32 | TVU44724 |
| LPERR02G | cds.KYUSt_ | ORUFI03G | Os02t020 | SECCE6Rv | TraesCS6A | scaffold1. | TVU32973 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t018 | SECCE7Rv | TraesCS4A | scaffold10 | TVU48187 |
| LPERR06G | genblast_C | ORUFI06G | Os06t062 | SECCE7Rv | TraesCS7A | scaffold12 | TVU08208 |
| genblast_C | cds.KYUSt_ | genblast_C | Os07t069 | SECCE2Rv | TraesCS2A | scaffold2. | TVT97792 |

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|---|---|---|---|---|---|---|---|
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t057 | SECCE2Rv | TraesCS2A | scaffold94 | TVT99727 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t016 | SECCE4Rv | TraesCS7D | scaffold34 | TVU12413 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t025 | SECCE7Rv | TraesCS4D | scaffold15 | genblast_C |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t037 | SECCE6Rv | TraesCS6A | scaffold21 | TVU20821 |
| LPERR08G | cds.KYUSt_ | ORUFI08G | Os08t054 | SECCE7Rv | TraesCS7D | scaffold54 | TVU04609 |
| LPERR06G | cds.KYUSt_ | ORUFI06G | Os06t065 | genblast_C | TraesCS7B | scaffold92 | TVU08395 |
| LPERR04G | cds.KYUSt_ | genblast_C | Os04t056 | SECCE2Rv | TraesCS2D | scaffold49 | TVU14881 |

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|---|---|---|---|---|---|---|---|
| genblast_C | cds.KYUSt_ | ORUFI04G | Os04t041 | SECCE2Rv | TraesCS2D | scaffold31 | TVU14635 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t068 | SECCE2Rv | TraesCS2A | scaffold30 | TVU16692 |
| LPERR12G | cds.KYUSt_ | genblast_C | Os12t018 | SECCE3Rv | TraesCS3D | scaffold17 | TVU35033 |
| LPERR07G | genblast_C | ORUFI07G | Os07t027 | SECCE3Rv | TraesCS3B | scaffold5. | TVU39592 |
| LPERR01G | cds.KYUSt_ | ORUFI01G | Os01t055 | SECCE3Rv | TraesCS3A | scaffold86 | TVT99562 |
| LPERR03G | cds.KYUSt_ | ORUFI03G | Os03t039 | SECCE5Rv | TraesCS5A | scaffold18 | TVU46664 |
| LPERR09G | cds.KYUSt_ | ORUFI09G | Os09t034 | SECCE5Rv | TraesCS5B | scaffold98 | TVU09240 |
| LPERR03G | cds.KYUSt_ | genblast_C | Os03t073 | SECCE4Rv | TraesCS4B | scaffold35 | TVU45146 |
| LPERR03G | genblast_C | ORUFI03G | Os03t033 | SECCE4Rv | TraesCS4B | scaffold22 | TVU47153 |

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|---|---|---|---|---|---|---|---|
| LPERR07G | cds.KYUSt_ | ORUFI07G | genblast_ | SECCE2Rv | TraesCS2B | scaffold86 | TVT96767 |
| LPERR01G | genblast_C | ORUFI01G | Os01t073 | SECCE3Rv | TraesCS3A | scaffold15 | TVU35227 |
| LPERR02G | cds.KYUSt_ | ORUFI02G | Os02t022 | SECCE6Rv | TraesCS7A | scaffold51 | TVU33127 |
| LPERR07G | cds.KYUSt_ | ORUFI07G | Os07t068 | SECCE2Rv | TraesCS2A | scaffold2. | genblast_ |
| LPERR08G | genblast_C | ORUFI08G | Os08t050 | SECCE5Rv | TraesCS5A | scaffold26 | TVU05226 |
| LPERR04G | cds.KYUSt_ | ORUFI04G | Os04t067 | SECCE2Rv | TraesCS2B | scaffold12 | TVU16503 |
| LPERR10G | genblast_C | ORUFI10G | Os10t055 | SECCE1Rv | TraesCS1A | scaffold70 | TVU31750 |

_HMMER_domains

| Panicum_h | Saccharum | Setaria_ital | Setaria_viri | Sorghum_l | Zea_mays | |
|---|---|---|---|---|---|---|
| PUZ52346 | Sspon.06G | KQL02610 | TKW11350 | KXG25545 | Zm00001eb036310_P001 | 0.921 |
| PUZ58614 | Sspon.03G | KQL04930 | TKW14117 | EES02268 | Zm00001eb120230_P001 | 0.933 |
| PUZ44933 | Sspon.05G | genblast_C | TKW03497 | EES10531 | Zm00001eb086820_P001 | 0.953 |
| PUZ61025 | genblast_C | KQL10362 | TKW21042 | KXG19831 | Zm00001eb281010_P001 | 0.890 |
| genblast_C | Sspon.01G | KQK87542 | TKV91847 | OQU91138 | Zm00001eb216770_P001 | 0.965 |
| PUZ47637 | Sspon.05G | KQK97720 | TKW04973 | EES12366 | Zm00001eb079650_P001 | 0.961 |
| PUZ37224 | Sspon.01G | KQK87317 | TKV91595 | EER93529 | Zm00001eb055960_P001 | 0.921 |
| PUZ76383 | Sspon.04G | KQL30316 | TKW40095 | OQU85248 | Zm00001eb246200_P002 | 0.906 |
| PUZ38275 | Sspon.01G | KQK88358 | TKV92889 | KXG38181 | Zm00001eb043520_P001 | 0.933 |
| PUZ40443 | Sspon.01G | KQK90235 | TKV95300 | KXG39044 | genblast_Os10t0522800-01_Ze | |
| PUZ74159 | Sspon.04G | KQL28646 | TKW37888 | EES04556 | Zm00001eb232670_P001 | 0.954 |
| PUZ66859 | Sspon.01G | KQL16318 | TKW28385 | KXG33698 | genblast_Os06t0294200-01 | Zm0 |
| PUZ62483 | Sspon.02G | KQL09005 | TKW19284 | EER98097 | Zm00001eb302270_P001 | 0.883 |
| PUZ62486 | Sspon.08G | KQK90670 | TKW19281 | OQU75714 | Zm00001eb378970_P001 | 0.871 |
| PUZ71207 | Sspon.02G | KQL24974 | TKW33721 | EER96944 | Zm00001eb316240_P001 | 0.815 |
| PUZ67536 | Sspon.02G | KQL16510 | TKW28622 | KXG23758 | Zm00001eb029260_P002 | 0.938 |
| PUZ57690 | Sspon.03G | KQL04079 | TKW13018 | OQU86505 | Zm00001eb126370_P003 | 0.999 |
| PUZ58972 | Sspon.08G | KQL12335 | TKW23584 | KXG20980 | Zm00001eb228790_P001 | 0.959 |
| PUZ60418 | Sspon.08G | KQL10876 | TKW21728 | EER88462 | Zm00001eb383490_P001 | 0.935 |
| PUZ64802 | Sspon.07G | KQL14337 | TKW25900 | EES18674 | Zm00001eb343620_P002 | 0.897 |
| PUZ59836 | Sspon.08G | KQL11297 | TKW22218 | EER88692 | Zm00001eb387410_P001 | 0.864 |
| PUZ78023 | Sspon.04G | KQL31892 | TKW42015 | EES07670 | Zm00001eb257720_P001 | 0.942 |
| PUZ70625 | Sspon.02G | KQL24401 | TKW33025 | EER98868 | Zm00001eb099200_P001 | 0.957 |
| PUZ71656 | genblast_C | KQL25426 | TKW34256 | EER99232 | Zm00001eb103340_P001 | 0.767 |
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| PUZ60011 | Sspon.08G | KQL11485 | TKW22483 | KXG20330 | Zm00001eb386530_P002 | 0.923 |
| PUZ36168 | Sspon.01G | KQK86265 | TKV90294 | KXG37177 | genblast_Os03t0838800-00_Ze | |
| PUZ62494 | Sspon.08G | KQL08991 | TKW19257 | EER87724 | Zm00001eb379060_P001 | 0.856 |
| PUZ44538 | Sspon.05G | KQK94290 | TKW00291 | KXG28247 | Zm00001eb168510_P001 | 0.945 |
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| PUZ43589 | Sspon.07G | KQK99778 | TKW07667 | EES15567 | Zm00001eb163470_P003 | 0.981 |
| PUZ55052 | Sspon.03G | KQL06711 | TKW16420 | KXG33252 | Zm00001eb154860_P006 | 0.920 |
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| PUZ73300 | Sspon.02G | KQL27017 | TKW36296 | genblast_C | genblast_Os07t0659600-00_Ze | |
| PUZ59849 | genblast_C | KQL11310 | TKW22243 | EER90079 | Zm00001eb387500_P001 | 0.960 |

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| PUZ42699 | Sspon.01G | KQK92434 | TKV98030 | EER92806 | Zm00001eb005020_P001 | 0.876 |
| PUZ72195 | genblast_C | genblast_C | TKW34923 | EER99436 | Zm00001eb105790_P001 | 0.956 |
| PUZ59242 | Sspon.08G | KQL11754 | TKW22840 | EER90327 | genblast_Os01t0532600-00_Zea | |
| PUZ70720 | Sspon.02G | KQL24498 | TKW33160 | OQU89497 | Zm00001eb099470_P004 | 0.896 |
| PUZ75865 | Sspon.04G | KQL29828 | TKW39428 | EES05156 | genblast_Os02t0518000-01_Zea | |

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| PUZ36173 | Sspon.01G | KQK86272 | TKV90301 | OQU90662 | Zm00001eb063900_P001 | 0.954 |
| PUZ41691 | Sspon.01G | KQK91473 | TKV96856 | EER95099 | Zm00001eb012350_P001 | 0.972 |
| PUZ70883 | Sspon.02G | KQL24682 | TKW33373 | EER98978 | Zm00001eb314180_P001 | 0.941 |
| PUZ49849 | Sspon.06G | KQL00259 | TKW21204 | KXG24241 | Zm00001eb260700_P001 | 0.880 |
| PUZ52604 | Sspon.06G | KQL02881 | TKW11661 | EES14111 | Zm00001eb202890_P002 | 0.927 |

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| PUZ46513 | Sspon.05G | KQK96673 | TKW03591 | EES14872 | Zm00001eb042710_P003 | 0.954 |
| PUZ67452 | Sspon.02G | KQL16603 | TKW28771 | EES17198 | Zm00001eb028480_P001 | 0.975 |
| PUZ42845 | Sspon.01G | KQK92579 | TKV98218 | genblast_C | Zm00001eb003850_P001 | 0.906 |
| PUZ74415 | Sspon.04G | KQL28393 | TKW37586 | EES06398 | Zm00001eb234560_P001 | 0.973 |

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| PUZ49249 | Sspon.05G | KQL13006 | TKW24180 | OQU82468 | Zm00001eb068050_P001 | 0.897 |
| PUZ65737 | genblast_C | KQL15249 | TKW26997 | KXG22121 | Zm00001eb347840_P001 | 0.896 |
| PUZ61627 | genblast_C | genblast_C | TKW20813 | EER89547 | Zm00001eb280750_P001 | 0.935 |
| PUZ58705 | Sspon.03G | KQL03394 | TKW12156 | EES02237 | Zm00001eb338730_P001 | 0.872 |

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|---|---|---|---|---|---|---|
| PUZ64992 | Sspon.04G | KQK92517 | TKV98138 | EES04713 | Zm00001eb235700_P002 | 0.976 |
| PUZ53522 | Sspon.03G | KQL08123 | TKW18229 | EES04034 | Zm00001eb365730_P001 | 0.970 |
| PUZ76263 | Sspon.04G | genblast_C | TKW39925 | EES07037 | Zm00001eb183170_P002 | 0.909 |
| PUZ60290 | genblast_C | KQL11735 | TKW22812 | OQU76578 | Zm00001eb384320_P005 | 0.889 |
| PUZ76376 | Sspon.01G | KQL30308 | TKW40083 | EER90667 | Zm00001eb212370_P001 | 0.847 |
| PUZ52392 | Sspon.06G | KQL02665 | TKW11403 | EES14189 | Zm00001eb036750_P001 | 0.941 |

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|---|---|---|---|---|---|---|
| PUZ44865 | Sspon.06G | KQK94612 | TKW00712 | EES08500 | Zm00001eb169480_P001 | 0.860 |
| PUZ44022 | Sspon.05G | KQK93915 | TKV99761 | KXG27959 | Zm00001eb091010_P002 | 0.934 |
| PUZ36143 | Sspon.01G | genblast_C | TKV90257 | KXG37171 | Zm00001eb064020_P001 | 0.987 |
| genblast_C | genblast_C | KQK89498 | TKV94383 | KXG38675 | genblast_Os10t0155400-00_Zea | |
| PUZ45259 | Sspon.06G | genblast_C | TKW01236 | EES08701 | Zm00001eb200060_P001 | 0.878 |
| PUZ65745 | genblast_C | KQL15264 | TKW27012 | EES18312 | Zm00001eb289020_P002 | 0.883 |

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|---|---|---|---|---|---|---|
| PUZ61901 | Sspon.08G | genblast_C | TKW19863 | EER89334 | Zm00001eb374700_P001 | 0.770 |
| PUZ65076 | genblast_C | KQL14631 | TKW26234 | EES19840 | Zm00001eb293320_P001 | 0.944 |
| PUZ72675 | genblast_C | KQL26430 | TKW35539 | KXG36561 | Zm00001eb325700_P001 | 0.768 |
| PUZ74645 | Sspon.04G | KQL28166 | TKW37319 | OQU84617 | Zm00001eb205430_P001 | 0.995 |
| PUZ74363 | Sspon.04G | KQL28455 | TKW37669 | KXG29622 | Zm00001eb233920_P002 | 0.907 |
| PUZ38733 | Sspon.01G | KQK88784 | TKV93466 | EER94108 | Zm00001eb046430_P001 | 0.962 |
| PUZ46854 | Sspon.05G | genblast_C | TKW04008 | EES12034 | Zm00001eb085410_P001 | 0.982 |
| PUZ37822 | Sspon.06G | KQK87959 | TKV92323 | KXG24984 | Zm00001eb042760_P002 | 1.004 |
| PUZ78241 | genblast_C | KQL32097 | TKW42256 | KXG31354 | Zm00001eb258900_P001 | 0.738 |
| PUZ77625 | Sspon.04G | KQL31512 | TKW41583 | KXG30756 | Zm00001eb194450_P001 | 0.968 |
| PUZ78068 | Sspon.04G | KQL31938 | TKW42060 | EES05961 | Zm00001eb192260_P001 | 0.964 |
| PUZ63552 | Sspon.04G | KQL13490 | TKW24839 | OQU84450 | genblast_Os01t0213100-00Zm0 | |
| PUZ56478 | Sspon.02G | genblast_C | TKW14668 | EES16141 | Zm00001eb137150_P001 | 1.000 |
| PUZ64685 | Sspon.07G | KQL14214 | TKW25765 | OQU78468 | Zm00001eb296510_P001 | 0.857 |

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|---|---|---|---|---|---|---|
| PUZ44564 | Sspon.05G | KQK94279 | TKW00282 | EES09641 | Zm00001eb168480_P001 | 0.991 |
| PUZ52983 | Sspon.03G | KQL28681 | TKW37933 | EES04226 | Zm00001eb140970_P002 | 0.970 |
| PUZ53911 | Sspon.03G | KQL07775 | TKW17776 | OQU8788 | Zm00001eb367330_P001 | 0.973 |
| PUZ52538 | Sspon.06G | KQL02811 | TKW11584 | EES14130 | Zm00001eb037550_P001 | 0.988 |
| PUZ77757 | Sspon.04G | KQL31626 | TKW41727 | EES05848 | Zm00001eb255750_P001 | 0.875 |
| PUZ70169 | Sspon.04G | KQL09077 | TKW19379 | OQU89206 | Zm00001eb097670_P001 | 0.967 |
| PUZ49090 | Sspon.05G | KQK99097 | TKW06803 | EES12922 | Zm00001eb069400_P001 | 0.959 |
| PUZ40103 | genblast_C | KQK89913 | TKV94918 | EER91928 | Zm00001eb023160_P001 | 0.981 |
| PUZ37491 | Sspon.01G | KQK87599 | TKV91909 | EER93620 | Zm00001eb053840_P001 | 0.936 |
| PUZ61212 | Sspon.08G | genblast_C | TKW21285 | KXG19938 | Zm00001eb281410_P001 | 0.935 |
| PUZ65889 | Sspon.07G | KQL15384 | TKW27156 | EES18272 | Zm00001eb348890_P001 | 0.867 |
| PUZ72294 | Sspon.02G | KQL26056 | TKW35072 | EER97319 | Zm00001eb323050_P002 | 0.965 |
| PUZ36607 | Sspon.01G | KQK86690 | TKV90859 | EER90745 | Zm00001eb213050_P001 | 0.892 |
| PUZ48970 | Sspon.05G | KQK98986 | TKW06669 | EES12884 | Zm00001eb014130_P001 | 0.737 |

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|---|---|---|---|---|---|
| PUZ72306 | Sspon.02GKQL26080 | TKW35095 | genblast_C | Zm00001eb106250_P004 | 0.878 |
| PUZ70683 | Sspon.02GKQL24466 | TKW33101 | KXG35617 | Zm00001eb099600_P001 | 0.991 |

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|---|---|---|---|---|---|
| PUZ66953 | genblast_CKQL23797 | TKW32210 | genblast_C | Zm00001eb095500_P001 | 0.934 |
| PUZ36445 | Sspon.01GKQK86520 | TKV90625 | OQU90774 | Zm00001eb212380_P001 | 0.952 |
| genblast_C | Sspon.01GKQK86911 | TKV91114 | EER93386 | Zm00001eb058800_P001 | 0.917 |
| PUZ75431 | Sspon.04GKQL29608 | TKW39139 | EES05022 | Zm00001eb240920_P001 | 0.921 |
| PUZ77848 | Sspon.04GKQL31701 | TKW41801 | EES07603 | Zm00001eb256290_P002 | 0.838 |
| PUZ61737 | Sspon.08G | genblast_C | TKW20374 | KXG19571 | Zm00001eb278880_P001 | 0.910 |
| PUZ64818 | Sspon.07GKQL14355 | TKW25921 | EES18667 | Zm00001eb295610_P001 | 0.920 |
| PUZ56166 | genblast_CKQL05623 | TKW15070 | EES00938 | genblast_Os01t0570500-01_Zea | |
| PUZ72592 | Sspon.02GKQL26353 | TKW35457 | EER97418 | Zm00001eb325090_P001 | 0.927 |
| PUZ50471 | genblast_CKQL00483 | TKW08472 | EES14682 | Zm00001eb171260_P001 | 0.927 |
| PUZ56964 | genblast_ZKQL03411 | TKW12171 | KXG32398 | Zm00001eb130600_P002 | 0.949 |
| PUZ63384 | Sspon.06GKQK99398 | TKW07162 | EES11757 | Zm00001eb418460_P001 | 0.851 |
| PUZ41137 | Sspon.01GKQK90927 | TKV96163 | EER92288 | Zm00001eb016560_P001 | 0.957 |

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| PUZ53065 | Sspon.03GKQL08552 | TKW18771 | EES02034 | Zm00001eb141610_P001 | 0.994 |
| PUZ41651 | genblast_CKQK91435 | TKV96810 | KXG39660 | Zm00001eb012690_P001 | 0.927 |

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| PUZ46481 | Sspon.01G | genblast_C | TKW03555 | OQU90885 | Zm00001eb059790_P001 | 0.880 |
| PUZ58144 | genblast_CKQL04494 | TKW13545 | KXG31821 | Zm00001eb336120_P002 | 0.813 |
| PUZ57513 | Sspon.03GKQL03939 | TKW12846 | EES02419 | Zm00001eb127370_P001 | 0.945 |
| PUZ75284 | Sspon.08GKQL29329 | TKW38738 | EER88893 | Zm00001eb203140_P002 | 0.916 |
| PUZ72059 | Sspon.02GKQL25799 | TKW34756 | EER99387 | Zm00001eb105020_P001 | 0.978 |
| genblast_C | Sspon.03GKQL08664 | TKW18914 | EES02072 | Zm00001eb362720_P001 | 0.916 |
| PUZ53698 | Sspon.03GKQL07964 | TKW18007 | KXG33803 | Zm00001eb366340_P002 | 0.960 |
| PUZ52232 | Sspon.06GKQL02489 | TKW11188 | EES15370 | Zm00001eb035450_P002 | 0.845 |

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| PUZ38929 | Sspon.04GKQK88957 | TKV93697 | KXG30541 | Zm00001eb245960_P001 | 0.975 |

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| PUZ64055 | Sspon.07GKQL13040 | TKW24216 | EES19030 | genblast_Os05t0150400-01_Zea | |
| PUZ55994 | Sspon.03GKQL05714 | TKW15178 | EES01003 | Zm00001eb161170_P003 | 0.930 |

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| PUZ70950 | Sspon.02GKQL24750 | TKW33447 | EER96834 | Zm00001eb314660_P001 | 0.952 |

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| PUZ69140 | Sspon.06G | KQL27318 | TKW36690 | EER92434 | Zm00001eb331630_P001 | 0.744 |
| PUZ76548 | Sspon.04G | KQL30482 | TKW40293 | EES05421 | Zm00001eb247110_P001 | 0.862 |
| PUZ68913 | Sspon.05G | genblast_C | TKW13088 | OQU86485 | Zm00001eb202030_P001 | 0.848 |
| PUZ52987 | Sspon.03G | KQL08621 | TKW18865 | EES04224 | Zm00001eb363050_P003 | 0.911 |

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| PUZ55897 | Sspon.03G | KQL05798 | TKW15278 | OQU87140 | Zm00001eb161690_P001 | 0.978 |
| PUZ55019 | genblast_C | KQL06754 | TKW16478 | EES01378 | Zm00001eb154610_P001 | 0.957 |
| PUZ66292 | Sspon.07G | KQL15777 | TKW27689 | OQU77881 | Zm00001eb365450_P001 | 0.910 |
| PUZ61517 | Sspon.08G | KQL10082 | TKW20650 | KXG19675 | Zm00001eb164580_P001 | 0.736 |
| PUZ60057 | Sspon.08G | KQL11524 | TKW22542 | EER88608 | Zm00001eb276830_P001 | 0.774 |
| PUZ61763 | Sspon.08G | KQL09887 | TKW20403 | KXG19557 | Zm00001eb278650_P001 | 1.005 |
| PUZ53693 | genblast_C | KQL07967 | TKW18012 | EES03975 | Zm00001eb145900_P001 | 0.869 |
| PUZ55845 | Sspon.03G | KQL05857 | TKW15346 | EES01068 | Zm00001eb161990_P001 | 0.971 |
| PUZ48649 | Sspon.05G | KQK98664 | TKW06223 | KXG27008 | Zm00001eb072510_P001 | 0.988 |
| PUZ47685 | Sspon.05G | KQK97766 | TKW05007 | EES11006 | Zm00001eb425100_P001 | 0.942 |
| PUZ49816 | Sspon.06G | KQL00222 | TKW08125 | EES13224 | Zm00001eb174180_P001 | 0.791 |

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| PUZ75127 | genblast_C | KQL29193 | TKW38587 | EES04932 | Zm00001eb203570_P004 | 0.982 |

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| PUZ42058 | Sspon.01G | KQL13895 | TKV97288 | KXG39824 | Zm00001eb009610_P001 | 0.885 |
| PUZ60374 | Sspon.08G | KQL10921 | TKW21782 | KXG20138 | Zm00001eb383720_P001 | 0.780 |
| PUZ48560 | Sspon.04G | KQK98558 | TKW06101 | EES11301 | Zm00001eb073350_P001 | 0.907 |
| PUZ57895 | Sspon.07G | KQL06109 | TKW15674 | KXG22470 | Zm00001eb294740_P002 | 0.960 |
| PUZ72489 | Sspon.02G | KQL26251 | TKW35306 | OQU90099 | Zm00001eb324310_P001 | 0.883 |

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| PUZ70944 | Sspon.02G | KQL24744 | TKW33440 | EER98995 | Zm00001eb314610_P001 | 0.972 |
| PUZ66774 | genblast_C | KQL16087 | TKW28070 | KXG32181 | Zm00001eb127520_P001 | 0.855 |
| PUZ37688 | Sspon.01G | genblast_C | TKV92181 | EER91121 | Zm00001eb052550_P001 | 0.906 |
| PUZ65007 | genblast_C | KQL14571 | TKW26162 | OQU78360 | Zm00001eb294190_P001 | 0.940 |
| PUZ54308 | Sspon.07G | KQL07402 | TKW17330 | EES01628 | Zm00001eb369270_P001 | 0.986 |
| PUZ38290 | Sspon.01G | KQL03296 | TKW12034 | EER90664 | Zm00001eb062050_P001 | 0.941 |
| PUZ74686 | Sspon.08G | KQL11623 | TKW22674 | EER88566 | Zm00001eb277260_P001 | 0.884 |
| PUZ52294 | Sspon.06G | KQL02572 | TKW11292 | EES14221 | Zm00001eb035910_P001 | 0.816 |
| genblast_C | genblast_C | KQK88275 | TKV92786 | KXG38149 | Zm00001eb219850_P001 | 0.933 |

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| PUZ53063 | Sspon.03G | KQL08554 | TKW18774 | EES02037 | Zm00001eb141570_P001 | 0.964 |
| PUZ46047 | Sspon.05G | KQK96174 | TKW02909 | EES10341 | Zm00001eb418750_P001 | 0.971 |
| PUZ39283 | Sspon.01G | KQK89252 | TKV94058 | OQU91899 | Zm00001eb027820_P001 | 0.902 |

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| PUZ58787 | Sspon.03G | KQL03282 | TKW12023 | KXG31510 | Zm00001eb339120_P001 | 0.892 |
| PUZ36287 | Sspon.01G | KQK86386 | TKV90428 | EER90606 | Zm00001eb063090_P002 | 0.983 |
| PUZ76278 | Sspon.04G | KQL30205 | TKW39945 | OQU85206 | Zm00001eb183250_P002 | 0.935 |
| PUZ36017 | Sspon.01G | KQK86118 | TKV90105 | EER90492 | Zm00001eb210560_P001 | 0.966 |
| PUZ68366 | Sspon.02G | genblast_C | TKW30381 | KXG34371 | Zm00001eb117740_P002 | 0.957 |
| PUZ65182 | genblast_C | KQL14731 | TKW26349 | EES18507 | Zm00001eb353100_P002 | 0.934 |
| PUZ38692 | genblast_C | KQK88734 | TKV93386 | EER94083 | Zm00001eb045890_P003 | 0.980 |
| PUZ65018 | Sspon.07G | KQL14582 | TKW26175 | KXG22415 | Zm00001eb294080_P001 | 0.905 |
| PUZ49669 | genblast_C | KQL12619 | TKW23680 | KXG27522 | Zm00001eb434500_P001 | 0.740 |
| PUZ69706 | Sspon.01G | KQL23663 | TKW32022 | KXG35151 | Zm00001eb307600_P001 | 0.952 |
| PUZ77576 | Sspon.04G | KQL31375 | TKW41425 | EES05581 | Zm00001eb253650_P002 | 0.901 |
| PUZ73267 | genblast_C | KQL26990 | TKW36261 | EER93704 | Zm00001eb217900_P001 | 0.977 |
| PUZ69603 | Sspon.02G | KQL23601 | TKW31931 | OQU89026 | Zm00001eb096040_P001 | 1.009 |
| PUZ38146 | Sspon.07G | KQK88245 | TKV92746 | KXG38123 | Zm00001eb048990_P001 | 0.922 |
| PUZ71450 | Sspon.02G | KQL25220 | TKW34013 | EER97013 | Zm00001eb102460_P001 | 0.881 |
| PUZ61899 | Sspon.08G | KQL09472 | TKW19859 | KXG19486 | Zm00001eb374680_P001 | 0.850 |
| PUZ72149 | Sspon.02G | KQL25889 | TKW34862 | EER97254 | Zm00001eb322110_P001 | 0.986 |

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| PUZ45908 | genblast_C | KQK96011 | TKW02762 | OQU84124 | genblast_Os11t0706801-00_Zea |  |
| PUZ64424 | Sspon.07G | KQL13959 | TKW25450 | EES20076 | Zm00001eb345570_P001 | 0.918 |
| PUZ77807 | genblast_C | KQL31677 | TKW41776 | EES05862 | Zm00001eb256150_P001 | 0.988 |
| PUZ61076 | Sspon.06G | KQK99877 | TKW07795 | OQU79960 | Zm00001eb172100_P001 | 0.899 |
| PUZ53467 | Sspon.03G | KQL08159 | TKW18284 | KXG33917 | Zm00001eb144510_P001 | 0.886 |
| PUZ43657 | Sspon.05G | KQK99840 | TKV99192 | EES16520 | Zm00001eb405060_P002 | 0.956 |
| PUZ49587 | genblast_C | KQL12709 | TKW23801 | EES11678 | Zm00001eb065720_P001 | 0.978 |
| PUZ72464 | Sspon.02G | KQL26223 | TKW35273 | EER97371 | Zm00001eb106740_P001 | 0.882 |
| PUZ44580 | Sspon.04G | KQK94265 | TKW00266 | EES08355 | Zm00001eb168410_P003 | 0.982 |
| PUZ76899 | Sspon.01G | KQL30802 | TKW40725 | KXG31085 | Zm00001eb186610_P001 | 0.940 |
| PUZ37689 | Sspon.01G | genblast_C | genblast_C | EER93715 | Zm00001eb052570_P001 | 0.835 |

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| PUZ47970 | Sspon.05G | KQK98039 | TKW05388 | OQU81949 | Zm00001eb077430_P001 | 0.829 |
| PUZ66123 | genblast_C | KQL15627 | TKW27482 | EES19481 | Zm00001eb287400_P001 | 0.962 |
| PUZ64880 | Sspon.07G | KQL14437 | TKW26006 | EES19914 | Zm00001eb343000_P001 | 0.912 |
| PUZ72346 | Sspon.02G | KQL26112 | TKW35137 | EER99490 | Zm00001eb323300_P001 | 0.946 |
| PUZ57932 | Sspon.03G | KQL04292 | TKW13308 | EES02528 | Zm00001eb335470_P002 | 0.918 |
| PUZ41514 | Sspon.01G | KQK91306 | TKV96672 | EER92412 | Zm00001eb013520_P001 | 0.982 |
| genblast_C | Sspon.04G | KQL29246 | TKW38645 | EES06700 | Zm00001eb345210_P002 | 0.734 |
| PUZ43493 | Sspon.05G | KQK99716 | TKW07579 | EES07900 | Zm00001eb093710_P001 | 0.969 |
| PUZ64423 | genblast_C | KQL13955 | TKW25443 | EES18815 | Zm00001eb345580_P001 | 0.831 |
| PUZ37236 | genblast_C | KQK87327 | TKV91608 | KXG37660 | Zm00001eb215660_P001 | 0.938 |
| PUZ47548 | Sspon.05G | KQK97631 | TKW04863 | EES12317 | Zm00001eb080310_P003 | 0.964 |
| PUZ48944 | Sspon.05G | KQK98961 | TKW06623 | EES12875 | Zm00001eb070460_P001 | 0.977 |
| PUZ41267 | Sspon.01G | KQK91056 | TKV96331 | KXG39465 | Zm00001eb015660_P003 | 0.990 |
| PUZ73429 | Sspon.02G | KQL27085 | TKW36376 | EER99876 | Zm00001eb330130_P001 | 0.973 |
| PUZ75143 | genblast_C | KQL29208 | TKW38606 | OQU84819 | Zm00001eb236860_P001 | 0.878 |
| PUZ40272 | Sspon.01G | KQK90082 | TKV95112 | EER94546 | Zm00001eb022760_P001 | 0.924 |
| PUZ73638 | Sspon.08G | KQL27715 | TKW36749 | EER89049 | Zm00001eb268660_P003 | 0.988 |
| PUZ49716 | Sspon.06G | genblast_C | TKW08018 | EES13173 | Zm00001eb198720_P002 | 0.893 |

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| PUZ56990 | genblast_C | KQL03433 | TKW12196 | EES00653 | Zm00001eb130450_P001 | 0.967 |
| PUZ54977 | genblast_C | KQL06792 | TKW16528 | EES01392 | Zm00001eb154460_P001 | 0.996 |
| PUZ37515 | Sspon.01G | KQK87622 | TKV91932 | EER93635 | Zm00001eb053670_P002 | 0.894 |
| PUZ63527 | genblast_C | KQL13513 | TKW24878 | genblast_C | Zm00001eb283830_P001 | 0.888 |
| PUZ55853 | genblast_C | KQL05844 | TKW15335 | KXG32884 | Zm00001eb161910_P001 | 0.961 |
| PUZ46949 | genblast_Z | KQK97062 | TKW04141 | KXG26174 | Zm00001eb084670_P001 | 0.968 |

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| PUZ62923 | Sspon.04G | KQK99894 | TKW07815 | OQU8469 | Zm00001eb163340_P001 | 0.992 |
| PUZ60330 | Sspon.08G | KQL10975 | TKW21856 | KXG20157 | genblast_Os06t0552700-01_Ze | |
| PUZ63765 | Sspon.07G | KQL13113 | TKW24312 | OQU7728 | Zm00001eb265740_P001 | 0.778 |
| PUZ45868 | Sspon.03G | KQL05181 | TKW14445 | EES15864 | Zm00001eb131870_P001 | 0.950 |
| PUZ52199 | Sspon.06G | KQL02453 | TKW11142 | EES15387 | Zm00001eb035270_P001 | 0.860 |

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| PUZ56938 | Sspon.03G | KQL04984 | TKW14199 | EES00676 | Zm00001eb340520_P001 | 0.981 |
| PUZ52948 | Sspon.03G | KQL08657 | TKW18910 | KXG34141 | Zm00001eb362730_P001 | 0.926 |
| PUZ74050 | Sspon.04G | genblast_C | TKW38018 | EES04515 | Zm00001eb232240_P001 | 0.894 |
| PUZ43888 | Sspon.06G | KQK93771 | TKV99552 | genblast_Z | Zm00001eb029740_P003 | 0.737 |
| PUZ52812 | Sspon.03G | KQL08791 | TKW19073 | EES02141 | Zm00001eb139840_P004 | 0.876 |
| PUZ61338 | Sspon.02G | KQL25193 | TKW33984 | EER99143 | Zm00001eb317630_P001 | 0.928 |

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| PUZ60474 | Sspon.08G | KQL10826 | TKW21675 | genblast_C | Zm00001eb383060_P004 | 0.915 |
| PUZ49474 | Sspon.05G | KQL12818 | TKW23933 | KXG27417 | Zm00001eb066500_P001 | 0.940 |
| PUZ47375 | Sspon.05G | KQK97472 | TKW04662 | EES10894 | Zm00001eb130250_P001 | 0.750 |
| PUZ72859 | Sspon.08G | KQL26606 | TKW35744 | EER88230 | Zm00001eb380530_P001 | 0.916 |
| PUZ52586 | Sspon.06G | KQL02857 | TKW11637 | EES15239 | Zm00001eb202700_P001 | 0.824 |
| PUZ45719 | Sspon.06G | KQK95732 | TKW02253 | KXG29076 | Zm00001eb165420_P001 | 0.974 |
| PUZ36284 | genblast_C | KQK86382 | TKV90423 | EER90604 | Zm00001eb211440_P001 | 0.866 |

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| PUZ63399 | genblast_C | genblast_C | TKW25009 | EES16964 | Zm00001eb069510_P001 | 0.987 |
| PUZ58756 | Sspon.03G | KQL03336 | TKW12083 | EES02220 | Zm00001eb119480_P001 | 0.947 |
| PUZ72073 | Sspon.02G | KQL01131 | TKW09409 | EER97216 | Zm00001eb105090_P002 | 0.968 |
| PUZ58309 | Sspon.03G | KQL04652 | TKW13750 | EES02372 | Zm00001eb122550_P001 | 0.885 |
| PUZ64235 | Sspon.07G | KQL13779 | TKW25228 | EES17796 | Zm00001eb283310_P001 | 0.939 |
| PUZ38220 | Sspon.01G | KQK88311 | TKV92830 | EER91347 | Zm00001eb043220_P002 | 0.912 |
| PUZ77834 | Sspon.04G | KQL31695 | TKW41796 | EES05867 | Zm00001eb256240_P001 | 0.945 |
| PUZ76957 | Sspon.04G | genblast_C | TKW40786 | OQU8567 | Zm00001eb186860_P002 | 0.751 |
| PUZ66895 | genblast_C | KQL16337 | TKW28404 | OQU7906 | Zm00001eb409000_P004 | 0.944 |
| PUZ69722 | Sspon.02G | KQL23678 | TKW32049 | EER96398 | Zm00001eb307490_P001 | 0.899 |
| PUZ40725 | Sspon.01G | KQK90462 | TKV95610 | EER92147 | Zm00001eb019650_P001 | 0.793 |
| PUZ64247 | Sspon.07G | KQL13790 | TKW25246 | EES19126 | Zm00001eb345720_P002 | 0.928 |
| PUZ66286 | Sspon.07G | KQL15775 | TKW27682 | EES19420 | Zm00001eb351000_P001 | 0.978 |

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| PUZ42109 | Sspon.01G | KQK91876 | TKV97357 | EER95242 | Zm00001eb399800_P001 | 0.947 |
| PUZ73961 | Sspon.04G | KQL28839 | TKW38136 | KXG29410 | Zm00001eb231500_P001 | 0.967 |
| PUZ62278 | Sspon.08G | KQL09210 | TKW19557 | EER87812 | Zm00001eb377500_P001 | 0.888 |
| PUZ69985 | Sspon.04G | KQL23869 | TKW32296 | OQU84734 | Zm00001eb238080_P002 | 0.952 |
| PUZ59120 | Sspon.08G | KQL12215 | TKW23421 | EER90388 | Zm00001eb272400_P001 | 0.830 |
| PUZ58360 | Sspon.03G | KQL04694 | TKW13821 | KXG31680 | Zm00001eb122170_P002 | 0.950 |
| PUZ36770 | Sspon.01G | KQK86835 | TKV91035 | EER90796 | Zm00001eb213670_P001 | 0.984 |
| PUZ63681 | Sspon.07G | KQL13370 | TKW24677 | EES18894 | Zm00001eb266760_P001 | 0.825 |
| PUZ70871 | Sspon.05G | KQL24665 | TKW33351 | EES09159 | Zm00001eb093750_P001 | 0.977 |
| PUZ47930 | Sspon.05G | genblast_C | TKW05343 | OQU81917 | Zm00001eb426240_P002 | 0.989 |
| PUZ52526 | Sspon.06G | genblast_C | TKW11571 | OQU80770 | Zm00001eb037480_P001 | 0.909 |
| PUZ72795 | genblast_C | KQL26536 | TKW35654 | KXG36622 | Zm00001eb108440_P001 | 0.969 |
| PUZ58947 | genblast_C | genblast_C | TKW23604 | EER89014 | Zm00001eb228930_P001 | 0.736 |
| PUZ55412 | Sspon.03G | KQL06356 | TKW15988 | OQU87312 | Zm00001eb157140_P001 | 0.915 |
| PUZ36969 | Sspon.01G | KQK87046 | TKV91288 | KXG37528 | Zm00001eb214620_P001 | 0.911 |
| PUZ45261 | Sspon.06G | KQK94997 | TKW01240 | KXG28714 | Zm00001eb200080_P002 | 0.812 |
| PUZ37617 | Sspon.01G | KQK87747 | TKV92081 | EER93679 | Zm00001eb052070_P001 | 0.886 |
| PUZ54884 | genblast_C | KQL06882 | TKW16645 | EES01445 | Zm00001eb153890_P001 | 0.891 |
| PUZ59601 | Sspon.04G | KQL11054 | TKW21935 | KXG20552 | Zm00001eb389770_P001 | 0.913 |
| PUZ52239 | Sspon.06G | KQL02497 | TKW11200 | EES15369 | Zm00001eb174570_P001 | 0.886 |
| PUZ78101 | Sspon.04G | KQL31972 | TKW42101 | KXG31293 | Zm00001eb192120_P003 | 0.920 |
| PUZ58537 | Sspon.03G | KQL04854 | TKW14017 | EES00115 | Zm00001eb337970_P001 | 0.949 |
| PUZ36814 | Sspon.01G | KQK86886 | TKV91082 | EER93376 | Zm00001eb213770_P001 | 0.969 |
| PUZ51993 | Sspon.06G | genblast_C | TKW10911 | EES15461 | Zm00001eb033700_P002 | 0.957 |
| PUZ65557 | genblast_C | KQL15066 | TKW26776 | EES18374 | Zm00001eb290160_P002 | 0.827 |
| PUZ67410 | Sspon.02G | genblast_C | TKW28803 | EES16144 | Zm00001eb410020_P001 | 0.927 |

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| PUZ78392 | Sspon.04G | KQL32251 | TKW42429 | KXG31424 | Zm00001eb259440_P001 | 0.958 |
| PUZ38745 | Sspon.01G | KQK88797 | TKV93482 | KXG38381 | Zm00001eb046390_P002 | 0.833 |
| PUZ78059 | Sspon.04G | KQL31928 | TKW42052 | OQU85887 | Zm00001eb192330_P002 | 0.926 |
| PUZ63865 | Sspon.07G | KQL13215 | TKW24449 | EES18961 | genblast_Os05t0131500-00_Zea | |
| PUZ70556 | Sspon.02G | KQL24315 | TKW32942 | KXG35530 | Zm00001eb311480_P001 | 0.916 |
| PUZ72745 | Sspon.02G | KQL26490 | TKW35602 | OQU90181 | Zm00001eb326290_P001 | 0.877 |
| PUZ59166 | Sspon.08G | KQL12157 | TKW23360 | KXG20827 | Zm00001eb227480_P001 | 0.987 |

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|---|---|---|---|---|---|---|
| PUZ46092 | genblast_C | KQK96214 | TKW02961 | EES11751 | Zm00001eb089470_P001 | 0.819 |
| PUZ36472 | genblast_C | KQK86542 | TKV90655 | EER93244 | Zm00001eb061750_P001 | 0.964 |
| PUZ57344 | Sspon.03G | genblast_Z | TKW12685 | EES00531 | Zm00001eb128260_P002 | 0.985 |
| PUZ47504 | genblast_C | KQK97588 | TKW04808 | EES10952 | Zm00001eb080620_P001 | 0.832 |
| PUZ61866 | Sspon.08G | KQK89944 | TKV94959 | EER91934 | Zm00001eb130050_P001 | 0.731 |
| PUZ62824 | Sspon.07G | KQK99762 | TKW07646 | OQU78645 | Zm00001eb132780_P001 | 0.805 |
| PUZ36035 | Sspon.01G | KQK86137 | TKV90128 | EER90503 | genblast_Zm00001eb210650_P0 | |
| PUZ41144 | genblast_C | KQK90932 | TKW08963 | OQU92610 | Zm00001eb416330_P002 | 0.849 |
| PUZ58858 | Sspon.03G | KQL04899 | TKW14074 | KXG31468 | genblast_Os01t0235100-01_Zea | |
| PUZ50749 | Sspon.01G | KQK92022 | TKV97526 | EER92057 | Zm00001eb021060_P001 | 0.820 |

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| PUZ40071 | Sspon.01G | genblast_C | TKV94875 | EER94473 | Zm00001eb023840_P001 | 0.927 |

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| PUZ69435 | Sspon.02G | KQL23395 | TKW31721 | KXG35000 | Zm00001eb306140_P002 | 0.982 |
| PUZ65167 | Sspon.07G | KQL14720 | TKW26336 | EES18513 | Zm00001eb293070_P002 | 0.951 |
| PUZ38938 | Sspon.01G | KQK88965 | TKV93708 | OQU91731 | Zm00001eb057350_P001 | 0.731 |
| PUZ57809 | Sspon.03G | genblast_C | TKW13177 | EES02591 | Zm00001eb334920_P001 | 0.986 |
| PUZ77465 | Sspon.04G | KQL31487 | TKW41561 | KXG30765 | Zm00001eb254480_P001 | 0.947 |
| PUZ71613 | Sspon.02G | KQL25393 | TKW34222 | EER97068 | Zm00001eb103160_P002 | 0.942 |
| PUZ43676 | Sspon.07G | KQK99857 | TKW07773 | EES16515 | Zm00001eb163360_P001 | 0.876 |
| genblast_C | Sspon.05G | genblast_C | genblast_C | EES11861 | genblast_Os04t0183300-01Zm0 | |
| PUZ69750 | genblast_C | KQL23693 | TKW32075 | KXG35160 | Zm00001eb095700_P001 | 0.914 |
| PUZ49792 | Sspon.06G | KQL00202 | TKW08093 | EES14371 | Zm00001eb260230_P001 | 0.965 |
| PUZ51931 | Sspon.06G | KQL02239 | TKW10833 | EES14342 | Zm00001eb033410_P005 | 0.934 |

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| PUZ72670 | Sspon.02G | KQL26425 | TKW35535 | EER97443 | Zm00001eb325630_P003 | 0.931 |
| PUZ47300 | Sspon.05G | KQK97407 | TKW04556 | EES12234 | Zm00001eb082040_P001 | 0.910 |
| PUZ37385 | Sspon.01G | genblast_C | TKV91749 | EER93586 | Zm00001eb216420_P001 | 0.989 |

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| PUZ38774 | Sspon.01G | KQK88820 | TKV93510 | EER91517 | Zm00001eb046510_P001 | 0.973 |
| PUZ46599 | Sspon.03G | KQK96731 | TKW03681 | EES03167 | Zm00001eb357000_P001 | 0.883 |
| PUZ54286 | Sspon.03G | KQL07417 | TKW17354 | OQU87732 | Zm00001eb150110_P001 | 0.828 |
| PUZ37455 | Sspon.01G | KQK87564 | TKV91868 | OQU91145 | Zm00001eb054110_P001 | 0.904 |
| PUZ68439 | genblast_C | KQL22475 | TKW30484 | EER97999 | Zm00001eb117470_P002 | 0.904 |
| PUZ70639 | genblast_Z | KQL24418 | TKW33048 | EER96709 | Zm00001eb312110_P001 | 0.730 |
| PUZ63317 | Sspon.07G | KQL13711 | TKW25133 | KXG23279 | Zm00001eb133860_P002 | 0.750 |
| PUZ71596 | Sspon.06G | KQL25375 | TKW34198 | EER99208 | Zm00001eb103060_P001 | 0.900 |
| PUZ42237 | Sspon.01G | genblast_C | TKV97505 | KXG39900 | Zm00001eb400430_P001 | 0.862 |
| PUZ43185 | Sspon.01G | KQK92962 | TKV98612 | EER95644 | Zm00001eb001070_P001 | 0.848 |
| PUZ38675 | Sspon.04G | KQK88749 | TKV93405 | KXG31316 | Zm00001eb258320_P002 | 0.975 |
| PUZ42329 | genblast_C | KQK92096 | TKV97618 | KXG39939 | genblast_Os03t0201000-01Zm0 | |
| PUZ36826 | Sspon.01G | genblast_C | TKV91101 | OQU90921 | Zm00001eb058930_P002 | 0.889 |
| PUZ49114 | genblast_Z | KQK99124 | TKW06835 | EES12936 | Zm00001eb431730_P002 | 0.941 |
| genblast_C | Sspon.03G | KQL05178 | TKW14443 | EES02961 | Zm00001eb152160_P001 | 0.961 |
| PUZ65264 | Sspon.07G | KQL14767 | TKW26396 | EES18493 | Zm00001eb292690_P001 | 0.897 |
| PUZ78385 | Sspon.04G | KQL32242 | TKW42425 | EES07812 | genblast_Os02t0829500-01_Zea | |

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| PUZ69800 | Sspon.02G | KQL23728 | TKW32114 | EER96424 | Zm00001eb307250_P001 | 0.963 |
| PUZ76677 | Sspon.04G | KQL30598 | TKW40467 | OQU85359 | genblast_Os02t0632500-01_Zea | |
| PUZ67507 | genblast_C | KQL16546 | TKW28678 | OQU79367 | genblast_Os12t0567500-00_Zea | |
| PUZ73977 | Sspon.04G | genblast_C | TKW38119 | EES04478 | Zm00001eb231640_P001 | 0.729 |
| PUZ67831 | Sspon.02G | KQL17123 | TKW29492 | EES17353 | Zm00001eb031310_P001 | 0.954 |
| PUZ72040 | Sspon.02G | KQL25781 | TKW34736 | EER99383 | genblast_Os08t0410266-00_Zea | |
| PUZ69674 | Sspon.02G | genblast_C | TKW32009 | KXG35145 | Zm00001eb307670_P001 | 0.943 |
| PUZ40665 | Sspon.01G | KQK90407 | TKV95530 | EER92124 | Zm00001eb020090_P001 | 0.938 |

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| PUZ47739 | Sspon.05G | KQK97811 | TKW05090 | EES11030 | Zm00001eb079000_P001 | 0.931 |
| PUZ36588 | Sspon.01G | KQK86676 | TKV90836 | EER90740 | Zm00001eb212970_P001 | 0.883 |

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| PUZ53997 | Sspon.03G | KQL07694 | TKW17690 | EES01744 | Zm00001eb148130_P001 | 0.962 |
| PUZ46983 | Sspon.04G | KQK97086 | TKW04175 | EES10713 | Zm00001eb084550_P001 | 0.861 |

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| PUZ54300 | Sspon.03G | KQL07410 | TKW17341 | EES01631 | Zm00001eb150260_P001 | 0.956 |

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| PUZ37397 | genblast_C | KQK87477 | TKV91761 | EER91007 | Zm00001eb054700_P001 | 0.966 |
| PUZ77763 | Sspon.04G | KQL31631 | TKW41733 | KXG31165 | Zm00001eb193710_P001 | 1.005 |

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| PUZ48479 | Sspon.05G | KQK98489 | TKW05999 | EES11274 | Zm00001eb073790_P002 | 0.804 |
| PUZ75176 | Sspon.04G | KQL29250 | TKW38651 | EES07521 | Zm00001eb249350_P001 | 0.978 |
| PUZ68890 | Sspon.01G | KQL22945 | TKW31059 | EER96047 | Zm00001eb094460_P001 | 1.002 |
| PUZ56585 | Sspon.07G | KQL05286 | TKW14622 | genblast_C | Zm00001eb341770_P001 | 0.949 |
| PUZ65142 | Sspon.07G | genblast_C | TKW26303 | EES19830 | Zm00001eb293750_P001 | 0.930 |

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| PUZ52039 | Sspon.02G | KQL02334 | TKW10984 | EES15444 | Zm00001eb033910_P001 | 0.979 |
| PUZ64879 | Sspon.07G | KQL14436 | TKW26005 | EES19915 | Zm00001eb343010_P001 | 0.849 |

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| PUZ57516 | Sspon.03G | KQL03942 | TKW12847 | genblast_C | Zm00001eb127350_P001 | 0.935 |
| PUZ72389 | Sspon.02G | KQL26147 | TKW35176 | KXG36431 | Zm00001eb323550_P002 | 0.936 |
| PUZ60230 | Sspon.08G | KQL11674 | TKW22746 | OQU76599 | genblast_Os06t0568000-01_Zea | |
| PUZ64604 | Sspon.07G | KQL14152 | TKW25672 | EES20007 | Zm00001eb344710_P001 | 0.775 |

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| PUZ58989 | Sspon.08GKQL12326 | TKW23573 | EER90434 | Zm00001eb271900_P001 | 0.981 |
| PUZ39892 | genblast_CKQK89723 | TKV94684 | KXG38808 | Zm00001eb025210_P001 | 0.995 |
| PUZ74653 | genblast_CKQL28157 | TKW37309 | KXG29776 | Zm00001eb240350_P002 | 0.972 |
| PUZ51977 | Sspon.06GKQL02288 | TKW10891 | KXG25721 | Zm00001eb199240_P001 | 0.944 |

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| PUZ38467 | Sspon.01GKQK88534 | TKV93134 | OQU91573 | Zm00001eb044790_P002 | 0.928 |
| PUZ73506 | Sspon.07GKQL16771 | genblast_C | EER91799 | Zm00001eb331110_P001 | 0.905 |
| PUZ76093 | Sspon.04GKQL30024 | TKW39720 | genblast_C | Zm00001eb182000_P001 | 0.972 |

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| PUZ66746 | genblast_CKQL16145 | TKW28125 | genblast_C | Zm00001eb327830_P001 | 0.946 |

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| PUZ45034 | Sspon.06GKQK94747 | TKW00923 | EES08566 | Zm00001eb170530_P001 | 0.947 |
| PUZ61877 | Sspon.08GKQL09446 | TKW19820 | EER89348 | Zm00001eb374500_P001 | 0.922 |
| PUZ58658 | genblast_CKQL04958 | TKW14153 | EES02259 | Zm00001eb338510_P001 | 0.951 |
| PUZ47029 | Sspon.05GKQK97160 | TKW04246 | EES12107 | Zm00001eb084110_P001 | 0.967 |
| PUZ57389 | Sspon.03GKQL03826 | TKW12714 | EES00518 | Zm00001eb333360_P001 | 0.964 |
| PUZ70709 | Sspon.02GKQK87498 | TKV91780 | EER96733 | Zm00001eb312640_P002 | 0.997 |
| PUZ78437 | Sspon.04GKQL32284 | TKW42464 | EES07831 | Zm00001eb259670_P001 | 0.857 |
| PUZ51424 | Sspon.06GKQL01772 | TKW10259 | OQU80426 | Zm00001eb178990_P001 | 0.925 |
| PUZ48134 | Sspon.04GKQK98202 | TKW05584 | EES11157 | Zm00001eb075850_P001 | 0.960 |
| PUZ54651 | Sspon.03GKQL07102 | TKW16931 | OQU87600 | Zm00001eb152300_P004 | 0.895 |
| PUZ74397 | Sspon.04GKQL28406 | TKW37603 | EES04649 | Zm00001eb234350_P001 | 0.966 |
| PUZ49346 | Sspon.05GKQL12921 | TKW24064 | EES11606 | Zm00001eb067350_P001 | 0.887 |
| PUZ63370 | genblast_CKQL13648 | TKW25057 | EES01150 | Zm00001eb158830_P002 | 0.989 |

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| PUZ66567 | genblast_CKQL16028 | TKW28000 | OQU77713 | Zm00001eb285050_P001 | 0.739 |
| PUZ38781 | Sspon.01GKQK88824 | TKV93519 | EER94119 | Zm00001eb222290_P003 | 0.927 |
| PUZ40856 | Sspon.03GKQK90599 | TKV95800 | EES02270 | Zm00001eb120260_P002 | 0.950 |
| PUZ67795 | Sspon.02GKQL17087 | TKW29462 | EES17331 | Zm00001eb135520_P001 | 0.838 |
| PUZ63992 | Sspon.07GKQL13308 | TKW24577 | EES18998 | Zm00001eb097070_P001 | 0.761 |

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| PUZ59192 | Sspon.08GKQL12116 | TKW23299 | EER88922 | genblast_Os06t0705000-01_Zea |

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| PUZ73767 | Sspon.04G | KQL08995 | TKW38367 | KXG29314 | Zm00001eb208200_P001 0.854 |
| PUZ68217 | genblast_C | KQL22143 | TKW30023 | EER97849 | Zm00001eb118180_P002 0.967 |

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| PUZ74003 | genblast_C | KQL28801 | TKW38088 | KXG29441 | Zm00001eb232000_P001 0.727 |
| PUZ40212 | genblast_C | KQK90001 | TKV95038 | OQU92173 | Zm00001eb391660_P001 0.961 |
| PUZ43432 | Sspon.07G | KQK93384 | TKV99042 | EES16626 | Zm00001eb163980_P001 0.920 |
| PUZ52374 | Sspon.06G | KQL02641 | TKW11386 | KXG25536 | Zm00001eb175120_P001 0.964 |
| PUZ61496 | genblast_C | KQL10057 | TKW20625 | OQU76123 | Zm00001eb372150_P001 0.934 |
| PUZ60245 | Sspon.08G | KQL11690 | TKW22766 | EER88542 | Zm00001eb383950_P004 0.925 |
| genblast_C | genblast_C | KQK88837 | TKV93527 | EER91521 | Zm00001eb046610_P001 0.932 |
| PUZ50915 | genblast_C | KQL01290 | TKW09636 | OQU80197 | Zm00001eb176760_P002 0.964 |

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| PUZ48731 | genblast_C | KQK98751 | TKW06329 | OQU82255 | Zm00001eb071850_P001 0.811 |
| PUZ63698 | Sspon.07G | KQL13352 | TKW24657 | EES18903 | Zm00001eb266460_P002 0.727 |

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| PUZ64356 | genblast_C | KQL13893 | TKW25363 | EES17849 | Zm00001eb284200_P002 0.966 |
| PUZ36310 | Sspon.01G | KQK86406 | TKV90452 | KXG37241 | Zm00001eb062850_P001 0.925 |
| PUZ52686 | Sspon.06G | KQL02906 | TKW11688 | EES14088 | Zm00001eb176050_P001 0.929 |

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| PUZ40261 | Sspon.01G | KQK90066 | TKV95098 | KXG38976 | Zm00001eb022830_P001 0.975 |
| PUZ58834 | genblast_C | KQL03245 | TKW11973 | KXG31483 | Zm00001eb123230_P001 0.981 |
| PUZ74364 | Sspon.04G | KQL28456 | TKW37670 | EES04633 | Zm00001eb206650_P005 0.959 |
| PUZ71471 | Sspon.02G | KQL25244 | TKW34041 | EER97018 | Zm00001eb317890_P001 0.843 |
| PUZ52209 | Sspon.06G | KQL02467 | TKW11157 | EES15381 | Zm00001eb199960_P002 0.982 |
| PUZ59883 | Sspon.08G | KQL11352 | TKW22297 | EER88673 | Zm00001eb387820_P001 0.859 |

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| PUZ38145 | Sspon.05G | KQK88243 | TKV92745 | KXG38121 | Zm00001eb219740_P001 0.827 |
| PUZ68858 | Sspon.05G | KQK87644 | TKV91955 | EES12041 | Zm00001eb067840_P001 0.985 |
| PUZ44613 | Sspon.05G | KQK94228 | TKW00200 | EES08340 | Zm00001eb169240_P001 0.942 |
| PUZ37587 | genblast_C | KQK87711 | TKV92034 | EER91075 | Zm00001eb053090_P001 0.962 |

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| PUZ43512 | Sspon.07G | KQK99735 | TKW07600 | KXG22877 | Zm00001eb163690_P001 | 0.943 |
| PUZ50143 | genblast_C | KQL00774 | TKW08926 | KXG24448 | Zm00001eb416180_P001 | 0.965 |
| PUZ64331 | Sspon.03G | KQL13863 | TKW25331 | KXG21487 | Zm00001eb283520_P003 | 0.899 |
| PUZ69599 | genblast_C | KQL23589 | TKW31909 | OQU89015 | Zm00001eb096080_P001 | 0.961 |
| PUZ43629 | Sspon.07G | KQK99825 | TKW07712 | EES07938 | Zm00001eb093320_P001 | 0.864 |
| PUZ58184 | genblast_C | KQL04537 | TKW13593 | KXG31798 | Zm00001eb336280_P003 | 0.876 |
| PUZ70563 | Sspon.02G | KQL24320 | TKW32946 | EER96678 | Zm00001eb311540_P001 | 0.900 |
| PUZ69522 | Sspon.02G | KQL23509 | TKW31813 | OQU88976 | Zm00001eb306570_P002 | 0.933 |
| PUZ61887 | genblast_C | KQL09457 | TKW19832 | EER89340 | genblast_Os06t0184800-01_Zea | |
| PUZ47730 | Sspon.05G | KQK97804 | TKW05082 | EES11025 | Zm00001eb079150_P001 | 0.978 |
| PUZ73607 | Sspon.04G | KQL27680 | TKW36716 | OQU84132 | Zm00001eb210150_P003 | 0.947 |
| PUZ75977 | Sspon.05G | KQL29926 | TKW39580 | EES06921 | Zm00001eb243040_P001 | 0.980 |
| PUZ42695 | Sspon.01G | KQK92430 | TKV98025 | EER92804 | Zm00001eb403420_P002 | 0.950 |
| PUZ60320 | genblast_C | KQL10995 | TKW21876 | EER88508 | Zm00001eb384710_P001 | 0.939 |
| PUZ64567 | Sspon.05G | KQL14093 | TKW25624 | KXG22633 | Zm00001eb344930_P001 | 0.917 |

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| PUZ72250 | Sspon.02G | KQL26011 | TKW35006 | genblast_C | Zm00001eb287840_P001 | 0.741 |
| PUZ36306 | genblast_C | KQK86402 | TKV90446 | KXG37239 | Zm00001eb062880_P001 | 0.897 |
| PUZ55289 | Sspon.03G | KQL06483 | TKW16130 | EES03453 | Zm00001eb156370_P002 | 0.903 |
| PUZ68025 | Sspon.02G | genblast_C | TKW29795 | OQU79716 | Zm00001eb134400_P001 | 0.817 |
| PUZ43894 | Sspon.05G | KQL04892 | TKV99559 | EES09372 | Zm00001eb091720_P001 | 0.947 |
| PUZ58169 | Sspon.03G | KQL04522 | TKW13576 | EES00265 | Zm00001eb123470_P001 | 0.865 |
| PUZ41148 | genblast_Z | KQK90941 | TKV96179 | EER94870 | Zm00001eb394920_P001 | 0.990 |
| PUZ38497 | Sspon.05G | genblast_C | TKV93180 | genblast_C | Zm00001eb068340_P001 | 0.937 |
| PUZ39540 | Sspon.02G | KQK89461 | TKV94334 | EES16927 | Zm00001eb409500_P001 | 0.976 |
| PUZ44110 | genblast_C | KQK94040 | TKV99919 | OQU83128 | Zm00001eb169080_P001 | 0.960 |
| PUZ78388 | Sspon.04G | KQL32249 | TKW42426 | EES07814 | Zm00001eb259410_P001 | 0.964 |
| PUZ64761 | genblast_C | genblast_C | TKW25855 | EES19955 | Zm00001eb296010_P001 | 0.887 |

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| PUZ48535 | Sspon.02G | KQK98530 | TKW06850 | OQU79144 | Zm00001eb110890_P001 | 0.936 |
| PUZ58747 | Sspon.03G | KQL03350 | TKW12095 | OQU86089 | Zm00001eb338960_P001 | 0.725 |
| PUZ54910 | Sspon.03G | KQL06850 | TKW16607 | EES03571 | Zm00001eb154050_P004 | 0.966 |
| PUZ63214 | Sspon.07G | KQK99406 | TKW07169 | KXG23155 | Zm00001eb138650_P001 | 0.982 |

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| PUZ76415 | Sspon.04G | KQL30357 | TKW40133 | EES05381 | genblast_Os02t0602100-02_Zea | |

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| PUZ53394 | Sspon.03G | KQL08229 | TKW18363 | EES01931 | Zm00001eb144120_P001 | 0.971 |
| PUZ62036 | genblast_C | KQL09597 | TKW20031 | EER87918 | Zm00001eb271500_P001 | 0.954 |
| PUZ71705 | Sspon.02G | KQL25463 | TKW34310 | EER99253 | Zm00001eb319720_P003 | 0.922 |
| PUZ70269 | Sspon.02G | KQL24068 | TKW32559 | EER96534 | Zm00001eb097880_P002 | 0.914 |
| PUZ72377 | Sspon.02G | KQL26134 | TKW35155 | EER97342 | Zm00001eb323480_P001 | 0.962 |
| PUZ57277 | genblast_C | KQL03687 | TKW12545 | OQU86693 | Zm00001eb128010_P002 | 0.907 |
| PUZ54117 | Sspon.03G | KQL07586 | TKW17558 | EES01709 | Zm00001eb368310_P001 | 0.928 |
| PUZ60313 | Sspon.08G | KQL11003 | TKW21882 | OQU76554 | Zm00001eb277540_P001 | 0.881 |
| PUZ54916 | Sspon.03G | KQL06844 | TKW16602 | EES01419 | Zm00001eb154100_P001 | 0.980 |
| PUZ44788 | Sspon.06G | KQK94564 | TKW00639 | EES08446 | Zm00001eb169850_P001 | 0.894 |
| PUZ55847 | Sspon.03G | KQL05850 | TKW15343 | EES01067 | Zm00001eb161980_P001 | 0.980 |
| PUZ66460 | genblast_C | KQL15909 | TKW27847 | EES18046 | Zm00001eb286120_P001 | 0.963 |

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| PUZ42429 | Sspon.01G | KQK92175 | TKV97713 | KXG39979 | Zm00001eb401240_P001 | 0.929 |
| PUZ68173 | Sspon.02G | KQK85885 | TKW29977 | EER97827 | Zm00001eb118300_P001 | 0.854 |
| PUZ57931 | Sspon.03G | KQL04294 | TKW13311 | OQU86379 | Zm00001eb124890_P001 | 0.727 |
| PUZ70712 | genblast_C | KQL24490 | TKW33149 | EER96734 | Zm00001eb312740_P001 | 0.770 |
| PUZ70794 | Sspon.02G | KQK94123 | TKW33273 | EER98944 | Zm00001eb313610_P001 | 0.883 |

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|---|---|---|---|---|---|---|
| PUZ41633 | genblast_C | KQK91418 | TKV96789 | EER95066 | Zm00001eb012800_P002 | 0.991 |
| PUZ66145 | Sspon.07G | KQL15637 | TKW27498 | EES18176 | Zm00001eb350890_P003 | 0.986 |
| PUZ46830 | Sspon.05G | KQK96951 | TKW03982 | OQU81391 | Zm00001eb421070_P001 | 0.882 |
| PUZ72543 | Sspon.02G | KQL26294 | TKW35391 | EER97396 | Zm00001eb324660_P001 | 0.943 |
| PUZ50844 | Sspon.06G | KQL00310 | TKW00293 | OQU83456 | genblast_Os11t0212100-00_Zea | |
| PUZ52313 | Sspon.06G | KQL02583 | TKW11313 | OQU80088 | Zm00001eb413910_P001 | 0.923 |

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|---|---|---|---|---|---|---|
| PUZ63920 | Sspon.07G | KQL13251 | TKW24501 | OQU77359 | Zm00001eb417440_P001 | 0.876 |
| PUZ77667 | Sspon.04G | KQL31546 | TKW41632 | EES07236 | genblast_Os02t0752600-00_Zea | |

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| PUZ58973 | Sspon.08G | genblast_C | TKW23580 | KXG20965 | Zm00001eb228770_P001 | 0.902 |
| PUZ53230 | Sspon.03G | KQL08372 | genblast_C | OQU88129 | Zm00001eb141250_P001 | 0.724 |
| PUZ40917 | Sspon.06G | KQK90878 | TKV96096 | KXG24269 | Zm00001eb143720_P003 | 0.843 |
| PUZ70150 | Sspon.02G | KQL24007 | TKW32460 | KXG35314 | Zm00001eb309040_P002 | 0.941 |
| PUZ62132 | genblast_C | KQL09695 | TKW20152 | EER87871 | Zm00001eb271060_P001 | 0.955 |
| PUZ58461 | Sspon.03G | KQL04798 | TKW13944 | EES00141 | Zm00001eb337410_P002 | 0.836 |
| PUZ64049 | Sspon.07G | KQL13049 | TKW24230 | EES17717 | Zm00001eb418150_P001 | 0.927 |
| PUZ73060 | Sspon.02G | KQL26799 | TKW36027 | EER97594 | Zm00001eb110240_P001 | 0.880 |
| PUZ66049 | Sspon.07G | KQL15532 | TKW27357 | EES18214 | Zm00001eb349640_P001 | 0.981 |
| PUZ68740 | Sspon.06G | KQL22771 | TKW30860 | KXG24853 | Zm00001eb180130_P003 | 0.852 |
| PUZ40073 | Sspon.03G | KQK89882 | TKV94876 | OQU86773 | Zm00001eb130070_P001 | 0.809 |
| PUZ48102 | Sspon.05G | KQK98161 | TKW05534 | EES12533 | Zm00001eb076870_P001 | 0.936 |

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| PUZ54136 | Sspon.03G | KQL07567 | TKW17538 | genblast_C | Zm00001eb148990_P001 | 0.897 |
| PUZ54075 | Sspon.03G | KQL07629 | TKW17605 | OQU87824 | Zm00001eb148650_P001 | 0.930 |
| PUZ55502 | genblast_C | KQL06196 | TKW15802 | EES01207 | genblast_Os01t0661000-01_Zea | |

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| PUZ57915 | Sspon.03G | KQL04280 | TKW13295 | EES00361 | Zm00001eb125060_P001 | 0.934 |
| PUZ76160 | Sspon.07G | KQL30096 | TKW39737 | KXG30452 | Zm00001eb244220_P001 | 0.724 |
| PUZ51894 | genblast_C | KQL02207 | TKW10798 | EES14023 | Zm00001eb038320_P001 | 0.922 |
| PUZ48519 | genblast_C | KQK98510 | TKW06046 | EES12687 | Zm00001eb073660_P001 | 0.912 |
| PUZ54723 | Sspon.03G | KQL07043 | TKW16850 | KXG33403 | Zm00001eb152790_P001 | 0.897 |
| PUZ59614 | Sspon.04G | genblast_C | TKW21951 | EER90166 | Zm00001eb389670_P002 | 0.879 |

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| PUZ49043 | Sspon.05G | genblast_C | genblast_C | genblast_C | Zm00001eb431470_P001 | 0.915 |
| PUZ58198 | Sspon.03G | KQL04550 | TKW13616 | EES00247 | Zm00001eb336370_P001 | 0.862 |
| PUZ36808 | Sspon.01G | KQK86879 | TKV91074 | EER90809 | Zm00001eb059150_P001 | 0.940 |

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| PUZ64753 | genblast_C | KQL14285 | TKW25844 | EES19960 | Zm00001eb296080_P001 | 0.929 |
| PUZ77971 | Sspon.04G | KQL31840 | TKW41960 | EES07648 | Zm00001eb257320_P001 | 0.902 |
| PUZ47241 | Sspon.05G | KQK97353 | TKW04500 | EES12206 | Zm00001eb082230_P001 | 0.954 |
| PUZ36398 | genblast_C | genblast_C | TKV90566 | EER90651 | Zm00001eb062220_P003 | 0.902 |
| PUZ57138 | Sspon.03G | KQL03561 | TKW12379 | EES02810 | Zm00001eb332330_P001 | 0.897 |
| PUZ59394 | Sspon.08G | KQL11931 | TKW23052 | KXG20670 | Zm00001eb273530_P001 | 0.878 |
| PUZ53048 | genblast_C | KQL14414 | TKW25976 | EES04195 | Zm00001eb141480_P006 | 0.950 |
| PUZ58384 | Sspon.03G | KQL04719 | TKW13851 | KXG31669 | Zm00001eb122000_P002 | 0.925 |
| PUZ64740 | Sspon.07G | KQL14267 | TKW25824 | EES19964 | Zm00001eb296230_P001 | 0.993 |
| PUZ38971 | Sspon.01G | KQK89214 | TKV94016 | EER91588 | Zm00001eb047910_P001 | 0.900 |
| PUZ41021 | Sspon.01G | KQK90810 | TKV96004 | KXG39328 | Zm00001eb017460_P003 | 0.943 |
| PUZ73252 | genblast_C | KQL26975 | TKW36243 | EER97649 | Zm00001eb329550_P001 | 0.885 |
| PUZ67817 | Sspon.01G | KQL17110 | TKW29484 | OQU79534 | Zm00001eb028720_P001 | 0.863 |
| PUZ52511 | genblast_C | KQK99924 | TKW07846 | EER99847 | Zm00001eb329770_P001 | 0.967 |
| PUZ65777 | Sspon.07G | KQL15287 | TKW27036 | KXG22105 | Zm00001eb288870_P001 | 0.886 |
| PUZ57551 | Sspon.03G | KQL03972 | TKW12872 | EES02669 | Zm00001eb334060_P001 | 0.933 |
| PUZ61521 | Sspon.04G | KQL10089 | TKW20671 | EES04435 | Zm00001eb208780_P001 | 0.928 |
| PUZ67062 | genblast_C | KQL16402 | TKW28494 | genblast_C | genblast_Os05t0293500-01_Zea | |
| PUZ77684 | Sspon.04G | genblast_C | TKW41652 | OQU85395 | Zm00001eb194140_P002 | 0.947 |
| PUZ55521 | Sspon.03G | KQL06176 | genblast_Z | EES01199 | Zm00001eb157880_P001 | 0.959 |
| PUZ75373 | Sspon.06G | genblast_C | TKW38824 | KXG24285 | Zm00001eb261130_P001 | 0.860 |
| PUZ38666 | Sspon.01G | genblast_C | TKV93416 | KXG38351 | Zm00001eb221910_P001 | 0.851 |
| PUZ37132 | Sspon.01G | KQK87217 | TKV91485 | OQU91037 | Zm00001eb056430_P002 | 0.872 |
| PUZ70957 | Sspon.02G | KQL24757 | TKW33454 | OQU89605 | genblast_Os09t0453300-01_Zea | |
| PUZ49379 | genblast_C | KQL23456 | TKW31755 | EER98441 | Zm00001eb096690_P004 | 0.949 |
| PUZ41522 | Sspon.01G | KQK91313 | TKV96679 | EER95033 | Zm00001eb013450_P001 | 0.960 |

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| PUZ71645 | Sspon.02G | KQL25420 | TKW34246 | KXG36047 | Zm00001eb103250_P002 | 0.922 |
| PUZ63385 | genblast_C | KQL13629 | TKW25030 | EER88965 | Zm00001eb418440_P002 | 0.847 |

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| PUZ61160 | Sspon.08G | KQL10444 | TKW21168 | OQU7632 | Zm00001eb189420_P001 | 0.722 |
| PUZ36690 | genblast_C | KQK86780 | TKV90960 | EER90772 | Zm00001eb059980_P001 | 0.904 |
| PUZ38796 | Sspon.01G | KQK88844 | TKV93536 | KXG38410 | genblast_Os10t0458700-02_Ze | |
| PUZ59103 | Sspon.08G | KQL12226 | TKW23437 | EER88960 | Zm00001eb228020_P001 | 0.840 |
| PUZ67314 | Sspon.02G | KQL16730 | TKW28930 | EES17129 | genblast_Os12t0534100-01_Ze | |
| PUZ69538 | Sspon.02G | KQL23530 | TKW31843 | EER96333 | Zm00001eb306680_P003 | 0.966 |
| PUZ72252 | Sspon.02G | KQL26014 | TKW35008 | EER99450 | Zm00001eb106050_P001 | 0.962 |
| PUZ73803 | Sspon.04G | KQL28968 | TKW38307 | OQU84251 | Zm00001eb230520_P001 | 0.941 |
| PUZ61328 | Sspon.08G | genblast_C | TKW20421 | OQU76059 | Zm00001eb372900_P001 | 0.990 |
| PUZ52376 | Sspon.06G | KQL02644 | TKW11385 | EES15312 | Zm00001eb036580_P002 | 0.983 |
| PUZ69017 | Sspon.02G | KQL23134 | TKW31323 | EER98268 | Zm00001eb304170_P001 | 0.861 |
| PUZ59150 | Sspon.08G | KQL12171 | TKW23374 | EER88944 | Zm00001eb227700_P004 | 0.862 |
| PUZ71351 | Sspon.02G | KQL25142 | TKW33919 | EER99125 | Zm00001eb102160_P001 | 0.864 |
| PUZ69582 | genblast_Z | KQL23569 | TKW31890 | KXG35096 | Zm00001eb096170_P003 | 0.972 |

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| PUZ68413 | Sspon.02G | KQL29785 | TKW30441 | EER95872 | Zm00001eb300050_P001 | 0.952 |
| PUZ76551 | Sspon.04G | KQL30484 | TKW40296 | EES07149 | Zm00001eb247120_P001 | 0.950 |
| PUZ70321 | Sspon.02G | KQL24106 | TKW32620 | EER96560 | Zm00001eb309720_P001 | 0.928 |
| PUZ42378 | Sspon.01G | KQK92127 | TKV97657 | EER95335 | Zm00001eb008080_P001 | 0.977 |
| PUZ40880 | Sspon.01G | KQK90632 | TKV95820 | OQU92502 | Zm00001eb018690_P001 | 0.892 |
| PUZ49201 | Sspon.05G | KQK99207 | TKW06939 | EES11546 | Zm00001eb068550_P001 | 0.904 |
| PUZ67727 | Sspon.02G | KQL17039 | TKW29381 | OQU79495 | genblast_Os12t0596300-01 | Zm0 |
| PUZ43953 | Sspon.05G | genblast_Z | TKV99686 | EES09411 | Zm00001eb201140_P002 | 0.922 |
| PUZ56427 | Sspon.03G | KQL05345 | TKW14712 | KXG32613 | Zm00001eb341910_P003 | 0.987 |
| PUZ65633 | Sspon.07G | KQL15143 | TKW26875 | KXG22169 | Zm00001eb351460_P001 | 0.827 |
| PUZ39890 | Sspon.01G | KQK89721 | TKV94680 | OQU92053 | Zm00001eb025290_P001 | 0.931 |

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| PUZ50806 | Sspon.06G | KQL01183 | TKW09491 | EES14801 | Zm00001eb178050_P001 | 0.809 |
| PUZ52338 | genblast_C | KQL02606 | TKW11338 | KXG25552 | Zm00001eb036250_P001 | 0.921 |

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| PUZ58684 | genblast_C | KQL04970 | TKW14178 | KXG22733 | Zm00001eb345600_P001 | 0.821 |

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| PUZ41667 | genblast_C | KQK91455 | TKV96830 | EER92465 | Zm00001eb012550_P001 | 0.933 |
| PUZ66465 | Sspon.07G | KQL15894 | TKW27832 | KXG21772 | Zm00001eb286040_P002 | 0.729 |
| PUZ77204 | genblast_C | genblast_C | TKW41050 | KXG30956 | Zm00001eb187880_P002 | 0.779 |
| PUZ66912 | genblast_Z | KQL16358 | TKW28437 | KXG22814 | Zm00001eb405010_P001 | 0.898 |

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| PUZ37711 | Sspon.01G | KQK87859 | TKV92203 | EER93724 | Zm00001eb218250_P001 | 0.933 |

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| PUZ62354 | Sspon.08G | KQL09134 | TKW19463 | EER87784 | Zm00001eb378150_P001 | 0.839 |
| PUZ69168 | Sspon.02G | KQL14382 | TKW25943 | EER97413 | Zm00001eb325060_P001 | 0.951 |
| PUZ39683 | Sspon.01G | KQK89325 | TKV94173 | KXG38231 | Zm00001eb220870_P001 | 0.936 |
| PUZ72269 | genblast_C | KQL26033 | TKW35035 | OQU90023 | Zm00001eb322840_P001 | 0.815 |
| PUZ41586 | genblast_C | KQK91377 | TKV96735 | EER95054 | Zm00001eb013030_P001 | 0.951 |
| PUZ37402 | Sspon.01G | KQK87485 | TKV91766 | EER91011 | Zm00001eb054670_P001 | 0.904 |
| PUZ52307 | Sspon.06G | KQL02576 | TKW11298 | EES15332 | Zm00001eb042740_P001 | 0.720 |
| PUZ59391 | Sspon.08G | KQL11934 | TKW14028 | OQU76929 | Zm00001eb225660_P001 | 0.863 |
| PUZ69620 | Sspon.03G | KQL23616 | TKW31949 | EES03744 | Zm00001eb369670_P001 | 0.937 |
| PUZ53358 | Sspon.03G | KQL08259 | TKW18412 | EES04083 | Zm00001eb365030_P001 | 0.974 |
| PUZ65520 | Sspon.07G | KQL15021 | TKW26728 | EES18393 | Zm00001eb290650_P001 | 0.719 |
| PUZ71189 | Sspon.02G | KQL24958 | TKW33692 | KXG35861 | Zm00001eb101560_P001 | 0.959 |
| PUZ38305 | Sspon.01G | KQK88388 | TKV92930 | KXG38193 | Zm00001eb043710_P001 | 0.980 |

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| PUZ68643 | Sspon.02G | KQL22667 | TKW30742 | OQU88534 | Zm00001eb301300_P001 | 0.983 |
| PUZ58120 | Sspon.03G | KQL04478 | TKW13527 | OQU86282 | Zm00001eb123770_P001 | 0.803 |
| PUZ36626 | Sspon.01G | genblast_C | TKV90867 | EER93305 | Zm00001eb060530_P001 | 0.930 |
| PUZ63740 | genblast_C | KQL13086 | TKW24279 | EES17607 | Zm00001eb266020_P001 | 0.984 |
| PUZ54183 | Sspon.03G | KQL07526 | TKW17485 | KXG33633 | Zm00001eb368690_P001 | 0.894 |

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| PUZ37887 | Sspon.01G | KQK88014 | TKV92396 | EER91204 | Zm00001eb051040_P002 | 0.924 |
| PUZ72120 | genblast_C | KQL25856 | TKW34829 | EER97244 | Zm00001eb321920_P001 | 0.909 |

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| PUZ73499 | Sspon.01G | KQL27230 | TKW36585 | OQU90496 | Zm00001eb111680_P001 | 0.788 |
| PUZ39800 | Sspon.01G | KQK89634 | TKV94568 | EER91818 | Zm00001eb025870_P001 | 0.840 |
| PUZ42136 | Sspon.01G | KQK91913 | TKV97397 | OQU92984 | Zm00001eb399930_P006 | 0.773 |
| PUZ47968 | Sspon.05G | KQK98038 | TKW05387 | KXG26693 | Zm00001eb426420_P002 | 0.861 |

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| PUZ60775 | genblast_C | KQL10253 | TKW20892 | genblast_C | Zm00001eb280480_P001 | 0.904 |
| PUZ53490 | genblast_C | KQL08147 | TKW18264 | EES01908 | Zm00001eb144580_P001 | 0.920 |
| PUZ41630 | genblast_C | KQK91417 | TKV96784 | KXG39648 | Zm00001eb012830_P001 | 0.912 |
| PUZ52490 | Sspon.06G | genblast_C | TKW11511 | EES15269 | Zm00001eb198350_P001 | 0.964 |
| PUZ49556 | Sspon.05G | KQL12736 | genblast_C | EES13119 | Zm00001eb065810_P001 | 0.923 |
| PUZ55688 | genblast_C | genblast_C | TKW15538 | EES01127 | Zm00001eb159140_P001 | 0.944 |

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| PUZ37234 | genblast_C | genblast_C | TKV91603 | EER90950 | Zm00001eb055920_P001 | 0.954 |
| genblast_C | Sspon.03G | genblast_C | TKW12778 | EES00507 | Zm00001eb127760_P002 | 0.947 |
| PUZ76499 | Sspon.04G | KQL30430 | TKW40228 | OQU85289 | Zm00001eb246800_P001 | 0.914 |
| PUZ49530 | Sspon.05G | KQL12768 | TKW23872 | genblast_C | Zm00001eb066030_P002 | 0.934 |
| PUZ54148 | genblast_C | KQL07552 | TKW17525 | genblast_C | Zm00001eb149070_P001 | 0.866 |
| PUZ48699 | genblast_C | genblast_C | genblast_C | OQU82235 | Zm00001eb072180_P001 | 0.880 |
| PUZ44500 | Sspon.05G | genblast_C | TKW00365 | EES08391 | Zm00001eb090760_P001 | 0.914 |
| PUZ47518 | Sspon.05G | KQK97604 | TKW04825 | EES10957 | Zm00001eb424390_P002 | 0.954 |
| PUZ71722 | Sspon.06G | KQL25478 | TKW34331 | OQU89832 | Zm00001eb103700_P001 | 0.980 |
| PUZ49181 | Sspon.05G | KQK99183 | TKW06906 | EES11537 | Zm00001eb068680_P001 | 0.866 |
| PUZ61830 | genblast_C | KQL09390 | TKW19737 | EER89369 | Zm00001eb278460_P001 | 0.831 |

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| PUZ53399 | Sspon.03G | KQL08224 | TKW18356 | KXG33953 | Zm00001eb365340_P001 | 0.766 |

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| PUZ61174 | Sspon.08G | KQL10483 | TKW21229 | EER88333 | genblast_Os06t0325200-01_Ze |

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| PUZ66552 | Sspon.05G | KQL16048 | TKW28027 | EES11497 | Zm00001eb069500_P001 | 0.935 |
| PUZ67475 | genblast_C | KQL16583 | TKW28728 | EES16173 | genblast_Os12t0565100-01_Ze | |
| PUZ42206 | genblast_C | KQK91977 | TKV97460 | EER95280 | Zm00001eb008570_P001 | 0.935 |
| PUZ45644 | Sspon.05G | KQK95635 | TKW02121 | KXG29017 | Zm00001eb165930_P001 | 0.904 |
| PUZ65124 | genblast_C | KQL14679 | TKW26281 | KXG22374 | Zm00001eb353550_P001 | 0.728 |
| PUZ73005 | Sspon.02G | KQL32120 | TKW42270 | EER99735 | Zm00001eb327930_P001 | 0.850 |
| PUZ61021 | Sspon.08G | KQL10358 | TKW21034 | genblast_C | genblast_Os06t0294000-01_Ze | |

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| PUZ40889 | Sspon.01G | genblast_C | TKV95836 | EER92197 | Zm00001eb018570_P001 | 0.832 |
| PUZ36643 | Sspon.01G | KQK86724 | TKV90903 | EER93317 | Zm00001eb300850_P001 | 0.718 |
| PUZ51007 | Sspon.07G | KQL01341 | TKW09709 | OQU78428 | Zm00001eb177450_P001 | 0.967 |
| PUZ72867 | genblast_C | KQL26596 | TKW35734 | EER99688 | Zm00001eb108930_P001 | 0.872 |
| PUZ61321 | genblast_C | KQL09781 | TKW20270 | EER88077 | Zm00001eb372960_P002 | 0.766 |
| PUZ66232 | Sspon.06G | KQL02475 | TKW11169 | OQU80904 | genblast_Os08t0515000-00 | Zm0 |
| PUZ67828 | Sspon.02G | genblast_C | TKW29489 | KXG23929 | Zm00001eb135720_P002 | 0.972 |
| PUZ41708 | Sspon.01G | genblast_C | TKV96963 | EER95110 | Zm00001eb214070_P002 | 0.900 |
| PUZ40358 | Sspon.01G | KQK90152 | TKV95202 | EER94583 | Zm00001eb022050_P001 | 0.965 |
| PUZ56536 | Sspon.04G | KQL05197 | TKW14475 | EES12862 | genblast_Os01t0371200-01_Zea | |
| PUZ77122 | Sspon.04G | genblast_C | TKW40978 | KXG30985 | Zm00001eb187650_P002 | 0.925 |
| PUZ55162 | Sspon.03G | KQL06611 | TKW16288 | KXG33209 | Zm00001eb155470_P001 | 0.780 |
| PUZ39307 | Sspon.01G | KQK89508 | TKV94394 | EER91738 | Zm00001eb026500_P001 | 0.894 |
| PUZ41386 | Sspon.01G | KQK91186 | TKV96505 | EER94973 | Zm00001eb014790_P001 | 0.754 |
| PUZ49549 | Sspon.05G | KQL12749 | TKW23854 | EES11665 | Zm00001eb433900_P001 | 0.979 |
| PUZ60579 | Sspon.04G | KQL10710 | TKW21549 | EES06772 | genblast_Os06t0341300-01 | Zm0 |
| PUZ71233 | genblast_C | KQL25006 | TKW33754 | genblast_C | Zm00001eb316430_P001 | 0.805 |
| PUZ47878 | Sspon.05G | KQK97954 | TKW05271 | EES11077 | Zm00001eb425990_P001 | 0.965 |
| PUZ54156 | Sspon.03G | KQL07545 | TKW17515 | genblast_C | Zm00001eb368550_P001 | 0.940 |
| PUZ63512 | Sspon.05G | KQL04722 | TKW13854 | KXG21572 | Zm00001eb424610_P001 | 0.973 |
| PUZ73439 | Sspon.02G | KQL27067 | TKW36355 | KXG36886 | Zm00001eb330030_P001 | 0.996 |
| PUZ60098 | Sspon.08G | KQL11559 | TKW22586 | EER89995 | Zm00001eb386000_P001 | 0.965 |
| PUZ70934 | Sspon.02G | KQL24733 | TKW33428 | KXG35739 | Zm00001eb314530_P003 | 0.779 |
| PUZ47322 | Sspon.05G | KQK97431 | TKW04603 | EES10871 | genblast_Os04t0445300-01_Zea | |

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| PUZ44960 | Sspon.01G | KQK94691 | TKW00826 | KXG28442 | Zm00001eb170150_P001 | 0.900 |
| PUZ53325 | Sspon.03G | KQL08291 | TKW18456 | EES04096 | Zm00001eb143540_P001 | 0.943 |
| PUZ58186 | Sspon.03G | KQL04544 | TKW13605 | EES02407 | Zm00001eb123380_P001 | 0.902 |
| PUZ37570 | Sspon.01G | KQK87695 | TKV92007 | EER91068 | Zm00001eb217240_P002 | 0.931 |
| PUZ36941 | genblast_C | KQK87015 | TKV91261 | KXG37509 | Zm00001eb057910_P002 | 0.929 |
| PUZ61707 | Sspon.07G | KQL09860 | TKW20367 | KXG19573 | Zm00001eb373450_P001 | 0.946 |
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| PUZ37828 | Sspon.01G | KQK87964 | TKV92333 | EER91176 | Zm00001eb050630_P001 | 0.998 |
| PUZ40083 | Sspon.01G | KQK89895 | TKV94893 | EER91921 | Zm00001eb023710_P001 | 0.939 |
| PUZ64214 | genblast_C | KQL13750 | TKW25191 | EES19111 | Zm00001eb281940_P001 | 0.939 |
| PUZ59941 | Sspon.08G | KQL11421 | TKW22404 | KXG20357 | Zm00001eb388300_P001 | 0.934 |
| PUZ77093 | Sspon.04G | KQL30970 | TKW40937 | EES05720 | Zm00001eb250800_P001 | 0.882 |
| PUZ76801 | Sspon.04G | KQL30710 | TKW40607 | KXG31117 | Zm00001eb248780_P001 | 0.816 |
| PUZ55633 | genblast_C | KQL06063 | TKW15603 | KXG32982 | Zm00001eb158740_P002 | 0.971 |
| PUZ42278 | Sspon.01G | KQK92045 | TKV97553 | OQU93034 | Zm00001eb007310_P001 | 0.945 |
| PUZ35986 | Sspon.01G | KQK86087 | TKV90066 | EER93057 | Zm00001eb251060_P003 | 0.965 |
| PUZ76356 | Sspon.04G | KQL30279 | TKW40050 | EES04714 | Zm00001eb205620_P001 | 0.965 |
| PUZ77114 | genblast_C | KQL30988 | TKW40963 | KXG30991 | Zm00001eb250990_P001 | 0.770 |
| PUZ44676 | genblast_C | genblast_C | TKW00535 | KXG30134 | Zm00001eb181140_P001 | 0.928 |
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| PUZ71186 | Sspon.06G | KQL24953 | TKW33685 | OQU8966 | Zm00001eb316120_P001 | 0.884 |
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| PUZ55653 | Sspon.03G | KQL06040 | TKW15576 | EES01143 | Zm00001eb158910_P001 | 0.878 |
| PUZ42077 | Sspon.01G | KQK91847 | TKV97318 | EER95218 | Zm00001eb399390_P002 | 0.808 |
| PUZ59812 | Sspon.08G | KQL11269 | TKW22176 | EER88702 | Zm00001eb275400_P001 | 0.900 |
| PUZ70834 | Sspon.04G | KQL24641 | TKW33324 | EER98967 | Zm00001eb100100_P001 | 0.987 |
| PUZ77298 | Sspon.04G | KQL31174 | TKW41185 | EES07383 | Zm00001eb188610_P001 | 0.797 |
| PUZ66614 | genblast_C | KQL15995 | TKW27958 | EES18011 | Zm00001eb350250_P001 | 0.850 |
| PUZ74992 | Sspon.04G | genblast_C | TKW36885 | OQU8474 | Zm00001eb237900_P003 | 0.951 |
| PUZ46596 | Sspon.05G | KQK96729 | TKW03677 | EES11974 | Zm00001eb420820_P002 | 0.983 |
| PUZ36801 | genblast_C | KQK86869 | TKV91063 | EER93367 | Zm00001eb213730_P001 | 0.849 |
| PUZ75888 | Sspon.04G | KQL29854 | TKW39458 | OQU8504 | Zm00001eb242410_P001 | 0.970 |
| PUZ72076 | Sspon.02G | KQL25819 | TKW34783 | EER97231 | Zm00001eb321620_P001 | 0.953 |
| PUZ48951 | Sspon.05G | KQK98966 | TKW06628 | EES11440 | Zm00001eb070430_P001 | 0.715 |
| PUZ64655 | Sspon.07G | KQL14193 | TKW25739 | KXG22587 | Zm00001eb296680_P001 | 0.970 |

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| PUZ36385 | genblast_C | KQK86473 | TKV90556 | EER93210 | Zm00001eb212020_P001 | 0.912 |
| PUZ75387 | Sspon.06G | KQL10640 | TKW21467 | OQU76438 | Zm00001eb384990_P001 | 0.878 |

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| PUZ76363 | Sspon.04G | KQL30294 | TKW40066 | EES07088 | Zm00001eb246010_P001 | 0.959 |
| PUZ59866 | Sspon.08G | KQL11331 | TKW22271 | EER88680 | Zm00001eb275610_P001 | 0.924 |
| PUZ46353 | Sspon.05G | KQK96387 | TKW03192 | OQU81175 | Zm00001eb419790_P001 | 0.867 |
| PUZ50034 | Sspon.06G | genblast_C | TKW09093 | EES13321 | Zm00001eb416890_P001 | 0.933 |
| PUZ69314 | Sspon.02G | KQL23287 | TKW31577 | EER98385 | Zm00001eb305560_P001 | 0.770 |
| PUZ51099 | genblast_C | KQL01425 | TKW09815 | KXG24940 | Zm00001eb177430_P001 | 0.935 |

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| PUZ66955 | Sspon.07G | KQL16248 | TKW28294 | EES16801 | Zm00001eb138690_P001 | 0.928 |
| PUZ65208 | Sspon.07G | KQL14816 | TKW26451 | EES18460 | Zm00001eb292310_P001 | 0.958 |
| PUZ52989 | Sspon.03G | KQL08620 | TKW18863 | EES02053 | Zm00001eb363070_P001 | 0.735 |
| PUZ48408 | Sspon.05G | KQK98429 | TKW05931 | KXG26891 | Zm00001eb074270_P001 | 0.912 |
| PUZ65256 | Sspon.07G | KQL14774 | TKW26407 | KXG22329 | Zm00001eb352950_P001 | 0.863 |
| PUZ77804 | genblast_C | KQL31672 | TKW41772 | EES05861 | Zm00001eb256090_P001 | 0.942 |
| PUZ77327 | Sspon.04G | KQL31200 | TKW41216 | EES07373 | Zm00001eb252550_P001 | 0.826 |
| PUZ55956 | Sspon.05G | KQL14402 | TKW25966 | EES07841 | Zm00001eb194870_P002 | 0.880 |
| PUZ40383 | genblast_C | KQK90185 | TKV95241 | OQU92249 | Zm00001eb021840_P001 | 0.902 |

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| PUZ60349 | genblast_C | genblast_C | TKW21822 | KXG20143 | Zm00001eb117090_P001 | 0.846 |
| PUZ48917 | Sspon.05G | KQK98942 | TKW06596 | OQU82335 | Zm00001eb070600_P001 | 0.901 |
| PUZ70239 | Sspon.02G | KQL13156 | TKW24366 | EER99320 | Zm00001eb104370_P001 | 0.927 |
| PUZ76473 | Sspon.04G | KQL30421 | TKW40212 | EES07130 | Zm00001eb246750_P005 | 0.934 |
| PUZ74737 | Sspon.04G | KQL28061 | TKW37178 | EES04776 | Zm00001eb239920_P004 | 0.971 |
| PUZ65417 | Sspon.07G | KQL14912 | TKW26580 | KXG22251 | Zm00001eb291380_P001 | 0.926 |
| PUZ75658 | genblast_C | KQL29484 | TKW38958 | OQU80721 | Zm00001eb176170_P001 | 0.986 |
| PUZ41515 | Sspon.01G | KQK91307 | TKV96673 | KXG39580 | Zm00001eb013510_P002 | 0.977 |

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| PUZ46793 | Sspon.05G | KQK96911 | TKW03938 | KXG26070 | Zm00001eb420910_P002 | 0.829 |

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| PUZ45561 | Sspon.06G | genblast_C | TKW01922 | EES08878 | Zm00001eb166540_P001 | 0.886 |
| PUZ71638 | Sspon.02G | KQL25412 | TKW34239 | EER97073 | Zm00001eb319220_P001 | 0.977 |
| genblast_C | genblast_C | KQL01042 | TKW09291 | EES13259 | Zm00001eb260890_P001 | 0.778 |
| PUZ63201 | genblast_C | KQK99421 | TKW07188 | EES16783 | Zm00001eb409100_P001 | 0.814 |

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| PUZ59719 | Sspon.08G | genblast_C | TKW22059 | EER88742 | genblast_Os06t0652100-00_Zea | |
| PUZ76524 | Sspon.04G | KQL30462 | TKW40270 | EES07141 | Zm00001eb184560_P003 | 0.890 |
| PUZ69345 | Sspon.02G | KQL23321 | TKW31616 | EER98400 | Zm00001eb094750_P001 | 0.885 |
| PUZ57641 | genblast_Z | KQL04057 | TKW12986 | EES02638 | Zm00001eb126660_P001 | 0.936 |

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| PUZ63847 | genblast_C | KQL13197 | TKW24421 | EES17650 | Zm00001eb264980_P001 | 0.991 |

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| PUZ48128 | Sspon.05G | KQK98194 | TKW05570 | OQU82009 | Zm00001eb075940_P002 | 0.991 |
| PUZ57306 | genblast_C | KQL03715 | TKW12585 | KXG32244 | Zm00001eb333030_P001 | 0.944 |
| PUZ78363 | Sspon.04G | KQL32220 | TKW42398 | EES07795 | Zm00001eb190770_P001 | 0.940 |
| PUZ61183 | Sspon.08G | genblast_C | TKW21250 | KXG19927 | Zm00001eb381980_P001 | 0.876 |

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| PUZ62568 | Sspon.06G | KQL08917 | TKW19186 | EER87695 | Zm00001eb379340_P001 | 0.908 |
| PUZ67968 | Sspon.02G | KQL04039 | TKW12963 | KXG24045 | Zm00001eb134480_P005 | 0.918 |

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| PUZ53088 | Sspon.03G | KQL08521 | TKW18738 | genblast_C | Zm00001eb141940_P002 | 0.964 |
| PUZ49527 | Sspon.05G | KQL12774 | TKW23877 | EES11654 | Zm00001eb097750_P001 | 0.954 |

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| PUZ71779 | genblast_C | KQL25527 | TKW34393 | OQU89853 | Zm00001eb104000_P001 | 0.770 |
| PUZ66217 | Sspon.07G | KQL15709 | TKW27606 | EES19439 | Zm00001eb286850_P001 | 0.982 |

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| PUZ65120 | Sspon.07G | KQL14676 | TKW26277 | KXG22376 | Zm00001eb293610_P004 | 0.769 |
| PUZ45524 | Sspon.06G | KQK95411 | TKW01823 | EES10116 | Zm00001eb166750_P005 | 0.713 |
| PUZ41700 | Sspon.01G | KQK91486 | TKV96864 | EER92483 | Zm00001eb012250_P001 | 0.968 |
| PUZ64808 | Sspon.07G | KQL14346 | TKW25910 | EES18672 | Zm00001eb295700_P001 | 0.944 |
| PUZ57290 | genblast_C | KQL03706 | TKW12567 | EES02750 | Zm00001eb128590_P001 | 0.869 |
| PUZ71077 | Sspon.02G | KQL24890 | TKW33609 | EER99036 | Zm00001eb315500_P002 | 0.970 |

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| PUZ46156 | Sspon.05G | KQK96296 | TKW03082 | EES10396 | Zm00001eb419430_P001 | 0.972 |
| PUZ55196 | Sspon.03G | KQL06579 | TKW16247 | EES01330 | Zm00001eb155670_P001 | 0.832 |
| PUZ69048 | genblast_C | KQL23100 | TKW31278 | EER96106 | Zm00001eb094890_P001 | 0.891 |
| PUZ38073 | Sspon.01G | KQK88156 | TKV92627 | EER91265 | Zm00001eb219310_P002 | 0.805 |
| PUZ36787 | Sspon.01G | KQK86861 | TKV91055 | EER90803 | Zm00001eb059240_P002 | 0.890 |

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| PUZ42092 | Sspon.01G | KQK91858 | TKV97334 | OQU9296 | Zm00001eb009380_P001 | 0.940 |

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| PUZ50098 | Sspon.06G | genblast_C | TKW08975 | EES13346 | Zm00001eb416400_P001 | 0.899 |
| PUZ45010 | Sspon.06G | KQK94736 | TKW00905 | EES08547 | Zm00001eb170360_P002 | 0.954 |
| PUZ53203 | Sspon.07G | KQL08404 | TKW18586 | EES04128 | Zm00001eb142840_P001 | 0.820 |
| PUZ55294 | Sspon.07G | KQL06471 | TKW16116 | OQU8735 | Zm00001eb360530_P001 | 0.864 |
| PUZ47972 | Sspon.05G | KQK98042 | TKW05391 | EES12490 | Zm00001eb077450_P001 | 0.944 |
| PUZ50001 | Sspon.06G | KQL00942 | TKW09147 | KXG24348 | Zm00001eb261800_P001 | 0.926 |
| PUZ71951 | Sspon.02G | KQL25704 | TKW34638 | EER97183 | Zm00001eb320310_P002 | 0.980 |
| PUZ64952 | Sspon.03G | KQL14515 | TKW26104 | KXG22458 | Zm00001eb294610_P001 | 0.894 |
| PUZ40297 | Sspon.01G | KQK90094 | TKV95130 | OQU9219 | Zm00001eb393970_P002 | 0.934 |
| PUZ45887 | Sspon.01G | KQK95978 | TKW0271 | EES09033 | Zm00001eb047690_P001 | 0.735 |
| PUZ50314 | Sspon.06G | KQL00633 | TKW08731 | OQU7997 | Zm00001eb414810_P001 | 0.943 |

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| PUZ54284 | genblast_C | KQL07420 | TKW17356 | EES01640 | Zm00001eb150050_P001 | 0.935 |

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| PUZ52087 | Sspon.04G | KQL27880 | TKW36965 | OQU8470 | Zm00001eb204370_P001 | 0.929 |
| PUZ63753 | Sspon.07G | KQL13096 | TKW24295 | EES18924 | Zm00001eb265820_P001 | 0.940 |
| PUZ65907 | Sspon.03G | KQL15405 | TKW2717 | EES19554 | Zm00001eb288410_P002 | 0.927 |
| PUZ41615 | Sspon.01G | KQK91405 | TKV96766 | KXG39644 | Zm00001eb012890_P001 | 0.788 |

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| PUZ72830 | Sspon.02G | KQL26575 | TKW35702 | EER97499 | Zm00001eb108840_P001 | 0.975 |

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| genblast_C | Sspon.02G | KQL17277 | TKW29655 | OQU7961 | Zm00001eb031760_P001 | 0.893 |

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| PUZ57270 | Sspon.03G | KQL03679 | TKW12535 | EES02758 | genblast_Os01t0274800-01_Zea | |
| PUZ56490 | Sspon.02G | KQL05192 | TKW14460 | EES06833 | Zm00001eb341380_P001 | 0.932 |
| PUZ65464 | Sspon.07G | KQL07436 | TKW26634 | EES19718 | Zm00001eb369130_P001 | 0.757 |
| PUZ49694 | genblast_Z | KQL12605 | TKW23657 | EES13169 | Zm00001eb434560_P001 | 1.004 |
| PUZ40233 | genblast_C | KQK90056 | TKV95068 | EER94531 | Zm00001eb022960_P001 | 0.868 |
| PUZ72874 | genblast_C | KQL26625 | TKW35774 | KXG36664 | Zm00001eb327260_P001 | 0.958 |
| PUZ70297 | Sspon.02G | KQL24082 | TKW32592 | OQU89259 | Zm00001eb097960_P001 | 0.916 |
| PUZ48281 | Sspon.05G | genblast_C | TKW05763 | EES12600 | Zm00001eb075010_P001 | 0.909 |
| PUZ56949 | Sspon.03G | KQL03403 | TKW12165 | EES00471 | Zm00001eb127170_P001 | 0.841 |
| PUZ65488 | Sspon.07G | KQL14973 | TKW26670 | EES18409 | Zm00001eb291030_P001 | 0.931 |

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| PUZ64057 | Sspon.07G | KQL13039 | TKW24215 | EES19031 | Zm00001eb354200_P001 | 0.989 |
| genblast_C | Sspon.05G | KQK99852 | TKW07752 | OQU82858 | Zm00001eb196540_P001 | 0.872 |

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| PUZ43092 | genblast_C | KQK92838 | TKV98493 | EER95599 | Zm00001eb001830_P001 | 0.954 |
| PUZ65475 | Sspon.07G | KQL14962 | TKW26651 | KXG22235 | Zm00001eb352190_P002 | 0.878 |
| PUZ56767 | Sspon.01G | KQK85934 | TKW14599 | EER93666 | Zm00001eb051840_P002 | 0.736 |
| PUZ48420 | Sspon.05G | KQK98442 | TKW05945 | EES12650 | Zm00001eb074120_P002 | 0.978 |

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| PUZ36012 | genblast_C | KQK86111 | TKV90095 | KXG37092 | Zm00001eb064880_P002 | 0.755 |
| genblast_C | Sspon.08G | KQL11543 | TKW22573 | EER88596 | Zm00001eb385910_P001 | 0.988 |
| PUZ69413 | Sspon.02G | KQL16859 | genblast_C | OQU79162 | Zm00001eb409490_P001 | 0.792 |
| PUZ72343 | Sspon.02G | KQL26110 | TKW35134 | EER97337 | Zm00001eb323280_P001 | 0.951 |

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| PUZ77056 | genblast_C | KQL30942 | TKW40898 | OQU85630 | Zm00001eb250670_P002 | 0.961 |

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| PUZ36986 | Sspon.01G | KQK87057 | TKV91302 | KXG37536 | Zm00001eb214740_P001 | 0.969 |
| PUZ49558 | Sspon.05G | KQL12731 | TKW23835 | EES11669 | Zm00001eb433960_P001 | 0.971 |
| PUZ63186 | Sspon.07G | KQK99446 | TKW07207 | EES15769 | Zm00001eb138480_P001 | 0.711 |

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| PUZ45345 | Sspon.06G | KQK95119 | TKW01406 | KXG28800 | Zm00001eb114700_P001 | 0.865 |
| PUZ74389 | Sspon.04G | KQL28419 | TKW37616 | EES04646 | Zm00001eb234260_P001 | 0.909 |
| PUZ71749 | Sspon.02G | genblast_C | TKW34369 | EER99274 | Zm00001eb331820_P001 | 0.907 |
| PUZ42177 | Sspon.08G | genblast_C | TKV97440 | EER88166 | Zm00001eb008650_P004 | 0.902 |
| PUZ76503 | Sspon.04G | KQL30434 | TKW40234 | OQU85291 | Zm00001eb184420_P003 | 0.952 |
| PUZ55650 | Sspon.03G | KQL06042 | TKW15584 | EES01147 | Zm00001eb158870_P001 | 0.821 |
| PUZ54950 | Sspon.03G | genblast_C | TKW16563 | EES03552 | Zm00001eb154270_P001 | 0.964 |
| PUZ37044 | Sspon.01G | KQK87121 | TKV91377 | OQU90997 | Zm00001eb214970_P003 | 0.884 |
| PUZ42436 | Sspon.01G | KQK92181 | TKV97719 | EER92712 | Zm00001eb007010_P002 | 0.928 |
| PUZ58268 | genblast_C | KQL04608 | TKW13698 | OQU8623( | Zm00001eb336740_P003 | 0.962 |
| PUZ48339 | Sspon.05G | KQK98379 | TKW05852 | EES11237 | Zm00001eb074590_P001 | 0.711 |
| PUZ49601 | genblast_C | KQL12694 | TKW23780 | EES13132 | Zm00001eb434170_P001 | 0.954 |

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| PUZ38350 | Sspon.01G | KQK88422 | TKV92977 | EER91397 | Zm00001eb220660_P001 | 0.885 |
| PUZ53884 | Sspon.03G | KQL07800 | TKW17801 | EES01777 | Zm00001eb367100_P001 | 0.984 |

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|---|---|---|---|---|---|---|
| genblast_C | genblast_C | KQL30588 | TKW40447 | KXG30676 | Zm00001eb247800_P001 | 0.905 |
| PUZ40002 | Sspon.01G | KQK89804 | TKV94784 | KXG38867 | Zm00001eb024570_P001 | 0.950 |

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|---|---|---|---|---|---|---|
| PUZ36258 | genblast_C | KQK86301 | TKV90336 | EER90590 | Zm00001eb063350_P001 | 0.921 |
| PUZ42435 | Sspon.01G | KQK92180 | TKV97718 | EER95353 | Zm00001eb007020_P001 | 0.954 |
| PUZ59121 | Sspon.08G | KQL12212 | TKW23419 | KXG20873 | Zm00001eb272410_P002 | 0.938 |

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|---|---|---|---|---|---|---|
| PUZ57714 | Sspon.03G | KQL04099 | TKW13041 | EES00435 | Zm00001eb334500_P001 | 0.762 |
| PUZ70908 | genblast_C | KQL24714 | TKW33405 | EER96812 | Zm00001eb314350_P001 | 0.938 |
| PUZ70717 | Sspon.02G | KQL24495 | TKW33157 | EER96737 | Zm00001eb312830_P001 | 0.950 |
| PUZ50164 | genblast_C | KQL00762 | TKW08911 | EES13369 | Zm00001eb172630_P001 | 0.955 |
| PUZ50802 | Sspon.06G | KQL01175 | TKW09484 | KXG24831 | Zm00001eb412910_P001 | 0.950 |

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|---|---|---|---|---|---|---|
| PUZ74596 | Sspon.08G | KQL28209 | TKW37379 | EES06486 | Zm00001eb235510_P001 | 0.945 |
| PUZ37712 | Sspon.01G | KQK87860 | TKV92204 | EER91129 | Zm00001eb052720_P001 | 0.972 |
| PUZ77878 | Sspon.04G | KQL31731 | TKW41832 | EES07614 | Zm00001eb193280_P001 | 0.918 |
| PUZ65636 | Sspon.05G | KQL15147 | TKW26879 | EES09432 | Zm00001eb091170_P001 | 0.932 |
| PUZ42368 | Sspon.01G | genblast_C | TKV97648 | EER92692 | Zm00001eb007990_P001 | 0.889 |
| PUZ51856 | genblast_C | KQL02160 | TKW10739 | OQU80628 | Zm00001eb037970_P001 | 0.886 |
| PUZ71589 | Sspon.02G | KQL25367 | TKW34189 | EER99204 | Zm00001eb318750_P001 | 0.881 |
| PUZ65341 | Sspon.07G | KQL14862 | TKW26508 | EES19761 | Zm00001eb291840_P001 | 0.884 |
| PUZ56022 | genblast_C | KQL05681 | TKW15139 | EES00987 | Zm00001eb357530_P002 | 0.985 |
| PUZ38909 | Sspon.06G | KQK88938 | TKV93669 | EER91566 | Zm00001eb222650_P001 | 0.947 |
| PUZ43281 | Sspon.01G | KQK93059 | genblast_C | EER93021 | Zm00001eb404360_P001 | 0.816 |
| PUZ50459 | Sspon.06G | KQL00496 | TKW08505 | KXG24674 | Zm00001eb413420_P001 | 0.841 |

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| PUZ64893 | Sspon.07G | KQL14456 | TKW26024 | KXG22495 | Zm00001eb294970_P001 | 0.880 |
| PUZ38716 | Sspon.01G | KQK88780 | TKV93461 | KXG38367 | Zm00001eb046220_P001 | 0.937 |
| PUZ40878 | Sspon.01G | KQK90626 | TKV95814 | EER94771 | genblast_Os03t0386500-01_Zea | |
| PUZ78002 | genblast_C | KQL31870 | TKW41989 | EES05937 | Zm00001eb192640_P001 | 0.980 |

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| PUZ55819 | genblast_C | KQL05897 | TKW15395 | EES03280 | Zm00001eb159790_P001 | 0.991 |

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| PUZ41420 | genblast_C | KQK91214 | TKV96543 | KXG39535 | Zm00001eb396360_P001 | 0.788 |
| PUZ74979 | Sspon.04G | KQL27791 | TKW36864 | OQU84758 | Zm00001eb237750_P001 | 0.959 |
| PUZ51470 | Sspon.06G | KQL01821 | TKW10321 | KXG25169 | Zm00001eb179120_P001 | 0.960 |

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| PUZ62286 | Sspon.08G | KQL09201 | TKW19546 | genblast_C | Zm00001eb377550_P001 | 0.944 |
| PUZ41882 | Sspon.01G | KQK91650 | TKV97051 | EER92539 | Zm00001eb010990_P001 | 0.979 |
| PUZ60269 | genblast_C | KQL11715 | TKW22791 | KXG20201 | Zm00001eb384230_P001 | 0.946 |
| genblast_C | Sspon.05G | KQK96151 | TKW02882 | OQU81046 | Zm00001eb418920_P002 | 0.914 |
| PUZ77810 | genblast_C | KQL31679 | TKW41778 | OQU85794 | Zm00001eb256160_P002 | 0.923 |
| genblast_C | Sspon.05G | genblast_C | genblast_C | EES11810 | Zm00001eb419890_P001 | 0.969 |
| PUZ65681 | Sspon.07G | KQL15188 | TKW26934 | EES18341 | Zm00001eb351250_P002 | 0.929 |

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| PUZ68687 | Sspon.02G | KQL22723 | TKW30786 | EER95959 | Zm00001eb301490_P001 | 0.819 |
| PUZ72565 | genblast_C | KQL26325 | TKW35421 | OQU90128 | Zm00001eb324930_P001 | 0.911 |
| PUZ62044 | Sspon.08G | genblast_C | TKW20040 | EER87917 | Zm00001eb271480_P001 | 0.989 |
| PUZ76046 | Sspon.04G | KQL29982 | TKW39664 | EER99457 | Zm00001eb181960_P001 | 0.803 |
| PUZ55253 | Sspon.03G | KQL06527 | TKW16179 | EES01305 | Zm00001eb156070_P002 | 0.953 |

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| PUZ43100 | Sspon.01G | KQK92848 | TKV98503 | KXG40302 | Zm00001eb001770_P001 | 0.824 |
| PUZ76380 | Sspon.04G | KQL30311 | TKW40087 | EES07097 | Zm00001eb183820_P004 | 0.950 |

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| PUZ75529 | Sspon.04G | KQL29652 | TKW39181 | OQU84937 | Zm00001eb241060_P002 | 0.947 |
| PUZ49473 | genblast_C | KQL12820 | TKW23934 | OQU82562 | Zm00001eb066510_P002 | 0.981 |
| PUZ52198 | Sspon.06G | KQL02452 | TKW11141 | EES14254 | Zm00001eb035260_P001 | 0.963 |
| PUZ40957 | Sspon.03G | KQK90746 | TKV95922 | EES09160 | Zm00001eb195620_P001 | 0.958 |
| PUZ44212 | Sspon.05G | KQK94133 | TKW00072 | EES08277 | Zm00001eb112210_P001 | 0.942 |
| PUZ55345 | Sspon.03G | KQL06428 | TKW16053 | genblast_C | Zm00001eb156680_P001 | 0.905 |
| PUZ73586 | Sspon.02G | KQL27308 | TKW36683 | genblast_C | Zm00001eb331600_P001 | 0.874 |
| PUZ75208 | Sspon.04G | KQL29274 | TKW38675 | EES04945 | Zm00001eb236980_P001 | 0.869 |
| PUZ51394 | Sspon.01G | genblast_C | TKW10220 | EER95647 | Zm00001eb001010_P001 | 0.918 |
| PUZ65655 | Sspon.03G | KQL15164 | TKW26901 | KXG22163 | Zm00001eb289700_P001 | 0.997 |
| PUZ74807 | Sspon.08G | genblast_C | TKW37096 | KXG29862 | Zm00001eb239380_P001 | 0.825 |

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| PUZ71255 | Sspon.02G | KQL25036 | TKW33793 | EER96968 | Zm00001eb101840_P001 | 0.878 |
| PUZ39502 | Sspon.05G | KQK89308 | TKV94132 | EES18321 | Zm00001eb027550_P001 | 0.982 |

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| PUZ41984 | Sspon.01G | KQK91747 | TKV97188 | EER92576 | Zm00001eb010210_P001 | 0.965 |

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| PUZ40768 | Sspon.01G | KQL26678 | TKV95681 | EER94726 | Zm00001eb327570_P001 | 0.751 |
| PUZ51689 | Sspon.06G | KQL01987 | TKW10533 | KXG25244 | Zm00001eb041050_P003 | 0.960 |
| PUZ41642 | Sspon.03G | KQK91426 | TKV96802 | EER95072 | genblast_Os03t0280400-01_Zea | |
| PUZ64514 | Sspon.07G | KQL14052 | TKW25557 | EES20042 | Zm00001eb297510_P001 | 0.954 |
| PUZ43397 | Sspon.07G | KQK99993 | TKV99098 | OQU82692 | Zm00001eb195070_P001 | 0.952 |
| PUZ53896 | genblast_C | KQK87793 | TKV92130 | EES03901 | Zm00001eb367170_P001 | 0.840 |
| PUZ68843 | Sspon.02G | KQL22886 | TKW30990 | EES09974 | Zm00001eb302740_P001 | 0.799 |
| PUZ58743 | genblast_C | KQL03355 | TKW12102 | KXG31530 | Zm00001eb338910_P001 | 0.892 |
| genblast_C | Sspon.04G | genblast_C | TKW41362 | KXG30840 | genblast_Os02t0726600-01_Zea | |
| PUZ56712 | Sspon.03G | genblast_C | TKW14356 | KXG32483 | Zm00001eb341220_P002 | 0.973 |
| PUZ43262 | Sspon.04G | genblast_C | TKV98723 | EES05105 | Zm00001eb241510_P001 | 0.870 |
| PUZ37046 | genblast_C | KQK87118 | TKV91373 | KXG37559 | Zm00001eb214960_P001 | 0.933 |
| PUZ63008 | Sspon.07G | KQK99643 | TKW07488 | EES15691 | Zm00001eb406920_P001 | 0.706 |
| PUZ47139 | Sspon.05G | KQK97250 | TKW04369 | OQU81571 | Zm00001eb422370_P001 | 0.959 |
| PUZ51801 | Sspon.08G | KQL02080 | TKW10648 | EES13971 | Zm00001eb040310_P001 | 0.985 |
| PUZ40095 | Sspon.01G | KQK89907 | TKV94908 | KXG38908 | Zm00001eb391080_P001 | 0.855 |
| PUZ73795 | Sspon.01G | KQL28978 | TKW38322 | OQU84248 | Zm00001eb230480_P001 | 0.821 |
| PUZ47841 | Sspon.05G | KQK97914 | TKW05225 | KXG26641 | Zm00001eb425800_P001 | 0.973 |
| PUZ52593 | Sspon.06G | KQL02866 | TKW11647 | KXG25432 | Zm00001eb202740_P001 | 0.874 |
| PUZ54087 | Sspon.03G | genblast_C | TKW17592 | EES03844 | Zm00001eb148750_P001 | 0.819 |
| PUZ40248 | Sspon.01G | KQK90041 | TKV95082 | KXG31052 | Zm00001eb186860_P001 | 0.753 |
| PUZ73431 | Sspon.02G | KQL27082 | TKW36373 | KXG36890 | Zm00001eb111000_P001 | 0.976 |
| PUZ51361 | Sspon.06G | KQL01696 | TKW10158 | OQU80407 | genblast_Os07t0664400-01_Zea | |
| PUZ42866 | Sspon.03G | KQK92603 | TKV98242 | EES02325 | Zm00001eb121510_P001 | 0.729 |

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| PUZ70752 | genblast_C | KQL24533 | TKW33209 | EER96750 | Zm00001eb099710_P002 | 0.997 |
| PUZ36839 | Sspon.01G | KQK86916 | TKV91121 | KXG37471 | Zm00001eb058760_P001 | 0.942 |

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| PUZ59743 | Sspon.08G | KQL11193 | TKW22094 | EER90127 | Zm00001eb275010_P001 | 0.747 |

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| genblast_C | Sspon.08G | KQL11666 | genblast_C | EER88550 | Zm00001eb385110_P001 | 0.767 |
| PUZ78432 | Sspon.04G | KQL15345 | TKW27105 | EES06084 | Zm00001eb259650_P001 | 0.819 |
| PUZ36285 | Sspon.01G | KQK86384 | TKV90425 | EER90605 | Zm00001eb063110_P001 | 0.950 |

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| PUZ47302 | Sspon.05G | KQK97410 | TKW04564 | KXG26384 | Zm00001eb081940_P001 | 0.908 |
| PUZ59266 | Sspon.08G | KQL11784 | TKW22874 | EER88899 | Zm00001eb226740_P002 | 0.952 |

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| PUZ48159 | genblast_C | KQK98222 | TKW05615 | EES11166 | Zm00001eb427230_P001 | 0.999 |
| PUZ68447 | Sspon.02G | KQL22489 | TKW30500 | EER95883 | Zm00001eb300280_P001 | 0.908 |
| PUZ77773 | genblast_C | KQL31643 | TKW41741 | EES05855 | Zm00001eb255840_P002 | 0.944 |
| PUZ73924 | Sspon.04G | KQL28878 | TKW38201 | KXG29383 | Zm00001eb231180_P002 | 0.912 |
| PUZ46722 | Sspon.05G | KQK96831 | TKW03800 | OQU81316 | genblast_Os04t0353000-01_Zea | |
| PUZ38301 | Sspon.01G | KQK88385 | TKV92928 | EER91380 | Zm00001eb220380_P002 | 0.891 |
| PUZ46869 | Sspon.05G | KQK96985 | TKW04026 | OQU81407 | Zm00001eb085310_P001 | 0.976 |

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| PUZ64896 | Sspon.07G | KQL14462 | TKW26035 | KXG22490 | Zm00001eb294950_P001 | 0.791 |
| PUZ55933 | Sspon.03G | KQL05766 | TKW15235 | EES03238 | Zm00001eb161470_P001 | 0.844 |
| PUZ72550 | Sspon.02G | KQL26302 | TKW35401 | EER97403 | Zm00001eb107220_P001 | 0.868 |
| PUZ75724 | Sspon.07G | KQL16007 | TKW27981 | EES15724 | Zm00001eb348360_P001 | 0.705 |
| PUZ38117 | Sspon.01G | KQK88206 | TKV92710 | KXG38096 | Zm00001eb219700_P002 | 0.859 |

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| PUZ59975 | Sspon.08G | KQL11455 | TKW22439 | OQU76691 | Zm00001eb388460_P001 | 0.962 |
| PUZ37879 | Sspon.01G | KQK88009 | TKV92388 | EER93770 | Zm00001eb050910_P001 | 0.899 |
| PUZ43858 | Sspon.05G | KQK93751 | TKV99490 | KXG27839 | Zm00001eb091800_P001 | 0.819 |
| PUZ69668 | Sspon.02G | KQL23646 | TKW31997 | OQU89044 | Zm00001eb307730_P001 | 0.962 |
| PUZ70463 | Sspon.02G | KQK98496 | TKW06014 | genblast_C | genblast_Os09t0362900-01_Zea | |
| PUZ53833 | Sspon.03G | KQL07841 | TKW17860 | KXG33743 | Zm00001eb366820_P001 | 0.939 |
| PUZ54889 | Sspon.03G | KQL06877 | TKW16640 | OQU87489 | Zm00001eb153930_P005 | 0.940 |
| PUZ69419 | Sspon.02G | KQL23387 | TKW31707 | OQU88903 | Zm00001eb096870_P001 | 0.959 |

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| PUZ73778 | Sspon.04G | KQL29853 | TKW39457 | EES04388 | Zm00001eb242390_P001 | 0.989 |
| PUZ76692 | genblast_C | KQL31099 | TKW41097 | EES05885 | Zm00001eb392820_P001 | 0.798 |

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| PUZ65379 | Sspon.03G | KQL14885 | TKW26542 | OQU78237 | genblast_Os05t0496400-00_Zea | |

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| PUZ70221 | Sspon.02G | KQL24047 | TKW32530 | genblast_C | Zm00001eb042980_P001 | 0.822 |
| PUZ64187 | genblast_C | KQK99321 | TKW07070 | EES19093 | Zm00001eb282290_P001 | 0.894 |
| PUZ63232 | Sspon.07G | KQK99389 | TKW07148 | KXG23190 | Zm00001eb264840_P001 | 0.929 |
| PUZ37626 | genblast_C | KQK87758 | TKV92090 | EER91091 | genblast_Os03t0672500-00 | Zm0 |
| PUZ44343 | Sspon.05G | KQK94216 | TKW00190 | EES09608 | Zm00001eb200750_P002 | 0.919 |
| PUZ53667 | genblast_C | KQL07994 | TKW18063 | KXG33819 | genblast_Os01t0881300-02_Zea | |
| PUZ55408 | Sspon.03G | KQL06359 | TKW15991 | OQU87315 | Zm00001eb360030_P001 | 0.957 |
| PUZ49903 | genblast_C | KQL01028 | TKW09277 | KXG24283 | Zm00001eb173650_P002 | 0.905 |
| PUZ57940 | Sspon.03G | KQL04308 | TKW13323 | EES02515 | Zm00001eb124880_P001 | 0.874 |
| PUZ36659 | genblast_C | KQK86739 | TKV90917 | OQU90855 | Zm00001eb060270_P001 | 0.704 |
| PUZ67849 | genblast_C | KQL17149 | TKW29513 | EES16326 | Zm00001eb031400_P001 | 0.981 |
| PUZ38217 | Sspon.01G | KQK88308 | TKV92827 | EER93919 | Zm00001eb043140_P002 | 0.947 |

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| PUZ77429 | genblast_Z | KQL31300 | TKW41346 | KXG30852 | Zm00001eb189200_P003 | 0.879 |
| PUZ65619 | Sspon.07G | KQL15135 | TKW26863 | EES19660 | Zm00001eb351520_P001 | 0.957 |
| PUZ69061 | Sspon.02G | KQL23090 | TKW31266 | EER98238 | Zm00001eb303850_P001 | 0.932 |
| PUZ51386 | Sspon.06G | KQL01731 | TKW10205 | EES13815 | Zm00001eb042260_P002 | 0.953 |
| PUZ54560 | genblast_C | KQL07176 | TKW17026 | genblast_C | genblast_Os01t0772200-02_Ze | |
| PUZ76333 | Sspon.04G | KQL30255 | TKW40023 | KXG30530 | Zm00001eb245730_P002 | 0.964 |
| PUZ58950 | Sspon.08G | KQL12347 | TKW23599 | EER89011 | Zm00001eb271790_P001 | 0.703 |
| PUZ44501 | genblast_C | KQK94345 | TKW00366 | KXG28265 | Zm00001eb168730_P005 | 0.929 |
| PUZ52417 | Sspon.06G | KQL02680 | TKW11423 | EES14180 | Zm00001eb036900_P001 | 0.986 |
| PUZ74029 | Sspon.04G | KQL28770 | TKW38041 | EES06262 | Zm00001eb208100_P001 | 0.874 |
| PUZ59839 | Sspon.08G | KQL11301 | TKW22225 | KXG20435 | Zm00001eb387450_P002 | 0.931 |
| PUZ55236 | genblast_Z | KQL06547 | TKW16199 | KXG33174 | genblast_Zm00001eb360810_P | |
| PUZ57087 | Sspon.03G | KQL03507 | TKW12308 | EES00623 | Zm00001eb130000_P002 | 0.938 |
| PUZ44203 | genblast_C | KQK94119 | TKW00055 | EES08270 | Zm00001eb167980_P001 | 0.923 |
| PUZ70842 | Sspon.02G | KQL24651 | TKW33333 | EER96791 | Zm00001eb314040_P001 | 0.967 |
| PUZ45272 | genblast_C | KQK95007 | TKW01252 | KXG28732 | Zm00001eb114200_P006 | 0.888 |
| PUZ53330 | Sspon.06G | KQL08287 | TKW18447 | EES04095 | Zm00001eb143560_P001 | 0.970 |

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| PUZ69202 | Sspon.06G | KQK89681 | TKV94629 | KXG24379 | Zm00001eb173050_P001 | 0.932 |
| PUZ40236 | genblast_C | KQK90050 | TKV95073 | KXG38961 | Zm00001eb391740_P002 | 0.911 |
| PUZ43981 | Sspon.05G | KQL03677 | TKW12527 | KXG27928 | Zm00001eb091250_P001 | 0.872 |
| PUZ67945 | Sspon.02G | KQL17230 | TKW29608 | KXG24027 | Zm00001eb032030_P003 | 0.866 |

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|---|---|---|---|---|---|---|
| PUZ59913 | genblast_C | KQL11381 | TKW22348 | KXG20383 | Zm00001eb275690_P003 | 0.900 |
| PUZ43961 | Sspon.05G | KQK93862 | TKV99692 | EES08096 | Zm00001eb201210_P003 | 0.990 |
| PUZ62235 | genblast_C | KQL09260 | TKW19617 | OQU75805 | Zm00001eb377200_P001 | 0.973 |

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| PUZ55011 | Sspon.03G | KQL06759 | TKW16484 | EES03537 | Zm00001eb154650_P001 | 0.917 |
| PUZ62574 | Sspon.08G | KQL08914 | TKW19183 | EER89037 | Zm00001eb379410_P003 | 0.927 |
| PUZ50825 | Sspon.07G | KQL11944 | TKW23104 | EES18579 | Zm00001eb294470_P001 | 0.938 |
| PUZ36289 | Sspon.01G | KQK86391 | TKV90433 | EER90609 | Zm00001eb063070_P001 | 0.937 |
| PUZ42155 | genblast_Z | KQK91934 | TKV97418 | EER95265 | Zm00001eb400030_P002 | 0.905 |
| PUZ54349 | Sspon.03G | KQL07361 | TKW17275 | KXG33562 | Zm00001eb291610_P001 | 0.894 |
| PUZ57668 | Sspon.03G | KQL04067 | TKW12998 | KXG32111 | Zm00001eb126610_P001 | 0.788 |

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| PUZ52810 | Sspon.03G | genblast_C | TKW19075 | EES04298 | Zm00001eb139810_P001 | 0.929 |
| PUZ49577 | genblast_C | KQK93371 | TKV99025 | OQU87747 | genblast_Os12t0114400-01_Ze | |
| PUZ49605 | genblast_C | KQL12688 | TKW23772 | OQU82599 | Zm00001eb434220_P001 | 0.931 |

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| PUZ74935 | Sspon.04G | KQL08877 | TKW19136 | KXG30018 | Zm00001eb237430_P002 | 0.947 |
| PUZ39727 | genblast_C | KQK89540 | TKV94412 | genblast_C | Zm00001eb224090_P001 | 0.820 |
| PUZ65338 | genblast_C | KQL14859 | TKW26503 | OQU78254 | Zm00001eb291870_P001 | 0.946 |
| PUZ59739 | Sspon.08G | genblast_C | TKW22079 | EES05389 | Zm00001eb388670_P001 | 0.875 |
| PUZ49354 | Sspon.05G | KQL12929 | TKW24070 | OQU82514 | Zm00001eb067310_P001 | 0.840 |
| PUZ57347 | Sspon.03G | KQL03796 | TKW12686 | EES02732 | Zm00001eb128290_P001 | 0.993 |
| PUZ68907 | Sspon.07G | KQK90682 | TKW31446 | KXG21489 | Zm00001eb304750_P001 | 0.701 |
| PUZ58533 | Sspon.03G | KQL04853 | TKW14014 | EES02291 | Zm00001eb120580_P001 | 0.868 |
| PUZ41989 | Sspon.01G | KQK91754 | TKV97194 | EER92577 | Zm00001eb010170_P001 | 0.897 |
| PUZ37510 | genblast_C | KQK87615 | TKV91927 | EER93631 | Zm00001eb053710_P002 | 0.983 |
| PUZ61897 | Sspon.08G | KQL09469 | TKW19854 | EER87977 | Zm00001eb374640_P001 | 0.908 |
| PUZ54443 | genblast_C | KQL07267 | TKW17152 | KXG33533 | Zm00001eb151270_P003 | 0.825 |
| PUZ75617 | genblast_C | KQL29528 | TKW39013 | EES12692 | Zm00001eb073540_P001 | 0.980 |

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| PUZ61443 | Sspon.04G | KQL10020 | TKW20574 | EER89472 | Zm00001eb279660_P001 | 0.961 |
| PUZ46420 | genblast_C | KQK96604 | TKW03516 | EER92536 | Zm00001eb420220_P001 | 0.828 |
| PUZ68501 | Sspon.02G | KQL22544 | TKW30568 | OQU88485 | Zm00001eb300710_P002 | 0.913 |
| PUZ65929 | Sspon.07G | KQL15425 | TKW27201 | KXG22030 | Zm00001eb349090_P001 | 0.908 |
| PUZ36443 | Sspon.01G | KQK86518 | TKV90621 | EER93230 | Zm00001eb062010_P002 | 0.987 |
| PUZ54740 | Sspon.08G | KQL07026 | TKW16833 | EER89030 | Zm00001eb379500_P001 | 0.867 |
| PUZ43812 | genblast_C | KQK99934 | TKW07853 | EES09272 | Zm00001eb406750_P001 | 0.953 |
| PUZ49727 | genblast_C | KQL00139 | TKW08029 | EES13178 | Zm00001eb198660_P001 | 0.880 |
| PUZ58830 | Sspon.03G | KQL03248 | TKW11981 | OQU86060 | Zm00001eb119210_P005 | 0.700 |
| PUZ49615 | genblast_C | KQL12676 | TKW23757 | EES13144 | Zm00001eb434290_P003 | 0.913 |
| PUZ73557 | genblast_C | KQL27272 | TKW36649 | EER97780 | Zm00001eb331410_P001 | 0.984 |
| PUZ77012 | Sspon.04G | genblast_C | TKW40848 | KXG31024 | Zm00001eb250300_P003 | 0.913 |
| PUZ72578 | Sspon.02G | KQL26340 | TKW35442 | KXG36525 | Zm00001eb325000_P001 | 0.971 |
| PUZ46279 | Sspon.05G | KQK96477 | TKW03321 | EES10501 | Zm00001eb419210_P001 | 0.984 |
| PUZ77715 | Sspon.04G | KQL31592 | TKW41687 | EES05494 | Zm00001eb255470_P001 | 0.765 |
| PUZ68032 | Sspon.02G | KQL17382 | TKW29803 | KXG24110 | Zm00001eb032670_P001 | 0.876 |
| PUZ60122 | Sspon.08G | KQL11587 | TKW22624 | EER89984 | Zm00001eb386170_P001 | 0.884 |
| PUZ53515 | Sspon.03G | KQL08128 | TKW18236 | KXG33896 | Zm00001eb144730_P005 | 0.961 |
| PUZ68772 | Sspon.02G | KQL22814 | TKW30911 | EER95990 | Zm00001eb116640_P001 | 0.879 |
| PUZ42830 | Sspon.01G | KQK92562 | TKV98193 | EER92849 | Zm00001eb003920_P001 | 0.939 |
| PUZ43567 | Sspon.05G | genblast_C | TKW07649 | OQU82802 | Zm00001eb196090_P001 | 0.865 |

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| PUZ73410 | Sspon.02G | KQL27124 | TKW36396 | KXG36907 | Zm00001eb330200_P001 | 0.895 |
| PUZ48569 | Sspon.05G | KQK98570 | TKW06117 | EES11306 | Zm00001eb073260_P001 | 0.814 |
| PUZ64178 | Sspon.07G | KQK99315 | TKW07061 | EES17770 | Zm00001eb282360_P001 | 0.940 |
| PUZ39935 | Sspon.01G | genblast_C | TKV94726 | EER91874 | Zm00001eb024820_P001 | 0.889 |
| PUZ64844 | Sspon.07G | genblast_C | TKW25939 | EES19929 | Zm00001eb295480_P003 | 0.958 |
| PUZ41704 | Sspon.01G | KQK91596 | TKV96970 | OQU92835 | Zm00001eb012210_P001 | 0.962 |
| PUZ70756 | Sspon.02G | KQL24538 | TKW33213 | OQU89518 | Zm00001eb313280_P001 | 0.874 |

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| genblast_C | Sspon.02G | KQL22985 | TKW31140 | OQU88697 | Zm00001eb303250_P003 | 0.760 |
| PUZ59696 | Sspon.08G | KQL11138 | TKW22037 | KXG20513 | Zm00001eb274940_P001 | 0.854 |
| PUZ37980 | Sspon.01G | KQK88083 | TKV92514 | EER91226 | Zm00001eb051450_P001 | 0.855 |
| PUZ65870 | Sspon.07G | KQL15363 | TKW27127 | genblast_C | Zm00001eb348780_P001 | 0.946 |
| PUZ59431 | Sspon.08G | KQL11938 | TKW23097 | OQU76902 | Zm00001eb225320_P001 | 0.913 |
| PUZ71808 | Sspon.02G | KQL25575 | TKW34442 | EER99304 | Zm00001eb321060_P001 | 0.960 |
| PUZ59704 | Sspon.08G | KQL11145 | TKW22046 | KXG20510 | Zm00001eb389070_P001 | 0.737 |
| PUZ75891 | genblast_C | genblast_C | TKW39463 | EES05166 | Zm00001eb242450_P001 | 0.971 |

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| PUZ40845 | Sspon.01GKQK90590 | TKV95789 | OQU92489 | Zm00001eb392460_P002 | 0.945 |
| PUZ65861 | Sspon.07GKQL15355 | TKW27113 | KXG22072 | Zm00001eb289280_P002 | 0.933 |
| PUZ43745 | Sspon.05GKQK93679 | TKV99388 | KXG27792 | Zm00001eb202180_P002 | 0.922 |
| PUZ40712 | Sspon.01GKQK90452 | TKV95597 | EER94701 | Zm00001eb393010_P001 | 0.758 |
| PUZ63567 | Sspon.07Ggenblast_C | TKW24819 | EES19205 | Zm00001eb347320_P001 | 0.958 |
| PUZ64179 | Sspon.01Ggenblast_C | TKV91674 | OQU91224 | Zm00001eb065440_P001 | 0.725 |

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| PUZ52806 | Sspon.07GKQL08795 | TKW19077 | EES04299 | Zm00001eb139800_P001 | 0.742 |

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| PUZ42628 | Sspon.01Ggenblast_C | TKV97980 | OQU93153 | Zm00001eb005390_P001 | 0.983 |
| PUZ64428 | Sspon.03GKQL13963 | TKW25453 | KXG22727 | Zm00001eb297840_P001 | 0.972 |
| PUZ58369 | Sspon.03GKQL04703 | TKW13837 | EES02347 | Zm00001eb337610_P001 | 0.938 |
| PUZ48098 | Sspon.05GKQK98157 | TKW05529 | EES11137 | Zm00001eb426920_P004 | 0.973 |
| PUZ66651 | Sspon.02GKQL16176 | genblast_C | EER99954 | Zm00001eb111820_P001 | 0.882 |

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| PUZ50370 | Sspon.01GKQL00588 | TKW08685 | KXG38196 | Zm00001eb220500_P001 | 0.900 |
| PUZ71141 | Sspon.02GKQL24913 | TKW33632 | EER96911 | Zm00001eb101340_P003 | 0.942 |
| PUZ40034 | Sspon.02GKQK89843 | TKV94821 | KXG38885 | Zm00001eb024150_P001 | 0.928 |
| PUZ43066 | Sspon.01GKQK92814 | TKV98465 | EER92945 | Zm00001eb403580_P001 | 0.907 |
| PUZ58557 | Sspon.03GKQL04877 | TKW14044 | EES02283 | Zm00001eb120740_P001 | 0.867 |

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| PUZ66253 | Sspon.07GKQL15738 | TKW27645 | EES18136 | genblast_Os05t0374200-00_Ze | |
| PUZ52620 | Sspon.06GKQL02955 | TKW11743 | EES15208 | Zm00001eb180420_P001 | 0.971 |
| PUZ68352 | Sspon.01GKQL22381 | TKW30369 | EER97948 | Zm00001eb299510_P001 | 0.957 |
| PUZ48493 | Sspon.04GKQK98492 | TKW06004 | EES12682 | Zm00001eb428870_P001 | 0.911 |
| PUZ59322 | Sspon.08GKQL11831 | TKW22935 | EER88877 | Zm00001eb226290_P001 | 0.963 |
| PUZ62534 | genblast_CKQL08950 | TKW19218 | EER89054 | Zm00001eb379210_P001 | 0.914 |

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| PUZ49123 | genblast_C | KQK99131 | TKW06842 | KXG27223 | Zm00001eb069150_P002 | 0.787 |
| PUZ47217 | Sspon.05G | genblast_C | TKW04475 | OQU81614 | Zm00001eb082390_P001 | 0.941 |
| PUZ54592 | Sspon.03G | KQL07152 | TKW16999 | EES03680 | genblast_Os01t0770000-01_Ze | |
| PUZ42049 | Sspon.01G | KQK91817 | TKV97274 | EER92600 | Zm00001eb009730_P002 | 0.979 |
| PUZ65962 | genblast_C | KQL15455 | TKW27250 | EES18240 | Zm00001eb288230_P001 | 0.937 |
| PUZ77832 | Sspon.04G | KQL31694 | TKW41793 | EES05866 | Zm00001eb256230_P001 | 0.872 |
| PUZ77562 | Sspon.04G | KQL31395 | TKW41444 | EES05570 | Zm00001eb253730_P001 | 0.937 |
| PUZ62357 | genblast_C | KQL09138 | TKW19470 | EER87781 | Zm00001eb269720_P001 | 0.965 |
| PUZ48606 | Sspon.05G | KQK98620 | TKW06171 | EES12724 | Zm00001eb072870_P003 | 0.828 |
| PUZ74868 | Sspon.04G | KQL27927 | TKW37026 | KXG29904 | Zm00001eb204590_P001 | 0.917 |
| PUZ51610 | Sspon.06G | genblast_C | TKW10455 | EES15045 | Zm00001eb041380_P001 | 0.966 |
| PUZ42375 | Sspon.01G | genblast_C | TKV97653 | EER95333 | Zm00001eb401000_P005 | 0.904 |
| PUZ65339 | genblast_C | KQL14860 | TKW26504 | EES18451 | Zm00001eb291860_P001 | 0.962 |
| PUZ53322 | Sspon.03G | KQL08295 | TKW18470 | EES04098 | Zm00001eb143520_P002 | 0.852 |
| PUZ68800 | Sspon.05G | KQK94042 | TKW30939 | EES11771 | genblast_Os11t0261600-01_Ze | |
| PUZ54544 | genblast_C | genblast_C | TKW17046 | OQU87632 | genblast_Os01t0772700-00_Ze | |
| PUZ58892 | Sspon.03G | KQL03181 | TKW11904 | EES02162 | Zm00001eb339500_P001 | 0.940 |
| PUZ40310 | genblast_C | KQK90104 | TKV95144 | EER94560 | Zm00001eb022630_P001 | 0.964 |
| PUZ45882 | Sspon.06G | KQK95935 | TKW02662 | KXG29192 | Zm00001eb164740_P001 | 0.930 |
| PUZ54763 | Sspon.03G | KQL07002 | TKW16799 | OQU87548 | Zm00001eb370880_P001 | 0.940 |
| PUZ46364 | Sspon.05G | KQK96577 | TKW03480 | EES10452 | Zm00001eb088090_P001 | 0.966 |
| PUZ37871 | Sspon.01G | KQK88005 | TKV92381 | KXG37968 | Zm00001eb050880_P001 | 0.973 |

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| PUZ69992 | Sspon.04G | KQL23886 | TKW32317 | EES07692 | Zm00001eb257980_P001 | 0.836 |
| PUZ54018 | Sspon.03G | KQL07677 | TKW17662 | EES03867 | Zm00001eb148270_P001 | 0.977 |
| PUZ57699 | Sspon.03G | KQL04088 | TKW13024 | KXG32101 | Zm00001eb334440_P001 | 0.963 |
| PUZ57750 | Sspon.03G | KQL04128 | TKW13096 | EES00429 | Zm00001eb334730_P001 | 0.914 |
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| PUZ44603 | genblast_C | KQK94237 | TKW00215 | EES09626 | Zm00001eb169210_P002 | 0.926 |
| PUZ37241 | Sspon.01G | KQK87335 | TKV91613 | EER93531 | Zm00001eb215670_P001 | 0.875 |
| PUZ66439 | Sspon.07G | KQL15888 | TKW27825 | EES19366 | genblast_Os05t0356700-01_Ze | |
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| PUZ36434 | genblast_C | KQK86508 | TKV90612 | EER93224 | Zm00001eb212270_P003 | 0.958 |
| PUZ40484 | Sspon.01G | KQK90281 | TKV95357 | EER92055 | Zm00001eb021070_P001 | 0.966 |
| PUZ38114 | Sspon.01G | KQK88204 | TKV92708 | EER91281 | Zm00001eb049160_P001 | 0.814 |
| genblast_C | Sspon.08G | KQL09802 | TKW20300 | OQU76052 | Zm00001eb373110_P005 | 0.963 |
| PUZ45487 | Sspon.06G | KQK95352 | TKW01730 | EES08828 | Zm00001eb115110_P001 | 0.828 |
| PUZ78230 | Sspon.04G | KQL32089 | TKW42243 | EES07753 | Zm00001eb191480_P001 | 0.960 |
| PUZ52025 | Sspon.06G | KQL02316 | TKW10937 | EES15451 | Zm00001eb199400_P001 | 0.977 |
| PUZ72990 | genblast_C | KQL26736 | TKW35917 | KXG36733 | Zm00001eb109680_P003 | 0.966 |
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| PUZ77300 | Sspon.04G | KQL31175 | TKW41186 | EES07382 | Zm00001eb188630_P001 | 0.934 |
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| PUZ68528 | Sspon.08G | KQL22573 | TKW30605 | KXG19170 | Zm00001eb269310_P001 | 0.895 |
| PUZ40496 | genblast_C | KQK90296 | TKV95374 | OQU92307 | Zm00001eb404720_P001 | 0.965 |
| PUZ63145 | Sspon.07G | KQK99504 | TKW07284 | KXG23086 | Zm00001eb408110_P001 | 0.800 |
| PUZ67166 | Sspon.02G | KQL16887 | TKW29154 | EES15993 | Zm00001eb066230_P003 | 0.943 |
| PUZ41967 | Sspon.01G | KQK91730 | TKV97163 | EER92571 | Zm00001eb010360_P001 | 0.973 |
| PUZ63379 | Sspon.07G | KQL13635 | TKW25036 | KXG23347 | Zm00001eb409890_P004 | 0.872 |
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| PUZ56422 | Sspon.03G | KQL05352 | TKW14723 | EES00586 | Zm00001eb129010_P001 | 0.958 |
| PUZ59111 | genblast_C | KQL09049 | TKW23428 | EER88959 | Zm00001eb272350_P002 | 0.935 |
| PUZ73316 | Sspon.02G | KQL27037 | TKW36319 | EER99855 | Zm00001eb110880_P001 | 0.814 |
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| PUZ47079 | Sspon.05G | KQK97210 | TKW04313 | EES10769 | Zm00001eb422000_P002 | 0.954 |

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| PUZ63090 | Sspon.07G | genblast_C | TKW07391 | EES16714 | Zm00001eb139260_P001 | 0.821 |
| PUZ45600 | Sspon.06G | KQK95530 | TKW01995 | OQU83898 | Zm00001eb166220_P001 | 0.905 |
| PUZ55756 | Sspon.03G | KQL05930 | TKW15453 | EES01090 | Zm00001eb358440_P001 | 0.944 |
| PUZ49464 | genblast_C | KQL12829 | TKW23945 | KXG27409 | Zm00001eb433490_P007 | 0.944 |
| PUZ44602 | Sspon.05G | KQK94238 | TKW00216 | KXG28215 | Zm00001eb169200_P002 | 0.801 |

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| PUZ77222 | Sspon.04G | KQL31082 | TKW41072 | EES07410 | Zm00001eb188060_P002 | 0.990 |
| PUZ47165 | Sspon.05G | genblast_C | TKW04406 | EES10820 | Zm00001eb082820_P001 | 0.864 |
| PUZ55254 | Sspon.03G | KQL06523 | TKW16181 | EES03469 | Zm00001eb156130_P001 | 0.938 |
| PUZ68258 | genblast_C | KQL22231 | TKW30133 | EES16625 | Zm00001eb406370_P001 | 0.970 |

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| PUZ37319 | Sspon.01G | KQK87409 | TKV91701 | EER90989 | Zm00001eb216130_P001 | 0.950 |
| PUZ37070 | Sspon.01G | KQK87142 | TKV91401 | EER90889 | Zm00001eb056980_P001 | 0.915 |
| PUZ44793 | genblast_C | KQK94549 | TKW00616 | KXG28339 | Zm00001eb169890_P001 | 0.855 |
| PUZ54234 | Sspon.07G | KQL07470 | TKW17420 | EES01655 | Zm00001eb149740_P001 | 0.887 |
| PUZ50199 | Sspon.06G | KQL00730 | TKW08862 | OQU79937 | Zm00001eb172410_P003 | 0.837 |
| genblast_C | Sspon.02G | KQL24704 | TKW33394 | KXG35731 | Zm00001eb100350_P001 | 0.697 |

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| PUZ67330 | Sspon.02G | KQL16715 | TKW28912 | EES16091 | Zm00001eb410510_P001 | 0.985 |
| PUZ39322 | Sspon.01G | KQK89523 | TKV94444 | EER91743 | Zm00001eb026430_P002 | 0.937 |
| PUZ76324 | Sspon.04G | KQL30247 | TKW40008 | EES05342 | Zm00001eb183390_P001 | 0.967 |
| PUZ60300 | Sspon.08G | KQL11014 | TKW21900 | EER88520 | Zm00001eb277420_P001 | 0.940 |
| PUZ58302 | Sspon.03G | KQL04647 | TKW13742 | KXG31729 | Zm00001eb122610_P001 | 0.962 |
| PUZ59048 | genblast_Z | KQL12269 | TKW23499 | EER88977 | Zm00001eb228320_P003 | 0.939 |
| PUZ46034 | Sspon.05G | KQK96164 | TKW02898 | EES10334 | Zm00001eb089580_P001 | 0.952 |
| PUZ56403 | Sspon.02G | KQL05363 | TKW14741 | KXG35330 | Zm00001eb398430_P001 | 0.985 |
| PUZ61006 | Sspon.08G | KQL10345 | TKW21011 | EER89617 | Zm00001eb280950_P001 | 0.941 |
| PUZ54883 | genblast_C | KQL06884 | TKW16647 | OQU87493 | Zm00001eb153880_P001 | 0.967 |
| genblast_C | Sspon.01G | KQK90483 | TKV95641 | KXG39179 | Zm00001eb392940_P001 | 0.959 |
| PUZ43628 | Sspon.07G | KQK99824 | TKW07711 | EES16534 | genblast_Os11t0139400-01_Ze | |
| PUZ37466 | genblast_C | KQK87569 | TKV91878 | KXG37780 | Zm00001eb054090_P004 | 0.986 |
| PUZ55625 | Sspon.03G | KQL06067 | TKW15611 | EES03342 | Zm00001eb158710_P001 | 0.940 |
| PUZ54880 | genblast_C | KQL06887 | TKW16653 | EES01447 | Zm00001eb371240_P002 | 0.943 |
| PUZ61152 | Sspon.08G | KQL10447 | TKW21171 | OQU76322 | Zm00001eb381530_P001 | 0.971 |
| PUZ77583 | Sspon.04G | KQL31364 | TKW41417 | EES05584 | Zm00001eb253570_P001 | 0.954 |
| PUZ67540 | Sspon.03G | KQL16509 | TKW28619 | OQU8632 | genblast_Os12t0571000-01Zm0 | |
| PUZ55275 | Sspon.03G | KQL06496 | TKW16147 | EES03458 | Zm00001eb360590_P002 | 0.903 |
| PUZ39422 | Sspon.01G | KQK89083 | TKV93851 | EER94293 | Zm00001eb048680_P001 | 0.957 |
| PUZ60990 | Sspon.08G | KQL10329 | TKW20990 | EER89628 | Zm00001eb280890_P001 | 0.833 |
| PUZ67167 | Sspon.02G | KQL16886 | TKW29150 | OQU79139 | Zm00001eb138240_P001 | 0.939 |
| PUZ36987 | genblast_C | KQK87061 | TKV91309 | EER93436 | Zm00001eb057530_P001 | 0.833 |

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| PUZ78358 | Sspon.04G | KQL32216 | TKW42391 | EES06059 | Zm00001eb259340_P004 | 0.956 |
| PUZ71288 | Sspon.02G | KQL25070 | TKW33841 | EER99094 | Zm00001eb316780_P001 | 0.955 |
| PUZ48768 | genblast_C | KQK98788 | TKW06379 | EES12801 | Zm00001eb071660_P001 | 0.926 |
| PUZ40554 | Sspon.01G | KQK90339 | TKV95454 | EER92090 | Zm00001eb020590_P001 | 0.990 |
| PUZ73877 | Sspon.04G | KQL28906 | TKW38238 | EES04434 | Zm00001eb208770_P001 | 0.962 |
| PUZ47949 | genblast_C | KQK98029 | TKW05365 | OQU81938 | Zm00001eb426330_P001 | 0.953 |
| PUZ77180 | Sspon.05G | KQL31045 | TKW41031 | EES05685 | Zm00001eb187810_P001 | 0.866 |
| PUZ68588 | Sspon.02G | KQL22628 | TKW30691 | EER98050 | Zm00001eb301160_P001 | 0.962 |
| PUZ51756 | Sspon.06G | KQL02045 | TKW10603 | KXG25271 | Zm00001eb040560_P001 | 0.862 |
| PUZ74798 | Sspon.04G | KQL27997 | TKW37105 | EES04799 | Zm00001eb239390_P001 | 0.877 |
| PUZ49692 | genblast_Z | KQL12607 | TKW23661 | EES19410 | Zm00001eb434530_P001 | 0.952 |
| PUZ66248 | Sspon.07G | KQL15737 | TKW27642 | KXG21869 | Zm00001eb285130_P001 | 0.822 |
| PUZ64748 | Sspon.07G | KQL14277 | TKW25836 | KXG22547 | Zm00001eb296130_P002 | 0.742 |
| PUZ41481 | genblast_C | KQK91279 | TKV96628 | EER95014 | Zm00001eb013810_P001 | 0.988 |
| PUZ57207 | Sspon.03G | KQL03653 | TKW12482 | EES02787 | Zm00001eb129050_P002 | 0.945 |
| PUZ76083 | Sspon.05G | KQK97327 | TKW04474 | KXG26346 | Zm00001eb082430_P002 | 0.866 |
| PUZ51833 | Sspon.06G | KQL02133 | TKW10707 | EES15112 | Zm00001eb037820_P001 | 0.906 |
| PUZ36073 | Sspon.01G | KQK86181 | TKV90188 | KXG37123 | Zm00001eb210800_P003 | 0.747 |
| PUZ52626 | Sspon.06G | KQL02949 | TKW11735 | KXG25416 | Zm00001eb039810_P005 | 0.940 |
| PUZ36885 | genblast_C | KQK86950 | TKV91182 | EER93395 | Zm00001eb058570_P001 | 0.960 |
| PUZ77380 | Sspon.04G | KQL31246 | TKW41271 | EES07356 | Zm00001eb252920_P001 | 0.885 |
| PUZ68126 | genblast_C | KQK85927 | TKW29928 | EER95712 | Zm00001eb297980_P001 | 0.880 |
| PUZ59491 | Sspon.08G | KQL11992 | TKW23154 | EER88814 | Zm00001eb224630_P001 | 0.928 |
| PUZ69837 | Sspon.05G | KQL23839 | TKW32260 | OQU82260 | Zm00001eb071600_P001 | 0.967 |
| PUZ76189 | Sspon.04G | KQL30121 | TKW39836 | EES05287 | Zm00001eb244500_P001 | 0.886 |
| PUZ66502 | Sspon.07G | KQL15941 | TKW27883 | EES19343 | Zm00001eb286410_P001 | 0.901 |
| PUZ45897 | Sspon.06G | KQK96002 | TKW02754 | OQU84105 | Zm00001eb164530_P001 | 0.862 |

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| PUZ75000 | Sspon.04G | genblast_C | TKW36893 | EES04879 | Zm00001eb237910_P002 | 0.873 |
| PUZ69563 | Sspon.02G | KQL23557 | TKW31873 | OQU88991 | Zm00001eb306870_P001 | 0.811 |

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| PUZ57857 | Sspon.03G | KQL04234 | TKW13225 | KXG31978 | Zm00001eb125440_P002 | 0.887 |
| PUZ36371 | genblast_C | KQK86466 | TKV90542 | EER90645 | Zm00001eb062390_P001 | 0.950 |
| PUZ72705 | Sspon.02G | KQL26454 | TKW35564 | KXG36580 | Zm00001eb325890_P001 | 0.885 |
| PUZ55249 | Sspon.03G | KQL06529 | TKW16185 | OQU87371 | Zm00001eb360730_P001 | 0.692 |

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|---|---|---|---|---|---|---|
| PUZ56136 | genblast_C | KQL05659 | TKW15110 | KXG32765 | Zm00001eb160220_P001 | 0.983 |
| PUZ42144 | Sspon.01G | KQK91920 | TKV97406 | EER95260 | Zm00001eb008890_P002 | 0.929 |
| PUZ66997 | Sspon.02G | KQL16202 | TKW28199 | OQU79254 | Zm00001eb137570_P002 | 0.819 |
| PUZ48304 | Sspon.05G | KQK98345 | TKW05796 | EES12610 | Zm00001eb074870_P001 | 0.959 |
| PUZ47589 | Sspon.05G | KQK97673 | TKW04911 | EES10973 | Zm00001eb079970_P001 | 0.925 |
| PUZ40643 | Sspon.01G | KQK90402 | TKV95526 | EER92116 | Zm00001eb393180_P001 | 0.806 |
| PUZ53132 | genblast_C | KQL08466 | TKW18674 | KXG34055 | Zm00001eb363620_P001 | 0.922 |
| PUZ66455 | Sspon.07G | KQL15902 | TKW27841 | EES18052 | Zm00001eb347480_P001 | 0.932 |

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| PUZ41094 | Sspon.01G | KQK90887 | TKV96108 | EER94860 | Zm00001eb016800_P002 | 0.892 |

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| PUZ65481 | genblast_C | KQL14969 | TKW26665 | KXG22231 | Zm00001eb291070_P002 | 0.965 |
| PUZ68739 | genblast_C | KQL22773 | TKW30859 | KXG24314 | Zm00001eb265310_P001 | 0.869 |
| PUZ72769 | Sspon.02G | KQL26506 | TKW35621 | EER97479 | Zm00001eb326490_P001 | 0.965 |
| PUZ55030 | genblast_C | KQL06740 | TKW16457 | EES01375 | Zm00001eb154570_P001 | 0.691 |
| PUZ69502 | genblast_C | KQL23324 | TKW31617 | EES18178 | genblast_Os01t0618000-01_Ze | |

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| PUZ68188 | Sspon.02G | KQL22120 | TKW29999 | EER95739 | Zm00001eb298390_P001 | 0.936 |
| PUZ73674 | genblast_C | KQL27751 | TKW36796 | KXG29267 | Zm00001eb209780_P001 | 0.850 |
| PUZ52113 | Sspon.06G | KQL02399 | TKW11067 | KXG25652 | Zm00001eb199700_P001 | 0.917 |

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| PUZ67519 | Sspon.02G | KQL16525 | TKW28641 | EES16188 | genblast_Os12t0569200-01_Zea | |
| PUZ48178 | Sspon.04G | KQK98241 | TKW05633 | EES11177 | Zm00001eb248560_P001 | 0.816 |
| PUZ59010 | Sspon.08G | KQL12305 | TKW23548 | OQU77163 | Zm00001eb228560_P001 | 0.844 |
| PUZ60228 | genblast_C | genblast_C | TKW22744 | EER89963 | Zm00001eb385060_P001 | 0.906 |
| PUZ40205 | genblast_C | KQK89996 | TKV95022 | EER94520 | Zm00001eb023100_P001 | 0.958 |
| PUZ76985 | genblast_C | KQL30880 | TKW40828 | KXG31041 | Zm00001eb186990_P001 | 0.711 |
| PUZ78133 | genblast_C | KQL32001 | TKW42141 | genblast_C | Zm00001eb258250_P001 | 0.940 |
| PUZ45287 | genblast_C | KQK95025 | TKW01281 | EES08727 | Zm00001eb114310_P001 | 0.690 |
| PUZ59280 | Sspon.08G | KQL11799 | TKW22893 | OQU76985 | Zm00001eb226650_P002 | 0.965 |
| PUZ76874 | Sspon.04G | KQL30781 | TKW40695 | EES05790 | Zm00001eb249390_P001 | 0.935 |
| PUZ36758 | genblast_C | KQK86822 | TKV91019 | EER90791 | Zm00001eb059510_P001 | 0.767 |
| PUZ53511 | Sspon.03G | KQL08130 | TKW18238 | KXG33898 | Zm00001eb144670_P001 | 0.968 |
| PUZ65439 | genblast_C | KQL14919 | TKW26597 | EES19716 | Zm00001eb291220_P001 | 0.870 |
| PUZ52310 | Sspon.06G | KQL02578 | TKW11304 | EES15330 | Zm00001eb036040_P001 | 0.865 |
| PUZ67587 | Sspon.02G | KQL16923 | TKW29205 | EES16218 | Zm00001eb136250_P001 | 0.970 |
| PUZ57564 | Sspon.03G | KQL03977 | TKW12877 | EES02665 | Zm00001eb334080_P001 | 0.860 |
| PUZ68046 | Sspon.02G | KQL17403 | TKW29840 | KXG24118 | Zm00001eb032890_P001 | 0.751 |
| PUZ69873 | genblast_C | KQK99510 | TKW07357 | KXG35179 | Zm00001eb095580_P001 | 0.904 |

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| genblast_C | genblast_C | KQL07539 | TKW17505 | OQU87774 | Zm00001eb149180_P001 | 0.999 |
| PUZ77748 | Sspon.08G | KQL31615 | TKW41714 | EES07566 | Zm00001eb193780_P001 | 0.820 |
| PUZ65876 | genblast_C | KQL15368 | TKW27132 | EES19570 | Zm00001eb288570_P001 | 0.924 |
| PUZ73154 | Sspon.02G | KQL26899 | TKW36133 | genblast_C | genblast_Os07t0641600-02_Zea | |
| PUZ59579 | Sspon.08G | KQL12070 | TKW23257 | EER88786 | Zm00001eb389890_P001 | 0.786 |
| PUZ37829 | genblast_C | KQK87965 | TKV92334 | EER91177 | Zm00001eb050650_P001 | 0.961 |
| PUZ66426 | Sspon.07G | KQL15878 | TKW27812 | KXG21791 | Zm00001eb285910_P003 | 0.960 |
| PUZ61816 | Sspon.08G | KQL09373 | TKW19723 | EER88003 | Zm00001eb374040_P001 | 0.868 |
| PUZ38025 | Sspon.01G | KQK88126 | TKV92572 | EER91249 | Zm00001eb050130_P001 | 0.940 |
| PUZ43609 | Sspon.05G | KQK99799 | TKV99143 | EES09210 | Zm00001eb093380_P003 | 0.954 |
| PUZ52185 | Sspon.06G | KQL02439 | TKW11125 | EES14263 | Zm00001eb035050_P002 | 0.818 |
| PUZ47998 | Sspon.05G | KQK98063 | TKW05408 | EES11112 | Zm00001eb426530_P002 | 0.920 |
| PUZ47677 | Sspon.05G | KQK97758 | TKW05016 | EES12388 | Zm00001eb425060_P001 | 0.963 |
| PUZ61741 | genblast_C | KQL09870 | TKW20380 | genblast_C | genblast_Os06t0207500-02_Zea | |
| PUZ53614 | Sspon.03G | KQL08043 | TKW18130 | OQU88003 | Zm00001eb145430_P001 | 0.979 |

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| PUZ45078 | genblast_C | KQK94809 | TKW01027 | OQU83580 | Zm00001eb113470_P001 | 0.827 |
| PUZ49840 | Sspon.06G | KQL00245 | TKW08144 | KXG24230 | Zm00001eb260510_P001 | 0.948 |
| PUZ42202 | Sspon.01G | genblast_Z | TKV97452 | EER92646 | Zm00001eb400240_P001 | 0.983 |
| genblast_C | Sspon.01G | KQL26118 | TKW35144 | OQU90056 | Zm00001eb217620_P001 | 0.857 |

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| PUZ55433 | Sspon.03G | KQL06337 | TKW15961 | EES02405 | genblast_Os01t0668901-00_Zea | |

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| PUZ42447 | genblast_C | KQK92195 | TKV97733 | EER92724 | Zm00001eb401390_P001 | 0.803 |
| PUZ56309 | Sspon.02G | KQL05469 | TKW14865 | EES03102 | Zm00001eb162650_P002 | 0.919 |
| PUZ46915 | Sspon.04G | KQL29811 | TKW39394 | KXG30289 | Zm00001eb180800_P001 | 0.962 |

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| PUZ72142 | genblast_C | KQL25875 | TKW34852 | EER97252 | Zm00001eb105540_P001 | 0.981 |

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| PUZ61767 | Sspon.04G | KQL09888 | TKW20404 | EER89390 | Zm00001eb278640_P001 | 0.984 |
| PUZ60396 | Sspon.08G | KQL10893 | TKW21748 | OQU7651 | Zm00001eb383570_P001 | 0.926 |
| PUZ47595 | Sspon.05G | KQK97676 | TKW04922 | OQU8176 | genblast_Os04t0472200-01_Ze | |
| PUZ60092 | genblast_C | KQL11557 | TKW22583 | KXG20277 | Zm00001eb385980_P003 | 0.972 |
| PUZ40759 | Sspon.01G | KQL16681 | TKW28857 | KXG39188 | Zm00001eb392870_P001 | 0.881 |
| PUZ38959 | Sspon.01G | KQK88980 | TKV93730 | EER91583 | Zm00001eb047580_P001 | 0.954 |
| PUZ75472 | Sspon.04G | KQL29581 | TKW39101 | KXG30162 | Zm00001eb240790_P001 | 0.756 |

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| PUZ47039 | Sspon.05G | KQK97172 | TKW04273 | KXG26229 | Zm00001eb083970_P001 | 0.766 |
| PUZ59084 | Sspon.06G | KQL12240 | TKW23451 | EER88964 | Zm00001eb228100_P001 | 0.854 |
| PUZ65783 | Sspon.02G | KQL15294 | TKW27048 | EES17104 | Zm00001eb410960_P002 | 0.894 |
| PUZ70753 | Sspon.02G | KQL24534 | TKW33210 | genblast_C | genblast_Os09t0422600-01_Ze | |

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| PUZ36245 | Sspon.01G | KQK86309 | TKV90348 | EER90585 | Zm00001eb211340_P002 | 0.936 |
| PUZ47230 | Sspon.05G | KQK97341 | TKW04488 | OQU8162 | Zm00001eb082300_P001 | 0.928 |
| PUZ59251 | Sspon.08G | genblast_C | TKW22855 | EER90318 | Zm00001eb226840_P001 | 0.921 |
| PUZ53953 | Sspon.03G | KQL07736 | TKW17727 | OQU8785 | Zm00001eb147960_P001 | 0.886 |
| PUZ75394 | Sspon.04G | genblast_C | TKW38857 | EES04844 | Zm00001eb238460_P002 | 0.912 |
| PUZ53185 | Sspon.03G | KQL08422 | TKW18623 | EES02001 | Zm00001eb142740_P001 | 0.960 |
| PUZ60447 | Sspon.01G | KQL10849 | TKW21697 | EER88443 | Zm00001eb383280_P001 | 0.870 |

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| PUZ59615 | Sspon.08G | KQL11072 | TKW21952 | EER90165 | Zm00001eb389660_P001 | 0.925 |
| PUZ38594 | Sspon.02G | KQK89389 | TKV94249 | EER97986 | Zm00001eb117530_P002 | 0.838 |
| PUZ54867 | genblast_C | KQL06911 | TKW16678 | genblast_C | Zm00001eb153710_P001 | 0.994 |
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| PUZ63197 | genblast_C | KQK99427 | TKW07193 | EES16782 | Zm00001eb409080_P001 | 0.956 |
| PUZ77291 | Sspon.04G | KQL31165 | TKW41173 | KXG30908 | Zm00001eb188560_P002 | 0.932 |
| PUZ36961 | Sspon.01G | KQK87042 | TKV91282 | KXG37524 | Zm00001eb057740_P001 | 0.955 |
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| PUZ73484 | Sspon.01G | KQL27219 | TKW36572 | EER97754 | Zm00001eb330910_P001 | 0.789 |
| PUZ65443 | genblast_C | KQL14927 | TKW26606 | OQU78227 | Zm00001eb352340_P001 | 0.998 |
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| PUZ53689 | Sspon.03G | KQL07970 | TKW18018 | KXG33808 | Zm00001eb366300_P002 | 0.961 |
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| PUZ55089 | Sspon.03G | KQL06691 | TKW16376 | KXG33236 | Zm00001eb361390_P001 | 0.911 |
| PUZ37751 | Sspon.01G | KQK87897 | TKV92251 | EER91148 | Zm00001eb218460_P001 | 0.877 |
| PUZ51514 | Sspon.07G | KQK93238 | TKV98848 | KXG22750 | Zm00001eb194930_P001 | 0.958 |
| PUZ55561 | Sspon.03G | KQL06130 | TKW15721 | EES01187 | Zm00001eb158160_P001 | 0.940 |
| PUZ64947 | Sspon.07G | KQL14510 | TKW26100 | EES18606 | Zm00001eb294650_P001 | 0.896 |
| PUZ76797 | Sspon.04G | KQL30706 | TKW40601 | EES05823 | Zm00001eb248740_P001 | 0.903 |
| PUZ68263 | Sspon.02G | KQL22246 | TKW30166 | EER95793 | Zm00001eb118010_P001 | 0.869 |
| PUZ53948 | Sspon.03G | KQL07743 | TKW17734 | EES01757 | Zm00001eb147910_P001 | 0.876 |
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| PUZ43506 | Sspon.05G | KQK99729 | TKW07593 | EES07907 | Zm00001eb405590_P001 | 0.729 |

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| PUZ62069 | Sspon.08G | KQL09627 | TKW20065 | EER89249 | Zm00001eb271370_P001 | 0.976 |
| PUZ65897 | Sspon.07G | KQL15392 | TKW27165 | KXG22042 | Zm00001eb288490_P001 | 0.826 |
| PUZ58490 | Sspon.03G | KQL04814 | TKW13963 | EES00131 | Zm00001eb121040_P001 | 0.968 |
| PUZ38491 | Sspon.01G | KQK88565 | TKV93173 | EER91441 | Zm00001eb221030_P001 | 0.888 |
| PUZ51271 | Sspon.05G | genblast_C | TKW41966 | KXG26221 | Zm00001eb312790_P001 | 0.777 |
| PUZ36446 | Sspon.01G | KQK86521 | TKV90626 | EER90673 | Zm00001eb061990_P002 | 0.880 |
| PUZ39820 | Sspon.01G | KQK89658 | TKV94601 | EER91823 | Zm00001eb025720_P001 | 0.950 |
| PUZ69458 | Sspon.02G | KQL23428 | genblast_C | EER96307 | Zm00001eb096710_P001 | 0.841 |
| PUZ71989 | Sspon.02G | KQL25742 | TKW34679 | EER97198 | Zm00001eb104820_P001 | 0.937 |
| PUZ71783 | genblast_C | KQL08406 | TKW18588 | EES04130 | Zm00001eb363970_P001 | 0.950 |
| PUZ52246 | Sspon.06G | KQL02502 | TKW11205 | EES14316 | Zm00001eb035580_P001 | 0.686 |
| PUZ63163 | Sspon.07G | KQK99477 | TKW07230 | EES16751 | Zm00001eb408270_P002 | 0.911 |
| PUZ59319 | genblast_C | KQL11830 | TKW22933 | EER90291 | Zm00001eb273240_P001 | 0.887 |
| PUZ53855 | genblast_C | KQL07827 | TKW17837 | KXG33735 | Zm00001eb147220_P003 | 0.950 |
| PUZ58777 | Sspon.03G | KQL03307 | TKW12046 | KXG31512 | Zm00001eb119430_P001 | 0.814 |
| PUZ49789 | genblast_C | KQL00201 | TKW08092 | OQU79763 | Zm00001eb260240_P001 | 0.979 |

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| PUZ68701 | Sspon.02GKQL24151 | TKW32689 | EER97823 | Zm00001eb116810_P001 | 0.972 |

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| PUZ51686 | Sspon.06GKQL01984 | TKW10528 | OQU80549 | Zm00001eb041070_P002 | 0.882 |
| PUZ77591 | genblast_CKQL31354 | TKW41409 | EES07314 | Zm00001eb253510_P004 | 0.958 |
| PUZ51219 | Sspon.06GKQL01546 | TKW09948 | EES14882 | Zm00001eb042780_P002 | 0.905 |
| PUZ57084 | Sspon.03GKQL03504 | TKW12303 | OQU86769 | genblast_Os01t0299300-00_Zea | |
| PUZ76919 | Sspon.04GKQL30821 | TKW40751 | EES05775 | Zm00001eb186660_P001 | 0.956 |
| PUZ52845 | Sspon.03GKQL08766 | TKW19046 | EES02126 | Zm00001eb140040_P001 | 0.977 |

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| PUZ65668 | Sspon.07GKQL15175 | TKW26915 | EES01738 | Zm00001eb148320_P001 | 0.747 |
| PUZ66045 | Sspon.07GKQL15538 | TKW27380 | KXG21969 | Zm00001eb349770_P001 | 0.938 |
| PUZ64259 | Sspon.07GKQL13803 | TKW25259 | EES17807 | Zm00001eb283000_P001 | 0.957 |
| PUZ36496 | Sspon.01GKQK86563 | TKV90702 | KXG37316 | Zm00001eb061520_P001 | 0.962 |
| PUZ37554 | Sspon.01GKQK87668 | TKV91986 | EER93647 | Zm00001eb053410_P001 | 0.888 |
| PUZ58389 | Sspon.03GKQL04725 | TKW13857 | EES02341 | Zm00001eb121920_P001 | 0.975 |
| PUZ37714 | Sspon.01GKQK87863 | genblast_C | EER91132 | Zm00001eb218310_P001 | 0.849 |
| PUZ44734 | genblast_CKQK94532 | TKW00595 | EES15633 | Zm00001eb163830_P001 | 0.685 |
| PUZ48455 | genblast_CKQK98466 | TKW05969 | OQU82135 | Zm00001eb429140_P001 | 0.982 |
| PUZ72378 | Sspon.02GKQL26136 | TKW35156 | EER97344 | Zm00001eb106450_P001 | 1.001 |

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| PUZ68500 | genblast_CKQL22542 | TKW30564 | EER98025 | Zm00001eb300700_P001 | 0.956 |
| PUZ69186 | Sspon.02GKQL22981 | TKW31133 | EER96063 | Zm00001eb303220_P001 | 0.954 |

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| PUZ52015 | Sspon.06Ggenblast_C | TKW10926 | OQU81002 | Zm00001eb199330_P003 | 0.934 |
| PUZ70974 | Sspon.02GKQL24770 | TKW33469 | OQU89611 | Zm00001eb100430_P002 | 0.962 |

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| PUZ58263 | Sspon.03G | KQL04596 | TKW13683 | EES02381 | Zm00001eb336730_P001 | 0.968 |
| PUZ60863 | Sspon.08G | KQL10270 | TKW20915 | KXG19779 | Zm00001eb280310_P001 | 0.855 |
| PUZ45216 | Sspon.06G | KQK94936 | TKW01190 | EES09947 | Zm00001eb114020_P001 | 0.761 |
| PUZ58949 | Sspon.08G | KQL12349 | TKW23601 | KXG20977 | Zm00001eb271770_P002 | 0.953 |
| PUZ55291 | Sspon.07G | KQL06476 | TKW16121 | EES18634 | Zm00001eb295010_P001 | 0.765 |
| PUZ53100 | Sspon.03G | KQL08505 | TKW18718 | EES04172 | Zm00001eb142060_P001 | 0.846 |

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| PUZ52749 | Sspon.06G | KQL01767 | TKW10251 | EES14037 | Zm00001eb038650_P001 | 0.982 |
| genblast_C | Sspon.01G | KQK87559 | TKV91865 | EER91033 | Zm00001eb054140_P001 | 0.948 |
| PUZ61869 | Sspon.04G | KQL09436 | TKW19806 | OQU75981 | Zm00001eb278370_P003 | 0.997 |
| PUZ52888 | Sspon.07G | KQL08722 | TKW18986 | EES02101 | Zm00001eb362500_P001 | 0.989 |
| PUZ42835 | Sspon.01G | KQK92570 | TKV98201 | OQU93225 | Zm00001eb403020_P001 | 0.768 |

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| PUZ62775 | Sspon.05G | genblast_C | TKW07581 | OQU82754 | Zm00001eb195650_P001 | 0.946 |
| PUZ67344 | genblast_C | KQL16702 | TKW28886 | EES16101 | Zm00001eb137610_P003 | 0.938 |
| PUZ63654 | Sspon.07G | KQL13388 | TKW24705 | EES18883 | Zm00001eb266910_P001 | 0.732 |
| PUZ48820 | Sspon.05G | KQK98826 | TKW06437 | OQU82277 | Zm00001eb430530_P001 | 0.956 |
| PUZ42809 | Sspon.01G | KQK92540 | TKV98171 | KXG40156 | Zm00001eb403130_P001 | 0.783 |
| PUZ56215 | Sspon.03G | KQL05545 | TKW14966 | EES00916 | Zm00001eb162250_P001 | 0.853 |
| PUZ63367 | Sspon.04G | KQK99939 | TKW07858 | EES06057 | Zm00001eb259310_P004 | 0.978 |
| PUZ59284 | Sspon.08G | KQL11802 | TKW22897 | EER90307 | Zm00001eb226590_P001 | 0.795 |
| PUZ43919 | genblast_C | KQK93823 | TKV99607 | EES08084 | Zm00001eb091540_P004 | 0.975 |
| PUZ51498 | Sspon.06G | KQL01855 | TKW10353 | EES15006 | Zm00001eb179280_P001 | 0.915 |
| PUZ43082 | Sspon.01G | KQK92823 | TKV98476 | genblast_C | Zm00001eb403650_P001 | 0.763 |
| PUZ68160 | Sspon.02G | KQK85897 | TKW29963 | EER95725 | Zm00001eb298220_P001 | 0.947 |

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| PUZ39101 | genblast_C | KQK89140 | TKV93916 | KXG29612 | Zm00001eb233800_P001 | 0.683 |

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| PUZ57617 | Sspon.03G | KQL24250 | TKW32834 | EES02651 | Zm00001eb334180_P002 | 0.832 |
| PUZ65911 | Sspon.03G | KQL29462 | TKW38900 | KXG31566 | Zm00001eb119950_P001 | 0.683 |
| PUZ66836 | genblast_C | KQL05512 | TKW14919 | EES17957 | Zm00001eb284860_P001 | 0.978 |
| PUZ64502 | Sspon.07G | KQL14042 | TKW25542 | EES18801 | Zm00001eb297420_P001 | 0.863 |
| PUZ36314 | genblast_C | KQK86410 | TKV90458 | EER93180 | Zm00001eb211640_P001 | 0.902 |
| PUZ61431 | Sspon.08G | KQL10006 | TKW20563 | EER88112 | Zm00001eb279580_P001 | 0.902 |
| PUZ52901 | Sspon.03G | KQL08708 | TKW18966 | EES04260 | Zm00001eb140420_P002 | 0.976 |
| PUZ47377 | Sspon.05G | genblast_C | TKW04664 | EES12252 | Zm00001eb423540_P001 | 0.972 |
| PUZ66586 | Sspon.07G | KQL16018 | TKW27991 | EES17993 | Zm00001eb347230_P001 | 0.860 |
| PUZ53903 | Sspon.03G | KQL07782 | TKW17783 | KXG33717 | Zm00001eb367290_P001 | 0.938 |
| PUZ73396 | Sspon.02G | KQL27111 | TKW36417 | OQU90456 | Zm00001eb330340_P002 | 0.725 |
| PUZ69375 | Sspon.02G | KQL23334 | TKW31631 | OQU81266 | Zm00001eb305790_P002 | 0.771 |
| PUZ68829 | Sspon.02G | KQL22863 | TKW30967 | EER98148 | Zm00001eb302670_P004 | 0.959 |
| PUZ76626 | Sspon.06G | KQL30558 | TKW40403 | KXG30662 | Zm00001eb247540_P001 | 0.962 |
| PUZ69465 | Sspon.02G | KQL23483 | TKW31753 | EER98440 | Zm00001eb306300_P001 | 0.933 |
| PUZ69156 | Sspon.02G | KQL23001 | TKW31161 | EER98208 | Zm00001eb095210_P001 | 0.912 |
| PUZ73342 | Sspon.02G | KQL27161 | TKW36492 | KXG36938 | genblast_Os07t0676600-01_Ze | |
| PUZ61539 | Sspon.08G | KQL10100 | TKW20684 | KXG19688 | Zm00001eb371890_P001 | 0.905 |
| PUZ64999 | Sspon.07G | KQL14555 | TKW26149 | EES18582 | Zm00001eb342330_P001 | 0.958 |
| PUZ75567 | Sspon.02G | KQL29486 | TKW38961 | KXG34983 | Zm00001eb306020_P001 | 0.966 |
| PUZ73603 | Sspon.01G | KQL27327 | TKW36707 | OQU91491 | Zm00001eb220000_P001 | 0.683 |
| PUZ50904 | Sspon.03G | KQL07613 | TKW17583 | EES01714 | genblast_Os09t0499400-01_Ze | |

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| PUZ77687 | genblast_C | KQL31563 | TKW41657 | KXG30729 | Zm00001eb255310_P002 | 0.974 |
| PUZ48189 | Sspon.05G | KQK98249 | TKW05642 | KXG26784 | Zm00001eb427410_P004 | 0.899 |

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| genblast_C | Sspon.08G | KQL11801 | TKW22896 | KXG20747 | Zm00001eb226550_P001 | 0.941 |
| PUZ37494 | Sspon.01G | genblast_C | TKV91913 | EER93624 | Zm00001eb053810_P001 | 0.923 |
| PUZ58225 | Sspon.03G | KQL04568 | TKW13650 | OQU8624 | Zm00001eb123160_P001 | 0.989 |
| PUZ36206 | genblast_C | genblast_C | TKV90384 | EER93146 | Zm00001eb063650_P001 | 0.913 |
| PUZ37291 | genblast_C | KQK87379 | TKV91665 | EER93554 | Zm00001eb055540_P001 | 0.938 |
| PUZ63239 | Sspon.07G | KQK99380 | TKW07140 | KXG23197 | Zm00001eb138730_P001 | 0.901 |
| PUZ70536 | Sspon.02G | KQL24296 | TKW32917 | EER96671 | Zm00001eb311430_P001 | 0.950 |
| PUZ47622 | Sspon.05G | KQK97706 | TKW04957 | OQU8179 | genblast_Os04t0476000-01 | Zm0 |

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| PUZ71068 | Sspon.02G | KQL24862 | TKW33571 | EER96888 | Zm00001eb315450_P001 | 0.788 |
| PUZ57526 | Sspon.03G | KQL03951 | TKW12855 | OQU86597 | Zm00001eb333940_P002 | 1.008 |
| PUZ38254 | Sspon.01G | KQK88336 | TKV92867 | EER93931 | Zm00001eb043360_P001 | 0.881 |
| PUZ76458 | Sspon.04G | KQL30339 | TKW40119 | EES05375 | Zm00001eb246680_P001 | 0.729 |
| PUZ66851 | Sspon.02G | KQL16123 | TKW28105 | KXG23698 | Zm00001eb137020_P002 | 0.995 |
| PUZ55167 | Sspon.03G | KQL06608 | TKW16283 | genblast_C | Zm00001eb155550_P001 | 0.936 |
| PUZ59449 | Sspon.08G | KQL11969 | TKW23131 | OQU76895 | Zm00001eb209620_P001 | 0.993 |
| PUZ68388 | Sspon.02G | KQL22415 | TKW30405 | KXG34386 | genblast_Os07t0143600-01_Zea |  |
| PUZ44737 | genblast_C | KQK94510 | TKW00584 | KXG36669 | Zm00001eb327290_P001 | 0.966 |
| PUZ70373 | Sspon.02G | KQL24179 | TKW32722 | EER96588 | Zm00001eb310220_P001 | 0.868 |
| PUZ40728 | Sspon.01G | KQK90468 | TKV95613 | EER92149 | Zm00001eb019620_P001 | 0.926 |
| PUZ61304 | Sspon.08G | KQL09801 | TKW20299 | EER88070 | Zm00001eb373100_P001 | 0.733 |

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| PUZ47508 | genblast_C | KQK97595 | TKW04818 | EES12301 | Zm00001eb424310_P001 | 0.993 |

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| PUZ36947 | Sspon.01G | KQK87022 | TKV91266 | KXG37513 | Zm00001eb057840_P001 | 0.977 |
| PUZ75979 | genblast_C | KQL29930 | TKW39585 | EES05202 | Zm00001eb243060_P001 | 0.978 |
| genblast_C | genblast_C | KQL01560 | TKW09967 | OQU8410 | genblast_Os06t0293500-01_Zea |  |
| PUZ43311 | genblast_C | KQK93086 | TKV98756 | EER93039 | genblast_Os01t0303100-01_Zea |  |
| PUZ50197 | genblast_C | KQL00731 | TKW08864 | OQU79936 | Zm00001eb415740_P001 | 0.846 |
| PUZ76421 | genblast_C | KQL30362 | TKW40136 | EES07109 | Zm00001eb246450_P001 | 0.990 |

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| PUZ57999 | Sspon.03GKQL04361 | TKW1339 | KXG31903 | Zm00001eb124500_P001 | 0.799 |
| PUZ61583 | Sspon.08GKQL10156 | TKW20762 | EER89524 | Zm00001eb280150_P001 | 0.902 |
| PUZ47096 | genblast_Z | KQK97223 | TKW04331 | EES10780 | Zm00001eb083520_P001 | 0.956 |
| PUZ62188 | Sspon.08GKQL09744 | TKW20214 | EER87855 | Zm00001eb376860_P001 | 0.953 |

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| PUZ60234 | Sspon.08GKQL11678 | TKW22755 | EER89958 | genblast_Os06t0567900-01_Ze | |
| PUZ76667 | Sspon.04GKQL30592 | TKW40452 | EES05462 | Zm00001eb185310_P002 | 0.946 |
| PUZ56733 | genblast_CKQL05137 | TKW14415 | KXG32496 | Zm00001eb131700_P001 | 0.986 |
| PUZ41383 | Sspon.01GKQK91182 | TKV96499 | genblast_C | Zm00001eb014820_P001 | 0.858 |
| PUZ56055 | Sspon.03GKQL06210 | TKW1581 | EES03184 | Zm00001eb160630_P001 | 0.792 |
| PUZ76256 | Sspon.04GKQL30178 | TKW39912 | KXG30492 | Zm00001eb183100_P001 | 0.985 |
| genblast_C | Sspon.01G | genblast_C | TKW00594 | EER94849 | Zm00001eb017070_P001 | 0.929 |
| PUZ45643 | Sspon.06G | genblast_C | TKW0212 | EES10182 | Zm00001eb165940_P001 | 0.935 |
| PUZ68676 | Sspon.02GKQL22711 | TKW30773 | OQU8857 | Zm00001eb301470_P001 | 0.967 |

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| PUZ50326 | Sspon.06GKQL00621 | TKW08725 | OQU8355 | Zm00001eb414770_P001 | 0.793 |

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| PUZ78289 | Sspon.04GKQL32156 | TKW42317 | EES07771 | Zm00001eb191170_P001 | 0.910 |

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| PUZ76522 | Sspon.04GKQL30458 | TKW40265 | EES07139 | Zm00001eb246940_P001 | 0.985 |
| PUZ68027 | Sspon.02GKQL17377 | TKW29796 | EES16437 | Zm00001eb134390_P001 | 0.796 |
| PUZ57879 | Sspon.03Ggenblast_C | TKW1324 | OQU8640 | Zm00001eb125310_P001 | 0.798 |

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| PUZ49000 | Sspon.05GKQK99018 | TKW06704 | KXG27152 | Zm00001eb070130_P004 | 0.972 |
| PUZ75689 | genblast_CKQL29577 | TKW39096 | OQU8489 | Zm00001eb392910_P001 | 0.747 |

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| PUZ36046 | Sspon.01GKQK86145 | TKV90137 | EER93088 | Zm00001eb064620_P001 | 0.961 |

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| PUZ57162 | Sspon.03GKQL03585 | TKW1240 | EES02806 | Zm00001eb129490_P001 | 0.963 |

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| PUZ72446 | Sspon.02GKQL26210 | TKW35259 | EER99518 | Zm00001eb323860_P001 | 0.882 |
| PUZ67441 | Sspon.02GKQL16621 | TKW28787 | EER98395 | genblast_Os03t0646400-01_Zea | |
| PUZ58026 | Sspon.03GKQL04388 | TKW13425 | EES00322 | Zm00001eb124430_P001 | 0.936 |
| PUZ54758 | genblast_CKQL07008 | TKW16812 | KXG33381 | Zm00001eb370830_P001 | 0.984 |

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| PUZ54028 | Sspon.03GKQL07672 | TKW17654 | KXG33676 | Zm00001eb367890_P001 | 0.996 |
| PUZ52369 | Sspon.06GKQL02635 | TKW11376 | EES15315 | Zm00001eb036550_P001 | 0.942 |
| PUZ64391 | Sspon.07GKQL13931 | TKW25413 | EES18828 | Zm00001eb356260_P002 | 0.818 |
| PUZ47821 | Sspon.05GKQK97897 | TKW05207 | OQU81865 | Zm00001eb425680_P001 | 0.868 |

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| PUZ49205 | Sspon.05GKQK99211 | TKW06944 | OQU82446 | Zm00001eb068520_P003 | 0.899 |
| PUZ64040 | Sspon.07GKQL13059 | TKW24238 | EES17713 | genblast_Os05t0148900-01_Zea | |

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| PUZ53732 | Sspon.07GKQL07939 | TKW17971 | KXG33790 | Zm00001eb146220_P003 | 0.914 |
| PUZ51417 | Sspon.06GKQL01765 | TKW10250 | EES13822 | Zm00001eb178980_P001 | 0.799 |
| PUZ47424 | Sspon.05GKQK97510 | TKW04716 | EES10915 | Zm00001eb081220_P001 | 0.819 |
| PUZ57598 | Sspon.03GKQL04014 | TKW12929 | KXG32139 | Zm00001eb334150_P001 | 0.900 |
| PUZ40367 | Sspon.01GKQK90164 | TKV95215 | EER94587 | Zm00001eb393630_P001 | 0.952 |
| PUZ63771 | genblast_CKQL13119 | TKW24325 | EES17623 | Zm00001eb265650_P001 | 0.960 |

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| PUZ50586 | Sspon.06GKQL00366 | TKW08312 | EES13537 | genblast_Os08t0223900-00_Zea | |
| PUZ40265 | genblast_CKQK90067 | TKV95099 | EER91984 | genblast_Os10t0548100-01_Zea | |

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| PUZ72982 | Sspon.02GKQL26733 | TKW35916 | genblast_C | Zm00001eb327860_P002 | 0.923 |
| PUZ36776 | genblast_CKQK86842 | TKV91041 | KXG37444 | Zm00001eb213700_P001 | 0.841 |
| PUZ55913 | Sspon.03GKQL05784 | TKW15259 | OQU87137 | Zm00001eb161570_P001 | 0.992 |
| PUZ37133 | Sspon.01GKQK87215 | TKV91484 | EER90911 | Zm00001eb215380_P002 | 1.003 |
| PUZ77243 | Sspon.04GKQL31113 | TKW41114 | OQU85554 | Zm00001eb251890_P001 | 0.927 |

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| PUZ57608 | Sspon.03G | genblast_C | TKW12941 | OQU8655 | Zm00001eb126900_P001 | 0.899 |
| PUZ61376 | Sspon.03G | KQL06777 | TKW16512 | EES01387 | Zm00001eb154550_P001 | 0.922 |
| PUZ60467 | Sspon.08G | KQL10827 | TKW21676 | KXG20091 | genblast_Os06t0526800-00_Ze | |
| PUZ48889 | Sspon.05G | KQK98900 | TKW06548 | EES11421 | Zm00001eb070840_P002 | 0.952 |
| PUZ40485 | Sspon.01G | KQK90283 | TKV95358 | OQU9229 | Zm00001eb021080_P001 | 0.916 |
| PUZ53794 | Sspon.03G | KQL07882 | TKW1790 | EES01814 | Zm00001eb146680_P002 | 0.987 |
| PUZ56653 | Sspon.03G | KQL05060 | TKW1430 | KXG32446 | Zm00001eb131340_P005 | 0.892 |
| genblast_C | Sspon.07G | KQL15063 | TKW26771 | EES18377 | Zm00001eb351920_P001 | 0.991 |
| PUZ67098 | Sspon.02G | genblast_C | TKW28538 | OQU7909 | Zm00001eb132990_P001 | 0.764 |
| PUZ59008 | Sspon.08G | genblast_C | TKW23553 | EER90432 | Zm00001eb228580_P003 | 0.978 |
| PUZ63709 | Sspon.07G | KQL13342 | TKW24642 | KXG21113 | Zm00001eb355600_P001 | 0.968 |
| PUZ41753 | genblast_C | KQK91552 | TKV96930 | EER92498 | Zm00001eb011960_P001 | 0.944 |
| PUZ56905 | Sspon.06G | KQL05029 | TKW14251 | KXG24185 | Zm00001eb260100_P001 | 0.871 |
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| PUZ67061 | Sspon.02G | genblast_C | TKW28493 | OQU7908 | Zm00001eb132960_P002 | 0.947 |
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| PUZ54730 | Sspon.03G | genblast_C | TKW16843 | OQU8757 | Zm00001eb152860_P001 | 0.901 |
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| PUZ53994 | Sspon.03G | KQL07696 | TKW1768 | KXG33685 | Zm00001eb148120_P003 | 0.863 |
| PUZ58395 | genblast_C | KQL04734 | TKW13863 | EES00161 | Zm00001eb121870_P002 | 0.989 |
| PUZ38605 | Sspon.01G | KQK88680 | TKV93321 | KXG38312 | Zm00001eb045580_P001 | 0.850 |
| PUZ53826 | Sspon.03G | KQL07849 | TKW1787 | EES03930 | Zm00001eb366780_P001 | 0.909 |
| PUZ54005 | Sspon.03G | KQL07688 | TKW1767 | EES03871 | Zm00001eb148210_P001 | 0.978 |

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| PUZ40491 | genblast_C | KQK90286 | TKV95365 | EER92060 | Zm00001eb404700_P002 | 0.955 |
| PUZ48876 | Sspon.05G | KQK98886 | TKW06534 | EES12850 | Zm00001eb430800_P001 | 0.853 |
| PUZ73106 | Sspon.02G | KQL26850 | TKW36080 | EER97614 | Zm00001eb328680_P002 | 0.950 |
| PUZ36191 | Sspon.01G | KQK87106 | TKV91352 | KXG37188 | Zm00001eb063770_P001 | 0.958 |
| PUZ74673 | Sspon.04G | KQL28144 | TKW37282 | EES06507 | Zm00001eb205310_P001 | 0.961 |
| PUZ66440 | Sspon.07G | KQL15889 | TKW27826 | EES18055 | Zm00001eb285980_P001 | 0.890 |
| PUZ76062 | Sspon.04G | KQL29995 | TKW39683 | EES05232 | Zm00001eb243540_P001 | 0.960 |
| PUZ54089 | genblast_C | genblast_C | TKW17588 | OQU87816 | Zm00001eb148770_P001 | 0.812 |
| PUZ51596 | Sspon.06G | KQL01921 | TKW10437 | EES15041 | Zm00001eb041480_P002 | 0.959 |
| PUZ55611 | Sspon.03G | KQL06088 | TKW15647 | OQU8723 | Zm00001eb158550_P001 | 0.940 |

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| PUZ75934 | Sspon.04GKQL29883 | TKW39498 | EES06908 | Zm00001eb242750_P001 | 0.965 |
| PUZ70993 | Sspon.02GKQL24789 | TKW33492 | EER99009 | Zm00001eb314880_P001 | 0.921 |
| PUZ48407 | Sspon.05GKQK98427 | TKW05928 | EER96520 | Zm00001eb074290_P001 | 0.947 |
| PUZ40077 | Sspon.01GKQK89886 | TKV94881 | KXG38901 | Zm00001eb391030_P001 | 0.903 |
| PUZ59422 | Sspon.08GKQL11916 | TKW23080 | EER88836 | Zm00001eb273600_P001 | 0.809 |
| PUZ55340 | Sspon.03GKQL06434 | TKW16061 | genblast_Z | Zm00001eb156640_P002 | 0.676 |
| PUZ62459 | Sspon.08GKQL09028 | TKW19318 | EER89085 | Zm00001eb269130_P001 | 0.874 |
| PUZ64699 | Sspon.07GKQK88465 | TKV93051 | KXG22562 | Zm00001eb296450_P001 | 0.973 |
| PUZ76948 | Sspon.04GKQL30846 | TKW40778 | EES07487 | Zm00001eb186830_P002 | 0.675 |
| PUZ52768 | Sspon.03GKQL08820 | TKW19119 | genblast_C | Zm00001eb362070_P002 | 0.961 |
| PUZ73514 | Sspon.02GKQL27241 | TKW36595 | KXG36991 | Zm00001eb111710_P001 | 0.909 |
| PUZ77614 | Sspon.04GKQL31321 | TKW41372 | OQU85475 | Zm00001eb189830_P001 | 0.909 |

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| PUZ77783 | genblast_CKQL31656 | TKW41752 | EES07580 | Zm00001eb255970_P001 | 0.912 |
| PUZ73842 | Sspon.04GKQL28933 | TKW38266 | KXG29351 | Zm00001eb230800_P002 | 0.910 |

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| PUZ65925 | Sspon.03GKQL15421 | TKW27195 | EES19547 | genblast_Os05t0421900-00_Ze | |
| PUZ54862 | Sspon.03GKQL06919 | TKW16684 | OQU87505 | Zm00001eb371210_P001 | 0.741 |
| PUZ59559 | Sspon.01GKQL12045 | TKW23222 | EER90203 | Zm00001eb274250_P002 | 0.834 |
| PUZ46575 | Sspon.01Ggenblast_C | TKW03645 | EER90679 | Zm00001eb212420_P001 | 0.970 |
| PUZ41834 | Sspon.01Ggenblast_C | TKV96977 | EER95148 | Zm00001eb011320_P001 | 0.976 |
| PUZ71809 | Sspon.02GKQL25577 | TKW34444 | EER97130 | Zm00001eb321050_P001 | 0.945 |
| PUZ52891 | Sspon.03GKQL08717 | TKW18981 | EES02099 | Zm00001eb140380_P001 | 0.821 |
| PUZ76975 | Sspon.04GKQL30872 | TKW40816 | EES05753 | Zm00001eb250040_P001 | 0.802 |

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| PUZ51580 | Sspon.03GKQL04034 | TKW12956 | EES00458 | Zm00001eb126780_P001 | 0.957 |

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| PUZ38452 | Sspon.01G | KQK88521 | TKV93117 | EER91427 | Zm00001eb044660_P002 | 0.788 |
| PUZ60992 | genblast_C | KQL10331 | TKW20995 | EER88261 | Zm00001eb280900_P005 | 0.941 |
| PUZ68256 | Sspon.02G | KQL22226 | TKW30126 | OQU88335 | Zm00001eb118020_P001 | 0.935 |
| PUZ45559 | Sspon.06G | KQK95475 | TKW01921 | EES10144 | Zm00001eb048670_P001 | 0.674 |
| PUZ73009 | genblast_C | KQL26756 | TKW35943 | genblast_C | Zm00001eb327950_P001 | 0.963 |
| PUZ72669 | Sspon.02G | KQL26424 | TKW35534 | genblast_C | Zm00001eb325590_P002 | 0.906 |
| PUZ64270 | Sspon.07G | KQL13810 | TKW25271 | EES17812 | Zm00001eb347000_P002 | 0.950 |
| PUZ54182 | genblast_C | KQL07527 | TKW17487 | KXG33634 | Zm00001eb149330_P001 | 0.917 |

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| PUZ40896 | genblast_C | KQK90653 | TKV95848 | KXG39270 | Zm00001eb018460_P001 | 0.938 |
| genblast_C | Sspon.07G | KQL14850 | TKW26494 | KXG22282 | Zm00001eb291950_P001 | 0.944 |
| PUZ57646 | genblast_C | KQL04058 | TKW12988 | OQU86527 | Zm00001eb334360_P005 | 0.964 |

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| PUZ45698 | genblast_C | KQK95708 | genblast_C | KXG29049 | Zm00001eb165510_P005 | 0.837 |
| PUZ73175 | genblast_C | KQL26921 | TKW36166 | EER99798 | genblast_Os07t0643700-01_Ze | |
| PUZ68535 | genblast_C | KQL22575 | TKW30613 | EER95909 | Zm00001eb117130_P001 | 0.936 |

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| PUZ69578 | Sspon.02G | genblast_C | TKW31883 | OQU88998 | Zm00001eb306930_P001 | 0.935 |
| PUZ52803 | Sspon.03G | KQL08797 | TKW19079 | EES02146 | Zm00001eb362210_P001 | 0.976 |
| PUZ57532 | Sspon.03G | KQL03958 | TKW12862 | KXG32163 | Zm00001eb127240_P001 | 0.911 |
| PUZ37433 | genblast_C | KQK87534 | TKV91841 | genblast_C | genblast_Os03t0703300-01_Ze | |

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| PUZ37392 | Sspon.02G | KQK87472 | TKV91755 | genblast_C | Zm00001eb133880_P001 | 0.895 |
| genblast_Z | Sspon.01G | KQL03604 | TKW12413 | KXG40414 | Zm00001eb000400_P001 | 0.798 |
| PUZ61247 | genblast_C | KQL10554 | TKW21328 | EER89737 | Zm00001eb382160_P001 | 0.882 |
| PUZ41430 | genblast_C | KQK91224 | TKV96563 | EER92386 | Zm00001eb014450_P001 | 0.945 |
| PUZ38268 | Sspon.01G | KQK88349 | TKV92878 | EER93935 | Zm00001eb220120_P001 | 0.968 |
| PUZ75026 | Sspon.04G | KQL27840 | TKW36912 | EES06611 | Zm00001eb238060_P001 | 0.953 |
| PUZ45377 | Sspon.01G | KQK95151 | TKW01447 | KXG37654 | Zm00001eb167580_P001 | 0.873 |

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| PUZ36421 | Sspon.01GKQK86499 | TKV90599 | EER90659 | Zm00001eb212180_P001 | 0.919 |
| PUZ73034 | Sspon.02GKQL26779 | TKW35989 | KXG36758 | Zm00001eb109810_P001 | 0.856 |
| PUZ38475 | Sspon.01GKQK88544 | TKV93151 | EER94019 | Zm00001eb044860_P002 | 0.972 |
| PUZ41240 | Sspon.01GKQK91028 | TKV96284 | OQU92657 | Zm00001eb015850_P001 | 0.878 |

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| PUZ73346 | Sspon.02GKQL27153 | genblast_C | EER99903 | Zm00001eb330500_P001 | 0.924 |

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| PUZ36988 | genblast_C | KQK87060 | TKV91307 | EER90862 | Zm00001eb057540_P001 | 0.958 |
| PUZ59611 | genblast_C | KQL11063 | TKW21946 | KXG20556 | Zm00001eb389680_P001 | 0.978 |
| PUZ40627 | genblast_C | KQK90381 | TKV95500 | EER94682 | Zm00001eb020180_P001 | 0.951 |

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| PUZ43702 | genblast_C | KQK93563 | TKW07785 | EES15662 | Zm00001eb196670_P002 | 0.877 |

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| PUZ42468 | genblast_C | KQK92214 | TKV97763 | OQU93095 | Zm00001eb006630_P001 | 0.956 |

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| PUZ43284 | Sspon.01GKQK93061 | TKV98731 | EER93022 | Zm00001eb404370_P001 | 0.973 |
| PUZ42163 | Sspon.01GKQK91941 | TKV97426 | EER92637 | Zm00001eb008770_P001 | 0.924 |
| PUZ70434 | genblast_CKQL24233 | genblast_C | KXG35475 | genblast_Os09t0359700-00_Ze | |
| PUZ41116 | Sspon.01GKQK90910 | TKV96142 | EER92281 | Zm00001eb016660_P001 | 0.902 |

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| PUZ76894 | Sspon.04Ggenblast_C | TKW40721 | EES05783 | Zm00001eb249520_P001 | 0.879 |
| PUZ49740 | Sspon.06GKQL00157 | TKW08042 | KXG24164 | Zm00001eb198810_P002 | 0.956 |
| PUZ71295 | Sspon.02GKQL25076 | TKW33848 | EER99099 | Zm00001eb101980_P003 | 0.906 |

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| PUZ62636 | Sspon.05GKQL00039 | TKW07976 | OQU82902 | Zm00001eb092480_P001 | 0.879 |
| PUZ46919 | Sspon.05GKQK97033 | TKW04089 | EES10681 | Zm00001eb084850_P004 | 0.934 |
| PUZ60494 | Sspon.08GKQL10803 | TKW21652 | EER89845 | Zm00001eb382790_P001 | 0.900 |
| PUZ59238 | Sspon.08GKQL11750 | TKW22836 | KXG20779 | Zm00001eb227030_P003 | 0.960 |
| PUZ47218 | Sspon.04GKQK97331 | TKW04477 | genblast_C | genblast_Os04t0437600-01_Zea | |
| PUZ51716 | Sspon.06GKQL02018 | TKW10561 | KXG25255 | Zm00001eb040870_P001 | 0.979 |
| PUZ43435 | Sspon.07GKQK93378 | TKV99034 | EES16622 | Zm00001eb406300_P001 | 0.725 |
| PUZ61725 | Sspon.05GKQL28716 | TKW37972 | OQU81534 | Zm00001eb276210_P001 | 0.829 |
| PUZ36344 | Sspon.01GKQK86444 | TKV90506 | OQU90727 | Zm00001eb211790_P001 | 0.878 |
| PUZ58851 | genblast_CKQL03220 | TKW11949 | KXG31475 | Zm00001eb119100_P001 | 0.922 |
| PUZ73809 | Sspon.04GKQL28964 | TKW38305 | KXG29333 | Zm00001eb208500_P004 | 0.943 |
| PUZ61450 | Sspon.08GKQL10026 | TKW20580 | genblast_Z | Zm00001eb372360_P001 | 0.952 |
| PUZ76031 | genblast_CKQL29897 | TKW39654 | KXG30376 | Zm00001eb243400_P003 | 0.953 |
| PUZ74252 | Sspon.04GKQL28567 | TKW37807 | EES06337 | Zm00001eb233000_P005 | 0.986 |
| PUZ75963 | Sspon.04Ggenblast_C | TKW39545 | EES05194 | Zm00001eb242950_P001 | 0.959 |
| PUZ58464 | Sspon.03GKQL04799 | TKW13947 | EES02317 | Zm00001eb121210_P002 | 0.834 |
| PUZ60276 | Sspon.08GKQL11721 | TKW22798 | KXG20197 | Zm00001eb384240_P002 | 0.789 |
| PUZ58059 | Sspon.03GKQL04407 | TKW13444 | EES02482 | Zm00001eb335930_P001 | 0.986 |
| PUZ67664 | Sspon.02GKQL16988 | TKW29313 | OQU79454 | Zm00001eb030400_P001 | 0.671 |
| PUZ50567 | Sspon.06GKQL00390 | TKW08355 | KXG24716 | Zm00001eb171060_P002 | 0.961 |
| PUZ36529 | Sspon.01GKQL26615 | TKV90748 | EER90714 | Zm00001eb212700_P001 | 0.911 |
| PUZ59198 | genblast_CKQL12114 | TKW23296 | KXG20804 | genblast_Os06t0704800-00Zm0 | |
| PUZ62094 | Sspon.08GKQL09660 | TKW20102 | OQU75871 | Zm00001eb271280_P002 | 0.869 |
| PUZ74232 | Sspon.04GKQL28585 | TKW37820 | OQU84433 | Zm00001eb207400_P001 | 0.864 |

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| PUZ59075 | Sspon.08G | KQL12248 | TKW23474 | KXG20897 | Zm00001eb228140_P001 | 0.955 |
| PUZ73436 | Sspon.02G | KQL27073 | TKW36361 | EER99873 | Zm00001eb110960_P001 | 0.841 |
| PUZ64153 | genblast_C | KQK99291 | TKW07037 | OQU77483 | Zm00001eb282550_P001 | 0.915 |
| PUZ54291 | Sspon.03G | KQL07415 | TKW17349 | KXG33583 | Zm00001eb150140_P001 | 0.964 |
| PUZ54586 | Sspon.03G | KQL07156 | TKW17001 | EES03683 | Zm00001eb152000_P001 | 0.935 |
| PUZ36915 | Sspon.01G | KQK86982 | TKV91219 | EER90842 | Zm00001eb058150_P001 | 0.974 |
| PUZ36227 | Sspon.01G | KQK86329 | TKV90367 | EER90577 | Zm00001eb063520_P001 | 0.915 |
| PUZ42459 | Sspon.01G | KQK92206 | TKV97752 | EER92730 | Zm00001eb006700_P001 | 0.875 |
| PUZ72179 | genblast_C | KQL25930 | TKW34904 | EER99428 | Zm00001eb322340_P001 | 0.984 |
| PUZ41098 | Sspon.02G | KQK90890 | TKV96112 | OQU92600 | Zm00001eb394760_P002 | 0.979 |

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| PUZ53201 | genblast_C | KQL08405 | TKW18587 | EES04124 | Zm00001eb142830_P002 | 0.894 |

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| PUZ53526 | Sspon.03G | KQL08120 | TKW18226 | EES01898 | Zm00001eb365750_P001 | 0.922 |
| PUZ56266 | genblast_C | genblast_C | TKW14912 | KXG32703 | Zm00001eb356500_P001 | 0.929 |
| PUZ44479 | Sspon.01G | genblast_Z | TKW00395 | OQU90647 | genblast_Zm00001eb064040_P | |
| PUZ36932 | Sspon.01G | KQK87002 | TKV91244 | EER93415 | Zm00001eb214440_P001 | 0.836 |
| PUZ57593 | genblast_C | KQL04013 | TKW12928 | OQU86555 | Zm00001eb126950_P001 | 0.933 |
| PUZ74163 | Sspon.04G | KQL28645 | TKW37886 | EES04558 | Zm00001eb207680_P001 | 0.976 |

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| PUZ53523 | Sspon.03G | KQL08121 | TKW18228 | KXG33892 | Zm00001eb365740_P002 | 0.954 |
| PUZ53199 | genblast_C | genblast_C | TKW23510 | EES09166 | Zm00001eb195760_P001 | 0.874 |
| PUZ76228 | Sspon.04G | KQL30150 | TKW39869 | OQU85192 | Zm00001eb182870_P001 | 0.973 |
| PUZ72554 | genblast_C | KQL26305 | TKW35404 | KXG36510 | Zm00001eb107240_P001 | 0.684 |
| PUZ72940 | Sspon.02G | KQL26696 | TKW35864 | EER97550 | Zm00001eb109480_P001 | 0.828 |

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| PUZ65995 | Sspon.07G | KQL15483 | TKW27302 | EES19526 | Zm00001eb288060_P001 | 0.934 |
| genblast_C | Sspon.07G | KQL11607 | TKW22650 | genblast_C | Zm00001eb345910_P001 | 0.864 |
| PUZ49266 | Sspon.05G | KQL12861 | TKW23988 | EES12999 | Zm00001eb432460_P001 | 0.873 |
| PUZ42922 | Sspon.01G | KQK92647 | TKV98293 | OQU93266 | Zm00001eb003210_P001 | 0.850 |

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| PUZ44951 | Sspon.06G | KQK94671 | TKW00793 | EES09768 | Zm00001eb170080_P001 | 0.906 |
| PUZ41415 | genblast_C | KQK91210 | TKV96537 | EER92376 | Zm00001eb014560_P001 | 0.912 |
| PUZ52451 | Sspon.06G | KQL02705 | TKW11448 | EES14167 | Zm00001eb198200_P001 | 0.943 |
| PUZ56436 | Sspon.03G | KQL05342 | TKW14707 | EES03984 | Zm00001eb366180_P001 | 0.913 |
| PUZ46094 | Sspon.03G | genblast_C | TKW22426 | EES01923 | Zm00001eb144250_P001 | 0.952 |
| PUZ36189 | Sspon.01G | KQK86289 | TKV90325 | EER93141 | Zm00001eb063730_P001 | 0.940 |

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| PUZ52234 | Sspon.06G | KQL02490 | TKW11189 | OQU80890 | Zm00001eb035470_P001 | 0.794 |
| PUZ40431 | Sspon.01G | KQK90220 | TKV95286 | EER92040 | Zm00001eb021530_P001 | 0.968 |
| PUZ64073 | Sspon.06G | KQL13030 | TKW24206 | EES15373 | Zm00001eb267900_P002 | 0.992 |
| PUZ48749 | Sspon.05G | KQK98770 | TKW06361 | EES12792 | Zm00001eb071770_P002 | 0.970 |
| PUZ68882 | Sspon.02G | KQL22936 | TKW31051 | genblast_C | Zm00001eb160900_P001 | 0.669 |
| PUZ66947 | Sspon.02G | KQL14142 | TKW25659 | EER98384 | Zm00001eb305490_P002 | 0.985 |
| PUZ53370 | Sspon.03G | KQL08248 | TKW18389 | EES04078 | Zm00001eb143910_P001 | 0.958 |
| PUZ51631 | genblast_C | KQL01949 | TKW10475 | KXG25228 | Zm00001eb041280_P002 | 0.932 |
| PUZ71213 | Sspon.02G | KQL24977 | TKW33729 | EER96947 | Zm00001eb316280_P002 | 0.965 |

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| PUZ48371 | genblast_C | KQK98402 | TKW05890 | EES12628 | Zm00001eb074420_P001 | 0.870 |
| PUZ55112 | genblast_Z | KQL06668 | TKW16353 | EES01359 | Zm00001eb361310_P002 | 0.986 |
| PUZ59970 | Sspon.08G | KQL11449 | TKW22433 | KXG20349 | Zm00001eb388430_P001 | 0.787 |
| PUZ47520 | genblast_C | KQK97607 | TKW04828 | EES12305 | Zm00001eb424400_P001 | 0.965 |

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| PUZ77896 | Sspon.04G | KQL31743 | TKW41850 | OQU85816 | Zm00001eb256650_P006 | 0.882 |
| PUZ77430 | Sspon.05G | KQL31301 | TKW41347 | EES11875 | Zm00001eb086650_P001 | 0.909 |
| PUZ69327 | genblast_C | KQL23300 | TKW31594 | EER98389 | Zm00001eb094690_P002 | 0.885 |

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| PUZ38450 | Sspon.01G | KQK88519 | TKV93116 | EER94008 | Zm00001eb044650_P001 | 0.977 |
| PUZ45282 | Sspon.06G | KQK95020 | TKW01270 | KXG28744 | Zm00001eb114280_P001 | 0.873 |
| PUZ67969 | genblast_C | KQL17197 | TKW29568 | KXG24044 | Zm00001eb032230_P002 | 0.986 |
| PUZ72942 | genblast_C | KQL26698 | TKW35867 | EER99712 | Zm00001eb109500_P002 | 0.981 |
| PUZ54432 | Sspon.03G | KQL07275 | TKW17166 | EES03734 | genblast_Os01t0786500-00_Zea | |
| PUZ37675 | Sspon.01G | KQK87828 | TKV92168 | EER93702 | Zm00001eb217890_P001 | 0.784 |

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| PUZ63942 | Sspon.07G | KQL13277 | TKW24528 | KXG21255 | Zm00001eb417610_P002 | 0.810 |

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| PUZ49928 | Sspon.06G | KQL01009 | TKW09252 | OQU79812 | Zm00001eb173490_P001 | 0.994 |

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| PUZ63243 | Sspon.07G | KQK99377 | TKW07136 | EES15803 | Zm00001eb264210_P001 | 0.953 |

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| PUZ65315 | Sspon.02G | genblast_C | TKW12100 | KXG31529 | Zm00001eb338920_P001 | 0.893 |
| PUZ50927 | Sspon.07G | KQL01287 | TKW09611 | OQU77706 | Zm00001eb346280_P002 | 0.859 |
| PUZ74939 | genblast_C | KQL29127 | TKW38512 | KXG30004 | Zm00001eb237510_P002 | 0.945 |

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| PUZ58174 | Sspon.06G | KQL04530 | TKW13582 | KXG32310 | Zm00001eb167270_P001 | 0.710 |
| PUZ59603 | Sspon.01G | genblast_C | TKW21936 | EER93311 | Zm00001eb060430_P001 | 0.922 |

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| PUZ56980 | Sspon.03G | genblast_C | TKW12189 | EES00658 | Zm00001eb130500_P001 | 0.957 |
| genblast_C | Sspon.02G | genblast_C | genblast_C | KXG35300 | Zm00001eb309060_P005 | 0.903 |
| PUZ69707 | Sspon.02G | KQL23665 | TKW32023 | KXG35152 | Zm00001eb307550_P001 | 0.855 |
| PUZ49995 | Sspon.06G | KQL00945 | TKW09152 | OQU79832 | Zm00001eb261760_P001 | 0.855 |
| PUZ41243 | genblast_C | KQL22637 | TKV96294 | KXG36093 | genblast_Os09t0326850-01_Ze |  |
| PUZ76875 | Sspon.04G | KQL30782 | TKW40696 | EES05789 | Zm00001eb249400_P001 | 0.826 |
| PUZ61199 | genblast_C | KQL10511 | TKW21270 | KXG37100 | Zm00001eb064820_P001 | 0.950 |
| PUZ58803 | Sspon.03G | KQL03269 | TKW12004 | KXG31498 | Zm00001eb339200_P001 | 0.794 |
| PUZ51532 | Sspon.06G | KQL01885 | TKW10389 | genblast_C | genblast_Os08t0430000-01_Ze |  |
| PUZ47373 | Sspon.05G | KQK97468 | TKW04652 | KXG26410 | Zm00001eb081530_P001 | 0.970 |
| PUZ47374 | Sspon.05G | KQK97470 | TKW04660 | EES10893 | Zm00001eb081510_P002 | 0.900 |
| PUZ45057 | Sspon.06G | KQK94788 | TKW00999 | OQU83559 | Zm00001eb198120_P002 | 0.958 |
| PUZ78208 | Sspon.04G | KQL32075 | TKW42227 | EES07746 | Zm00001eb191530_P001 | 0.927 |
| PUZ51297 | Sspon.06G | KQL01562 | TKW09969 | EES14943 | Zm00001eb042470_P002 | 0.899 |

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| PUZ67083 | Sspon.02G | KQL16415 | genblast_C | OQU79047 | Zm00001eb408950_P001 | 0.907 |
| PUZ70005 | Sspon.07G | KQL23757 | TKW32151 | EES19735 | genblast_Os09t0115900-01_Ze |  |
| PUZ67285 | Sspon.02G | KQL16767 | TKW28984 | KXG23585 | Zm00001eb137780_P002 | 0.887 |
| PUZ76751 | Sspon.04G | KQL30668 | TKW40552 | EES07211 | Zm00001eb248510_P001 | 0.800 |

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| PUZ46628 | Sspon.07G | KQL30939 | TKW40894 | EES19977 | Zm00001eb296470_P001 | 0.975 |
| PUZ77519 | Sspon.04G | KQL31434 | TKW41487 | EES05563 | Zm00001eb253960_P001 | 0.931 |
| PUZ71541 | Sspon.02G | KQL25320 | TKW34137 | EER99183 | Zm00001eb318730_P003 | 0.911 |
| PUZ78309 | Sspon.04G | KQL32170 | TKW42330 | EES06036 | Zm00001eb191090_P001 | 0.980 |
| PUZ72715 | genblast_C | KQK85157 | TKV94926 | OQU9017 | Zm00001eb325950_P001 | 0.823 |
| PUZ61762 | Sspon.08G | KQL09885 | TKW20401 | OQU7602 | Zm00001eb373670_P001 | 0.837 |
| PUZ54622 | Sspon.03G | KQL07124 | TKW16970 | KXG33445 | Zm00001eb370260_P001 | 0.846 |
| PUZ65037 | Sspon.07G | KQL14600 | TKW26198 | EES18564 | Zm00001eb293150_P001 | 0.929 |

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| PUZ55748 | Sspon.03GKQL05939 | TKW15468 | EES03302 | Zm00001eb358500_P001 | 0.955 |
| PUZ36566 | Sspon.01GKQK86649 | TKV90807 | EER90731 | Zm00001eb212870_P001 | 0.944 |
| PUZ57998 | Sspon.02GKQL23517 | TKW31821 | EES00329 | Zm00001eb124520_P001 | 0.932 |
| PUZ52236 | Sspon.06GKQL02493 | TKW11198 | OQU80887 | Zm00001eb035500_P002 | 0.908 |

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| PUZ77872 | Sspon.04GKQL31726 | TKW41827 | KXG31193 | Zm00001eb256470_P002 | 0.965 |
| PUZ44592 | Sspon.02GKQL22236 | TKW30156 | KXG21358 | Zm00001eb352290_P001 | 0.665 |
| PUZ77434 | Sspon.04GKQL31304 | TKW41350 | KXG30849 | Zm00001eb253240_P001 | 0.866 |
| PUZ62682 | genblast_CKQK99987 | TKV99094 | EES15526 | Zm00001eb163290_P001 | 0.964 |

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| PUZ52384 | genblast_CKQL02649 | TKW11391 | EES15309 | Zm00001eb036590_P001 | 0.978 |

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| PUZ61256 | genblast_CKQL06885 | TKW21341 | OQU76395 | Zm00001eb153850_P005 | 0.672 |
| genblast_C | Sspon.02GKQL26018 | TKW35016 | genblast_C | Zm00001eb322760_P002 | 0.727 |
| PUZ40472 | Sspon.01GKQK90269 | TKV95346 | EER92053 | Zm00001eb021170_P001 | 0.864 |

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| PUZ38888 | Sspon.01GKQK88915 | TKV93644 | OQU91719 | Zm00001eb047140_P003 | 0.870 |
| PUZ66360 | Sspon.07GKQL15840 | TKW27762 | OQU77852 | Zm00001eb346560_P001 | 0.904 |
| PUZ48940 | Sspon.05GKQK98956 | TKW06617 | OQU82346 | Zm00001eb070490_P002 | 0.877 |

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|---|---|---|---|---|---|---|
| PUZ52929 | genblast_C | KQL08684 | TKW18938 | OQU83034 | Zm00001eb140520_P001 | 0.911 |
| PUZ46785 | Sspon.05G | KQK96901 | TKW03922 | OQU81360 | Zm00001eb085760_P005 | 0.964 |
| PUZ39925 | Sspon.01G | KQK89751 | TKV94717 | OQU92064 | Zm00001eb024900_P002 | 0.943 |
| PUZ44461 | Sspon.07G | KQK94376 | TKW00406 | EES16654 | Zm00001eb406800_P001 | 0.990 |
| PUZ52719 | genblast_C | KQL03006 | TKW11805 | OQU80699 | Zm00001eb038920_P001 | 0.958 |
| PUZ43392 | Sspon.05G | KQL00004 | TKW07938 | EES15509 | Zm00001eb195030_P001 | 0.961 |
| PUZ52517 | genblast_C | KQL02786 | TKW11590 | EES14143 | genblast_Os08t0542200-01_Zea | |
| PUZ77952 | genblast_C | KQL31819 | TKW41937 | EES05910 | Zm00001eb192910_P004 | 0.972 |
| PUZ49331 | Sspon.05G | KQL12906 | TKW24045 | OQU82499 | Zm00001eb067460_P003 | 0.895 |
| PUZ49271 | Sspon.05G | KQL12865 | TKW23992 | EES11579 | Zm00001eb067740_P001 | 0.880 |
| PUZ53390 | Sspon.03G | KQL08235 | TKW18371 | EES01933 | Zm00001eb144010_P001 | 0.995 |
| PUZ41835 | Sspon.01G | KQK91607 | TKV96978 | EER95145 | Zm00001eb398220_P001 | 0.896 |
| PUZ49404 | Sspon.05G | KQL12961 | TKW24120 | EES11614 | Zm00001eb433150_P001 | 0.878 |
| PUZ37060 | genblast_C | KQK87133 | TKV91391 | EER90883 | Zm00001eb215010_P001 | 0.807 |
| PUZ55455 | Sspon.03G | KQL06313 | TKW15936 | EES03400 | Zm00001eb359800_P001 | 0.945 |
| PUZ75920 | genblast_C | KQL29878 | TKW39489 | KXG30331 | Zm00001eb242720_P001 | 0.980 |

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| PUZ65401 | Sspon.07G | KQL14896 | TKW26556 | KXG22258 | Zm00001eb291590_P003 | 0.959 |
| PUZ72436 | Sspon.07G | KQL26170 | TKW35239 | EER97364 | Zm00001eb323800_P001 | 0.924 |
| PUZ70779 | genblast_C | KQL24560 | TKW33235 | EER98931 | Zm00001eb313500_P001 | 0.944 |
| PUZ60346 | Sspon.05G | KQL10951 | TKW21825 | EER89907 | Zm00001eb384930_P001 | 0.971 |
| PUZ39053 | Sspon.01G | KQK89179 | TKV93958 | EER94252 | Zm00001eb048140_P001 | 0.933 |

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|---|---|---|---|---|---|---|
| PUZ47542 | Sspon.05G | KQK97623 | TKW04851 | EES10963 | Zm00001eb080370_P001 | 0.978 |
| PUZ70659 | Sspon.02G | KQL24441 | TKW33075 | EER96715 | Zm00001eb312330_P001 | 0.965 |

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| PUZ55867 | Sspon.03G | KQL05831 | TKW15322 | OQU87155 | Zm00001eb161870_P001 | 0.956 |
| PUZ74107 | Sspon.06G | KQL01024 | TKW37931 | KXG25421 | Zm00001eb039870_P001 | 0.873 |
| PUZ46694 | Sspon.05G | KQK96401 | TKW03207 | EES11890 | Zm00001eb086830_P002 | 0.955 |
| PUZ49943 | Sspon.06G | KQL00997 | TKW09239 | EES14525 | Zm00001eb416650_P001 | 0.797 |
| PUZ55410 | Sspon.03G | KQL06357 | TKW15989 | EES03419 | Zm00001eb157130_P001 | 0.914 |

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|---|---|---|---|---|---|---|
| PUZ67679 | Sspon.02G | KQL16994 | TKW29324 | EES17296 | Zm00001eb135040_P001 | 0.663 |
| PUZ38445 | Sspon.01G | genblast_C | TKV93113 | KXG38246 | Zm00001eb220920_P002 | 0.959 |
| PUZ55545 | Sspon.03G | KQL06149 | TKW15737 | genblast_C | Zm00001eb158050_P004 | 0.871 |
| PUZ47914 | Sspon.07G | KQK97995 | TKW05321 | OQU81911 | Zm00001eb077990_P001 | 0.957 |
| PUZ78234 | Sspon.04G | KQL32091 | TKW42247 | KXG31351 | Zm00001eb258860_P003 | 0.937 |
| PUZ55272 | Sspon.03G | KQL06500 | TKW16152 | KXG33163 | Zm00001eb156230_P002 | 0.745 |
| PUZ42867 | Sspon.01G | KQK92605 | TKV98243 | EER95503 | Zm00001eb402960_P002 | 0.951 |

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| PUZ73459 | genblast_C | KQL27188 | TKW36525 | EER99917 | Zm00001eb330710_P001 | 0.779 |

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| PUZ53237 | Sspon.03G | KQL08368 | TKW18549 | EES01979 | Zm00001eb143110_P001 | 0.829 |
| PUZ62625 | Sspon.05G | KQK93224 | TKV98825 | OQU78623 | Zm00001eb163070_P003 | 0.876 |
| PUZ77915 | Sspon.04G | KQL31769 | TKW41877 | EES05891 | Zm00001eb256950_P001 | 0.915 |
| PUZ78419 | Sspon.01G | KQL32270 | TKW42450 | EES07825 | Zm00001eb190560_P001 | 0.832 |
| PUZ59691 | Sspon.04G | KQL11132 | TKW22032 | EER90145 | Zm00001eb389540_P003 | 0.939 |
| PUZ38311 | Sspon.01G | KQK88392 | TKV92937 | KXG38195 | Zm00001eb043750_P002 | 0.987 |
| PUZ48322 | Sspon.05G | KQK98364 | TKW05829 | OQU82093 | Zm00001eb429760_P001 | 0.898 |

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| PUZ68695 | genblast_C | KQL22730 | TKW30810 | OQU88577 | Zm00001eb301620_P001 | 0.977 |
| PUZ76370 | genblast_C | KQL30298 | TKW40071 | EES07093 | Zm00001eb246080_P001 | 0.995 |
| PUZ70667 | Sspon.02G | KQL24448 | TKW33084 | EER96723 | Zm00001eb099370_P001 | 0.904 |
| PUZ72409 | Sspon.02G | KQL26167 | TKW35200 | OQU90065 | Zm00001eb106620_P001 | 0.948 |
| PUZ58886 | Sspon.03G | KQL03187 | TKW11912 | EES02165 | Zm00001eb064830_P001 | 0.993 |
| PUZ76281 | Sspon.04G | KQL30208 | TKW39947 | EES07042 | Zm00001eb245220_P001 | 0.923 |
| PUZ44529 | Sspon.08G | KQL05379 | TKW14756 | KXG27747 | Zm00001eb250820_P001 | 0.709 |
| PUZ47481 | Sspon.05G | KQK97568 | TKW04787 | EES10941 | Zm00001eb080790_P001 | 0.706 |
| PUZ47289 | Sspon.05G | KQK97399 | TKW04547 | KXG26379 | Zm00001eb423130_P001 | 0.931 |
| PUZ78310 | Sspon.04G | KQL32172 | TKW42331 | KXG31390 | Zm00001eb191080_P001 | 0.662 |
| PUZ58997 | Sspon.08G | KQL12318 | TKW23567 | OQU77168 | genblast_Os06t0728500-01_Zea |  |
| PUZ73634 | genblast_C | KQL27713 | TKW36746 | EES06101 | Zm00001eb229360_P002 | 0.919 |
| PUZ43507 | Sspon.05G | KQK99730 | TKW07594 | EES07908 | Zm00001eb093650_P001 | 0.698 |
| PUZ48082 | genblast_C | KQK98142 | TKW05511 | EES12528 | Zm00001eb077010_P005 | 0.956 |
| genblast_C | Sspon.05G | KQK99089 | TKW06794 | EES11501 | Zm00001eb069410_P003 | 0.894 |
| PUZ36485 | genblast_C | KQK86549 | TKV90679 | KXG37311 | Zm00001eb061570_P001 | 0.993 |
| PUZ77285 | Sspon.04G | genblast_C | TKW41165 | EES07392 | Zm00001eb252230_P001 | 0.841 |
| PUZ51412 | Sspon.06G | KQL01764 | TKW10248 | EES13821 | Zm00001eb178960_P005 | 0.847 |
| PUZ51817 | Sspon.06G | KQL02113 | TKW10687 | OQU80613 | genblast_Os08t0464400-01 | Zm0 |
| PUZ74765 | genblast_C | KQL28037 | TKW37150 | KXG29840 | Zm00001eb205030_P001 | 0.971 |
| PUZ57296 | genblast_C | KQL03710 | TKW12570 | EES00556 | Zm00001eb332980_P001 | 0.918 |

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| PUZ41740 | Sspon.01G | KQK91567 | TKV96938 | EER92495 | Zm00001eb012000_P001 | 0.974 |
| PUZ65090 | Sspon.07G | KQL14651 | TKW26250 | EES18546 | Zm00001eb293460_P001 | 0.967 |
| PUZ74749 | Sspon.04G | KQL28050 | TKW37169 | EES04781 | Zm00001eb239750_P001 | 0.889 |
| PUZ70791 | Sspon.02G | KQL24579 | TKW33263 | EER98942 | Zm00001eb313580_P002 | 0.903 |
| PUZ47604 | Sspon.05G | KQK97686 | TKW04932 | KXG26529 | Zm00001eb079910_P001 | 0.894 |
| PUZ62451 | Sspon.08G | KQL09039 | TKW19324 | EER89092 | Zm00001eb269160_P001 | 0.972 |
| PUZ44137 | Sspon.05G | KQK94064 | TKV99964 | OQU82593 | Zm00001eb434100_P001 | 0.952 |
| PUZ54694 | Sspon.03G | KQL07065 | TKW16886 | KXG33413 | Zm00001eb152520_P001 | 0.878 |
| PUZ74064 | Sspon.04G | KQL28735 | TKW37996 | EES04526 | Zm00001eb208000_P001 | 0.835 |

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| PUZ68376 | Sspon.02G | KQL22402 | TKW30392 | EER92773 | Zm00001eb005570_P001 | 0.913 |
| PUZ52332 | Sspon.06G | KQL02597 | TKW11333 | EES14212 | Zm00001eb036160_P001 | 0.945 |
| PUZ66489 | Sspon.07G | KQL15934 | TKW27874 | KXG21749 | Zm00001eb286460_P003 | 0.914 |
| PUZ75862 | Sspon.04G | KQL29826 | TKW39426 | KXG30309 | Zm00001eb180680_P004 | 0.989 |

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| PUZ60390 | Sspon.01G | genblast_C | TKW21755 | OQU92760 | Zm00001eb013670_P001 | 0.888 |
| PUZ45367 | Sspon.06G | KQK95138 | TKW01432 | KXG28808 | Zm00001eb167670_P001 | 0.764 |
| PUZ57297 | Sspon.03G | KQL03711 | TKW12571 | OQU86683 | Zm00001eb128620_P001 | 0.973 |
| PUZ45837 | Sspon.06G | KQK95862 | TKW02527 | EES08977 | Zm00001eb165040_P001 | 0.870 |
| PUZ68861 | genblast_C | KQL22914 | TKW31030 | EER96032 | Zm00001eb302760_P001 | 0.805 |
| PUZ65610 | Sspon.07G | KQL15128 | TKW26851 | KXG22177 | Zm00001eb351670_P003 | 0.969 |
| PUZ72525 | genblast_C | KQL26281 | TKW35374 | EER99561 | Zm00001eb324560_P001 | 0.921 |
| PUZ64021 | Sspon.07G | KQL13078 | TKW24264 | EES19016 | Zm00001eb354310_P002 | 0.888 |
| PUZ69285 | Sspon.02G | KQL00788 | TKW08953 | OQU88866 | Zm00001eb305010_P001 | 0.659 |
| PUZ60263 | Sspon.07G | KQL11707 | TKW22778 | KXG22891 | Zm00001eb405660_P001 | 0.968 |

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| PUZ41215 | Sspon.01G | KQK90998 | TKV96248 | EER94905 | Zm00001eb395130_P001 | 0.800 |

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| PUZ41321 | Sspon.01G | KQK91100 | TKV96396 | EER94940 | Zm00001eb015320_P003 | 0.899 |

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| PUZ42173 | genblast_C | KQK91951 | TKV97435 | OQU93000 | Zm00001eb400120_P001 | 0.922 |

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| PUZ58687 | Sspon.03G | KQL04972 | TKW14180 | KXG31555 | Zm00001eb119900_P001 | 0.834 |
| PUZ52055 | Sspon.06G | KQL02348 | TKW11000 | EES14309 | Zm00001eb199500_P001 | 0.659 |
| PUZ68259 | Sspon.02G | KQL22228 | TKW30127 | EER97891 | genblast_Os07t0118900-01 | Zm0 |
| PUZ58004 | Sspon.03G | KQL04365 | TKW13393 | OQU86333 | Zm00001eb124490_P001 | 0.883 |

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| PUZ75790 | Sspon.04G | KQL29739 | TKW39301 | EES05115 | Zm00001eb241620_P001 | 0.968 |

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| PUZ49503 | Sspon.05G | KQL12789 | TKW23899 | EES13099 | Zm00001eb066260_P001 | 0.960 |
| PUZ53870 | genblast_C | KQL07813 | TKW17823 | KXG33728 | Zm00001eb147340_P002 | 0.949 |
| PUZ55120 | Sspon.03G | KQL06660 | TKW16344 | KXG33227 | Zm00001eb361260_P001 | 0.942 |
| PUZ38295 | Sspon.01G | KQK88378 | TKV92921 | EER93943 | Zm00001eb043630_P001 | 0.954 |
| PUZ41475 | Sspon.01G | KQK91269 | TKV96617 | EER92402 | Zm00001eb396680_P002 | 0.871 |
| PUZ43303 | Sspon.01G | KQK93079 | TKV98752 | EER95699 | Zm00001eb404430_P006 | 0.884 |
| PUZ45712 | genblast_C | KQK95728 | TKW02247 | EES08933 | Zm00001eb115800_P001 | 0.863 |
| PUZ55754 | Sspon.05G | KQL05931 | TKW15454 | OQU82448 | Zm00001eb432120_P001 | 0.726 |
| PUZ41221 | Sspon.01G | KQK91005 | TKV96256 | EER94909 | Zm00001eb395190_P001 | 0.769 |

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| PUZ37697 | Sspon.01G | KQK87843 | TKV92186 | EER93717 | Zm00001eb218120_P001 | 0.985 |
| PUZ66350 | Sspon.03G | KQL15823 | TKW27742 | EES18089 | Zm00001eb130690_P001 | 0.698 |
| PUZ59027 | Sspon.08G | KQL12284 | TKW23520 | KXG20919 | Zm00001eb228410_P001 | 0.777 |
| PUZ74558 | Sspon.04G | genblast_C | TKW37417 | EES06466 | Zm00001eb205830_P002 | 0.949 |

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| PUZ71562 | Sspon.07G | KQL25345 | TKW34163 | EER97052 | Zm00001eb102900_P001 | 0.915 |
| PUZ70488 | Sspon.02G | KQL24269 | TKW32864 | EER96652 | Zm00001eb311150_P001 | 0.899 |
| PUZ76297 | Sspon.04G | KQL30220 | TKW39969 | EES07046 | Zm00001eb245390_P002 | 0.712 |
| PUZ73344 | Sspon.02G | KQL27160 | TKW36491 | EER97724 | Zm00001eb330520_P001 | 0.853 |
| PUZ76623 | Sspon.04G | KQL30554 | TKW40398 | EES07168 | Zm00001eb185100_P001 | 0.952 |

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| PUZ54755 | Sspon.03G | genblast_C | TKW16814 | KXG33383 | genblast_Os01t0753300-00Zm0 | |

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| PUZ70618 | Sspon.02G | KQL24390 | TKW33014 | KXG35581 | Zm00001eb311960_P001 | 0.927 |
| PUZ60815 | Sspon.08G | KQL10312 | TKW20968 | EER88231 | Zm00001eb380550_P003 | 0.936 |

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| PUZ47784 | Sspon.05G | KQK97876 | TKW05179 | EES12431 | Zm00001eb078770_P001 | 0.908 |
| PUZ73263 | Sspon.02G | KQL26985 | TKW36255 | EER97669 | Zm00001eb329600_P001 | 0.959 |
| PUZ77410 | Sspon.04G | KQL31276 | TKW41321 | EES07345 | Zm00001eb253110_P001 | 0.943 |
| PUZ67294 | genblast_C | KQL16755 | TKW28971 | KXG23587 | Zm00001eb047930_P001 | 0.901 |
| PUZ66463 | Sspon.07G | KQL15911 | TKW27850 | EES03481 | Zm00001eb155830_P002 | 0.902 |
| PUZ73679 | Sspon.04G | KQL27756 | TKW36800 | OQU84173 | Zm00001eb229620_P002 | 0.903 |
| PUZ63861 | Sspon.07G | KQL00459 | TKW24447 | OQU77339 | Zm00001eb417110_P001 | 0.931 |

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| PUZ37614 | Sspon.01G | KQK87743 | TKV92078 | EER91088 | Zm00001eb217420_P001 | 0.898 |
| PUZ55152 | Sspon.03G | KQL06623 | TKW16297 | EES01345 | Zm00001eb155410_P001 | 0.907 |
| PUZ65489 | genblast_C | KQL07468 | TKW17418 | EES03799 | Zm00001eb149750_P005 | 0.976 |
| PUZ37993 | Sspon.01G | genblast_C | TKV92527 | genblast_C | Zm00001eb051490_P001 | 0.926 |
| PUZ45176 | Sspon.01G | KQK96264 | TKW01155 | EER99645 | Zm00001eb350070_P001 | 0.671 |
| PUZ77970 | Sspon.04G | KQL31839 | TKW41959 | EES05918 | Zm00001eb257310_P001 | 0.932 |
| PUZ47184 | genblast_Z | KQK97295 | TKW04428 | KXG26332 | Zm00001eb082690_P004 | 0.974 |
| genblast_C | genblast_C | KQL12797 | TKW23917 | OQU82566 | Zm00001eb066340_P001 | 0.965 |

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| PUZ68600 | Sspon.02G | KQL22634 | TKW30702 | KXG34507 | Zm00001eb301200_P001 | 0.937 |
| PUZ38772 | genblast_C | genblast_C | TKV93509 | KXG38400 | Zm00001eb046450_P001 | 0.716 |
| PUZ76128 | genblast_C | KQL30053 | TKW39775 | EES06976 | Zm00001eb244070_P002 | 0.807 |
| PUZ54756 | Sspon.03G | KQL07009 | TKW16813 | EES03623 | genblast_Os01t0753200-01Zm0 | |

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| PUZ52041 | Sspon.06G | KQL02336 | TKW10987 | OQU80992 | Zm00001eb033930_P001 | 0.736 |

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| PUZ55535 | genblast_C | genblast_C | TKW15745 | KXG33023 | Zm00001eb158020_P001 | 0.885 |
| PUZ67297 | Sspon.02G | KQL16746 | TKW28958 | EES17114 | Zm00001eb410730_P001 | 0.981 |
| PUZ36528 | Sspon.02G | KQK86600 | TKV90744 | KXG37334 | Zm00001eb061290_P001 | 0.903 |

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|---|---|---|---|---|---|---|
| PUZ77311 | genblast_C | KQL31182 | TKW41193 | EES07379 | Zm00001eb252380_P001 | 0.952 |
| PUZ55371 | genblast_C | KQL06396 | TKW16023 | EES01250 | Zm00001eb156850_P001 | 0.971 |
| PUZ71552 | Sspon.02G | KQK95924 | TKW02647 | genblast_C | Zm00001eb318600_P001 | 0.840 |
| PUZ52949 | Sspon.03G | KQL08656 | TKW18909 | KXG34140 | Zm00001eb362740_P001 | 0.932 |

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| PUZ74453 | Sspon.04G | KQL28347 | TKW37540 | EES06428 | Zm00001eb235050_P001 | 0.839 |
| PUZ73486 | Sspon.02G | KQL27220 | TKW36574 | KXG36973 | Zm00001eb330920_P001 | 0.898 |
| PUZ75938 | Sspon.04G | KQL29885 | TKW39501 | EES05179 | Zm00001eb181420_P001 | 0.675 |

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| PUZ71256 | Sspon.02G | KQL25037 | TKW33794 | EER99080 | Zm00001eb101850_P001 | 0.913 |
| PUZ54360 | genblast_Z | KQL07352 | TKW17262 | EES01611 | Zm00001eb369440_P001 | 0.949 |

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| PUZ76655 | Sspon.04G | KQL30584 | TKW40441 | OQU85350 | genblast_Os02t0628800-01_Ze | |
| PUZ70500 | Sspon.02G | KQL24275 | TKW32878 | OQU89415 | Zm00001eb098660_P001 | 0.874 |
| PUZ73185 | Sspon.02G | KQK90775 | TKW36171 | OQU90363 | Zm00001eb329210_P001 | 0.951 |

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| PUZ48514 | Sspon.01G | KQK98506 | TKW06028 | KXG26935 | Zm00001eb428740_P003 | 0.915 |
| PUZ69446 | genblast_C | KQL23416 | TKW31732 | OQU8891 | Zm00001eb306220_P001 | 0.962 |
| PUZ39113 | Sspon.01G | KQK89149 | TKV93930 | genblast_C | Zm00001eb223210_P001 | 0.804 |
| PUZ54289 | genblast_C | KQL07416 | TKW17350 | EES01637 | Zm00001eb150130_P001 | 0.899 |
| PUZ72819 | Sspon.02G | KQL26564 | TKW35687 | EER97493 | Zm00001eb108570_P002 | 0.962 |
| PUZ53134 | genblast_C | KQL08462 | TKW18670 | EES04150 | genblast_Os01t0930500-01_Ze | |
| PUZ54962 | Sspon.03G | genblast_C | TKW16558 | OQU8745 | Zm00001eb361830_P001 | 0.697 |
| PUZ49555 | Sspon.05G | KQL12739 | TKW23839 | EES13117 | genblast_Os04t0681900-02_Ze | |
| PUZ70272 | genblast_C | KQL24070 | TKW32561 | OQU8924 | Zm00001eb309540_P001 | 0.910 |
| PUZ50384 | genblast_Z | KQL00582 | TKW08670 | KXG24589 | Zm00001eb171770_P002 | 0.800 |
| PUZ38602 | Sspon.01G | KQK88675 | TKV93316 | EER91473 | Zm00001eb045560_P002 | 0.874 |
| PUZ40203 | Sspon.01G | KQK89991 | TKV95016 | KXG38948 | Zm00001eb023120_P002 | 0.710 |
| PUZ62231 | genblast_C | KQL09267 | TKW19625 | EER87834 | Zm00001eb270470_P002 | 0.951 |
| PUZ45347 | genblast_C | KQK95121 | TKW01409 | EES10014 | Zm00001eb200650_P004 | 0.855 |
| PUZ39914 | Sspon.01G | KQK89747 | TKV94711 | EER91870 | Zm00001eb224920_P001 | 0.763 |

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| PUZ45614 | Sspon.06G | KQK95581 | TKW02050 | EES08899 | Zm00001eb115340_P001 | 0.946 |

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| PUZ74209 | Sspon.08G | KQL28597 | TKW37836 | EES04579 | Zm00001eb232850_P001 | 0.920 |
| PUZ51370 | Sspon.06G | KQL01710 | TKW10177 | EES14967 | Zm00001eb168930_P001 | 0.654 |
| PUZ46064 | Sspon.05G | KQK96192 | genblast_C | EES11739 | Zm00001eb418620_P001 | 0.654 |
| PUZ63369 | genblast_C | KQL13650 | TKW25059 | EES03335 | Zm00001eb158840_P001 | 0.985 |
| PUZ49016 | Sspon.05G | KQK99032 | TKW06723 | EES12893 | Zm00001eb069720_P001 | 0.809 |
| PUZ55759 | Sspon.03G | KQL05926 | TKW15449 | EES03295 | Zm00001eb159570_P001 | 0.927 |
| genblast_C | Sspon.06G | KQK95514 | TKW01967 | KXG29137 | Zm00001eb164960_P001 | 0.872 |
| PUZ73216 | Sspon.02G | KQL26943 | TKW36197 | EER99809 | Zm00001eb110450_P001 | 0.951 |
| PUZ60748 | genblast_C | KQL28737 | TKW37999 | EER93352 | Zm00001eb213510_P001 | 0.883 |

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|---|---|---|---|---|---|---|
| PUZ78119 | genblast_C | KQL31988 | TKW42126 | EES05976 | genblast_Os02t0804900-01_Zea | |
| PUZ42733 | Sspon.01G | KQK92469 | TKV98070 | KXG40135 | Zm00001eb403360_P001 | 0.814 |
| PUZ77608 | Sspon.04G | KQL31329 | TKW41379 | EES07322 | Zm00001eb253420_P002 | 0.927 |
| PUZ77450 | Sspon.04G | KQL31503 | TKW41575 | EES07255 | Zm00001eb194480_P001 | 0.889 |
| PUZ66197 | Sspon.07G | KQL15689 | TKW27587 | EES18150 | Zm00001eb286970_P001 | 0.938 |
| PUZ71286 | Sspon.02G | KQL25067 | TKW33830 | EER99093 | Zm00001eb101930_P001 | 0.755 |

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| PUZ71448 | genblast_C | KQL25217 | TKW34011 | EER97012 | Zm00001eb102450_P001 | 0.997 |

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| PUZ70606 | Sspon.02G | genblast_C | TKW32996 | KXG35568 | Zm00001eb311850_P001 | 0.892 |
| PUZ36207 | Sspon.01G | KQK86342 | TKV90379 | KXG37197 | Zm00001eb211200_P006 | 0.917 |
| PUZ60810 | Sspon.08G | KQL10315 | TKW20972 | EER88243 | Zm00001eb380630_P001 | 0.879 |

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| PUZ72276 | Sspon.02G | KQL26040 | TKW35053 | EER97313 | Zm00001eb106130_P001 | 0.961 |
| PUZ42584 | genblast_C | genblast_C | TKV97911 | KXG40061 | genblast_Os03t0176100-00_Zea | |

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| PUZ73092 | Sspon.02G | KQL26830 | TKW36062 | EER97589 | Zm00001eb328540_P001 | 0.844 |
| PUZ70489 | Sspon.02G | KQL24270 | TKW32869 | KXG35505 | Zm00001eb311160_P001 | 0.889 |
| PUZ54912 | Sspon.03G | KQL06849 | TKW16606 | EES01424 | Zm00001eb154060_P001 | 0.876 |
| PUZ49223 | Sspon.05G | KQK99226 | TKW06962 | KXG27192 | Zm00001eb068410_P001 | 0.938 |
| PUZ50464 | Sspon.06G | KQL00494 | TKW08502 | EES14679 | Zm00001eb413520_P001 | 0.652 |
| PUZ50654 | Sspon.02G | KQL00331 | TKW08266 | EES15959 | genblast_Os04t0208400-01_Zea | |
| PUZ51247 | Sspon.06G | KQL01626 | TKW10069 | KXG24980 | Zm00001eb170720_P002 | 0.976 |
| PUZ72245 | Sspon.02G | KQL26006 | TKW35002 | EER97293 | Zm00001eb322670_P001 | 0.838 |
| PUZ46413 | genblast_C | KQK93467 | TKW07698 | OQU89836 | Zm00001eb293550_P002 | 0.896 |
| PUZ47731 | Sspon.05G | KQK97805 | TKW05084 | EES11026 | Zm00001eb079130_P001 | 0.961 |
| PUZ58270 | Sspon.03G | KQL04609 | TKW13700 | EES00224 | Zm00001eb336750_P001 | 0.899 |
| PUZ64453 | Sspon.07G | KQL14004 | TKW25485 | EES18809 | Zm00001eb297250_P001 | 0.652 |
| PUZ36107 | Sspon.01G | KQK86202 | TKV90217 | OQU90635 | Zm00001eb064330_P001 | 0.790 |
| PUZ59483 | Sspon.08G | KQL11982 | TKW23146 | EER90224 | Zm00001eb224600_P004 | 0.802 |
| PUZ54913 | Sspon.03G | KQL06848 | TKW16605 | KXG33312 | Zm00001eb154070_P001 | 0.873 |
| PUZ72736 | genblast_C | KQL26483 | TKW35593 | KXG36592 | Zm00001eb108180_P001 | 0.924 |
| PUZ65785 | Sspon.07G | KQL15295 | TKW27051 | EES18302 | genblast_Os05t0440000-00_Zea | |
| PUZ46212 | Sspon.05G | KQK96447 | TKW03254 | KXG25932 | Zm00001eb086790_P001 | 0.979 |
| PUZ52941 | genblast_C | KQL08667 | TKW18917 | EES02075 | Zm00001eb362700_P002 | 0.948 |
| PUZ43109 | Sspon.01G | KQK92868 | TKV98522 | OQU93352 | Zm00001eb403750_P001 | 0.967 |
| PUZ50618 | Sspon.08G | KQL00341 | TKW08282 | EES14728 | genblast_Os08t0226400-00_Zea | |
| PUZ40241 | Sspon.01G | KQK90045 | TKV95076 | OQU92181 | Zm00001eb022920_P001 | 0.923 |
| PUZ41638 | Sspon.01G | KQK91423 | TKV96798 | KXG39653 | Zm00001eb397390_P002 | 0.849 |

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| PUZ55711 | Sspon.03G | KQL05984 | TKW15517 | EES01116 | Zm00001eb358780_P001 | 0.932 |
| PUZ47035 | genblast_C | KQK97167 | TKW04265 | EES10732 | Zm00001eb421890_P001 | 0.832 |
| PUZ54208 | genblast_C | KQL07501 | TKW17451 | KXG33620 | Zm00001eb368820_P001 | 0.818 |
| PUZ69401 | genblast_C | KQL00464 | TKW08458 | OQU92318 | Zm00001eb164950_P001 | 0.909 |
| PUZ52129 | Sspon.02G | KQL02411 | TKW11084 | EES15412 | Zm00001eb034700_P001 | 0.872 |
| PUZ60280 | Sspon.08G | KQL11724 | TKW22803 | KXG20196 | genblast_Os06t0561800-00_Zea | |
| PUZ71672 | Sspon.02G | KQL25437 | TKW34272 | OQU89813 | Zm00001eb103420_P001 | 0.677 |
| PUZ54875 | Sspon.03G | KQL06899 | TKW16668 | EES03581 | Zm00001eb153780_P001 | 0.678 |
| PUZ74675 | Sspon.04G | KQL28142 | TKW37280 | KXG29797 | Zm00001eb240230_P001 | 0.892 |
| PUZ65502 | genblast_C | KQL14997 | TKW26699 | EES19705 | Zm00001eb290900_P001 | 0.960 |
| PUZ54217 | Sspon.03G | KQL07485 | TKW17436 | OQU87761 | Zm00001eb149620_P001 | 0.955 |
| PUZ36456 | genblast_C | KQK86525 | TKV90633 | EER90680 | Zm00001eb061870_P001 | 0.931 |
| PUZ53690 | Sspon.03G | KQL07968 | TKW18015 | EES01852 | Zm00001eb145890_P001 | 0.961 |
| PUZ58338 | genblast_C | KQL04676 | TKW13794 | EES02356 | Zm00001eb122280_P001 | 0.944 |
| PUZ41568 | Sspon.01G | KQK91355 | TKV96718 | EER95047 | Zm00001eb013140_P003 | 0.952 |

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| PUZ72425 | Sspon.02G | genblast_C | TKW35222 | EER99514 | Zm00001eb323700_P002 | 0.952 |
| PUZ40600 | Sspon.01G | KQK87847 | genblast_C | EER91122 | Zm00001eb218160_P001 | 0.955 |
| PUZ36333 | Sspon.01G | KQK86434 | TKV90496 | EER90626 | Zm00001eb211730_P001 | 0.972 |
| PUZ58927 | Sspon.08G | genblast_C | TKW23627 | EER89017 | Zm00001eb229030_P002 | 0.826 |

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| PUZ75029 | Sspon.04G | KQL27844 | TKW36916 | EES04870 | Zm00001eb238170_P001 | 0.943 |

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| PUZ45983 | Sspon.05G | KQK96113 | TKW37006 | EES11725 | Zm00001eb089700_P001 | 0.967 |
| PUZ63720 | genblast_C | KQL13330 | TKW24625 | EES17598 | genblast_Os05t0116700-01_Zea | |

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| PUZ47274 | Sspon.05G | KQK97383 | TKW04531 | EES10856 | Zm00001eb082130_P002 | 0.882 |

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| PUZ49371 | Sspon.05G | KQL12945 | TKW24085 | EES13043 | Zm00001eb067190_P001 | 0.775 |
| PUZ69001 | Sspon.02G | genblast_C | TKW31342 | EER96136 | Zm00001eb304350_P001 | 0.797 |
| PUZ53395 | genblast_C | KQL08230 | TKW18364 | EES04070 | Zm00001eb365410_P001 | 0.650 |
| PUZ42706 | Sspon.01G | KQK92442 | TKV98036 | EER92810 | Zm00001eb403390_P001 | 0.861 |
| PUZ75434 | Sspon.04G | genblast_C | TKW39134 | EES05020 | Zm00001eb240910_P001 | 0.970 |

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| PUZ68961 | Sspon.02G | KQL23182 | TKW31387 | EER96156 | Zm00001eb097100_P001 | 0.992 |
| PUZ59582 | Sspon.08G | KQL07868 | TKW17888 | OQU76841 | genblast_Os06t0666500-00_Zea | |
| PUZ73497 | Sspon.04G | KQL27229 | TKW36584 | EES05515 | Zm00001eb194230_P001 | 0.924 |

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| PUZ65212 | Sspon.07G | KQL14811 | TKW26448 | KXG22304 | genblast_Os05t0508500-01_Zea | |
| PUZ36964 | Sspon.01G | KQK87043 | TKV91285 | KXG37527 | Zm00001eb214580_P002 | 0.865 |
| PUZ75426 | Sspon.04G | KQL29614 | TKW39142 | EES05024 | Zm00001eb180650_P001 | 0.816 |
| PUZ68244 | Sspon.02G | KQL22206 | TKW30109 | EER95777 | Zm00001eb118040_P001 | 0.904 |
| PUV26687 | Sspon.05G | KQK96572 | TKW03472 | EES10453 | Zm00001eb161220_P001 | 0.791 |
| PUZ46153 | Sspon.01G | KQK96290 | TKW03073 | OQU81123 | Zm00001eb221180_P001 | 0.853 |
| PUZ72772 | Sspon.02G | KQL26509 | TKW35624 | EER99642 | Zm00001eb326510_P001 | 0.916 |
| PUZ71997 | Sspon.02G | KQL25747 | TKW34689 | KXG36200 | Zm00001eb104840_P001 | 0.929 |

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| PUZ60911 | genblast_C | KQL07015 | TKW16819 | genblast_C | Zm00001eb014970_P001 | 0.930 |
| PUZ72283 | Sspon.02G | KQL26044 | TKW35060 | EER97316 | Zm00001eb322970_P002 | 0.846 |
| PUZ47687 | genblast_C | KQK97767 | TKW05036 | EES12396 | Zm00001eb425110_P001 | 0.863 |
| PUZ64900 | Sspon.07G | KQL14466 | TKW26038 | EES19908 | Zm00001eb342900_P001 | 0.743 |
| PUZ56153 | Sspon.03G | KQL05639 | TKW15088 | EES00943 | Zm00001eb160100_P001 | 0.842 |
| PUZ55971 | Sspon.02G | KQL05745 | TKW15218 | OQU84510 | genblast_Os02t0178200-00 | Zm0 |
| PUZ42596 | Sspon.01G | KQK92341 | TKV97934 | KXG40074 | Zm00001eb402070_P002 | 0.915 |
| PUZ53621 | genblast_C | KQL08031 | TKW18117 | EES03998 | Zm00001eb145500_P003 | 0.925 |

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| PUZ77502 | Sspon.04G | KQL31452 | TKW41512 | EES07286 | Zm00001eb254110_P001 | 0.960 |
| PUZ36828 | Sspon.01G | KQK86905 | TKV91104 | EER90819 | Zm00001eb213820_P001 | 0.865 |
| PUZ70818 | Sspon.02G | KQL24613 | TKW33299 | KXG35699 | Zm00001eb099990_P001 | 0.921 |
| PUZ49456 | Sspon.07G | KQL12840 | TKW23958 | EES15499 | Zm00001eb194830_P004 | 0.907 |
| PUZ71837 | genblast_C | KQL25595 | genblast_C | EER97140 | Zm00001eb320930_P001 | 0.928 |
| PUZ52605 | Sspon.06G | KQL02882 | TKW11662 | EES15222 | Zm00001eb202900_P001 | 0.984 |
| PUZ55000 | Sspon.03G | KQL06773 | TKW16504 | EES01382 | Zm00001eb361650_P001 | 0.787 |
| PUZ36712 | Sspon.01G | KQK86799 | TKV90987 | KXG37420 | Zm00001eb059840_P001 | 0.937 |
| PUZ71155 | Sspon.02G | KQL24929 | TKW33646 | EER96917 | Zm00001eb315970_P001 | 0.942 |
| PUZ66341 | Sspon.07G | KQL15814 | TKW27733 | EES18090 | Zm00001eb285530_P001 | 0.944 |
| PUZ68396 | genblast_C | KQL22423 | TKW30415 | OQU88434 | Zm00001eb420620_P001 | 0.933 |

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| PUZ72826 | genblast_C | KQL26571 | TKW35699 | KXG36646 | Zm00001eb326930_P001 | 0.906 |
| PUZ48000 | Sspon.05G | KQK98065 | TKW05414 | OQU81973 | Zm00001eb077540_P002 | 0.938 |
| PUZ50004 | Sspon.06G | KQL00939 | TKW09144 | EES14493 | Zm00001eb261820_P001 | 0.929 |
| PUZ64559 | Sspon.07G | KQL14088 | TKW25618 | KXG22639 | Zm00001eb344970_P001 | 0.894 |
| PUZ55953 | Sspon.03G | KQL05747 | TKW15219 | EES01020 | Zm00001eb357710_P006 | 0.938 |

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| PUZ43458 | Sspon.05G | KQK93358 | TKV99012 | OQU82728 | Zm00001eb195420_P002 | 0.862 |
| genblast_Z | genblast_Z | KQL07146 | TKW16994 | OQU87616 | Zm00001eb152060_P001 | 0.894 |
| PUZ36906 | Sspon.01G | KQK86973 | TKV91209 | OQU90937 | Zm00001eb058300_P003 | 0.963 |

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| PUZ63039 | Sspon.05G | KQK99606 | TKW07447 | EES15701 | Zm00001eb407240_P001 | 0.957 |
| PUZ51633 | Sspon.06G | KQL01950 | TKW10476 | EES15051 | Zm00001eb332480_P001 | 0.935 |
| PUZ68981 | Sspon.02G | KQL23167 | TKW31370 | EER96145 | Zm00001eb304500_P001 | 0.969 |
| PUZ76229 | Sspon.04G | KQL30153 | TKW39875 | OQU85191 | Zm00001eb244810_P001 | 0.890 |
| PUZ40859 | Sspon.01G | genblast_C | TKV95804 | KXG39240 | Zm00001eb018850_P003 | 0.911 |
| PUZ57484 | Sspon.03G | KQL03901 | TKW12805 | EES00502 | Zm00001eb333680_P001 | 0.925 |
| PUZ67829 | Sspon.02G | KQL17122 | TKW29491 | EES17352 | Zm00001eb031300_P001 | 0.895 |
| PUZ60488 | Sspon.08G | KQL10808 | TKW21658 | EER88427 | Zm00001eb382900_P001 | 0.922 |
| PUZ64492 | genblast_C | KQL14025 | TKV90024 | KXG39541 | Zm00001eb212750_P002 | 0.860 |
| PUZ70125 | Sspon.02G | KQL23962 | TKW32390 | EER98648 | Zm00001eb097310_P001 | 0.880 |
| PUZ53207 | Sspon.03G | KQL08393 | TKW18575 | KXG34019 | Zm00001eb364090_P002 | 0.925 |
| PUZ46727 | genblast_C | KQK96837 | TKW03804 | EES11937 | Zm00001eb087230_P001 | 0.914 |
| PUZ42411 | Sspon.01G | KQK92164 | TKV97697 | EER92706 | Zm00001eb008310_P001 | 0.939 |

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| PUZ76450 | Sspon.04G | KQL30391 | TKW40170 | KXG30593 | Zm00001eb184150_P001 | 0.909 |

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| PUZ47510 | Sspon.05G | KQK97598 | TKW04821 | OQU81717 | Zm00001eb080540_P001 | 0.889 |
| PUZ76400 | Sspon.04G | KQL30335 | TKW40116 | EES05373 | Zm00001eb246290_P001 | 0.930 |
| PUZ70533 | Sspon.02G | KQL24294 | TKW32910 | KXG35522 | Zm00001eb311420_P001 | 0.965 |

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| PUZ64833 | Sspon.07G | KQL14372 | TKW25931 | EES18661 | Zm00001eb343360_P001 | 0.960 |
| PUZ48225 | Sspon.05G | KQK98291 | TKW05691 | EES12573 | Zm00001eb075330_P002 | 0.898 |
| PUZ75307 | Sspon.04G | genblast_C | TKW38759 | KXG30143 | Zm00001eb203200_P004 | 0.913 |
| genblast_C | Sspon.01G | KQL05660 | TKW15111 | EES11676 | genblast_Os10t0133166-00_Ze | |
| PUZ49264 | genblast_C | KQL12860 | TKW23987 | OQU82477 | Zm00001eb067810_P002 | 0.867 |
| PUZ71216 | Sspon.02G | KQL24980 | TKW33731 | EER96942 | Zm00001eb101670_P001 | 0.921 |
| PUZ56334 | Sspon.08G | KQL23253 | TKW31531 | EER88656 | Zm00001eb388210_P001 | 0.897 |

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| PUZ60206 | Sspon.08G | KQL11659 | TKW22725 | EER88552 | Zm00001eb385190_P001 | 0.874 |
| PUZ40221 | Sspon.01G | KQK90060 | TKV95053 | KXG38955 | Zm00001eb022970_P001 | 0.915 |
| PUZ75024 | Sspon.04G | KQL27839 | TKW36910 | KXG29961 | Zm00001eb238050_P001 | 0.936 |
| PUZ42556 | Sspon.01G | KQK92304 | TKV97879 | KXG40048 | Zm00001eb005950_P001 | 0.958 |

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| PUZ76331 | genblast_C | KQL30252 | TKW40016 | EES05344 | Zm00001eb245710_P001 | 0.849 |

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| PUZ75959 | Sspon.04G | KQL29909 | TKW39544 | EES05193 | Zm00001eb242940_P001 | 0.937 |

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| PUZ69778 | Sspon.02G | KQL23716 | TKW32099 | EER98557 | Zm00001eb307290_P002 | 0.914 |
| PUZ62441 | Sspon.08G | KQL09050 | TKW19337 | KXG19160 | Zm00001eb269260_P001 | 0.890 |
| PUZ54968 | Sspon.03G | KQL06802 | TKW16540 | KXG33295 | Zm00001eb154390_P001 | 0.849 |

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| PUZ42518 | Sspon.01G | KQK92271 | TKV97830 | EER92744 | Zm00001eb006260_P001 | 0.849 |
| PUZ66475 | Sspon.03G | KQL15921 | TKW27859 | KXG34096 | Zm00001eb141460_P003 | 0.931 |
| PUZ76218 | Sspon.04G | KQL30139 | TKW39861 | KXG30480 | Zm00001eb182800_P001 | 0.767 |
| PUZ60764 | Sspon.08G | KQL10612 | TKW21419 | EER88389 | Zm00001eb382480_P003 | 0.955 |

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| PUZ54213 | Sspon.03G | KQL07494 | TKW17445 | EES01667 | Zm00001eb149580_P001 | 0.824 |
| PUZ38380 | Sspon.01G | KQK88444 | TKV93011 | KXG38217 | Zm00001eb044090_P001 | 0.974 |
| PUZ53998 | Sspon.03G | KQL07693 | TKW17688 | EES03872 | Zm00001eb367860_P001 | 0.964 |
| PUZ75580 | Sspon.06G | KQL29490 | TKW38963 | EES14386 | Zm00001eb174200_P004 | 0.859 |
| PUZ41921 | Sspon.01G | KQK91680 | TKV97086 | KXG39773 | Zm00001eb398600_P001 | 0.926 |
| PUZ47414 | Sspon.05G | KQK97508 | TKW04706 | OQU81682 | Zm00001eb081260_P003 | 0.845 |
| PUZ42885 | Sspon.01G | KQK92619 | TKV98259 | KXG40198 | Zm00001eb003540_P007 | 0.925 |
| PUZ54199 | Sspon.03G | KQL07510 | TKW17466 | OQU87764 | Zm00001eb368790_P001 | 0.855 |
| PUZ73762 | Sspon.04G | KQL29010 | TKW38375 | EES06175 | Zm00001eb230250_P001 | 0.889 |

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| PUZ61829 | Sspon.08G | KQL09388 | TKW19735 | KXG19523 | Zm00001eb374120_P001 | 0.965 |
| PUZ67238 | genblast_C | KQL16819 | TKW29061 | KXG23548 | Zm00001eb264720_P001 | 0.897 |
| PUZ70830 | Sspon.02G | KQL24635 | TKW33315 | KXG35705 | Zm00001eb313970_P001 | 0.800 |
| PUZ60040 | Sspon.08G | KQL11510 | TKW22519 | EER90015 | Zm00001eb276740_P001 | 0.771 |
| PUZ73406 | genblast_Z | KQL27119 | TKW36400 | OQU90452 | Zm00001eb330260_P001 | 0.928 |
| PUZ67888 | Sspon.02G | KQL17309 | TKW29707 | EES17383 | Zm00001eb136010_P002 | 0.915 |
| PUZ63471 | Sspon.05G | KQL13549 | TKW24930 | OQU81844 | Zm00001eb078960_P001 | 0.877 |
| PUZ50097 | Sspon.06G | KQL00812 | TKW08977 | EES14540 | Zm00001eb416370_P001 | 0.927 |
| PUZ67486 | Sspon.02G | KQL16568 | TKW28713 | KXG23721 | Zm00001eb028750_P002 | 0.925 |
| PUZ56988 | Sspon.03G | KQL03432 | TKW12193 | OQU86795 | Zm00001eb340180_P001 | 0.967 |
| PUZ76891 | Sspon.04G | KQL30792 | TKW40715 | KXG31088 | Zm00001eb186540_P001 | 0.899 |
| PUZ65768 | Sspon.07G | KQL15278 | TKW27027 | EES19612 | Zm00001eb288940_P002 | 0.972 |
| PUZ76844 | Sspon.04G | KQL30752 | TKW40666 | EES05795 | Zm00001eb186310_P001 | 0.907 |
| PUZ59257 | Sspon.08G | KQL11775 | TKW22864 | KXG20763 | Zm00001eb226810_P001 | 0.807 |
| PUZ77228 | genblast_C | KQL31091 | TKW41079 | EES05674 | Zm00001eb188160_P001 | 0.924 |
| PUZ36889 | Sspon.01G | KQK86957 | TKV91190 | EER93396 | Zm00001eb214130_P001 | 0.975 |
| PUZ52355 | Sspon.06G | KQL02628 | TKW11370 | EES15318 | Zm00001eb036470_P001 | 0.861 |
| PUZ45673 | Sspon.06G | KQK95659 | TKW02157 | EES10193 | Zm00001eb165830_P001 | 0.909 |
| PUZ52614 | Sspon.06G | KQL02959 | TKW11745 | EES14104 | Zm00001eb039890_P001 | 0.973 |
| PUZ73351 | Sspon.02G | KQL27147 | TKW36476 | EER97719 | Zm00001eb111390_P001 | 0.972 |
| PUZ49453 | Sspon.05G | KQL12843 | TKW23963 | EES13074 | Zm00001eb433430_P001 | 0.845 |
| PUZ61854 | Sspon.08G | genblast_C | TKW19779 | EER89358 | Zm00001eb374330_P002 | 0.843 |
| PUZ66558 | genblast_C | KQL16040 | TKW28012 | EES12857 | Zm00001eb284970_P002 | 0.862 |
| PUZ71270 | Sspon.02G | KQL25054 | TKW33811 | EER96974 | Zm00001eb101890_P002 | 0.943 |
| PUZ41848 | Sspon.01G | KQK91617 | TKV96997 | EER92527 | Zm00001eb011220_P002 | 0.862 |

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| PUZ71421 | Sspon.02G | KQL25195 | TKW33986 | EER99145 | Zm00001eb102350_P001 | 0.943 |
| PUZ52389 | Sspon.06G | KQL02662 | TKW11401 | EES15303 | Zm00001eb175250_P001 | 0.913 |

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| PUZ76784 | genblast_C | KQL30695 | TKW40588 | KXG31129 | Zm00001eb248620_P001 | 0.917 |
| PUZ53336 | Sspon.03G | KQL08284 | TKW18443 | KXG33973 | genblast_Os01t0914000-01_Ze | |
| PUZ67573 | Sspon.02G | KQL16913 | TKW29191 | KXG23785 | Zm00001eb136280_P002 | 0.920 |

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| PUZ41461 | Sspon.05G | KQK91259 | TKV96603 | EER95007 | Zm00001eb013990_P001 | 0.977 |
| PUZ38757 | Sspon.01G | KQK88801 | TKV93487 | KXG38393 | Zm00001eb046350_P003 | 0.874 |
| PUZ77307 | Sspon.04G | KQL31178 | TKW41189 | KXG30901 | Zm00001eb188670_P001 | 0.948 |
| PUZ67483 | Sspon.02G | KQL16574 | TKW28718 | KXG23720 | Zm00001eb136860_P001 | 0.872 |
| PUZ40812 | Sspon.01G | KQK90566 | TKV95755 | EER92178 | Zm00001eb019140_P001 | 0.928 |
| PUZ42234 | Sspon.01G | KQK92004 | TKV97501 | KXG39897 | Zm00001eb400390_P002 | 0.892 |

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| PUZ54967 | Sspon.03G | KQL06803 | TKW16543 | KXG33296 | Zm00001eb361790_P001 | 0.957 |
| PUZ41604 | Sspon.01G | KQK91391 | TKV96752 | EER92438 | Zm00001eb397270_P003 | 0.785 |
| PUZ38496 | Sspon.05G | KQK88573 | TKV93181 | EES11553 | Zm00001eb068330_P001 | 0.926 |
| PUZ61744 | Sspon.08G | KQL09872 | TKW20385 | KXG19566 | Zm00001eb373580_P001 | 0.955 |
| PUZ70782 | Sspon.02G | KQL24563 | TKW33238 | KXG35667 | Zm00001eb313520_P001 | 0.855 |
| PUZ68096 | Sspon.02G | KQL17458 | TKW29906 | EES16463 | Zm00001eb133960_P001 | 0.990 |
| PUZ58944 | Sspon.08G | KQL12353 | TKW23605 | KXG20978 | Zm00001eb228940_P001 | 0.914 |

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| PUZ76933 | Sspon.04G | KQL30838 | TKW40769 | EES05768 | Zm00001eb186770_P003 | 0.964 |
| PUZ45299 | Sspon.08G | KQL22899 | TKW31011 | genblast_C | Zm00001eb069540_P001 | 0.828 |
| PUZ76798 | Sspon.04G | KQL30707 | TKW40602 | EES05821 | Zm00001eb186120_P001 | 0.963 |
| PUZ50102 | genblast_C | KQL00804 | TKW08971 | KXG24411 | Zm00001eb416420_P001 | 0.921 |
| PUZ54142 | genblast_C | genblast_C | TKW17530 | KXG33643 | Zm00001eb368420_P001 | 0.870 |
| PUZ62256 | genblast_C | KQL15679 | TKW27567 | KXG20615 | Zm00001eb390310_P001 | 0.955 |

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| PUZ39909 | Sspon.01G | KQK89743 | TKV94703 | KXG38822 | Zm00001eb025040_P001 | 0.959 |

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| PUZ56005 | Sspon.03G | KQL05698 | TKW15156 | EES00998 | Zm00001eb161050_P001 | 0.871 |
| PUZ42040 | Sspon.01G | KQK91808 | TKV97263 | EER95210 | Zm00001eb009870_P002 | 0.945 |

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| PUZ49202 | Sspon.05GKQK99209 | TKW06940 | EES11547 | Zm00001eb432070_P001 | 0.943 |

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| PUZ77021 | Sspon.04GKQL30908 | TKW40859 | EES07467 | Zm00001eb250370_P002 | 0.902 |
| PUZ59153 | Sspon.08GKQL12170 | TKW23372 | OQU77081 | Zm00001eb227690_P001 | 0.849 |
| PUZ62187 | Sspon.08GKQL09741 | TKW20211 | OQU75836 | Zm00001eb270810_P001 | 0.978 |
| PUZ60016 | Sspon.08GKQL11490 | TKW22493 | KXG20324 | Zm00001eb386490_P003 | 0.959 |
| PUZ42308 | Sspon.01GKQK92077 | TKV97598 | EER92678 | Zm00001eb007690_P003 | 0.822 |
| PUZ71021 | Sspon.02GKQL24814 | TKW33518 | EER96866 | Zm00001eb100900_P001 | 0.910 |
| PUZ71891 | genblast_CKQL25650 | TKW34565 | EER99333 | Zm00001eb320610_P001 | 0.951 |

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| PUZ60762 | Sspon.08GKQL10610 | TKW21417 | EER88393 | Zm00001eb382490_P001 | 0.971 |
| PUZ42925 | Sspon.01GKQK92652 | TKV98297 | KXG40218 | Zm00001eb003190_P001 | 0.877 |
| PUZ53835 | Sspon.03GKQL07840 | TKW17859 | EES01796 | Zm00001eb147080_P001 | 0.992 |

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| PUZ70295 | Sspon.02GKQL24084 | TKW32595 | EER98690 | Zm00001eb309590_P001 | 0.913 |
| PUZ54461 | Sspon.03GKQL07257 | TKW17135 | EES01570 | Zm00001eb369800_P001 | 0.966 |
| PUZ49900 | Sspon.06GKQL01033 | TKW09282 | OQU79802 | genblast_Os08t0117800-01_Zea | |
| PUZ43883 | Sspon.05GKQK93769 | TKV99538 | EES09367 | Zm00001eb200890_P001 | 0.922 |
| PUZ55150 | genblast_CKQL06626 | TKW16300 | EES03498 | Zm00001eb361140_P001 | 0.847 |
| PUZ58750 | genblast_CKQL03347 | TKW12090 | EES00028 | Zm00001eb192850_P001 | 0.957 |
| PUZ77619 | Sspon.05GKQK96865 | TKW03872 | OQU81241 | Zm00001eb086720_P001 | 0.884 |
| PUZ39336 | Sspon.04GKQK86153 | TKV90149 | EES05483 | Zm00001eb248330_P002 | 0.889 |
| PUZ69235 | Sspon.02GKQL23213 | TKW31489 | EER98353 | Zm00001eb304880_P001 | 0.829 |
| PUZ65597 | Sspon.07GKQL15112 | TKW26828 | KXG22181 | genblast_Os05t0466100-01_Zea | |
| PUZ65057 | Sspon.07GKQL14613 | TKW26215 | EES18555 | Zm00001eb293200_P001 | 0.911 |

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| PUZ57110 | Sspon.03GKQL03523 | TKW12326 | EES02826 | Zm00001eb332170_P001 | 0.880 |
| PUZ37740 | Sspon.01GKQK87887 | TKV92240 | EER91149 | Zm00001eb052910_P001 | 0.978 |
| PUZ42489 | genblast_CKQK92246 | TKV97796 | KXG40020 | Zm00001eb006470_P002 | 0.908 |
| PUZ56637 | genblast_CKQL05044 | TKW14280 | EES02901 | Zm00001eb131200_P001 | 0.923 |
| PUZ37211 | Sspon.01GKQK87306 | TKV91579 | EER90943 | Zm00001eb055990_P001 | 0.944 |
| PUZ37857 | Sspon.01GKQK87993 | TKV92363 | EER91191 | genblast_Os03t0638900-01_Zea | |
| PUZ75964 | Sspon.04GKQL29911 | TKW39546 | EES05195 | Zm00001eb242990_P001 | 0.875 |

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| PUZ78159 | genblast_C | KQL32027 | TKW4217 | KXG31320 | Zm00001eb258380_P001 | 0.920 |
| PUZ72445 | Sspon.02G | KQL26209 | TKW35256 | EER99528 | Zm00001eb323840_P002 | 0.947 |

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| PUZ72904 | genblast_C | KQL26655 | TKW35807 | KXG36684 | Zm00001eb327470_P001 | 0.922 |

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| PUZ75992 | Sspon.04G | KQL29936 | TKW3959 | EES04344 | Zm00001eb209740_P002 | 0.902 |
| PUZ44289 | Sspon.05G | KQK94175 | TKW00126 | EES09588 | Zm00001eb200700_P001 | 0.919 |
| PUZ72716 | genblast_C | KQL26465 | TKW35574 | EER99622 | Zm00001eb325970_P002 | 0.834 |
| PUZ72549 | Sspon.02G | KQL26301 | TKW3540 | EER99570 | Zm00001eb107210_P001 | 0.867 |
| PUZ37167 | Sspon.02G | KQK87254 | TKV91521 | EER93510 | Zm00001eb056330_P001 | 0.879 |
| PUZ46756 | genblast_C | KQK96873 | TKW03881 | KXG30872 | Zm00001eb420720_P004 | 0.888 |
| PUZ57238 | Sspon.01G | KQL03666 | TKW12501 | EER93025 | Zm00001eb000500_P001 | 0.869 |
| PUZ38935 | Sspon.01G | KQK88962 | TKV93704 | EER94186 | Zm00001eb222770_P001 | 0.825 |
| PUZ75978 | Sspon.04G | KQL29927 | TKW39581 | EES06922 | Zm00001eb243050_P001 | 0.927 |
| PUZ43733 | Sspon.05G | KQK93703 | TKV99415 | EES09317 | Zm00001eb202370_P001 | 0.942 |
| PUZ77207 | Sspon.04G | KQL31062 | TKW41052 | KXG30955 | Zm00001eb251400_P003 | 0.870 |
| PUZ73245 | Sspon.02G | KQL26973 | TKW36241 | OQU9039 | Zm00001eb329530_P002 | 0.920 |
| PUZ59224 | Sspon.08G | KQL11737 | TKW22814 | EER88914 | Zm00001eb227160_P003 | 0.946 |

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| PUZ59907 | Sspon.04G | KQL11377 | TKW22341 | OQU7671 | Zm00001eb388050_P002 | 0.915 |
| PUZ47897 | Sspon.05G | KQK97982 | TKW05305 | OQU8190 | Zm00001eb078060_P001 | 0.919 |
| PUZ37348 | Sspon.03G | KQL03160 | TKW11875 | EER99981 | Zm00001eb118790_P001 | 0.923 |
| PUZ70473 | Sspon.02G | KQL24255 | TKW32845 | KXG35486 | Zm00001eb098610_P001 | 0.915 |

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| PUZ65515 | Sspon.07GKQL15016 | TKW26724 | EES19695 | Zm00001eb352050_P002 | 0.751 |
| PUZ46772 | Sspon.05GKQK96890 | TKW03899 | KXG26087 | Zm00001eb085850_P001 | 0.930 |
| PUZ54970 | genblast_CKQL06800 | TKW16538 | EES03545 | Zm00001eb361780_P001 | 0.899 |
| PUZ76213 | genblast_CKQL30135 | TKW39853 | genblast_C | Zm00001eb244640_P001 | 0.925 |
| PUZ44133 | Sspon.05GKQK94058 | TKV99954 | KXG28091 | Zm00001eb201350_P002 | 0.873 |
| PUZ59421 | Sspon.08GKQL11917 | TKW23079 | EER90247 | Zm00001eb225480_P001 | 0.982 |
| PUZ47690 | Sspon.05GKQK97769 | TKW05039 | KXG26579 | Zm00001eb079340_P001 | 0.972 |
| PUZ68178 | Sspon.02GKQL22109 | TKW29982 | KXG34255 | Zm00001eb298300_P001 | 0.895 |
| PUZ54894 | genblast_CKQL06870 | TKW16635 | EES01438 | Zm00001eb153970_P001 | 0.924 |

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| PUZ75682 | genblast_CKQL29395 | TKW38813 | OQU84860 | Zm00001eb203240_P002 | 0.942 |
| PUZ53094 | genblast_CKQL08511 | TKW18728 | EES04173 | Zm00001eb142010_P003 | 0.913 |

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| PUZ62739 | Sspon.05GKQK99681 | TKW07534 | EES09138 | Zm00001eb195440_P001 | 0.778 |
| PUZ41652 | genblast_C | genblast_C | genblast_COQU92806 | Zm00001eb012680_P001 | 0.834 |
| PUZ55683 | Sspon.03G | genblast_C | TKW15546EES01130 | Zm00001eb358990_P001 | 0.879 |

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| PUZ64814 | Sspon.07G | genblast_C | TKW25915EES19938 | Zm00001eb295650_P001 | 0.946 |
| PUZ58363 | Sspon.03GKQL04699 | TKW13831 | EES00175 | Zm00001eb122120_P001 | 0.896 |
| PUZ41369 | genblast_CKQK91159 | TKV96475 | KXG39511 | Zm00001eb015000_P001 | 0.888 |
| PUZ77308 | Sspon.04GKQL31179 | TKW41190 | EES07380 | Zm00001eb252370_P004 | 0.945 |
| PUZ52942 | Sspon.03GKQL08666 | TKW18916 | KXG34144 | Zm00001eb362710_P001 | 0.875 |

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| PUZ63692 | Sspon.07GKQL13358 | TKW24663 | KXG21107 | Zm00001eb266560_P005 | 0.833 |
| genblast_C | Sspon.05GKQK94075 | TKV99981 | EES09544 | Zm00001eb168220_P001 | 0.958 |
| PUZ76971 | Sspon.04GKQL30870 | TKW40810 | EES07481 | Zm00001eb250010_P001 | 0.942 |
| PUZ64579 | Sspon.07GKQL14104 | TKW25639 | KXG22624 | Zm00001eb297190_P001 | 0.859 |
| PUZ49939 | Sspon.06GKQL01000 | TKW09242 | EES13286 | Zm00001eb173470_P001 | 0.887 |
| PUZ65222 | Sspon.07GKQL14802 | TKW26438 | EES19781 | Zm00001eb292380_P001 | 0.974 |
| PUZ67358 | Sspon.02GKQL16677 | TKW28850 | EES17166 | Zm00001eb410260_P001 | 0.834 |

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| PUZ50195 | Sspon.06G | genblast_C | TKW08867 | EES13385 | Zm00001eb172450_P005 | 0.947 |
| PUZ71291 | Sspon.06G | KQL25073 | TKW33844 | EER99096 | Zm00001eb316810_P001 | 0.925 |
| PUZ65399 | Sspon.07G | KQL14894 | TKW26554 | EES18435 | Zm00001eb291600_P001 | 0.901 |
| PUZ39042 | Sspon.01G | KQK89186 | TKV93966 | EER94248 | Zm00001eb223080_P002 | 0.896 |

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| PUZ42659 | Sspon.01G | KQK92400 | TKV97997 | KXG40098 | Zm00001eb005280_P001 | 0.954 |
| PUZ62383 | Sspon.08G | KQL09118 | TKW19440 | KXG19192 | Zm00001eb378330_P003 | 0.893 |
| PUZ36999 | Sspon.01G | genblast_C | TKV91320 | EER93441 | Zm00001eb057470_P001 | 0.868 |
| PUZ76547 | Sspon.04G | KQL30480 | TKW40289 | EES05420 | Zm00001eb247090_P003 | 0.921 |
| PUZ55271 | Sspon.03G | KQL06503 | TKW16156 | EES01296 | genblast_Os01t0690200-00_Ze |  |

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| PUZ63944 | Sspon.07G | KQL13279 | TKW24531 | OQU77372 | Zm00001eb417620_P001 | 0.997 |
| PUZ49214 | Sspon.06G | KQK94772 | TKW00958 | EES08582 | Zm00001eb276920_P001 | 0.763 |
| PUZ58571 | Sspon.03G | KQL04886 | TKW14054 | EES00099 | Zm00001eb120780_P002 | 0.941 |
| PUZ54222 | Sspon.03G | KQL07481 | TKW17431 | EES01661 | Zm00001eb149660_P003 | 0.927 |
| PUZ74791 | genblast_C | KQL28005 | TKW37116 | OQU84673 | genblast_Os02t0230000-01_Ze |  |
| PUZ44860 | Sspon.06G | KQK94617 | TKW00723 | KXG28403 | Zm00001eb169450_P001 | 0.941 |
| PUZ64845 | Sspon.07G | KQL14380 | TKW25940 | EES19928 | Zm00001eb343270_P002 | 0.972 |

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| PUZ37057 | Sspon.01G | KQK87130 | TKV91388 | EER93464 | Zm00001eb057090_P001 | 0.906 |
| PUZ50945 | Sspon.06G | KQL01270 | TKW09601 | EES14907 | Zm00001eb176740_P001 | 0.919 |
| PUZ40352 | Sspon.01G | KQK90146 | TKV95194 | KXG39009 | Zm00001eb022130_P001 | 0.868 |
| PUZ71371 | Sspon.02G | genblast_C | TKW33940 | EER99130 | Zm00001eb317350_P001 | 0.898 |
| PUZ42933 | Sspon.01G | KQK92663 | TKV98306 | OQU93273 | Zm00001eb402780_P001 | 0.926 |
| PUZ39040 | Sspon.01G | KQK89187 | TKV93967 | KXG38537 | Zm00001eb223070_P002 | 0.800 |
| PUZ70750 | Sspon.02G | KQL01980 | TKW33202 | EER98920 | Zm00001eb041100_P001 | 0.950 |
| PUZ48717 | Sspon.04G | KQK98733 | TKW06303 | EES05673 | Zm00001eb251650_P001 | 0.867 |
| PUZ75656 | Sspon.04G | KQL29553 | TKW39047 | KXG30106 | Zm00001eb236740_P001 | 0.904 |
| genblast_C | Sspon.08G | KQK91749 | TKV97190 | EER95193 | Zm00001eb399070_P001 | 0.927 |
| PUZ37419 | Sspon.01G | KQK87515 | TKV91809 | EER93596 | Zm00001eb054430_P001 | 0.886 |
| PUZ59632 | genblast_C | KQL11080 | TKW21960 | KXG20536 | Zm00001eb389630_P001 | 0.936 |
| PUZ48935 | Sspon.05G | KQK98953 | TKW06614 | EES11436 | Zm00001eb070520_P001 | 0.942 |
| PUZ65015 | genblast_C | KQL14580 | TKW26173 | KXG22416 | Zm00001eb356480_P001 | 0.943 |
| PUZ65026 | Sspon.07G | KQL14586 | TKW26185 | KXG22409 | Zm00001eb294000_P003 | 0.979 |
| PUZ67671 | Sspon.02G | KQL16991 | TKW29320 | EES17294 | Zm00001eb134990_P001 | 0.926 |
| PUZ49718 | Sspon.06G | KQL00132 | TKW08019 | EES14344 | Zm00001eb198710_P002 | 0.909 |
| PUZ59181 | Sspon.04G | KQL12135 | TKW23315 | EER88926 | Zm00001eb227380_P002 | 0.967 |
| PUZ74857 | Sspon.04G | KQL27938 | TKW37041 | EES04827 | Zm00001eb238710_P001 | 0.789 |
| PUZ63025 | Sspon.07G | KQK99620 | TKW07462 | EES15698 | Zm00001eb407080_P002 | 0.966 |
| PUZ52291 | Sspon.06G | KQL02551 | TKW11262 | KXG25581 | Zm00001eb174750_P001 | 0.842 |
| PUZ70986 | Sspon.02G | KQL24786 | TKW33488 | KXG35763 | Zm00001eb314840_P004 | 0.953 |
| PUZ71323 | Sspon.02G | KQL25108 | TKW33880 | KXG35935 | Zm00001eb317030_P001 | 0.897 |
| PUZ61418 | Sspon.08G | genblast_C | TKW20540 | OQU7609 | Zm00001eb107280_P004 | 0.933 |

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| PUZ74002 | genblast_C | KQL28803 | TKW38091 | EES04493 | Zm00001eb209220_P001 | 0.894 |
| PUZ39129 | Sspon.03G | KQK89296 | TKV94109 | KXG34176 | Zm00001eb140390_P002 | 0.951 |
| PUZ48630 | Sspon.05G | KQK98644 | TKW06193 | EES12738 | Zm00001eb072680_P001 | 0.973 |

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| PUZ66142 | Sspon.07G | KQL15635 | TKW27493 | OQU77942 | genblast_Os05t0392400-01_Ze | |
| PUZ38553 | Sspon.01G | KQK88637 | TKV93259 | EER94055 | Zm00001eb221300_P001 | 0.959 |
| PUZ48400 | genblast_C | KQK98419 | TKW05919 | EER89206 | Zm00001eb429350_P001 | 0.954 |
| PUZ78148 | Sspon.04G | KQL32015 | TKW42154 | EES05983 | Zm00001eb191940_P001 | 0.840 |
| PUZ36667 | genblast_C | KQK86754 | TKV90938 | EER90763 | Zm00001eb213200_P001 | 0.939 |
| PUZ46780 | Sspon.05G | KQK96896 | TKW03909 | EES12001 | Zm00001eb085780_P001 | 0.829 |

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| PUZ72682 | Sspon.02G | KQL26438 | TKW35548 | KXG36569 | Zm00001eb325760_P001 | 0.970 |
| PUZ64751 | Sspon.03G | KQL14282 | TKW25840 | KXG22544 | Zm00001eb296100_P002 | 0.913 |
| PUZ61560 | Sspon.08G | KQL10123 | TKW20714 | EER88152 | Zm00001eb280030_P002 | 0.906 |
| PUZ67109 | Sspon.03G | KQL03232 | TKW28549 | KXG31480 | Zm00001eb339320_P001 | 0.852 |
| genblast_C | Sspon.02G | KQL25789 | TKW34748 | KXG36225 | Zm00001eb321440_P001 | 0.933 |
| PUZ46918 | Sspon.05G | KQK97030 | TKW04085 | KXG26154 | Zm00001eb421370_P001 | 0.939 |
| genblast_C | Sspon.03G | genblast_C | genblast_C | EES01323 | Zm00001eb360910_P003 | 0.839 |

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| PUZ54210 | genblast_C | KQL07498 | TKW17449 | EES01669 | Zm00001eb368850_P001 | 0.863 |
| PUZ37055 | Sspon.01G | KQK87129 | TKV91387 | EER90880 | Zm00001eb057100_P001 | 0.938 |
| PUZ74051 | genblast_C | KQL28751 | TKW38015 | EES04516 | Zm00001eb232250_P002 | 0.910 |
| PUZ67695 | Sspon.02G | KQL17019 | TKW29346 | EES17302 | Zm00001eb030510_P003 | 0.879 |
| PUZ55483 | Sspon.03G | KQL06282 | TKW15906 | KXG33052 | Zm00001eb157580_P001 | 0.935 |
| PUZ44686 | Sspon.02G | KQK94489 | TKW00554 | KXG34919 | Zm00001eb305070_P001 | 0.809 |
| PUZ68594 | Sspon.02G | KQL22631 | TKW30697 | OQU88523 | Zm00001eb301170_P002 | 0.861 |
| PUZ42511 | Sspon.01G | KQK92263 | TKV97824 | KXG40032 | Zm00001eb006310_P002 | 0.920 |
| PUZ58333 | Sspon.07G | KQL04673 | TKW13789 | EES00189 | Zm00001eb122300_P001 | 0.942 |
| PUZ53713 | Sspon.03G | KQL07950 | TKW17984 | EES01846 | Zm00001eb146070_P003 | 0.935 |

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|---|---|---|---|---|---|---|
| PUZ64098 | Sspon.03G | KQK99253 | TKW06996 | EES19051 | Zm00001eb282730_P001 | 0.923 |
| PUZ51272 | Sspon.06G | KQL01500 | TKW09905 | EES13759 | Zm00001eb170770_P001 | 0.823 |
| PUZ69379 | Sspon.02G | KQL23359 | TKW31657 | EER98417 | Zm00001eb305950_P004 | 0.885 |
| PUZ78245 | Sspon.04G | KQL32103 | TKW42257 | EES06017 | Zm00001eb191410_P001 | 0.889 |
| PUZ57393 | Sspon.03G | KQL03830 | TKW12719 | EES00516 | Zm00001eb127990_P001 | 0.971 |
| PUZ63031 | Sspon.07G | KQK99612 | TKW07453 | EES16681 | Zm00001eb139560_P001 | 0.858 |

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| PUZ78315 | Sspon.04G | KQL32180 | TKW42343 | EES06041 | Zm00001eb191020_P001 | 0.903 |
| PUZ45774 | Sspon.06G | KQK95799 | TKW02379 | OQU83991 | Zm00001eb165250_P001 | 0.961 |
| PUZ77543 | genblast_C | KQL31410 | TKW41459 | EES07298 | Zm00001eb190360_P001 | 0.938 |

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| PUZ59341 | Sspon.08G | KQL11854 | TKW22973 | KXG20709 | Zm00001eb273340_P002 | 0.918 |
| PUZ41693 | genblast_C | KQK91475 | TKV96858 | EER95101 | Zm00001eb012330_P001 | 0.929 |

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| PUZ73482 | Sspon.01G | KQL27217 | TKW36570 | EER99920 | Zm00001eb330880_P003 | 0.944 |
| PUZ66996 | genblast_C | KQL16204 | TKW28201 | EES17203 | Zm00001eb409030_P001 | 0.847 |
| PUZ78028 | Sspon.04G | genblast_C | TKW42019 | EES07673 | Zm00001eb192480_P001 | 0.912 |

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| PUZ67555 | Sspon.02G | KQL16496 | TKW28605 | KXG23773 | Zm00001eb029370_P002 | 0.950 |

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| PUZ53916 | Sspon.07G | KQL07772 | TKW17773 | EES03894 | Zm00001eb147740_P001 | 0.940 |
| PUZ55379 | Sspon.03G | KQL06389 | TKW16015 | EES03429 | Zm00001eb156920_P001 | 0.976 |

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| PUZ40040 | Sspon.01G | KQK89848 | TKV94833 | EER91904 | Zm00001eb390680_P001 | 0.965 |
| PUZ47194 | genblast_C | KQK97308 | TKW04449 | EES12185 | Zm00001eb082620_P002 | 0.903 |
| PUZ41890 | Sspon.01G | KQK91656 | TKV97057 | EER92543 | Zm00001eb398470_P001 | 0.911 |
| PUZ65429 | Sspon.07G | KQL14914 | TKW26581 | KXG22249 | Zm00001eb291370_P001 | 0.970 |
| PUZ55568 | Sspon.03G | KQL06121 | TKW15711 | genblast_C | Zm00001eb158240_P001 | 0.954 |
| PUZ58866 | Sspon.03G | KQL03209 | TKW11936 | EER99993 | Zm00001eb119000_P002 | 0.962 |
| genblast_C | Sspon.05G | KQK93761 | TKV99524 | KXG27846 | Zm00001eb414490_P001 | 0.894 |
| PUZ65981 | Sspon.07G | KQL15471 | TKW27277 | KXG22004 | Zm00001eb349360_P001 | 0.925 |
| PUZ47015 | genblast_C | KQK97123 | TKW04212 | EES10723 | Zm00001eb421730_P001 | 0.934 |
| PUZ38035 | Sspon.01G | KQK88134 | TKV92588 | genblast_C | Zm00001eb212440_P001 | 0.975 |
| PUZ61757 | Sspon.08G | KQL09880 | TKW20397 | EER88029 | Zm00001eb373630_P002 | 0.942 |
| PUZ59760 | Sspon.08G | KQL11196 | TKW22098 | OQU76787 | Zm00001eb388610_P001 | 0.887 |

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| PUZ37145 | Sspon.01GKQK87233 | TKV91500 | EER90917 | Zm00001eb215410_P001 | 0.964 |

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| PUZ53897 | Sspon.03GKQL07785 | TKW17786 | OQU87881 | Zm00001eb147630_P001 | 0.918 |
| PUZ56363 | Sspon.03GKQL05411 | TKW14790 | EES03075 | Zm00001eb162950_P003 | 0.794 |
| PUZ63577 | Sspon.07GKQL13463 | TKW24806 | EES19201 | Zm00001eb284070_P001 | 0.894 |
| PUZ65269 | Sspon.07GKQL14764 | TKW26388 | EER89928 | Zm00001eb292700_P001 | 0.867 |
| PUZ65298 | Sspon.08GKQL14831 | TKW26466 | KXG20605 | Zm00001eb390260_P003 | 0.909 |
| PUZ66156 | Sspon.07Ggenblast_C | TKW27514 | EES19478 | Zm00001eb350830_P001 | 0.916 |
| PUZ40791 | Sspon.01GKQK90546 | TKV95733 | OQU92465 | Zm00001eb019260_P001 | 0.917 |

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| PUZ74087 | Sspon.04GKQL28708 | TKW37966 | EES06292 | Zm00001eb207900_P001 | 0.789 |
| PUZ40167 | Sspon.01GKQK89963 | TKV94984 | EER94500 | genblast_Os10t0556100-01Zm0 | |
| PUZ53913 | genblast_Cgenblast_C | TKW17775 | EES03897 | Zm00001eb367410_P002 | 0.913 |
| PUZ67318 | Sspon.02Ggenblast_Z | TKW28926 | KXG23975 | Zm00001eb410560_P006 | 0.857 |

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| PUZ45426 | Sspon.06GKQK95245 | TKW01562 | EES10057 | Zm00001eb167310_P002 | 0.793 |
| PUZ69641 | Sspon.02GKQL23633 | TKW31983 | EER96375 | Zm00001eb095890_P002 | 0.965 |
| PUZ60125 | Sspon.08Ggenblast_C | TKW22630 | EER88574 | Zm00001eb386190_P001 | 0.928 |
| PUZ66294 | genblast_ZKQL15780 | TKW27690 | KXG21855 | Zm00001eb350990_P002 | 0.869 |
| PUZ58496 | Sspon.07GKQL04819 | TKW13972 | EES00128 | Zm00001eb337830_P001 | 0.851 |
| PUZ64783 | Sspon.07GKQL14320 | TKW25880 | EES19949 | Zm00001eb295870_P001 | 0.924 |
| PUZ76566 | Sspon.04GKQL30510 | TKW40350 | EES07150 | Zm00001eb247160_P001 | 0.892 |
| PUZ49131 | Sspon.05GKQK99135 | TKW06849 | EES12940 | Zm00001eb069110_P001 | 0.927 |
| PUZ77275 | Sspon.04GKQL31141 | TKW41147 | EES07395 | Zm00001eb252120_P001 | 0.970 |
| PUZ42367 | Sspon.01GKQK92119 | TKV97647 | EER95331 | Zm00001eb400990_P003 | 0.944 |
| PUZ40945 | Sspon.01GKQK90733 | TKV95904 | EER94794 | Zm00001eb394130_P001 | 0.848 |
| PUZ42348 | Sspon.01Ggenblast_C | TKV97634 | OQU93054 | Zm00001eb007900_P002 | 0.899 |

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| PUZ48956 | genblast_C | KQK98969 | TKW06634 | EES11442 | Zm00001eb070390_P001 | 0.901 |
| PUZ42929 | Sspon.04G | KQK92657 | TKV98301 | EES04386 | genblast_Os03t0138900-01_Ze | |
| PUZ42478 | Sspon.01G | KQK92224 | TKV97778 | EER95365 | Zm00001eb006560_P001 | 0.919 |
| PUZ57638 | genblast_C | KQL04052 | TKW12984 | KXG32119 | Zm00001eb126680_P002 | 0.825 |
| PUZ50846 | Sspon.06G | KQL01223 | TKW09545 | EES13636 | Zm00001eb177940_P001 | 0.928 |
| PUZ77005 | Sspon.04G | KQL30895 | TKW40841 | EES07470 | Zm00001eb250230_P002 | 0.842 |
| PUZ36882 | Sspon.01G | KQK86943 | TKV91167 | EER93393 | Zm00001eb214030_P002 | 0.828 |
| PUZ48628 | Sspon.04G | KQK98642 | TKW06191 | KXG27001 | Zm00001eb428170_P001 | 0.935 |

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| PUZ59673 | Sspon.08G | KQL11113 | TKW22007 | EER88765 | Zm00001eb389360_P001 | 0.851 |

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| PUZ37103 | Sspon.01G | KQK87172 | TKV91433 | EER93478 | Zm00001eb056780_P001 | 0.967 |
| PUZ37096 | Sspon.01G | KQK87169 | TKV91430 | EER93477 | Zm00001eb215180_P001 | 0.882 |
| PUZ76857 | Sspon.04G | KQL30761 | TKW40680 | KXG31098 | Zm00001eb249280_P001 | 0.894 |
| PUZ63742 | Sspon.07G | KQL13087 | TKW24281 | EES17609 | Zm00001eb265980_P001 | 0.910 |
| PUZ41694 | Sspon.01G | KQK91476 | TKV96860 | KXG39690 | Zm00001eb012310_P001 | 0.942 |
| PUZ74316 | Sspon.04G | KQL28498 | TKW37725 | EES06357 | Zm00001eb206900_P001 | 0.884 |
| PUZ64721 | Sspon.07G | KQL14249 | TKW25803 | EES18712 | Zm00001eb296340_P001 | 0.923 |
| PUZ70059 | Sspon.02G | KQL23931 | TKW32347 | KXG35239 | Zm00001eb308670_P001 | 0.896 |
| PUZ36560 | Sspon.01G | KQK86644 | TKV90801 | EER93281 | Zm00001eb061070_P001 | 0.944 |
| PUZ53287 | Sspon.03G | KQL08330 | TKW18506 | EES01962 | Zm00001eb143350_P001 | 0.846 |
| PUZ68205 | Sspon.02G | KQL22132 | TKW30011 | EER95743 | Zm00001eb298480_P001 | 0.979 |
| PUZ70714 | Sspon.02G | KQL24492 | TKW33154 | KXG35635 | Zm00001eb099490_P001 | 0.855 |

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| PUZ52508 | Sspon.06G | KQL02758 | TKW11528 | KXG25466 | Zm00001eb198450_P003 | 0.876 |
| PUZ73595 | genblast_C | KQL27324 | TKW36697 | KXG36969 | Zm00001eb112090_P001 | 0.869 |
| PUZ41211 | Sspon.01G | KQK90993 | TKV96242 | EER94902 | Zm00001eb016080_P001 | 0.926 |

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| PUZ65994 | Sspon.07GKQL15481 | TKW27295 | KXG21997 | Zm00001eb349480_P002 | 0.954 |
| PUZ78072 | Sspon.04GKQL31941 | TKW42063 | KXG31281 | Zm00001eb192250_P002 | 0.908 |
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| PUZ70219 | Sspon.02GKQL24039 | TKW32525 | OQU8922 | Zm00001eb309320_P001 | 0.905 |
| PUZ74723 | Sspon.04GKQL28104 | genblast_C | KXG29821 | Zm00001eb240050_P001 | 0.864 |
| PUZ41166 | Sspon.01GKQK90958 | TKV96197 | EER92298 | Zm00001eb016390_P001 | 0.857 |
| PUZ50275 | Sspon.06GKQL00662 | TKW08771 | EES14615 | genblast_Os08t0167400-00_Ze | |
| PUZ73946 | Sspon.04GKQL28856 | TKW38169 | OQU8430 | Zm00001eb231310_P001 | 0.941 |
| PUZ65985 | Sspon.07GKQL15476 | TKW27284 | EES19522 | Zm00001eb349390_P004 | 0.933 |
| PUZ55216 | Sspon.03GKQL06563 | TKW16222 | KXG33191 | Zm00001eb155870_P001 | 0.903 |
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| PUZ71473 | Sspon.02GKQL25247 | TKW34044 | EER97020 | Zm00001eb317920_P001 | 0.937 |
| PUZ48581 | genblast_C | KQK98583 | TKW06133 | KXG26973 | genblast_Os04t0580500-01_Ze |
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| PUZ42115 | Sspon.01GKQK91883 | TKV97360 | EER95243 | Zm00001eb009140_P001 | 0.966 |
| PUZ70260 | Sspon.02GKQL24063 | TKW32554 | OQU8924 | Zm00001eb309450_P001 | 0.960 |
| PUZ43235 | Sspon.01GKQK93012 | TKV98671 | EER95660 | Zm00001eb404180_P001 | 0.858 |
| PUZ49227 | Sspon.05GKQK99231 | TKW06966 | EES12978 | Zm00001eb068390_P003 | 0.963 |
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| PUZ49762 | Sspon.06GKQL00193 | TKW08062 | KXG24174 | Zm00001eb260200_P001 | 0.854 |
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| PUZ57040 | genblast_CKQL03456 | TKW12233 | KXG32375 | Zm00001eb130290_P001 | 0.920 |
| PUZ55921 | Sspon.03GKQL05779 | TKW15253 | OQU8713 | Zm00001eb357790_P001 | 0.934 |
| PUZ54139 | Sspon.03GKQL07562 | TKW17532 | EES03831 | Zm00001eb149010_P002 | 0.930 |
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| PUZ71330 | Sspon.02GKQL25118 | TKW33889 | KXG35937 | Zm00001eb317060_P001 | 0.847 |
| PUZ43267 | Sspon.01GKQK93044 | TKV98730 | KXG40395 | Zm00001eb000590_P001 | 0.983 |
| PUZ55597 | Sspon.03GKQL06093 | TKW15654 | EES01166 | Zm00001eb158500_P001 | 0.927 |
| PUZ73116 | genblast_CKQL26862 | TKW36096 | EER99772 | Zm00001eb328720_P002 | 0.931 |
| PUZ41060 | Sspon.01GKQK90841 | TKV96046 | EER94844 | Zm00001eb017140_P001 | 0.838 |
| PUZ66767 | genblast_CKQL16136 | TKW28112 | genblast_C | Zm00001eb350760_P002 | 0.938 |

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| PUZ48244 | Sspon.04G | KQK98308 | TKW05711 | EES11198 | Zm00001eb075230_P001 | 0.899 |
| PUZ36844 | Sspon.01G | KQK86928 | TKV91151 | EER93387 | Zm00001eb213950_P001 | 0.816 |

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| PUZ74378 | Sspon.08G | KQL28437 | TKW37644 | EES04642 | Zm00001eb234120_P001 | 0.890 |
| PUZ70516 | Sspon.02G | KQL24287 | TKW32901 | KXG35515 | Zm00001eb311380_P001 | 0.954 |
| PUZ76413 | genblast_C | KQL30352 | TKW40131 | EES07108 | Zm00001eb246410_P001 | 0.939 |
| PUZ72604 | Sspon.02G | KQL26368 | TKW35477 | EER99590 | Zm00001eb325180_P001 | 0.913 |
| PUZ49207 | Sspon.05G | KQK99212 | TKW06947 | KXG27258 | Zm00001eb432130_P001 | 0.942 |

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| PUZ37102 | Sspon.01G | KQK87174 | TKV91434 | EER93480 | Zm00001eb056760_P001 | 0.828 |

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| PUZ56137 | Sspon.03G | KQL05658 | TKW15109 | EES00948 | Zm00001eb160210_P001 | 0.801 |
| PUZ64512 | Sspon.07G | KQL14049 | TKW25555 | EES18778 | Zm00001eb297490_P003 | 0.847 |
| PUZ63868 | Sspon.07G | KQL13218 | TKW24455 | EES17657 | Zm00001eb354820_P001 | 0.927 |
| PUZ36070 | Sspon.01G | KQK86178 | TKV90185 | KXG37122 | Zm00001eb210780_P001 | 0.940 |
| PUZ71615 | Sspon.02G | KQL25396 | TKW34224 | EER99218 | Zm00001eb319010_P001 | 0.971 |

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| PUZ74875 | Sspon.04G | KQL27925 | TKW37024 | KXG29907 | Zm00001eb204560_P001 | 0.977 |
| PUZ64605 | Sspon.07G | KQL14154 | TKW25677 | KXG22612 | Zm00001eb297070_P002 | 0.918 |
| PUZ64158 | Sspon.07G | KQK99295 | TKW07040 | EES19076 | Zm00001eb353850_P002 | 0.960 |
| PUZ55835 | Sspon.03G | KQL05876 | TKW15369 | KXG32891 | Zm00001eb358170_P001 | 0.989 |
| PUZ57992 | Sspon.03G | KQL04353 | TKW13382 | EES00333 | Zm00001eb335790_P001 | 0.912 |

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| PUZ43758 | Sspon.05G | genblast_C | TKV99370 | EES08014 | Zm00001eb092230_P002 | 0.887 |
| PUZ72405 | Sspon.02G | KQL26165 | TKW35195 | EER99509 | Zm00001eb323610_P001 | 0.881 |
| PUZ75621 | Sspon.01G | KQL29530 | TKW39015 | EER95613 | Zm00001eb403760_P001 | 0.952 |
| PUZ71943 | genblast_C | KQL25687 | TKW34617 | EER99353 | Zm00001eb320350_P001 | 0.970 |
| PUZ73372 | Sspon.02G | KQL27140 | TKW36463 | EER97716 | Zm00001eb111340_P001 | 0.966 |
| PUZ47788 | Sspon.05G | KQK97880 | TKW05182 | KXG26625 | genblast_Os04t0493300-01_Ze | |
| PUZ62125 | Sspon.08G | KQL09684 | TKW20138 | EER89228 | Zm00001eb376530_P004 | 0.977 |
| PUZ46042 | Sspon.05G | genblast_C | TKW02902 | EES10336 | Zm00001eb089560_P001 | 0.851 |
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| PUZ53417 | Sspon.03G | KQL08207 | TKW18334 | EES04061 | Zm00001eb365420_P002 | 0.966 |
| genblast_C | Sspon.05G | genblast_C | TKW04283 | EES10743 | Zm00001eb083820_P001 | 0.955 |
| PUZ55473 | Sspon.03G | KQL06294 | TKW15915 | KXG33059 | Zm00001eb157520_P001 | 0.938 |
| PUZ73068 | Sspon.02G | KQL26802 | TKW36029 | EER97595 | Zm00001eb328350_P001 | 0.899 |
| PUZ64321 | Sspon.05G | KQL13857 | TKW25323 | OQU77566 | Zm00001eb283600_P001 | 0.957 |
| PUZ42740 | Sspon.01G | KQK92480 | TKV98084 | EER95466 | Zm00001eb403300_P001 | 0.923 |
| PUZ43107 | Sspon.01G | KQK92858 | TKV98512 | genblast_C | Zm00001eb001700_P001 | 0.933 |
| PUZ54832 | genblast_C | KQL06947 | TKW16719 | EES01465 | Zm00001eb153550_P001 | 0.848 |
| PUZ66021 | Sspon.07G | KQL15511 | TKW27337 | EES19519 | Zm00001eb287870_P001 | 0.967 |
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| PUZ42066 | Sspon.01G | KQK91835 | TKV97306 | EER92605 | Zm00001eb399340_P001 | 0.885 |
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| PUZ73973 | Sspon.04G | KQL28830 | TKW38124 | EES04470 | Zm00001eb231570_P004 | 0.958 |
| PUZ43748 | Sspon.05G | KQK93674 | TKV99385 | EES08020 | Zm00001eb202130_P002 | 0.907 |
| PUZ60480 | Sspon.08G | KQL10821 | TKW21667 | OQU76485 | Zm00001eb382950_P001 | 0.905 |
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| genblast_C | Sspon.02G | KQL24371 | TKW33001 | KXG35573 | Zm00001eb099090_P002 | 0.961 |
| PUZ75896 | Sspon.04G | KQL29862 | TKW39469 | EES06898 | Zm00001eb242480_P002 | 0.962 |
| PUZ47095 | Sspon.05G | KQK97222 | TKW04330 | EES12138 | Zm00001eb083540_P001 | 0.963 |
| PUZ78407 | Sspon.04G | KQL32259 | TKW42439 | EES06072 | Zm00001eb190610_P001 | 0.771 |
| genblast_C | Sspon.05G | KQK96318 | TKW03107 | EES10406 | Zm00001eb418250_P001 | 0.931 |
| PUZ56179 | Sspon.03G | KQL05609 | TKW15053 | OQU87026 | Zm00001eb356930_P002 | 0.853 |
| PUZ74640 | genblast_C | KQL28173 | TKW37326 | EES04731 | Zm00001eb205470_P001 | 0.888 |
| PUZ78171 | Sspon.04G | KQL32040 | TKW42189 | KXG31328 | Zm00001eb191660_P001 | 0.951 |
| PUZ65337 | Sspon.07G | KQL14855 | TKW26500 | EES19767 | Zm00001eb291890_P001 | 0.930 |

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| PUZ50124 | Sspon.06GKQL00787 | TKW08952 | EES14552 | Zm00001eb416240_P001 | 0.944 |
| PUZ62128 | Sspon.08GKQL09692 | TKW20147 | KXG19336 | Zm00001eb376570_P002 | 0.982 |
| PUZ54108 | Sspon.03GKQL07598 | TKW17566 | KXG33654 | Zm00001eb148880_P004 | 0.981 |
| PUZ45584 | Sspon.06GKQK95510 | TKW01960 | KXG28988 | Zm00001eb282850_P001 | 0.825 |
| PUZ60519 | Sspon.08GKQL10790 | TKW21640 | EER89831 | Zm00001eb278050_P001 | 0.920 |
| PUZ48576 | Sspon.04GKQK98580 | TKW06128 | genblast_C | Zm00001eb073130_P001 | 0.951 |
| PUZ66391 | Sspon.01GKQL15852 | TKW27784 | OQU7784 | Zm00001eb285770_P001 | 0.870 |
| PUZ50394 | Sspon.06GKQL00560 | TKW08639 | EES14664 | Zm00001eb171710_P001 | 0.933 |
| PUZ59917 | Sspon.08GKQL11398 | TKW22371 | EER90053 | Zm00001eb388100_P001 | 0.816 |
| PUZ73871 | Sspon.04GKQL28908 | TKW38241 | EES04433 | Zm00001eb231010_P001 | 0.912 |
| PUZ58215 | Sspon.03GKQL04562 | TKW13631 | EES02394 | Zm00001eb123220_P001 | 0.878 |

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| PUZ71143 | genblast_CKQL24914 | TKW33633 | EER96905 | Zm00001eb101350_P001 | 0.903 |
| PUZ53295 | Sspon.03GKQL08322 | TKW18497 | EES04108 | Zm00001eb143390_P002 | 0.940 |

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|---|---|---|---|---|---|
| PUZ59183 | Sspon.08GKQL12123 | TKW23308 | EER90349 | genblast_Os06t0707000-00_Ze | |
| PUZ60025 | Sspon.08GKQL11503 | TKW22506 | EER88620 | Zm00001eb386320_P001 | 0.874 |
| PUZ71415 | Sspon.02GKQL12669 | TKW23746 | EER99142 | Zm00001eb317590_P001 | 0.934 |
| PUZ64094 | Sspon.07GKQK99247 | TKW06986 | EES19045 | Zm00001eb353970_P002 | 0.965 |
| PUZ52714 | Sspon.06GKQL03001 | TKW11798 | OQU8070 | Zm00001eb175850_P001 | 0.921 |
| PUZ71786 | Sspon.02GKQL25539 | TKW34408 | EER99290 | Zm00001eb104050_P001 | 0.934 |
| PUZ60797 | Sspon.08GKQL10320 | TKW20977 | EER88246 | Zm00001eb380690_P001 | 0.957 |
| PUZ56175 | Sspon.02GKQL05604 | TKW15051 | EER96725 | Zm00001eb312410_P001 | 0.957 |
| PUZ52425 | Sspon.06GKQL02688 | TKW11430 | EES15295 | Zm00001eb036950_P001 | 0.951 |
| PUZ43102 | Sspon.01GKQK92849 | TKV98507 | EER95608 | Zm00001eb001760_P001 | 0.884 |
| PUZ68326 | Sspon.01GKQL22353 | TKW30329 | EER95824 | Zm00001eb299290_P001 | 0.906 |
| PUZ55842 | Sspon.03GKQL05862 | TKW15351 | EES03272 | Zm00001eb162020_P003 | 0.956 |
| PUZ68306 | Sspon.02GKQL22324 | TKW30282 | EER95817 | Zm00001eb117910_P001 | 0.806 |

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| PUZ72548 | Sspon.02GKQL26300 | TKW35399 | EER99569 | Zm00001eb324700_P001 | 0.947 |
| PUZ37251 | genblast_CKQK87348 | TKV91634 | KXG37677 | Zm00001eb055800_P001 | 0.842 |
| PUZ63111 | Sspon.05GKQK99511 | TKW07354 | KXG23067 | Zm00001eb407890_P002 | 0.930 |
| PUZ74173 | Sspon.04GKQL28635 | TKW37875 | KXG29521 | Zm00001eb207650_P001 | 0.948 |
| PUZ73222 | Sspon.02GKQL26950 | TKW36206 | KXG36823 | Zm00001eb329400_P001 | 0.922 |

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| PUZ49064 | Sspon.05G | KQK99074 | TKW06769 | EES11495 | Zm00001eb069700_P002 | 0.846 |
| PUZ62465 | genblast_C | KQL09023 | TKW19313 | EER89081 | Zm00001eb269050_P001 | 0.969 |
| PUZ52959 | Sspon.03G | KQL08647 | TKW18898 | KXG34133 | Zm00001eb362800_P001 | 0.947 |
| PUZ43700 | Sspon.05G | KQK99868 | TKW07783 | OQU87033 | Zm00001eb406520_P001 | 0.887 |
| PUZ76978 | Sspon.04G | KQL30874 | TKW40819 | OQU85669 | genblast_Os02t0667600-03_Zea | |
| PUZ47081 | Sspon.05G | KQK97211 | TKW04315 | EES10771 | Zm00001eb422010_P002 | 0.982 |
| PUZ52225 | Sspon.06G | KQL02478 | TKW11174 | KXG25613 | Zm00001eb174520_P001 | 0.854 |
| PUZ36014 | Sspon.01G | KQK86112 | TKV90096 | EER90487 | Zm00001eb210510_P002 | 0.907 |
| PUZ50591 | Sspon.06G | KQL00361 | TKW08308 | EES14722 | Zm00001eb414030_P001 | 0.947 |
| PUZ65468 | genblast_C | KQL14956 | TKW26641 | KXG22238 | Zm00001eb291150_P001 | 0.925 |
| PUZ77346 | Sspon.04G | genblast_C | TKW41237 | EES07366 | Zm00001eb252690_P001 | 0.962 |
| PUZ41888 | Sspon.01G | KQK91653 | TKV97054 | EER92541 | Zm00001eb398460_P002 | 0.970 |
| PUZ71493 | Sspon.02G | KQL25270 | TKW34069 | EER99166 | Zm00001eb318100_P001 | 0.880 |
| PUZ72733 | Sspon.02G | KQL26481 | TKW35591 | EER97466 | Zm00001eb326130_P004 | 0.933 |
| PUZ52068 | Sspon.06G | KQL02362 | TKW11015 | genblast_Z | Zm00001eb199550_P002 | 0.909 |
| PUZ47786 | genblast_C | KQK97877 | TKW05180 | KXG26623 | Zm00001eb425590_P004 | 0.953 |
| PUZ67570 | Sspon.07G | KQL16485 | TKW28591 | EES15849 | Zm00001eb136300_P001 | 0.952 |
| PUZ76923 | Sspon.04G | KQL30823 | TKW40756 | EES05773 | Zm00001eb249700_P001 | 0.980 |
| PUZ55374 | Sspon.07G | KQL06395 | TKW16021 | KXG33106 | Zm00001eb156860_P001 | 0.894 |
| PUZ64402 | Sspon.07G | genblast_C | TKW25424 | KXG20996 | Zm00001eb356320_P004 | 0.943 |
| PUZ54965 | Sspon.03G | genblast_C | TKW16549 | KXG33297 | Zm00001eb154360_P002 | 0.907 |
| PUZ42664 | Sspon.01G | KQK92404 | TKV98000 | EER92797 | Zm00001eb402430_P001 | 0.864 |
| PUZ72763 | Sspon.02G | KQL26502 | TKW35615 | EER99638 | Zm00001eb326410_P001 | 0.953 |

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| PUZ57409 | Sspon.03G | KQL03846 | TKW12742 | EES00509 | Zm00001eb127900_P001 | 0.938 |
| PUZ60792 | Sspon.08G | KQL10255 | TKW20896 | KXG19762 | Zm00001eb280540_P002 | 0.955 |

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| PUZ73046 | Sspon.02G | genblast_C | genblast_C | EER99751 | Zm00001eb328250_P001 | 0.944 |
| PUZ36286 | Sspon.01G | genblast_C | TKV90426 | EER93171 | Zm00001eb063100_P001 | 0.961 |
| PUZ57064 | Sspon.03G | KQL03488 | TKW12261 | EES02848 | Zm00001eb340320_P002 | 0.936 |

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| PUZ74082 | Sspon.04G | KQL28718 | TKW37975 | KXG29488 | Zm00001eb232450_P002 | 0.946 |
| PUZ41200 | Sspon.01G | KQK90985 | TKV96230 | KXG39422 | Zm00001eb016120_P001 | 0.895 |
| PUZ68686 | Sspon.02G | KQL22724 | TKW30787 | EER98073 | Zm00001eb301500_P001 | 0.961 |
| PUZ74465 | Sspon.04G | KQL28331 | TKW37526 | EES06442 | Zm00001eb236550_P001 | 0.879 |
| PUZ41783 | Sspon.01G | KQK91519 | TKV96902 | EER92505 | Zm00001eb011680_P001 | 0.910 |
| PUZ38462 | Sspon.01G | KQK88533 | TKV93127 | KXG38256 | Zm00001eb044780_P005 | 0.922 |
| PUZ73062 | Sspon.02G | KQL26801 | TKW36028 | KXG36766 | Zm00001eb328340_P001 | 0.749 |
| PUZ59771 | genblast_C | KQL11220 | TKW22123 | EER88721 | Zm00001eb386840_P001 | 0.951 |

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| PUZ44832 | Sspon.06G | KQK94645 | TKW00761 | EES08518 | Zm00001eb112950_P001 | 0.981 |
| PUZ77293 | Sspon.04G | KQL31168 | TKW41178 | genblast_C | Zm00001eb188580_P001 | 0.912 |
| PUZ76965 | Sspon.04G | KQL30865 | TKW40803 | EES07483 | Zm00001eb249980_P001 | 0.934 |
| PUZ36170 | Sspon.01G | KQK86266 | TKV90296 | genblast_C | Zm00001eb211080_P001 | 0.938 |
| PUZ58346 | Sspon.03G | KQL04684 | TKW13807 | OQU86191 | Zm00001eb122200_P003 | 0.932 |
| PUZ41987 | Sspon.01G | KQK91751 | TKV97191 | KXG39800 | Zm00001eb399090_P003 | 0.954 |
| PUZ44041 | Sspon.05G | KQK93945 | TKV99793 | EES09471 | Zm00001eb202050_P001 | 0.869 |

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| PUZ35978 | Sspon.01G | KQK86077 | TKV90056 | KXG37075 | Zm00001eb210370_P004 | 0.879 |
| PUZ76806 | Sspon.04G | KQL30718 | TKW40617 | OQU85751 | Zm00001eb186170_P001 | 0.958 |

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| PUZ42551 | Sspon.01G | KQK92298 | TKV97868 | EER92749 | Zm00001eb005980_P001 | 0.807 |
| PUZ41622 | Sspon.01G | KQK91409 | TKV96775 | KXG39646 | Zm00001eb012870_P001 | 0.940 |
| PUZ38715 | Sspon.01G | KQK88778 | TKV93460 | genblast_C | Zm00001eb222040_P001 | 0.879 |
| PUZ38693 | Sspon.01G | KQK88733 | TKV93385 | EER91487 | Zm00001eb045880_P001 | 0.906 |

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| PUZ59336 | Sspon.08G | KQL11840 | TKW22955 | KXG20722 | Zm00001eb226240_P001 | 0.986 |
| PUZ67715 | genblast_C | KQL17031 | TKW29366 | OQU79487 | Zm00001eb030680_P001 | 0.927 |
| PUZ46891 | genblast_C | KQK97007 | TKW04052 | EES12043 | Zm00001eb085110_P001 | 0.914 |
| PUZ49585 | genblast_C | KQL12712 | TKW23807 | KXG27470 | Zm00001eb065740_P001 | 0.863 |
| PUZ46753 | Sspon.05G | genblast_C | TKW03878 | EES11972 | Zm00001eb420850_P001 | 0.948 |

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| PUZ72430 | Sspon.02G | KQL26191 | TKW35232 | KXG36449 | Zm00001eb323760_P001 | 0.980 |
| PUZ74247 | genblast_C | KQL28573 | TKW37810 | KXG29551 | Zm00001eb207380_P002 | 0.799 |
| PUZ49008 | Sspon.05G | KQK99019 | TKW06705 | EES11463 | Zm00001eb070120_P001 | 0.933 |

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| PUZ45129 | Sspon.06G | KQK94856 | TKW01087 | EES08635 | Zm00001eb197620_P001 | 0.937 |
| PUZ60339 | Sspon.08G | KQL10957 | TKW21836 | OQU76539 | Zm00001eb384870_P001 | 0.828 |
| PUZ78212 | Sspon.04G | KQL32078 | TKW42229 | KXG31345 | Zm00001eb191520_P001 | 0.805 |
| PUZ71478 | Sspon.02G | genblast_C | TKW34050 | KXG35983 | Zm00001eb317930_P004 | 0.889 |
| PUZ78207 | Sspon.04G | KQL32071 | TKW42221 | OQU85937 | Zm00001eb191560_P001 | 0.935 |

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| PUZ72479 | Sspon.02GKQL26240 | TKW35294 | EER99544 | Zm00001eb106850_P001 | 0.853 |
| PUZ69373 | Sspon.02GKQL23355 | TKW31650 | EER96281 | Zm00001eb305940_P001 | 0.933 |
| PUZ52255 | Sspon.06GKQL02512 | TKW11220 | EES15358 | Zm00001eb035650_P002 | 0.920 |
| PUZ57768 | Sspon.03GKQL04150 | TKW13136 | KXG32065 | Zm00001eb125930_P001 | 0.915 |
| PUZ61413 | Sspon.03GKQL09952 | TKW20495 | EER96626 | Zm00001eb062820_P002 | 0.850 |
| PUZ78311 | genblast_CKQL32174 | TKW42333 | EES06038 | Zm00001eb191070_P001 | 0.968 |
| PUZ58815 | Sspon.03GKQL03262 | TKW11998 | EES02196 | Zm00001eb109700_P001 | 0.914 |
| PUZ42579 | Sspon.01GKQK92324 | TKV97907 | KXG40058 | Zm00001eb401920_P001 | 0.953 |
| PUZ71791 | Sspon.02Ggenblast_C | TKW34416 | OQU89856 | Zm00001eb321150_P001 | 0.986 |
| PUZ45510 | Sspon.06GKQK95389 | TKW01791 | OQU83842 | Zm00001eb166800_P001 | 0.885 |
| PUZ37944 | Sspon.01GKQK88063 | TKV92470 | EER93797 | Zm00001eb051330_P001 | 0.750 |
| PUZ71973 | Sspon.02GKQL25725 | TKW34660 | EER99361 | Zm00001eb320200_P001 | 0.928 |
| PUZ63708 | Sspon.07Ggenblast_C | TKW24643 | EES17594 | Zm00001eb355620_P001 | 0.775 |
| PUZ65923 | Sspon.03GKQL15420 | TKW27192 | EES02297 | Zm00001eb337940_P001 | 0.953 |
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| PUZ75075 | Sspon.04GKQL27878 | TKW36964 | EES04851 | Zm00001eb238330_P001 | 0.980 |
| PUZ69598 | Sspon.02GKQL23588 | TKW31908 | OQU89013 | Zm00001eb096100_P001 | 0.891 |
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| PUZ50856 | Sspon.06GKQL01248 | TKW09568 | EES13643 | Zm00001eb412050_P003 | 0.916 |
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| PUZ52428 | Sspon.06Ggenblast_C | TKW11433 | EES14176 | Zm00001eb036970_P001 | 0.895 |
| PUZ60433 | Sspon.08GKQL10867 | TKW21718 | EER89868 | Zm00001eb383330_P002 | 0.990 |

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| PUZ71831 | Sspon.02G | KQL25593 | TKW34473 | KXG36124 | Zm00001eb320950_P001 | 0.966 |
| PUZ44539 | Sspon.05G | KQK94289 | TKW00290 | EES09651 | Zm00001eb166630_P001 | 0.842 |
| PUZ76908 | Sspon.04G | KQL30811 | TKW40743 | OQU8569 | Zm00001eb186650_P001 | 0.847 |
| PUZ37597 | genblast_C | KQK87723 | TKV92046 | EER91079 | Zm00001eb217350_P002 | 0.943 |
| PUZ72176 | Sspon.02G | KQL25927 | TKW34901 | EER97266 | Zm00001eb322310_P001 | 0.925 |
| PUZ72729 | Sspon.02G | KQL26478 | TKW35588 | EER97465 | Zm00001eb326080_P001 | 0.999 |

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| PUZ48855 | Sspon.06G | KQK98863 | TKW06503 | EES11405 | Zm00001eb071110_P001 | 0.917 |
| PUZ74643 | genblast_C | KQL28169 | TKW37322 | KXG29768 | Zm00001eb240400_P002 | 0.936 |

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| PUZ49623 | genblast_C | KQL12668 | TKW23740 | KXG27496 | Zm00001eb076140_P004 | 0.951 |
| PUZ76354 | Sspon.04G | KQL30275 | TKW40048 | EES07083 | Zm00001eb245950_P002 | 0.881 |
| PUZ65596 | Sspon.07G | KQL15111 | TKW26827 | genblast_C | Zm00001eb351580_P001 | 0.946 |

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| PUZ63549 | Sspon.07G | KQL13494 | TKW24852 | KXG21541 | Zm00001eb350690_P003 | 0.964 |
| PUZ48682 | Sspon.05G | KQK98699 | TKW06254 | EES11350 | Zm00001eb429900_P001 | 0.919 |
| PUZ53006 | Sspon.03G | KQL08591 | TKW18836 | KXG34114 | Zm00001eb363090_P002 | 0.891 |
| PUZ46331 | Sspon.05G | KQK96352 | TKW03153 | EES11807 | Zm00001eb418330_P001 | 0.896 |
| PUZ67982 | Sspon.02G | KQL17322 | TKW29725 | EES17441 | Zm00001eb032360_P001 | 0.749 |
| PUZ55634 | Sspon.03G | KQL06061 | TKW15602 | EES01157 | Zm00001eb359230_P001 | 0.901 |

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| PUZ60372 | Sspon.08G | KQL10926 | TKW21790 | EER88491 | Zm00001eb383780_P001 | 0.941 |
| PUZ61913 | Sspon.04G | KQL09485 | TKW19877 | KXG19480 | Zm00001eb374760_P002 | 0.916 |
| PUZ58814 | Sspon.03G | KQL03265 | TKW12000 | EES02200 | Zm00001eb339240_P001 | 0.911 |
| PUZ58835 | Sspon.03G | KQL03244 | TKW11972 | EES02188 | Zm00001eb339280_P001 | 0.918 |
| PUZ53433 | Sspon.02G | KQL22562 | TKW18319 | KXG23864 | Zm00001eb135220_P001 | 0.916 |
| PUZ48629 | Sspon.05G | KQK98643 | TKW06192 | EES12737 | Zm00001eb072690_P001 | 0.916 |
| PUZ60397 | Sspon.08G | KQL10891 | TKW21746 | OQU76516 | Zm00001eb383560_P001 | 0.835 |
| PUZ74796 | Sspon.04G | KQL27999 | TKW37109 | EES04798 | genblast_Zm00001eb239400_P0 | |
| PUZ57391 | Sspon.03G | KQL03828 | TKW12717 | KXG32209 | Zm00001eb128000_P005 | 0.879 |
| PUZ42359 | Sspon.01G | KQK92115 | TKV97642 | EER92693 | Zm00001eb007950_P001 | 0.944 |
| PUZ37403 | Sspon.01G | KQK87486 | TKV91770 | OQU91119 | Zm00001eb216510_P002 | 0.909 |
| PUZ54401 | Sspon.03G | KQL07308 | TKW17206 | OQU87706 | Zm00001eb369620_P001 | 0.752 |
| PUZ72724 | Sspon.02G | KQL26471 | TKW35583 | KXG36586 | Zm00001eb326040_P001 | 0.903 |
| PUZ69715 | Sspon.03G | KQL07942 | TKW32029 | EES01840 | Zm00001eb146180_P001 | 0.915 |
| PUZ48523 | genblast_C | KQK98518 | TKW06053 | EES11283 | genblast_Os04t0571200-01_Ze | |
| PUZ77899 | genblast_C | KQL31746 | TKW41855 | KXG31207 | Zm00001eb256690_P009 | 0.903 |
| PUZ51409 | Sspon.06G | genblast_C | TKW10239 | OQU80420 | Zm00001eb178940_P001 | 0.953 |
| PUZ42434 | Sspon.01G | KQK92178 | TKV97716 | EER92710 | Zm00001eb008380_P001 | 0.877 |
| PUZ53829 | genblast_C | genblast_C | TKW17865 | EES01798 | Zm00001eb147040_P001 | 0.931 |

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| PUZ72897 | Sspon.02G | KQL26651 | TKW35803 | EER97533 | Zm00001eb109190_P001 | 0.918 |
| PUZ64360 | Sspon.01G | KQL27256 | TKW36623 | EER99929 | Zm00001eb111790_P001 | 0.931 |
| PUZ60827 | Sspon.08G | KQL10302 | TKW20954 | KXG19790 | Zm00001eb380500_P002 | 0.983 |

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|---|---|---|---|---|---|---|
| PUZ36246 | genblast_C | KQK86307 | TKV90346 | EER93157 | Zm00001eb063390_P001 | 0.963 |
| PUZ52670 | Sspon.02G | KQL02917 | TKW11698 | genblast_Z | genblast_Zm00001eb039600_P | |
| PUZ42277 | Sspon.01G | KQK92042 | TKV97548 | EER95307 | Zm00001eb400600_P001 | 0.981 |

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| PUZ59805 | Sspon.08G | KQL11259 | TKW22163 | EER90100 | genblast_Os06t0643000-01_Ze | |
| PUZ57136 | Sspon.03G | KQL03559 | TKW12377 | EES02817 | Zm00001eb129650_P001 | 0.903 |
| PUZ39622 | Sspon.01G | KQK89492 | TKV94375 | EES08537 | Zm00001eb026600_P001 | 0.789 |
| PUZ43157 | Sspon.01G | KQK92914 | TKV98566 | OQU93372 | Zm00001eb001350_P001 | 0.941 |
| PUZ64698 | Sspon.07G | KQL14224 | TKW25775 | EES19976 | Zm00001eb344230_P001 | 0.930 |
| PUZ73163 | Sspon.01G | KQL26911 | TKW36155 | OQU90351 | Zm00001eb110330_P001 | 0.852 |
| PUZ74906 | Sspon.08G | KQL27896 | TKW36983 | EES06586 | Zm00001eb383460_P001 | 0.865 |
| PUZ63876 | Sspon.07G | KQL13222 | TKW24466 | EES18962 | Zm00001eb354850_P002 | 0.952 |
| PUZ41707 | Sspon.01G | KQK91593 | TKV96965 | EER95109 | Zm00001eb397770_P001 | 0.993 |
| PUZ55358 | genblast_C | KQL06412 | TKW16036 | EES01260 | Zm00001eb160040_P001 | 0.963 |

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| PUZ53328 | genblast_C | KQL08286 | TKW18449 | EES01947 | Zm00001eb143570_P001 | 0.953 |
| PUZ43010 | Sspon.01G | KQK92752 | TKV98402 | EER95573 | Zm00001eb002440_P001 | 0.905 |
| PUZ59549 | Sspon.08G | KQL12039 | TKW23216 | OQU7686 | Zm00001eb390100_P001 | 0.923 |
| PUZ68365 | Sspon.02G | genblast_C | TKW30379 | EER95850 | genblast_Os07t0137900-01 | Zm |
| PUZ50090 | Sspon.06G | KQK95018 | TKW01267 | EES09981 | Zm00001eb200230_P001 | 0.814 |
| PUZ38933 | Sspon.01G | KQK88960 | TKV93701 | EER91576 | Zm00001eb222750_P002 | 0.819 |

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| PUZ77077 | Sspon.04G | KQL30959 | TKW40916 | EES05726 | Zm00001eb187340_P001 | 0.863 |
| PUZ72290 | Sspon.02G | KQL26052 | TKW35068 | EER99465 | Zm00001eb323000_P004 | 0.964 |
| PUZ77249 | Sspon.04G | KQL31120 | TKW41124 | EES07401 | Zm00001eb251950_P002 | 0.964 |
| PUZ70242 | Sspon.02G | KQL24055 | TKW32542 | EER96530 | Zm00001eb309420_P001 | 0.890 |
| PUZ70217 | Sspon.02G | KQL24038 | TKW32522 | EER98666 | Zm00001eb309310_P001 | 0.952 |
| PUZ47959 | Sspon.05G | KQK98033 | TKW05373 | EES11106 | Zm00001eb077390_P003 | 0.884 |
| PUZ76683 | Sspon.04G | KQL30609 | TKW40476 | KXG30688 | genblast_Os02t0633100-02_Ze | |
| PUZ73788 | Sspon.04G | KQL28982 | TKW38325 | KXG29328 | Zm00001eb230400_P001 | 0.953 |
| PUZ44776 | Sspon.01G | KQL03557 | TKW12371 | KXG40278 | Zm00001eb002000_P001 | 0.959 |
| PUZ60087 | Sspon.08G | KQL11550 | TKW22578 | EER88592 | Zm00001eb385970_P002 | 0.955 |
| PUZ60088 | Sspon.08G | KQL11551 | TKW22580 | EER89996 | genblast_Os06t0594600-01_Ze | |
| PUZ37671 | Sspon.01G | KQK87825 | TKV92162 | EER91113 | Zm00001eb217860_P001 | 0.861 |
| PUZ64287 | Sspon.08G | KQL12263 | TKW23491 | EER88975 | Zm00001eb272190_P002 | 0.918 |
| PUZ67112 | Sspon.02G | KQL16458 | TKW28554 | EES17014 | Zm00001eb133050_P001 | 0.964 |
| PUZ76141 | Sspon.08G | KQL30065 | TKW39763 | EER89201 | Zm00001eb377000_P001 | 0.906 |
| PUZ48247 | Sspon.05G | KQK98310 | TKW05713 | EES11199 | Zm00001eb427660_P002 | 0.895 |
| PUZ49360 | genblast_C | KQL12936 | TKW24076 | EES13038 | Zm00001eb433020_P001 | 0.955 |
| genblast_C | Sspon.02G | KQL22746 | TKW30833 | EER98085 | Zm00001eb301730_P001 | 0.950 |
| PUZ48821 | Sspon.05G | KQK98827 | TKW06438 | EES11391 | genblast_Os04t0608400-01_Ze | |
| PUZ42095 | genblast_C | KQK91860 | TKV97339 | EER92614 | Zm00001eb009360_P002 | 0.938 |
| PUZ60437 | Sspon.08G | KQL10865 | TKW21717 | EER89867 | Zm00001eb277860_P002 | 0.947 |
| PUZ65470 | Sspon.07G | KQL14958 | TKW26642 | KXG22236 | Zm00001eb291140_P001 | 0.952 |
| PUZ64821 | Sspon.07G | KQL14362 | TKW25924 | EES18664 | Zm00001eb343490_P001 | 0.991 |
| PUZ53067 | Sspon.03G | KQL08551 | TKW18769 | OQU88178 | Zm00001eb363260_P003 | 0.818 |
| PUZ61043 | genblast_C | KQL10368 | TKW21049 | OQU76275 | Zm00001eb281160_P002 | 0.911 |

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| PUZ54784 | Sspon.03GKQL06983 | TKW16772 | EES01479 | Zm00001eb371000_P001 | 0.925 |

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| PUZ71100 | Sspon.02GKQL24868 | TKW33577 | EER96901 | Zm00001eb315750_P001 | 0.922 |
| PUZ71144 | Sspon.02GKQL24916 | TKW33635 | KXG35834 | Zm00001eb315870_P001 | 0.918 |
| PUZ54230 | Sspon.03GKQL07475 | TKW17425 | EES01658 | Zm00001eb149710_P001 | 0.957 |

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| PUZ77759 | Sspon.04GKQL31629 | TKW41729 | OQU85783 | Zm00001eb255760_P003 | 0.818 |
| PUZ36886 | Sspon.01GKQK86951 | TKV91183 | EER90829 | Zm00001eb214110_P001 | 0.949 |
| PUZ46813 | Sspon.05GKQK96924 | TKW03957 | EES11990 | Zm00001eb085630_P001 | 0.936 |

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| PUZ58484 | Sspon.03GKQL04810 | TKW13958 | KXG31635 | Zm00001eb121110_P003 | 0.894 |

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| PUZ76812 | Sspon.04GKQL30723 | TKW40627 | EES05814 | Zm00001eb248930_P001 | 0.893 |
| PUZ77131 | Sspon.04GKQL31003 | TKW40982 | EES05698 | Zm00001eb251070_P001 | 0.885 |
| PUZ72545 | Sspon.02GKQL26298 | TKW35396 | EER99552 | Zm00001eb324670_P002 | 0.991 |

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| PUZ45511 | Sspon.06GKQK95391 | TKW01792 | EES10114 | Zm00001eb166790_P001 | 0.917 |
| PUZ43478 | Sspon.05GKQK99705 | TKW07564 | EES09151 | Zm00001eb195530_P001 | 0.868 |
| PUZ63021 | Sspon.05GKQK99624 | TKW07466 | EES15696 | Zm00001eb407030_P001 | 0.805 |
| PUZ40954 | Sspon.01GKQL26847 | TKV95915 | EER92218 | Zm00001eb394180_P001 | 0.889 |

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| PUZ73645 | genblast_C | KQL27724 | TKW36763 | genblast_C | genblast_Os02t0104800-01_Zea | |
| PUZ70858 | Sspon.02G | KQL24654 | TKW33339 | KXG35709 | Zm00001eb314060_P001 | 0.801 |
| PUZ58576 | Sspon.03G | KQL04890 | TKW14062 | EES00098 | Zm00001eb120810_P001 | 0.929 |
| PUZ42956 | Sspon.01G | KQK92683 | TKV98323 | EER92900 | Zm00001eb002940_P002 | 0.949 |
| PUZ42629 | Sspon.01G | KQK92382 | TKV97982 | EER95426 | Zm00001eb005380_P001 | 0.808 |
| PUZ74070 | genblast_C | KQL28727 | TKW37988 | EES04530 | Zm00001eb232400_P001 | 0.862 |
| PUZ49930 | Sspon.06G | KQL01008 | TKW09251 | EES13283 | Zm00001eb173480_P001 | 0.956 |
| PUZ66330 | Sspon.08G | KQL16098 | TKW28088 | EER88905 | Zm00001eb227010_P001 | 0.838 |
| PUZ59305 | Sspon.08G | KQL11820 | TKW22919 | EER90299 | Zm00001eb226390_P002 | 0.916 |
| PUZ41074 | Sspon.01G | KQK92957 | TKV98605 | EER94852 | Zm00001eb394590_P002 | 0.918 |
| PUZ77785 | Sspon.04G | KQL31660 | TKW41756 | KXG31173 | Zm00001eb255980_P003 | 0.955 |
| PUZ51280 | Sspon.06G | KQL01587 | TKW10013 | KXG25075 | genblast_Os08t0379000-01Zm0 | |
| PUZ75159 | Sspon.04G | genblast_C | TKW38627 | EES06385 | Zm00001eb234150_P001 | 0.865 |
| PUZ53912 | Sspon.03G | KQL07777 | TKW17778 | EES03898 | Zm00001eb367320_P001 | 0.979 |
| PUZ72738 | genblast_C | KQL26484 | TKW35594 | EER99632 | Zm00001eb108190_P001 | 0.868 |
| PUZ45577 | genblast_C | KQK95495 | TKW01941 | KXG28986 | Zm00001eb253770_P001 | 0.954 |

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| PUZ54927 | Sspon.03GKQL06831 | TKW16581 | EES03563 | Zm00001eb154170_P001 | 0.784 |
| PUZ61057 | genblast_CKQL10389 | TKW21084 | EER88287 | Zm00001eb381130_P001 | 0.902 |
| PUZ78140 | genblast_CKQL32006 | TKW42145 | EES07716 | Zm00001eb191980_P001 | 0.922 |

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| PUZ44037 | Sspon.05GKQK93941 | TKV99788 | EES08158 | Zm00001eb090980_P004 | 0.936 |
| PUZ54625 | Sspon.03GKQL07120 | TKW16964 | OQU87608 | Zm00001eb152180_P003 | 0.933 |
| PUZ58483 | Sspon.03GKQL04811 | TKW13957 | EES00132 | Zm00001eb121070_P001 | 0.848 |
| PUZ64285 | genblast_CKQL13832 | TKW25291 | OQU77553 | Zm00001eb283650_P001 | 0.963 |
| PUZ77261 | Sspon.04GKQL31129 | TKW41136 | EES05659 | Zm00001eb252010_P001 | 0.940 |
| PUZ55252 | genblast_CKQL06522 | TKW16178 | EES01304 | Zm00001eb156080_P001 | 0.946 |
| PUZ51275 | Sspon.06GKQL01589 | TKW10018 | OQU80360 | Zm00001eb170760_P001 | 0.872 |
| PUZ48441 | Sspon.05GKQK98459 | TKW05959 | KXG26898 | Zm00001eb073990_P001 | 0.932 |
| PUZ60450 | genblast_CKQL10843 | TKW21693 | EER88440 | Zm00001eb277870_P002 | 0.968 |
| PUZ52228 | Sspon.06GKQL02483 | TKW11184 | EES14249 | Zm00001eb174530_P001 | 0.920 |
| PUZ70418 | Sspon.02GKQL24218 | TKW32780 | EER96610 | Zm00001eb310480_P001 | 0.969 |

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| PUZ58403 | Sspon.03GKQL04742 | TKW13871 | EES02334 | Zm00001eb121650_P001 | 0.969 |

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| PUZ58316 | Sspon.03GKQL04660 | TKW13768 | EES00202 | Zm00001eb122500_P001 | 0.970 |
| PUZ52824 | Sspon.03GKQL08777 | TKW19057 | EES04290 | Zm00001eb139960_P001 | 0.934 |
| PUZ72358 | genblast_CKQL26116 | TKW35141 | KXG36409 | Zm00001eb323380_P003 | 0.939 |
| PUZ43116 | Sspon.01GKQK92878 | TKV98527 | OQU93358 | Zm00001eb001630_P001 | 0.923 |
| PUZ67710 | genblast_CKQL17029 | TKW29361 | OQU79486 | Zm00001eb030660_P001 | 0.954 |

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| PUZ39357 | Sspon.01G | KQK89373 | TKV94227 | EER91779 | Zm00001eb026110_P001 | 0.949 |
| PUZ52499 | Sspon.06G | KQL02766 | TKW11535 | EES14150 | Zm00001eb037300_P001 | 0.949 |
| PUZ67749 | Sspon.02G | KQL17043 | TKW29385 | EES16275 | Zm00001eb030880_P001 | 0.939 |

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| PUZ42589 | Sspon.01G | KQK92334 | TKV97919 | EER92762 | Zm00001eb005690_P002 | 0.928 |
| PUZ57760 | Sspon.03G | KQL04142 | TKW13127 | EES00420 | Zm00001eb125980_P001 | 0.914 |

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| PUZ40079 | Sspon.01G | KQK89889 | TKV94883 | EER94477 | Zm00001eb023780_P004 | 0.871 |
| PUZ61985 | Sspon.08G | KQL09553 | TKW19967 | OQU75928 | Zm00001eb375320_P001 | 0.755 |
| PUZ64276 | Sspon.07G | genblast_C | TKW25280 | KXG21461 | Zm00001eb283760_P001 | 0.941 |
| PUZ65234 | Sspon.07G | KQL14793 | TKW26426 | KXG22316 | Zm00001eb352840_P001 | 0.899 |
| PUZ76687 | Sspon.04G | genblast_C | TKW40480 | EES07193 | Zm00001eb248040_P001 | 0.925 |
| PUZ72319 | Sspon.02G | KQL26085 | TKW35100 | EER97326 | Zm00001eb323180_P002 | 0.942 |

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| PUZ71604 | Sspon.02G | KQL25383 | TKW34208 | EER99213 | Zm00001eb318900_P001 | 0.917 |

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| PUZ41251 | Sspon.01G | KQK91043 | TKV96314 | KXG39447 | Zm00001eb015750_P002 | 0.893 |

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| genblast_C | genblast_C | KQL09484 | TKW19876 | KXG19481 | Zm00001eb268260_P001 | 0.883 |
| PUZ54288 | Sspon.03G | KQL07394 | TKW17317 | EES03776 | Zm00001eb150380_P001 | 0.926 |
| PUZ77816 | Sspon.04G | KQL31683 | TKW41779 | KXG31179 | Zm00001eb193530_P001 | 0.940 |
| PUZ37450 | Sspon.01G | KQK87555 | TKV91862 | EER91031 | Zm00001eb054160_P001 | 0.960 |
| PUZ73976 | Sspon.03G | KQL28828 | TKW38123 | EES06247 | Zm00001eb231620_P001 | 0.969 |
| PUZ55732 | Sspon.03G | KQL05968 | TKW15489 | EES01103 | Zm00001eb159390_P001 | 0.863 |
| PUZ66015 | Sspon.07G | KQL15503 | TKW27327 | EES18222 | Zm00001eb287890_P002 | 0.918 |
| PUZ62050 | genblast_C | KQL09611 | TKW20049 | KXG19385 | Zm00001eb375680_P002 | 0.920 |
| PUZ47540 | Sspon.05G | KQK97621 | TKW04849 | EES12315 | Zm00001eb424460_P001 | 0.928 |
| PUZ37270 | Sspon.01G | KQK87364 | TKV91651 | EER93545 | Zm00001eb215860_P002 | 0.909 |
| PUZ51258 | Sspon.06G | KQL01617 | TKW10059 | EES13689 | Zm00001eb178470_P001 | 0.923 |
| PUZ43138 | genblast_C | KQK92894 | TKV98546 | KXG40319 | Zm00001eb001510_P002 | 0.952 |

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| PUZ71010 | Sspon.02G | KQL24805 | TKW33507 | EER96862 | Zm00001eb314970_P001 | 0.921 |
| PUZ66356 | Sspon.07G | KQL15832 | TKW27756 | OQU7785 | Zm00001eb285640_P003 | 0.970 |
| PUZ50922 | Sspon.08G | genblast_C | TKW09628 | EER88733 | Zm00001eb174980_P001 | 0.900 |
| PUZ36383 | Sspon.01G | KQK86471 | TKV90553 | EER90648 | Zm00001eb062300_P001 | 0.996 |
| PUZ42055 | Sspon.01G | KQK91823 | TKV97282 | EER92602 | Zm00001eb234310_P001 | 0.921 |
| PUZ53617 | Sspon.03G | KQL08038 | TKW18123 | EES03999 | Zm00001eb366020_P003 | 0.943 |

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| PUZ74310 | Sspon.04G | KQL28509 | TKW37734 | KXG29589 | Zm00001eb233420_P004 | 0.928 |
| PUZ65092 | Sspon.07G | KQL14652 | TKW26251 | EES19842 | Zm00001eb353610_P001 | 0.870 |
| PUZ73822 | Sspon.04G | KQL28949 | TKW38290 | KXG29339 | Zm00001eb230680_P001 | 0.952 |
| PUZ77890 | Sspon.04G | KQL31738 | TKW41841 | EES07618 | Zm00001eb256560_P001 | 0.851 |
| PUZ62206 | Sspon.08G | KQK86808 | TKV90997 | EER87853 | Zm00001eb376990_P001 | 0.927 |
| PUZ53696 | Sspon.03G | KQL07965 | TKW18008 | EES01851 | Zm00001eb366330_P001 | 0.974 |
| PUZ58649 | Sspon.03G | KQL04952 | TKW14143 | EES02258 | Zm00001eb119980_P001 | 0.964 |
| PUZ57781 | Sspon.03G | KQL04156 | TKW13144 | KXG32050 | Zm00001eb125880_P004 | 0.910 |
| PUZ53108 | genblast_C | KQL08496 | TKW18711 | OQU88162 | Zm00001eb142180_P004 | 0.871 |
| PUZ77416 | Sspon.04G | KQL31282 | TKW41330 | KXG30857 | Zm00001eb189090_P001 | 0.938 |
| PUZ37389 | Sspon.01G | KQK87470 | TKV91752 | EER91002 | Zm00001eb216440_P001 | 0.983 |
| PUZ75803 | Sspon.04G | KQL29760 | TKW39331 | EES05123 | Zm00001eb180910_P002 | 0.907 |
| PUZ52487 | Sspon.03G | KQL07449 | TKW17391 | KXG31790 | Zm00001eb123340_P001 | 0.933 |
| PUZ48268 | genblast_C | KQL23918 | TKW05749 | EES12592 | Zm00001eb075140_P001 | 0.986 |
| PUZ74201 | Sspon.04G | KQL28611 | TKW37853 | KXG29538 | Zm00001eb207310_P001 | 0.956 |
| genblast_C | Sspon.08G | KQL10576 | TKW21369 | KXG19988 | Zm00001eb382320_P001 | 0.958 |

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| PUZ58874 | Sspon.03G | KQL03202 | TKW11924 | EES02169 | Zm00001eb339390_P002 | 0.959 |
| PUZ42842 | Sspon.02G | KQK92578 | TKV98217 | EER92854 | Zm00001eb003860_P002 | 0.974 |
| PUZ62203 | genblast_C | KQL09756 | TKW20237 | EER87849 | genblast_Os06t0149500-01_Ze | |
| PUZ36894 | Sspon.01G | KQK86962 | TKV91196 | KXG37487 | Zm00001eb058460_P002 | 0.877 |

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| PUZ44436 | Sspon.05G | KQK94431 | TKW00489 | EES09646 | Zm00001eb090830_P001 | 0.926 |
| PUZ56011 | Sspon.01G | KQL05692 | TKW15153 | EES00995 | Zm00001eb161010_P001 | 0.880 |

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| PUZ78129 | genblast_C | KQL31997 | TKW42138 | KXG31309 | Zm00001eb258240_P001 | 0.852 |
| PUZ36426 | genblast_C | KQK86503 | TKV90604 | EER90662 | Zm00001eb062140_P001 | 0.925 |
| PUZ48986 | Sspon.05G | KQK99006 | TKW06691 | EES12886 | Zm00001eb431290_P001 | 0.946 |
| PUZ37139 | Sspon.01G | KQK87224 | TKV91490 | EER93499 | Zm00001eb056380_P001 | 0.979 |

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| PUZ52149 | Sspon.02G | KQL02425 | TKW11106 | OQU80938 | Zm00001eb323880_P001 | 0.871 |
| PUZ66320 | Sspon.07G | KQL15799 | TKW27718 | OQU77870 | Zm00001eb285480_P001 | 0.895 |
| PUZ65095 | Sspon.07G | KQL14655 | TKW26256 | KXG22385 | Zm00001eb293490_P004 | 0.944 |
| PUZ72695 | genblast_C | KQL26448 | TKW35558 | KXG36570 | Zm00001eb325820_P001 | 0.939 |
| PUZ46111 | Sspon.05G | KQK96239 | TKW02996 | KXG25783 | Zm00001eb089230_P001 | 0.822 |
| PUZ48610 | Sspon.05G | KQK98622 | TKW06173 | OQU82211 | Zm00001eb072830_P001 | 0.908 |
| PUZ42281 | Sspon.01G | KQK92048 | TKV97556 | EER92670 | Zm00001eb400610_P001 | 0.978 |

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| PUZ43369 | Sspon.05G | KQK93250 | TKV98861 | EES15497 | Zm00001eb404750_P001 | 0.886 |

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| PUZ67939 | Sspon.02G | KQL17234 | TKW29611 | OQU79642 | Zm00001eb032000_P001 | 0.819 |
| PUZ75672 | Sspon.07G | KQL29407 | TKW38836 | EES17669 | Zm00001eb354560_P001 | 0.974 |
| PUZ77369 | Sspon.04G | KQL31235 | TKW41258 | OQU85515 | Zm00001eb189290_P001 | 0.974 |

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| PUZ73481 | Sspon.01G | KQL27216 | TKW36569 | KXG36963 | genblast_Os07t0683600-00_Ze | |
| PUZ64548 | Sspon.07G | KQL14073 | TKW25592 | EES18784 | Zm00001eb297580_P001 | 0.933 |
| PUZ76992 | Sspon.04G | KQL30886 | TKW40833 | OQU85656 | Zm00001eb250180_P001 | 0.940 |
| PUZ37592 | Sspon.01G | KQK87712 | TKV92035 | KXG37841 | Zm00001eb217310_P001 | 0.959 |
| PUZ50319 | Sspon.05G | KQK91082 | TKV96368 | KXG27423 | Zm00001eb066360_P001 | 0.882 |
| PUZ53077 | Sspon.03G | KQL08534 | TKW18753 | EES04187 | Zm00001eb363360_P001 | 0.852 |
| PUZ47145 | Sspon.05G | KQK97257 | TKW04378 | KXG26298 | Zm00001eb083170_P002 | 0.924 |
| PUZ39662 | Sspon.01G | KQK91585 | TKV96954 | EER92488 | Zm00001eb397810_P001 | 0.927 |

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| PUZ49639 | Sspon.05G | KQL12645 | TKW23708 | KXG27505 | Zm00001eb076340_P003 | 0.936 |
| PUZ72367 | Sspon.02G | KQL26123 | TKW35148 | EER97339 | Zm00001eb323430_P001 | 0.871 |
| PUZ46322 | genblast_C | KQK96408 | TKW03216 | KXG25957 | Zm00001eb087090_P001 | 0.961 |
| PUZ38806 | Sspon.01G | KQK88850 | TKV93552 | KXG38420 | Zm00001eb046680_P001 | 0.897 |
| PUZ53176 | genblast_Z | KQL08431 | TKW18640 | OQU88149 | Zm00001eb142600_P001 | 0.878 |
| PUZ68181 | Sspon.02G | KQK88312 | TKV92831 | EER95734 | Zm00001eb043230_P001 | 0.885 |
| PUZ37690 | Sspon.01G | KQK87840 | TKV92182 | KXG37890 | Zm00001eb218080_P001 | 0.903 |
| PUZ47368 | Sspon.05G | KQK97467 | TKW04651 | KXG26409 | Zm00001eb423480_P001 | 0.913 |
| PUZ74409 | Sspon.04G | genblast_C | TKW37593 | EES06399 | Zm00001eb206500_P001 | 0.946 |
| PUZ53172 | genblast_C | KQL08432 | TKW18642 | EES04138 | Zm00001eb363820_P001 | 0.892 |

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| PUZ58156 | Sspon.03G | KQL04511 | TKW13565 | EES00272 | Zm00001eb123570_P001 | 0.849 |
| PUZ55666 | Sspon.03G | KQL06026 | TKW15562 | EES01138 | genblast_Os01t0634900-00_Ze | |
| PUZ40613 | Sspon.07G | KQL14856 | TKW26501 | EES19764 | Zm00001eb291880_P001 | 0.893 |

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| PUZ77101 | Sspon.04G | KQL30975 | TKW40946 | EES05718 | Zm00001eb250940_P001 | 0.794 |
| PUZ41850 | Sspon.01G | KQK91622 | TKV97006 | EER92528 | Zm00001eb057660_P001 | 0.942 |
| PUZ72743 | Sspon.02G | KQL26489 | TKW35601 | KXG36602 | Zm00001eb326230_P002 | 0.933 |
| PUZ67389 | Sspon.02G | KQL16645 | TKW28812 | KXG23666 | Zm00001eb410060_P002 | 0.932 |
| PUZ37779 | Sspon.01G | KQK87917 | TKV92278 | EER93744 | Zm00001eb050260_P001 | 0.772 |
| PUZ38531 | Sspon.01G | KQK88614 | TKV93227 | EER94048 | Zm00001eb221260_P001 | 0.880 |
| PUZ43633 | Sspon.07G | KQK99826 | TKW07716 | EES15558 | Zm00001eb405200_P001 | 0.893 |
| PUZ75281 | genblast_C | KQL29322 | TKW38731 | KXG29401 | Zm00001eb231330_P005 | 0.902 |

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| PUZ71985 | Sspon.02G | KQL25738 | TKW34674 | EER97196 | Zm00001eb320100_P001 | 0.937 |
| PUZ64268 | Sspon.07G | genblast_C | TKW25268 | OQU77548 | Zm00001eb282950_P002 | 0.982 |
| PUZ55577 | Sspon.03G | KQL06114 | TKW15687 | OQU87242 | Zm00001eb158320_P001 | 0.969 |
| PUZ40764 | Sspon.01G | KQK90516 | TKV95680 | EER94725 | Zm00001eb392850_P001 | 0.952 |
| PUZ77447 | Sspon.04G | KQL31316 | TKW41367 | EES07326 | Zm00001eb189550_P004 | 0.964 |
| PUZ73813 | Sspon.04G | KQL28959 | TKW38302 | EES06203 | Zm00001eb230550_P001 | 0.925 |

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| PUZ77272 | genblast_C | KQL31140 | TKW41146 | EES05656 | Zm00001eb188380_P001 | 0.883 |

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| PUZ72428 | Sspon.02G | KQL26188 | TKW35226 | KXG36446 | Zm00001eb323710_P002 | 0.968 |
| PUZ45659 | Sspon.06G | KQK95648 | TKW02147 | KXG29029 | Zm00001eb165880_P002 | 0.921 |

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| PUZ68995 | Sspon.02G | KQL23151 | TKW31347 | EER96139 | Zm00001eb097030_P001 | 0.943 |
| PUZ41789 | genblast_C | genblast_C | TKV96889 | EER95135 | Zm00001eb011620_P001 | 0.978 |
| PUZ45539 | Sspon.06G | KQK95450 | TKW01855 | EES08871 | Zm00001eb166690_P001 | 0.942 |
| PUZ59065 | Sspon.08G | KQL12251 | TKW23480 | EER88969 | Zm00001eb228180_P002 | 0.948 |

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| PUZ36581 | genblast_C | KQK86671 | TKV90830 | EER90738 | Zm00001eb060860_P001 | 0.927 |
| PUZ61181 | Sspon.08G | KQL10491 | TKW21246 | EER88336 | Zm00001eb381960_P001 | 0.927 |

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| PUZ43002 | Sspon.01G | KQK92747 | TKV98380 | EER92921 | Zm00001eb002490_P001 | 0.954 |
| PUZ37269 | Sspon.01G | KQK87362 | TKV91649 | EER93543 | Zm00001eb215850_P002 | 0.956 |
| PUZ36078 | Sspon.01G | genblast_C | TKV90193 | EER90535 | Zm00001eb064460_P001 | 0.898 |
| PUZ47103 | Sspon.05G | KQK97228 | TKW04336 | EES10782 | Zm00001eb422140_P001 | 0.935 |

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| PUZ73642 | genblast_C | KQL27722 | TKW36759 | OQU84149 | Zm00001eb229390_P001 | 0.913 |
| PUZ76718 | Sspon.04G | KQL30639 | TKW40511 | EES07199 | Zm00001eb185580_P001 | 0.919 |
| PUZ51433 | Sspon.06G | KQL01780 | TKW10269 | EES14986 | Zm00001eb179030_P001 | 0.913 |
| PUZ53277 | Sspon.03G | KQK99069 | TKW18513 | EES01966 | Zm00001eb364520_P001 | 0.839 |
| PUZ78287 | Sspon.04G | KQL32155 | TKW42316 | OQU85970 | Zm00001eb191180_P001 | 0.909 |
| PUZ69790 | Sspon.02G | KQL23718 | TKW32104 | EER98560 | Zm00001eb221750_P001 | 0.944 |
| PUZ39338 | Sspon.06G | KQL22950 | TKW31066 | EES06818 | Zm00001eb026860_P001 | 0.946 |
| PUZ48729 | Sspon.05G | KQK98750 | TKW06327 | EES12784 | Zm00001eb071860_P001 | 0.986 |
| PUZ76193 | Sspon.04G | KQL30125 | TKW39841 | EES05285 | Zm00001eb244530_P001 | 0.887 |
| PUZ72718 | Sspon.02G | KQL26466 | TKW35576 | EER99623 | Zm00001eb326000_P001 | 0.957 |

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| PUZ49942 | Sspon.06G | KQL00999 | TKW09241 | EES14466 | Zm00001eb173440_P001 | 0.934 |
| PUZ48871 | Sspon.05G | KQK98879 | TKW06528 | KXG27102 | Zm00001eb070970_P001 | 0.931 |
| PUZ40068 | genblast_C | KQK89878 | TKV94871 | EER94471 | Zm00001eb390910_P001 | 0.987 |

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| PUZ71557 | Sspon.02G | KQL25333 | TKW34152 | EER97050 | Zm00001eb318590_P001 | 0.878 |
| PUZ61797 | Sspon.08G | KQL09339 | TKW19694 | EER89379 | Zm00001eb278590_P002 | 0.929 |
| PUZ64870 | Sspon.07G | KQL14418 | TKW25982 | EES18642 | Zm00001eb295130_P002 | 0.956 |
| PUZ73456 | Sspon.02G | KQL27184 | TKW36522 | EER99914 | Zm00001eb330690_P001 | 0.960 |
| PUZ72288 | Sspon.02G | KQL26051 | TKW35067 | EER99464 | Zm00001eb322980_P002 | 0.948 |
| PUZ35953 | Sspon.01G | KQK86065 | TKV90045 | OQU90581 | Zm00001eb065300_P001 | 0.917 |
| PUZ72324 | Sspon.02G | KQL26092 | TKW35112 | EER99480 | Zm00001eb106300_P001 | 0.957 |
| PUZ43011 | genblast_C | KQK92753 | TKV98404 | EER92924 | Zm00001eb002430_P005 | 0.950 |
| PUZ48967 | Sspon.05G | KQK85592 | TKW06664 | genblast_C | Zm00001eb070320_P002 | 0.903 |
| PUZ78343 | Sspon.04G | KQL32201 | TKW42371 | OQU85994 | Zm00001eb259240_P002 | 0.889 |
| PUZ70971 | Sspon.02G | KQL24769 | TKW33468 | EER99004 | Zm00001eb100440_P001 | 0.901 |
| PUZ42473 | Sspon.01G | KQK92221 | TKV97771 | EER95363 | Zm00001eb006590_P001 | 0.889 |
| PUZ52148 | Sspon.06G | KQL02423 | TKW11102 | KXG25642 | Zm00001eb034900_P001 | 0.932 |

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| PUZ71839 | Sspon.02G | KQL25597 | TKW34482 | EER99310 | Zm00001eb320910_P001 | 0.922 |
| PUZ52930 | genblast_C | KQL08685 | TKW18939 | EES04251 | genblast_Os01t0957900-01_Zea |  |
| PUZ59568 | genblast_C | KQL12058 | TKW23245 | OQU76854 | Zm00001eb274180_P003 | 0.945 |
| PUZ35988 | Sspon.01G | KQK86088 | TKV90067 | OQU90591 | Zm00001eb210440_P001 | 0.974 |
| PUZ77162 | Sspon.04G | KQL31030 | TKW41013 | OQU85578 | genblast_Zm00001eb187750_P0 |  |
| PUZ72133 | genblast_C | KQL25869 | TKW34843 | KXG27288 | Zm00001eb432440_P001 | 0.943 |
| PUZ73711 | genblast_C | KQL29079 | TKW38461 | EES06149 | Zm00001eb229830_P001 | 0.956 |
| PUZ36888 | Sspon.01G | KQK86955 | TKV91189 | EER90831 | Zm00001eb058520_P002 | 0.933 |
| PUZ36217 | Sspon.01G | KQK86335 | TKV90371 | EER90568 | Zm00001eb211220_P001 | 0.877 |
| PUZ52262 | Sspon.06G | KQL02519 | TKW11226 | KXG25600 | Zm00001eb174630_P001 | 0.942 |

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| PUZ45576 | Sspon.06G | KQK95492 | TKW01937 | KXG28983 | Zm00001eb166460_P001 | 0.971 |
| PUZ37654 | Sspon.01G | KQK87801 | TKV92136 | EER91103 | genblast_Os03t0669600-01_Zea |  |
| PUZ59413 | Sspon.02G | KQL11923 | TKW23068 | KXG37011 | Zm00001eb331260_P002 | 0.939 |

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| PUZ72183 | Sspon.02G | KQK93818 | TKW34908 | EER97261 | Zm00001eb091620_P002 | 0.862 |
| PUZ42305 | genblast_C | KQK92074 | TKV97597 | KXG39927 | Zm00001eb007680_P001 | 0.950 |
| PUZ73273 | Sspon.02G | KQL26995 | TKW36265 | KXG36846 | Zm00001eb110710_P002 | 0.995 |
| PUZ39384 | genblast_C | KQL31511 | TKW41581 | KXG32381 | Zm00001eb028000_P001 | 0.943 |

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| PUZ73178 | Sspon.02G | KQL26925 | TKW36170 | EER97638 | Zm00001eb110370_P002 | 0.919 |
| PUZ52775 | Sspon.03G | KQL08814 | TKW19113 | EES02152 | Zm00001eb139670_P002 | 0.894 |
| PUZ45309 | Sspon.06G | KQK95061 | TKW01331 | EES08735 | Zm00001eb200470_P001 | 0.951 |
| PUZ76741 | Sspon.04G | KQL30657 | TKW40540 | KXG30704 | Zm00001eb248370_P001 | 0.952 |
| PUZ71466 | Sspon.02G | KQL25233 | TKW34026 | EER99162 | Zm00001eb317830_P001 | 0.915 |
| PUZ54650 | Sspon.03G | KQL07103 | TKW16932 | EES03661 | Zm00001eb370330_P001 | 0.999 |

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| PUZ65708 | Sspon.07G | KQL15221 | TKW26967 | EES18336 | Zm00001eb289480_P001 | 0.904 |
| PUZ36368 | genblast_C | KQK86463 | TKV90539 | EER93206 | Zm00001eb211990_P001 | 0.921 |
| PUZ57709 | Sspon.03G | KQL04096 | TKW13037 | EES02617 | Zm00001eb334480_P002 | 0.933 |

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| PUZ54482 | Sspon.03G | KQL07243 | TKW17115 | OQU8767 | Zm00001eb369860_P004 | 0.968 |
| genblast_C | Sspon.08G | KQL11121 | TKW22021 | EER90151 | Zm00001eb274860_P001 | 0.867 |
| PUZ42725 | Sspon.01G | KQK92456 | TKV98055 | EER95459 | Zm00001eb004750_P001 | 0.940 |
| PUZ64889 | Sspon.07G | KQL14447 | TKW26012 | EES18633 | Zm00001eb295000_P001 | 0.919 |
| PUZ77232 | Sspon.04G | KQL31100 | TKW41098 | EES07407 | Zm00001eb251670_P001 | 0.927 |
| PUZ63056 | Sspon.05G | KQK99590 | TKW07435 | EES15709 | Zm00001eb139480_P001 | 0.895 |

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| PUZ47599 | Sspon.05G | KQK97681 | TKW04927 | KXG26527 | Zm00001eb424740_P002 | 0.901 |
| PUZ58218 | Sspon.03G | KQL04564 | TKW13641 | EES00241 | Zm00001eb123210_P001 | 0.851 |
| PUZ40885 | Sspon.01G | KQK90639 | genblast_C | KXG39259 | Zm00001eb392330_P001 | 0.897 |
| PUZ45406 | genblast_C | KQK95200 | TKW01495 | EES10045 | Zm00001eb167410_P001 | 0.824 |
| PUZ52524 | Sspon.06G | KQL02799 | TKW11568 | EES15257 | Zm00001eb037460_P001 | 0.968 |

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| PUZ53502 | Sspon.03G | KQL08141 | TKW18252 | EES04041 | Zm00001eb365670_P001 | 0.773 |

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| PUZ62968 | Sspon.05G | KQK99921 | TKW07841 | EES09268 | Zm00001eb196980_P001 | 0.952 |
| PUZ71243 | Sspon.02G | KQL25021 | TKW33776 | KXG35895 | Zm00001eb101780_P001 | 0.977 |
| PUZ78332 | Sspon.04G | KQL32190 | TKW42362 | EES06049 | Zm00001eb190930_P002 | 0.946 |
| PUZ56149 | Sspon.03G | KQL05643 | TKW15095 | EES03153 | Zm00001eb357210_P001 | 0.933 |
| PUZ70892 | Sspon.02G | KQL24693 | TKW33383 | EES19953 | Zm00001eb295990_P002 | 0.780 |
| PUZ70441 | Sspon.02G | KQL24237 | TKW32808 | EER96625 | Zm00001eb098520_P001 | 0.987 |

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| PUZ47820 | Sspon.05G | KQL02966 | TKW11751 | KXG26633 | Zm00001eb425660_P001 | 0.943 |
| PUZ61564 | Sspon.04G | KQL10126 | TKW20723 | KXG19701 | Zm00001eb280060_P003 | 0.960 |
| PUZ42132 | Sspon.01G | KQK91910 | TKV97387 | EER92626 | Zm00001eb008950_P001 | 0.948 |
| PUZ42569 | Sspon.01G | KQK92313 | TKV97896 | KXG40055 | Zm00001eb005860_P001 | 0.971 |

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| PUZ74328 | Sspon.04G | genblast_C | TKW37706 | EES06365 | Zm00001eb233650_P001 | 0.890 |
| PUZ58861 | genblast_C | KQL03210 | TKW11937 | OQU86053 | Zm00001eb119020_P001 | 0.855 |
| PUZ43063 | Sspon.01G | KQK92810 | TKV98463 | EER92944 | Zm00001eb002020_P001 | 0.934 |
| PUZ44653 | Sspon.04G | KQK94406 | TKW00450 | EES07206 | Zm00001eb248350_P001 | 0.936 |
| PUZ58230 | Sspon.03G | KQL04571 | TKW13656 | EES00238 | Zm00001eb336490_P003 | 0.927 |
| PUZ71396 | Sspon.02G | KQL25176 | TKW33959 | OQU89735 | Zm00001eb317460_P004 | 0.911 |
| PUZ66168 | genblast_C | KQL15662 | TKW27535 | EES18166 | Zm00001eb287150_P002 | 0.931 |
| PUZ49831 | genblast_C | KQL00240 | TKW08135 | EES14394 | Zm00001eb260450_P001 | 0.851 |
| PUZ51263 | Sspon.06G | genblast_C | TKW10039 | OQU80348 | Zm00001eb178450_P001 | 0.899 |

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| PUZ70341 | Sspon.02G | KQL24132 | TKW32667 | EER98732 | Zm00001eb309900_P002 | 0.974 |

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| PUZ52272 | Sspon.06G | KQL02529 | TKW11246 | KXG25590 | Zm00001eb035750_P001 | 0.944 |
| PUZ61008 | Sspon.08G | genblast_Z | TKW21012 | KXG19820 | Zm00001eb280970_P002 | 0.848 |
| PUZ48723 | Sspon.05G | KQK98741 | TKW06319 | EES11372 | Zm00001eb071930_P001 | 0.951 |
| PUZ55053 | Sspon.03G | KQL06710 | TKW16419 | EES03527 | Zm00001eb140740_P001 | 0.969 |
| PUZ77147 | Sspon.04G | KQL31015 | TKW40992 | EES07426 | Zm00001eb251170_P001 | 0.981 |
| PUZ77656 | Sspon.04G | KQL31538 | TKW41623 | KXG30742 | Zm00001eb194270_P001 | 0.897 |

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| PUZ36900 | Sspon.01G | KQK86966 | TKV91203 | EER90834 | Zm00001eb058370_P002 | 0.854 |
| PUZ39995 | Sspon.01G | KQK89800 | TKV94781 | KXG38864 | Zm00001eb390450_P001 | 0.909 |

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| PUZ63559 | Sspon.02G | KQL13481 | TKW24827 | EER99154 | Zm00001eb317730_P001 | 0.955 |
| PUZ71544 | Sspon.02G | KQL25323 | TKW34140 | EER99185 | Zm00001eb102790_P003 | 0.984 |
| PUZ62134 | genblast_C | KQL09697 | TKW20155 | EER87873 | Zm00001eb376600_P001 | 0.973 |
| PUZ63191 | Sspon.03G | KQL04376 | TKW13404 | EES02538 | Zm00001eb125080_P001 | 0.940 |
| PUZ39396 | Sspon.01G | KQK89060 | TKV93820 | KXG38634 | Zm00001eb203360_P003 | 0.884 |

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| PUZ54759 | Sspon.03G | KQL07006 | TKW16808 | KXG33380 | Zm00001eb153520_P002 | 0.938 |

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| PUZ66062 | Sspon.07G | KQK92110 | TKV97635 | EER88697 | Zm00001eb349860_P001 | 0.839 |
| PUZ72005 | Sspon.02G | KQL25753 | TKW34698 | EER99371 | Zm00001eb234990_P001 | 0.908 |
| genblast_C | Sspon.06G | KQL02613 | TKW11354 | EES14202 | Zm00001eb175070_P001 | 0.946 |
| PUZ51644 | Sspon.06G | KQL01961 | TKW10492 | EES13907 | Zm00001eb041210_P001 | 0.941 |
| PUZ38421 | Sspon.01G | KQK88487 | TKV93073 | EER93990 | Zm00001eb044450_P002 | 0.970 |
| PUZ41584 | Sspon.01G | KQK91375 | TKV96732 | EER92428 | Zm00001eb397200_P003 | 0.968 |
| PUZ58754 | genblast_Z | KQL03340 | TKW12086 | OQU86087 | Zm00001eb119510_P001 | 0.909 |
| PUZ61282 | Sspon.08G | KQL09818 | TKW20327 | EER89410 | Zm00001eb373180_P002 | 0.996 |
| PUZ62537 | genblast_C | KQL08941 | TKW19207 | EER87705 | Zm00001eb379260_P001 | 0.969 |
| PUZ54548 | genblast_C | KQL07186 | TKW17042 | EES03695 | Zm00001eb370070_P002 | 0.947 |

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| PUZ48465 | Sspon.05G | KQK98473 | TKW05977 | KXG26906 | Zm00001eb073900_P001 | 0.814 |
| PUZ72880 | Sspon.02G | KQL26642 | TKW35796 | EER99692 | Zm00001eb327310_P001 | 0.980 |
| PUZ57159 | Sspon.03G | KQL03581 | TKW12396 | EES00603 | Zm00001eb129510_P005 | 0.905 |
| PUZ42345 | Sspon.01G | KQK92107 | TKV97632 | KXG39943 | Zm00001eb007870_P002 | 0.887 |
| PUZ40395 | Sspon.01G | KQK90194 | TKV95250 | genblast_C | Zm00001eb021750_P001 | 0.873 |
| PUZ60123 | Sspon.08G | KQL11588 | genblast_C | EER88575 | Zm00001eb386180_P003 | 0.965 |
| PUZ76081 | Sspon.04G | KQL30016 | TKW39702 | EES05239 | Zm00001eb243740_P001 | 0.978 |
| PUZ49921 | Sspon.06G | KQL01016 | TKW09262 | EES13280 | Zm00001eb261190_P002 | 0.921 |
| PUZ38412 | Sspon.01G | KQK88470 | TKV93055 | EER92330 | Zm00001eb015540_P002 | 0.950 |
| PUZ38471 | Sspon.01G | KQK88537 | TKV93142 | EER91435 | Zm00001eb044820_P001 | 0.994 |
| PUZ59496 | Sspon.08G | KQL11999 | TKW23162 | EER88811 | Zm00001eb224710_P001 | 0.955 |
| PUZ63290 | Sspon.07G | KQL13735 | TKW25167 | OQU78931 | Zm00001eb411140_P003 | 0.929 |

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| PUZ59209 | Sspon.08G | KQL12099 | TKW23285 | OQU77022 | Zm00001eb227200_P003 | 0.898 |
| PUZ59721 | Sspon.08G | KQL11161 | TKW22061 | EER88740 | Zm00001eb388800_P001 | 0.988 |

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| PUZ72111 | Sspon.02G | KQL25849 | TKW34818 | EER99403 | genblast_Os07t0500300-01 | Zm0 |
| PUZ73059 | Sspon.02G | KQL26798 | TKW36024 | KXG36765 | Zm00001eb328330_P003 | 0.959 |
| PUZ70570 | Sspon.02G | KQL24329 | TKW32952 | KXG35540 | Zm00001eb311590_P001 | 0.968 |
| PUZ65913 | Sspon.07G | KQL15410 | TKW27183 | EES19545 | Zm00001eb288380_P001 | 0.917 |

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| PUZ38151 | Sspon.01G | KQK88253 | TKV92754 | EER91310 | Zm00001eb048950_P001 | 0.969 |
| PUZ76926 | Sspon.04G | genblast_C | TKW40762 | KXG31078 | Zm00001eb249710_P001 | 0.869 |

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| PUZ58766 | Sspon.03GKQL03331 | TKW12069 | EES00022 | Zm00001eb119470_P001 | 0.763 |
| PUZ46032 | Sspon.05GKQK96156 | TKW02884 | EES11733 | Zm00001eb418910_P001 | 0.984 |
| PUZ52765 | Sspon.06GKQL03051 | TKW11857 | KXG25344 | Zm00001eb038510_P002 | 0.918 |
| genblast_C | genblast_CKQL05075 | TKW14326 | OQU86827 | Zm00001eb131470_P002 | 0.966 |
| PUZ43097 | genblast_CKQK92845 | TKV98498 | EER95601 | Zm00001eb001810_P001 | 0.973 |
| PUZ38556 | Sspon.01GKQK88645 | TKV93263 | EER91463 | Zm00001eb221340_P001 | 0.942 |
| PUZ37333 | genblast_CKQK87432 | TKV91727 | EER93570 | Zm00001eb055080_P001 | 0.982 |

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| PUZ42973 | Sspon.01GKQK92702 | TKV98344 | EER92911 | Zm00001eb002780_P001 | 0.915 |

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| PUZ56271 | Sspon.03GKQL05499 | TKW14909 | OQU87002 | Zm00001eb356350_P001 | 0.977 |

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|---|---|---|---|---|---|
| PUZ72979 | Sspon.02GKQL26731 | TKW35914 | KXG36730 | Zm00001eb327840_P001 | 0.961 |
| PUZ68182 | Sspon.02GKQL22115 | TKW29987 | OQU88298 | Zm00001eb118270_P001 | 0.783 |

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| PUZ54344 | Sspon.03GKQL07366 | TKW17284 | EES03766 | Zm00001eb150590_P001 | 0.916 |
| PUZ75522 | Sspon.04GKQL29655 | TKW39190 | EES05060 | Zm00001eb241100_P001 | 0.909 |

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|---|---|---|---|---|---|
| PUZ72976 | Sspon.02GKQL26729 | TKW35910 | OQU90285 | Zm00001eb327820_P001 | 0.986 |
| PUZ51364 | genblast_CKQL01702 | TKW10164 | EES13807 | Zm00001eb167210_P001 | 0.951 |
| PUZ68061 | Sspon.02GKQL17419 | TKW29864 | EES17492 | Zm00001eb032780_P001 | 0.823 |
| PUZ36689 | genblast_CKQK86779 | TKV90959 | EER90771 | genblast_Os03t0786600-01_Zea |  |

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| PUZ67897 | Sspon.02GKQL17301 | TKW29694 | EES17387 | Zm00001eb031690_P001 | 0.975 |
| PUZ62615 | Sspon.08GKQL08886 | TKW19148 | KXG19082 | Zm00001eb268390_P001 | 0.931 |
| PUZ58563 | Sspon.03GKQL04884 | TKW14051 | EES00100 | Zm00001eb120760_P001 | 0.909 |
| PUZ50982 | Sspon.06G | genblast_Z | TKW09555 | OQU80224 | genblast_Zm00001eb269020_P0 |
| PUZ43237 | Sspon.01GKQK93013 | TKV98678 | KXG40376 | Zm00001eb404190_P001 | 0.804 |
| PUZ63773 | Sspon.07GKQL13123 | TKW24330 | EES18932 | Zm00001eb355270_P001 | 0.972 |
| PUZ44581 | Sspon.05GKQK94264 | TKW00261 | KXG28232 | Zm00001eb169130_P001 | 0.914 |
| PUZ55316 | Sspon.08GKQL06448 | TKW16088 | EER90269 | Zm00001eb225820_P001 | 0.953 |
| PUZ48340 | genblast_CKQK98380 | TKW05853 | EES11238 | Zm00001eb074570_P001 | 0.869 |

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| PUZ48696 | Sspon.05GKQK98711 | TKW06275 | EES12768 | Zm00001eb430000_P001 | 0.842 |
| PUZ72404 | Sspon.02GKQL26164 | TKW35194 | KXG36439 | Zm00001eb323600_P001 | 0.941 |

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| PUZ64715 | Sspon.07G | KQL14235 | TKW25792 | KXG22559 | Zm00001eb245440_P001 | 0.926 |
| genblast_C | Sspon.02G | KQL26647 | TKW35802 | OQU9025 | Zm00001eb109140_P003 | 0.958 |

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| PUZ47624 | Sspon.08G | KQK97707 | TKW04958 | EER88897 | Zm00001eb226800_P001 | 0.952 |
| PUZ41976 | genblast_C | KQK91736 | TKV97174 | KXG39792 | genblast_Os03t0241900-02_Ze | |
| PUZ42294 | Sspon.01G | KQK92059 | TKV97578 | EER95311 | Zm00001eb007570_P003 | 0.936 |
| PUZ42681 | Sspon.01G | KQK92416 | TKV98013 | EER95447 | Zm00001eb005130_P001 | 0.956 |
| PUZ54419 | Sspon.03G | KQL07288 | TKW17178 | EES01586 | Zm00001eb369700_P001 | 0.912 |
| PUZ39940 | genblast_C | KQK89761 | TKV94730 | EER91876 | Zm00001eb024740_P001 | 0.841 |
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| PUZ74298 | genblast_C | KQL28519 | TKW37746 | EES04609 | Zm00001eb233320_P001 | 0.925 |
| PUZ61251 | genblast_C | KQL10555 | TKW21331 | KXG19969 | Zm00001eb382170_P003 | 0.959 |

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| PUZ60020 | Sspon.08G | KQL11495 | TKW22497 | EER90022 | Zm00001eb276590_P001 | 0.927 |
| PUZ40537 | genblast_C | KQK90323 | TKV95425 | OQU9233 | Zm00001eb020720_P001 | 0.878 |
| PUZ66763 | genblast_C | KQL16414 | TKW28511 | EES19623 | Zm00001eb347780_P001 | 0.958 |

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| PUZ71683 | Sspon.02G | KQL25444 | TKW34286 | EER99234 | Zm00001eb319590_P001 | 0.945 |

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| PUZ38006 | Sspon.01G | KQK88105 | TKV92545 | KXG38039 | Zm00001eb051620_P001 | 0.872 |

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| PUZ37557 | Sspon.01G | KQK87677 | TKV91991 | OQU9118 | Zm00001eb217200_P002 | 0.913 |
| PUZ47582 | Sspon.05G | KQK97665 | TKW04902 | EES12340 | Zm00001eb424650_P001 | 0.950 |
| PUZ58500 | Sspon.04G | genblast_C | TKW13978 | OQU8550 | Zm00001eb253100_P001 | 0.945 |
| PUZ42302 | Sspon.01G | KQK92067 | TKV97590 | KXG39925 | Zm00001eb007640_P001 | 0.890 |
| PUZ77399 | Sspon.04G | KQL31259 | TKW41303 | EES07349 | Zm00001eb253030_P001 | 0.970 |
| PUZ47647 | Sspon.05G | KQK97734 | TKW04997 | EES10998 | Zm00001eb424960_P001 | 0.925 |

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| PUZ36898 | Sspon.01G | KQK86964 | TKV91201 | EER90833 | Zm00001eb058410_P002 | 0.965 |

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| PUZ36739 | Sspon.01G | KQK86812 | TKV91008 | genblast_C | Zm00001eb059460_P001 | 0.895 |
| PUZ65562 | Sspon.07G | KQL15069 | TKW26779 | KXG20080 | Zm00001eb290190_P003 | 0.950 |
| PUZ47509 | Sspon.05G | KQK97596 | TKW04819 | KXG26481 | Zm00001eb080550_P001 | 0.974 |
| PUZ71815 | Sspon.02G | KQL25587 | TKW34459 | EER97124 | Zm00001eb321000_P001 | 0.928 |
| PUZ43936 | genblast_C | KQK93843 | TKV99655 | EES12385 | Zm00001eb124210_P001 | 0.902 |

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| PUZ46527 | genblast_C | KQK96681 | TKW03607 | OQU78814 | Zm00001eb139070_P001 | 0.855 |
| PUZ47602 | genblast_C | KQK97682 | TKW04928 | EES10976 | Zm00001eb424770_P002 | 0.921 |
| PUZ77574 | Sspon.04G | KQL31378 | TKW41431 | EES07310 | Zm00001eb190130_P001 | 0.965 |
| PUZ53193 | Sspon.03G | KQL08410 | TKW18599 | EES04133 | Zm00001eb142750_P001 | 0.968 |
| PUZ62479 | genblast_C | KQL09008 | TKW19287 | EER89074 | Zm00001eb268890_P001 | 0.982 |
| PUZ51534 | Sspon.05G | KQL01887 | TKW10390 | EES09236 | Zm00001eb196520_P001 | 0.926 |

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| PUZ59759 | Sspon.08G | KQL11195 | TKW22097 | EER90124 | Zm00001eb388620_P001 | 0.857 |
| PUZ71952 | Sspon.02G | KQL25702 | TKW34637 | EER99355 | Zm00001eb104690_P001 | 0.956 |

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| PUZ73491 | Sspon.02G | KQL27223 | TKW36577 | OQU90492 | Zm00001eb331000_P001 | 0.845 |
| PUZ41069 | Sspon.01G | KQK90846 | TKV96062 | EER92266 | Zm00001eb394570_P001 | 0.919 |
| genblast_C | Sspon.01G | KQK92188 | TKV97724 | EER92715 | Zm00001eb401340_P001 | 0.833 |
| PUZ71653 | Sspon.02G | KQL25425 | TKW34255 | EER99231 | Zm00001eb319390_P001 | 0.937 |
| PUZ39277 | Sspon.01G | KQK89253 | TKV94060 | OQU91902 | Zm00001eb027810_P001 | 0.908 |
| PUZ66100 | Sspon.07G | KQL15605 | TKW27451 | KXG21940 | Zm00001eb287500_P001 | 0.902 |

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| PUZ36771 | Sspon.01G | KQK86839 | TKV91038 | EER93358 | Zm00001eb213680_P001 | 0.931 |
| PUZ42301 | Sspon.01G | KQK92066 | TKV97589 | KXG39923 | Zm00001eb400670_P001 | 0.950 |
| PUZ53225 | Sspon.03G | KQL08376 | TKW18557 | EES01985 | Zm00001eb143060_P002 | 0.953 |
| PUZ78304 | Sspon.04G | KQL32166 | TKW42326 | EES06029 | Zm00001eb259210_P003 | 0.923 |
| PUZ36584 | Sspon.01G | KQK86672 | TKV90833 | EER93295 | Zm00001eb060780_P006 | 0.923 |
| PUZ71543 | Sspon.02G | KQL25321 | TKW34139 | EER99184 | Zm00001eb318720_P001 | 0.937 |
| PUZ72286 | genblast_C | KQL26049 | TKW35065 | EER99462 | Zm00001eb106190_P001 | 0.908 |
| PUZ37492 | genblast_C | KQK87600 | TKV91910 | KXG37796 | Zm00001eb053830_P001 | 0.901 |
| PUZ70995 | Sspon.02G | KQL24791 | TKW33493 | EER96851 | Zm00001eb314890_P001 | 0.902 |
| PUZ41513 | Sspon.01G | KQK91305 | TKV96671 | KXG39579 | Zm00001eb396920_P001 | 0.966 |
| PUZ64279 | Sspon.04G | KQL13825 | TKW25286 | EES07049 | Zm00001eb283780_P001 | 0.954 |
| PUZ73879 | Sspon.04G | KQL28905 | TKW38237 | EES04436 | Zm00001eb208800_P001 | 0.919 |
| PUZ71658 | Sspon.02G | KQL25428 | TKW34259 | EER97080 | Zm00001eb319470_P001 | 1.002 |
| PUZ50225 | Sspon.06G | KQL00702 | TKW08816 | EES14597 | Zm00001eb172230_P001 | 0.976 |
| PUZ53153 | genblast_C | KQL08446 | TKW18655 | KXG34044 | Zm00001eb363750_P004 | 0.938 |
| PUZ64855 | Sspon.07G | KQL14398 | TKW25956 | EES18654 | Zm00001eb343220_P002 | 0.970 |
| PUZ70594 | Sspon.02G | KQL24344 | TKW32974 | EER98844 | Zm00001eb098980_P002 | 0.961 |
| PUZ75651 | Sspon.04G | genblast_C | TKW39036 | EES04892 | Zm00001eb236670_P001 | 0.967 |
| PUZ66214 | Sspon.07G | KQL15704 | TKW27602 | EES18143 | Zm00001eb347150_P002 | 0.853 |
| PUZ59156 | Sspon.08G | KQL12166 | TKW23368 | EER90359 | Zm00001eb227630_P001 | 0.883 |
| PUZ37248 | Sspon.01G | KQK87345 | TKV91627 | KXG37671 | Zm00001eb055830_P001 | 0.928 |

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| PUZ43920 | Sspon.05G | KQK93824 | TKV99609 | KXG27890 | Zm00001eb201080_P003 | 0.951 |
| PUZ54498 | Sspon.03G | KQL07232 | TKW17098 | EES01558 | Zm00001eb151570_P006 | 0.769 |
| PUZ53260 | genblast_C | KQL08349 | TKW18526 | OQU88118 | Zm00001eb364420_P001 | 0.865 |

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| PUZ53859 | Sspon.03G | KQL07825 | TKW17834 | KXG33733 | Zm00001eb366900_P002 | 0.891 |

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| PUZ58703 | Sspon.03G | KQL03397 | TKW12160 | EES02240 | genblast_Os01t0219200-01_Zea | |
| PUZ56125 | Sspon.03G | KQL06261 | TKW15875 | EES00952 | Zm00001eb357050_P001 | 0.879 |
| PUZ42507 | genblast_C | KQK92261 | TKV97822 | EER95370 | Zm00001eb006320_P001 | 0.826 |
| PUZ71007 | Sspon.02G | KQL24803 | TKW33505 | EER96860 | Zm00001eb314950_P001 | 0.958 |
| PUZ55218 | Sspon.03G | KQL06562 | TKW16220 | EES03480 | Zm00001eb155880_P001 | 0.974 |

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| PUZ54145 | genblast_C | KQL07554 | TKW17527 | OQU87786 | Zm00001eb368450_P001 | 0.985 |

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| PUZ55651 | Sspon.03G | KQL06043 | TKW15582 | genblast_C | genblast_Os01t0639200-01_Zea | |

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| PUZ63547 | Sspon.07G | KQL13495 | TKW24853 | EES17880 | genblast_Os05t0210100-01_Zea | |
| PUZ62463 | Sspon.08G | KQK87521 | TKV91822 | KXG19156 | Zm00001eb378880_P001 | 0.916 |
| PUZ65158 | Sspon.07G | KQL14711 | TKW26320 | EES18520 | Zm00001eb353340_P001 | 0.948 |
| PUZ43637 | Sspon.05G | KQK93503 | TKV99177 | OQU82838 | Zm00001eb093280_P001 | 0.962 |
| PUZ42081 | genblast_C | genblast_C | TKV97325 | EER92608 | Zm00001eb399450_P001 | 0.759 |
| PUZ67621 | genblast_C | KQL16944 | TKW29238 | EES16230 | Zm00001eb134850_P001 | 0.905 |
| PUZ48670 | Sspon.04G | KQK98692 | TKW06246 | EES12753 | Zm00001eb072390_P001 | 0.845 |
| PUZ35946 | Sspon.01G | genblast_Z | TKV90039 | genblast_Z | Zm00001eb065330_P001 | 0.827 |
| genblast_C | genblast_C | KQK92184 | TKV97722 | genblast_C | Zm00001eb006950_P001 | 0.781 |
| PUZ40933 | Sspon.01G | KQK90729 | TKV95899 | OQU92533 | Zm00001eb394100_P001 | 0.950 |
| PUZ64759 | Sspon.07G | KQL14303 | TKW25857 | EES18691 | Zm00001eb296050_P001 | 0.953 |

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| PUZ55562 | Sspon.03GKQL06128 | TKW15719 | EES03360 | Zm00001eb158170_P001 | 0.995 |
| PUZ41563 | Sspon.01GKQK91350 | TKV96714 | EER95046 | Zm00001eb013180_P002 | 0.912 |
| PUZ52745 | Sspon.06GKQL03033 | TKW11833 | EES14038 | Zm00001eb175670_P001 | 0.924 |
| PUZ52903 | Sspon.03GKQL08705 | TKW18964 | EES02089 | Zm00001eb362550_P001 | 0.982 |
| PUZ47172 | Sspon.05GKQK97285 | TKW04414 | EES12177 | Zm00001eb082750_P001 | 0.937 |
| PUZ36026 | Sspon.01GKQK86122 | TKV90111 | KXG37101 | Zm00001eb064800_P001 | 0.952 |

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| PUZ52413 | Sspon.06GKQL02677 | TKW11420 | EES14183 | genblast_Os08t0535200-01_Zea | |
| PUZ54597 | Sspon.03GKQL07147 | TKW16995 | EES01527 | Zm00001eb152050_P001 | 0.974 |
| PUZ42916 | Sspon.01GKQK92641 | TKV98288 | EER92881 | genblast_Os03t0140700-01_Zea | |
| PUZ75509 | Sspon.08GKQL29667 | TKW39201 | OQU84946 | Zm00001eb202950_P004 | 0.949 |

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| PUZ65009 | Sspon.03GKQL14572 | TKW26164 | EES18577 | Zm00001eb294180_P001 | 0.916 |
| PUZ51551 | Sspon.02GKQL01893 | TKW10403 | EER95910 | Zm00001eb300940_P001 | 0.919 |
| PUZ49872 | Sspon.06GKQL01076 | TKW09334 | EES14411 | Zm00001eb173940_P001 | 0.964 |
| PUZ36212 | Sspon.01GKQK86336 | TKV90372 | KXG37199 | Zm00001eb063580_P002 | 0.819 |
| PUZ72630 | Sspon.03GKQL03883 | TKW12791 | EES06999 | Zm00001eb127690_P002 | 0.865 |
| PUZ68289 | Sspon.02GKQL22300 | TKW30253 | EER95805 | Zm00001eb117930_P001 | 0.908 |
| PUZ37313 | genblast_CKQK87406 | TKV91699 | EER93563 | Zm00001eb055220_P001 | 0.976 |
| PUZ73974 | Sspon.04GKQL28827 | TKW38122 | EES04472 | Zm00001eb231630_P001 | 0.939 |

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| PUZ65495 | Sspon.07G | genblast_C | TKW26683 | KXG22230 | Zm00001eb290950_P001 | 0.965 |
| PUZ54020 | Sspon.03G | KQL07675 | TKW17657 | EES01740 | Zm00001eb148290_P001 | 0.944 |
| PUZ64159 | Sspon.07G | KQK99296 | TKW07041 | OQU77484 | Zm00001eb282510_P001 | 0.940 |
| PUZ36775 | Sspon.01G | KQK86840 | TKV91039 | EER90798 | Zm00001eb059370_P001 | 0.966 |
| PUZ71915 | genblast_C | KQL25665 | TKW34592 | EER99339 | Zm00001eb320530_P001 | 0.937 |

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| PUZ71487 | Sspon.02G | genblast_C | TKW34060 | EER99171 | Zm00001eb318020_P003 | 0.847 |
| PUZ60479 | Sspon.08G | KQL10823 | TKW21669 | OQU76487 | Zm00001eb383000_P001 | 0.894 |

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| PUZ37787 | Sspon.01G | KQK87926 | TKV92286 | KXG37939 | Zm00001eb050320_P001 | 0.811 |
| PUZ55680 | Sspon.03G | KQL06015 | TKW15549 | EES03324 | Zm00001eb159080_P001 | 0.984 |
| PUZ62389 | Sspon.08G | KQL09110 | TKW19423 | EER87768 | Zm00001eb378390_P001 | 0.885 |
| PUZ54361 | genblast_C | KQL07351 | TKW17260 | EES01610 | Zm00001eb369450_P001 | 0.892 |
| PUZ68514 | genblast_C | KQL22557 | TKW30584 | KXG27340 | Zm00001eb067410_P001 | 0.914 |
| PUZ72207 | genblast_C | KQL25959 | TKW34934 | OQU89996 | Zm00001eb322480_P003 | 0.949 |

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| PUZ47431 | Sspon.05G | KQK97520 | TKW04725 | KXG26440 | Zm00001eb423930_P003 | 0.968 |
| PUZ42959 | Sspon.01G | genblast_Z | TKV98324 | KXG40233 | Zm00001eb002930_P001 | 0.973 |
| PUZ55016 | Sspon.04G | KQL06755 | TKW16479 | EES04464 | Zm00001eb209080_P003 | 0.898 |
| PUZ61607 | Sspon.08G | KQL10171 | TKW20783 | EER89540 | Zm00001eb280720_P001 | 0.907 |

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| PUZ63921 | Sspon.07G | KQL13256 | TKW24505 | EES17668 | Zm00001eb417450_P001 | 0.928 |
| PUZ41816 | Sspon.01G | genblast_C | TKV96866 | OQU92885 | Zm00001eb011360_P001 | 0.864 |
| PUZ68441 | genblast_C | KQL22485 | TKW30495 | EER98001 | Zm00001eb300260_P001 | 0.907 |

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| PUZ41981 | Sspon.01G | KQK91744 | TKV97184 | KXG40230 | Zm00001eb399030_P003 | 0.930 |
| PUZ77152 | Sspon.04G | KQL31020 | TKW40997 | EES05692 | Zm00001eb251210_P001 | 0.883 |
| PUZ74458 | Sspon.04G | KQL28342 | TKW37535 | EES06432 | Zm00001eb206250_P001 | 0.887 |
| PUZ41341 | Sspon.01G | KQK91125 | TKV96434 | EER94948 | Zm00001eb015170_P002 | 0.984 |
| PUZ58299 | Sspon.03G | KQL04645 | TKW13741 | KXG31730 | Zm00001eb122630_P001 | 0.912 |
| PUZ61438 | Sspon.08G | KQL10012 | TKW20568 | EER89471 | Zm00001eb372390_P001 | 0.975 |
| PUZ76511 | Sspon.04G | KQL30446 | TKW40247 | EES05410 | Zm00001eb246850_P001 | 0.945 |
| PUZ67305 | Sspon.02G | KQL16741 | TKW28950 | EES17120 | Zm00001eb410680_P002 | 0.897 |
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| PUZ49836 | Sspon.06G | KQL00242 | TKW08137 | EES14396 | Zm00001eb174100_P001 | 0.965 |
| PUZ48218 | genblast_C | KQK98286 | TKW05684 | KXG26789 | Zm00001eb427560_P003 | 0.949 |
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| PUZ41794 | genblast_C | KQK91504 | TKV96883 | OQU92876 | Zm00001eb011560_P001 | 0.978 |
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| PUZ77239 | Sspon.04G | KQL31105 | TKW41105 | OQU85559 | Zm00001eb251710_P001 | 0.923 |
| PUZ48601 | Sspon.05G | KQK98614 | TKW06160 | EES12722 | Zm00001eb072900_P001 | 0.893 |
| PUZ46195 | Sspon.02G | KQK96339 | TKW03135 | EER97064 | Zm00001eb318800_P001 | 0.925 |
| PUZ52162 | Sspon.06G | KQL02430 | TKW11112 | EES15398 | Zm00001eb034980_P001 | 0.886 |
| PUZ59515 | Sspon.08G | KQL12014 | TKW23180 | OQU76879 | Zm00001eb273960_P005 | 0.948 |
| PUZ76694 | Sspon.04G | KQL30622 | TKW40492 | OQU85364 | Zm00001eb185430_P001 | 0.844 |
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| PUZ48114 | Sspon.04G | KQK98176 | TKW05552 | KXG26758 | Zm00001eb427040_P002 | 0.935 |
| PUZ66277 | Sspon.07G | KQL15766 | TKW27675 | EES18130 | Zm00001eb285420_P001 | 0.933 |
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| PUZ52383 | Sspon.06G | KQL02648 | TKW11390 | KXG25534 | Zm00001eb175150_P003 | 0.779 |
| PUZ36447 | Sspon.01G | KQK86522 | TKV90627 | EER90674 | Zm00001eb061960_P001 | 0.948 |
| PUZ41940 | genblast_C | KQK91695 | TKV97111 | EER95178 | Zm00001eb398680_P001 | 0.959 |
| PUZ57548 | Sspon.03G | KQL03970 | TKW12870 | EES02670 | Zm00001eb334030_P003 | 0.954 |
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| PUZ37384 | Sspon.01G | KQK87465 | TKV91748 | EER93585 | Zm00001eb216410_P001 | 0.880 |
| PUZ44544 | Sspon.06G | KQK94246 | TKW00226 | EES09025 | genblast_Os11t0306400-01Zm |  |
| PUZ66450 | genblast_C | KQL15898 | TKW27836 | KXG38815 | Zm00001eb025110_P001 | 0.932 |
| PUZ63791 | Sspon.07G | genblast_C | TKW24345 | OQU77296 | Zm00001eb265540_P004 | 0.920 |

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|---|---|---|---|---|---|---|
| PUZ77942 | Sspon.04G | KQL31805 | TKW41919 | EES05905 | Zm00001eb257130_P001 | 0.900 |
| PUZ72766 | genblast_C | KQL26504 | TKW35618 | EER97478 | Zm00001eb326450_P001 | 0.943 |
| PUZ50860 | genblast_C | KQL01361 | TKW09726 | EER89855 | Zm00001eb028220_P005 | 0.936 |
| PUZ41916 | Sspon.01G | KQK91675 | TKV97079 | EER92551 | Zm00001eb398560_P001 | 0.951 |
| PUZ72853 | Sspon.02G | KQL26612 | TKW35756 | EER99682 | Zm00001eb327110_P001 | 0.975 |
| PUZ70377 | Sspon.02G | KQL24182 | TKW32729 | EER96590 | Zm00001eb310270_P001 | 0.758 |
| PUZ50878 | Sspon.07G | KQL01346 | TKW09711 | EES19087 | Zm00001eb282320_P001 | 0.954 |
| PUZ52367 | Sspon.06G | KQL02632 | TKW11374 | EES15316 | Zm00001eb036510_P001 | 0.879 |
| PUZ51527 | Sspon.06G | KQL01876 | TKW10384 | EES15018 | Zm00001eb041840_P003 | 0.952 |
| PUZ53642 | Sspon.03G | KQL08014 | TKW18093 | EES01869 | Zm00001eb145640_P001 | 0.932 |
| PUZ59514 | Sspon.04G | KQL12013 | TKW23176 | EER90210 | Zm00001eb224830_P001 | 0.890 |
| PUZ38205 | Sspon.01G | KQK88292 | TKV92809 | EER91340 | Zm00001eb043080_P001 | 0.858 |
| PUZ58836 | Sspon.03G | KQL03242 | TKW11970 | KXG31482 | Zm00001eb339300_P001 | 0.956 |
| PUZ67983 | Sspon.02G | KQL17328 | TKW29727 | KXG24063 | Zm00001eb032370_P001 | 0.810 |
| PUZ66646 | Sspon.07G | genblast_C | TKW28077 | EES15804 | Zm00001eb264250_P001 | 0.950 |
| PUZ70885 | Sspon.02G | KQL24686 | TKW33376 | KXG35720 | Zm00001eb314230_P001 | 0.949 |
| PUZ71264 | Sspon.02G | KQL25045 | TKW33801 | KXG35903 | Zm00001eb316660_P001 | 0.889 |
| PUZ37008 | Sspon.01G | KQK87076 | TKV91328 | EER90867 | Zm00001eb057420_P001 | 0.915 |
| PUZ70032 | genblast_C | KQL23771 | TKW32175 | EER96413 | Zm00001eb308130_P001 | 0.949 |
| PUZ55608 | Sspon.03G | KQL06081 | TKW15643 | OQU87232 | Zm00001eb359300_P001 | 0.867 |
| PUZ61775 | Sspon.08G | KQL09894 | TKW20412 | KXG19555 | genblast_Os06t0203600-01Zm0 | |
| PUZ63769 | Sspon.07G | KQL13116 | TKW24321 | EES17622 | Zm00001eb265670_P001 | 0.915 |
| PUZ78141 | genblast_C | KQL32007 | TKW42146 | KXG31315 | Zm00001eb258280_P003 | 0.938 |
| PUZ73719 | Sspon.04G | KQL29085 | TKW38468 | EES04357 | Zm00001eb229900_P004 | 0.941 |
| PUZ76618 | Sspon.04G | KQL30548 | TKW40393 | EES05467 | Zm00001eb248020_P001 | 0.951 |
| PUZ68166 | Sspon.02G | KQK85890 | TKW29970 | EER95729 | Zm00001eb298270_P001 | 0.912 |
| PUZ77247 | Sspon.04G | KQL31117 | TKW41120 | EES05665 | Zm00001eb251920_P001 | 0.947 |

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| PUZ72721 | genblast_C | KQL26469 | TKW35579 | EER97462 | Zm00001eb326020_P001 0.969 |
| PUZ59636 | Sspon.08G | KQL11083 | TKW21961 | OQU76825 | Zm00001eb389150_P003 0.963 |
| PUZ71784 | Sspon.02G | KQL25538 | TKW34406 | EER99288 | Zm00001eb321200_P003 0.964 |
| PUZ56085 | Sspon.03G | KQL06225 | TKW15839 | EES00973 | Zm00001eb357310_P001 0.864 |
| PUZ46388 | Sspon.05G | KQK96550 | TKW03446 | KXG25874 | Zm00001eb419690_P001 0.905 |
| PUZ55939 | Sspon.03G | KQL05764 | TKW15230 | EES01026 | Zm00001eb161460_P001 0.864 |
| PUZ47407 | genblast_C | KQK97502 | TKW04698 | OQU81672 | genblast_Os04t0450500-01Zm0 |

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| PUZ73820 | Sspon.04G | KQL28950 | TKW38291 | EES04407 | Zm00001eb208560_P001 0.964 |
| PUZ70458 | genblast_C | KQL24248 | TKW32830 | EER98795 | Zm00001eb310860_P001 0.974 |
| PUZ76456 | genblast_C | KQL30401 | TKW40180 | EES05396 | Zm00001eb246660_P001 0.959 |
| PUZ74742 | Sspon.04G | KQL28057 | TKW37174 | EES04777 | Zm00001eb239890_P001 0.947 |
| PUZ51429 | Sspon.06G | genblast_C | TKW10267 | EES13830 | Zm00001eb042410_P001 0.907 |

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| PUZ52817 | Sspon.03G | KQL08783 | TKW19065 | KXG34214 | Zm00001eb139880_P003 0.817 |
| PUZ46851 | Sspon.05G | KQK96969 | TKW04006 | OQU81398 | Zm00001eb085420_P002 0.947 |
| PUZ55818 | Sspon.03G | KQL05900 | TKW15398 | EES03281 | Zm00001eb159770_P001 0.957 |
| PUZ47519 | Sspon.05G | KQK97606 | TKW04827 | EES12304 | Zm00001eb080490_P002 0.853 |
| PUZ70960 | Sspon.02G | KQL24758 | TKW33456 | EER99001 | Zm00001eb314690_P001 0.957 |
| PUZ64366 | Sspon.07G | genblast_C | TKW25376 | EES19193 | genblast_Os05t0199100-01_Zea |
| PUZ70475 | Sspon.02G | KQL24257 | TKW32851 | KXG35488 | Zm00001eb310990_P001 0.934 |
| PUZ50906 | Sspon.07G | KQL04909 | TKW14089 | EES18696 | Zm00001eb296150_P001 0.961 |
| PUZ36152 | Sspon.06G | KQK86253 | TKV90278 | KXG25445 | Zm00001eb202650_P002 0.951 |
| PUZ77513 | genblast_Z | KQL31441 | TKW41501 | EES05554 | Zm00001eb254040_P001 0.934 |
| PUZ55133 | genblast_C | KQL06651 | TKW16326 | EES03502 | Zm00001eb155230_P001 0.901 |
| PUZ77368 | Sspon.04G | KQL31234 | TKW41257 | EES05620 | genblast_Os02t0717900-01Zm0 |
| PUZ72861 | Sspon.02G | KQL26604 | TKW35743 | EER97519 | Zm00001eb327170_P001 0.867 |

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| PUZ74823 | Sspon.04G | KQL27968 | TKW37073 | EES04812 | Zm00001eb239050_P001 0.977 |
| PUZ36838 | Sspon.01G | KQK86915 | TKV91120 | EER90822 | Zm00001eb058770_P001 0.943 |
| PUZ63788 | Sspon.07G | KQL13129 | TKW24340 | EES17627 | genblast_Os05t0122400-00_Zea |

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| PUZ59513 | Sspon.08GKQL12012 | TKW23175 | EER88807 | Zm00001eb224800_P001 | 0.915 |
| PUZ56203 | Sspon.03GKQL05574 | TKW14994 | EES00919 | Zm00001eb356770_P001 | 0.926 |
| PUZ60058 | Sspon.08GKQL11525 | TKW22543 | EER88607 | Zm00001eb385620_P001 | 0.935 |

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| PUZ52178 | Sspon.02GKQL02433 | TKW11116 | EES14266 | Zm00001eb035030_P002 | 0.829 |
| PUZ37572 | Sspon.01GKQK87703 | TKV92022 | OQU91192 | Zm00001eb053190_P002 | 0.972 |
| PUZ46985 | Sspon.05GKQK97089 | TKW04178 | KXG26203 | Zm00001eb084530_P001 | 0.944 |

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| PUZ54568 | Sspon.03G | KQL07170 | TKW17018 | EES01533 | Zm00001eb151930_P001 | 0.954 |
| PUZ54754 | Sspon.03G | KQL07012 | TKW16817 | KXG33384 | Zm00001eb370810_P003 | 0.943 |
| PUZ42295 | Sspon.01G | KQK92060 | TKV97581 | KXG39918 | Zm00001eb400660_P001 | 0.848 |
| PUZ67269 | Sspon.02G | KQL16784 | TKW29007 | EES16065 | Zm00001eb004090_P001 | 0.947 |
| PUZ76318 | Sspon.04G | KQL30242 | TKW39999 | EES05335 | Zm00001eb245580_P001 | 0.902 |
| PUZ43711 | Sspon.05G | KQK99887 | TKW07808 | KXG27738 | Zm00001eb092730_P001 | 0.784 |
| PUZ69845 | Sspon.07G | KQL23829 | TKW32251 | EES04018 | Zm00001eb308400_P001 | 0.913 |
| PUZ41979 | Sspon.01G | KQK91740 | TKV97179 | EER92574 | Zm00001eb010320_P001 | 0.958 |
| PUZ51875 | Sspon.06G | KQL02188 | TKW10773 | KXG25323 | Zm00001eb180330_P001 | 0.977 |
| PUZ37077 | genblast_C | KQK87155 | TKV91413 | KXG37585 | Zm00001eb056920_P002 | 0.975 |
| genblast_C | Sspon.02G | KQK85888 | TKW29973 | EER95730 | Zm00001eb118320_P001 | 0.870 |
| PUZ45180 | Sspon.06G | genblast_C | TKW01153 | EES10304 | Zm00001eb201750_P002 | 0.900 |
| PUZ58245 | genblast_C | KQL04578 | TKW13664 | EES02391 | Zm00001eb123050_P003 | 0.955 |

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| PUZ71285 | Sspon.02G | KQL25066 | TKW33829 | EER99092 | Zm00001eb316740_P001 | 0.854 |

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|---|---|---|---|---|---|---|
| PUZ41288 | Sspon.01G | KQK91069 | TKV96349 | KXG39473 | Zm00001eb395430_P001 | 0.930 |
| PUZ43980 | Sspon.05G | KQK93881 | TKV99710 | OQU83025 | Zm00001eb091260_P002 | 0.970 |
| PUZ46323 | Sspon.05G | KQK96409 | TKW03217 | EES11922 | Zm00001eb087100_P001 | 0.930 |

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| PUZ76790 | Sspon.05G | KQL30698 | TKW40591 | EES05828 | Zm00001eb248640_P001 | 0.931 |
| PUZ54140 | genblast_Z | KQL07560 | TKW17531 | EES03827 | Zm00001eb149030_P001 | 0.760 |

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| PUZ55834 | Sspon.03G | KQL05878 | TKW15371 | EES03275 | Zm00001eb162060_P001 | 0.984 |
| PUZ45306 | Sspon.06G | KQK95055 | TKW01327 | OQU83721 | Zm00001eb200440_P001 | 0.922 |
| PUZ39668 | Sspon.01G | KQK91578 | TKV96948 | genblast_C | Zm00001eb012070_P002 | 0.956 |
| PUZ67510 | Sspon.02G | KQL16539 | TKW28670 | EES16183 | Zm00001eb028930_P001 | 0.971 |
| PUZ58601 | Sspon.03G | KQL04918 | TKW14102 | OQU86128 | Zm00001eb221460_P001 | 0.922 |

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| PUZ72973 | Sspon.02G | KQL26727 | TKW35909 | KXG36727 | Zm00001eb327810_P001 | 0.964 |
| PUZ65626 | Sspon.07G | KQL15140 | TKW26871 | OQU78144 | Zm00001eb289820_P003 | 0.940 |
| PUZ64851 | Sspon.03G | genblast_C | TKW25950 | EES19926 | Zm00001eb343260_P001 | 0.918 |
| PUZ53310 | Sspon.01G | KQL08311 | TKW18480 | EER93718 | Zm00001eb218130_P001 | 0.948 |
| PUZ49970 | Sspon.06G | KQL00970 | TKW09199 | EES14475 | Zm00001eb261540_P001 | 0.958 |

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| PUZ54899 | Sspon.03G | KQL06864 | TKW16628 | EES01430 | Zm00001eb154000_P001 | 0.915 |
| PUZ38373 | genblast_C | KQK88432 | TKV92995 | OQU91536 | Zm00001eb044040_P006 | 0.949 |
| PUZ58069 | Sspon.03G | KQL04422 | TKW13458 | EES02477 | Zm00001eb335990_P001 | 0.948 |
| PUZ73021 | Sspon.02G | KQL26764 | TKW35960 | KXG36751 | Zm00001eb327990_P001 | 0.969 |
| PUZ48467 | genblast_C | KQK98475 | TKW05979 | KXG26908 | Zm00001eb073880_P003 | 0.968 |
| PUZ67164 | genblast_C | KQL16890 | TKW29158 | EES16200 | Zm00001eb136360_P005 | 0.943 |
| PUZ61925 | genblast_C | KQL09499 | TKW19893 | OQU75963 | Zm00001eb268080_P004 | 0.909 |
| PUZ56264 | Sspon.03G | KQL05505 | TKW14914 | genblast_C | Zm00001eb162480_P002 | 0.854 |
| PUZ47648 | Sspon.05G | KQK97737 | TKW05035 | EES10999 | Zm00001eb079510_P002 | 0.932 |
| PUZ60940 | Sspon.08G | KQL10694 | TKW21529 | KXG20038 | Zm00001eb382660_P001 | 0.956 |
| PUZ58996 | Sspon.08G | KQL12321 | TKW23568 | EER89004 | Zm00001eb278770_P001 | 0.963 |
| PUZ55674 | Sspon.03G | genblast_C | TKW15557 | KXG32947 | Zm00001eb159030_P001 | 0.926 |
| PUZ51257 | Sspon.06G | KQL01618 | TKW10060 | EES13250 | Zm00001eb260770_P001 | 0.933 |
| PUZ77965 | genblast_C | KQL31834 | TKW41955 | KXG31236 | Zm00001eb257270_P001 | 0.966 |
| PUZ58036 | Sspon.03G | KQL04394 | TKW13430 | EES02483 | Zm00001eb124390_P004 | 0.965 |
| PUZ78361 | Sspon.04G | KQL32219 | TKW42397 | KXG31404 | Zm00001eb190790_P001 | 0.945 |
| PUZ73896 | Sspon.04G | KQL28898 | TKW38226 | EES04444 | Zm00001eb208880_P002 | 0.974 |
| PUZ67172 | Sspon.02G | KQL16882 | TKW29147 | EES15998 | Zm00001eb409750_P002 | 0.876 |
| PUZ72218 | Sspon.01G | KQL25967 | TKW34952 | EER99440 | Zm00001eb322560_P001 | 0.974 |

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| PUZ70838 | genblast_C | KQL24645 | TKW33326 | EER98969 | Zm00001eb314010_P001 | 0.749 |
| PUZ38617 | genblast_Z | KQK88702 | TKV93335 | EER94071 | Zm00001eb045730_P001 | 0.979 |
| PUZ48697 | genblast_Z | KQK98712 | TKW06276 | EES11357 | Zm00001eb430030_P001 | 0.959 |

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| PUZ43301 | Sspon.01G | KQK93072 | TKV98744 | KXG40416 | Zm00001eb000380_P001 | 0.932 |

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| PUZ56234 | Sspon.03GKQL05535 | TKW14940 | OQU87011 | Zm00001eb162310_P001 | 0.947 |
| PUZ61883 | Sspon.08GKQL09453 | TKW19826 | EER87979 | Zm00001eb374550_P001 | 0.946 |
| PUZ56901 | Sspon.03GKQL05030 | TKW14253 | EES00696 | Zm00001eb131130_P001 | 0.941 |
| PUZ57304 | Sspon.03GKQL03719 | TKW12588 | OQU86680 | Zm00001eb128680_P001 | 0.938 |
| PUZ47983 | Sspon.05GKQK98046 | TKW05396 | EES11110 | Zm00001eb426500_P001 | 0.931 |
| PUZ63894 | Sspon.07GKQL13231 | TKW24479 | OQU77343 | Zm00001eb354720_P003 | 0.870 |
| PUZ55353 | Sspon.03GKQL06418 | TKW16046 | OQU87332 | Zm00001eb360390_P004 | 0.912 |
| PUZ44057 | Sspon.05GKQK93965 | TKV99821 | EES09482 | Zm00001eb168920_P002 | 0.964 |
| PUZ38105 | Sspon.01GKQK88186 | TKV92693 | EER91274 | Zm00001eb049330_P002 | 0.890 |
| PUZ66643 | Sspon.04GKQL16169 | TKW28157 | KXG30910 | Zm00001eb253040_P002 | 0.980 |
| PUZ62946 | Sspon.07GKQK99872 | TKV99254 | EES15664 | Zm00001eb164020_P001 | 0.965 |

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| PUZ53569 | Sspon.03GKQL08074 | genblast_C | KXG33862 | Zm00001eb145140_P002 | 0.942 |
| PUZ75860 | Sspon.04GKQL29825 | TKW39424 | EES05153 | Zm00001eb242200_P001 | 0.921 |
| PUZ75791 | Sspon.04GKQL29741 | TKW39303 | EES06855 | Zm00001eb181000_P001 | 0.749 |
| PUZ37519 | Sspon.01GKQK87629 | TKV91937 | EER91054 | Zm00001eb217080_P001 | 0.975 |
| PUZ63798 | Sspon.07GKQL13143 | TKW24354 | KXG21174 | Zm00001eb265430_P001 | 0.947 |
| PUZ52444 | Sspon.06GKQL02768 | genblast_C | OQU80781 | Zm00001eb037410_P001 | 0.862 |
| PUZ72316 | genblast_C | genblast_C | TKW35097 | EER97325 | Zm00001eb106290_P001 | 0.932 |
| PUZ43778 | Sspon.05GKQK93626 | TKV99337 | EES08005 | Zm00001eb197370_P001 | 0.802 |
| PUZ41612 | genblast_C | genblast_C | TKV96763 | EER95061 | Zm00001eb397290_P001 | 0.963 |

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| PUZ48555 | Sspon.05GKQK98549 | TKW06091 | EES11298 | Zm00001eb073400_P001 | 0.927 |

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| PUZ41277 | Sspon.01GKQK91059 | TKV96333 | EER92327 | genblast_Os03t0327600-01 | Zm0 |

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| PUZ62412 | Sspon.08G | KQL09087 | TKW19392 | EER87757 | Zm00001eb378590_P001 | 0.947 |

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| PUZ66207 | Sspon.07G | KQL15696 | TKW27594 | KXG21898 | Zm00001eb286920_P001 | 0.930 |
| PUZ58508 | Sspon.03G | KQL04835 | TKW13990 | KXG31612 | Zm00001eb120860_P001 | 0.975 |

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| PUZ43149 | Sspon.01G | KQK92901 | TKV98558 | EER95621 | Zm00001eb403880_P001 | 0.890 |
| PUZ65454 | Sspon.08G | KQL14937 | TKW26614 | EER90367 | Zm00001eb227770_P001 | 0.926 |

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| PUZ42982 | Sspon.01G | KQK92711 | TKV98353 | genblast_C | Zm00001eb002690_P001 | 0.903 |
| PUZ64124 | Sspon.07G | KQK99272 | TKW07017 | EES17751 | Zm00001eb345660_P001 | 0.910 |
| PUZ76892 | Sspon.04G | KQL30798 | TKW40716 | KXG31087 | Zm00001eb186550_P001 | 0.912 |
| PUZ50824 | Sspon.05G | KQL16093 | TKW28083 | EES09169 | Zm00001eb093630_P001 | 0.936 |
| PUZ41427 | Sspon.01G | KQK91221 | TKV96558 | EER92383 | Zm00001eb014470_P002 | 0.987 |
| PUZ70790 | Sspon.02G | KQL24578 | TKW33261 | KXG35672 | Zm00001eb099820_P001 | 0.943 |
| PUZ74413 | genblast_C | KQL28395 | TKW37589 | EES04658 | Zm00001eb234510_P002 | 0.969 |
| PUZ72523 | Sspon.02G | KQL26279 | TKW35372 | EER99560 | Zm00001eb324550_P003 | 0.906 |
| PUZ65683 | Sspon.07G | genblast_C | TKW26937 | EES19643 | Zm00001eb351230_P002 | 0.956 |
| PUZ42175 | Sspon.01G | KQK91955 | TKV97438 | KXG39869 | Zm00001eb400130_P001 | 0.942 |
| PUZ48713 | Sspon.05G | KQK98728 | TKW06298 | EES12779 | Zm00001eb430170_P001 | 0.928 |
| PUZ36021 | genblast_C | KQK86121 | TKV90108 | EER90494 | Zm00001eb210590_P001 | 0.943 |
| PUZ70464 | Sspon.02G | KQL24253 | TKW32839 | EER96635 | Zm00001eb310960_P001 | 0.946 |
| PUZ42878 | Sspon.01G | KQK92615 | TKV98255 | KXG40196 | Zm00001eb003580_P002 | 0.946 |
| PUZ52666 | Sspon.01G | KQL02921 | TKW11703 | KXG38995 | Zm00001eb364590_P003 | 0.972 |
| PUZ62429 | Sspon.08G | KQL09063 | TKW19356 | KXG19166 | Zm00001eb378700_P001 | 0.861 |

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|---|---|---|---|---|---|---|
| PUZ73834 | genblast_C | KQL28926 | TKW38260 | EES06209 | Zm00001eb230740_P001 | 0.963 |
| PUZ58002 | Sspon.03G | KQL04366 | TKW13394 | EES02496 | Zm00001eb124480_P003 | 0.926 |

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| PUZ72986 | Sspon.08G | KQL10256 | TKW20897 | KXG19763 | Zm00001eb280460_P001 | 0.947 |

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|---|---|---|---|---|---|---|
| PUZ36816 | Sspon.01G | KQK86892 | TKV91088 | EER90813 | Zm00001eb059030_P001 | 0.952 |
| PUZ38569 | Sspon.06G | KQK88653 | TKV93279 | KXG25632 | Zm00001eb360500_P002 | 0.912 |
| PUZ43736 | Sspon.05G | KQK93699 | TKV99411 | genblast_C | Zm00001eb202270_P001 | 0.922 |
| PUZ54605 | Sspon.03G | KQL07139 | TKW16986 | EES01521 | Zm00001eb370180_P002 | 0.983 |
| PUZ47814 | Sspon.05G | KQK97895 | TKW05203 | EES11058 | Zm00001eb078640_P001 | 0.964 |
| PUZ69874 | genblast_Z | KQL23801 | TKW32214 | EER96429 | Zm00001eb307020_P002 | 0.881 |
| PUZ58843 | Sspon.03G | KQL03228 | TKW11955 | KXG31479 | Zm00001eb119130_P004 | 0.879 |

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| PUZ74568 | Sspon.08G | KQL28235 | TKW37403 | EES06473 | Zm00001eb235810_P001 | 0.962 |
| PUZ62023 | genblast_C | KQL09581 | TKW20009 | KXG19400 | Zm00001eb375240_P001 | 0.970 |
| PUZ42038 | Sspon.01G | KQK91805 | TKV97255 | EER92594 | Zm00001eb009880_P001 | 0.934 |
| PUZ41991 | Sspon.01G | KQK91757 | TKV97196 | KXG39803 | Zm00001eb010150_P003 | 0.920 |
| PUZ50411 | Sspon.06G | KQL00533 | TKW08611 | OQU80028 | Zm00001eb413270_P002 | 0.948 |
| PUZ70982 | Sspon.02G | KQL24781 | TKW33484 | KXG35761 | Zm00001eb314830_P001 | 0.903 |

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| PUZ54496 | genblast_Z | KQL07233 | TKW17099 | EES03711 | Zm00001eb151550_P001 | 0.962 |
| PUZ57684 | Sspon.03G | KQL04072 | TKW13007 | EES02630 | Zm00001eb126560_P001 | 0.960 |
| PUZ76565 | Sspon.04G | KQL30498 | TKW40342 | EES05426 | Zm00001eb247140_P001 | 0.894 |
| PUZ65367 | Sspon.07G | KQL14874 | TKW26524 | EES19752 | Zm00001eb291760_P001 | 0.934 |
| PUZ60099 | genblast_C | KQL11560 | TKW22587 | EES00793 | Zm00001eb131880_P001 | 0.799 |

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| PUZ46373 | Sspon.05G | KQK96562 | TKW03461 | genblast_C | Zm00001eb419710_P001 | 0.961 |

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| PUZ39912 | Sspon.01G | KQK89745 | TKV94706 | OQU92059 | Zm00001eb025020_P002 | 0.933 |
| PUZ41712 | Sspon.01G | KQK91588 | TKV96958 | EER95113 | Zm00001eb012130_P004 | 0.943 |
| PUZ38054 | Sspon.01G | KQK88149 | TKV92604 | EER93844 | Zm00001eb049930_P001 | 0.853 |
| PUZ49988 | Sspon.06G | KQL00953 | TKW09164 | EES14488 | Zm00001eb261720_P001 | 0.983 |
| PUZ72552 | genblast_C | KQL26304 | TKW35403 | EER97404 | Zm00001eb324730_P001 | 0.948 |

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| PUZ52939 | Sspon.03G | KQL08669 | TKW18923 | EES04242 | Zm00001eb362690_P001 | 0.892 |

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| PUZ63716 | Sspon.07GKQL13335 | TKW24630 | OQU77254 | Zm00001eb266320_P001 | 0.963 |
| PUZ54402 | Sspon.03GKQL07305 | TKW17203 | EES03747 | Zm00001eb151030_P001 | 0.870 |
| PUZ37805 | Sspon.01GKQK87946 | TKV92314 | EER93754 | Zm00001eb050490_P001 | 0.951 |
| PUZ42572 | Sspon.01GKQK92317 | TKV97900 | EER92756 | genblast_Os03t0178300-01_Ze | |
| PUZ49806 | Sspon.06Ggenblast_C | TKW08115 | KXG24203 | Zm00001eb260350_P003 | 0.951 |
| PUZ70364 | Sspon.02GKQL24170 | TKW32709 | EER96586 | Zm00001eb310130_P001 | 0.955 |
| PUZ52798 | Sspon.03GKQL08800 | TKW19091 | OQU88268 | Zm00001eb139780_P002 | 0.824 |
| PUZ59318 | Sspon.08GKQL11828 | TKW22930 | genblast_C | Zm00001eb226310_P001 | 0.964 |
| PUZ65738 | Sspon.07GKQL15251 | TKW26998 | OQU78113 | Zm00001eb288790_P002 | 0.917 |
| PUZ72044 | Sspon.02GKQL25786 | TKW34741 | EER99384 | Zm00001eb321410_P001 | 0.972 |
| PUZ40126 | Sspon.01GKQK89936 | TKV94951 | EER94492 | Zm00001eb391240_P002 | 0.909 |
| PUZ59128 | Sspon.08GKQL12200 | TKW23403 | EER90373 | Zm00001eb227830_P001 | 0.871 |

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| PUZ40252 | Sspon.01GKQK90040 | TKV95084 | EER94537 | Zm00001eb391800_P001 | 0.969 |
| PUZ57622 | Sspon.03GKQL04043 | TKW12969 | EES02643 | Zm00001eb334260_P002 | 0.961 |

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| PUZ66101 | Sspon.01GKQL15604 | TKW27449 | EES19489 | Zm00001eb287520_P002 | 0.952 |
| PUZ61842 | Sspon.02GKQL09404 | TKW19748 | EER96624 | Zm00001eb310710_P002 | 0.939 |
| PUZ69296 | genblast_CKQL23261 | TKW31545 | EER96240 | Zm00001eb305200_P001 | 1.001 |
| PUZ46834 | Sspon.05GKQK96957 | TKW03988 | KXG26102 | Zm00001eb421100_P001 | 0.879 |
| PUZ64835 | genblast_CKQK92567 | TKW25934 | KXG22518 | Zm00001eb343350_P001 | 0.889 |
| PUZ68229 | Sspon.01GKQL22161 | TKW30045 | EER93404 | Zm00001eb058270_P001 | 0.874 |
| PUZ55187 | Sspon.03GKQL06587 | TKW16256 | EES03488 | Zm00001eb155650_P001 | 0.972 |
| PUZ55111 | Sspon.03GKQL06669 | TKW16354 | KXG33230 | Zm00001eb361320_P001 | 0.950 |
| PUZ73786 | Sspon.04GKQL28983 | TKW38327 | KXG29327 | Zm00001eb230410_P001 | 0.897 |
| PUZ35947 | genblast_CKQK86063 | TKV90038 | EER93051 | Zm00001eb065320_P001 | 0.967 |

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| PUZ48706 | genblast_CKQK98722 | TKW06289 | KXG27029 | Zm00001eb430130_P001 | 0.845 |
| PUZ41174 | Sspon.01GKQK90967 | TKV96205 | EER94884 | Zm00001eb016320_P001 | 0.957 |
| PUZ76412 | Sspon.04GKQL30349 | TKW40130 | EES05379 | Zm00001eb246400_P001 | 0.943 |
| PUZ62814 | Sspon.05GKQK86923 | TKV91145 | EES09184 | Zm00001eb093540_P001 | 0.918 |

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| PUZ36298 | Sspon.01G | KQK86396 | TKV90439 | OQU90703 | Zm00001eb331750_P003 | 0.969 |
| PUZ49525 | Sspon.05G | KQL12776 | TKW23878 | EES11653 | Zm00001eb066110_P001 | 0.944 |
| PUZ59088 | Sspon.08G | KQL12239 | TKW23460 | KXG20892 | Zm00001eb228090_P003 | 0.949 |
| PUZ57858 | Sspon.03G | KQL04235 | TKW13227 | KXG31977 | Zm00001eb125430_P001 | 0.880 |
| PUZ42814 | Sspon.01G | KQK92544 | TKV98176 | EER92841 | Zm00001eb004140_P001 | 0.981 |
| PUZ76850 | Sspon.04G | KQL30757 | TKW40672 | EES07528 | Zm00001eb249230_P001 | 0.972 |
| PUZ59354 | Sspon.08G | KQL11865 | TKW22989 | EER90284 | Zm00001eb226020_P001 | 0.949 |
| PUZ78408 | genblast_C | KQL32262 | TKW42442 | EES07822 | Zm00001eb259540_P002 | 0.950 |
| PUZ76668 | Sspon.04G | KQL30594 | TKW40453 | KXG30680 | Zm00001eb185330_P001 | 0.962 |

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| PUZ42550 | Sspon.01G | KQK92297 | TKV97867 | EER95398 | Zm00001eb005990_P001 | 0.817 |
| genblast_C | Sspon.02G | KQL24751 | TKW33448 | EER96835 | Zm00001eb100590_P001 | 0.946 |

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| PUZ49212 | Sspon.05G | KQK99214 | TKW06948 | OQU82449 | Zm00001eb432140_P001 | 0.872 |
| PUZ43221 | genblast_C | KQK92998 | TKV98652 | EER95656 | Zm00001eb404090_P002 | 0.944 |
| PUZ72758 | Sspon.02G | KQL26499 | TKW35612 | EER97475 | genblast_Os07t0592000-01_Zea | |
| PUZ59506 | Sspon.08G | KQL12006 | TKW23168 | EER90215 | Zm00001eb224740_P001 | 0.966 |
| PUZ73469 | Sspon.02G | KQL27201 | TKW36545 | EER97744 | Zm00001eb111630_P002 | 0.969 |
| PUZ73951 | genblast_C | KQL28851 | TKW38148 | OQU84311 | Zm00001eb231370_P001 | 0.954 |
| PUZ74088 | Sspon.04G | KQL28707 | TKW37963 | OQU84388 | Zm00001eb232490_P002 | 0.963 |
| PUZ75834 | Sspon.04G | KQL29798 | TKW39377 | KXG30287 | Zm00001eb241910_P001 | 0.950 |
| genblast_C | Sspon.08G | KQL11553 | TKW22581 | EER88591 | Zm00001eb277050_P001 | 0.883 |
| PUZ41709 | genblast_C | KQK91590 | TKV96960 | KXG39704 | Zm00001eb012150_P001 | 0.949 |
| PUZ40783 | genblast_C | KQK90534 | TKV95714 | KXG39199 | Zm00001eb019330_P003 | 0.927 |
| PUZ36027 | Sspon.01G | KQK86126 | TKV90115 | EER90496 | Zm00001eb064780_P001 | 0.899 |
| PUZ63005 | Sspon.04G | KQL32238 | TKW07505 | EES07806 | Zm00001eb259380_P002 | 0.923 |
| PUZ58488 | Sspon.03G | KQL04812 | TKW13961 | OQU8615( | Zm00001eb121060_P004 | 0.956 |
| PUZ42824 | Sspon.01G | KQK92556 | TKV98189 | EER95495 | Zm00001eb003970_P001 | 0.923 |
| PUZ42816 | Sspon.01G | KQK92546 | TKV98181 | KXG40161 | Zm00001eb403060_P001 | 0.926 |
| PUZ67349 | genblast_Z | KQL16694 | TKW28877 | EES17142 | Zm00001eb410330_P001 | 0.899 |
| PUZ61277 | Sspon.08G | KQL09824 | TKW20333 | OQU76045 | Zm00001eb373220_P001 | 0.942 |
| PUZ37304 | Sspon.01G | KQK87396 | TKV91682 | EER90980 | Zm00001eb055410_P001 | 0.958 |
| PUZ77246 | Sspon.04G | KQL31116 | TKW41119 | EES05664 | Zm00001eb251910_P006 | 0.954 |
| PUZ53890 | Sspon.07G | KQL07792 | TKW17793 | EES01775 | Zm00001eb147530_P001 | 0.943 |

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| PUZ42991 | Sspon.01G | KQK92734 | TKV98371 | OQU93303 | genblast_Os03t0131900-01_Zea | |
| PUZ58304 | genblast_C | KQL04650 | TKW13745 | EES00205 | Zm00001eb122560_P002 | 0.932 |
| PUZ37888 | genblast_C | KQK88015 | TKV92397 | EER91205 | Zm00001eb218850_P001 | 0.959 |
| PUZ71616 | genblast_C | KQL25397 | TKW34225 | OQU89797 | Zm00001eb319020_P001 | 0.875 |
| PUZ64570 | Sspon.07G | KQL14096 | TKW25632 | KXG22631 | Zm00001eb344890_P003 | 0.944 |
| PUZ55746 | Sspon.03G | KQL05941 | TKW15470 | EES03303 | Zm00001eb159520_P004 | 0.949 |
| PUZ36018 | Sspon.01G | KQK86117 | TKV90104 | EER93075 | Zm00001eb210550_P001 | 0.927 |
| PUZ74304 | Sspon.04G | KQL28513 | TKW37741 | EES04613 | Zm00001eb233410_P001 | 0.838 |
| PUZ37523 | Sspon.01G | KQK87631 | TKV91942 | EER91056 | Zm00001eb053610_P003 | 0.889 |
| PUZ36519 | Sspon.01G | genblast_Z | TKV90731 | OQU90807 | Zm00001eb061370_P001 | 0.945 |
| PUZ49197 | Sspon.05G | KQK99205 | TKW06936 | OQU82439 | Zm00001eb068570_P002 | 0.940 |
| PUZ47912 | Sspon.05G | KQK97994 | TKW05320 | KXG26667 | Zm00001eb426150_P001 | 0.962 |
| PUZ38891 | Sspon.01G | KQK88918 | TKV93649 | KXG40213 | Zm00001eb003340_P001 | 0.968 |
| PUZ41661 | Sspon.01G | genblast_C | TKV96822 | KXG40160 | Zm00001eb397530_P001 | 0.965 |

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| PUZ70585 | Sspon.02G | KQL24335 | TKW32962 | OQU89437 | Zm00001eb311660_P003 | 0.979 |

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| PUZ70429 | Sspon.02G | KQL24226 | TKW32794 | EER96613 | Zm00001eb310550_P001 | 0.951 |
| PUZ58476 | Sspon.03G | KQL04805 | TKW13952 | KXG31637 | Zm00001eb121140_P001 | 0.954 |
| PUZ77719 | genblast_C | KQL31507 | TKW41577 | KXG30761 | Zm00001eb254860_P007 | 0.907 |
| PUZ58203 | Sspon.03G | KQL04553 | TKW13621 | EES00246 | Zm00001eb123270_P001 | 0.979 |
| PUZ64249 | Sspon.07G | KQL13793 | TKW25249 | EES19127 | Zm00001eb283070_P001 | 0.876 |

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| PUZ62422 | Sspon.08G | KQL09069 | TKW19364 | EER87751 | Zm00001eb378640_P001 | 0.864 |
| PUZ63237 | Sspon.07G | KQK99382 | TKW07141 | EES16633 | Zm00001eb164030_P001 | 0.867 |
| PUZ41551 | Sspon.01G | KQK91337 | TKV96703 | EER95042 | Zm00001eb397080_P001 | 0.974 |

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| PUZ41389 | Sspon.01G | KQK91189 | TKV96508 | EER92370 | Zm00001eb014760_P003 | 0.964 |
| PUZ73944 | Sspon.04G | KQL28857 | TKW38171 | OQU84306 | Zm00001eb209030_P001 | 0.977 |
| PUZ76543 | Sspon.04G | KQL30478 | TKW40287 | EES07148 | Zm00001eb247070_P001 | 0.907 |

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| PUZ42101 | Sspon.01G | KQK91870 | TKV97350 | EER95238 | Zm00001eb399630_P002 | 0.955 |
| PUZ57418 | Sspon.03G | KQL03853 | TKW12749 | OQU86624 | Zm00001eb333460_P001 | 0.935 |
| PUZ47853 | Sspon.05G | KQK97924 | TKW05240 | OQU81881 | Zm00001eb078390_P001 | 0.943 |
| PUZ37152 | Sspon.01G | KQK87242 | TKV91507 | EER90915 | Zm00001eb215440_P001 | 0.932 |
| PUZ55156 | Sspon.03G | KQL06617 | TKW16294 | KXG33213 | Zm00001eb361120_P001 | 0.992 |
| PUZ64971 | Sspon.07G | KQL14530 | TKW26115 | EES18597 | Zm00001eb294520_P002 | 0.952 |

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| PUZ77284 | genblast_C | KQL31154 | TKW41162 | EES05649 | Zm00001eb252220_P001 | 0.914 |

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| PUZ52435 | Sspon.02G | KQL02697 | TKW11439 | EES14175 | Zm00001eb036990_P003 | 0.851 |

PUZ37205 Sspon.01GKQK87300TKV91572 EER90936 Zm00001eb056050_P001 0.930
PUZ77316 Sspon.04GKQL31188 TKW41203KXG30894 Zm00001eb252430_P001 0.955
PUZ77508 Sspon.04GKQL31449 TKW41507EES05553 Zm00001eb254080_P001 0.960
PUZ49231 Sspon.05Ggenblast_CTKW07322OQU82463Zm00001eb068290_P002 0.945
PUZ61841 Sspon.08GKQL09401 genblast_Cgenblast_Cgenblast_Os06t0192400-01Zm0
PUZ77100 Sspon.04GKQL30974 TKW40945OQU85620Zm00001eb187440_P001 0.921
PUZ61880 Sspon.08GKQL09449 TKW19823KXG19489 Zm00001eb374510_P001 0.979
PUZ47435 Sspon.03GKQL13664 TKW25075OQU87213Zm00001eb359130_P001 0.963
PUZ41438 Sspon.01GKQK91232TKV96574 EER94992 Zm00001eb396430_P001 0.870
PUZ41335 Sspon.01GKQK91112TKV96418 EER92349 Zm00001eb015230_P001 0.975

genblast_CSspon.03GKQL06577 TKW16244EES03486 Zm00001eb155690_P001 0.849
PUZ42316 genblast_CKQK92084TKV97608 EER95317 Zm00001eb007750_P002 0.982
PUZ72267 Sspon.02GKQL26031 TKW35032EER99458 Zm00001eb322820_P001 0.960

PUZ43988 genblast_CKQK93890TKV99726 EES09417 Zm00001eb091230_P001 0.963
PUZ49046 Sspon.05GKQK99052TKW06744OQU82388Zm00001eb431490_P001 0.944
PUZ42170 Sspon.01GKQK91948TKV97433 EER95273 Zm00001eb008710_P001 0.925
PUZ61801 Sspon.08GKQL09346 TKW19698EER88010 Zm00001eb373950_P001 0.991
PUZ76678 genblast_CKQL30599 TKW40475OQU80963Zm00001eb034290_P004 0.879

PUZ41244 Sspon.01GKQK91032TKV96288 EER92317 Zm00001eb015820_P001 0.989
PUZ59686 Sspon.08GKQL28477 TKW22023EER88760 Zm00001eb389430_P001 0.974
PUZ61567 Sspon.08GKQL10130 TKW20727EER88156 Zm00001eb280090_P001 0.940
PUZ54871 Sspon.03GKQL06907 TKW16673EES01453 Zm00001eb153750_P001 0.956
PUZ55958 Sspon.03GKQL05732 TKW15197EES01018 Zm00001eb357660_P001 0.912
PUZ41170 Sspon.01GKQK90960TKV96199 EER92299 Zm00001eb016350_P001 0.931
PUZ60571 Sspon.08Ggenblast_CTKW21595OQU76450Zm00001eb382580_P002 0.940
PUZ59324 Sspon.08GKQL11832 TKW22936KXG20728 Zm00001eb226280_P002 0.964
PUZ57711 Sspon.03GKQL04097 TKW13038OQU86498genblast_Zm00001eb126330_P0
PUZ63314 Sspon.07GKQL13712 TKW25135EES16891 Zm00001eb133870_P001 0.945

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| PUZ55940 | Sspon.05GKQK94249 | TKV94617 | EES09632 | Zm00001eb169190_P001 | 0.946 |
| PUZ48865 | Sspon.06GKQL25656 | TKW06522 | EES11411 | Zm00001eb071020_P001 | 0.999 |
| PUZ50515 | Sspon.06GKQL00430 | TKW08403 | KXG24704 | Zm00001eb171180_P002 | 0.961 |
| PUZ62603 | Sspon.08GKQL08897 | TKW19159 | EER87686 | Zm00001eb268440_P002 | 0.894 |
| PUZ76731 | genblast_CKQL30649 | TKW40529 | KXG30699 | Zm00001eb185620_P001 | 0.980 |
| PUZ48265 | genblast_CKQL23921 | TKW05746 | EES12588 | Zm00001eb075120_P001 | 0.918 |
| PUZ77935 | Sspon.04GKQL31798 | TKW41909 | KXG31228 | Zm00001eb257110_P004 | 0.976 |
| PUZ48081 | Sspon.05GKQK98139 | TKW05507 | OQU81997 | Zm00001eb426760_P001 | 0.900 |

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| PUZ40178 | Sspon.01GKQK89968 | TKV94992 | EER91943 | Zm00001eb391360_P001 | 0.961 |

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| PUZ72884 | Sspon.02GKQL26637 | TKW35791 | EER97528 | Zm00001eb327340_P001 | 0.979 |
| PUZ71738 | genblast_CKQL25497 | TKW34356 | EER97106 | Zm00001eb331950_P004 | 0.950 |
| PUZ72253 | Sspon.02GKQL26022 | TKW35020 | EER99454 | Zm00001eb322790_P001 | 0.920 |

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|---|---|---|---|---|---|
| PUZ39454 | Sspon.02GKQK89112 | TKV93889 | EES17403 | Zm00001eb031810_P001 | 0.900 |
| PUZ54061 | Sspon.03GKQL07643 | TKW17621 | EES03852 | Zm00001eb368070_P001 | 0.798 |
| PUZ74367 | Sspon.04GKQL28451 | TKW37666 | EES06381 | Zm00001eb233940_P001 | 0.971 |

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| PUZ63309 | Sspon.07GKQL13714 | TKW25139 | EES15848 | Zm00001eb411250_P001 | 0.964 |
| PUZ37117 | genblast_ZKQK87195 | TKV91458 | KXG37601 | Zm00001eb056540_P001 | 0.957 |
| PUZ49855 | Sspon.06GKQL00269 | TKW08175 | KXG24248 | Zm00001eb260600_P002 | 0.985 |
| PUZ76807 | Sspon.04GKQL30719 | TKW40618 | EES05816 | Zm00001eb248880_P001 | 0.919 |
| PUZ78151 | Sspon.04GKQL32019 | TKW42160 | EES07720 | Zm00001eb191930_P002 | 0.927 |
| PUZ47874 | Sspon.05GKQK97946 | TKW05265 | EES11076 | Zm00001eb425930_P001 | 0.955 |
| PUZ48788 | Sspon.05GKQK98814 | TKW06407 | EES11389 | Zm00001eb071460_P001 | 0.975 |
| PUZ53660 | genblast_ZKQL08002 | TKW18074 | KXG33822 | Zm00001eb145720_P002 | 0.959 |

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| PUZ36338 | Sspon.01GKQK86437 | TKV90499 | EER93193 | Zm00001eb211750_P001 | 0.792 |
| PUZ47032 | Sspon.05GKQK97164 | TKW04256 | EES10731 | Zm00001eb084070_P001 | 0.911 |
| PUZ77414 | Sspon.04GKQL31279 | TKW41327 | EES05610 | Zm00001eb253140_P001 | 0.963 |
| PUZ47960 | Sspon.05Ggenblast_C | TKW05375 | EES12482 | genblast_Os04t0510600-01_Ze | |
| PUZ47106 | Sspon.05Ggenblast_C | TKW04338 | KXG26281 | Zm00001eb181570_P001 | 0.797 |

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| PUZ42741 | Sspon.01G | KQK92483 | TKV98085 | EER95467 | Zm00001eb004500_P001 | 0.942 |

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| PUZ41927 | Sspon.01G | KQK91687 | TKV97096 | EER95176 | Zm00001eb398620_P002 | 0.954 |

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| PUZ36568 | Sspon.01G | genblast_C | TKV90810 | KXG37357 | Zm00001eb060990_P003 | 0.925 |
| PUZ54152 | Sspon.03G | KQL07549 | TKW17522 | EES03825 | Zm00001eb368510_P001 | 0.953 |
| PUZ56600 | Sspon.08G | KQL05266 | TKW14572 | OQU7612 | Zm00001eb371930_P001 | 0.872 |
| PUZ65345 | Sspon.03G | genblast_Z | genblast_Z | EES19759 | Zm00001eb291820_P001 | 0.918 |
| PUZ77458 | Sspon.04G | KQL31495 | TKW4156 | EES07261 | Zm00001eb254560_P003 | 0.969 |

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| PUZ61171 | Sspon.08G | KQL10480 | TKW2122 | KXG19910 | Zm00001eb381840_P001 | 0.913 |
| PUZ77035 | Sspon.04G | KQL30922 | TKW40877 | KXG31014 | Zm00001eb187170_P001 | 0.940 |

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| PUZ36209 | Sspon.01G | KQK86339 | TKV90374 | EER93149 | Zm00001eb063610_P002 | 0.916 |
| PUZ66607 | genblast_C | KQL15990 | TKW27952 | EES05886 | Zm00001eb286710_P001 | 0.938 |
| PUZ48627 | Sspon.05G | KQK98640 | TKW0619 | EES12735 | Zm00001eb428160_P001 | 0.979 |
| PUZ70688 | Sspon.02G | KQL24470 | TKW33104 | EER98894 | Zm00001eb312480_P002 | 0.979 |
| PUZ38347 | Sspon.01G | KQK88415 | TKV92967 | EER91393 | genblast_Os10t0508700-01_Ze | |
| PUZ46144 | Sspon.05G | KQK96280 | TKW0306 | EES11780 | Zm00001eb419470_P001 | 0.935 |

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| PUZ72951 | Sspon.02G | KQL26707 | TKW35881 | EER97558 | Zm00001eb327750_P002 | 0.912 |
| PUZ64026 | genblast_C | KQL13073 | TKW24260 | EES11768 | Zm00001eb089080_P002 | 0.941 |
| PUZ53402 | Sspon.03G | KQL08221 | TKW18351 | EES01924 | Zm00001eb365220_P001 | 0.865 |

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| PUZ57353 | Sspon.03G | KQL03801 | TKW12691 | EES02731 | Zm00001eb128310_P001 | 0.861 |

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| PUZ42577 | Sspon.01G | KQK92322 | TKV97906 | EER95404 | Zm00001eb401910_P002 | 0.953 |
| PUZ57687 | Sspon.03G | genblast_C | TKW13014 | KXG32106 | Zm00001eb334280_P001 | 0.919 |

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| PUZ40084 | Sspon.01G | KQK89897 | TKV94896 | EER94480 | Zm00001eb023690_P001 | 0.965 |
| PUZ71619 | genblast_C | KQL25398 | TKW34226 | EER99219 | Zm00001eb319030_P003 | 0.915 |
| PUZ60186 | Sspon.08G | KQL11642 | TKW22703 | EER89976 | Zm00001eb385260_P001 | 0.951 |
| PUZ51274 | Sspon.06G | genblast_C | TKW10022 | OQU80358 | Zm00001eb042620_P001 | 0.964 |
| PUZ68357 | Sspon.02G | genblast_C | TKW30370 | EER95842 | Zm00001eb299520_P001 | 0.926 |
| PUZ75300 | Sspon.05G | KQL29335 | TKW38752 | EES13118 | Zm00001eb065850_P001 | 0.888 |
| PUZ67874 | Sspon.02G | KQL17182 | TKW29547 | EES17365 | Zm00001eb031580_P001 | 0.838 |
| PUZ38552 | Sspon.01G | KQK88643 | TKV93260 | KXG38297 | Zm00001eb221310_P001 | 0.944 |
| PUZ56943 | Sspon.06G | KQL03466 | TKW12239 | genblast_C | Zm00001eb040130_P002 | 0.910 |
| PUZ42574 | Sspon.01G | KQK92320 | TKV97903 | EER95402 | Zm00001eb005830_P001 | 0.924 |

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| PUZ67499 | Sspon.02G | KQL16549 | TKW28685 | KXG23736 | Zm00001eb028820_P001 | 0.978 |
| PUZ72694 | Sspon.02G | KQL26447 | TKW35557 | EER97453 | Zm00001eb325810_P001 | 0.989 |
| PUZ39975 | genblast_C | KQK89788 | TKV94769 | OQU92086 | Zm00001eb024430_P001 | 0.908 |
| PUZ54323 | Sspon.03G | KQL07381 | TKW17300 | EES01622 | Zm00001eb150460_P001 | 0.937 |
| PUZ37602 | Sspon.01G | KQK87731 | TKV92064 | EER93673 | Zm00001eb051980_P001 | 0.982 |
| PUZ39352 | genblast_C | genblast_C | TKV94326 | OQU91931 | Zm00001eb027100_P003 | 0.946 |
| PUZ70501 | Sspon.02G | KQL24276 | TKW32880 | EER96662 | Zm00001eb098670_P001 | 0.856 |
| PUZ71720 | Sspon.02G | KQL25477 | TKW34326 | EER99260 | genblast_Os09t0536000-01_Zea | |

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| PUZ47631 | Sspon.05G | KQK97715 | TKW04970 | EES10994 | Zm00001eb424850_P001 | 0.947 |

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| PUZ41278 | Sspon.01G | KQK91060 | TKV96334 | EER92328 | Zm00001eb015570_P001 | 0.898 |
| PUZ71051 | Sspon.06G | KQL24849 | TKW33556 | EER96881 | Zm00001eb315330_P001 | 0.977 |
| PUZ43375 | Sspon.05G | KQK93448 | TKV99119 | EES15502 | Zm00001eb094300_P001 | 0.977 |
| PUZ38449 | genblast_C | KQK88517 | TKV93115 | KXG38248 | Zm00001eb044640_P004 | 0.930 |
| PUZ77045 | Sspon.04G | KQL30934 | TKW40890 | KXG31012 | Zm00001eb250630_P001 | 0.973 |
| PUZ37186 | Sspon.01G | KQK87282 | TKV91547 | EER93515 | Zm00001eb056210_P001 | 0.830 |

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| PUZ71499 | genblast_C | KQL25277 | TKW34078 | EER97031 | Zm00001eb318160_P001 | 0.942 |
| PUZ41900 | Sspon.01G | KQK91665 | TKV97066 | OQU92904 | Zm00001eb010820_P001 | 0.949 |
| PUZ37730 | Sspon.01G | KQK87880 | TKV92231 | EER91145 | Zm00001eb052850_P002 | 0.936 |
| PUZ75914 | Sspon.04G | KQL29873 | TKW39482 | EES06904 | genblast_Os02t0529900-01_Zea | |
| PUZ76434 | Sspon.04G | KQL30378 | TKW40159 | KXG30583 | Zm00001eb246550_P001 | 0.989 |
| PUZ49583 | Sspon.05G | KQL12716 | TKW23812 | EES11675 | Zm00001eb065760_P001 | 0.969 |
| PUZ54942 | Sspon.03G | KQL06820 | TKW16567 | EES01405 | Zm00001eb361880_P001 | 0.927 |

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| PUZ77476 | Sspon.04G | KQL31476 | TKW41550 | EES07274 | Zm00001eb254410_P001 | 0.876 |
| PUZ43313 | Sspon.01G | KQK93096 | TKV98768 | OQU93494 | Zm00001eb000330_P001 | 0.916 |

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| PUZ67998 | Sspon.05G | KQL11349 | TKW22294 | KXG27689 | Zm00001eb093290_P001 | 0.959 |

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| PUZ77407 | genblast_C | KQL31271 | TKW41315 | KXG30865 | Zm00001eb253080_P004 | 0.962 |
| PUZ41688 | genblast_C | KQK91471 | TKV96849 | KXG39683 | Zm00001eb012380_P004 | 0.997 |
| PUZ57831 | genblast_C | KQL04207 | TKW13198 | EES02568 | Zm00001eb334990_P002 | 0.946 |
| PUZ74701 | Sspon.04G | KQL28080 | TKW37204 | KXG29810 | Zm00001eb205240_P002 | 0.984 |
| PUZ41926 | Sspon.01G | KQK91686 | TKV97094 | EER92555 | Zm00001eb010620_P001 | 0.977 |
| PUZ37363 | Sspon.01G | KQK87449 | TKV91739 | KXG37731 | Zm00001eb216320_P001 | 0.938 |
| PUZ68375 | Sspon.02G | KQL22399 | TKW30390 | KXG34372 | Zm00001eb299750_P001 | 0.808 |
| PUZ48615 | genblast_C | KQK98627 | TKW06177 | EES11323 | Zm00001eb072790_P001 | 0.965 |
| PUZ45002 | genblast_C | KQK94721 | TKW00887 | EES09797 | Zm00001eb112990_P001 | 0.943 |
| PUZ42590 | Sspon.01G | KQK92337 | TKV97920 | KXG40067 | Zm00001eb402020_P001 | 0.995 |
| PUZ53291 | genblast_Z | KQL08326 | TKW18500 | KXG33990 | Zm00001eb364640_P001 | 0.954 |
| PUZ73475 | Sspon.02G | KQL27204 | TKW36552 | OQU90486 | Zm00001eb330830_P001 | 0.828 |
| PUZ40792 | Sspon.01G | genblast_C | TKV95734 | EER92167 | Zm00001eb019250_P001 | 0.939 |
| PUZ67346 | Sspon.02G | KQL16700 | TKW28884 | KXG23614 | Zm00001eb410210_P001 | 0.946 |
| PUZ73837 | Sspon.04G | KQL28930 | TKW38263 | EES04420 | Zm00001eb230760_P001 | 0.924 |

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| PUZ65185 | Sspon.03G | KQL14732 | TKW26350 | EES18506 | Zm00001eb292900_P002 | 0.934 |
| PUZ64531 | genblast_C | genblast_C | TKW25567 | KXG37265 | Zm00001eb062420_P003 | 0.962 |
| PUZ55413 | Sspon.03G | KQL06352 | TKW15986 | KXG33085 | Zm00001eb157160_P003 | 0.980 |
| PUZ71929 | Sspon.02G | KQL25678 | TKW34606 | KXG36174 | Zm00001eb320470_P001 | 0.960 |

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| PUZ54507 | Sspon.03G | KQL07226 | TKW17089 | OQU87654 | Zm00001eb151620_P001 | 0.912 |

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| PUZ77586 | Sspon.04G | KQL31362 | TKW41414 | EES05585 | Zm00001eb189980_P002 | 0.968 |

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| PUZ65368 | Sspon.03G | KQL14876 | TKW26527 | KXG22271 | Zm00001eb352600_P002 | 0.943 |
| PUZ71916 | genblast_C | genblast_C | TKW34593 | KXG36169 | Zm00001eb104560_P001 | 0.953 |
| PUZ62606 | Sspon.08G | KQL08893 | TKW19156 | EER87685 | Zm00001eb268400_P001 | 0.922 |
| PUZ43192 | Sspon.01G | KQK92968 | TKV98620 | EER95646 | Zm00001eb001040_P001 | 0.943 |
| PUZ52277 | genblast_C | KQL02530 | TKW11247 | EES15346 | Zm00001eb035760_P002 | 0.945 |
| PUZ62504 | Sspon.05G | KQL08989 | TKW19254 | EES11310 | Zm00001eb379020_P001 | 0.883 |
| PUZ69558 | Sspon.02G | KQL23551 | TKW31866 | EER98482 | Zm00001eb096480_P003 | 0.946 |
| PUZ56567 | Sspon.03G | KQL05263 | TKW14562 | KXG32269 | Zm00001eb332680_P001 | 0.952 |
| PUZ38456 | Sspon.08G | KQK88526 | TKV93122 | KXG38251 | Zm00001eb220970_P002 | 0.955 |
| PUZ75841 | Sspon.04G | KQL29809 | TKW39391 | EES06877 | Zm00001eb242020_P001 | 0.950 |

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| PUZ64713 | Sspon.07G | KQL14233 | TKW25787 | EES19971 | Zm00001eb344140_P001 | 0.934 |
| PUZ61369 | Sspon.08G | KQL09924 | TKW20459 | OQU76072 | Zm00001eb279350_P001 | 0.971 |
| PUZ37481 | genblast_C | KQK87587 | TKV91897 | EER91037 | Zm00001eb216890_P003 | 0.967 |
| PUZ74488 | Sspon.04G | KQL28304 | TKW37486 | KXG29699 | Zm00001eb206050_P001 | 0.966 |
| PUZ61615 | Sspon.03G | KQL10177 | TKW20792 | EER89546 | Zm00001eb121990_P001 | 0.921 |
| PUZ54121 | Sspon.03G | KQL07580 | TKW17551 | EES01706 | Zm00001eb368340_P002 | 0.962 |

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| genblast_C | genblast_C | KQL26003 | TKW35000 | EER99449 | Zm00001eb322660_P001 | 0.875 |
| PUZ73195 | Sspon.02G | KQL26933 | TKW36178 | EER97640 | Zm00001eb110390_P001 | 0.946 |
| PUZ42430 | Sspon.01G | KQK92176 | TKV97712 | EER92708 | Zm00001eb401230_P001 | 0.808 |
| PUZ38432 | genblast_C | KQK88497 | TKV93094 | KXG38242 | Zm00001eb044500_P001 | 0.974 |
| PUZ76749 | Sspon.04G | KQL30664 | TKW40550 | EES05487 | Zm00001eb248470_P001 | 0.910 |
| PUZ47555 | Sspon.05G | KQK97637 | TKW04874 | EER99940 | Zm00001eb433700_P001 | 0.824 |
| PUZ69462 | Sspon.02G | KQL23431 | TKW31748 | EER98436 | Zm00001eb306280_P002 | 0.970 |
| PUZ42276 | genblast_C | KQK92041 | TKV97550 | EER92668 | Zm00001eb007250_P001 | 0.972 |
| PUZ60188 | Sspon.08G | KQL11644 | TKW22709 | EER89974 | Zm00001eb385250_P001 | 0.938 |

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| PUZ58242 | Sspon.03G | KQL04577 | TKW13662 | EES00235 | Zm00001eb123060_P001 | 0.928 |
| PUZ71582 | Sspon.02G | KQL25363 | TKW34183 | EER99203 | Zm00001eb318480_P001 | 0.968 |
| PUZ72863 | Sspon.02G | KQL26602 | TKW35739 | EER99687 | Zm00001eb108720_P001 | 0.911 |
| PUZ66012 | Sspon.07G | KQL15500 | genblast_C | EES18226 | Zm00001eb287910_P001 | 0.972 |
| PUZ69730 | Sspon.02G | KQL23686 | TKW32062 | EER96403 | Zm00001eb307410_P001 | 0.897 |
| PUZ48671 | Sspon.05G | KQK98693 | TKW06247 | EES12754 | Zm00001eb072370_P002 | 0.883 |
| PUZ47225 | Sspon.05G | KQK97333 | TKW04480 | EES12202 | Zm00001eb082320_P003 | 0.919 |

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| PUZ66027 | Sspon.07G | genblast_C | TKW27344 | EES18220 | Zm00001eb349730_P002 | 0.945 |
| PUZ36069 | Sspon.01G | KQK86177 | TKV90184 | EER93098 | Zm00001eb064490_P001 | 0.820 |
| PUZ70804 | Sspon.02G | KQL24597 | TKW33284 | EER98950 | Zm00001eb313740_P001 | 0.964 |
| PUZ38528 | genblast_C | KQK88610 | TKV93225 | genblast_C | Zm00001eb221240_P001 | 0.945 |
| PUZ65971 | Sspon.07G | KQL15460 | TKW27256 | EES19534 | Zm00001eb349270_P002 | 0.946 |

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| PUZ65091 | Sspon.07G | KQL14650 | TKW26249 | EES14846 | Zm00001eb293450_P001 | 0.913 |
| PUZ37400 | Sspon.01G | KQK87484 | TKV91765 | EER93589 | Zm00001eb216480_P002 | 0.863 |
| PUZ65568 | Sspon.07G | KQL15076 | TKW26791 | KXG22192 | Zm00001eb290130_P001 | 0.881 |
| PUZ48659 | Sspon.05G | KQK98681 | TKW06238 | OQU82226 | Zm00001eb428370_P001 | 0.916 |
| genblast_C | Sspon.04G | KQL31448 | TKW41506 | KXG30794 | Zm00001eb194770_P001 | 0.919 |
| PUZ50289 | Sspon.06G | KQL00648 | TKW08755 | OQU79970 | Zm00001eb414960_P001 | 0.961 |
| PUZ63248 | Sspon.07G | KQK99374 | TKW07128 | EES15811 | Zm00001eb264300_P001 | 0.974 |
| PUZ69137 | Sspon.05G | KQK99008 | TKW06694 | OQU80511 | Zm00001eb303580_P001 | 0.970 |
| PUZ53070 | Sspon.03G | KQL08547 | TKW18764 | EES04190 | Zm00001eb141710_P001 | 0.903 |

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| PUZ74269 | Sspon.04G | KQL28549 | TKW37778 | EES06346 | Zm00001eb233110_P002 | 0.951 |
| PUZ37837 | Sspon.01G | KQK87976 | TKV92341 | EER93762 | Zm00001eb050700_P001 | 0.916 |
| PUZ75020 | Sspon.04G | KQL27835 | TKW36906 | EES06612 | Zm00001eb238000_P001 | 0.895 |
| PUZ55279 | Sspon.03G | KQL06492 | TKW16142 | EES03457 | Zm00001eb156330_P001 | 0.884 |
| PUZ44845 | Sspon.07G | KQK94632 | TKW00375 | OQU83293 | Zm00001eb174770_P001 | 0.790 |
| PUZ52829 | genblast_C | KQL08773 | TKW19053 | genblast_C | genblast_Os01t0968600-00_Ze | |
| PUZ45848 | Sspon.06G | KQK95865 | TKW02531 | EES08981 | Zm00001eb198880_P001 | 0.930 |
| PUZ67993 | Sspon.01G | KQL17338 | TKW29745 | EES02737 | Zm00001eb128180_P001 | 0.969 |
| PUZ38468 | Sspon.01G | genblast_C | TKV93139 | EER94013 | Zm00001eb221140_P002 | 0.930 |
| genblast_C | Sspon.06G | KQK93805 | genblast_C | genblast_C | Zm00001eb375000_P001 | 0.789 |
| PUZ70041 | Sspon.02G | KQL23777 | TKW32179 | KXG35212 | Zm00001eb097300_P002 | 0.941 |
| PUZ52852 | Sspon.03G | KQL08761 | TKW19039 | EES04285 | Zm00001eb140080_P001 | 0.906 |
| PUZ51715 | Sspon.06G | KQL02016 | TKW10560 | OQU80568 | Zm00001eb040880_P001 | 0.961 |
| PUZ54428 | Sspon.03G | KQL07278 | TKW17168 | KXG33537 | Zm00001eb151200_P001 | 0.902 |
| PUZ56172 | Sspon.03G | KQL05600 | TKW15049 | EES03140 | Zm00001eb356950_P001 | 0.887 |

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| PUZ68568 | Sspon.02GKQL22612 | TKW30663 | KXG34492 | Zm00001eb301060_P001 | 0.822 |
| PUZ36176 | Sspon.01GKQK86276 | TKV90306 | EER90561 | Zm00001eb063880_P001 | 0.950 |
| PUZ50015 | Sspon.06GKQL00924 | TKW09129 | EES14492 | Zm00001eb173150_P004 | 0.904 |
| PUZ63551 | Sspon.07GKQL13491 | TKW24840 | EES17873 | Zm00001eb350700_P002 | 0.956 |
| PUZ64294 | Sspon.07GKQL13844 | TKW25307 | EES17821 | Zm00001eb282930_P002 | 0.898 |
| PUZ67807 | Sspon.02GKQL17092 | TKW29470 | EES16316 | Zm00001eb031210_P001 | 0.878 |
| PUZ68440 | Sspon.03GKQK87572 | TKV91882 | KXG37781 | Zm00001eb119690_P001 | 0.943 |

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| PUZ65606 | Sspon.07GKQL15121 | TKW26843 | EES19664 | Zm00001eb289880_P001 | 0.964 |
| PUZ78089 | Sspon.04GKQL31957 | TKW42082 | KXG31290 | Zm00001eb258090_P001 | 0.982 |

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| PUZ62372 | Sspon.08GKQL09124 | TKW19451 | EER89121 | Zm00001eb378270_P001 | 0.972 |
| PUZ59784 | Sspon.02GKQL11232 | TKW22142 | KXG23701 | Zm00001eb136970_P001 | 0.965 |
| PUZ54247 | Sspon.03GKQL07456 | TKW17403 | EES01649 | Zm00001eb369070_P001 | 0.954 |

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| PUZ47614 | Sspon.05GKQK97701 | TKW04950 | EES10982 | Zm00001eb079800_P002 | 0.991 |
| PUZ48590 | Sspon.05GKQK98591 | genblast_C | EES11314 | Zm00001eb427960_P001 | 0.931 |
| PUZ51318 | genblast_C | KQL01636 TKW10084 | EES13777 | Zm00001eb042060_P002 | 0.922 |
| PUZ76984 | Sspon.04GKQL30879 | TKW40826 | EES05749 | Zm00001eb250110_P002 | 0.996 |
| PUZ38346 | Sspon.01GKQK88417 | TKV92968 | EER93964 | Zm00001eb043910_P001 | 0.967 |

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| PUZ67302 | Sspon.02GKQL16743 | TKW28953 | EES17116 | Zm00001eb137870_P001 | 0.962 |
| PUZ73714 | Sspon.04GKQL29080 | TKW38462 | EES04356 | Zm00001eb229850_P001 | 0.916 |

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| PUZ41879 | Sspon.01GKQK91648 | TKV97042 | EER95163 | Zm00001eb011000_P001 | 0.983 |
| PUZ63821 | Sspon.07GKQL13168 | TKW24377 | EES18943 | Zm00001eb265250_P001 | 0.966 |
| PUZ63546 | Sspon.07GKQL13497 | TKW24856 | EES17881 | Zm00001eb350680_P001 | 0.899 |
| PUZ64905 | Sspon.07GKQL14469 | TKW26048 | EES18626 | Zm00001eb294880_P001 | 0.894 |
| PUZ58539 | Sspon.03GKQL04857 | TKW14019 | EES02290 | Zm00001eb337990_P001 | 0.972 |

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|---|---|---|---|---|---|
| PUZ61403 | Sspon.08GKQL09962 | TKW20504 | OQU7608 | Zm00001eb372600_P001 | 0.823 |
| PUZ67327 | Sspon.02GKQL16717 | TKW28914 | EES17134 | Zm00001eb137700_P001 | 0.906 |
| PUZ48190 | Sspon.05GKQK98253 | TKW05646 | EES11183 | Zm00001eb427420_P002 | 0.922 |
| PUZ55696 | Sspon.03GKQL05992 | TKW15528 | KXG32935 | Zm00001eb358870_P005 | 0.974 |

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| PUZ56025 | Sspon.03G | KQL05674 | TKW15130 | EES00985 | Zm00001eb357510_P002 | 0.973 |
| PUZ37782 | Sspon.01G | KQK87920 | TKV92281 | EER91163 | Zm00001eb050290_P001 | 0.929 |
| PUZ54893 | genblast_C | KQL06871 | TKW16636 | OQU87487 | Zm00001eb153950_P001 | 0.936 |
| PUZ37798 | genblast_C | KQK87940 | TKV92303 | KXG37944 | Zm00001eb050370_P001 | 0.964 |
| PUZ68410 | Sspon.02G | KQL22439 | TKW30435 | KXG34403 | Zm00001eb300000_P001 | 0.956 |
| PUZ55901 | Sspon.03G | KQL05796 | TKW15276 | KXG32852 | Zm00001eb357890_P003 | 0.950 |
| PUZ58431 | Sspon.03G | KQL04772 | TKW13909 | EES00152 | Zm00001eb332340_P001 | 0.945 |

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| PUZ37170 | Sspon.01G | KQK87259 | TKV91526 | EER90925 | Zm00001eb056300_P001 | 0.954 |
| PUZ66927 | Sspon.07G | KQL16267 | TKW28316 | KXG23267 | Zm00001eb411230_P002 | 0.966 |
| PUZ71360 | genblast_C | KQL25149 | TKW33925 | KXG35952 | Zm00001eb102180_P002 | 0.956 |
| PUZ41185 | genblast_C | KQK90974 | TKV96214 | EER94890 | Zm00001eb016190_P001 | 0.935 |
| PUZ40392 | Sspon.01G | KQK90191 | TKV95247 | EER94594 | Zm00001eb021760_P001 | 0.934 |
| PUZ70668 | Sspon.02G | KQL24449 | TKW33085 | EER98886 | Zm00001eb099390_P001 | 0.904 |
| PUZ39928 | Sspon.01G | KQK89752 | TKV94719 | EER91872 | Zm00001eb024890_P001 | 0.976 |

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| PUZ76835 | Sspon.05G | KQL30740 | TKW40649 | genblast_C | Zm00001eb249100_P001 | 0.962 |
| PUZ60919 | Sspon.08G | KQL10651 | TKW21484 | EER88779 | Zm00001eb299930_P004 | 0.935 |
| PUZ66054 | Sspon.07G | KQL15556 | TKW27396 | EES18200 | Zm00001eb349820_P001 | 0.916 |
| PUZ40727 | Sspon.01G | KQK90466 | TKV95612 | EER94702 | Zm00001eb019630_P001 | 0.974 |

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| PUZ38608 | Sspon.01GKQK88684 | TKV93324 | KXG38314 | Zm00001eb045620_P001 | 0.912 |
| PUZ62176 | genblast_CKQL09732 | TKW20203 | KXG19323 | Zm00001eb376730_P001 | 0.947 |
| PUZ67137 | Sspon.02GKQL16898 | TKW29168 | EES17032 | Zm00001eb310390_P001 | 0.963 |
| PUZ37104 | Sspon.01GKQL29306 | TKV91432 | OQU78728 | Zm00001eb394890_P002 | 0.968 |
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| PUZ61962 | Sspon.08GKQL09530 | TKW19938 | EER87955 | genblast_Os06t0176300-00Zm0 | |
| PUZ77790 | genblast_CKQL31662 | TKW41763 | EES05859 | Zm00001eb255990_P003 | 0.952 |
| PUZ39472 | Sspon.07GKQK89317 | TKV94155 | KXG22066 | Zm00001eb288630_P001 | 0.961 |
| PUZ48614 | genblast_CKQK98629 | TKW06178 | EES12727 | Zm00001eb072780_P001 | 0.927 |
| PUZ43274 | Sspon.01GKQK93049 | genblast_C | OQU93459 | Zm00001eb402900_P001 | 0.939 |
| PUZ53665 | genblast_CKQL07997 | TKW18064 | EES01862 | Zm00001eb145740_P001 | 0.922 |
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| PUZ39374 | Sspon.01GKQK89047 | TKV93797 | OQU86787 | Zm00001eb027950_P001 | 0.957 |

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| PUZ45127 | Sspon.06G | KQK94854 | TKW01086 | EES08634 | Zm00001eb113700_P001 | 0.887 |
| PUZ60039 | Sspon.08G | KQK99544 | TKW07370 | EER90016 | Zm00001eb386260_P001 | 0.960 |
| PUZ42379 | Sspon.01G | KQK92128 | TKV97660 | OQU93065 | Zm00001eb008090_P002 | 0.970 |
| PUZ59350 | Sspon.08G | KQL11862 | TKW22984 | EER88869 | Zm00001eb225970_P001 | 0.957 |
| PUZ40370 | Sspon.08G | KQK90172 | TKV95222 | EER92019 | Zm00001eb021950_P001 | 0.971 |
| PUZ74822 | Sspon.04G | KQL27969 | TKW37074 | OQU84683 | Zm00001eb239070_P001 | 0.938 |
| PUZ59827 | Sspon.08G | KQL11282 | TKW22201 | EER90087 | Zm00001eb387310_P001 | 0.956 |
| PUZ38243 | Sspon.01G | KQK88327 | TKV92855 | EER93927 | Zm00001eb043330_P001 | 0.923 |
| PUZ64490 | genblast_C | KQL14024 | TKW25520 | EES18806 | Zm00001eb297330_P001 | 0.900 |
| PUZ41290 | Sspon.01G | KQK91070 | TKV96350 | EER94931 | Zm00001eb015490_P001 | 0.981 |
| PUZ41046 | Sspon.02G | KQK90829 | TKV96033 | EER92252 | Zm00001eb394490_P001 | 0.860 |
| PUZ41108 | Sspon.01G | KQK90899 | TKV96123 | KXG39389 | Zm00001eb016730_P002 | 0.916 |
| PUZ58493 | Sspon.03G | KQL04818 | TKW13970 | OQU86148 | Zm00001eb121000_P001 | 0.941 |
| PUZ56026 | Sspon.03G | KQL05672 | TKW15129 | EES03193 | Zm00001eb160760_P001 | 0.924 |
| PUZ72824 | Sspon.02G | KQL26568 | TKW35694 | EER99676 | Zm00001eb326900_P001 | 0.755 |
| PUZ55168 | Sspon.03G | KQL06607 | TKW16281 | KXG33207 | Zm00001eb155560_P003 | 0.973 |
| PUZ77440 | Sspon.04G | KQL31312 | TKW41360 | EES07330 | Zm00001eb189530_P002 | 0.943 |
| PUZ42091 | Sspon.01G | genblast_C | TKV97332 | EER92612 | Zm00001eb399520_P001 | 0.951 |
| PUZ55181 | Sspon.01G | KQL06594 | TKW16263 | OQU90735 | Zm00001eb062490_P003 | 0.927 |
| PUZ43829 | genblast_C | KQK93722 | TKV99451 | KXG27818 | Zm00001eb202460_P002 | 0.814 |
| PUZ59147 | Sspon.08G | KQL12176 | TKW23379 | EER88947 | Zm00001eb227720_P001 | 0.896 |
| PUZ70502 | Sspon.02G | KQL24277 | TKW32883 | EER98811 | Zm00001eb098680_P001 | 0.959 |
| PUZ65365 | Sspon.07G | KQL14875 | TKW26523 | EES18444 | Zm00001eb352610_P002 | 0.943 |
| PUZ76110 | Sspon.04G | KQL30031 | TKW39730 | EES05244 | Zm00001eb182090_P003 | 0.974 |
| PUZ55862 | Sspon.03G | KQL05834 | TKW15325 | EES03268 | Zm00001eb358010_P001 | 0.794 |
| PUZ72936 | Sspon.02G | KQL26692 | TKW35859 | KXG36701 | Zm00001eb327640_P001 | 0.927 |
| PUZ77007 | Sspon.04G | KQL30896 | TKW40844 | KXG31026 | Zm00001eb250240_P001 | 0.928 |

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| PUZ36577 | Sspon.01G | KQK86658 | TKV90818 | KXG37359 | Zm00001eb212930_P002 | 0.964 |
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| PUZ72893 | Sspon.02G | KQL26628 | TKW35779 | OQU90252 | Zm00001eb392960_P001 | 0.768 |
| PUZ38296 | genblast_C | KQK88380 | TKV92924 | EER93946 | Zm00001eb043640_P001 | 0.797 |
| PUZ62777 | Sspon.07G | KQK93315 | TKW07584 | EES15601 | Zm00001eb405650_P001 | 0.936 |
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| PUZ65063 | Sspon.07G | KQL14622 | TKW26223 | EES18551 | Zm00001eb353710_P001 | 0.904 |
| PUZ44100 | Sspon.05G | KQK94025 | TKV99889 | KXG28056 | Zm00001eb112550_P001 | 0.912 |
| PUZ55775 | Sspon.03G | KQL05915 | TKW15412 | KXG32911 | Zm00001eb159650_P002 | 0.947 |
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| PUZ63479 | Sspon.07G | genblast_C | TKW24922 | OQU77655 | Zm00001eb284290_P001 | 0.794 |
| PUZ64728 | Sspon.07G | KQL14253 | TKW25806 | OQU78447 | Zm00001eb296310_P001 | 0.925 |
| PUZ64404 | genblast_C | KQL13942 | TKW25429 | KXG20994 | Zm00001eb267700_P004 | 0.910 |
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| PUZ46117 | Sspon.01G | KQK96244 | TKW03000 | KXG39311 | Zm00001eb089360_P001 | 0.918 |
| PUZ66807 | genblast_C | KQL16070 | TKW28053 | KXG21632 | Zm00001eb350730_P001 | 0.994 |
| PUZ58275 | genblast_C | genblast_C | TKW13706 | KXG31745 | Zm00001eb122830_P001 | 0.930 |
| PUZ71766 | Sspon.02G | KQL25520 | TKW34386 | EER99282 | Zm00001eb103960_P001 | 0.943 |
| PUZ74468 | Sspon.04G | KQL28324 | TKW37519 | KXG29690 | Zm00001eb236520_P002 | 0.913 |
| PUZ58967 | Sspon.08G | KQL12341 | TKW23592 | EER90440 | Zm00001eb228900_P002 | 0.832 |
| PUZ62767 | Sspon.07G | KQK99709 | TKW07569 | EES15616 | Zm00001eb405720_P001 | 0.913 |
| PUZ64221 | Sspon.03G | KQL13761 | TKW25210 | EES19114 | genblast_Os05t0169400-01_Ze | |
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| PUZ48267 | Sspon.05G | KQL23920 | TKW05747 | EES12591 | Zm00001eb075130_P003 | 0.920 |
| PUZ38291 | Sspon.01G | KQK88371 | TKV92909 | EER91375 | Zm00001eb043610_P001 | 0.984 |
| PUZ63033 | Sspon.05G | KQK99610 | TKW07451 | EES16682 | Zm00001eb407150_P001 | 0.955 |
| PUZ66215 | Sspon.07G | KQL15706 | TKW27604 | EES19444 | Zm00001eb286870_P001 | 0.957 |
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| PUZ72429 | Sspon.02G | KQL26189 | TKW35229 | OQU90069 | Zm00001eb323730_P002 | 0.930 |
| PUZ61885 | genblast_C | KQL09454 | TKW19828 | EER89341 | Zm00001eb374560_P001 | 0.955 |
| PUZ67552 | Sspon.07G | KQL29913 | TKW39551 | KXG25836 | Zm00001eb112980_P001 | 0.828 |
| genblast_C | Sspon.03G | KQL06867 | TKW16632 | EES01437 | Zm00001eb371290_P001 | 0.955 |
| PUZ75198 | Sspon.08G | KQL29268 | TKW38670 | EER87769 | Zm00001eb378420_P002 | 0.940 |

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| PUZ74180 | genblast_C | KQL28622 | TKW37867 | EES04566 | Zm00001eb232750_P001 | 0.899 |
| PUZ74855 | Sspon.04G | KQL27941 | TKW37043 | EES06570 | Zm00001eb204660_P001 | 0.900 |
| PUZ64076 | genblast_C | KQL13027 | TKW24204 | EES19040 | Zm00001eb354140_P003 | 0.967 |
| PUZ72157 | Sspon.02G | KQL25900 | TKW34871 | EER97258 | Zm00001eb105590_P001 | 0.979 |
| PUZ68307 | Sspon.02G | KQL22327 | TKW30287 | EER97906 | Zm00001eb299190_P001 | 0.836 |
| PUZ48916 | Sspon.05G | KQK98939 | TKW06594 | EES12865 | Zm00001eb431070_P001 | 0.970 |
| PUZ55993 | genblast_C | KQL05716 | TKW15180 | OQU8710 | Zm00001eb357630_P001 | 0.925 |

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| PUZ64613 | Sspon.07G | KQL14159 | TKW25683 | KXG22609 | genblast_Os05t0580500-01_Ze | |
| PUZ64825 | Sspon.07G | KQL14369 | TKW25929 | EES18670 | Zm00001eb295680_P001 | 0.959 |

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| PUZ46795 | Sspon.05G | KQK96915 | TKW03943 | KXG26069 | Zm00001eb420920_P001 | 0.967 |
| PUZ65541 | Sspon.07G | KQL15039 | TKW26754 | EES18382 | Zm00001eb290480_P001 | 0.946 |
| PUZ74145 | genblast_C | KQL28657 | TKW37900 | EES06314 | Zm00001eb232600_P001 | 0.966 |

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| PUZ36594 | Sspon.02G | KQK86679 | TKV90840 | EER93298 | Zm00001eb060670_P001 | 0.955 |

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| PUZ41449 | Sspon.01G | KQK91243 | TKV96588 | EER95000 | Zm00001eb014120_P001 | 0.978 |
| PUZ37982 | Sspon.01G | genblast_C | TKV92515 | EER91229 | Zm00001eb051460_P001 | 0.955 |
| PUZ63885 | Sspon.07G | KQL13227 | TKW24472 | KXG21224 | Zm00001eb354730_P003 | 0.964 |
| PUZ38313 | Sspon.01G | KQK88393 | TKV92941 | EER91385 | Zm00001eb043760_P001 | 0.929 |
| PUZ74073 | Sspon.04G | KQL28725 | TKW37980 | EES06280 | genblast_Os02t0150900-01_Ze | |

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| PUZ76507 | Sspon.04G | KQL30439 | TKW40239 | EES05409 | Zm00001eb184470_P001 | 0.937 |
| PUZ72081 | Sspon.02G | KQL25826 | TKW34795 | KXG36241 | Zm00001eb105190_P001 | 0.929 |
| PUZ39887 | genblast_C | KQK89719 | TKV94677 | EER94417 | Zm00001eb025400_P002 | 0.954 |
| PUZ69816 | Sspon.01G | KQL23782 | TKW32184 | EER91847 | Zm00001eb025560_P003 | 0.968 |

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| PUZ70936 | Sspon.02GKQL24736 | TKW33432 | EER96823 | Zm00001eb314550_P001 | 0.983 |
| PUZ41501 | Sspon.01GKQK91296 | TKV96651 | KXG39573 | Zm00001eb396880_P002 | 0.970 |

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| PUZ55836 | Sspon.03GKQL05868 | TKW15356 | EES03274 | Zm00001eb358160_P003 | 0.961 |
| PUZ65564 | Sspon.02GKQL16604 | TKW28772 | EES17197 | Zm00001eb136960_P002 | 0.881 |
| PUZ64850 | Sspon.07GKQL14385 | TKW25948 | EES18659 | Zm00001eb295460_P001 | 0.975 |
| PUZ38315 | Sspon.01GKQK88395 | TKV92943 | EER91386 | Zm00001eb043780_P001 | 0.976 |
| PUZ64069 | Sspon.07GKQL13033 | genblast_C | KXG21314 | Zm00001eb267820_P001 | 0.983 |
| PUZ73422 | Sspon.02GKQL27089 | TKW36381 | EER99881 | Zm00001eb330150_P002 | 0.970 |
| PUZ36351 | Sspon.01GKQK86446 | TKV90511 | EER90630 | Zm00001eb062500_P001 | 0.899 |
| PUZ44967 | Sspon.06GKQL13682 | TKW25090 | EES13627 | Zm00001eb411900_P001 | 0.918 |
| PUZ41396 | Sspon.01GKQK91195 | TKV96516 | EER94977 | Zm00001eb014720_P003 | 0.954 |
| genblast_C | Sspon.01GKQK91849 | TKV97324 | KXG39831 | Zm00001eb399440_P001 | 0.891 |
| PUZ42972 | Sspon.01GKQK92701 | TKV98343 | EER92910 | Zm00001eb002790_P001 | 0.955 |
| PUZ54509 | Sspon.03GKQL07224 | TKW17085 | EES01554 | Zm00001eb369950_P001 | 0.966 |

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| PUZ45558 | Sspon.06GKQK95473 | TKW01919 | EES10143 | Zm00001eb166550_P001 | 0.756 |
| PUZ69151 | Sspon.02GKQL23017 | TKW31179 | EER96079 | Zm00001eb303530_P001 | 0.992 |
| PUZ71008 | Sspon.02GKQL24804 | TKW33506 | EER96861 | Zm00001eb100840_P001 | 0.977 |
| PUZ71034 | genblast_CKQL24832 | TKW33534 | EER99019 | Zm00001eb100960_P001 | 0.969 |
| PUZ73437 | Sspon.01GKQL27072 | TKW36359 | EER99872 | genblast_Os07t0667100-00_Ze | |
| PUZ76998 | Sspon.04GKQL30890 | TKW40837 | OQU85655 | Zm00001eb250190_P002 | 0.944 |
| PUZ53391 | Sspon.03GKQL08231 | TKW18365 | EES04071 | Zm00001eb144080_P001 | 0.994 |

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| PUZ70991 | Sspon.02GKQL24788 | TKW33491 | EER96850 | Zm00001eb314860_P001 | 0.903 |
| PUZ77084 | Sspon.07GKQL14601 | TKW26199 | EES19865 | Zm00001eb293160_P001 | 0.966 |
| PUZ74372 | Sspon.04GKQL28445 | TKW37652 | KXG29625 | genblast_Os02t0180400-00_Ze | |
| PUZ49148 | Sspon.05GKQK99158 | TKW06875 | EES11524 | Zm00001eb431860_P001 | 0.973 |

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| PUZ54830 | Sspon.03G | KQL06949 | TKW16722 | EES03595 | Zm00001eb371070_P001 | 0.769 |
| PUZ70691 | Sspon.02G | KQL24474 | TKW33110 | genblast_C | Zm00001eb312530_P001 | 0.947 |
| PUZ61957 | Sspon.01G | KQL09526 | TKW19932 | KXG19442 | Zm00001eb027940_P001 | 0.926 |
| PUZ59604 | genblast_C | KQL11058 | TKW21941 | KXG20550 | Zm00001eb389710_P003 | 0.955 |
| PUZ41973 | genblast_C | KQK91733 | TKV97170 | EER95187 | Zm00001eb398900_P003 | 0.929 |
| PUZ64819 | Sspon.07G | KQL14359 | TKW25922 | KXG22523 | Zm00001eb295600_P001 | 0.943 |
| PUZ39528 | Sspon.01G | KQK89386 | TKV94247 | OQU91935 | genblast_Os10t0324900-01_Zea | |
| PUZ67792 | genblast_C | KQL17082 | TKW29455 | OQU79520 | Zm00001eb031130_P001 | 0.892 |
| PUZ76719 | Sspon.04G | KQL30640 | TKW40512 | EES07200 | Zm00001eb185590_P001 | 0.880 |
| PUZ45961 | Sspon.03G | KQK96100 | TKW02813 | OQU77799 | Zm00001eb284870_P001 | 0.937 |
| PUZ67371 | Sspon.02G | KQL16673 | TKW28842 | EES17168 | Zm00001eb137290_P001 | 0.900 |
| PUZ67219 | Sspon.02G | KQL16840 | TKW29098 | EES16019 | Zm00001eb409280_P002 | 0.931 |
| PUZ74871 | genblast_C | KQL27926 | TKW37025 | EES06573 | Zm00001eb238660_P002 | 0.954 |
| PUZ77260 | Sspon.04G | genblast_C | TKW41135 | EES07399 | Zm00001eb188310_P001 | 0.930 |
| PUZ59134 | Sspon.08G | KQL12190 | TKW23388 | EER88950 | Zm00001eb272520_P001 | 0.975 |
| PUZ54613 | Sspon.03G | KQL07130 | TKW16976 | EES01520 | Zm00001eb370220_P001 | 0.923 |
| PUZ48307 | Sspon.05G | KQK98348 | TKW05799 | EES12613 | Zm00001eb074830_P003 | 0.926 |
| PUZ55926 | Sspon.03G | KQL05774 | TKW15243 | EES01034 | Zm00001eb161500_P001 | 0.920 |

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| PUZ58147 | Sspon.03G | KQL04501 | TKW13553 | EES00285 | Zm00001eb336160_P002 | 0.969 |
| PUZ67902 | Sspon.02G | KQL17290 | TKW29686 | KXG23993 | Zm00001eb136120_P001 | 0.753 |

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| PUZ42444 | Sspon.01G | KQK92190 | TKV97726 | OQU93088 | Zm00001eb006890_P002 | 0.933 |
| PUZ77431 | Sspon.04G | KQL31302 | TKW41349 | EES07336 | Zm00001eb189470_P001 | 0.928 |
| PUZ37695 | Sspon.01G | KQK87841 | TKV92184 | KXG37893 | Zm00001eb218090_P003 | 0.984 |
| PUZ67056 | Sspon.02G | KQL16393 | TKW28489 | EER99787 | Zm00001eb328980_P001 | 0.973 |

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|---|---|---|---|---|---|---|
| PUZ65905 | Sspon.07G | KQL07987 | TKW27177 | KXG22035 | Zm00001eb288420_P001 | 0.887 |
| PUZ59031 | Sspon.08G | KQL12279 | TKW23513 | OQU77135 | Zm00001eb228340_P001 | 0.938 |

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| PUZ73567 | Sspon.02G | KQL27287 | TKW36664 | KXG37026 | Zm00001eb331510_P001 | 0.923 |
| PUZ50752 | Sspon.06G | KQL01120 | TKW09394 | EES14778 | Zm00001eb414690_P001 | 0.992 |

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|---|---|---|---|---|---|---|
| PUZ54176 | Sspon.03G | KQL07532 | TKW17495 | KXG33637 | Zm00001eb149300_P001 | 0.879 |
| genblast_C | Sspon.01G | genblast_C | TKW40727 | EES05781 | Zm00001eb249570_P002 | 0.964 |
| PUZ38418 | Sspon.01G | KQK88478 | TKV93061 | EER91421 | Zm00001eb220850_P001 | 0.919 |
| PUZ77801 | genblast_C | KQL31673 | TKW41773 | EES07589 | Zm00001eb256100_P002 | 0.893 |
| PUZ44660 | genblast_C | KQK94410 | TKW00453 | OQU83341 | genblast_Os11t0293900-01 | Zm0 |

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|---|---|---|---|---|---|---|
| PUZ73732 | genblast_C | KQL29100 | TKW38481 | KXG29296 | Zm00001eb209480_P001 | 0.974 |
| PUZ76611 | Sspon.04G | KQL30541 | TKW40387 | KXG30654 | Zm00001eb247460_P003 | 0.934 |
| PUZ61163 | Sspon.08G | KQL10443 | TKW21161 | EER88310 | Zm00001eb381490_P001 | 0.962 |

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| PUZ74015 | Sspon.04G | genblast_C | TKW38077 | EES04495 | Zm00001eb232050_P001 | 0.786 |

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| PUZ66010 | Sspon.07G | KQL15495 | TKW27318 | EES18228 | Zm00001eb287940_P001 | 0.956 |
| PUZ76595 | Sspon.04G | genblast_C | TKW40377 | OQU85324 | Zm00001eb247390_P001 | 0.955 |
| PUZ41819 | Sspon.01G | genblast_C | TKV96973 | KXG39739 | Zm00001eb398210_P001 | 0.974 |
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| PUZ42006 | Sspon.08G | KQK91772 | TKV97214 | EER87932 | Zm00001eb036170_P001 | 0.895 |
| PUZ42921 | Sspon.01G | KQK92645 | TKV98292 | EER92886 | Zm00001eb003230_P001 | 0.956 |
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| PUZ67873 | Sspon.02G | KQL17181 | TKW29546 | OQU79579 | Zm00001eb135910_P002 | 0.834 |
| PUZ60576 | Sspon.08G | genblast_C | TKW21587 | EER89807 | Zm00001eb281570_P003 | 0.928 |
| PUZ77146 | Sspon.04G | KQL31014 | TKW40991 | EES07427 | Zm00001eb251160_P001 | 0.914 |
| PUZ58516 | Sspon.03G | KQL04839 | TKW13995 | EES00124 | Zm00001eb337900_P001 | 0.992 |
| PUZ76139 | Sspon.04G | KQL30064 | TKW39764 | EES05262 | Zm00001eb182330_P001 | 0.920 |
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| PUZ43728 | genblast_C | KQK93707 | TKV99418 | OQU82934 | Zm00001eb092040_P001 | 0.941 |
| PUZ53166 | Sspon.03G | KQL08435 | TKW18647 | EES02007 | Zm00001eb142560_P001 | 0.966 |
| PUZ65381 | Sspon.07G | KQL14887 | TKW26545 | EES18439 | Zm00001eb291660_P001 | 0.880 |
| PUZ78025 | Sspon.04G | KQL31896 | TKW42017 | EES07672 | genblast_Os06t0184900-01_Zea | |
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| PUZ71496 | Sspon.02G | KQL25274 | TKW34072 | KXG35991 | Zm00001eb318150_P001 | 0.939 |
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| PUZ50705 | Sspon.04G | KQL00288 | TKW08206 | OQU80180 | Zm00001eb414340_P001 | 0.965 |
| PUZ67454 | Sspon.02G | KQL16599 | TKW28767 | EES16159 | Zm00001eb028500_P001 | 0.978 |
| PUZ40038 | Sspon.01G | KQK89846 | TKV94830 | KXG40133 | Zm00001eb004590_P001 | 0.937 |
| PUZ38761 | Sspon.01G | KQK88809 | TKV93496 | EER91507 | Zm00001eb046310_P001 | 0.971 |
| PUZ43699 | Sspon.05G | KQK93571 | TKV99262 | OQU82869 | Zm00001eb092840_P001 | 0.952 |
| PUZ67563 | Sspon.02G | KQL16487 | TKW28593 | EES17245 | Zm00001eb029450_P001 | 0.962 |
| PUZ71015 | Sspon.02G | KQL24812 | TKW33515 | EER99015 | Zm00001eb100880_P001 | 0.871 |
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| PUZ76878 | Sspon.04G | KQL30784 | TKW40699 | KXG31090 | Zm00001eb186450_P001 | 0.961 |

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| PUZ59176 | genblast_C | KQL12144 | TKW23350 | KXG20822 | Zm00001eb227420_P002 | 0.936 |
| PUZ72703 | Sspon.02G | KQL26457 | TKW35566 | EER97457 | Zm00001eb325870_P001 | 0.883 |
| PUZ42369 | Sspon.01G | KQK92121 | TKV97650 | EER95332 | Zm00001eb008010_P001 | 0.915 |
| PUZ51211 | Sspon.06G | genblast_C | TKW09942 | EES14887 | Zm00001eb042820_P001 | 0.865 |
| PUZ78253 | genblast_C | KQL32118 | TKW42267 | KXG31364 | Zm00001eb191350_P001 | 0.913 |
| PUZ41946 | Sspon.01G | KQK91698 | TKV97116 | EER95179 | Zm00001eb010530_P001 | 0.934 |
| PUZ77977 | genblast_Z | KQL31847 | TKW41968 | KXG31241 | Zm00001eb257360_P001 | 0.971 |
| PUZ61294 | Sspon.08G | KQL09804 | TKW20303 | EER88069 | Zm00001eb373120_P001 | 0.968 |
| PUZ55021 | Sspon.03G | KQL06752 | TKW16474 | EES01377 | Zm00001eb154600_P001 | 0.948 |
| PUZ76186 | Sspon.04G | KQL30119 | TKW39834 | KXG30470 | Zm00001eb244460_P001 | 0.955 |
| PUZ75212 | Sspon.03G | KQL29276 | TKW38677 | KXG34073 | Zm00001eb142150_P001 | 0.925 |
| PUZ62489 | Sspon.08G | KQL10516 | TKW21282 | KXG19937 | Zm00001eb281400_P002 | 0.945 |
| PUZ48900 | Sspon.05G | KQK98909 | TKW06561 | KXG27113 | Zm00001eb070760_P001 | 0.919 |
| PUZ57401 | Sspon.03G | KQL03838 | TKW12727 | OQU86633 | Zm00001eb127940_P001 | 0.940 |
| PUZ71333 | Sspon.02G | KQL25121 | TKW33894 | KXG35939 | Zm00001eb102090_P007 | 0.912 |
| PUZ48232 | Sspon.05G | KQK98298 | TKW05696 | OQU82040 | Zm00001eb427600_P002 | 0.893 |
| PUZ46765 | Sspon.05G | KQK96881 | TKW03891 | EES12019 | Zm00001eb420700_P002 | 0.944 |
| PUZ65240 | Sspon.07G | KQL14789 | TKW26420 | EES18483 | Zm00001eb292490_P001 | 0.882 |

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| PUZ48709 | Sspon.05GKQK98724 | TKW06295 | EES11361 | Zm00001eb430150_P001 | 0.968 |
| PUZ41357 | Sspon.01GKQK91146 | TKV96460 | EER94955 | Zm00001eb395770_P001 | 0.970 |
| PUZ76300 | Sspon.04GKQL30221 | TKW39971 | EES07047 | Zm00001eb183340_P003 | 0.968 |

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| PUZ48866 | Sspon.05GKQK98877 | TKW06523 | EES12842 | Zm00001eb071010_P001 | 0.977 |
| PUZ38479 | Sspon.01GKQK88547 | TKV93155 | OQU91581 | Zm00001eb044900_P004 | 0.953 |
| PUZ59240 | Sspon.08GKQL11751 | TKW22837 | EER90331 | Zm00001eb227020_P001 | 0.898 |
| PUZ43443 | Sspon.05GKQK93343 | TKW07556 | EES09127 | Zm00001eb195280_P001 | 0.914 |
| PUZ63563 | Sspon.07GKQL13477 | TKW24823 | EES19209 | Zm00001eb347360_P001 | 0.884 |
| PUZ66896 | Sspon.07GKQL16334 | TKW27815 | KXG21784 | genblast_Os11t0279750-00_Zea | |
| PUZ77366 | Sspon.04GKQL31232 | TKW41255 | EES07361 | Zm00001eb189250_P001 | 0.968 |
| PUZ58659 | Sspon.03GKQL04962 | TKW14160 | EES02257 | genblast_Os01t0215700-01_Zea | |
| PUZ74710 | Sspon.04GKQL28089 | genblast_C | EES06519 | Zm00001eb240120_P001 | 0.900 |
| PUZ49859 | Sspon.06GKQL01089 | TKW09355 | KXG24255 | Zm00001eb260720_P005 | 0.942 |

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| PUZ76253 | Sspon.04GKQL30172 | TKW39906 | EES07034 | Zm00001eb244930_P001 | 0.971 |
| PUZ38932 | Sspon.01GKQK88959 | TKV93699 | EER94184 | Zm00001eb047460_P004 | 0.951 |
| PUZ49356 | Sspon.05GKQL12931 | TKW24072 | EES13035 | Zm00001eb067290_P001 | 0.962 |

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| PUZ49190 | Sspon.05GKQK99192 | TKW06923 | KXG27246 | Zm00001eb068620_P001 | 0.965 |
| PUZ56697 | Sspon.03GKQL05080 | TKW14342 | EES02923 | Zm00001eb131510_P001 | 0.997 |
| PUZ43782 | Sspon.05GKQK93622 | TKV99329 | KXG27770 | genblast_Os11t0155100-01_Zea | |
| PUZ36513 | Sspon.01GKQK86581 | TKV90726 | EER93260 | Zm00001eb061400_P001 | 0.931 |
| PUZ77857 | Sspon.04GKQL31713 | TKW41809 | EES07602 | Zm00001eb256350_P001 | 0.969 |

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| PUZ65462 | Sspon.07GKQL14946 | TKW26629 | EES18419 | Zm00001eb352240_P001 | 0.930 |

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| PUZ60761 | Sspon.03GKQL10608 | TKW21416 | KXG33919 | Zm00001eb144500_P002 | 0.979 |
| PUZ47454 | Sspon.04GKQK97539 | TKW04760 | KXG26452 | Zm00001eb081010_P001 | 0.822 |

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| PUZ77342 | Sspon.04G | KQL31215 | TKW41227 | KXG30884 | Zm00001eb252650_P001 | 0.979 |
| PUZ42565 | Sspon.01G | KQK92309 | TKV97888 | KXG40052 | Zm00001eb401880_P001 | 0.941 |
| genblast_C | Sspon.03G | KQK91208 | TKV96535 | EES00270 | Zm00001eb123560_P001 | 0.929 |

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| PUZ63065 | Sspon.07G | KQK99582 | TKW07429 | EES15711 | genblast_Os12t0163600-01_Ze |

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| PUZ46661 | genblast_C | KQK96785 | TKW03745 | OQU76853 | Zm00001eb389920_P001 | 0.798 |
| PUZ36883 | Sspon.01G | KQK86946 | TKV91169 | EER93394 | Zm00001eb058590_P001 | 0.966 |
| PUZ70310 | Sspon.02G | KQL24092 | TKW32604 | EER96549 | Zm00001eb098030_P002 | 0.949 |
| PUZ43848 | genblast_Z | KQK93742 | TKV99480 | KXG27836 | Zm00001eb202020_P001 | 0.933 |

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| PUZ67704 | Sspon.02G | KQL17025 | TKW29357 | EES17308 | Zm00001eb030570_P001 | 0.961 |
| PUZ60834 | genblast_C | KQL10296 | TKW20939 | OQU76225 | Zm00001eb280270_P001 | 0.945 |
| PUZ73799 | Sspon.04G | KQL28971 | TKW38312 | EES06197 | Zm00001eb208440_P001 | 0.953 |
| PUZ48269 | genblast_C | KQL23917 | TKW05751 | KXG37847 | Zm00001eb427850_P001 | 0.922 |
| PUZ65154 | Sspon.07G | KQL14709 | TKW26317 | OQU78316 | Zm00001eb353440_P001 | 0.924 |
| PUZ76628 | Sspon.01G | KQL30560 | TKW40405 | KXG37080 | Zm00001eb210420_P001 | 0.918 |
| PUZ52849 | Sspon.03G | KQL08763 | TKW19042 | OQU88249 | Zm00001eb140050_P001 | 0.922 |
| PUZ73735 | genblast_C | KQL29102 | TKW38483 | EES06158 | Zm00001eb209450_P003 | 0.894 |
| PUZ37100 | Sspon.01G | KQK87175 | TKV91436 | EER93482 | Zm00001eb056730_P001 | 0.920 |
| PUZ43136 | Sspon.01G | KQK92886 | TKV98540 | EER92967 | Zm00001eb001530_P001 | 0.927 |
| PUZ49538 | Sspon.05G | KQL12766 | TKW23870 | EES11661 | Zm00001eb433860_P001 | 0.928 |

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| PUZ49880 | Sspon.06GKQL01062 | TKW09308 | EES14418 | Zm00001eb173930_P001 | 0.859 |
| PUZ43677 | Sspon.05GKQK99858 | TKW07775 | OQU82861 | Zm00001eb165410_P001 | 0.848 |
| PUZ40874 | Sspon.01GKQK90624 | TKV95811 | OQU92499 | Zm00001eb018750_P002 | 0.971 |
| PUZ73243 | Sspon.02GKQL26968 | TKW36234 | KXG36838 | Zm00001eb110610_P001 | 0.958 |

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| PUZ42966 | Sspon.01GKQK92689 | TKV98331 | EER92904 | Zm00001eb002830_P001 | 0.880 |
| PUZ65862 | Sspon.07GKQL15356 | TKW27114 | EES18281 | Zm00001eb348710_P001 | 0.973 |

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| PUZ77309 | Sspon.04GKQL31180 | TKW41192 | EES07381 | Zm00001eb252360_P001 | 0.878 |
| PUZ76928 | Sspon.04GKQL30828 | TKW40763 | EES07505 | Zm00001eb186700_P001 | 0.946 |

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| PUZ65553 | Sspon.07GKQL15058 | TKW26767 | KXG22202 | Zm00001eb290310_P001 | 0.981 |

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| PUZ61807 | Sspon.08GKQL09361 | TKW19708 | KXG19536 | Zm00001eb373970_P003 | 0.988 |
| PUZ77867 | Sspon.04GKQL31719 | TKW41820 | EES05875 | Zm00001eb256430_P002 | 0.958 |
| PUZ42046 | Sspon.01GKQK94083 | TKV99992 | EER95211 | Zm00001eb009780_P001 | 0.961 |

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| PUZ42059 | Sspon.01G | KQK91826 | TKV97289 | KXG39827 | Zm00001eb009600_P001 | 0.953 |
| PUZ69562 | Sspon.02G | KQL23553 | TKW31868 | KXG35088 | Zm00001eb096340_P001 | 0.961 |

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| PUZ54418 | genblast_C | KQL07289 | TKW17179 | EES01587 | Zm00001eb151130_P001 | 0.910 |

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| PUZ47557 | genblast_C | KQK97638 | TKW04875 | OQU81751 | Zm00001eb080260_P001 | 0.970 |
| PUZ61562 | Sspon.08G | KQL10125 | TKW20717 | KXG19700 | Zm00001eb280040_P001 | 0.941 |
| PUZ53444 | Sspon.03G | KQL08191 | TKW18314 | OQU88055 | Zm00001eb365570_P001 | 0.979 |
| PUZ42005 | genblast_C | KQK91770 | TKV97213 | EER95199 | Zm00001eb010060_P001 | 0.993 |

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| PUZ38976 | Sspon.01G | KQK89013 | TKV93759 | EER94213 | Zm00001eb047760_P002 | 0.909 |
| PUZ61999 | Sspon.08G | genblast_Z | TKW19984 | OQU75924 | Zm00001eb375410_P001 | 0.951 |
| PUZ65209 | Sspon.07G | KQL14814 | TKW26450 | EES18470 | Zm00001eb292320_P001 | 0.959 |
| PUZ40281 | Sspon.01G | KQK90086 | TKV95119 | EER94547 | Zm00001eb392000_P001 | 0.972 |

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| PUZ56444 | Sspon.08G | KQL05335 | TKW21792 | EES00813 | Zm00001eb132550_P001 | 0.926 |
| PUZ71625 | Sspon.02G | KQL25406 | TKW34232 | OQU89801 | Zm00001eb319350_P002 | 0.920 |

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| PUZ53081 | Sspon.03G | KQL08530 | TKW18749 | EES04185 | Zm00001eb141880_P001 | 0.907 |

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| PUZ37851 | genblast_C | KQK87990 | TKV92353 | OQU80289 | Zm00001eb042720_P001 | 0.916 |
| PUZ71222 | Sspon.02G | KQL24992 | TKW33740 | KXG35874 | Zm00001eb316320_P001 | 0.922 |
| PUZ73169 | Sspon.02G | KQL26915 | TKW36161 | KXG36805 | Zm00001eb329140_P001 | 0.934 |
| PUZ65436 | Sspon.07G | KQL14918 | TKW26591 | EES19732 | Zm00001eb291350_P002 | 0.931 |
| PUZ44861 | Sspon.06G | KQK94618 | TKW00724 | genblast_C | genblast_Os11t0491500-00_Ze | |
| PUZ41601 | genblast_C | KQK91392 | TKV96754 | EER95058 | Zm00001eb012950_P001 | 0.897 |
| PUZ76180 | Sspon.04G | KQL30114 | TKW39819 | OQU85171 | Zm00001eb182650_P001 | 0.790 |
| PUZ42156 | genblast_C | KQK91935 | TKV97420 | OQU92992 | Zm00001eb400040_P001 | 0.937 |
| PUZ47243 | Sspon.05G | KQK97356 | TKW04502 | KXG26361 | Zm00001eb082220_P001 | 0.935 |

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| PUZ40581 | Sspon.01G | KQK90358 | TKV95482 | OQU92373 | Zm00001eb393290_P001 | 0.984 |
| PUZ54989 | Sspon.03G | KQL06783 | TKW16514 | KXG33274 | Zm00001eb361690_P001 | 0.926 |

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| PUZ42919 | Sspon.01G | KQK92644 | TKV98291 | EER92887 | Zm00001eb003240_P001 | 0.960 |
| PUZ65333 | Sspon.07G | KQL14852 | TKW26496 | EES18454 | Zm00001eb291920_P001 | 0.963 |
| PUZ48168 | Sspon.05G | KQK98230 | TKW05624 | EES11171 | Zm00001eb427300_P003 | 0.913 |
| PUZ46989 | Sspon.05G | KQK97093 | TKW04183 | EES12087 | Zm00001eb084510_P001 | 0.990 |
| PUZ63159 | Sspon.05G | KQK99483 | TKW07235 | KXG23105 | Zm00001eb408250_P004 | 0.902 |
| PUZ37565 | Sspon.01G | KQK87691 | TKV92004 | EER93657 | Zm00001eb053350_P003 | 0.968 |
| PUZ67283 | Sspon.02G | KQL16769 | TKW28987 | KXG23584 | Zm00001eb137800_P001 | 0.956 |
| PUZ67954 | Sspon.02G | KQL17222 | TKW29593 | KXG24034 | Zm00001eb134560_P001 | 0.938 |
| PUZ62616 | Sspon.08G | KQL08884 | TKW19147 | EER89027 | Zm00001eb379590_P001 | 0.897 |
| genblast_C | Sspon.05G | KQL12783 | TKW23893 | KXG27433 | Zm00001eb433740_P003 | 0.965 |
| PUZ58350 | Sspon.03G | genblast_C | TKW13814 | KXG31683 | Zm00001eb122180_P003 | 0.896 |
| PUZ78257 | Sspon.04G | KQL32126 | TKW42287 | EES06019 | Zm00001eb258980_P001 | 0.947 |
| PUZ54257 | Sspon.03G | KQL07454 | TKW17399 | EES01648 | genblast_Os01t0815800-01_Ze | |
| PUZ58005 | Sspon.03G | KQL04368 | TKW13397 | EES02495 | genblast_Os01t0144700-01_Ze | |

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| PUZ67315 | Sspon.02GKQL16729 | TKW28929 | EES17130 | Zm00001eb137740_P002 | 0.929 |
| PUZ67188 | Sspon.02GKQL16869 | TKW29133 | EES17047 | Zm00001eb409620_P002 | 0.896 |
| PUZ47699 | Sspon.04GKQK97777 | TKW05048 | EES11014 | Zm00001eb079310_P001 | 0.977 |

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| PUZ78168 | Sspon.04GKQL32037 | TKW42186 | genblast_C | Zm00001eb258470_P002 | 0.925 |
| PUZ52520 | Sspon.06GKQL02789 | TKW11555 | EES14142 | Zm00001eb037420_P005 | 0.911 |

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| PUZ76328 | Sspon.04GKQL30249 | TKW40014 | EES07068 | Zm00001eb245690_P002 | 0.980 |
| PUZ71532 | Sspon.02GKQL25306 | TKW34108 | EER97043 | Zm00001eb102740_P001 | 0.955 |
| PUZ36534 | genblast_CKQK86611 | genblast_C | OQU90818 | Zm00001eb061240_P001 | 0.963 |
| PUZ63975 | Sspon.07GKQL13298 | TKW24565 | KXG21275 | Zm00001eb417780_P001 | 0.940 |
| PUZ46860 | Sspon.05GKQK96976 | TKW04016 | EES10633 | Zm00001eb421150_P001 | 0.976 |
| PUZ71032 | Sspon.02GKQL24828 | TKW33532 | KXG35783 | Zm00001eb100950_P001 | 0.974 |
| PUZ77679 | Sspon.04GKQL31554 | TKW41646 | KXG30730 | Zm00001eb194170_P002 | 0.946 |
| PUZ54741 | Sspon.03GKQL07018 | TKW16821 | EES01490 | genblast_Os01t0754000-01_Zea | |
| PUZ50849 | Sspon.06GKQL01225 | TKW09546 | EES13637 | Zm00001eb177980_P001 | 0.966 |
| PUZ71761 | Sspon.02GKQL25515 | TKW34381 | OQU89843 | Zm00001eb103900_P001 | 0.983 |
| PUZ53814 | Sspon.02GKQL07865 | TKW17885 | OQU8791 | Zm00001eb146840_P001 | 0.956 |
| PUZ49420 | Sspon.05GKQL12980 | TKW24139 | EES13057 | Zm00001eb066900_P001 | 0.893 |
| PUZ72692 | Sspon.02GKQL26445 | TKW35555 | EER97452 | Zm00001eb325800_P001 | 0.966 |
| PUZ64195 | Sspon.07GKQK99327 | TKW07075 | EES19097 | Zm00001eb282210_P001 | 0.869 |
| PUZ58253 | Sspon.03GKQL04588 | TKW13672 | OQU86234 | Zm00001eb122970_P002 | 0.912 |

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| PUZ50040 | Sspon.06G | genblast_C | TKW09087 | EES13322 | Zm00001eb416900_P001 | 0.846 |
| PUZ55436 | genblast_Z | KQL06327 | TKW15956 | OQU87303 | Zm00001eb157300_P001 | 0.876 |
| PUZ41295 | Sspon.01GKQK91074 | TKV96356 | EER92335 | Zm00001eb015470_P001 | 0.983 |
| PUZ71744 | genblast_CKQL25501 | TKW34363 | EER99271 | Zm00001eb103820_P001 | 0.931 |
| PUZ77357 | Sspon.04GKQL31226 | TKW41248 | EES07363 | Zm00001eb252770_P001 | 0.941 |
| PUZ68612 | genblast_CKQL22643 | TKW30715 | KXG34512 | Zm00001eb301230_P001 | 0.944 |
| PUZ73923 | Sspon.04GKQL28880 | TKW38202 | KXG29381 | Zm00001eb231170_P001 | 0.814 |
| PUZ53455 | genblast_CKQL08174 | TKW18298 | EES04050 | Zm00001eb144430_P001 | 0.979 |
| PUZ49407 | Sspon.05GKQL12966 | TKW24124 | EES11616 | Zm00001eb433160_P001 | 0.889 |
| PUZ38570 | Sspon.03GKQK88654 | TKV93280 | genblast_C | Zm00001eb121820_P001 | 0.854 |
| PUZ57804 | Sspon.03GKQL04177 | TKW13171 | EES00405 | Zm00001eb125860_P002 | 0.957 |
| PUZ40183 | Sspon.01GKQK89972 | TKV94995 | EER91947 | Zm00001eb391400_P001 | 0.893 |
| PUZ37009 | Sspon.01GKQK87077 | TKV91329 | EER90868 | Zm00001eb057410_P001 | 0.975 |
| PUZ47714 | Sspon.05GKQK97787 | TKW05061 | EES11019 | Zm00001eb425170_P002 | 0.929 |

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| PUZ65447 | Sspon.07GKQL14930 | TKW26608 | EES19725 | Zm00001eb291310_P002 | 0.968 |
| PUZ41160 | Sspon.01GKQK90952 | TKV96190 | EER92294 | Zm00001eb016420_P001 | 0.981 |

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| PUZ42106 | Sspon.01G | KQK91874 | TKV97354 | OQU92973 | Zm00001eb399650_P001 | 0.872 |
| PUZ65590 | Sspon.07G | KQL15107 | TKW26819 | OQU78157 | Zm00001eb351740_P001 | 0.906 |
| PUZ48020 | Sspon.05G | KQK98097 | TKW05449 | EES11116 | Zm00001eb077670_P001 | 0.968 |
| PUZ73566 | Sspon.02G | KQL27286 | TKW36661 | KXG37024 | Zm00001eb331480_P001 | 0.874 |
| PUZ49851 | Sspon.06G | KQL00263 | TKW08171 | KXG24242 | Zm00001eb174030_P001 | 0.967 |
| PUZ41364 | Sspon.01G | KQK91154 | TKV96469 | OQU92698 | Zm00001eb015030_P005 | 0.986 |
| PUZ60568 | genblast_C | KQL10754 | TKW21600 | EER92161 | Zm00001eb019420_P002 | 0.960 |
| PUZ50830 | Sspon.06G | genblast_C | TKW09516 | EES14816 | Zm00001eb411880_P002 | 0.996 |
| PUZ44009 | Sspon.05G | KQK93912 | TKV99754 | OQU83042 | Zm00001eb201360_P003 | 0.896 |
| PUZ58281 | genblast_C | KQL13788 | TKW13720 | EES00218 | Zm00001eb122730_P001 | 0.853 |
| PUZ36124 | Sspon.01G | KQK86215 | TKV90232 | OQU90639 | genblast_Os03t0844000-01_Zea | |
| PUZ69200 | Sspon.02G | KQK90681 | TKW31444 | EER96202 | Zm00001eb304740_P001 | 0.910 |
| PUZ70823 | Sspon.02G | KQL24627 | TKW33306 | genblast_C | genblast_Os09t0437500-01_Zea | |
| PUZ77712 | Sspon.04G | KQL31588 | TKW41683 | OQU85385 | Zm00001eb193940_P001 | 0.944 |

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| PUZ77764 | Sspon.04G | KQL31632 | TKW41734 | EES05849 | Zm00001eb193700_P001 | 0.961 |
| PUZ59856 | Sspon.01G | genblast_C | TKW22251 | genblast_C | Zm00001eb387540_P001 | 0.953 |
| PUZ53249 | Sspon.03G | KQL08357 | TKW18535 | EES01976 | Zm00001eb364390_P001 | 0.928 |
| PUZ52567 | Sspon.02G | KQL02838 | TKW11619 | KXG35516 | Zm00001eb311320_P002 | 0.906 |
| PUZ47162 | Sspon.05G | KQK97277 | TKW04401 | KXG26320 | Zm00001eb082830_P001 | 0.966 |
| PUZ54761 | Sspon.03G | genblast_C | TKW16803 | KXG33379 | Zm00001eb153480_P001 | 0.978 |
| PUZ48083 | Sspon.05G | KQK98141 | TKW05512 | KXG26739 | Zm00001eb077030_P001 | 0.904 |
| PUZ42571 | genblast_C | KQK92315 | TKV97898 | EER92755 | Zm00001eb005850_P001 | 0.961 |
| PUZ70905 | Sspon.02G | KQL24712 | TKW33402 | EER98987 | Zm00001eb314330_P001 | 0.977 |
| PUZ62442 | Sspon.08G | KQL09054 | TKW19344 | OQU84087 | Zm00001eb269230_P001 | 0.865 |
| PUZ40283 | Sspon.01G | KQK90087 | TKV95124 | EER94552 | Zm00001eb022730_P001 | 0.900 |
| PUZ63073 | genblast_Z | KQK99574 | TKW07418 | EES16701 | Zm00001eb139410_P004 | 0.967 |
| PUZ64608 | Sspon.07G | KQL14156 | TKW25679 | KXG22611 | Zm00001eb344620_P001 | 0.947 |
| PUZ40369 | Sspon.01G | KQK90169 | TKV95220 | EER92018 | Zm00001eb021970_P001 | 0.848 |
| PUZ38557 | Sspon.01G | KQK88646 | TKV93267 | OQU91613 | Zm00001eb221360_P003 | 0.927 |
| PUZ72522 | Sspon.02G | KQL26278 | TKW35370 | EER99559 | Zm00001eb324540_P001 | 0.982 |
| PUZ46426 | Sspon.02G | genblast_C | TKW03511 | OQU89677 | Zm00001eb420200_P002 | 0.935 |

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| PUZ78300 | Sspon.04G | KQL32162 | TKW42323 | OQU85974 | Zm00001eb191130_P001 | 0.920 |
| PUZ63079 | Sspon.05G | KQK99569 | TKW07409 | EES16704 | Zm00001eb407590_P001 | 0.951 |
| PUZ52843 | Sspon.01G | KQL08768 | TKW19048 | EER94663 | Zm00001eb393470_P001 | 0.939 |
| PUZ57912 | Sspon.03G | KQL04278 | TKW13291 | EES02539 | Zm00001eb125120_P003 | 0.927 |

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| PUZ74878 | Sspon.04G | KQL27922 | TKW37020 | EES06576 | Zm00001eb238620_P004 | 0.967 |
| PUZ51024 | genblast_C | KQL01326 | TKW09682 | OQU87621 | Zm00001eb151970_P001 | 0.919 |
| PUZ61337 | Sspon.02G | KQL25192 | TKW33983 | KXG31640 | Zm00001eb102310_P001 | 0.934 |
| PUZ59736 | Sspon.08G | KQL11170 | TKW22077 | EES14013 | Zm00001eb038160_P004 | 0.933 |
| PUZ48698 | Sspon.05G | KQK98713 | TKW06278 | EES12769 | Zm00001eb072190_P002 | 0.940 |
| PUZ67662 | Sspon.02G | KQL16986 | TKW29311 | EES16256 | Zm00001eb134970_P001 | 0.966 |
| PUZ73633 | Sspon.04G | KQL27711 | TKW36745 | EES06100 | Zm00001eb229350_P001 | 0.935 |
| PUZ37447 | genblast_C | KQK87550 | TKV91856 | KXG37770 | Zm00001eb054190_P005 | 0.982 |
| PUZ52572 | Sspon.02G | KQL02841 | TKW11626 | KXG25440 | Zm00001eb202660_P001 | 0.922 |
| PUZ37282 | Sspon.05G | KQK87371 | TKV91658 | EER93546 | Zm00001eb215910_P003 | 0.944 |
| PUZ66847 | genblast_C | KQK85602 | TKW28122 | EES12764 | Zm00001eb429950_P001 | 0.960 |
| PUZ61031 | Sspon.08G | KQL10365 | TKW21047 | EER88270 | Zm00001eb380950_P002 | 0.972 |
| PUZ72533 | Sspon.02G | genblast_C | TKW35377 | EER97384 | Zm00001eb324590_P001 | 0.959 |
| PUZ65191 | Sspon.07G | genblast_C | TKW26358 | KXG22343 | Zm00001eb292830_P002 | 0.921 |
| PUZ59252 | Sspon.08G | KQL11771 | TKW22856 | KXG20766 | Zm00001eb226830_P001 | 0.828 |
| PUZ49222 | Sspon.05G | genblast_C | TKW06960 | KXG27266 | Zm00001eb068440_P001 | 0.934 |
| PUZ54184 | genblast_C | KQL07525 | TKW17484 | EES03814 | Zm00001eb368700_P002 | 0.917 |
| PUZ43832 | Sspon.05G | KQK93723 | TKV99452 | EES09328 | Zm00001eb202470_P001 | 0.938 |
| PUZ56238 | Sspon.03G | KQL05530 | TKW14935 | EES00907 | Zm00001eb162330_P002 | 0.954 |
| PUZ53464 | Sspon.03G | genblast_Z | TKW18285 | OQU88047 | Zm00001eb144480_P001 | 0.949 |
| genblast_C | Sspon.08G | KQL13905 | TKW25382 | EER89168 | Zm00001eb270290_P001 | 0.888 |
| PUZ78076 | Sspon.04G | KQL31944 | TKW42067 | EES05963 | Zm00001eb257970_P002 | 0.973 |
| PUZ43176 | Sspon.01G | KQK92952 | TKV98599 | OQU9338 | Zm00001eb001130_P002 | 0.898 |
| PUZ73995 | Sspon.04G | KQL28810 | TKW38101 | EES04485 | Zm00001eb231840_P004 | 0.936 |
| PUZ72011 | Sspon.02G | KQL25757 | TKW34704 | EER97205 | Zm00001eb319960_P004 | 0.971 |
| PUZ77768 | Sspon.08G | KQL31636 | TKW41736 | EES05850 | Zm00001eb193690_P001 | 0.935 |

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| PUZ42606 | Sspon.01G | KQK92357 | TKV97956 | EER95418 | Zm00001eb402160_P001 | 0.964 |
| PUZ63350 | genblast_C | KQL13669 | TKW25079 | EES15886 | Zm00001eb411630_P001 | 0.875 |

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| PUZ50057 | Sspon.06G | KQL00869 | TKW09053 | EES14521 | Zm00001eb416700_P001 | 0.992 |
| PUZ65936 | Sspon.07G | KQL15430 | TKW27214 | EES18248 | Zm00001eb349200_P002 | 0.907 |
| PUZ70924 | Sspon.02G | KQL24731 | TKW32158 | OQU89596 | Zm00001eb314510_P002 | 0.827 |
| genblast_C | Sspon.02G | KQL26285 | TKW35379 | OQU90112 | Zm00001eb107160_P001 | 0.981 |

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| PUZ52861 | genblast_C | KQL08755 | TKW19028 | EES19096 | Zm00001eb282230_P001 | 0.957 |
| PUZ55184 | Sspon.02G | KQL06589 | TKW16260 | KXG23846 | Zm00001eb135130_P001 | 0.902 |
| PUZ48297 | Sspon.05G | KQK98336 | TKW05786 | EES11215 | Zm00001eb074890_P002 | 0.974 |

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| PUZ54052 | Sspon.03G | KQL07648 | TKW17626 | EES03854 | Zm00001eb368040_P001 | 0.771 |
| PUZ42905 | Sspon.01G | genblast_C | TKV98274 | OQU93256 | Zm00001eb003460_P002 | 0.945 |
| PUZ44027 | Sspon.05G | KQK93926 | TKV99770 | KXG27975 | Zm00001eb201440_P001 | 0.971 |
| PUZ46857 | Sspon.06G | KQK96973 | TKW04013 | EES13584 | Zm00001eb414570_P003 | 0.939 |
| PUZ48571 | genblast_C | KQK98574 | TKW06122 | EES11308 | Zm00001eb073200_P001 | 0.975 |
| PUZ71444 | Sspon.02G | KQL25213 | TKW34008 | genblast_C | Zm00001eb102430_P003 | 0.915 |
| PUZ47078 | Sspon.05G | KQK97209 | TKW04312 | KXG26268 | Zm00001eb083670_P001 | 0.966 |
| PUZ59001 | genblast_C | KQL12313 | TKW23559 | OQU77165 | Zm00001eb228610_P001 | 0.921 |
| PUZ74302 | Sspon.04G | KQL28515 | TKW37743 | EES04611 | Zm00001eb206980_P001 | 0.970 |
| PUZ52056 | Sspon.06G | KQL02349 | TKW11002 | EES14304 | Zm00001eb199520_P001 | 0.958 |
| PUZ78335 | Sspon.04G | KQL32194 | TKW42365 | EES06044 | Zm00001eb190880_P001 | 0.960 |

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| PUZ72369 | Sspon.02G | KQL26125 | TKW35149 | EER99495 | Zm00001eb323440_P004 | 0.945 |
| PUZ44972 | genblast_C | KQK94712 | TKW00870 | KXG28467 | Zm00001eb170190_P001 | 0.984 |
| PUZ58376 | Sspon.03G | KQL04711 | TKW13844 | EES02345 | genblast_Os01t0183500-01_Ze | |
| PUZ53763 | genblast_Z | KQL07910 | TKW17935 | OQU87945 | Zm00001eb146450_P003 | 0.911 |

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| PUZ56928 | genblast_C | KQL05001 | TKW14220 | KXG32417 | Zm00001eb130860_P001 | 0.979 |
| PUZ41919 | Sspon.01G | KQK91678 | TKV97082 | EER95173 | Zm00001eb010690_P002 | 0.940 |

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| PUZ72092 | genblast_C | KQL25829 | TKW34801 | KXG36244 | Zm00001eb321680_P001 | 0.948 |
| PUZ57285 | Sspon.03G | KQL30526 | TKW40371 | EES02752 | Zm00001eb184900_P001 | 0.839 |
| PUZ49901 | Sspon.06G | KQL01031 | TKW09279 | KXG24282 | Zm00001eb173660_P001 | 0.885 |

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| PUZ64853 | Sspon.07G | KQL14390 | TKW25953 | OQU78406 | Zm00001eb295400_P001 | 0.939 |
| PUZ65938 | Sspon.07G | KQL15433 | TKW27217 | OQU78023 | Zm00001eb349170_P001 | 0.899 |

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| PUZ52217 | genblast_C | KQL02470 | TKW11161 | KXG25620 | Zm00001eb035370_P002 | 0.939 |
| PUZ61084 | Sspon.08G | KQL10410 | TKW21107 | OQU76291 | Zm00001eb381210_P001 | 0.946 |
| PUZ46749 | Sspon.05G | KQK96869 | TKW03874 | EES10576 | Zm00001eb086040_P002 | 0.986 |
| PUZ59154 | Sspon.08G | KQL12168 | TKW23370 | OQU77076 | Zm00001eb227640_P001 | 0.979 |
| PUZ77770 | Sspon.04G | KQL31641 | TKW41739 | KXG31166 | Zm00001eb255830_P001 | 0.929 |
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| PUZ52044 | genblast_C | KQL02339 | TKW10990 | EES15442 | Zm00001eb033960_P001 | 0.950 |
| PUZ75511 | genblast_C | KQL29663 | TKW39199 | KXG30212 | Zm00001eb202940_P001 | 0.983 |
| PUZ41542 | Sspon.01G | KQK91329 | TKV96697 | KXG39609 | Zm00001eb397070_P001 | 0.984 |
| PUZ48830 | Sspon.05G | KQK98836 | TKW06455 | EES11396 | Zm00001eb430610_P001 | 0.942 |
| PUZ73993 | Sspon.04G | KQL28811 | TKW38102 | EES04484 | Zm00001eb231830_P002 | 0.979 |
| PUZ71825 | Sspon.02G | KQL25590 | TKW34464 | EER99305 | Zm00001eb320970_P001 | 0.948 |
| PUZ59918 | Sspon.08G | KQL11400 | TKW22372 | EER88661 | genblast_Os06t0618300-01_Zea | |
| PUZ59885 | Sspon.08G | KQL11356 | TKW22300 | OQU76729 | Zm00001eb387830_P001 | 0.953 |
| PUZ42216 | Sspon.01G | KQK91988 | TKV97475 | genblast_C | genblast_Os03t0212600-01_Zea | |
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| PUZ67768 | Sspon.01G | KQL17064 | TKW29426 | EES17321 | Zm00001eb135400_P002 | 0.941 |
| PUZ36204 | Sspon.01G | genblast_C | TKV90388 | OQU90674 | Zm00001eb211170_P001 | 0.852 |
| PUZ71047 | Sspon.02G | KQL24846 | TKW33553 | KXG35796 | Zm00001eb101010_P002 | 0.883 |
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| PUZ72190 | Sspon.02G | KQL25943 | TKW34914 | KXG36290 | Zm00001eb322380_P004 | 0.956 |
| PUZ72727 | Sspon.02G | KQL26475 | TKW35586 | EER97464 | Zm00001eb326060_P001 | 0.999 |
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| PUZ71731 | Sspon.02G | KQL25488 | TKW34347 | EER97101 | Zm00001eb103750_P001 | 0.963 |
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| PUZ46893 | Sspon.05G | KQK97010 | TKW04062 | EES12044 | Zm00001eb085100_P001 | 0.917 |

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| PUZ55392 | Sspon.03G | KQL06382 | TKW16005 | EES01242 | Zm00001eb360170_P001 | 0.922 |
| PUZ69515 | Sspon.02G | KQL23501 | TKW31801 | EER96324 | Zm00001eb306530_P002 | 0.981 |
| PUZ39943 | Sspon.01G | KQK89765 | TKV94738 | KXG38835 | Zm00001eb224850_P001 | 0.954 |

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| PUZ48550 | Sspon.05G | KQK98545 | TKW06086 | OQU82187 | Zm00001eb073440_P001 | 0.955 |
| PUZ74080 | Sspon.04G | KQL28720 | TKW37976 | KXG29487 | Zm00001eb207960_P002 | 0.786 |
| PUZ76119 | Sspon.04G | KQL30040 | TKW39791 | EES05250 | Zm00001eb243920_P001 | 0.904 |

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| PUZ44726 | genblast_C | genblast_C | TKW00560 | EES09695 | Zm00001eb112700_P001 | 0.960 |
| PUZ74144 | Sspon.08G | KQL28658 | TKW37901 | OQU84413 | Zm00001eb232590_P001 | 0.960 |
| PUZ46445 | genblast_C | KQK96620 | TKW03539 | KXG23193 | Zm00001eb086220_P001 | 0.950 |
| PUZ37701 | Sspon.01G | KQK87845 | TKV92189 | EER91125 | Zm00001eb052640_P001 | 0.983 |
| PUZ36872 | genblast_C | KQK86934 | TKV91158 | EER90826 | Zm00001eb213980_P001 | 0.919 |

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| PUZ76588 | Sspon.04G | KQL30521 | TKW40367 | EES05438 | Zm00001eb184870_P002 | 0.951 |
| PUZ41936 | genblast_Z | KQK91694 | TKV97106 | EER90701 | Zm00001eb061430_P002 | 0.947 |
| PUZ45488 | Sspon.06G | KQK95353 | TKW01733 | EES10100 | Zm00001eb166990_P002 | 0.936 |
| PUZ71622 | Sspon.02G | KQL25401 | TKW34228 | OQU89800 | Zm00001eb319060_P001 | 0.972 |
| PUZ78130 | Sspon.01G | KQL31992 | TKW42136 | EER95457 | Zm00001eb004770_P001 | 0.948 |
| PUZ56024 | genblast_Z | KQL05675 | TKW15132 | EES00986 | Zm00001eb160790_P001 | 0.963 |
| PUZ61820 | Sspon.08G | KQL09377 | TKW19725 | EER89373 | Zm00001eb278480_P003 | 0.980 |
| PUZ55054 | genblast_C | KQL06709 | TKW16418 | EES03526 | genblast_Os01t0715800-01Zm0 | |
| PUZ71546 | Sspon.02G | KQL25325 | TKW34142 | EER99187 | Zm00001eb318630_P002 | 0.964 |
| genblast_C | Sspon.01G | KQK87922 | TKV92284 | KXG37936 | Zm00001eb218590_P001 | 0.977 |
| PUZ70939 | Sspon.02G | KQL24739 | TKW33436 | EER96829 | genblast_Os09t0450200-01Zm0 | |

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| PUZ39821 | Sspon.01G | KQK89661 | TKV94603 | KXG19248 | Zm00001eb025730_P001 | 0.939 |

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| PUZ76747 | Sspon.04G | KQL30661 | TKW40545 | EES05486 | Zm00001eb185700_P004 | 0.960 |

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| PUZ41908 | Sspon.01G | KQK91670 | TKV97069 | KXG39762 | Zm00001eb010770_P002 | 0.955 |
| PUZ78233 | Sspon.04G | KQL32090 | TKW42244 | EES06009 | Zm00001eb258850_P002 | 0.901 |
| PUZ58897 | genblast_C | KQL03178 | TKW1190 | EER99984 | Zm00001eb118850_P005 | 0.936 |
| PUZ75137 | Sspon.04G | KQL29214 | TKW38617 | EES06683 | Zm00001eb237200_P001 | 0.970 |
| genblast_C | Sspon.06G | KQL02760 | TKW1153 | EES15262 | Zm00001eb037330_P002 | 0.976 |
| PUZ68384 | Sspon.05G | KQK93749 | TKV99488 | EES18766 | Zm00001eb297610_P003 | 0.968 |
| PUZ73389 | genblast_C | KQL27099 | TKW36437 | OQU90457 | Zm00001eb111230_P001 | 0.928 |

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| PUZ63641 | Sspon.07G | KQL13403 | TKW24723 | EES18868 | Zm00001eb355990_P001 | 0.937 |
| PUZ48147 | Sspon.05G | KQK98207 | TKW05597 | EER95620 | Zm00001eb001470_P001 | 0.945 |

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| PUZ69818 | Sspon.02G | KQL23781 | TKW32182 | KXG35204 | Zm00001eb095560_P002 | 0.933 |
| PUZ78185 | Sspon.04G | KQL32053 | TKW42205 | genblast_C | Zm00001eb258590_P001 | 0.911 |

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| PUZ37659 | Sspon.01G | KQK87813 | TKV92148 | EER91108 | Zm00001eb065420_P002 | 0.920 |

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| PUZ49261 | Sspon.05G | KQL12855 | TKW23979 | OQU82472 | Zm00001eb067900_P001 | 0.955 |
| PUZ63270 | Sspon.07G | genblast_C | TKW25184 | EES15823 | Zm00001eb411120_P001 | 0.917 |
| PUZ58322 | Sspon.03G | KQL04665 | TKW13778 | EES02364 | Zm00001eb336920_P003 | 0.956 |
| PUZ41570 | genblast_C | KQK91357 | TKV96720 | EER95048 | Zm00001eb013130_P001 | 0.878 |
| PUZ58327 | Sspon.03G | KQL04671 | TKW13784 | KXG31704 | Zm00001eb122400_P001 | 0.953 |
| PUZ37502 | Sspon.01G | KQK87608 | TKV91921 | EER91047 | Zm00001eb053760_P001 | 0.989 |
| PUZ48635 | Sspon.05G | KQK98649 | TKW06198 | EES12745 | Zm00001eb072650_P001 | 0.945 |
| PUZ77829 | Sspon.04G | KQL31691 | TKW41789 | EES07597 | Zm00001eb193500_P001 | 0.962 |

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| PUZ66791 | Sspon.01G | KQL16090 | TKW28073 | KXG39981 | Zm00001eb007030_P002 | 0.916 |

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| PUZ72124 | Sspon.02G | KQL25858 | TKW34832 | KXG36264 | genblast_Os07t0497100-01Zm0 |
| PUZ71612 | Sspon.06G | KQL25392 | TKW34220 | KXG36034 | Zm00001eb318990_P002 | 0.956 |
| PUZ69651 | Sspon.02G | KQL23634 | TKW31984 | KXG35136 | Zm00001eb095880_P002 | 0.901 |
| PUZ41153 | Sspon.01G | KQK90949 | TKV96188 | EER94878 | Zm00001eb016440_P001 | 0.944 |
| PUZ45821 | Sspon.06G | KQK95831 | TKW02434 | EES08969 | Zm00001eb115970_P001 | 0.912 |
| PUZ55723 | Sspon.05G | KQL05977 | TKW15506 | EES01111 | Zm00001eb358750_P003 | 0.948 |
| PUZ54119 | Sspon.03G | KQL07582 | TKW17553 | EES03838 | Zm00001eb368330_P001 | 0.959 |
| PUZ46715 | genblast_Z | KQK96827 | TKW03792 | KXG19925 | Zm00001eb420510_P001 | 0.950 |
| PUZ40524 | genblast_C | KQK90315 | TKV95411 | EER87817 | Zm00001eb377380_P001 | 0.954 |
| PUZ68261 | genblast_C | KQL22245 | TKW30162 | EER97885 | Zm00001eb117980_P001 | 0.918 |
| PUZ36682 | genblast_C | KQK86772 | TKV90950 | EER90769 | Zm00001eb060040_P001 | 0.911 |
| PUZ67860 | Sspon.02G | KQL17165 | TKW29524 | EES16340 | Zm00001eb031520_P001 | 0.976 |

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| PUZ70209 | Sspon.03G | KQL07114 | TKW16955 | KXG33442 | Zm00001eb152210_P002 | 0.931 |

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| PUZ40849 | Sspon.01G | KQK90595 | TKV95794 | EER92185 | Zm00001eb018900_P001 | 0.920 |
| PUZ36800 | genblast_C | KQK86871 | TKV91064 | EER93368 | Zm00001eb059220_P001 | 0.996 |
| PUZ39884 | genblast_C | genblast_C | TKV94671 | EER94415 | Zm00001eb025350_P001 | 0.910 |
| PUZ53545 | Sspon.03G | KQL08108 | TKW18213 | KXG33884 | Zm00001eb144880_P001 | 0.912 |
| PUZ52080 | Sspon.06G | KQL02375 | TKW11034 | EES15426 | Zm00001eb034180_P001 | 0.909 |

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| PUZ72491 | Sspon.02G | KQL26249 | TKW35305 | KXG36480 | Zm00001eb324300_P002 | 0.945 |
| PUZ53753 | Sspon.03G | KQL07919 | TKW17942 | EES01830 | Zm00001eb146390_P001 | 0.962 |
| PUZ50894 | Sspon.06G | KQL01309 | TKW09665 | EES00977 | Zm00001eb028210_P001 | 0.941 |
| PUZ47471 | Sspon.05G | KQK97555 | TKW04777 | OQU84779 | Zm00001eb424010_P002 | 0.913 |

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| PUZ55072 | Sspon.03G | KQL06699 | TKW16389 | KXG33244 | Zm00001eb154960_P001 | 0.866 |
| PUZ42003 | Sspon.01G | KQK91769 | TKV97212 | EER92583 | Zm00001eb010070_P001 | 0.972 |
| PUZ73164 | Sspon.02G | KQL26912 | TKW36156 | EER97634 | Zm00001eb329080_P001 | 0.964 |
| PUZ69805 | genblast_Z | KQL23732 | TKW32120 | EER98568 | Zm00001eb307130_P001 | 0.959 |
| PUZ37003 | Sspon.01G | KQK87073 | TKV91324 | KXG37543 | Zm00001eb057430_P001 | 0.968 |
| PUZ64201 | Sspon.07G | KQK99337 | TKW07081 | KXG21405 | Zm00001eb282100_P003 | 0.895 |
| PUZ37223 | genblast_C | KQK87315 | TKV91589 | EER93527 | Zm00001eb215650_P003 | 0.960 |

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| PUZ40070 | Sspon.01G | KQK89880 | TKV94874 | EER94472 | Zm00001eb391060_P001 | 0.938 |
| genblast_C | genblast_C | KQK90761 | TKV95939 | EER92221 | Zm00001eb394240_P001 | 0.941 |
| PUZ43322 | genblast_C | KQK93105 | TKV98778 | EER95707 | Zm00001eb000190_P001 | 0.955 |
| PUZ68735 | Sspon.02G | KQL22765 | TKW30855 | EER95978 | Zm00001eb226700_P001 | 0.823 |
| PUZ75833 | genblast_C | KQL29802 | TKW39380 | EES06872 | Zm00001eb180810_P001 | 0.914 |

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| PUZ54719 | Sspon.03G | KQL07047 | TKW16854 | EES01498 | Zm00001eb152710_P001 | 0.981 |
| PUZ42229 | Sspon.01G | KQK92002 | TKV97495 | EER95295 | Zm00001eb008430_P001 | 0.956 |
| PUZ78054 | Sspon.04G | KQL31922 | TKW42047 | EES07683 | Zm00001eb192360_P001 | 0.922 |
| PUZ43653 | Sspon.07G | KQK99837 | TKW07739 | KXG22822 | Zm00001eb405110_P001 | 0.789 |
| PUZ68449 | Sspon.02G | KQL22490 | TKW30504 | genblast_C | Zm00001eb300310_P005 | 0.891 |

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| PUZ43247 | Sspon.01G | KQK93024 | TKV98691 | EER95670 | Zm00001eb404280_P001 | 0.978 |
| PUZ46143 | Sspon.05G | KQK96278 | TKW03059 | EES11779 | Zm00001eb088960_P001 | 0.930 |
| PUZ41250 | Sspon.01G | KQK91041 | TKV96311 | EER92321 | Zm00001eb015760_P002 | 0.944 |
| PUZ61065 | Sspon.02G | KQL10395 | TKW21096 | EER98049 | Zm00001eb301150_P004 | 0.807 |
| PUZ63266 | Sspon.07G | KQK99353 | TKW07100 | EES15821 | Zm00001eb411070_P002 | 0.888 |
| PUZ54817 | Sspon.06G | KQL06961 | TKW16739 | EES14980 | Zm00001eb042350_P001 | 0.959 |

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| PUZ64500 | Sspon.07G | KQL14038 | TKW25540 | EES20049 | Zm00001eb297410_P001 | 0.905 |

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| PUZ61422 | Sspon.04G | KQL31516 | TKW41589 | KXG30755 | Zm00001eb254940_P001 | 0.951 |

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| PUZ54329 | Sspon.03G | KQL07380 | TKW17299 | KXG33573 | Zm00001eb150470_P002 | 0.942 |

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| PUZ44729 | genblast_C | KQK94491 | TKW00557 | OQU83379 | Zm00001eb169360_P001 | 0.970 |
| PUZ48946 | Sspon.05G | KQK98965 | TKW06627 | EES12876 | Zm00001eb070450_P001 | 0.954 |
| PUZ68151 | Sspon.02G | KQK85903 | TKW29952 | EER97821 | Zm00001eb298140_P001 | 0.868 |
| PUZ49979 | Sspon.06G | genblast_C | TKW09195 | KXG24329 | Zm00001eb261680_P001 | 0.941 |
| PUZ58868 | Sspon.03G | KQL03207 | TKW11935 | EES02175 | Zm00001eb339370_P005 | 0.908 |

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| PUZ39858 | Sspon.01G | KQK89693 | TKV94643 | EER91848 | Zm00001eb025550_P001 | 0.966 |
| PUZ48327 | Sspon.05G | KQK98369 | TKW05838 | OQU82096 | Zm00001eb429690_P001 | 0.826 |

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| PUZ38549 | Sspon.01G | KQK88633 | TKV93254 | OQU91611 | Zm00001eb045380_P001 | 0.932 |
| PUZ51418 | Sspon.02G | KQL24319 | TKW10252 | EES14978 | Zm00001eb311500_P001 | 0.930 |
| PUZ40317 | Sspon.01G | KQK90111 | TKV95153 | KXG38989 | Zm00001eb022570_P001 | 0.955 |

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| PUZ52705 | Sspon.06G | genblast_C | TKW11782 | genblast_C | genblast_Os08t0559900-01_Ze | |
| PUZ60117 | Sspon.08G | KQK85356 | TKW22618 | OQU7664 | Zm00001eb386120_P001 | 0.916 |
| PUZ44882 | Sspon.06G | KQK94607 | TKW00702 | genblast_C | Zm00001eb112820_P001 | 0.953 |
| PUZ52680 | Sspon.06G | KQL02911 | TKW11693 | OQU8071 | Zm00001eb176110_P003 | 0.954 |
| genblast_C | genblast_C | KQL06599 | TKW16271 | OQU8739 | Zm00001eb155600_P002 | 0.938 |

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| PUZ71276 | genblast_C | KQL25058 | TKW33818 | KXG35912 | Zm00001eb316720_P002 | 0.956 |
| PUZ37772 | Sspon.01G | KQK87909 | TKV92268 | KXG37933 | Zm00001eb053010_P001 | 0.943 |
| PUZ51276 | Sspon.06G | KQL01591 | TKW10021 | OQU8035 | Zm00001eb042610_P003 | 0.960 |
| PUZ73985 | Sspon.04G | KQL28818 | TKW38112 | KXG29427 | Zm00001eb231790_P002 | 0.968 |
| PUZ38652 | Sspon.01G | KQK88756 | TKV93423 | KXG38354 | Zm00001eb046100_P001 | 0.978 |
| PUZ72181 | genblast_C | KQL25931 | TKW34906 | OQU8999 | Zm00001eb322350_P003 | 0.912 |
| PUZ47654 | Sspon.05G | KQK97742 | TKW05031 | EES12375 | Zm00001eb079490_P001 | 0.964 |

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| PUZ61656 | Sspon.08G | KQL10228 | TKW20855 | EER88191 | Zm00001eb280600_P002 | 0.891 |

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| PUZ45893 | Sspon.06G | KQK95998 | TKW0275 | EES10308 | Zm00001eb091470_P001 | 0.918 |
| PUZ59961 | Sspon.08G | KQL11443 | TKW22422 | EER88643 | Zm00001eb275910_P001 | 0.961 |
| PUZ47023 | Sspon.05G | KQK97142 | TKW04234 | EES12098 | Zm00001eb421850_P002 | 0.986 |
| PUZ60507 | Sspon.08G | genblast_C | TKW21617 | OQU7645 | Zm00001eb382730_P003 | 0.924 |
| PUZ65555 | Sspon.03G | KQL15059 | TKW26768 | EES19684 | Zm00001eb351930_P001 | 0.984 |
| PUZ66834 | Sspon.07G | genblast_C | TKV92335 | OQU9216 | Zm00001eb284530_P001 | 0.916 |
| PUZ70426 | Sspon.02G | KQL24225 | TKW32792 | EER98782 | genblast_Os09t0349100-00_Ze | |
| PUZ40894 | Sspon.01G | KQK90649 | TKV95844 | EER92199 | Zm00001eb018480_P003 | 0.981 |
| PUZ49735 | genblast_C | KQL00153 | TKW0803 | EES14353 | Zm00001eb259950_P001 | 0.968 |
| PUZ67892 | Sspon.02G | KQL17307 | TKW29705 | EES17384 | Zm00001eb031650_P001 | 0.992 |
| PUZ61547 | Sspon.08G | KQL10115 | TKW20702 | EER88150 | Zm00001eb280010_P002 | 0.971 |

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| PUZ77500 | Sspon.04G | KQL31455 | TKW41515 | OQU8543 | genblast_Os02t0740700-01_Ze | |

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| PUZ67672 | Sspon.02G | KQL16992 | TKW29321 | EES17295 | Zm00001eb135000_P001 | 0.940 |
| PUZ40648 | genblast_C | KQK90397 | TKV95514 | EER92119 | Zm00001eb020130_P001 | 0.982 |

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| PUZ35984 | Sspon.01G | KQK86083 | TKV90063 | KXG37081 | Zm00001eb210430_P001 | 0.893 |
| PUZ40093 | Sspon.01G | KQK89906 | TKV94906 | EER94483 | Zm00001eb391070_P001 | 0.957 |
| PUZ48657 | Sspon.05G | KQK98674 | TKW06232 | EES11341 | Zm00001eb428320_P001 | 0.951 |
| PUZ77457 | Sspon.08G | KQL31496 | TKW41569 | EES07260 | Zm00001eb194520_P001 | 0.991 |
| PUZ67189 | genblast_C | KQL16867 | TKW29132 | EES17048 | Zm00001eb409580_P001 | 0.944 |
| PUZ50839 | Sspon.06G | KQL01213 | TKW09534 | EES13631 | Zm00001eb177920_P001 | 0.963 |
| PUZ71988 | Sspon.02G | KQL25739 | TKW34676 | EER97197 | Zm00001eb320090_P001 | 0.950 |
| PUZ41598 | genblast_C | KQK91390 | TKV96753 | EER92437 | genblast_Os03t0283500-01_Ze |  |

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| PUZ36755 | Sspon.01G | KQK86820 | TKV91018 | EER90692 | Zm00001eb212530_P001 | 0.978 |
| PUZ41669 | Sspon.03G | KQK91458 | TKV96834 | KXG39673 | Zm00001eb012540_P001 | 0.987 |

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| PUZ52103 | genblast_C | KQL02388 | TKW11049 | genblast_C | Zm00001eb199620_P001 | 0.866 |
| PUZ54333 | genblast_C | KQL07378 | TKW17297 | KXG33570 | Zm00001eb150530_P002 | 0.956 |
| PUZ65133 | Sspon.03G | KQL14695 | TKW26301 | EES18524 | Zm00001eb293740_P001 | 0.901 |
| PUZ78193 | Sspon.04G | KQL32056 | TKW42207 | KXG31336 | Zm00001eb258610_P001 | 0.983 |

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| PUZ53937 | genblast_C | KQL07758 | TKW17752 | EES01764 | Zm00001eb147840_P001 | 0.955 |
| PUZ67717 | Sspon.02G | genblast_C | TKW29367 | EES16277 | Zm00001eb135280_P001 | 0.883 |
| PUZ46695 | genblast_C | KQK96810 | TKW03778 | KXG25952 | Zm00001eb420500_P003 | 0.973 |
| PUZ54425 | Sspon.03G | KQL07282 | TKW17172 | EES01583 | Zm00001eb151170_P001 | 0.971 |
| PUZ36240 | Sspon.01G | KQK86314 | TKV90355 | EER90581 | Zm00001eb063450_P001 | 0.951 |
| PUZ75214 | Sspon.04G | KQL29278 | TKW38679 | KXG30072 | Zm00001eb237040_P001 | 0.922 |

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| genblast_C | Sspon.05G | KQL05819 | TKW15307 | EES07890 | Zm00001eb195380_P004 | 0.917 |

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| PUZ40433 | Sspon.01G | KQK90222 | TKV95288 | EER94621 | Zm00001eb021500_P001 | 0.977 |
| PUZ44474 | Sspon.01G | KQL02835 | TKW11615 | EER90542 | Zm00001eb064030_P002 | 0.970 |

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| PUZ47734 | Sspon.05G | KQK97807 | TKW05086 | EES12415 | Zm00001eb079010_P001 | 0.928 |
| PUZ43182 | Sspon.01G | KQK92960 | TKV98608 | EER95643 | genblast_Os03t0116300-01Zm0 | |
| PUZ76108 | Sspon.04G | KQL30029 | TKW39727 | EER98543 | Zm00001eb243870_P001 | 0.961 |
| PUZ73188 | Sspon.02G | KQL26928 | TKW36172 | EER97639 | Zm00001eb329220_P001 | 0.979 |
| PUZ55891 | Sspon.03G | KQL05803 | TKW15283 | EES03251 | Zm00001eb161710_P002 | 0.949 |
| PUZ40129 | Sspon.01G | KQK89939 | TKV94955 | EER91932 | Zm00001eb023250_P002 | 0.883 |
| PUZ59167 | Sspon.08G | KQL12155 | TKW23358 | KXG20824 | Zm00001eb272640_P003 | 0.915 |
| PUZ48463 | Sspon.05G | KQK98471 | TKW05976 | KXG26904 | Zm00001eb429120_P003 | 0.983 |
| PUZ61873 | Sspon.08G | KQL09441 | TKW19815 | KXG19496 | Zm00001eb374460_P001 | 0.959 |
| PUZ36154 | Sspon.01G | KQK86254 | TKV90279 | OQU90655 | Zm00001eb211020_P001 | 0.871 |
| PUZ68742 | Sspon.02G | KQL22775 | TKW30862 | EER95980 | Zm00001eb302210_P001 | 0.883 |
| PUZ71128 | genblast_Z | KQL24912 | TKW33631 | OQU89648 | Zm00001eb315840_P001 | 0.916 |

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| PUZ56120 | Sspon.03G | KQL06257 | TKW15872 | OQU87044 | Zm00001eb357070_P001 | 0.958 |
| PUZ68540 | Sspon.02G | KQL16812 | TKW30618 | EER95911 | Zm00001eb264660_P001 | 0.921 |
| PUZ37911 | Sspon.01G | KQK88032 | TKV92427 | genblast_C | Zm00001eb218890_P001 | 0.942 |
| PUZ38226 | Sspon.01G | KQK88315 | TKV92844 | EER93922 | Zm00001eb043240_P003 | 0.949 |
| PUZ40953 | Sspon.01G | genblast_C | TKV95913 | EER94799 | genblast_Os03t0370400-01_Ze | |
| PUZ57010 | Sspon.03G | KQL03439 | TKW12212 | EES00648 | Zm00001eb339890_P001 | 0.975 |
| PUZ49343 | Sspon.05G | KQL12917 | TKW24060 | KXG27351 | Zm00001eb067370_P001 | 0.932 |
| PUZ64986 | Sspon.07G | KQL14540 | TKW26132 | EES18592 | Zm00001eb342360_P001 | 0.951 |
| PUZ47507 | Sspon.05G | KQK97593 | TKW04815 | EES10953 | Zm00001eb080560_P001 | 0.890 |
| PUZ65104 | Sspon.07G | KQL14662 | TKW26262 | KXG22383 | Zm00001eb290700_P001 | 0.818 |

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| PUZ62461 | Sspon.08G | KQL09027 | TKW19317 | EER87740 | Zm00001eb378870_P001 | 0.965 |

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| PUZ46608 | Sspon.01G | KQK86712 | TKV90885 | OQU9084 | Zm00001eb060460_P001 | 0.927 |

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| PUZ41209 | Sspon.01G | KQK90991 | TKV96240 | KXG39426 | Zm00001eb395100_P002 | 0.964 |
| PUZ53825 | Sspon.07G | KQL07850 | TKW27035 | EES19598 | Zm00001eb288880_P001 | 0.957 |
| PUZ75589 | Sspon.04G | KQL29722 | TKW39273 | OQU84967 | Zm00001eb241420_P001 | 0.989 |

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| PUZ63026 | Sspon.07G | KQK99618 | TKW07460 | genblast_C | Zm00001eb407120_P002 | 0.950 |
| PUZ53059 | Sspon.01G | KQK92836 | TKV98489 | EER95598 | Zm00001eb001860_P002 | 0.974 |

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| PUZ66178 | genblast_C | KQL15673 | TKW27548 | EES19464 | Zm00001eb287100_P001 | 0.971 |
| PUZ54646 | Sspon.03G | KQL07106 | TKW16934 | EES01515 | Zm00001eb152270_P003 | 0.967 |
| PUZ36515 | Sspon.01G | KQK86582 | TKV90728 | EER93261 | Zm00001eb061390_P002 | 0.924 |
| genblast_C | genblast_C | KQL14545 | TKW26136 | KXG22437 | Zm00001eb294360_P001 | 0.864 |
| PUZ48902 | Sspon.05G | KQK98912 | TKW06564 | EES12856 | Zm00001eb430930_P002 | 0.942 |
| PUZ48643 | Sspon.05G | KQK98658 | TKW06210 | EES11334 | Zm00001eb072600_P001 | 0.954 |
| PUZ67871 | Sspon.02G | KQL17178 | TKW29544 | EES16348 | Zm00001eb135900_P003 | 0.972 |

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| PUZ56367 | Sspon.03G | KQL05404 | TKW14786 | EES03073 | Zm00001eb341960_P001 | 0.978 |

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| PUZ65761 | genblast_C | KQL15275 | TKW27024 | OQU78097 | Zm00001eb288970_P001 | 0.951 |
| PUZ67847 | Sspon.02G | KQL17147 | TKW29510 | OQU76587 | Zm00001eb031390_P001 | 0.951 |

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| PUZ49397 | Sspon.05G | genblast_C | TKW24107 | KXG27374 | Zm00001eb067040_P001 | 0.966 |

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| PUZ53343 | Sspon.03G | KQL08276 | TKW18430 | EES04090 | Zm00001eb143640_P001 | 0.898 |
| PUZ55677 | Sspon.03G | KQL08673 | TKW18927 | EES01133 | Zm00001eb159040_P002 | 0.969 |
| PUZ51037 | Sspon.03G | genblast_C | genblast_C | EES02295 | Zm00001eb120460_P002 | 0.913 |
| PUZ39519 | genblast_C | KQK89451 | TKV94331 | KXG24418 | Zm00001eb416360_P001 | 0.958 |

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| PUZ37747 | Sspon.01G | KQK87895 | TKV92250 | OQU91254 | Zm00001eb052950_P001 | 0.969 |
| PUZ66242 | Sspon.07G | KQL15729 | TKW27635 | EES18140 | Zm00001eb286770_P001 | 0.964 |

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| PUZ72665 | Sspon.02G | KQL26418 | TKW35529 | EER99605 | Zm00001eb107690_P002 | 0.978 |
| PUZ59345 | Sspon.08G | KQL11856 | TKW22975 | OQU76955 | Zm00001eb273360_P002 | 0.812 |
| PUZ69455 | Sspon.02G | KQL23426 | TKW31741 | OQU75659 | Zm00001eb306260_P002 | 0.970 |
| PUZ72095 | Sspon.02G | KQL25833 | TKW34805 | KXG36251 | Zm00001eb321720_P004 | 0.960 |
| PUZ59919 | Sspon.08G | KQL11401 | TKW22375 | OQU76714 | Zm00001eb275720_P001 | 0.959 |
| PUZ72102 | Sspon.02G | KQL25840 | TKW34812 | KXG36256 | Zm00001eb321770_P001 | 0.950 |
| PUZ42762 | genblast_C | KQK92496 | TKV98105 | EER95473 | Zm00001eb004400_P002 | 0.978 |
| PUZ48770 | Sspon.05G | KQK98790 | TKW06381 | EES11382 | Zm00001eb071640_P001 | 0.938 |
| PUZ48409 | Sspon.05G | KQK98428 | TKW05929 | EES11256 | Zm00001eb074280_P001 | 0.956 |
| genblast_C | Sspon.01G | KQK86705 | TKV90872 | EER93307 | Zm00001eb060490_P003 | 0.802 |
| PUZ76711 | Sspon.04G | KQL30632 | TKW40505 | EES05475 | Zm00001eb248280_P001 | 0.942 |

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| PUZ74717 | Sspon.04G | KQL28096 | TKW37222 | OQU84648 | Zm00001eb205140_P002 | 0.958 |
| PUZ44032 | Sspon.05G | KQL03817 | TKW12707 | EES17133 | Zm00001eb024240_P001 | 0.890 |
| PUZ47052 | Sspon.05G | KQK97176 | TKW04279 | EES10742 | Zm00001eb083840_P002 | 0.916 |
| PUZ62901 | Sspon.05G | KQK94117 | TKW07743 | EES07950 | genblast_Os12t0138800-01_Zea | |
| PUZ54371 | Sspon.03G | KQL07337 | TKW17246 | KXG33555 | Zm00001eb150740_P001 | 0.951 |
| PUZ58913 | Sspon.08G | KQL12366 | TKW23630 | OQU77190 | Zm00001eb229050_P001 | 0.934 |
| PUZ71852 | Sspon.02G | KQL25617 | TKW34509 | OQU89892 | Zm00001eb320860_P001 | 0.933 |
| PUZ43117 | Sspon.01G | KQK92879 | TKV98530 | OQU93362 | Zm00001eb001590_P001 | 0.822 |

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| PUZ64800 | genblast_C | KQL14332 | TKW25897 | KXG33081 | Zm00001eb343660_P001 | 0.921 |
| PUZ61351 | Sspon.08G | KQL09908 | TKW20432 | EER88088 | Zm00001eb279290_P001 | 0.897 |

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| PUZ45366 | Sspon.06G | KQK95137 | TKW01431 | OQU83762 | Zm00001eb114780_P001 | 0.921 |
| PUZ70778 | Sspon.02G | KQL24556 | TKW33233 | EER96762 | Zm00001eb313490_P001 | 0.906 |
| PUZ41735 | Sspon.01G | KQK91572 | TKV96943 | EER92493 | Zm00001eb012040_P002 | 0.928 |
| PUZ63834 | Sspon.07G | KQL13181 | TKW24407 | OQU77320 | Zm00001eb265200_P001 | 0.902 |
| PUZ41328 | Sspon.01G | KQK91105 | TKV96404 | EER94942 | Zm00001eb015270_P001 | 0.931 |
| genblast_C | genblast_C | KQK88868 | TKV93573 | EER94138 | Zm00001eb046840_P001 | 0.980 |
| PUZ42397 | Sspon.01G | KQK92152 | TKV97686 | EER95343 | Zm00001eb401140_P001 | 0.925 |
| PUZ67492 | Sspon.02G | KQL16560 | TKW28699 | KXG23278 | Zm00001eb411300_P003 | 0.864 |

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| PUZ75822 | Sspon.04G | KQL29789 | TKW39368 | EES06868 | Zm00001eb241930_P002 | 0.915 |
| PUZ42290 | Sspon.01G | KQK92056 | TKV97571 | EER95309 | Zm00001eb400640_P001 | 0.953 |
| PUZ75902 | genblast_C | KQL29865 | TKW39472 | KXG30327 | Zm00001eb242570_P001 | 0.940 |
| PUZ51208 | Sspon.06G | KQL01540 | TKW09941 | EES13710 | Zm00001eb042860_P001 | 0.914 |
| PUZ55928 | Sspon.01G | KQL05771 | TKW15241 | EES03239 | Zm00001eb161480_P001 | 0.960 |
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| PUZ42338 | Sspon.01G | KQK92102 | TKV97627 | EER92689 | Zm00001eb007830_P001 | 0.988 |
| PUZ46677 | genblast_C | KQK96792 | TKW03758 | EES10564 | Zm00001eb086320_P002 | 0.954 |
| PUZ63797 | genblast_C | KQL13142 | TKW24352 | genblast_C | Zm00001eb355140_P001 | 0.945 |
| PUZ36968 | Sspon.01G | KQK87045 | TKV91287 | EER90856 | Zm00001eb057710_P001 | 0.969 |
| PUZ50733 | genblast_C | KQL01108 | TKW09381 | EER95666 | Zm00001eb000710_P001 | 0.963 |
| PUZ71710 | Sspon.02G | KQL25469 | TKW34314 | EER99255 | Zm00001eb319780_P001 | 0.948 |
| PUZ68329 | genblast_C | KQL22357 | TKW30332 | EER97928 | Zm00001eb299310_P002 | 0.974 |
| PUZ52416 | Sspon.06G | genblast_C | TKW11424 | KXG25516 | Zm00001eb036910_P001 | 0.933 |
| PUZ63905 | Sspon.07G | KQL26956 | TKW07026 | EES17755 | Zm00001eb282600_P001 | 1.011 |
| PUZ48755 | Sspon.05G | KQK98775 | TKW06366 | KXG27048 | Zm00001eb430360_P003 | 0.916 |
| PUZ61645 | Sspon.08G | KQL10217 | TKW20835 | KXG19726 | Zm00001eb280640_P002 | 0.926 |
| PUZ74728 | Sspon.08G | genblast_C | TKW37238 | EES06526 | Zm00001eb205130_P001 | 0.909 |
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| PUZ45007 | genblast_C | KQK94730 | TKW00900 | KXG28488 | genblast_Os11t0521900-02_Ze | |
| PUZ53305 | Sspon.03G | KQL08316 | TKW18484 | EES01956 | Zm00001eb143450_P001 | 0.963 |
| PUZ62770 | Sspon.05G | KQK99713 | TKW07576 | OQU82749 | Zm00001eb093770_P001 | 0.787 |
| PUZ59000 | Sspon.08G | KQL12312 | TKW23558 | KXG20954 | Zm00001eb228600_P001 | 0.989 |
| PUZ37298 | Sspon.01G | KQK87389 | TKV91676 | KXG37702 | Zm00001eb055450_P001 | 0.969 |
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| PUZ77461 | Sspon.04G | KQL31494 | TKW41567 | EES07262 | Zm00001eb254540_P001 | 0.975 |

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| PUZ47541 | Sspon.05G | KQK97622 | TKW04850 | EES10962 | Zm00001eb080380_P001 | 0.982 |
| PUZ52061 | Sspon.06G | KQL02360 | TKW11009 | OQU80981 | Zm00001eb199530_P003 | 0.810 |
| PUZ64620 | Sspon.01G | KQK87790 | TKV92125 | EES18742 | Zm00001eb062710_P001 | 0.877 |
| PUZ72182 | genblast_C | genblast_C | TKW34907 | EER99430 | Zm00001eb322360_P002 | 0.966 |
| PUZ72053 | Sspon.05G | KQL12718 | TKW23815 | EES11590 | Zm00001eb067600_P001 | 0.924 |
| PUZ41856 | Sspon.08G | KQK91625 | TKV97011 | KXG39749 | Zm00001eb398340_P001 | 0.922 |
| PUZ56799 | genblast_C | KQL05228 | TKW14523 | KXG32424 | Zm00001eb132020_P001 | 0.949 |
| PUZ48237 | Sspon.04G | genblast_C | TKW05702 | OQU82045 | Zm00001eb075250_P001 | 0.909 |
| PUZ49649 | Sspon.05G | KQL12632 | TKW23696 | EES16355 | Zm00001eb031640_P001 | 0.936 |
| PUZ67261 | Sspon.02G | KQL16796 | TKW29018 | OQU79210 | Zm00001eb411000_P001 | 0.956 |
| PUZ57339 | Sspon.03G | KQL03784 | TKW12680 | EES02736 | Zm00001eb128200_P004 | 0.895 |
| PUZ42483 | Sspon.01G | KQK92229 | TKV97785 | KXG40013 | Zm00001eb006530_P001 | 0.983 |
| PUZ37432 | Sspon.01G | KQK87531 | TKV91832 | genblast_C | Zm00001eb054290_P004 | 0.823 |
| PUZ69541 | Sspon.04G | KQL32289 | TKW42470 | EES04355 | Zm00001eb249970_P001 | 0.943 |

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| PUZ38335 | Sspon.01G | KQK88408 | TKV92961 | EER93963 | Zm00001eb220610_P003 | 0.985 |
| PUZ38061 | genblast_C | KQK88151 | TKV92617 | EER91262 | Zm00001eb049910_P001 | 0.951 |
| PUZ59380 | Sspon.08G | KQL11906 | TKW23043 | EER88850 | Zm00001eb225830_P001 | 0.923 |

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| PUZ46038 | Sspon.05G | KQK96166 | TKW02901 | EES10335 | Zm00001eb418870_P001 | 0.816 |

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| PUZ70814 | Sspon.02G | KQL24607 | TKW33294 | EER98955 | genblast_Os09t0434200-01_Ze | |
| PUZ49634 | genblast_C | KQL12657 | TKW23720 | KXG27500 | Zm00001eb076230_P001 | 0.980 |

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| PUZ77693 | Sspon.04G | KQL31567 | TKW41662 | KXG30728 | Zm00001eb255340_P001 | 0.988 |
| PUZ63172 | Sspon.07G | KQK99465 | genblast_C | OQU78841 | Zm00001eb408320_P002 | 0.868 |
| PUZ42975 | Sspon.01G | KQK92704 | TKV98346 | EER92912 | Zm00001eb002760_P001 | 0.952 |
| PUZ35942 | genblast_C | KQK86060 | TKV90034 | EER93049 | Zm00001eb065340_P001 | 0.920 |
| PUZ62186 | Sspon.08G | genblast_C | TKW20209 | KXG19320 | Zm00001eb270800_P001 | 0.961 |

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| PUZ54279 | Sspon.07G | KQL07423 | TKW17361 | EES03785 | Zm00001eb150010_P001 | 0.929 |
| PUZ54652 | Sspon.06G | KQL07101 | TKW16930 | EES03659 | Zm00001eb370340_P004 | 0.998 |

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| PUZ41990 | Sspon.01GKQK91755 | TKV97195 | EER95194 | Zm00001eb010160_P002 | 0.963 |
| PUZ62000 | Sspon.06GKQL09564 | TKW19982 | EES15357 | Zm00001eb215170_P001 | 0.984 |
| PUZ61113 | Sspon.08GKQL10435 | TKW21149 | EER88303 | Zm00001eb281190_P001 | 0.846 |
| PUZ55546 | Sspon.03GKQL06148 | TKW15736 | OQU87254 | Zm00001eb359430_P003 | 0.955 |
| PUZ66805 | Sspon.02GKQL16138 | TKW28114 | KXG24148 | Zm00001eb134020_P001 | 0.948 |
| PUZ36493 | Sspon.01GKQK86561 | TKV90699 | EER93252 | Zm00001eb061530_P003 | 0.970 |
| PUZ78341 | Sspon.04GKQL02774 | TKW11545 | genblast_C | Zm00001eb190860_P002 | 0.963 |
| PUZ37155 | Sspon.01GKQK87245 | TKV91508 | EER93504 | Zm00001eb215450_P001 | 0.973 |
| PUZ47940 | Sspon.05GKQK98019 | TKW05352 | EES11097 | Zm00001eb077820_P001 | 0.987 |

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| genblast_C | Sspon.04GKQL31665 | genblast_C | EES07585 | Zm00001eb256030_P001 | 0.943 |
| PUZ39333 | Sspon.02GKQK89321 | TKV94164 | KXG34533 | Zm00001eb027580_P001 | 0.974 |
| PUZ36259 | genblast_CKQK86299 | TKV90335 | EER90592 | Zm00001eb063340_P001 | 0.943 |
| PUZ70903 | Sspon.02GKQL24708 | TKW33399 | EER98982 | Zm00001eb314320_P001 | 0.953 |
| PUZ41910 | Sspon.01GKQK91672 | TKV97073 | KXG39766 | Zm00001eb398540_P001 | 0.958 |
| PUZ59143 | Sspon.08GKQL12181 | TKW23383 | KXG20844 | Zm00001eb227740_P001 | 0.919 |
| PUZ61448 | Sspon.08GKQL10025 | TKW20579 | KXG19645 | Zm00001eb372370_P001 | 0.922 |
| PUZ36473 | genblast_CKQK86543 | TKV90656 | OQU90794 | Zm00001eb212510_P001 | 0.913 |
| PUZ73866 | Sspon.04GKQL28912 | TKW38245 | EES04430 | Zm00001eb230920_P001 | 0.928 |
| PUZ56910 | genblast_CKQL05023 | TKW14244 | EES02890 | Zm00001eb131080_P002 | 0.959 |
| PUZ58838 | genblast_CKQL03238 | TKW11965 | KXG31481 | Zm00001eb119150_P003 | 0.901 |
| PUZ73097 | Sspon.02GKQL26839 | TKW36073 | EER99768 | Zm00001eb110040_P001 | 0.932 |
| PUZ72993 | genblast_CKQL26742 | TKW35926 | EER99728 | Zm00001eb109710_P001 | 0.975 |
| PUZ65712 | Sspon.05GKQL15226 | TKW26973 | KXG27371 | Zm00001eb065860_P002 | 1.015 |
| PUZ61997 | Sspon.08GKQL09563 | TKW19981 | KXG19418 | Zm00001eb375390_P001 | 0.926 |
| PUZ76197 | Sspon.04GKQK97492 | TKW39844 | EES05288 | Zm00001eb182740_P001 | 0.954 |

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| PUZ58610 | Sspon.03GKQL04928 | TKW14113 | EES00081 | Zm00001eb338340_P001 | 0.915 |
| PUZ37561 | genblast_CKQK87682 | TKV91998 | OQU91185 | genblast_Os03t0685750-00_Zea | |
| PUZ59798 | Sspon.08GKQL11253 | TKW22155 | EER90104 | Zm00001eb275250_P001 | 0.976 |
| PUZ54138 | Sspon.03Ggenblast_C | TKW17533 | EES01702 | Zm00001eb149000_P001 | 0.958 |
| PUZ44342 | Sspon.05GKQK94211 | TKW00187 | EES09607 | Zm00001eb200730_P001 | 0.957 |
| PUZ64907 | genblast_CKQL14471 | TKW26050 | EES19907 | Zm00001eb294860_P001 | 0.925 |
| PUZ38033 | Sspon.01GKQK88131 | TKV92585 | genblast_C | Zm00001eb219250_P001 | 0.948 |

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| PUZ38671 | Sspon.01G | KQK88751 | TKV93409 | EER94093 | Zm00001eb046050_P001 | 0.989 |
| PUZ50784 | Sspon.06G | KQL01159 | TKW09467 | genblast_C | Zm00001eb412800_P002 | 0.954 |
| PUZ42347 | Sspon.01G | KQK92108 | TKV97633 | EER95325 | Zm00001eb007880_P001 | 0.940 |
| PUZ58697 | Sspon.03G | KQL04978 | TKW14193 | EES00052 | Zm00001eb119840_P001 | 0.938 |
| PUZ78350 | Sspon.04G | KQL32208 | TKW42379 | EES07789 | Zm00001eb259260_P001 | 0.939 |
| PUZ74250 | genblast_C | KQL28568 | TKW37808 | genblast_C | Zm00001eb232980_P001 | 0.986 |
| PUZ38974 | Sspon.01G | KQK89012 | TKV93757 | KXG38489 | Zm00001eb047750_P001 | 0.881 |
| PUZ40838 | Sspon.01G | genblast_C | TKV95781 | OQU92485 | Zm00001eb018970_P001 | 0.982 |
| PUZ69604 | Sspon.02G | KQL23602 | TKW31932 | EER96353 | Zm00001eb308150_P005 | 0.949 |
| PUZ42758 | Sspon.01G | KQK92495 | TKV98098 | KXG40139 | Zm00001eb004420_P002 | 0.930 |
| PUZ63418 | Sspon.07G | KQL13589 | TKW24984 | EES19280 | Zm00001eb347520_P001 | 0.947 |
| PUZ48167 | Sspon.05G | KQL22561 | TKW05621 | genblast_C | Zm00001eb427290_P001 | 0.961 |
| PUZ76688 | Sspon.04G | KQL30615 | TKW40483 | KXG30689 | Zm00001eb248070_P005 | 0.820 |
| PUZ71649 | Sspon.02G | KQL25422 | TKW34250 | EER97077 | Zm00001eb103300_P001 | 0.990 |
| PUZ62926 | Sspon.05G | KQK93535 | TKV99212 | EES07965 | Zm00001eb342980_P003 | 0.941 |
| PUZ59654 | Sspon.08G | KQL11098 | TKW21992 | EER88892 | Zm00001eb226640_P005 | 0.944 |
| PUZ47177 | Sspon.05G | KQK97288 | TKW04420 | KXG26353 | Zm00001eb082370_P001 | 0.925 |
| PUZ68058 | genblast_C | KQL17415 | TKW29860 | EES16449 | Zm00001eb032800_P001 | 0.874 |
| PUZ40944 | Sspon.01G | KQK90732 | TKV95903 | EER92216 | Zm00001eb018070_P001 | 0.899 |
| PUZ51265 | Sspon.02G | KQL01600 | genblast_C | OQU79685 | Zm00001eb032320_P001 | 0.943 |
| PUZ54574 | Sspon.03G | genblast_C | TKW17016 | EES03690 | Zm00001eb151950_P001 | 0.963 |

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| PUZ64859 | Sspon.07GKQL14401 | TKW25963 | EES18651 | Zm00001eb295350_P001 | 0.965 |
| PUZ37069 | Sspon.01GKQK87141 | TKV91400 | KXG37575 | Zm00001eb056990_P001 | 0.918 |
| PUZ71273 | genblast_CKQL25055 | TKW33815 | EER99087 | Zm00001eb316710_P001 | 0.914 |

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| PUZ73517 | genblast_CKQL03392 | TKW12153 | OQU90503 | Zm00001eb331140_P001 | 0.965 |

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| PUZ62272 | Sspon.08GKQL09217 | TKW19568 | EER89167 | Zm00001eb377420_P002 | 0.973 |
| PUZ38020 | Sspon.01GKQK88121 | TKV92567 | OQU91388 | Zm00001eb051810_P001 | 0.977 |
| PUZ39609 | Sspon.06GKQK89501 | TKV94389 | OQU80948 | Zm00001eb034800_P002 | 0.873 |
| PUZ66020 | Sspon.01GKQL15509 | TKW27336 | EER94478 | Zm00001eb023730_P001 | 0.947 |
| PUZ66365 | Sspon.07GKQL15844 | TKW27768 | KXG21823 | Zm00001eb346550_P002 | 0.980 |
| PUZ38369 | Sspon.01GKQK88428 | TKV92985 | EER91402 | Zm00001eb043990_P002 | 0.932 |
| genblast_C | genblast_CKQL25914 | TKW34885 | EER97262 | Zm00001eb105610_P001 | 0.941 |

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| PUZ54587 | Sspon.03GKQK92249 | TKV97802 | EES03681 | Zm00001eb006440_P001 | 0.956 |
| PUZ62015 | Sspon.08GKQK96675 | TKW03594 | OQU75905 | Zm00001eb375500_P001 | 0.948 |
| PUZ74033 | genblast_CKQL28766 | TKW38036 | EES06266 | Zm00001eb208090_P001 | 0.896 |
| genblast_C | Sspon.05GKQK93841 | TKV99638 | EES09408 | Zm00001eb201130_P001 | 0.920 |
| PUZ57656 | Sspon.01GKQL04059 | TKW12992 | EES02632 | Zm00001eb334320_P002 | 0.982 |
| PUZ62330 | Sspon.08GKQL09158 | TKW19491 | EER89139 | Zm00001eb377970_P001 | 0.960 |
| PUZ77566 | Sspon.04GKQL31390 | TKW41440 | EES05573 | Zm00001eb253710_P001 | 0.942 |

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| PUZ71930 | Sspon.02GKQL25679 | TKW34607 | EER97175 | Zm00001eb320460_P001 | 0.986 |
| PUZ67752 | genblast_CKQL17058 | TKW29413 | KXG36666 | Zm00001eb327280_P001 | 0.949 |
| PUZ61610 | genblast_CKQL10172 | TKW20784 | EER89542 | Zm00001eb371550_P001 | 0.947 |
| PUZ65722 | Sspon.07GKQL15234 | TKW26980 | EES18331 | Zm00001eb289390_P001 | 0.949 |

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| PUZ56711 | genblast_CKQL05092 | TKW14352 | EES02933 | Zm00001eb131540_P001 | 0.914 |
| PUZ50721 | Sspon.06GKQL00270 | TKW08176 | EES13581 | Zm00001eb414530_P002 | 0.924 |

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| PUZ55428 | Sspon.07GKQL06344 | TKW15975 | EES03412 | Zm00001eb157270_P004 | 0.941 |
| PUZ53083 | Sspon.03GKQL08528 | TKW18747 | EES04183 | Zm00001eb141890_P003 | 0.883 |
| PUZ58597 | Sspon.03GKQL04914 | TKW14098 | EES00085 | Zm00001eb338270_P001 | 0.954 |
| PUZ61799 | Sspon.08GKQL09345 | TKW19697 | EER88011 | Zm00001eb373880_P001 | 0.941 |
| PUZ54205 | Sspon.03GKQL07504 | TKW17456 | EES03807 | Zm00001eb149520_P002 | 0.952 |

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| PUZ58999 | Sspon.08GKQL12315 | TKW23563 | KXG20955 | Zm00001eb228620_P001 | 0.964 |
| PUZ73635 | Sspon.04GKQL27714 | TKW36748 | OQU84141 | Zm00001eb209920_P001 | 0.925 |
| PUZ50290 | Sspon.06GKQL00649 | TKW08756 | KXG24534 | Zm00001eb414950_P004 | 0.936 |

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| PUZ77018 | Sspon.04GKQL30905 | TKW40857 | EES05741 | Zm00001eb250340_P002 | 0.952 |
| PUZ59157 | Sspon.08GKQL12164 | TKW23367 | OQU77073 | Zm00001eb227610_P001 | 0.886 |
| PUZ76944 | Sspon.04GKQL30842 | TKW40773 | EES05764 | Zm00001eb249870_P001 | 0.940 |
| PUZ65849 | genblast_CKQL15347 | TKW27107 | KXG22076 | Zm00001eb289240_P001 | 0.983 |
| PUZ76336 | Sspon.04GKQL30258 | TKW40027 | EES07073 | Zm00001eb183460_P004 | 0.951 |
| PUZ68721 | genblast_CKQL23217 | TKW31071 | KXG21363 | Zm00001eb112770_P001 | 0.750 |
| PUZ69532 | genblast_CKQL23523 | TKW31830 | OQU88983 | Zm00001eb306640_P001 | 0.889 |
| PUZ74356 | Sspon.04GKQL28462 | TKW37676 | KXG29620 | Zm00001eb206610_P002 | 0.970 |
| PUZ69881 | Sspon.03GKQL23878 | TKW32307 | EES02294 | Zm00001eb094390_P001 | 0.962 |
| PUZ47655 | Sspon.05GKQK97746 | TKW05025 | EES11002 | Zm00001eb424990_P001 | 0.933 |
| PUZ50857 | Sspon.06GKQL01250 | TKW09570 | EES14825 | Zm00001eb178000_P001 | 0.911 |
| PUZ76394 | Sspon.04Ggenblast_C | TKW40105 | KXG30556 | Zm00001eb246250_P001 | 0.992 |
| PUZ38408 | Sspon.01GKQK88466 | TKV93052 | EER93980 | Zm00001eb029410_P001 | 0.903 |

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| PUZ63276 | Sspon.07G | KQL13742 | TKW25179 | EES15827 | Zm00001eb411130_P001 | 0.969 |
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| PUZ36444 | Sspon.01G | KQK86519 | TKV90622 | OQU90773 | Zm00001eb062000_P001 | 0.923 |
| PUZ77019 | genblast_C | KQL30907 | TKW40858 | EES05742 | Zm00001eb250330_P001 | 0.949 |
| PUZ75112 | Sspon.04G | KQL29184 | TKW38577 | EES04926 | Zm00001eb237240_P001 | 0.953 |
| PUZ56113 | Sspon.03G | KQL06254 | TKW15867 | KXG32775 | Zm00001eb160430_P003 | 0.950 |
| PUZ52573 | Sspon.06G | KQL02842 | TKW11628 | EES14122 | Zm00001eb040190_P001 | 0.939 |
| PUZ47016 | Sspon.05G | genblast_Z | TKW04221 | EES12096 | Zm00001eb084290_P001 | 0.878 |
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| PUZ49516 | genblast_C | KQL12779 | TKW23886 | KXG27434 | Zm00001eb433770_P001 | 0.941 |
| PUZ49256 | Sspon.05G | KQL12999 | TKW24173 | KXG27285 | Zm00001eb067980_P001 | 0.855 |
| PUZ69728 | Sspon.02G | KQL29035 | TKW32060 | KXG35159 | Zm00001eb307420_P004 | 0.958 |
| PUZ77555 | Sspon.04G | KQL31399 | TKW41448 | OQU85454 | Zm00001eb253740_P001 | 0.977 |
| PUZ73470 | Sspon.01G | KQL27203 | TKW36548 | EER97746 | Zm00001eb330810_P003 | 0.937 |
| PUZ75018 | Sspon.04G | KQL27833 | TKW36904 | EES06613 | Zm00001eb237980_P001 | 0.975 |
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| PUZ55305 | Sspon.03G | KQL06458 | TKW16106 | OQU87349 | Zm00001eb360520_P001 | 0.984 |
| PUZ47120 | Sspon.05G | KQK97236 | TKW04348 | OQU81550 | genblast_Os04t0419550-01_Ze | |
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| PUZ48734 | Sspon.05G | KQK98754 | TKW06334 | EES12787 | Zm00001eb071830_P001 | 0.888 |
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| PUZ71807 | Sspon.02G | KQL25569 | TKW34429 | EER97128 | Zm00001eb104170_P001 | 0.904 |
| PUZ55177 | Sspon.03G | KQL06598 | TKW16270 | EES03490 | Zm00001eb361040_P001 | 0.888 |
| PUZ67284 | Sspon.02G | KQL16768 | TKW28986 | OQU79216 | Zm00001eb410850_P001 | 0.948 |
| genblast_C | Sspon.07G | KQL14979 | TKW26680 | EES19708 | Zm00001eb290990_P001 | 0.902 |
| PUZ35982 | Sspon.01G | KQK86080 | TKV90060 | EER90469 | Zm00001eb065120_P002 | 0.907 |
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| PUZ49327 | Sspon.05G | KQL12904 | TKW24040 | OQU82498 | Zm00001eb067480_P001 | 0.915 |

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| PUZ36995 | genblast_C | KQK87066 | TKV91313 | KXG37538 | Zm00001eb057500_P001 | 0.975 |
| PUZ39880 | Sspon.01G | KQK89711 | TKV94667 | EER91853 | Zm00001eb025300_P001 | 0.986 |

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| PUZ72400 | Sspon.02G | KQL26160 | TKW35189 | EER99505 | Zm00001eb323580_P001 | 0.993 |
| PUZ36134 | Sspon.01G | KQK86229 | TKV90250 | EER93115 | Zm00001eb064130_P001 | 0.934 |

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| PUZ55439 | Sspon.03G | KQL06325 | TKW15954 | EES03406 | Zm00001eb359850_P001 | 0.923 |
| PUZ67453 | Sspon.02G | KQL16601 | TKW28770 | EES17199 | Zm00001eb028490_P004 | 0.979 |
| PUZ53198 | Sspon.03G | KQL08407 | TKW18589 | KXG34022 | Zm00001eb363960_P001 | 0.953 |

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| PUZ46499 | Sspon.06G | KQK96660 | TKW03575 | EES14602 | Zm00001eb415520_P002 | 0.770 |
| PUZ71711 | Sspon.02G | KQL25472 | TKW34316 | EER97094 | Zm00001eb103610_P001 | 0.934 |

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| PUZ54201 | Sspon.03G | KQL07508 | TKW17462 | EES03810 | Zm00001eb149490_P001 | 0.996 |
| PUZ68714 | Sspon.02G | KQL22749 | TKW30840 | EER95974 | Zm00001eb301770_P001 | 0.954 |
| PUZ56281 | Sspon.03G | KQL05490 | TKW14893 | KXG32696 | Zm00001eb162560_P001 | 0.957 |
| PUZ47402 | Sspon.05G | KQK97499 | TKW04695 | EES10908 | Zm00001eb081350_P001 | 0.873 |
| PUZ42993 | Sspon.01G | KQK92736 | TKV98372 | OQU93304 | Zm00001eb002560_P001 | 0.956 |

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| PUZ66244 | Sspon.07G | KQL15732 | TKW27639 | KXG21871 | Zm00001eb286760_P001 | 0.985 |
| PUZ58792 | genblast_C | KQL03278 | TKW12015 | EES00019 | Zm00001eb339180_P001 | 0.950 |
| PUZ40348 | genblast_C | KQK90141 | TKV95189 | EER94579 | genblast_Os10t0539700-01_Zea | |
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| PUZ53164 | genblast_C | KQL08439 | TKW18650 | KXG34038 | Zm00001eb142540_P001 | 0.932 |
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| PUZ40801 | Sspon.01G | KQK90559 | TKV95745 | EER94748 | Zm00001eb019170_P002 | 0.960 |
| PUZ58547 | Sspon.03G | KQL04870 | TKW14030 | EES00110 | Zm00001eb338020_P001 | 0.943 |
| PUZ41464 | genblast_C | KQK91261 | TKV96605 | EER95008 | Zm00001eb013980_P001 | 0.948 |
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| PUZ70082 | Sspon.02G | KQL23984 | TKW32421 | OQU89155 | Zm00001eb094570_P001 | 0.891 |
| PUZ58192 | genblast_C | genblast_C | TKW13614 | EES02400 | Zm00001eb123330_P001 | 0.934 |
| genblast_C | Sspon.03G | KQL03750 | TKW12627 | OQU86668 | Zm00001eb333150_P001 | 0.906 |
| PUZ68120 | Sspon.02G | KQL17473 | TKW29921 | KXG24155 | Zm00001eb033230_P002 | 0.910 |
| PUZ47192 | Sspon.05G | KQK97307 | TKW04447 | KXG26334 | Zm00001eb422670_P003 | 0.919 |
| PUZ61844 | Sspon.08G | KQL09406 | TKW19751 | EER87993 | Zm00001eb374230_P001 | 0.957 |
| PUZ49433 | Sspon.05G | KQL12986 | TKW24154 | EES11624 | Zm00001eb433320_P001 | 0.993 |
| PUZ67912 | Sspon.08G | genblast_C | TKW29652 | OQU79616 | Zm00001eb134810_P002 | 0.944 |
| PUZ62288 | Sspon.08G | KQL09197 | TKW19542 | KXG19249 | Zm00001eb377750_P002 | 0.924 |
| PUZ56240 | genblast_C | KQL05528 | TKW14931 | KXG32714 | Zm00001eb162370_P006 | 0.950 |
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| PUZ37889 | genblast_C | KQK88017 | TKV92398 | EER93778 | Zm00001eb051060_P001 | 0.912 |
| PUZ73353 | Sspon.02G | KQL27146 | TKW36473 | EER99899 | Zm00001eb111370_P002 | 0.920 |
| PUZ77181 | Sspon.04G | KQL31050 | TKW41036 | OQU85574 | Zm00001eb187840_P001 | 0.948 |
| PUZ68163 | Sspon.02G | KQK85891 | TKW29968 | EER95728 | Zm00001eb298250_P001 | 0.853 |
| PUZ37338 | Sspon.03G | KQL03172 | TKW11893 | EES00193 | Zm00001eb336950_P001 | 0.964 |
| PUZ59135 | Sspon.08G | KQL12192 | TKW23392 | EER90369 | Zm00001eb227790_P001 | 0.917 |
| PUZ71522 | genblast_C | genblast_C | TKW34094 | EER97038 | Zm00001eb318320_P007 | 0.952 |
| PUZ73885 | Sspon.04G | KQL28903 | TKW38235 | EES04438 | Zm00001eb231030_P001 | 0.855 |
| PUZ70592 | Sspon.02G | KQL24342 | TKW32973 | OQU89443 | Zm00001eb311740_P001 | 0.890 |
| PUZ72493 | Sspon.02G | KQL26254 | TKW35307 | EER99548 | Zm00001eb106960_P003 | 0.963 |
| PUZ55195 | Sspon.03G | KQL06582 | TKW16248 | EES01331 | Zm00001eb155660_P003 | 0.986 |
| PUZ41957 | Sspon.01G | KQK91708 | TKV97125 | EER92567 | Zm00001eb398820_P001 | 0.971 |
| PUZ57419 | Sspon.03G | KQL03855 | TKW12751 | EES02712 | Zm00001eb127840_P001 | 0.948 |
| PUZ54816 | Sspon.03G | KQL14710 | TKW26319 | EES19824 | Zm00001eb153020_P003 | 0.855 |

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| PUZ37122 | Sspon.01G | KQK87205 | TKV91468 | KXG37613 | Zm00001eb056490_P002 | 0.967 |
| PUZ44024 | Sspon.05G | KQK93917 | TKV99763 | EES08133 | Zm00001eb201410_P002 | 0.956 |

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| PUZ54296 | Sspon.03G | KQL07413 | TKW17346 | EES01635 | Zm00001eb150160_P001 | 0.959 |
| PUZ71240 | Sspon.06G | genblast_C | TKW33774 | EER99079 | Zm00001eb316510_P001 | 0.965 |
| PUZ38077 | genblast_Z | KQK88168 | TKV92659 | KXG38074 | Zm00001eb049730_P001 | 0.935 |
| PUZ36930 | Sspon.01G | KQK86997 | TKV91239 | KXG37498 | Zm00001eb058100_P001 | 0.958 |
| PUZ72589 | Sspon.02G | KQL26350 | TKW35452 | EER97415 | Zm00001eb107370_P001 | 0.977 |
| PUZ73327 | genblast_C | KQL27047 | TKW36328 | EER97684 | Zm00001eb110920_P001 | 0.967 |
| PUZ67022 | Sspon.02G | genblast_C | TKW28463 | KXG22873 | Zm00001eb200430_P001 | 0.904 |
| PUZ56954 | Sspon.03G | KQL03406 | TKW12166 | EES00478 | Zm00001eb127180_P001 | 0.960 |
| PUZ73496 | Sspon.02G | KQL27228 | genblast_C | KXG36051 | Zm00001eb103350_P004 | 0.929 |
| PUZ36260 | Sspon.01G | KQK86298 | TKV90334 | OQU90687 | genblast_Os03t0828300-01_Ze | |
| PUZ49247 | Sspon.05G | KQL13011 | TKW24187 | EES12992 | Zm00001eb432350_P001 | 0.980 |
| PUZ51936 | genblast_C | KQL02247 | TKW10840 | EES15481 | Zm00001eb199070_P001 | 0.976 |
| PUZ77584 | Sspon.04G | KQL31363 | TKW41415 | KXG30823 | Zm00001eb253560_P002 | 0.940 |
| PUZ38866 | Sspon.01G | KQK88896 | TKV93617 | KXG36465 | Zm00001eb093300_P001 | 0.942 |

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| PUZ71572 | Sspon.02G | KQL25353 | TKW34174 | EER99199 | Zm00001eb318540_P001 | 0.955 |
| PUZ67381 | Sspon.02G | KQL16652 | TKW28830 | KXG23663 | Zm00001eb410120_P003 | 0.973 |
| PUZ76436 | Sspon.04G | KQL30375 | TKW40161 | OQU85266 | Zm00001eb246540_P001 | 0.796 |

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| PUZ70976 | Sspon.02G | KQL24774 | TKW33475 | EER96846 | Zm00001eb314780_P001 | 0.952 |
| PUZ38644 | Sspon.01G | KQK88731 | TKV93383 | EER94081 | Zm00001eb045870_P001 | 0.986 |
| PUZ77688 | Sspon.04G | KQL31566 | TKW41661 | EES05510 | Zm00001eb255320_P001 | 0.949 |
| PUZ68887 | Sspon.02G | KQL22938 | TKW31054 | EER98182 | Zm00001eb302930_P001 | 0.970 |
| PUZ71236 | Sspon.02G | KQL25013 | TKW33769 | KXG35886 | Zm00001eb316450_P001 | 0.969 |
| PUZ76740 | Sspon.04G | KQL30656 | TKW40539 | KXG30703 | Zm00001eb248360_P001 | 0.908 |
| PUZ56150 | Sspon.03G | KQL05642 | TKW15093 | EES00944 | Zm00001eb357220_P001 | 0.870 |
| PUZ73623 | genblast_C | KQL27696 | TKW36733 | genblast_C | Zm00001eb210000_P003 | 0.903 |
| PUZ45686 | Sspon.06G | KQK95699 | TKW02200 | EES08917 | Zm00001eb165770_P001 | 0.978 |

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| PUZ67461 | Sspon.02G | KQL16593 | TKW28756 | EES17205 | Zm00001eb136900_P001 | 0.961 |
| PUZ38641 | Sspon.01G | KQK88727 | TKV93376 | EER94078 | Zm00001eb221840_P001 | 0.961 |
| PUZ37113 | Sspon.01G | KQK87183 | TKV91449 | OQU91026 | Zm00001eb056580_P003 | 0.949 |
| PUZ48724 | Sspon.05G | KQK98743 | TKW06320 | KXG27037 | Zm00001eb071920_P001 | 0.898 |
| PUZ74734 | Sspon.04G | KQL28112 | TKW37249 | EES04771 | Zm00001eb240010_P003 | 0.981 |
| PUZ53012 | Sspon.03G | KQL08588 | TKW18828 | KXG34107 | Zm00001eb141210_P001 | 0.968 |
| PUZ70789 | Sspon.02G | genblast_C | TKW33259 | KXG35671 | Zm00001eb099810_P001 | 0.941 |

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| PUZ72164 | Sspon.02G | KQL25912 | TKW34883 | OQU89985 | Zm00001eb322260_P001 | 0.977 |
| PUZ72510 | Sspon.02G | KQL26270 | TKW35355 | KXG36488 | Zm00001eb324480_P001 | 0.934 |
| genblast_C | Sspon.06G | KQK95114 | TKW01397 | KXG28797 | genblast_Os11t0586001-00_Zea | |
| PUZ66527 | Sspon.07G | KQL15966 | TKW27921 | EES19329 | Zm00001eb286320_P001 | 0.978 |
| PUZ59323 | Sspon.08G | KQL11833 | TKW22937 | EER88876 | Zm00001eb226270_P001 | 0.962 |
| PUZ66130 | Sspon.07G | KQL15632 | TKW27489 | KXG21925 | Zm00001eb350920_P003 | 0.966 |
| PUZ53726 | Sspon.03G | KQL07944 | TKW17979 | KXG33794 | Zm00001eb146160_P001 | 0.975 |
| PUZ73812 | genblast_C | KQL28960 | TKW38303 | EES04404 | Zm00001eb208530_P002 | 0.983 |
| PUZ50976 | Sspon.06G | KQL01227 | TKW09550 | EES14834 | Zm00001eb177870_P001 | 0.955 |
| PUZ51979 | Sspon.06G | genblast_C | TKW10897 | EES15471 | Zm00001eb033650_P001 | 0.987 |
| PUZ59493 | Sspon.08G | KQL11996 | TKW23157 | EER88812 | Zm00001eb224690_P001 | 0.965 |
| PUZ70767 | Sspon.02G | KQL24551 | TKW33224 | EER98924 | Zm00001eb313400_P001 | 0.949 |
| PUZ36187 | Sspon.01G | KQK86287 | TKV90321 | EER90563 | Zm00001eb211110_P001 | 0.921 |

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| PUZ38277 | Sspon.01G | KQK88360 | TKV92891 | EER93937 | Zm00001eb043540_P003 | 0.974 |
| PUZ42158 | genblast_C | KQL07764 | TKW17761 | KXG39856 | Zm00001eb400080_P001 | 0.888 |

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| PUZ62919 | Sspon.05G | KQK99862 | TKV99205 | EES07962 | Zm00001eb092900_P001 | 0.906 |
| PUZ60084 | Sspon.08G | KQL11547 | TKW22576 | EER88593 | Zm00001eb385960_P001 | 0.979 |
| PUZ65880 | genblast_C | KQL15373 | TKW27136 | EES19566 | Zm00001eb288550_P002 | 0.898 |
| PUZ41478 | Sspon.01G | KQK91276 | TKV96624 | genblast_C | Zm00001eb396690_P002 | 0.926 |

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| PUZ44634 | Sspon.05G | KQK94389 | TKW00431 | KXG28299 | genblast_Os11t0283500-01Zm0 | |

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| PUZ69795 | Sspon.02G | KQL23723 | TKW32110 | EER96428 | Zm00001eb307260_P001 | 0.945 |

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| PUZ77325 | Sspon.04G | KQL31199 | TKW41213 | KXG30889 | Zm00001eb252540_P001 | 0.907 |
| PUZ51053 | Sspon.01G | KQL01379 | TKW09752 | EER90461 | Zm00001eb065200_P001 | 0.947 |
| PUZ56564 | genblast_C | KQL05255 | TKW14548 | KXG29404 | Zm00001eb231410_P001 | 0.969 |

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| PUZ49143 | Sspon.05G | KQK99155 | TKW06869 | EES12946 | Zm00001eb069000_P001 | 0.900 |
| PUZ49488 | Sspon.05G | KQL12799 | TKW23919 | EES11644 | Zm00001eb433640_P001 | 0.901 |
| PUZ77210 | Sspon.04G | KQL31068 | TKW41059 | EES05677 | Zm00001eb251500_P001 | 0.962 |
| PUZ64378 | Sspon.01G | KQL13916 | TKW25399 | EES18831 | Zm00001eb356210_P001 | 0.911 |
| PUZ52908 | Sspon.03G | KQL08700 | TKW18958 | EES02087 | Zm00001eb140440_P001 | 0.901 |
| PUZ48617 | genblast_C | KQK98631 | TKW06180 | EES11324 | Zm00001eb072760_P001 | 0.966 |
| PUZ67688 | Sspon.02G | KQL17013 | TKW29334 | EES16260 | Zm00001eb030470_P001 | 0.980 |
| PUZ66120 | Sspon.07G | genblast_C | TKW27475 | EES18173 | Zm00001eb350970_P001 | 0.955 |

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| PUZ54485 | Sspon.03G | KQL07240 | TKW17111 | OQU87667 | Zm00001eb369880_P003 | 0.902 |
| PUZ72633 | Sspon.02G | KQL26397 | TKW35501 | EER97435 | Zm00001eb325370_P001 | 0.973 |

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| PUZ41113 | Sspon.01G | KQK90904 | TKV96131 | EER92278 | Zm00001eb016690_P001 | 0.923 |
| PUZ53708 | Sspon.03G | KQL07958 | TKW17999 | EES03974 | Zm00001eb145970_P001 | 0.952 |

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| PUZ37682 | Sspon.01G | KQK87831 | TKV92171 | OQU91232 | Zm00001eb052450_P001 | 0.888 |
| PUZ57795 | Sspon.03G | KQL04175 | TKW13165 | EES02593 | Zm00001eb334840_P002 | 0.958 |
| PUZ41963 | Sspon.01G | KQK91717 | TKV97155 | EER95184 | Zm00001eb010420_P003 | 0.980 |
| PUZ77034 | Sspon.04G | KQL30919 | TKW40876 | EES07463 | Zm00001eb250520_P001 | 0.977 |

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| PUZ42117 | Sspon.01G | KQK91884 | TKV97365 | EER95244 | Zm00001eb009130_P003 | 0.971 |
| PUZ48125 | Sspon.05G | KQK98190 | TKW05567 | KXG26764 | Zm00001eb075960_P002 | 0.979 |
| PUZ57477 | Sspon.03G | KQL03895 | TKW12797 | OQU86618 | Zm00001eb333620_P001 | 0.869 |
| PUZ47860 | Sspon.05G | KQK97930 | TKW05245 | EES11071 | Zm00001eb078320_P001 | 0.884 |

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|---|---|---|---|---|---|---|
| PUZ49183 | genblast_C | KQK99184 | TKW06907 | EES11538 | Zm00001eb068670_P001 | 0.938 |
| PUZ39166 | genblast_C | KQK89259 | TKV94066 | EES08846 | genblast_Os10t0375000-01_Zea | |
| PUZ41837 | Sspon.01G | KQK91608 | TKV96982 | EER92523 | Zm00001eb011310_P002 | 0.978 |
| PUZ65847 | genblast_C | KQL15342 | TKW27102 | EES19588 | Zm00001eb289210_P001 | 0.870 |

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| PUZ47836 | Sspon.05G | KQK97911 | TKW05221 | EES12447 | Zm00001eb425750_P001 | 0.944 |
| PUZ57216 | Sspon.03G | KQL03634 | TKW12453 | KXG32283 | Zm00001eb129090_P001 | 0.946 |
| PUZ50128 | Sspon.06G | genblast_C | TKW08947 | KXG24432 | Zm00001eb172780_P002 | 0.932 |
| PUZ41120 | Sspon.01G | KQK90916 | TKV96146 | EER92280 | Zm00001eb394830_P003 | 0.962 |
| PUZ70598 | Sspon.02G | KQL24346 | TKW32976 | EER98846 | Zm00001eb099000_P001 | 0.961 |
| PUZ73321 | genblast_C | KQL27043 | TKW36324 | EER99861 | Zm00001eb329920_P001 | 0.990 |

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| PUZ52723 | Sspon.06G | KQL03013 | TKW11813 | EES14067 | Zm00001eb038890_P001 | 0.974 |
| PUZ65509 | genblast_C | genblast_C | TKW26717 | EES19700 | Zm00001eb290730_P001 | 0.969 |
| PUZ69242 | Sspon.02G | genblast_C | TKW27657 | EER98656 | Zm00001eb308860_P002 | 0.970 |
| PUZ68511 | Sspon.02G | KQL22552 | TKW30579 | EER98028 | Zm00001eb300770_P002 | 0.951 |
| PUZ42273 | Sspon.01G | KQK92038 | TKV97544 | EER95305 | Zm00001eb007230_P001 | 0.949 |
| PUZ61054 | Sspon.08G | KQL10386 | TKW21080 | EER89643 | Zm00001eb381100_P001 | 0.987 |
| PUZ53347 | genblast_C | KQL08272 | TKW18426 | EES01944 | Zm00001eb365000_P003 | 0.939 |
| PUZ68276 | Sspon.02G | KQL23234 | TKW31508 | EER95811 | Zm00001eb299020_P001 | 0.917 |
| PUZ63539 | Sspon.07G | genblast_C | TKW24861 | KXG21545 | Zm00001eb284850_P001 | 0.963 |
| PUZ77208 | Sspon.04G | KQL01604 | TKW10043 | EES05679 | Zm00001eb187950_P001 | 0.964 |
| PUZ56475 | Sspon.06G | KQL05293 | TKW14629 | EES14354 | Zm00001eb259960_P001 | 0.983 |
| PUZ69292 | genblast_C | genblast_C | TKW31533 | EER96237 | Zm00001eb305180_P001 | 0.973 |

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| PUZ36777 | Sspon.01G | KQK86843 | TKV91042 | EER93360 | genblast_Os03t0777000-01_Zea | |
| PUZ47768 | Sspon.05G | KQK97858 | TKW05138 | OQU81851 | Zm00001eb078860_P001 | 0.895 |
| PUZ48594 | Sspon.05G | KQK98596 | TKW06150 | EES12717 | Zm00001eb072980_P001 | 0.901 |

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| PUZ73957 | Sspon.04G | KQL28847 | TKW38141 | OQU84321 | Zm00001eb231470_P001 | 0.965 |

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| PUZ60049 | Sspon.08G | KQL11517 | genblast_C | EER90006 | Zm00001eb385600_P001 0.982 |

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| PUZ64364 | Sspon.07G | KQL13898 | TKW25373 | EES17852 | Zm00001eb284160_P002 0.973 |

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| PUZ58698 | genblast_C | KQL04979 | TKW14194 | KXG31547 | Zm00001eb119830_P001 0.960 |
| PUZ64661 | Sspon.03G | KQL14200 | TKW25746 | EES18731 | Zm00001eb296640_P002 0.794 |
| PUZ36389 | Sspon.01G | KQK86474 | TKV90558 | EER90650 | Zm00001eb062270_P001 0.953 |
| PUZ55989 | genblast_C | KQL24157 | TKW32699 | KXG39851 | Zm00001eb008900_P001 0.936 |

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| PUZ49454 | genblast_C | KQL12842 | TKW23962 | KXG27404 | Zm00001eb433460_P002 0.977 |
| PUZ70064 | genblast_C | KQL23992 | TKW32437 | KXG35280 | Zm00001eb094370_P001 0.948 |
| PUZ40311 | Sspon.01G | KQK90107 | TKV95147 | KXG38988 | Zm00001eb393900_P001 0.940 |
| PUZ62501 | Sspon.08G | KQL08990 | TKW19255 | OQU75704 | Zm00001eb378990_P001 0.940 |
| PUZ48508 | genblast_C | KQK98499 | TKW06023 | KXG26932 | Zm00001eb073730_P001 0.972 |
| PUZ56242 | genblast_C | KQL05526 | TKW14929 | EES00906 | Zm00001eb162380_P004 0.950 |
| PUZ47750 | Sspon.04G | KQK97830 | TKW05113 | EES12419 | Zm00001eb078950_P001 0.956 |

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| PUZ72337 | Sspon.02G | KQL26101 | TKW35125 | OQU90048 | Zm00001eb323240_P003 0.943 |
| PUZ41562 | Sspon.01G | KQK91343 | TKV96708 | EER95045 | Zm00001eb397100_P001 0.970 |
| PUZ59816 | Sspon.08G | KQL11276 | TKW22186 | KXG20460 | Zm00001eb387270_P001 0.963 |
| PUZ67641 | Sspon.02G | KQL16969 | TKW29291 | OQU79441 | Zm00001eb030220_P001 0.974 |
| PUZ48551 | Sspon.05G | KQK98546 | TKW06087 | KXG26960 | Zm00001eb073430_P002 0.954 |

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| PUZ77364 | Sspon.04GKQL31231 | TKW41254 | EES07359 | Zm00001eb252800_P001 | 0.934 |
| PUZ67240 | genblast_CKQL16818 | TKW29060 | OQU79191 | Zm00001eb137960_P001 | 0.939 |

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| PUZ44135 | Sspon.05GKQK94062 | TKV99960 | EES08245 | Zm00001eb250900_P001 | 0.968 |
| PUZ65743 | Sspon.07GKQL15262 | TKW27004 | EES19618 | Zm00001eb348230_P002 | 0.949 |

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| PUZ70104 | Sspon.02GKQL23975 | TKW32403 | EER98622 | Zm00001eb097360_P001 | 0.961 |
| PUZ74405 | Sspon.04GKQL28413 | TKW37610 | KXG29640 | Zm00001eb234400_P003 | 0.992 |
| PUZ76593 | Sspon.04GKQL30527 | TKW40372 | EES05440 | Zm00001eb247380_P001 | 0.938 |
| PUZ59371 | Sspon.08GKQL11887 | TKW23025 | OQU76934 | Zm00001eb225770_P001 | 0.982 |
| PUZ48466 | Sspon.03GKQK98474 | TKW05978 | KXG34040 | Zm00001eb142530_P001 | 0.950 |
| PUZ55121 | Sspon.03GKQL06659 | TKW16335 | EES01356 | Zm00001eb361250_P002 | 0.950 |
| PUZ42218 | Sspon.01GKQK91990 | TKV97477 | EER95289 | Zm00001eb008520_P002 | 0.913 |
| PUZ65585 | Sspon.07GKQL15087 | TKW26806 | OQU78161 | Zm00001eb351770_P001 | 0.925 |
| PUZ40999 | Sspon.01GKQK90791 | TKV95981 | EER94819 | Zm00001eb017660_P001 | 0.950 |

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| PUZ71849 | Sspon.02GKQK85213 | TKW34500 | KXG35417 | Zm00001eb104300_P001 | 0.813 |
| PUZ42128 | Sspon.01GKQK91897 | TKV97378 | EER95247 | Zm00001eb399900_P002 | 0.970 |
| PUZ41807 | Sspon.01GKQK91494 | TKV96874 | OQU92882 | Zm00001eb011460_P001 | 0.977 |
| PUZ62945 | Sspon.07GKQK99871 | TKW07786 | KXG22962 | Zm00001eb406490_P001 | 0.984 |
| PUZ72354 | genblast_CKQL05585 | TKW15025 | EER99486 | Zm00001eb106380_P001 | 0.862 |
| PUZ77943 | Sspon.04GKQL31806 | TKW41921 | EES05906 | Zm00001eb257160_P001 | 0.963 |
| PUZ71895 | genblast_CKQL25654 | TKW34570 | EER97166 | Zm00001eb320580_P002 | 0.978 |
| PUZ36820 | Sspon.02GKQK86896 | TKV91092 | EER90815 | Zm00001eb058970_P001 | 0.982 |
| PUZ39116 | Sspon.01GKQK89153 | TKV93933 | KXG38560 | Zm00001eb223190_P001 | 0.951 |
| PUZ41769 | genblast_CKQK91534 | TKV96914 | EER92501 | Zm00001eb011820_P002 | 0.947 |
| PUZ66051 | Sspon.07GKQL15547 | TKW27391 | EES19509 | Zm00001eb349800_P001 | 0.973 |
| PUZ56104 | genblast_CKQL06241 | TKW15854 | KXG32782 | Zm00001eb357010_P006 | 0.927 |
| PUZ78286 | genblast_CKQL32154 | TKW42315 | EES07769 | Zm00001eb191190_P001 | 0.964 |

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| PUZ50045 | Sspon.06GKQL00884 | TKW09077 | KXG24376 | Zm00001eb416800_P001 | 0.956 |

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| PUZ76115 | Sspon.04GKQL30039 | TKW39792 | OQU85120 | Zm00001eb243910_P001 | 0.918 |
| PUZ46723 | Sspon.05Ggenblast_C | TKW15217 | EES10525 | Zm00001eb420100_P001 | 0.956 |
| PUZ60128 | genblast_CKQL11590 | TKW22631 | EER89983 | Zm00001eb277060_P004 | 0.969 |
| PUZ45636 | Sspon.06GKQK95621 | TKW02109 | EES08902 | Zm00001eb127360_P002 | 0.802 |
| PUZ52140 | Sspon.02GKQL02419 | TKW11095 | EES14276 | Zm00001eb034840_P002 | 0.958 |
| PUZ67180 | Sspon.02GKQL16878 | TKW29141 | EES17039 | Zm00001eb138130_P001 | 0.978 |

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| PUZ48203 | Sspon.05GKQK98267 | TKW05658 | EES12563 | Zm00001eb075520_P003 | 0.816 |

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| PUZ53175 | genblast_CKQL08430 | TKW18638 | OQU88147 | Zm00001eb363830_P001 | 0.958 |
| PUZ65628 | Sspon.03GKQL15141 | TKW26872 | EES18358 | Zm00001eb289810_P001 | 0.981 |

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| PUZ36951 | Sspon.01GKQK87030 | TKV91271 | EER93424 | Zm00001eb057770_P001 | 0.930 |
| PUZ53285 | Sspon.03GKQL08333 | TKW18507 | EES01963 | Zm00001eb143340_P001 | 0.954 |

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| PUZ60577 | Sspon.08GKQL10665 | TKW21498 | EER88132 | Zm00001eb371980_P001 | 0.860 |
| PUZ62276 | Sspon.08GKQL09213 | TKW19560 | KXG19254 | Zm00001eb377470_P001 | 0.946 |
| PUZ58924 | Sspon.08GKQL12375 | TKW23639 | EER89022 | Zm00001eb013700_P002 | 0.786 |
| PUZ42768 | Sspon.01GKQK92502 | TKV98108 | KXG40145 | Zm00001eb403230_P001 | 0.926 |
| PUZ51647 | Sspon.06GKQL01963 | TKW10498 | EES13909 | Zm00001eb179840_P001 | 0.965 |
| PUZ40461 | Sspon.01GKQK90253 | TKV95328 | EER94633 | Zm00001eb021300_P001 | 0.948 |
| PUZ55403 | Sspon.03GKQL06367 | TKW15995 | KXG33095 | Zm00001eb360100_P005 | 0.980 |
| PUZ47097 | Sspon.05GKQK96177 | TKW04332 | KXG26278 | Zm00001eb083510_P001 | 0.919 |
| PUZ71567 | Sspon.02GKQL25350 | TKW34169 | EER97054 | Zm00001eb318560_P001 | 0.989 |
| PUZ77531 | Sspon.04GKQK92892 | TKW41470 | KXG30805 | Zm00001eb253900_P003 | 0.948 |

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| PUZ49475 | Sspon.05GKQL12814 | TKW23931 | KXG27420 | Zm00001eb066420_P001 | 0.987 |
| PUZ52150 | genblast_CKQL02428 | TKW11109 | EES14272 | Zm00001eb034970_P003 | 0.912 |
| PUZ63630 | Sspon.07GKQL13413 | TKW24738 | EES17549 | Zm00001eb267130_P001 | 0.927 |
| PUZ62607 | Sspon.08GKQL08895 | TKW19155 | EER89028 | Zm00001eb268420_P001 | 0.950 |
| PUZ55224 | genblast_CKQL06557 | TKW16211 | KXG33187 | Zm00001eb155910_P004 | 0.939 |
| PUZ63001 | Sspon.05GKQK99951 | TKW07875 | EES16664 | Zm00001eb406860_P001 | 0.957 |
| PUZ77511 | Sspon.04GKQL31446 | TKW41504 | EES05556 | Zm00001eb254050_P001 | 0.967 |

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| PUZ72676 | Sspon.02G | KQL26432 | TKW35541 | EER97446 | Zm00001eb107900_P002 | 0.967 |
| PUZ36332 | Sspon.01G | genblast_C | TKV90495 | EER90625 | Zm00001eb211720_P002 | 0.955 |
| PUZ70604 | Sspon.02G | KQL24365 | TKW32995 | KXG35566 | Zm00001eb099080_P004 | 0.986 |
| PUZ42691 | Sspon.01G | KQK92426 | TKV98021 | EER92802 | Zm00001eb403450_P001 | 0.944 |

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| PUZ42980 | Sspon.01G | KQK92714 | TKV98357 | EER92917 | Zm00001eb002660_P002 | 0.890 |
| PUZ72466 | Sspon.02G | KQL26228 | TKW35278 | KXG36472 | Zm00001eb106770_P001 | 0.996 |
| PUZ65490 | Sspon.03G | KQL14978 | TKW26677 | EES19709 | Zm00001eb291010_P001 | 0.984 |
| PUZ66205 | Sspon.07G | KQL15695 | TKW27593 | EES18149 | Zm00001eb286930_P002 | 0.930 |
| PUZ53942 | Sspon.03G | KQL07747 | TKW17743 | OQU87862 | Zm00001eb367660_P002 | 0.880 |
| PUZ67956 | Sspon.02G | KQL17210 | TKW29582 | OQU79660 | Zm00001eb134530_P002 | 0.958 |
| PUZ78269 | Sspon.04G | KQL32143 | TKW42302 | EES07765 | Zm00001eb259070_P003 | 0.967 |
| PUZ53548 | Sspon.03G | KQL08104 | TKW18212 | KXG33882 | Zm00001eb144890_P001 | 0.867 |

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| PUZ52589 | Sspon.02G | KQL02861 | TKW11644 | EES15233 | Zm00001eb040100_P003 | 0.948 |
| PUZ41453 | Sspon.01G | KQL22585 | TKW30624 | KXG39549 | Zm00001eb014050_P001 | 0.934 |
| PUZ64038 | Sspon.07G | KQL13062 | TKW24241 | EES17708 | Zm00001eb418060_P001 | 0.945 |
| PUZ59815 | Sspon.08G | KQL11274 | TKW22182 | EER88700 | Zm00001eb275420_P001 | 0.965 |
| PUZ68363 | Sspon.02G | KQK86359 | TKV90400 | OQU88410 | Zm00001eb299540_P001 | 0.958 |
| PUZ59850 | Sspon.08G | KQL11312 | TKW22244 | EER90078 | Zm00001eb387510_P001 | 0.873 |
| PUZ41948 | Sspon.01G | KQK91699 | TKV97118 | KXG39781 | Zm00001eb010500_P001 | 0.983 |
| PUZ65496 | Sspon.07G | KQL14988 | TKW26686 | EES18402 | Zm00001eb290940_P001 | 0.945 |
| PUZ69044 | Sspon.02G | KQL23110 | TKW31294 | genblast_Z | Zm00001eb096940_P001 | 0.930 |
| PUZ47189 | Sspon.05G | KQK97302 | TKW04442 | EES10830 | Zm00001eb082660_P001 | 0.968 |

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| PUZ36827 | Sspon.01G | KQK86904 | TKV91102 | EER90818 | Zm00001eb058880_P002 | 0.849 |
| PUZ54181 | Sspon.01G | KQL07528 | TKW17489 | EER93643 | Zm00001eb217160_P001 | 0.965 |
| PUZ67465 | Sspon.02G | KQL16590 | TKW28748 | EES16171 | Zm00001eb136750_P001 | 0.889 |
| PUZ38926 | Sspon.01G | KQK88954 | TKV93691 | KXG38463 | Zm00001eb047430_P001 | 0.791 |
| PUZ53681 | genblast_C | KQL07977 | TKW18032 | OQU87983 | Zm00001eb145840_P001 | 0.835 |

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| PUZ56376 | genblast_C | KQL12184 | TKW23386 | EES03066 | Zm00001eb163010_P001 | 0.965 |

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| PUZ41143 | Sspon.01G | KQK90931 | TKV96168 | EER92289 | Zm00001eb016540_P004 | 0.913 |

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| PUZ48736 | Sspon.05G | KQK98756 | TKW06335 | EES12788 | Zm00001eb071820_P001 | 0.981 |
| PUZ59161 | Sspon.08G | KQL12161 | TKW23364 | KXG20829 | Zm00001eb227600_P002 | 0.948 |
| PUZ47074 | genblast_C | KQK97203 | TKW04309 | EES10764 | Zm00001eb083720_P001 | 0.924 |

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| PUZ40551 | Sspon.01G | KQK90337 | TKV95445 | EER92089 | Zm00001eb393460_P001 | 0.820 |
| PUZ73079 | Sspon.02G | KQL26813 | TKW36039 | OQU9032 | Zm00001eb328430_P003 | 0.939 |
| PUZ41213 | Sspon.01G | KQK90994 | TKV96243 | EER94903 | Zm00001eb016040_P001 | 0.983 |
| PUZ63456 | Sspon.07G | KQL13559 | TKW24947 | EES17913 | Zm00001eb284350_P002 | 0.984 |
| PUZ53114 | Sspon.03G | KQL08488 | TKW18700 | KXG34068 | Zm00001eb142220_P001 | 0.968 |
| PUZ70589 | Sspon.02G | KQL24339 | TKW32969 | EER96686 | genblast_Os09t0381600-01_Ze |  |
| PUZ63080 | Sspon.07G | KQK99567 | TKW07408 | EES16705 | Zm00001eb407610_P006 | 0.911 |
| PUZ72476 | Sspon.02G | KQL26238 | TKW35291 | OQU90088 | Zm00001eb106840_P001 | 0.918 |
| PUZ62514 | Sspon.08G | KQL08980 | TKW19247 | KXG19127 | Zm00001eb379090_P005 | 0.899 |
| PUZ61636 | Sspon.08G | KQL10206 | TKW20825 | EER88181 | Zm00001eb280670_P001 | 0.933 |
| PUZ55709 | Sspon.03G | KQL05986 | TKW15519 | EES01118 | Zm00001eb358860_P001 | 0.951 |
| PUZ47235 | Sspon.05G | KQK97350 | TKW04496 | KXG26359 | Zm00001eb082280_P001 | 0.961 |
| PUZ77189 | Sspon.04G | KQL31057 | TKW41044 | EES07417 | Zm00001eb251370_P001 | 0.966 |
| PUZ74183 | genblast_Z | KQL28620 | TKW37865 | EES06328 | Zm00001eb207560_P001 | 0.946 |
| PUZ72864 | Sspon.02G | KQL26600 | TKW35736 | EER97507 | Zm00001eb327210_P001 | 0.940 |
| PUZ71401 | Sspon.02G | KQL25180 | TKW33969 | EER99139 | Zm00001eb317500_P001 | 0.979 |

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| PUZ71813 | genblast_C | genblast_C | TKW34455 | KXG24588 | Zm00001eb171780_P003 | 0.924 |
| PUZ65788 | Sspon.05G | KQL15298 | TKW27056 | EES11141 | Zm00001eb076830_P001 | 0.955 |
| PUZ49244 | Sspon.05G | KQL13014 | TKW24190 | EES11561 | Zm00001eb068120_P001 | 0.982 |
| PUZ70292 | Sspon.05G | genblast_C | TKW32589 | KXG25915 | Zm00001eb163600_P001 | 0.782 |
| PUZ59077 | Sspon.08G | KQL12247 | TKW23473 | EER90399 | Zm00001eb228160_P001 | 0.964 |
| PUZ51751 | Sspon.06G | KQL02044 | TKW10601 | KXG25268 | Zm00001eb040580_P001 | 0.936 |
| PUZ77806 | Sspon.04G | KQL31676 | TKW41775 | EES07591 | Zm00001eb256120_P002 | 0.950 |

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| PUZ75971 | genblast_C | KQL29919 | TKW39573 | OQU85083 | Zm00001eb243000_P001 | 0.941 |
| PUZ40420 | Sspon.01G | KQK90214 | TKV95271 | EER92032 | Zm00001eb021600_P001 | 0.944 |
| PUZ56581 | genblast_C | KQL05298 | TKW14634 | EES03035 | Zm00001eb341740_P001 | 0.941 |
| PUZ72351 | Sspon.02G | KQL05586 | TKW15026 | KXG36403 | Zm00001eb323330_P001 | 0.903 |
| PUZ47573 | Sspon.05G | KQK97658 | TKW04892 | OQU81758 | Zm00001eb424590_P001 | 0.967 |

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| PUZ77708 | Sspon.04GKQL31582 | TKW41680 | EES07216 | Zm00001eb193970_P001 | 0.941 |
| PUZ43172 | Sspon.01GKQK92939 | TKV98587 | EER95637 | Zm00001eb001180_P001 | 0.954 |
| PUZ73445 | Sspon.02GKQL27172 | TKW36505 | EER97734 | Zm00001eb111490_P002 | 0.945 |
| PUZ52016 | Sspon.06GKQL02308 | TKW10927 | EES15456 | Zm00001eb033780_P003 | 0.975 |

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| PUZ52630 | genblast_CKQL26785 | TKW36002 | KXG25415 | Zm00001eb180360_P001 | 0.954 |
| PUZ42256 | Sspon.01GKQK92020 | TKV97524 | EER92659 | Zm00001eb007090_P004 | 0.949 |
| PUZ71343 | Sspon.02GKQL25137 | TKW33913 | KXG35943 | Zm00001eb102130_P001 | 0.961 |
| PUZ71271 | Sspon.02GKQL25056 | TKW33814 | EER96975 | Zm00001eb316700_P001 | 0.964 |

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| PUZ44463 | Sspon.07GKQK94375 | TKW00405 | KXG22978 | Zm00001eb406810_P001 | 0.885 |
| PUZ64643 | Sspon.07GKQL14178 | TKW25716 | EES18736 | Zm00001eb344520_P002 | 0.957 |
| PUZ53404 | genblast_CKQL08220 | TKW18350 | EES04067 | Zm00001eb144210_P001 | 0.985 |

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| PUZ65192 | Sspon.07GKQL14739 | TKW26356 | EES19802 | Zm00001eb353110_P001 | 0.901 |
| PUZ52598 | Sspon.06GKQL02873 | TKW11655 | EES14114 | Zm00001eb040040_P001 | 0.920 |

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| PUZ72590 | Sspon.02GKQL26351 | TKW35455 | EER97416 | Zm00001eb107400_P001 | 0.964 |
| PUZ66454 | Sspon.01GKQL15901 | TKW27840 | EES19361 | Zm00001eb286060_P003 | 0.852 |
| PUZ68522 | Sspon.02GKQL22567 | TKW30599 | KXG34464 | Zm00001eb300880_P001 | 0.931 |
| PUZ64091 | genblast_CKQK99245 | TKW06984 | EES19046 | Zm00001eb353980_P001 | 0.924 |
| PUZ67586 | Sspon.02Ggenblast_C | TKW29203 | KXG23791 | Zm00001eb029580_P001 | 0.952 |
| PUZ40571 | Sspon.01GKQK90350 | TKV95473 | EER94674 | Zm00001eb020430_P001 | 0.947 |
| PUZ42844 | Sspon.01GKQK92580 | TKV98219 | EER92855 | Zm00001eb003840_P002 | 0.925 |
| PUZ72016 | Sspon.02GKQL25760 | TKW34711 | KXG36212 | Zm00001eb104970_P001 | 0.988 |

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| PUZ42727 | genblast_C | KQK92461 | TKV98060 | OQU93186 | Zm00001eb004710_P002 | 0.944 |

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| PUZ54246 | Sspon.02G | KQL07457 | TKW17404 | EES03797 | Zm00001eb149810_P001 | 0.880 |
| PUZ70835 | genblast_C | KQL24644 | TKW33325 | KXG35706 | Zm00001eb100110_P001 | 0.913 |
| PUZ50820 | Sspon.06G | KQL01188 | TKW09508 | EES14803 | Zm00001eb178040_P001 | 0.988 |

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| PUZ77244 | Sspon.04G | KQL31112 | TKW41113 | EES07403 | Zm00001eb251880_P001 | 0.947 |
| PUZ54506 | Sspon.05G | KQK89319 | TKV94161 | EES11253 | Zm00001eb224370_P001 | 0.994 |
| PUZ70549 | Sspon.02G | KQL24314 | TKW32940 | EER96675 | Zm00001eb311470_P001 | 0.944 |
| PUZ74475 | Sspon.04G | KQL28317 | TKW37510 | EES04686 | Zm00001eb206120_P001 | 0.959 |
| PUZ49537 | Sspon.05G | KQL12763 | TKW23869 | KXG27447 | Zm00001eb066010_P001 | 0.964 |
| PUZ47596 | Sspon.05G | KQK97677 | TKW04923 | EES10974 | Zm00001eb424720_P001 | 0.978 |
| PUZ72237 | Sspon.02G | KQL25990 | TKW34983 | KXG36320 | Zm00001eb322630_P002 | 0.945 |
| PUZ43196 | Sspon.01G | KQK92973 | TKV98624 | EER95648 | Zm00001eb000990_P001 | 0.901 |
| PUZ60323 | Sspon.08G | genblast_Z | TKW21869 | EER89919 | Zm00001eb384760_P002 | 0.940 |

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|---|---|---|---|---|---|---|
| genblast_C | Sspon.08G | KQL11909 | TKW23093 | EER88832 | Zm00001eb225410_P001 | 0.966 |
| PUZ51730 | Sspon.06G | KQL02029 | TKW10577 | EES13944 | Zm00001eb177150_P001 | 0.940 |

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| PUZ41299 | genblast_C | KQK91078 | TKV96366 | EER94933 | Zm00001eb015440_P001 | 0.959 |
| PUZ41114 | Sspon.01G | KQK90747 | TKV95923 | KXG39404 | Zm00001eb016530_P001 | 0.973 |
| PUZ73223 | genblast_Z | KQL26949 | TKW36205 | OQU90375 | Zm00001eb329390_P001 | 0.954 |
| PUZ58910 | Sspon.03G | KQL03154 | TKW11870 | EER99977 | genblast_Os01t0247900-01Zm0 |  |
| PUZ58917 | Sspon.08G | KQL12372 | TKW23635 | KXG20990 | Zm00001eb229120_P001 | 0.957 |
| PUZ77558 | Sspon.04G | KQL31396 | TKW41446 | EES07306 | Zm00001eb190260_P001 | 0.954 |
| PUZ47782 | Sspon.05G | KQK97875 | TKW05177 | KXG26557 | Zm00001eb078780_P001 | 0.969 |
| PUZ41613 | genblast_C | KQK91399 | TKV96764 | EER92441 | Zm00001eb397300_P003 | 0.917 |
| PUZ53728 | Sspon.03G | KQL07941 | TKW17973 | OQU87964 | Zm00001eb146190_P002 | 0.925 |
| PUZ66171 | Sspon.07G | KQL15665 | TKW27538 | EES18165 | Zm00001eb287130_P001 | 0.992 |
| PUZ58170 | Sspon.03G | genblast_C | TKW13577 | KXG31803 | Zm00001eb336220_P001 | 0.928 |
| PUZ49492 | genblast_C | KQL12796 | TKW23916 | EES13095 | Zm00001eb066330_P001 | 0.967 |
| PUZ50949 | Sspon.02G | KQL00765 | TKW08916 | KXG25022 | Zm00001eb198650_P001 | 0.971 |
| PUZ54302 | genblast_C | genblast_C | TKW17340 | OQU87729 | Zm00001eb150270_P001 | 0.971 |
| PUZ77978 | Sspon.04G | KQL31850 | TKW41970 | KXG31244 | Zm00001eb257400_P001 | 0.900 |
| PUZ60288 | Sspon.08G | KQL11734 | TKW22811 | EER89945 | Zm00001eb384300_P001 | 0.966 |
| PUZ61836 | Sspon.06G | KQL09397 | TKW19743 | OQU80376 | Zm00001eb108610_P001 | 0.950 |
| PUZ41662 | Sspon.01G | KQK91447 | TKV96823 | EER92462 | Zm00001eb012610_P001 | 0.975 |
| PUZ71235 | Sspon.02G | KQL25011 | TKW33758 | EER99078 | Zm00001eb316440_P001 | 0.973 |
| PUZ61508 | Sspon.08G | KQL10072 | TKW20634 | EER88133 | Zm00001eb279860_P001 | 0.844 |

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| PUZ78170 | Sspon.04G | KQL32039 | TKW42191 | EES07731 | Zm00001eb258520_P002 | 0.943 |
| PUZ71536 | genblast_C | genblast_C | TKW34116 | OQU89773 | Zm00001eb318410_P002 | 0.918 |
| PUZ36031 | Sspon.01G | KQK86131 | TKV90120 | EER90499 | Zm00001eb210620_P001 | 0.864 |
| PUZ71176 | Sspon.02G | KQL24946 | TKW33667 | OQU89663 | Zm00001eb101470_P002 | 0.978 |
| PUZ77126 | Sspon.04G | KQL31002 | TKW40979 | EES05697 | Zm00001eb187660_P001 | 0.987 |
| PUZ64765 | Sspon.07G | KQL14292 | TKW25848 | EES18688 | Zm00001eb295960_P001 | 0.909 |
| PUZ65382 | Sspon.07G | KQL14888 | TKW26546 | OQU78235 | Zm00001eb291640_P001 | 0.941 |
| PUZ77931 | Sspon.04G | KQL31787 | TKW41897 | KXG31223 | Zm00001eb257050_P001 | 0.959 |
| PUZ78281 | Sspon.04G | KQL32147 | TKW42306 | EES07768 | Zm00001eb259110_P001 | 0.894 |
| PUZ78058 | genblast_C | KQL31926 | TKW42051 | EES07686 | Zm00001eb192340_P002 | 0.966 |
| PUZ78154 | Sspon.04G | KQL32020 | TKW42162 | EES07722 | Zm00001eb258360_P002 | 0.939 |
| PUZ76372 | Sspon.04G | KQL30300 | TKW40075 | EES05367 | Zm00001eb246120_P001 | 0.937 |
| PUZ40986 | Sspon.01G | genblast_C | TKV95964 | KXG39307 | Zm00001eb017780_P002 | 0.924 |
| PUZ47941 | genblast_C | genblast_C | TKW05354 | OQU81931 | Zm00001eb426300_P001 | 0.952 |
| PUZ57425 | Sspon.03G | KQL03862 | TKW12770 | KXG32198 | Zm00001eb333510_P002 | 0.943 |

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| PUZ66720 | Sspon.07GKQL16163 | TKW28150 | EES17948 | genblast_Os05t0267800-01_Ze | |
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| PUZ59834 | Sspon.04GKQL11294 | TKW22213 | EER90085 | Zm00001eb387370_P001 | 0.903 |
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| PUZ54109 | Sspon.03GKQL07600 | TKW17562 | KXG33650 | Zm00001eb148890_P001 | 0.945 |
| PUZ37059 | genblast_CKQK87132 | TKV91390 | EER90882 | Zm00001eb215000_P001 | 0.978 |
| PUZ65662 | Sspon.07GKQL15169 | TKW26906 | EES19637 | Zm00001eb289670_P001 | 0.955 |
| PUZ71468 | Sspon.02GKQL25235 | TKW34029 | EER99164 | Zm00001eb317860_P001 | 0.991 |
| PUZ71732 | Sspon.02GKQL25490 | TKW34348 | KXG36086 | Zm00001eb332010_P001 | 0.930 |
| PUZ68308 | Sspon.02GKQL22328 | TKW30288 | KXG34314 | genblast_Zm00001eb299200_P0 | |
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| PUZ55298 | Sspon.05GKQL06463 | TKW16114 | KXG26016 | Zm00001eb420250_P001 | 0.934 |
| PUZ46394 | Sspon.05GKQK96536 | TKW03423 | KXG25878 | Zm00001eb419670_P001 | 0.969 |
| PUZ65343 | Sspon.07GKQL14863 | TKW26509 | EES19760 | Zm00001eb352680_P001 | 0.946 |
| PUZ67087 | Sspon.02GKQL16422 | TKW28524 | EES15958 | Zm00001eb133070_P001 | 0.966 |
| PUZ49180 | Sspon.05GKQK99182 | TKW06905 | EES11536 | Zm00001eb431980_P001 | 0.956 |
| PUZ59953 | Sspon.02GKQL11429 | TKW22412 | EER99032 | Zm00001eb315460_P002 | 0.940 |
| PUZ60140 | Sspon.08GKQL11599 | TKW22642 | KXG20259 | genblast_Os06t0586150-00Zm0 | |
| PUZ42996 | Sspon.01Ggenblast_C | TKV98376 | OQU93309 | Zm00001eb002540_P001 | 0.928 |
| PUZ45083 | Sspon.06GKQK94814 | TKW01039 | EES09869 | Zm00001eb197970_P003 | 0.938 |
| PUZ58107 | Sspon.03GKQL04469 | TKW13515 | OQU86289 | Zm00001eb123910_P001 | 0.919 |
| PUZ37233 | genblast_CKQK87321 | TKV91600 | KXG37658 | Zm00001eb055930_P001 | 0.972 |
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| PUZ37150 | genblast_CKQK87238 | TKV91505 | KXG37626 | Zm00001eb215430_P001 | 0.965 |
| PUZ49320 | Sspon.05GKQL12901 | TKW24038 | EES13021 | Zm00001eb432750_P001 | 0.893 |
| PUZ65440 | Sspon.07GKQL14922 | TKW26601 | EES19730 | Zm00001eb352470_P001 | 0.895 |
| PUZ37666 | Sspon.01GKQK87823 | TKV92158 | OQU91227 | Zm00001eb065520_P002 | 0.954 |
| PUZ48256 | Sspon.05GKQK98322 | TKW05733 | KXG26818 | Zm00001eb075060_P001 | 0.950 |
| PUZ42145 | Sspon.01GKQK91921 | TKV97408 | OQU92989 | Zm00001eb008880_P001 | 0.975 |
| PUZ70647 | Sspon.02GKQL24426 | TKW33060 | genblast_C | Zm00001eb099250_P001 | 0.925 |
| PUZ36768 | Sspon.01GKQK86834 | TKV91031 | EER93357 | Zm00001eb213650_P001 | 0.957 |
| PUZ76800 | Sspon.04GKQL30709 | TKW40606 | KXG31119 | Zm00001eb186130_P001 | 0.975 |

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| PUZ61426 | Sspon.08GKQL10001 | TKW20558 | EER88111 | Zm00001eb372510_P001 | 0.971 |
| PUZ74026 | Sspon.04GKQL28772 | TKW38044 | OQU84350 | Zm00001eb232120_P001 | 0.956 |
| PUZ72687 | genblast_CKQL26443 | TKW35554 | EER97451 | Zm00001eb325790_P001 | 0.948 |
| PUZ57769 | Sspon.03GKQL04151 | TKW13137 | EES00415 | Zm00001eb125920_P001 | 0.892 |
| PUZ68036 | genblast_CKQL17391 | TKW29811 | OQU90203 | Zm00001eb108430_P001 | 0.950 |
| PUZ76417 | Sspon.04GKQL30361 | TKW40135 | KXG30576 | Zm00001eb246440_P001 | 0.969 |
| PUZ42396 | Sspon.01GKQK92151 | TKV97685 | OQU93075 | Zm00001eb401130_P001 | 0.870 |
| PUZ39448 | Sspon.01GKQK89109 | TKV93884 | EER94287 | Zm00001eb048600_P002 | 0.937 |
| PUZ45690 | Sspon.04GKQK95703 | TKW02204 | EES10204 | Zm00001eb165710_P003 | 0.941 |
| PUZ66494 | Sspon.07GKQL26017 | TKW35012 | EER97300 | Zm00001eb322750_P001 | 0.918 |

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| PUZ53577 | Sspon.03Ggenblast_C | TKW18160 | OQU88010 | Zm00001eb365870_P002 | 0.956 |
| PUZ48453 | Sspon.05GKQK98463 | TKW05964 | EES12663 | Zm00001eb073930_P003 | 0.986 |
| PUZ63538 | Sspon.07GKQL13502 | TKW24864 | KXG21547 | Zm00001eb350650_P001 | 0.961 |
| PUZ54805 | Sspon.03GKQL06969 | TKW16752 | OQU87537 | Zm00001eb153120_P001 | 0.778 |

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| PUZ73259 | Sspon.02GKQL26984 | TKW36253 | KXG36842 | Zm00001eb110650_P001 | 0.964 |

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| PUZ77702 | Sspon.04GKQL31574 | TKW41672 | EES05501 | Zm00001eb194040_P001 | 0.874 |

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| PUZ37038 | Sspon.01GKQK87113 | TKV91364 | EER93461 | Zm00001eb057150_P003 | 0.962 |
| PUZ61484 | Sspon.08GKQL10050 | TKW20612 | KXG19659 | Zm00001eb372210_P001 | 0.949 |
| PUZ50621 | Sspon.05GKQL01200 | TKW09517 | EES08104 | Zm00001eb201250_P005 | 0.934 |
| PUZ53731 | Sspon.03GKQL07940 | TKW17972 | EES01763 | Zm00001eb367560_P001 | 0.970 |

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| PUZ50815 | Sspon.02GKQL01186 | TKW09499 | KXG34762 | Zm00001eb304110_P001 | 0.956 |
| PUZ37242 | genblast_CKQK87336 | TKV91616 | KXG37663 | Zm00001eb215680_P001 | 0.930 |

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| PUZ70793 | Sspon.02G | KQL24586 | TKW33270 | EER96769 | Zm00001eb099850_P004 | 0.970 |
| PUZ78003 | genblast_C | KQL31871 | TKW41993 | EES05939 | Zm00001eb192600_P001 | 0.743 |
| PUZ36009 | Sspon.01G | genblast_C | TKV90091 | EER93070 | Zm00001eb210500_P001 | 0.966 |
| PUZ59408 | Sspon.03G | KQL11926 | TKW23058 | EER93581 | Zm00001eb122600_P001 | 0.979 |
| PUZ72194 | Sspon.02G | KQL25950 | TKW34922 | EER97273 | Zm00001eb105780_P001 | 0.948 |
| PUZ62393 | Sspon.08G | KQL09106 | TKW19418 | EER87766 | Zm00001eb378440_P001 | 0.971 |

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| PUZ47616 | Sspon.05G | KQK97703 | TKW04951 | EES12363 | Zm00001eb079790_P002 | 0.977 |
| PUZ45695 | Sspon.06G | KQK95705 | TKW02206 | EES10205 | Zm00001eb115680_P003 | 0.927 |
| PUZ54180 | Sspon.03G | KQL07529 | TKW17490 | KXG33635 | Zm00001eb368680_P001 | 0.962 |
| PUZ74519 | Sspon.08G | genblast_Z | TKW37455 | OQU84570 | Zm00001eb236200_P001 | 0.973 |
| PUZ73305 | Sspon.02G | KQL27021 | TKW36300 | KXG36862 | Zm00001eb329850_P005 | 0.894 |
| PUZ39866 | Sspon.01G | KQK89697 | TKV94649 | EER91850 | Zm00001eb025510_P001 | 0.941 |
| PUZ37299 | Sspon.01G | KQK87390 | TKV91677 | EER90977 | Zm00001eb055430_P001 | 0.965 |
| PUZ59715 | Sspon.04G | KQL11154 | TKW22055 | EER90136 | Zm00001eb388960_P002 | 0.886 |
| PUZ45079 | genblast_C | KQK94811 | TKW01031 | EES08607 | Zm00001eb113490_P001 | 0.926 |
| PUZ49326 | Sspon.05G | KQK97834 | TKW05114 | EES11033 | Zm00001eb078940_P001 | 0.968 |
| PUZ36936 | Sspon.01G | KQK87006 | TKV91248 | EER90852 | Zm00001eb214500_P001 | 0.933 |
| PUZ71873 | genblast_C | KQL25640 | TKW34538 | KXG36159 | Zm00001eb320680_P002 | 0.971 |
| PUZ68020 | Sspon.02G | KQL17374 | TKW29792 | EES17469 | Zm00001eb032750_P001 | 0.982 |
| PUZ54457 | Sspon.06G | KQL07261 | TKW17144 | EES01574 | Zm00001eb151360_P001 | 0.937 |
| PUZ42969 | Sspon.01G | KQK92698 | TKV98340 | EER92906 | Zm00001eb402660_P003 | 0.991 |
| PUZ73524 | genblast_C | genblast_C | TKW36603 | OQU90515 | Zm00001eb331190_P001 | 0.971 |
| PUZ62980 | Sspon.05G | KQK93605 | TKV99312 | KXG27755 | Zm00001eb092650_P001 | 0.955 |
| PUZ69318 | genblast_C | KQL23289 | TKW31580 | KXG34939 | Zm00001eb305570_P001 | 0.997 |
| PUZ35992 | Sspon.01G | KQK86093 | TKV90073 | EER93060 | Zm00001eb065000_P001 | 0.930 |
| PUZ66073 | Sspon.07G | KQL15575 | TKW27420 | KXG21947 | Zm00001eb287610_P001 | 1.004 |
| PUZ66162 | Sspon.08G | KQL15651 | TKW27520 | OQU76788 | Zm00001eb287220_P002 | 0.910 |
| PUZ63495 | Sspon.07G | KQL13530 | TKW24907 | EES19244 | Zm00001eb350490_P001 | 0.942 |
| PUZ64388 | genblast_C | KQL13925 | TKW25408 | EES18829 | Zm00001eb267600_P001 | 0.936 |
| genblast_C | Sspon.02G | KQL01394 | TKW09773 | EER99174 | Zm00001eb102590_P001 | 0.884 |
| PUZ60368 | Sspon.08G | KQL10929 | TKW21796 | OQU76534 | Zm00001eb383800_P001 | 0.957 |
| PUZ69317 | Sspon.02G | KQL23292 | TKW31583 | KXG34940 | Zm00001eb094630_P001 | 0.983 |

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| PUZ67822 | Sspon.02G | KQL17115 | TKW29487 | OQU79537 | Zm00001eb135710_P001 | 0.972 |
| PUZ73701 | Sspon.04G | KQL24766 | TKW33464 | OQU84199 | Zm00001eb229760_P001 | 0.943 |
| PUZ62266 | Sspon.08G | KQL09224 | TKW19575 | EER89169 | Zm00001eb377390_P001 | 1.002 |
| PUZ39767 | Sspon.05G | KQK96386 | TKW03191 | EES10446 | Zm00001eb088290_P001 | 0.953 |
| PUZ71024 | Sspon.02G | KQL24817 | TKW33521 | OQU89623 | Zm00001eb315060_P001 | 0.911 |
| PUZ55595 | Sspon.03G | KQL06095 | TKW15656 | EES00535 | Zm00001eb128190_P001 | 0.963 |
| PUZ75926 | Sspon.01G | KQK89819 | TKV94796 | genblast_C | Zm00001eb390550_P002 | 0.927 |

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| PUZ68212 | Sspon.02G | KQL22147 | TKW30027 | EER97846 | Zm00001eb298570_P001 | 0.967 |

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| PUZ52834 | Sspon.03GKQL08770 | TKW19050 | OQU88251 | Zm00001eb140020_P001 | 0.884 |
| PUZ49803 | Sspon.06GKQL00210 | TKW08111 | EES13221 | Zm00001eb260310_P001 | 0.939 |
| PUZ64982 | Sspon.07GKQL14539 | TKW26129 | KXG22439 | Zm00001eb342390_P002 | 0.891 |
| PUZ42665 | Sspon.01GKQK92406 | TKV98004 | EER95441 | Zm00001eb402450_P001 | 0.962 |
| PUZ42799 | Sspon.01GKQK92530 | TKV98157 | OQU93210 | Zm00001eb004250_P003 | 0.984 |
| PUZ62821 | Sspon.07GKQK99757 | TKV98906 | EES15580 | Zm00001eb405320_P001 | 0.933 |
| PUZ37924 | Sspon.01GKQK88050 | TKV92448 | EER93790 | Zm00001eb218920_P001 | 0.907 |

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| PUZ66978 | Sspon.07GKQL16231 | TKW28255 | OQU79081 | Zm00001eb133420_P001 | 0.955 |
| PUZ49459 | genblast_CKQL12837 | TKW23953 | EES13077 | Zm00001eb433480_P001 | 0.971 |
| PUZ66656 | Sspon.07GKQL16182 | TKW28173 | OQU79020 | Zm00001eb133280_P001 | 0.968 |
| PUZ74510 | Sspon.03GKQL28263 | TKW01343 | KXG34083 | genblast_Os11t0583200-01_Ze | |

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| PUZ73741 | Sspon.04GKQL29040 | TKW38407 | KXG29299 | Zm00001eb209370_P002 | 0.961 |

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| PUZ71965 | Sspon.02GKQL25714 | TKW34651 | EER99357 | genblast_Os09t0560900-01_Ze | |
| PUZ62530 | genblast_CKQL08955 | TKW19224 | OQU75691 | Zm00001eb379170_P001 | 0.935 |

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| genblast_C | Sspon.01Ggenblast_C | TKV97587 | genblast_C | genblast_Os03t0205000-01_Ze | |
| PUZ43548 | Sspon.05GKQK86921 | TKV91138 | KXG22867 | Zm00001eb405340_P001 | 0.928 |
| PUZ72804 | genblast_CKQL26545 | TKW35662 | EER99662 | Zm00001eb326760_P001 | 0.962 |
| PUZ59062 | Sspon.08GKQL12254 | TKW23482 | EER88970 | Zm00001eb228230_P001 | 0.883 |
| PUZ47077 | Sspon.05GKQK97207 | TKW04311 | EES10765 | Zm00001eb083680_P002 | 0.997 |
| PUZ62687 | Sspon.05GKQK93409 | TKW07906 | KXG22797 | Zm00001eb276220_P001 | 0.961 |
| PUZ43495 | Sspon.07GKQK99718 | TKW07582 | KXG22890 | Zm00001eb163750_P001 | 0.969 |
| PUZ48959 | Sspon.05GKQK98972 | TKW06638 | EES12880 | Zm00001eb070350_P001 | 0.759 |
| PUZ42917 | Sspon.01GKQK92643 | TKV98289 | EER92884 | genblast_Os03t0140500-01_Ze | |
| PUZ57237 | Sspon.03GKQL03665 | TKW12500 | EES02765 | Zm00001eb332720_P001 | 0.961 |
| PUZ78238 | genblast_Cgenblast_C | TKW42252 | EES07756 | genblast_Os02t0816700-01_Ze | |

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| PUZ54835 | genblast_CKQL06943 | TKW16718 | OQU87522 | Zm00001eb153560_P004 | 0.964 |
| PUZ41392 | genblast_CKQK91193 | TKV96514 | OQU92717 | Zm00001eb396090_P001 | 0.871 |
| PUZ76864 | Sspon.04GKQL30766 | TKW40684 | KXG31095 | Zm00001eb186370_P001 | 0.830 |
| PUZ61325 | Sspon.08GKQL09778 | TKW20268 | EER88082 | Zm00001eb372950_P001 | 0.948 |
| PUZ59806 | genblast_CKQL11262 | TKW22168 | EER90099 | Zm00001eb387140_P001 | 0.966 |
| PUZ66289 | Sspon.07GKQL15776 | TKW27687 | KXG21857 | Zm00001eb285380_P002 | 0.969 |
| PUZ59776 | Sspon.08GKQL11226 | TKW22134 | EER90111 | Zm00001eb386900_P001 | 0.956 |
| PUZ47696 | Sspon.05GKQK97775 | TKW05046 | EES11012 | Zm00001eb079320_P001 | 0.861 |
| PUZ39845 | genblast_CKQK89679 | TKV94626 | EER91839 | Zm00001eb025620_P001 | 0.963 |
| PUZ71065 | Sspon.02GKQL24860 | TKW33567 | EER96886 | Zm00001eb101120_P001 | 0.905 |
| PUZ77664 | genblast_CKQL31541 | TKW41626 | KXG30738 | Zm00001eb255130_P002 | 0.957 |
| PUZ45315 | Sspon.05GKQK95075 | TKW01351 | EES07915 | Zm00001eb195840_P001 | 0.947 |
| PUZ72165 | Sspon.02GKQK87633 | TKV91945 | genblast_C | Zm00001eb105580_P001 | 0.916 |
| PUZ74129 | Sspon.01GKQK92230 | TKV97786 | KXG40016 | Zm00001eb006510_P004 | 0.981 |
| PUZ60440 | Sspon.08GKQL10858 | TKW21708 | OQU76502 | Zm00001eb277910_P002 | 0.929 |
| PUZ78364 | Sspon.04GKQL32222 | TKW42399 | EES07796 | Zm00001eb259350_P001 | 0.949 |

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| PUZ48275 | genblast_CKQL23914 | TKW05756 | KXG26823 | Zm00001eb075170_P001 | 0.859 |

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| PUZ59152 | Sspon.08GKQL12169 | TKW23371 | OQU77078 | Zm00001eb227670_P003 | 0.974 |
| PUZ65051 | Sspon.03GKQL14608 | TKW26211 | KXG22397 | genblast_Os05t0533100-01_Zea | |
| PUZ75154 | Sspon.04GKQL29217 | TKW38622 | EES04943 | Zm00001eb203780_P002 | 0.967 |
| PUZ70438 | Sspon.02GKQL24235 | TKW32805 | KXG35476 | Zm00001eb098490_P001 | 0.949 |
| PUZ60331 | genblast_CKQL10974 | TKW21853 | EER89914 | Zm00001eb384810_P003 | 0.962 |
| PUZ73397 | genblast_Cgenblast_C | TKW36416 | EER99880 | Zm00001eb111120_P001 | 0.958 |
| PUZ47726 | Sspon.05GKQK97797 | TKW05074 | EES12342 | Zm00001eb425250_P001 | 0.959 |

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| PUZ38019 | Sspon.05GKQK88122 | TKV92568 | EES12199 | Zm00001eb082380_P001 | 0.958 |
| PUZ56109 | Sspon.03GKQL06247 | TKW15862 | EES00964 | Zm00001eb160470_P002 | 0.971 |
| PUZ70349 | Sspon.02GKQL24153 | TKW32693 | EER98746 | Zm00001eb309940_P001 | 0.949 |
| PUZ54342 | Sspon.03GKQL07369 | TKW17287 | KXG33568 | Zm00001eb369350_P001 | 0.938 |
| PUZ78177 | Sspon.04GKQL32048 | TKW42199 | EES05993 | Zm00001eb258570_P001 | 0.977 |
| PUZ65039 | Sspon.07GKQL14602 | TKW26200 | KXG22401 | Zm00001eb293170_P003 | 0.944 |
| PUZ63192 | Sspon.03GKQK99437 | TKW07197 | EES01184 | Zm00001eb359370_P001 | 0.965 |
| genblast_C | Sspon.04Ggenblast_C | genblast_C | OQU84273 | Zm00001eb230840_P001 | 0.808 |
| PUZ72625 | Sspon.02GKQL26392 | TKW35496 | EER97431 | Zm00001eb325330_P001 | 0.956 |

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| PUZ40107 | Sspon.01G | KQK89918 | TKV94931 | EER90668 | Zm00001eb023170_P001 | 0.966 |
| PUZ43982 | Sspon.05G | KQK93885 | TKV99719 | OQU83031 | Zm00001eb201260_P002 | 0.957 |
| PUZ63807 | Sspon.07G | KQL13148 | TKW24357 | EES18940 | Zm00001eb265420_P001 | 0.937 |
| PUZ64493 | genblast_C | KQL14026 | TKW25526 | EES20050 | Zm00001eb297340_P001 | 0.987 |
| PUZ76133 | Sspon.04G | KQL30058 | TKW39772 | EES05258 | Zm00001eb244050_P002 | 0.923 |
| genblast_C | Sspon.01G | KQK92391 | genblast_C | EER92793 | Zm00001eb005310_P001 | 0.947 |
| PUZ47314 | Sspon.05G | KQK97417 | TKW04578 | EES10867 | Zm00001eb081810_P001 | 0.973 |
| PUZ49557 | Sspon.05G | KQL12733 | TKW23836 | KXG27461 | Zm00001eb065800_P001 | 0.952 |
| PUZ47210 | Sspon.05G | KQK97323 | TKW04470 | OQU81612 | Zm00001eb082470_P001 | 0.995 |
| PUZ37456 | genblast_C | KQK87566 | TKV91869 | KXG37775 | Zm00001eb054100_P001 | 0.882 |
| PUZ74271 | genblast_C | KQL28543 | TKW37776 | EES13455 | Zm00001eb413100_P001 | 0.889 |
| PUZ40078 | Sspon.01G | KQK89888 | TKV94882 | EER94476 | Zm00001eb391020_P001 | 0.886 |
| PUZ41506 | genblast_C | KQK91300 | TKV96656 | KXG39575 | Zm00001eb013610_P005 | 0.937 |
| PUZ47073 | Sspon.05G | KQK97201 | TKW04308 | KXG26266 | Zm00001eb083750_P001 | 0.931 |
| PUZ42849 | Sspon.01G | KQK92588 | TKV98225 | KXG40170 | Zm00001eb003830_P002 | 0.998 |
| PUZ47445 | Sspon.05G | KQK97531 | TKW04748 | EES12276 | Zm00001eb081110_P001 | 0.978 |
| PUZ72075 | Sspon.02G | KQL25818 | TKW34781 | OQU89962 | Zm00001eb105130_P005 | 0.970 |
| PUZ46515 | Sspon.05G | KQK96676 | TKW03597 | EES09254 | Zm00001eb029080_P001 | 0.985 |

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| PUZ54450 | Sspon.03G | KQL07265 | TKW17149 | EES03731 | Zm00001eb369770_P001 | 0.973 |
| PUZ73013 | genblast_C | KQL26753 | TKW35941 | EER97576 | Zm00001eb109770_P002 | 0.950 |

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| PUZ36920 | Sspon.01G | KQK86985 | TKV91225 | KXG37497 | Zm00001eb058130_P001 | 0.969 |
| PUZ46277 | Sspon.05G | KQK96480 | genblast_Z | EES10500 | Zm00001eb176980_P001 | 0.924 |
| PUZ78006 | Sspon.04G | KQL31876 | TKW41997 | KXG31257 | Zm00001eb257610_P003 | 0.986 |
| PUZ36574 | genblast_C | KQK86656 | TKV90816 | EER93291 | Zm00001eb212900_P001 | 0.970 |
| PUZ42314 | genblast_C | KQK92085 | TKV97606 | EER92685 | Zm00001eb007760_P001 | 0.964 |
| PUZ46768 | genblast_C | KQK96889 | TKW03895 | OQU8138 | Zm00001eb420660_P003 | 0.965 |
| PUZ59648 | Sspon.08G | KQL11092 | TKW21982 | OQU7682 | Zm00001eb389210_P005 | 0.959 |
| PUZ61835 | Sspon.08G | KQL09392 | TKW19740 | EER89368 | Zm00001eb278450_P001 | 0.985 |
| PUZ66355 | Sspon.07G | KQL15831 | TKW27753 | EES19404 | Zm00001eb346590_P001 | 0.991 |
| PUZ36799 | Sspon.01G | KQK86866 | TKV91061 | EER95390 | Zm00001eb006140_P001 | 0.967 |

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| PUZ38193 | Sspon.01G | KQK88289 | TKV92804 | EER91338 | Zm00001eb043060_P001 | 0.980 |
| PUZ69293 | Sspon.02G | KQL23258 | TKW31540 | EER96238 | Zm00001eb094610_P001 | 0.962 |
| PUZ54460 | Sspon.03G | KQL07258 | TKW17142 | EES01573 | Zm00001eb369790_P001 | 0.957 |

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| PUZ46372 | Sspon.05G | KQK96560 | TKW03459 | EES11834 | Zm00001eb419720_P001 | 0.965 |

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| PUZ65735 | Sspon.07G | KQL15247 | TKW26994 | EES18318 | Zm00001eb347860_P001 | 0.991 |
| PUZ47433 | Sspon.05G | KQK97524 | TKW04730 | EES10919 | genblast_Os04t0453266-00_Ze | |

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| PUZ39945 | Sspon.01GKQK89768 | TKV94743 | KXG38837 | Zm00001eb024680_P002 | 0.962 |

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| PUZ74095 | Sspon.04GKQL28704 | TKW37960 | KXG29501 | Zm00001eb232500_P001 | 0.954 |
| PUZ36539 | Sspon.01GKQK86616 | TKV90764 | KXG37340 | Zm00001eb061200_P002 | 0.963 |
| PUZ60732 | Sspon.08GKQL10258 | TKW20899 | EER89585 | Zm00001eb380200_P001 | 0.960 |
| PUZ42242 | Sspon.01GKQK92010 | TKV97506 | EER92656 | Zm00001eb400460_P003 | 0.941 |
| PUZ54399 | Sspon.03GKQL07310 | TKW17210 | EES01593 | Zm00001eb369590_P002 | 0.945 |
| PUZ44766 | Sspon.06GKQK88475 | TKV93059 | KXG28331 | Zm00001eb169740_P002 | 0.975 |

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| PUZ48242 | Sspon.05GKQK98306 | TKW05709 | OQU82050 | Zm00001eb427640_P002 | 0.983 |
| PUZ52030 | Sspon.06GKQL02322 | TKW10950 | EES15449 | Zm00001eb199410_P001 | 0.945 |
| PUZ73455 | Sspon.02GKQL27183 | TKW36521 | OQU90478 | Zm00001eb330680_P002 | 0.972 |
| PUZ49107 | Sspon.05GKQK99118 | TKW06823 | EES11508 | Zm00001eb069220_P001 | 0.990 |
| PUZ37905 | Sspon.01GKQK88026 | TKV92410 | KXG37982 | Zm00001eb051090_P001 | 0.914 |
| PUZ54031 | genblast_CKQL07670 | TKW17649 | EES01737 | Zm00001eb148330_P001 | 0.970 |
| PUZ73405 | Sspon.02GKQL27117 | TKW36401 | EER99887 | Zm00001eb330270_P001 | 0.959 |
| PUZ77280 | Sspon.04GKQL31149 | TKW41153 | KXG30912 | Zm00001eb252190_P002 | 0.975 |
| PUZ76859 | Sspon.02GKQL30765 | TKW40683 | genblast_C | Zm00001eb028360_P004 | 0.941 |
| PUZ42970 | Sspon.01GKQK92699 | TKV98341 | EER92907 | Zm00001eb002810_P001 | 0.991 |

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| PUZ40239 | Sspon.01GKQK90046 | TKV95075 | EER91972 | Zm00001eb391750_P001 | 0.969 |

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| PUZ60182 | Sspon.08GKQL11638 | TKW22700 | OQU76615 | Zm00001eb385300_P001 | 0.934 |
| PUZ53741 | Sspon.07GKQL07929 | TKW17959 | EES03962 | Zm00001eb146310_P001 | 0.987 |
| PUZ52751 | Sspon.06GKQL03040 | TKW11843 | EES14036 | Zm00001eb038640_P002 | 0.957 |
| PUZ71277 | genblast_CKQL25059 | TKW33819 | EER99089 | Zm00001eb316730_P001 | 0.959 |
| PUZ51881 | Sspon.06GKQL02192 | TKW10778 | EES15132 | Zm00001eb038230_P002 | 0.966 |
| PUZ64371 | Sspon.07GKQL13908 | TKW25390 | EES19198 | Zm00001eb284110_P001 | 0.905 |

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| PUZ66135 | genblast_CKQL08351 | TKW18528 | OQU88120 | Zm00001eb143210_P003 | 0.967 |
| PUZ69473 | Sspon.02GKQL23466 | TKW31765 | EER98449 | Zm00001eb306350_P001 | 0.949 |
| PUZ50827 | Sspon.06GKQL01193 | TKW09512 | OQU80206 | Zm00001eb412590_P002 | 0.945 |

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| PUZ58248 | Sspon.03G | KQL04579 | TKW13667 | KXG31764 | Zm00001eb123040_P001 | 0.907 |
| PUZ68787 | Sspon.02G | KQL22832 | TKW30927 | EER96004 | Zm00001eb302360_P002 | 0.924 |
| PUZ42707 | Sspon.01G | KQK92443 | TKV98038 | OQU9317 | Zm00001eb004990_P003 | 0.956 |
| PUZ42395 | genblast_C | KQK92149 | TKV97683 | EER95339 | Zm00001eb008200_P001 | 0.948 |
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| PUZ39889 | Sspon.01G | KQK89720 | TKV94678 | EER94418 | genblast_Os10t0579600-01_Ze | |
| PUZ52921 | Sspon.03G | KQL08692 | TKW18946 | EES02081 | Zm00001eb140480_P002 | 0.958 |
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| PUZ49678 | genblast_C | KQL12620 | TKW23682 | EES11712 | Zm00001eb434490_P003 | 0.875 |
| PUZ59708 | Sspon.08G | KQL23580 | TKW3190 | EER88055 | Zm00001eb373330_P001 | 0.970 |
| PUZ47214 | Sspon.05G | KQK97326 | TKW04473 | OQU8161 | genblast_Os04t0436800-01_Ze | |
| PUZ43468 | Sspon.05G | KQK93348 | TKW0754 | EES09148 | Zm00001eb093870_P001 | 0.949 |
| PUZ49522 | Sspon.05G | KQL12778 | TKW23881 | EES13106 | Zm00001eb066140_P003 | 0.940 |
| PUZ61605 | Sspon.08G | KQL10169 | TKW20781 | EER89539 | Zm00001eb371530_P001 | 0.952 |

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| PUZ74375 | Sspon.04G | KQL28442 | TKW37649 | EES04640 | Zm00001eb234090_P001 | 0.951 |
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| PUZ53827 | Sspon.07G | KQL07848 | TKW17869 | EES01800 | Zm00001eb147010_P001 | 0.923 |
| PUZ43499 | Sspon.07G | KQK99721 | TKW07586 | KXG22889 | Zm00001eb405640_P002 | 0.919 |
| PUZ76999 | Sspon.05G | KQL30891 | TKW40838 | EES07473 | Zm00001eb250210_P001 | 0.969 |
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| PUZ54828 | Sspon.03G | KQL06952 | TKW16725 | EES01466 | Zm00001eb152980_P003 | 0.972 |
| PUZ72730 | genblast_C | KQL26479 | TKW35589 | OQU90179 | Zm00001eb326090_P001 | 0.979 |
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| PUZ54024 | Sspon.03G | KQL07673 | TKW17656 | EES01739 | Zm00001eb148310_P001 | 0.978 |
| PUZ52789 | Sspon.06G | KQL08801 | TKW19093 | EES13267 | Zm00001eb260950_P001 | 0.974 |
| PUZ67038 | Sspon.03G | KQL16382 | TKW28474 | EES03242 | Zm00001eb161520_P001 | 0.902 |
| PUZ38376 | Sspon.01G | KQK88436 | TKV93002 | genblast_C | Zm00001eb044070_P001 | 0.969 |
| PUZ53782 | Sspon.03G | KQL07896 | TKW17917 | EES03950 | genblast_Os01t0869000-01 | Zm0 |
| PUZ70759 | Sspon.02G | KQL24541 | TKW33216 | EER96754 | Zm00001eb313300_P003 | 0.913 |
| PUZ46295 | Sspon.05G | KQK96422 | TKW03227 | KXG37650 | Zm00001eb086910_P001 | 0.971 |
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| PUZ64816 | genblast_C | KQL14352 | TKW25916 | EES19937 | Zm00001eb343580_P002 | 0.876 |
| PUZ55744 | Sspon.03G | KQL05943 | TKW15472 | OQU87187 | Zm00001eb159490_P001 | 0.895 |
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| PUZ57034 | Sspon.03G | KQL03452 | TKW12226 | EES02854 | Zm00001eb130310_P001 | 0.900 |
| PUZ66888 | genblast_C | KQL16340 | TKW28407 | OQU79067 | Zm00001eb409880_P002 | 0.960 |
| PUZ46905 | Sspon.05G | KQK97018 | TKW04067 | KXG26145 | Zm00001eb084970_P002 | 0.983 |

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| genblast_C | Sspon.05GKQK96495 | TKW03353 | EES10489 | Zm00001eb419580_P001 | 0.945 |
| PUZ76670 | genblast_CKQL30593 | TKW40458 | EES05463 | genblast_Os02t0631100-01_Ze | |
| PUZ41686 | Sspon.01GKQK91468 | TKV96844 | EER92480 | Zm00001eb012390_P001 | 0.965 |

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| PUZ65008 | Sspon.07GKQL14570 | TKW26161 | KXG22422 | Zm00001eb294200_P002 | 0.938 |

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| PUZ57909 | Sspon.03GKQL04273 | TKW13283 | EES02541 | Zm00001eb125150_P001 | 0.981 |

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| PUZ70153 | Sspon.02GKQL24011 | TKW32465 | EER96489 | Zm00001eb309030_P001 | 0.977 |
| PUZ43916 | Sspon.05GKQK93821 | TKV99604 | KXG27887 | Zm00001eb201010_P001 | 0.997 |
| PUZ70862 | Sspon.02GKQL24656 | TKW33340 | KXG35712 | Zm00001eb314080_P001 | 0.957 |
| PUZ46361 | Sspon.05GKQK96583 | TKW03487 | EES11831 | Zm00001eb419770_P001 | 0.976 |
| PUZ53943 | Sspon.03Ggenblast_C | TKW17740 | genblast_C | Zm00001eb147890_P001 | 0.880 |

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| PUZ70886 | Sspon.02GKQL24687 | TKW33377 | EER96802 | Zm00001eb100250_P002 | 0.953 |
| PUZ71048 | Sspon.02GKQL24847 | TKW33554 | OQU8962 | Zm00001eb315310_P001 | 0.958 |
| PUZ74770 | Sspon.04GKQL28021 | TKW37139 | EES06536 | Zm00001eb205020_P001 | 0.854 |
| PUZ71876 | Sspon.02GKQL25644 | TKW34543 | EER99329 | Zm00001eb320660_P001 | 0.946 |

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| PUZ60830 | genblast_C | genblast_C | TKW20948 | EER88227 | Zm00001eb380460_P001 | 0.834 |
| PUZ77603 | Sspon.04G | KQL31335 | TKW41391 | EES05589 | Zm00001eb189890_P001 | 0.938 |
| PUZ77495 | Sspon.04G | KQL31463 | TKW41527 | KXG30787 | Zm00001eb194730_P004 | 0.928 |
| PUZ52257 | Sspon.06G | KQL02515 | TKW11222 | KXG25603 | Zm00001eb035670_P001 | 0.971 |
| PUZ48669 | Sspon.04G | KQK98689 | TKW06244 | KXG27015 | Zm00001eb428400_P002 | 0.858 |
| PUZ68872 | genblast_C | KQL22931 | TKW31046 | KXG34638 | Zm00001eb302830_P004 | 0.969 |
| PUZ73754 | genblast_C | KQL29018 | TKW38384 | EES04381 | Zm00001eb209310_P002 | 0.972 |
| PUZ63830 | Sspon.07G | KQL13175 | TKW24402 | genblast_C | Zm00001eb354990_P001 | 0.740 |
| PUZ53178 | Sspon.03G | KQL08429 | TKW18634 | EES02004 | Zm00001eb142620_P001 | 0.989 |
| PUZ36942 | Sspon.01G | KQK87014 | TKV91260 | OQU9095 | Zm00001eb057920_P002 | 0.939 |
| PUZ69672 | Sspon.02G | KQL23648 | TKW32006 | OQU89047 | Zm00001eb307760_P001 | 0.955 |
| PUZ58413 | Sspon.03G | KQL04758 | TKW13884 | KXG31655 | Zm00001eb121590_P008 | 0.936 |
| PUZ51709 | Sspon.06G | KQL02006 | TKW10553 | KXG25252 | Zm00001eb040920_P001 | 0.958 |

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| PUZ41840 | Sspon.01G | KQK91611 | TKV96988 | EER95151 | Zm00001eb011280_P001 | 0.941 |
| PUZ49809 | Sspon.06G | genblast_C | TKW08116 | KXG24206 | Zm00001eb260360_P001 | 0.987 |
| PUZ59440 | Sspon.08G | KQL11958 | TKW23117 | KXG20650 | Zm00001eb273630_P001 | 0.961 |
| PUZ44399 | Sspon.05G | KQK94416 | TKW00457 | OQU83360 | Zm00001eb199050_P002 | 0.968 |
| PUZ67729 | genblast_C | KQL17040 | TKW29382 | KXG23878 | Zm00001eb288690_P001 | 0.919 |
| PUZ73684 | Sspon.04G | KQL29117 | TKW38499 | EES06126 | Zm00001eb229640_P001 | 0.971 |
| PUZ55851 | genblast_C | KQL05846 | TKW15337 | genblast_C | genblast_Os01t0612600-01_Ze | |
| PUZ48053 | Sspon.05G | KQK98122 | TKW05482 | genblast_C | Zm00001eb426720_P001 | 0.960 |
| genblast_C | Sspon.06G | KQL25391 | TKW34219 | genblast_C | Zm00001eb318940_P001 | 0.977 |
| PUZ57502 | Sspon.01G | KQL03926 | TKW12837 | OQU86609 | Zm00001eb127450_P001 | 0.978 |
| PUZ41473 | Sspon.01G | KQK91267 | TKV96615 | EER95011 | Zm00001eb013890_P001 | 0.940 |
| PUZ69912 | genblast_C | KQL23802 | TKW32215 | EER98613 | Zm00001eb095450_P001 | 0.990 |
| PUZ52549 | Sspon.06G | KQL02814 | TKW11588 | KXG25451 | Zm00001eb198600_P001 | 0.944 |
| PUZ61834 | Sspon.08G | KQL09394 | TKW19741 | KXG19520 | Zm00001eb374160_P001 | 0.932 |
| PUZ68180 | Sspon.02G | KQL22113 | TKW29986 | EER95733 | Zm00001eb118290_P002 | 0.971 |
| PUZ42288 | Sspon.01G | KQK92055 | TKV97570 | EER92674 | Zm00001eb007490_P001 | 0.934 |
| PUZ63873 | Sspon.07G | KQL13219 | genblast_C | EES17658 | Zm00001eb354830_P001 | 0.952 |
| PUZ67231 | Sspon.02G | KQL16824 | TKW29073 | EES16036 | Zm00001eb264780_P001 | 0.971 |
| PUZ41488 | Sspon.01G | KQK91285 | TKV96636 | OQU92753 | Zm00001eb013730_P001 | 0.991 |
| PUZ77654 | genblast_C | KQL31536 | TKW41620 | KXG30744 | Zm00001eb255090_P003 | 0.964 |
| PUZ62417 | Sspon.08G | KQL09080 | TKW19385 | KXG19172 | Zm00001eb269430_P001 | 0.938 |
| PUZ60950 | Sspon.08G | KQL10734 | TKW21573 | EER88406 | Zm00001eb278130_P001 | 0.942 |
| PUZ72381 | Sspon.02G | KQL26140 | TKW35163 | EER97346 | Zm00001eb106490_P001 | 0.984 |
| PUZ51427 | Sspon.06G | KQL01777 | TKW10265 | KXG25141 | Zm00001eb179020_P002 | 0.899 |
| PUZ42318 | genblast_C | KQK92087 | TKV97611 | KXG39936 | Zm00001eb400780_P001 | 0.972 |

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| PUZ73585 | genblast_C | KQL27307 | TKW36682 | EER99968 | Zm00001eb112000_P001 | 0.863 |
| PUZ42748 | Sspon.01G | KQK92488 | TKV98093 | OQU93195 | Zm00001eb403270_P001 | 0.758 |
| PUZ45854 | Sspon.06G | KQK95878 | TKW02548 | KXG29064 | Zm00001eb165460_P001 | 0.937 |
| PUZ67649 | Sspon.02G | KQL16979 | TKW29300 | KXG23827 | Zm00001eb030300_P001 | 0.967 |
| PUZ70322 | Sspon.02G | KQL24107 | TKW32622 | EER98701 | Zm00001eb309730_P001 | 0.987 |
| PUZ54221 | Sspon.03G | KQL07483 | TKW17433 | EES01662 | Zm00001eb149650_P002 | 0.964 |
| PUZ72474 | Sspon.02G | KQL26236 | TKW35287 | EER99539 | Zm00001eb324170_P002 | 0.918 |

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| PUZ73084 | Sspon.02G | KQL26823 | TKW36052 | EER99762 | Zm00001eb328490_P001 | 0.978 |
| PUZ39764 | Sspon.01G | KQK89586 | TKV94501 | KXG38741 | Zm00001eb026090_P001 | 0.977 |
| PUZ76840 | Sspon.04G | KQL30750 | TKW40663 | KXG31101 | Zm00001eb249190_P001 | 0.961 |

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| PUZ41539 | Sspon.06G | KQK91325 | TKV96694 | EER92419 | Zm00001eb013360_P002 | 0.962 |
| PUZ67460 | Sspon.02G | KQL16594 | TKW28757 | KXG23710 | Zm00001eb136910_P001 | 0.912 |
| PUZ69303 | Sspon.02G | KQL23275 | TKW31562 | EER96246 | Zm00001eb305370_P001 | 0.953 |
| PUZ47999 | Sspon.05G | KQK98064 | TKW05409 | OQU81970 | genblast_Os04t0514500-01_Zea | |
| PUZ64334 | Sspon.07G | KQL13866 | TKW25334 | EES17840 | Zm00001eb283470_P001 | 0.953 |
| PUZ51531 | Sspon.02G | KQL01883 | TKW10388 | OQU80479 | Zm00001eb179460_P001 | 0.975 |

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| PUZ64430 | Sspon.07G | KQL13967 | TKW25458 | KXG22724 | Zm00001eb345540_P001 | 0.868 |
| PUZ63129 | Sspon.07G | KQL06678 | TKW16364 | EES15737 | genblast_Os08t0365500-00_Zea | |
| PUZ62259 | Sspon.08G | KQL09236 | TKW19588 | EER87824 | Zm00001eb377350_P001 | 0.951 |
| PUZ42637 | Sspon.01G | KQK92387 | TKV97987 | EER95433 | Zm00001eb005350_P001 | 0.970 |
| PUZ36072 | Sspon.01G | KQK86180 | TKV90186 | EER90517 | Zm00001eb210790_P002 | 0.955 |
| PUZ54725 | Sspon.03G | KQL07038 | TKW16848 | EES01493 | Zm00001eb152810_P001 | 0.901 |
| PUZ41051 | Sspon.01G | KQK90835 | TKV96038 | EER94841 | Zm00001eb017230_P001 | 0.980 |
| PUZ70980 | Sspon.02G | KQL24779 | TKW33482 | KXG35759 | Zm00001eb314820_P001 | 0.917 |

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| PUZ52539 | Sspon.06G | KQL02812 | TKW11585 | EES14129 | Zm00001eb037570_P001 | 0.915 |
| PUZ54385 | Sspon.05G | KQL07326 | TKW17230 | EES03752 | Zm00001eb150860_P001 | 0.934 |

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| PUZ61708 | Sspon.08G | KQL09861 | TKW20371 | EER88039 | Zm00001eb278940_P002 | 0.964 |
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| PUZ37886 | Sspon.01G | KQK88013 | TKV92395 | KXG37976 | genblast_Os03t0634400-01Zm0 | |
| PUZ52122 | Sspon.06G | KQL02403 | TKW11074 | KXG36695 | Zm00001eb327550_P001 | 0.935 |
| PUZ37812 | Sspon.01G | KQK87951 | TKV92318 | EER91171 | Zm00001eb218700_P001 | 0.938 |
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| PUZ76921 | Sspon.04G | KQL30822 | TKW40753 | KXG31079 | Zm00001eb249690_P001 | 0.952 |
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| PUZ68165 | genblast_C | KQK85889 | TKW29971 | OQU88296 | Zm00001eb298280_P001 | 0.976 |
| PUZ77505 | Sspon.04G | KQL31450 | TKW41510 | KXG30792 | Zm00001eb254090_P002 | 0.944 |
| PUZ69584 | Sspon.02G | KQL23572 | TKW31893 | EER98490 | Zm00001eb096140_P001 | 0.981 |
| PUZ48701 | Sspon.05G | KQK98717 | TKW06283 | EES12774 | Zm00001eb430070_P002 | 0.978 |
| PUZ65779 | Sspon.07G | KQL15289 | TKW27038 | KXG22104 | Zm00001eb288850_P001 | 0.942 |
| PUZ54712 | Sspon.03G | KQL07054 | TKW16868 | EES01500 | Zm00001eb152650_P005 | 0.954 |
| PUZ36605 | Sspon.01G | KQK86688 | TKV90857 | EER90744 | Zm00001eb060610_P001 | 0.960 |
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| PUZ76664 | genblast_C | KQL30589 | TKW40448 | EES05460 | Zm00001eb247810_P001 | 0.980 |
| PUZ68823 | Sspon.02G | KQL22861 | TKW30964 | OQU88645 | Zm00001eb116440_P003 | 0.887 |
| PUZ52753 | Sspon.06G | KQL03043 | TKW11846 | OQU80666 | Zm00001eb175630_P001 | 0.974 |
| PUZ78314 | Sspon.04G | KQL32179 | TKW42341 | EES06040 | Zm00001eb259230_P003 | 0.975 |
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| PUZ60473 | Sspon.08G | KQL10121 | TKW20707 | EER88151 | Zm00001eb371800_P002 | 0.875 |
| PUZ67446 | Sspon.02G | KQL16609 | TKW28779 | EER99601 | Zm00001eb137010_P001 | 0.954 |
| PUZ37360 | Sspon.01G | KQK87446 | TKV91737 | EER90996 | Zm00001eb216290_P001 | 0.939 |
| PUZ77874 | Sspon.04G | KQL31729 | TKW41828 | EES05879 | Zm00001eb256480_P001 | 0.967 |

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| PUZ38039 | Sspon.01GKQK88140 | TKV92599 | EER93838 | Zm00001eb050040_P001 | 0.946 |
| PUZ46950 | Sspon.05GKQK97065 | TKW04144 | EES10698 | Zm00001eb084630_P002 | 0.991 |
| PUZ58738 | Sspon.03GKQL03360 | TKW12109 | EES02226 | genblast_Os01t0223000-01Zm |  |
| PUZ59500 | Sspon.08GKQL12003 | TKW23166 | EER88810 | Zm00001eb224730_P001 | 0.975 |
| PUZ58651 | Sspon.03GKQL04951 | TKW14142 | EES00064 | Zm00001eb119990_P001 | 0.967 |
| PUZ36871 | Sspon.01GKQK86935 | TKV91160 | EER93390 | Zm00001eb213970_P001 | 0.971 |
| PUZ56260 | Sspon.03GKQL05515 | TKW14920 | EES00901 | Zm00001eb356520_P001 | 0.864 |
| PUZ60388 | Sspon.08GKQL10907 | TKW21764 | EER88476 | Zm00001eb277830_P001 | 0.984 |
| PUZ42738 | Sspon.01GKQK92478 | TKV98081 | EER92824 | Zm00001eb403310_P001 | 0.926 |
| PUZ45613 | Sspon.06GKQK95580 | TKW02049 | EES08897 | Zm00001eb115370_P001 | 0.918 |
| PUZ52512 | Sspon.06GKQL02783 | TKW11550 | EES15259 | Zm00001eb037360_P001 | 0.974 |
| PUZ56933 | Sspon.03GKQL04992 | TKW14208 | EES00678 | Zm00001eb340460_P001 | 0.947 |
| PUZ44362 | Sspon.06GKQK94447 | TKW00505 | EES15299 | Zm00001eb036840_P003 | 0.976 |
| PUZ66107 | Sspon.07GKQL15613 | TKW27458 | EES18180 | Zm00001eb287440_P001 | 0.980 |
| PUZ63455 | Sspon.07GKQL13562 | TKW24948 | EES17914 | genblast_Os05t0232500-01_Ze |  |
| PUZ47345 | Sspon.05GKQK97453 | TKW04635 | KXG26406 | Zm00001eb423450_P002 | 0.943 |
| PUZ61679 | Sspon.08GKQL09832 | TKW20340 | EER89404 | genblast_Os06t0211600-01_Ze |  |
| PUZ71382 | Sspon.02GKQL25169 | genblast_ | KXG35959 | Zm00001eb102240_P001 | 0.983 |
| PUZ70073 | Sspon.02GKQL23987 | TKW32429 | EER98620 | Zm00001eb308420_P002 | 0.954 |
| PUZ48942 | Sspon.02GKQK98957 | TKW06619 | OQU9032 | Zm00001eb140630_P001 | 0.935 |
| PUZ62425 | Sspon.04GKQL09067 | TKW19362 | EES07675 | Zm00001eb269370_P001 | 0.874 |
| PUZ69700 | Sspon.02GKQL23659 | TKW32018 | KXG35149 | Zm00001eb095800_P002 | 0.950 |
| PUZ54999 | Sspon.03GKQL06774 | TKW16505 | EES03538 | Zm00001eb154690_P001 | 0.956 |
| PUZ72927 | Sspon.02GKQL26685 | TKW35847 | EER97545 | Zm00001eb327610_P002 | 0.943 |
| PUZ40188 | Sspon.01GKQK89979 | TKV95001 | KXG38939 | Zm00001eb023510_P003 | 0.948 |
| PUZ38853 | Sspon.01GKQK88883 | TKV93602 | KXG38434 | Zm00001eb222430_P004 | 0.970 |
| PUZ59479 | Sspon.08GKQL11978 | TKW23141 | EER90225 | Zm00001eb224560_P004 | 0.976 |
| PUZ54941 | Sspon.06GKQK87418 | TKV91712 | EES14606 | Zm00001eb172160_P003 | 0.977 |
| PUZ75980 | Sspon.01GKQL29931 | TKW39586 | EES06924 | Zm00001eb219540_P001 | 0.860 |
| PUZ57490 | Sspon.03GKQL03907 | TKW12815 | KXG32183 | Zm00001eb127550_P002 | 0.962 |

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| PUZ63250 | Sspon.07G | KQK99373 | TKW07127 | EES16841 | Zm00001eb264310_P001 | 0.902 |
| PUZ74248 | genblast_C | KQL28569 | TKW37809 | EES04587 | Zm00001eb232970_P001 | 0.932 |

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| PUZ63336 | Sspon.07G | KQL13693 | TKW25096 | EES15873 | Zm00001eb133780_P005 | 0.972 |
| PUZ57519 | Sspon.03G | KQL03947 | TKW12852 | KXG32168 | Zm00001eb127300_P001 | 0.956 |

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| PUZ75947 | Sspon.04G | KQL29898 | TKW39524 | KXG30339 | Zm00001eb242820_P001 | 0.933 |
| PUZ76827 | genblast_C | KQL09211 | TKW40642 | KXG31106 | Zm00001eb249040_P001 | 0.979 |

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| PUZ40905 | Sspon.01G | KQK90660 | TKV95857 | EER94784 | Zm00001eb018380_P002 | 0.936 |
| PUZ55349 | Sspon.07G | KQL06427 | TKW16052 | EES03440 | Zm00001eb156690_P001 | 0.962 |
| PUZ57286 | Sspon.03G | KQL03698 | TKW12556 | EES00560 | Zm00001eb128490_P003 | 0.946 |
| PUZ74406 | Sspon.04G | KQL28415 | TKW37611 | EES04652 | Zm00001eb234410_P002 | 0.930 |
| PUZ69176 | Sspon.02G | KQL22989 | TKW31145 | genblast_C | Zm00001eb303290_P001 | 0.925 |
| PUZ57707 | Sspon.03G | KQL04095 | TKW13036 | EES00436 | Zm00001eb334490_P001 | 0.917 |
| PUZ45760 | genblast_C | KQK95775 | TKW02342 | KXG29090 | Zm00001eb115940_P001 | 0.896 |
| PUZ38943 | Sspon.01G | KQK88970 | TKV93716 | KXG38471 | Zm00001eb047520_P004 | 0.958 |
| genblast_C | genblast_C | KQK94045 | TKV99928 | genblast_C | Zm00001eb169040_P001 | 0.957 |

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| PUZ49161 | Sspon.05G | KQK99167 | TKW06885 | EES12951 | Zm00001eb068900_P001 | 0.941 |
| PUZ64260 | Sspon.07G | KQL13805 | TKW25262 | EES17808 | Zm00001eb282990_P001 | 0.939 |
| PUZ59916 | Sspon.08G | KQL11383 | TKW22354 | EER88662 | Zm00001eb388080_P001 | 0.984 |
| PUZ76053 | Sspon.04G | KQL29989 | TKW39672 | EES05228 | Zm00001eb181970_P001 | 0.950 |

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| PUZ53909 | Sspon.07G | KQL07778 | TKW17779 | EES01769 | Zm00001eb367310_P001 | 0.984 |
| PUZ60309 | Sspon.08G | KQL11006 | TKW21887 | OQU76563 | Zm00001eb384640_P002 | 0.944 |
| PUZ47480 | Sspon.05G | KQK97563 | TKW04785 | KXG26469 | Zm00001eb080820_P001 | 0.962 |
| PUZ68620 | Sspon.02G | KQL22647 | TKW30724 | EER95940 | Zm00001eb301280_P001 | 0.962 |
| PUZ42693 | Sspon.01G | genblast_C | TKV98024 | OQU93169 | Zm00001eb005070_P001 | 0.841 |
| PUZ61307 | Sspon.08G | KQL09800 | TKW20298 | EER89414 | Zm00001eb373090_P002 | 0.958 |

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| PUZ44607 | Sspon.07G | genblast_C | TKW24901 | KXG21128 | genblast_Os04t0356600-01 | Zm0 |
| PUZ73266 | genblast_C | KQL26987 | TKW36257 | EER97670 | Zm00001eb110680_P001 | 0.955 |
| PUZ61412 | Sspon.08G | KQL09971 | TKW20512 | EER89459 | Zm00001eb279490_P001 | 0.954 |

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| PUZ41491 | Sspon.01G | KQK91288 | TKV96639 | EER95019 | Zm00001eb396810_P001 | 0.919 |
| PUZ38252 | Sspon.01G | KQK88335 | TKV92866 | EER91355 | Zm00001eb220030_P001 | 0.958 |
| PUZ36082 | Sspon.01G | genblast_Z | TKV90195 | OQU90616 | Zm00001eb064440_P001 | 0.960 |
| PUZ40786 | Sspon.01G | KQK90541 | TKV95723 | genblast_C | Zm00001eb019320_P001 | 0.983 |

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| PUZ42168 | genblast_C | KQK91946 | TKV97431 | EER92639 | Zm00001eb008730_P001 | 0.966 |
| PUZ64746 | Sspon.07G | KQL14275 | TKW25833 | EES18697 | Zm00001eb296160_P001 | 0.962 |
| PUZ36835 | genblast_C | KQK86910 | TKV91113 | KXG37470 | Zm00001eb213890_P002 | 0.961 |
| PUZ44492 | Sspon.05G | KQK94360 | TKW00386 | EES09667 | Zm00001eb168760_P004 | 0.962 |
| PUZ54130 | Sspon.03G | KQL07577 | TKW17545 | EES03837 | Zm00001eb368380_P001 | 0.936 |
| PUZ57855 | Sspon.03G | KQL04230 | TKW13222 | KXG31980 | Zm00001eb125460_P001 | 0.957 |
| genblast_C | Sspon.02G | KQL26257 | TKW35332 | OQU90105 | Zm00001eb324400_P001 | 0.976 |
| PUZ39428 | Sspon.01G | KQK89088 | TKV93861 | OQU91850 | Zm00001eb048660_P002 | 0.963 |
| PUZ73322 | genblast_C | KQL27045 | TKW36326 | EER99862 | Zm00001eb329950_P001 | 0.901 |
| PUZ56424 | Sspon.05G | KQL05351 | TKW14721 | EES12606 | Zm00001eb427930_P001 | 0.934 |
| PUZ41985 | Sspon.01G | KQK91748 | TKV97189 | KXG39799 | Zm00001eb010200_P001 | 0.980 |

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| PUZ49846 | Sspon.02GKQL00258 | TKW0815 | KXG24238 | Zm00001eb174070_P001 | 0.938 |
| PUZ72537 | Sspon.02GKQL26288 | TKW3538 | KXG36500 | Zm00001eb324620_P002 | 0.932 |
| PUZ47467 | Sspon.04GKQK97552 | TKW04774 | EES10934 | Zm00001eb080890_P001 | 0.953 |
| PUZ60518 | Sspon.08GKQL10785 | TKW2163 | EER89830 | Zm00001eb278060_P001 | 0.984 |
| PUZ76393 | Sspon.04GKQL30323 | TKW40104 | EES05371 | Zm00001eb246230_P001 | 0.930 |
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| PUZ48544 | Sspon.05GKQK98542 | TKW0608 | KXG26957 | Zm00001eb428560_P001 | 0.939 |
| genblast_Z | Sspon.03GKQL08239 | TKW1837 | KXG33958 | genblast_Zm00001eb143980_P |  |
| PUZ66768 | genblast_CKQL16117 | TKW28101 | OQU8547 | Zm00001eb284630_P001 | 0.949 |
| PUZ71204 | Sspon.02GKQL24972 | TKW3371 | EER96936 | Zm00001eb101530_P002 | 0.939 |
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| PUZ62359 | Sspon.08GKQL09133 | TKW19462 | EER87780 | Zm00001eb378200_P001 | 0.936 |
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| PUZ53645 | Sspon.07GKQL08013 | TKW1809 | EES01864 | Zm00001eb145660_P001 | 0.990 |
| PUZ50206 | Sspon.06GKQL00719 | TKW08834 | EES14591 | Zm00001eb415700_P004 | 0.946 |
| PUZ41252 | genblast_CKQK91045 | TKV96316 | KXG39450 | Zm00001eb015730_P002 | 0.986 |
| PUZ57322 | Sspon.03GKQL03749 | TKW1262 | EES02742 | Zm00001eb333140_P001 | 0.928 |
| PUZ63688 | Sspon.07GKQL13362 | TKW24667 | OQU7724 | Zm00001eb266620_P001 | 0.952 |
| PUZ44199 | Sspon.05GKQK94112 | TKW0003 | EES09560 | Zm00001eb168010_P001 | 0.903 |
| PUZ54922 | Sspon.03GKQL06840 | TKW16597 | EES03566 | Zm00001eb154120_P001 | 0.922 |
| PUZ52403 | Sspon.06GKQL02674 | TKW11417 | KXG25524 | Zm00001eb175430_P002 | 0.958 |
| PUZ42745 | Sspon.01GKQK92484 | TKV98086 | EER92826 | Zm00001eb004490_P001 | 0.883 |
| PUZ78007 | genblast_CKQL31875 | TKW4199 | EES05936 | Zm00001eb257600_P001 | 0.954 |
| PUZ47208 | Sspon.05GKQK97320 | TKW04464 | EES12192 | Zm00001eb082540_P001 | 0.990 |
| PUZ37976 | Sspon.01GKQK88075 | TKV92506 | OQU9136 | Zm00001eb219040_P001 | 0.978 |

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| PUZ47491 | Sspon.04G | KQK97576 | TKW04800 | EES10946 | Zm00001eb080700_P001 | 0.816 |
| PUZ53933 | Sspon.03G | KQL07763 | TKW17760 | EES03892 | Zm00001eb367490_P003 | 0.953 |
| PUZ46065 | Sspon.05G | KQK96157 | TKW02927 | EES11740 | Zm00001eb338070_P001 | 0.924 |
| PUZ67445 | Sspon.02G | KQL16611 | TKW28782 | KXG23694 | Zm00001eb137040_P002 | 0.938 |
| PUZ64585 | Sspon.07G | KQL14135 | TKW25644 | KXG22620 | Zm00001eb297180_P001 | 0.951 |
| PUZ55040 | Sspon.03G | KQL06726 | TKW16437 | KXG33254 | Zm00001eb154790_P001 | 0.941 |
| PUZ47891 | Sspon.07G | KQK97969 | TKW05293 | KXG26660 | Zm00001eb078080_P004 | 0.972 |

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| PUZ64220 | genblast_C | KQL13759 | TKW25207 | EES17788 | Zm00001eb281900_P001 | 0.939 |
| PUZ67721 | Sspon.02G | KQL17034 | TKW29373 | EES16281 | Zm00001eb135300_P001 | 0.900 |

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|---|---|---|---|---|---|---|
| PUZ40726 | Sspon.01G | KQK90465 | TKV95611 | OQU92409 | Zm00001eb019640_P001 | 0.931 |
| PUZ48191 | Sspon.05G | genblast_C | TKW05645 | KXG26785 | Zm00001eb075560_P005 | 0.948 |
| PUZ76714 | Sspon.04G | KQL30635 | TKW40508 | EES07197 | Zm00001eb248240_P001 | 0.981 |
| PUZ71875 | Sspon.02G | genblast_C | TKW34542 | EER97165 | Zm00001eb320670_P001 | 0.923 |

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| PUZ52189 | Sspon.06G | KQL02443 | TKW11128 | EES14261 | Zm00001eb035180_P001 | 0.911 |

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| PUZ52049 | Sspon.06G | KQL02344 | TKW10995 | EES14313 | Zm00001eb199490_P002 | 0.973 |
| PUZ68393 | Sspon.02G | KQL22419 | TKW30409 | EER97969 | Zm00001eb117610_P001 | 0.969 |
| PUZ43826 | genblast_C | KQK93589 | TKV99288 | KXG27743 | Zm00001eb196970_P003 | 0.973 |
| PUZ77468 | Sspon.04G | KQL31485 | TKW41558 | KXG30767 | Zm00001eb194590_P001 | 0.943 |
| PUZ54790 | Sspon.03G | KQL06976 | TKW16764 | EES01475 | Zm00001eb153200_P004 | 0.979 |
| PUZ70735 | genblast_C | KQL24511 | TKW33175 | EER98910 | Zm00001eb312980_P002 | 0.977 |
| PUZ37676 | Sspon.01G | KQK87829 | TKV92165 | EER91115 | Zm00001eb217880_P001 | 0.967 |
| PUZ71356 | Sspon.02G | KQL25147 | TKW33924 | EER99127 | Zm00001eb317190_P002 | 0.961 |

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| PUZ60305 | Sspon.08G | KQL11007 | TKW21890 | EER88513 | Zm00001eb384620_P001 | 0.981 |
| PUZ44257 | Sspon.05G | KQK94160 | TKW00107 | EES08296 | Zm00001eb167820_P001 | 0.960 |
| PUZ50867 | Sspon.06G | KQL01368 | TKW09740 | KXG24955 | genblast_Zm00001eb177380_P( | |
| PUZ36297 | genblast_C | KQK86395 | TKV90437 | EER93176 | Zm00001eb211470_P001 | 0.950 |
| PUZ64945 | Sspon.07G | KQL14508 | TKW26098 | EES18607 | Zm00001eb294670_P001 | 0.970 |
| PUZ49018 | Sspon.05G | KQK99033 | TKW06724 | EES12896 | Zm00001eb069710_P001 | 0.775 |
| PUZ64767 | Sspon.07G | KQL14310 | TKW25865 | EES18686 | Zm00001eb295940_P001 | 0.876 |
| PUZ56111 | Sspon.03G | KQL01694 | TKW10155 | EES03161 | Zm00001eb160460_P002 | 0.963 |

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| PUZ57836 | Sspon.06G | KQL04212 | TKW13204 | KXG31997 | Zm00001eb125620_P001 | 0.947 |
| PUZ38199 | Sspon.01G | KQK88291 | TKV92807 | EER91339 | Zm00001eb043070_P001 | 0.965 |
| PUZ41523 | Sspon.01G | genblast_C | TKV96682 | EER95036 | genblast_Os03t0291800-01_Zea | |
| PUZ70622 | Sspon.02G | KQL24399 | TKW33024 | KXG35583 | Zm00001eb312040_P001 | 0.976 |
| PUZ40202 | Sspon.01G | KQK89989 | TKV95013 | EER91955 | Zm00001eb391540_P001 | 0.956 |
| PUZ36316 | genblast_C | genblast_C | TKV90459 | KXG37249 | Zm00001eb062790_P002 | 0.986 |

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| PUZ46684 | genblast_C | KQK96800 | TKW03766 | genblast_C | genblast_Os04t0348400-01_Zea | |
| PUZ60294 | Sspon.08G | KQL11037 | TKW21915 | EER89942 | Zm00001eb277460_P001 | 0.933 |
| PUZ40641 | genblast_Z | KQK91901 | TKV97381 | OQU92981 | Zm00001eb009060_P001 | 0.926 |

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| PUZ49854 | Sspon.06G | KQL00268 | TKW08174 | EES13239 | Zm00001eb260590_P001 | 0.918 |
| PUZ47008 | genblast_C | KQL29600 | TKW39129 | KXG29420 | genblast_Os02t0489500-01_Ze | |
| PUZ40467 | Sspon.01G | KQK90265 | TKV95341 | EER92050 | Zm00001eb021220_P001 | 0.972 |
| PUZ64547 | Sspon.07G | KQL14072 | TKW25590 | EES20031 | Zm00001eb297570_P002 | 0.928 |
| PUZ66000 | Sspon.07G | KQL15487 | TKW27306 | EES19524 | Zm00001eb288020_P003 | 0.960 |
| PUZ66164 | genblast_C | KQL15654 | TKW27524 | EES18169 | Zm00001eb287190_P003 | 0.955 |
| genblast_C | Sspon.05G | KQK97992 | TKW05319 | EES12461 | Zm00001eb426130_P001 | 0.938 |

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| PUZ40633 | Sspon.01G | KQK90384 | TKV95505 | OQU92371 | Zm00001eb284380_P002 | 0.888 |
| PUZ71595 | Sspon.02G | KQL25374 | TKW34197 | OQU89793 | Zm00001eb318810_P001 | 0.943 |
| PUZ36730 | Sspon.01G | genblast_C | TKV90993 | EER90785 | Zm00001eb059800_P002 | 0.838 |
| PUZ68862 | Sspon.01G | KQL22915 | TKW31031 | EER96033 | Zm00001eb302800_P001 | 0.988 |
| PUZ48898 | Sspon.05G | KQK98906 | TKW06559 | KXG27108 | Zm00001eb070770_P001 | 0.975 |
| PUZ78012 | genblast_C | KQL31881 | TKW42000 | EES07665 | Zm00001eb257650_P001 | 0.948 |
| PUZ56258 | Sspon.03G | KQL05516 | TKW14921 | EES03116 | Zm00001eb356530_P001 | 0.963 |
| PUZ69086 | Sspon.02G | genblast_C | TKW31241 | EER98235 | Zm00001eb303770_P003 | 0.982 |
| PUZ54508 | Sspon.03G | KQL07225 | TKW17088 | KXG33497 | Zm00001eb369940_P001 | 0.971 |
| PUZ59306 | Sspon.08G | KQL11821 | TKW22920 | EER88883 | Zm00001eb226380_P001 | 0.947 |
| PUZ67293 | Sspon.02G | KQL16756 | TKW28972 | EES16076 | Zm00001eb410800_P001 | 0.953 |
| genblast_C | Sspon.02G | KQL31204 | TKW41218 | EES05630 | Zm00001eb252580_P001 | 0.966 |
| PUZ48952 | Sspon.05G | KQK98967 | TKW06629 | EES11441 | Zm00001eb070410_P001 | 0.952 |
| PUZ74155 | Sspon.04G | genblast_Z | TKW37890 | KXG29518 | Zm00001eb232660_P002 | 0.977 |
| genblast_Z | Sspon.01G | genblast_Z | TKW03462 | EER92066 | Zm00001eb020970_P003 | 0.966 |
| PUZ76787 | Sspon.04G | KQL30696 | TKW40589 | EES07545 | Zm00001eb185970_P001 | 0.974 |

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| PUZ76931 | Sspon.04G | KQL30835 | TKW40767 | OQU85684 | Zm00001eb249830_P001 | 0.988 |
| PUZ36878 | Sspon.01G | KQK86941 | TKV91163 | OQU90932 | Zm00001eb058630_P001 | 0.987 |

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| PUZ50433 | Sspon.06G | KQL00513 | TKW08597 | EES13486 | Zm00001eb413390_P001 | 0.956 |
| PUZ53751 | genblast_C | KQL07920 | TKW17946 | EES01831 | Zm00001eb366570_P001 | 0.962 |
| PUZ76148 | Sspon.04G | KQL30076 | TKW39754 | EES05267 | Zm00001eb244130_P002 | 0.964 |
| PUZ69159 | Sspon.02G | KQL23009 | TKW31174 | EER96074 | Zm00001eb303420_P001 | 0.990 |

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| PUZ40576 | Sspon.01G | KQK90355 | TKV95478 | EER94675 | Zm00001eb393300_P001 | 0.896 |
| PUZ70822 | Sspon.02G | KQL24625 | TKW33305 | EER96781 | Zm00001eb313930_P002 | 0.914 |

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| PUZ54602 | Sspon.03G | KQL07142 | TKW16989 | EES01524 | Zm00001eb370160_P001 | 0.975 |
| PUZ68221 | genblast_C | KQL22135 | TKW30014 | EER95753 | Zm00001eb298680_P001 | 0.953 |
| PUZ72831 | genblast_C | KQL26577 | TKW35705 | EER97500 | Zm00001eb108830_P001 | 0.980 |
| PUZ52998 | Sspon.03G | KQL08618 | TKW18860 | EES04223 | Zm00001eb141030_P001 | 0.899 |
| PUZ51287 | Sspon.06G | KQL01584 | TKW10008 | OQU80369 | genblast_Os08t0379300-01_Zea | |
| PUZ39349 | genblast_C | KQK89370 | TKV94224 | OQU91876 | Zm00001eb027390_P001 | 0.963 |
| PUZ43491 | Sspon.05G | KQK93322 | TKV98974 | EES09162 | Zm00001eb195640_P001 | 0.946 |
| PUZ69324 | Sspon.02G | KQL23298 | TKW31592 | EER98388 | Zm00001eb305600_P001 | 0.937 |
| PUZ53197 | Sspon.03G | KQL08408 | TKW18591 | KXG34023 | Zm00001eb363950_P001 | 0.973 |
| PUZ72450 | Sspon.07G | KQL26214 | TKW35264 | EES09081 | Zm00001eb094310_P001 | 0.959 |
| PUZ66329 | Sspon.07G | KQL15812 | TKW27730 | EES19406 | Zm00001eb285510_P001 | 0.939 |
| PUZ44136 | Sspon.05G | KQK94063 | TKV99961 | EES08246 | Zm00001eb112400_P001 | 0.917 |
| PUZ68741 | Sspon.03G | KQL22776 | TKW30863 | EES15494 | Zm00001eb194920_P001 | 0.927 |
| PUZ68043 | Sspon.02G | KQL17401 | TKW29833 | OQU79722 | Zm00001eb134200_P002 | 0.985 |
| PUZ60813 | Sspon.08G | genblast_C | TKW40425 | EER89263 | Zm00001eb380580_P003 | 0.957 |
| PUZ51672 | Sspon.06G | KQL01976 | TKW10511 | EES13917 | Zm00001eb179760_P001 | 0.927 |
| PUZ67158 | Sspon.02G | KQL16894 | TKW29163 | EES17034 | Zm00001eb408660_P002 | 0.889 |
| PUZ68548 | Sspon.02G | KQL22589 | TKW30629 | KXG34475 | Zm00001eb300970_P001 | 0.912 |
| PUZ38963 | Sspon.01G | KQK88983 | TKV93736 | OQU91735 | Zm00001eb047610_P002 | 0.937 |
| PUZ49275 | Sspon.05G | KQL12870 | TKW23998 | EES11581 | genblast_Os04t0657900-01_Zea | |
| PUZ40410 | Sspon.01G | KQK90207 | TKV95263 | EER94605 | Zm00001eb021640_P001 | 0.936 |
| PUZ69631 | Sspon.02G | KQL23629 | TKW31964 | EER98523 | Zm00001eb307960_P001 | 0.916 |
| PUZ37709 | Sspon.01G | KQK87856 | TKV92200 | KXG37901 | Zm00001eb052690_P003 | 0.975 |

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| PUZ44163 | Sspon.05G | KQK94078 | TKV99988 | EES08260 | Zm00001eb168170_P001 | 0.941 |
| PUZ63304 | genblast_C | KQL13718 | TKW25144 | genblast_C | Zm00001eb411200_P001 | 0.944 |
| PUZ35993 | Sspon.01G | KQK86094 | TKV90074 | KXG37083 | Zm00001eb210460_P001 | 0.983 |

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| PUZ73173 | Sspon.02G | KQL26920 | TKW36168 | OQU90362 | Zm00001eb329160_P001 | 0.889 |
| PUZ40305 | Sspon.01G | KQK90101 | TKV95139 | EER91996 | Zm00001eb022650_P001 | 0.957 |
| PUZ55273 | Sspon.03G | KQL06498 | TKW16148 | EES01292 | Zm00001eb360610_P001 | 0.969 |

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| PUZ62032 | genblast_C | KQL09593 | TKW20027 | EER87920 | Zm00001eb271540_P006 | 0.965 |
| PUZ71999 | Sspon.02G | KQL25748 | TKW34691 | EER99364 | Zm00001eb320030_P001 | 0.938 |

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| genblast_C | Sspon.03G | KQL03747 | TKW12622 | OQU86672 | Zm00001eb128110_P001 | 0.933 |
| PUZ58491 | Sspon.07G | KQL04815 | TKW13964 | EES02308 | Zm00001eb121020_P001 | 0.964 |
| PUZ52779 | Sspon.03G | KQL08807 | TKW19106 | EES04301 | Zm00001eb139720_P001 | 0.979 |
| genblast_C | genblast_C | KQL26841 | TKW36076 | EER97612 | Zm00001eb328630_P001 | 0.934 |

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| PUZ70305 | Sspon.02G | KQL24087 | TKW32600 | OQU89261 | Zm00001eb097990_P001 | 0.951 |
| PUZ54559 | genblast_C | KQL07177 | TKW17027 | EES01534 | Zm00001eb104980_P001 | 0.956 |
| PUZ46866 | Sspon.05G | KQK96980 | TKW04021 | KXG26117 | Zm00001eb085330_P002 | 0.807 |

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| PUZ48586 | Sspon.05G | KQK98590 | TKW06140 | EES12710 | Zm00001eb073030_P002 | 0.990 |

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| PUZ36335 | Sspon.01G | KQK86436 | TKV90498 | KXG37257 | Zm00001eb062580_P001 | 0.913 |

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| PUZ36679 | genblast_C | KQK86766 | TKV90946 | OQU90864 | Zm00001eb060070_P001 | 0.903 |
| PUZ67787 | Sspon.02G | KQL17077 | TKW29451 | KXG23895 | Zm00001eb031110_P003 | 0.879 |
| PUZ70158 | Sspon.02G | KQL24014 | TKW32469 | EER98637 | Zm00001eb309080_P003 | 0.962 |
| PUZ43259 | Sspon.01G | KQK93032 | TKV98718 | EER95677 | Zm00001eb000640_P001 | 0.969 |
| PUZ51850 | Sspon.02G | KQL02155 | TKW10733 | EES15124 | Zm00001eb176650_P001 | 0.889 |
| PUZ37061 | genblast_C | KQK87134 | TKV91393 | KXG37566 | Zm00001eb057050_P001 | 0.980 |

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| PUZ64998 | Sspon.07G | KQL14554 | TKW26147 | EES18583 | Zm00001eb342340_P001 | 0.981 |
| PUZ58589 | Sspon.03G | KQL04906 | TKW14084 | EES02274 | Zm00001eb338230_P001 | 0.911 |
| PUZ41960 | Sspon.01G | KQK91712 | TKV97129 | KXG39784 | Zm00001eb010450_P001 | 0.919 |
| PUZ58310 | genblast_C | genblast_C | TKW13755 | OQU86218 | Zm00001eb122520_P001 | 0.931 |
| PUZ36767 | Sspon.01G | KQK86833 | TKV91030 | genblast_C | Zm00001eb213660_P001 | 0.935 |
| PUZ49063 | Sspon.05G | KQK99072 | TKW06767 | EER91282 | Zm00001eb069640_P002 | 0.956 |
| PUZ51630 | Sspon.05G | KQL01948 | TKW10473 | EES07922 | Zm00001eb196080_P001 | 0.966 |
| PUZ71799 | Sspon.02G | KQL25568 | TKW34437 | OQU89869 | Zm00001eb104120_P001 | 0.929 |
| PUZ59100 | Sspon.08G | KQL12230 | TKW23442 | EER88961 | Zm00001eb272310_P001 | 0.965 |

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| PUZ53679 | Sspon.03G | KQL07980 | TKW18038 | EES01856 | Zm00001eb366250_P001 | 0.976 |
| PUZ38509 | Sspon.01G | KQK88590 | TKV93200 | EER94037 | Zm00001eb045180_P001 | 0.862 |

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| PUZ44010 | Sspon.05G | KQK93913 | TKV99755 | EES09442 | Zm00001eb201390_P001 | 0.961 |
| PUZ42901 | genblast_C | KQK92627 | TKV98270 | EER92868 | Zm00001eb003480_P001 | 0.965 |
| PUZ51797 | Sspon.06G | KQL02078 | TKW10645 | KXG25288 | Zm00001eb177310_P001 | 0.915 |

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| PUZ77420 | Sspon.04G | KQL31286 | TKW41334 | EES07342 | Zm00001eb189080_P001 | 0.960 |

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| PUZ48646 | Sspon.05G | KQK98661 | TKW06218 | KXG27006 | Zm00001eb072560_P003 | 0.956 |
| PUZ53331 | genblast_C | KQL08288 | genblast_C | OQU88099 | Zm00001eb143550_P002 | 0.963 |
| PUZ45139 | Sspon.06G | KQK94870 | TKW01103 | KXG28623 | Zm00001eb197580_P003 | 0.883 |
| PUZ40340 | genblast_C | KQK90138 | TKV95184 | EER92006 | Zm00001eb022280_P005 | 0.970 |
| PUZ52645 | genblast_C | KQL02943 | TKW11731 | KXG25412 | Zm00001eb039740_P003 | 0.925 |

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| PUZ46897 | Sspon.05GKQL07698 | TKW17693 | EES10658 | Zm00001eb085050_P002 | 0.944 |
| PUZ53119 | Sspon.03GKQL08482 | TKW18693 | EES02018 | Zm00001eb363540_P002 | 0.962 |
| PUZ71584 | Sspon.02GKQL25365 | TKW34187 | OQU89788 | Zm00001eb102980_P002 | 0.941 |
| PUZ41763 | Sspon.01Ggenblast_C | TKV96922 | EER95122 | Zm00001eb011910_P001 | 0.991 |
| PUZ48663 | Sspon.05Ggenblast_C | TKW06240 | EES12751 | Zm00001eb072420_P001 | 0.948 |
| PUZ43419 | Sspon.05GKQK99965 | TKW07897 | EES09114 | Zm00001eb276280_P001 | 0.907 |

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| PUZ48773 | Sspon.05GKQK98795 | TKW06389 | EES12808 | Zm00001eb071570_P001 | 0.956 |
| PUZ51043 | Sspon.08GKQL01383 | TKW09756 | EES13732 | Zm00001eb028200_P002 | 0.969 |
| PUZ41871 | Sspon.01GKQK91642 | TKV97033 | EER92535 | Zm00001eb011040_P001 | 0.954 |
| PUZ75742 | Sspon.04GKQL29707 | TKW39245 | EES05094 | Zm00001eb241300_P001 | 0.921 |
| PUZ74348 | Sspon.04GKQL28468 | TKW37682 | EES06374 | Zm00001eb233840_P001 | 0.986 |
| PUZ74057 | Sspon.04GKQL28745 | TKW38006 | EES04520 | Zm00001eb232320_P001 | 0.939 |
| PUZ37411 | Sspon.01GKQK87507 | TKV91796 | EER91017 | Zm00001eb054500_P003 | 0.975 |
| PUZ54093 | Sspon.03Ggenblast_C | TKW17580 | EES03843 | Zm00001eb148790_P001 | 0.950 |

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| PUZ55513 | genblast_CKQL06181 | TKW15779 | EES01202 | Zm00001eb157830_P001 | 0.976 |

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| PUZ72422 | Sspon.02Ggenblast_C | TKW35218 | EER99512 | Zm00001eb323660_P001 | 0.932 |

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| PUZ44248 | Sspon.05G | KQK94154 | TKW00092 | KXG28147 | Zm00001eb167840_P003 | 0.908 |

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|---|---|---|---|---|---|---|
| PUZ38581 | Sspon.01G | KQK88657 | TKV93289 | KXG38303 | Zm00001eb045490_P001 | 0.887 |
| PUZ62977 | Sspon.05G | KQL02773 | TKV99310 | OQU82891 | Zm00001eb197040_P002 | 0.954 |
| PUZ65730 | Sspon.07G | KQL15244 | TKW26990 | EES19627 | Zm00001eb288730_P001 | 0.893 |
| PUZ63646 | Sspon.07G | KQL13397 | TKW24715 | EES18877 | Zm00001eb355970_P001 | 0.978 |
| PUZ49850 | Sspon.06G | KQL00261 | TKW08160 | EES14404 | Zm00001eb260550_P001 | 0.850 |
| PUZ64744 | Sspon.07G | KQL14273 | TKW25831 | EES19962 | Zm00001eb296180_P001 | 0.948 |
| PUZ53326 | Sspon.03G | KQL08290 | TKW18454 | KXG33976 | Zm00001eb364910_P001 | 0.963 |

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| PUZ67903 | Sspon.02G | KQL17289 | TKW29683 | EES17392 | Zm00001eb136130_P001 | 0.948 |
| PUZ77830 | Sspon.04G | KQL31693 | TKW41790 | EES07598 | Zm00001eb193490_P004 | 0.930 |
| PUZ52514 | Sspon.06G | KQL02781 | TKW11547 | EES15258 | Zm00001eb037380_P001 | 0.892 |
| PUZ61518 | Sspon.04G | KQL10086 | TKW20655 | KXG19676 | Zm00001eb279890_P001 | 0.838 |
| PUZ41776 | Sspon.01G | KQK91523 | TKV96907 | EER92502 | Zm00001eb011730_P001 | 0.946 |
| PUZ50234 | Sspon.06G | KQL00695 | TKW08804 | EES14600 | Zm00001eb415590_P001 | 0.959 |
| PUZ61278 | Sspon.08G | KQL09825 | TKW20334 | EER88060 | Zm00001eb279130_P002 | 0.916 |
| PUZ69340 | Sspon.02G | KQL23312 | TKW31606 | EER98397 | Zm00001eb305690_P001 | 0.954 |
| PUZ55506 | Sspon.03G | KQL06190 | TKW15793 | EES03384 | Zm00001eb359560_P001 | 0.935 |
| PUZ68140 | Sspon.01G | KQK85909 | TKW29944 | OQU88287 | Zm00001eb118350_P002 | 0.828 |
| PUZ59309 | Sspon.08G | KQL11823 | TKW22923 | EER88880 | Zm00001eb226360_P001 | 0.950 |
| PUZ37091 | Sspon.01G | KQK87161 | TKV91425 | EER93475 | Zm00001eb215130_P001 | 0.992 |
| PUZ43086 | Sspon.01G | genblast_C | TKV98483 | EER92954 | Zm00001eb001890_P001 | 0.957 |
| PUZ70614 | Sspon.02G | KQL24382 | TKW33008 | OQU89459 | Zm00001eb311920_P001 | 0.874 |
| PUZ61231 | Sspon.08G | KQL10534 | TKW21302 | KXG19959 | Zm00001eb382090_P002 | 0.927 |

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| PUZ67214 | Sspon.08G | KQL16846 | TKW29102 | KXG23504 | Zm00001eb409420_P004 | 0.905 |
| PUZ58911 | genblast_C | KQL03153 | TKW11869 | EER99976 | Zm00001eb339550_P001 | 0.904 |
| PUZ41204 | genblast_C | KQK90988 | TKV96234 | EER92307 | Zm00001eb395080_P001 | 0.935 |
| PUZ45898 | genblast_C | KQK96003 | TKW02756 | OQU84113 | Zm00001eb164480_P001 | 0.841 |
| genblast_C | Sspon.01G | KQK91266 | genblast_C | OQU92745 | Zm00001eb396640_P001 | 0.812 |
| PUZ62526 | Sspon.08G | KQL08959 | TKW19228 | EER89057 | Zm00001eb379140_P001 | 0.971 |

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| PUZ56054 | Sspon.03G | KQL06209 | TKW15818 | EES03185 | Zm00001eb357390_P001 | 0.981 |

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| PUZ39151 | Sspon.01G | KQK89263 | TKV94072 | OQU9192 | Zm00001eb027760_P001 | 0.941 |
| PUZ39436 | Sspon.01G | KQK89093 | TKV93870 | EER94290 | Zm00001eb048620_P001 | 0.918 |
| PUZ46796 | Sspon.05G | KQK96918 | TKW03947 | KXG26065 | Zm00001eb085680_P001 | 0.978 |
| PUZ41540 | Sspon.01G | KQK91327 | TKV96695 | genblast_C | Zm00001eb013380_P002 | 0.952 |
| PUZ72595 | Sspon.02G | KQL26355 | TKW3545 | EER97421 | Zm00001eb325110_P002 | 0.789 |
| PUZ67120 | Sspon.02G | KQL16471 | TKW2856 | OQU7911 | genblast_Os12t0484600-02_Ze | |

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| PUZ62362 | Sspon.08G | genblast_C | TKW1945 | EER89125 | Zm00001eb378210_P001 | 0.969 |
| PUZ56004 | Sspon.03G | KQL05699 | TKW15157 | EES03203 | Zm00001eb357570_P001 | 0.931 |
| PUZ36015 | Sspon.01G | KQK86116 | TKV90102 | EER93074 | Zm00001eb210530_P001 | 0.823 |

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| PUZ51906 | Sspon.06G | KQL02222 | TKW10811 | EES15144 | Zm00001eb038450_P001 | 0.910 |
| PUZ40462 | Sspon.01G | genblast_C | TKV95331 | KXG39048 | Zm00001eb021290_P002 | 0.967 |
| PUZ49731 | Sspon.06G | KQL00144 | TKW0803 | EES14361 | Zm00001eb260210_P004 | 0.967 |
| PUZ74469 | Sspon.04G | KQL28323 | TKW3751 | EES04683 | Zm00001eb236510_P001 | 0.887 |
| PUZ38612 | Sspon.01G | KQK88686 | TKV93328 | EER94066 | Zm00001eb045640_P002 | 0.941 |
| PUZ47627 | Sspon.05G | KQK97712 | TKW0496 | KXG26549 | Zm00001eb079750_P005 | 0.965 |
| PUZ51390 | Sspon.02G | KQL01739 | TKW1020 | EES13816 | Zm00001eb042270_P002 | 0.981 |
| PUZ57214 | Sspon.03G | KQL03636 | TKW12454 | EES02789 | Zm00001eb129080_P002 | 0.949 |

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| PUZ77303 | Sspon.04G | KQL31176 | TKW41187 | EES05641 | Zm00001eb188660_P003 | 0.973 |
| PUZ68437 | Sspon.02G | KQL22472 | TKW3047 | EER97998 | Zm00001eb117500_P004 | 0.950 |
| PUZ73023 | Sspon.02G | KQL26766 | TKW35964 | EER99739 | Zm00001eb328010_P001 | 0.963 |
| PUZ43738 | Sspon.05G | KQK93695 | TKV99409 | EES08023 | Zm00001eb202260_P001 | 0.941 |
| PUZ41354 | Sspon.01G | KQK91144 | TKV96457 | EER94953 | Zm00001eb015070_P001 | 0.948 |
| PUZ40977 | Sspon.01G | KQK90772 | TKV95953 | EER92224 | Zm00001eb017810_P001 | 0.995 |
| PUZ61125 | genblast_C | KQL10473 | TKW21212 | OQU7633 | Zm00001eb381660_P002 | 0.962 |
| PUZ70961 | Sspon.02G | KQL24759 | TKW33457 | KXG35750 | Zm00001eb314700_P002 | 0.927 |
| PUZ71764 | Sspon.02G | KQL25516 | TKW34382 | EER97113 | Zm00001eb331740_P001 | 0.943 |
| PUZ70896 | Sspon.02G | KQL24696 | TKW3338 | KXG35726 | Zm00001eb314270_P001 | 0.968 |
| PUZ73669 | Sspon.04G | KQL27744 | TKW36782 | EES04335 | Zm00001eb209800_P001 | 0.967 |
| PUZ41752 | Sspon.01G | KQK91550 | TKV96929 | EER95119 | Zm00001eb011950_P001 | 0.980 |

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| PUZ51426 | Sspon.06G | KQL01924 | TKW10442 | KXG25217 | Zm00001eb211140_P001 | 0.961 |

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| PUZ47343 | Sspon.05G | KQK97447 | genblast_C | EES10882 | Zm00001eb081610_P002 | 0.977 |
| PUZ38398 | Sspon.01G | KQK88458 | TKV93040 | OQU91545 | Zm00001eb044180_P002 | 0.999 |
| PUZ63133 | Sspon.07G | KQK99523 | TKW07333 | KXG23078 | Zm00001eb408070_P001 | 0.959 |
| PUZ36543 | Sspon.02G | KQK86619 | TKV90767 | EER93233 | Zm00001eb212410_P001 | 0.988 |
| PUZ51399 | Sspon.03G | KQL28796 | TKW38083 | KXG34110 | Zm00001eb178930_P002 | 0.974 |

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| PUZ59993 | Sspon.08G | KQL11467 | TKW22463 | KXG20338 | Zm00001eb386670_P001 | 0.975 |
| PUZ73750 | genblast_C | KQL29022 | TKW38386 | EES06170 | Zm00001eb230170_P001 | 0.969 |
| PUZ59051 | Sspon.08G | KQL12266 | TKW23495 | OQU77124 | Zm00001eb272160_P001 | 0.870 |
| PUZ38786 | Sspon.01G | KQK88833 | TKV93524 | OQU91685 | Zm00001eb222310_P001 | 0.968 |

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| PUZ75273 | Sspon.04G | KQL29318 | TKW38723 | EES06723 | Zm00001eb236820_P003 | 0.983 |
| PUZ68084 | Sspon.02G | KQL17446 | TKW29894 | EES17501 | Zm00001eb033110_P001 | 0.961 |

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| PUZ51381 | Sspon.06G | KQL01727 | TKW10201 | EES13813 | Zm00001eb042230_P001 | 0.992 |
| PUZ38385 | Sspon.01G | KQK88446 | TKV93016 | EER91407 | Zm00001eb044100_P001 | 1.016 |

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| PUZ40417 | Sspon.01G | KQK90213 | TKV95270 | EER94614 | Zm00001eb021620_P001 | 0.910 |
| PUZ53905 | Sspon.03G | KQL07779 | TKW17780 | KXG33716 | Zm00001eb147710_P001 | 0.828 |
| PUZ77041 | Sspon.04G | KQL30925 | TKW40882 | OQU85640 | Zm00001eb187200_P001 | 0.908 |
| PUZ39420 | Sspon.01G | KQK89081 | TKV93848 | OQU91856 | Zm00001eb223550_P002 | 0.911 |
| PUZ72187 | Sspon.02G | KQL25942 | TKW34913 | EER99434 | Zm00001eb105750_P001 | 0.984 |
| PUZ78152 | Sspon.04G | genblast_C | TKW42161 | OQU85917 | Zm00001eb191920_P002 | 0.985 |
| PUZ61155 | Sspon.08G | KQL10446 | TKW21169 | EER89678 | Zm00001eb381520_P001 | 0.972 |

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| PUZ42837 | Sspon.01G | KQK92573 | TKV98204 | EER95499 | Zm00001eb003890_P001 | 0.980 |
| PUZ53552 | Sspon.03G | KQL08097 | TKW18195 | OQU88024 | Zm00001eb144980_P001 | 0.970 |
| PUZ71760 | genblast_C | KQL25512 | TKW34380 | EER99278 | Zm00001eb331760_P001 | 0.928 |
| PUZ47038 | Sspon.05G | KQK97171 | TKW04272 | EES10737 | Zm00001eb083980_P001 | 0.944 |
| PUZ55163 | Sspon.03G | KQL06610 | TKW16285 | KXG33208 | Zm00001eb155530_P003 | 0.965 |

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| PUZ66406 | Sspon.07G | KQL16083 | TKW28067 | OQU77613 | Zm00001eb350660_P004 | 0.940 |
| PUZ41236 | Sspon.01G | KQK91025 | TKV96276 | KXG39440 | Zm00001eb015870_P001 | 0.960 |
| PUZ44952 | Sspon.06G | KQL10044 | TKW20607 | EES09770 | Zm00001eb256370_P001 | 0.975 |
| PUZ61676 | Sspon.08G | KQL10251 | TKW20888 | EER89582 | Zm00001eb380140_P001 | 0.916 |

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| PUZ54266 | Sspon.03G | KQL07439 | TKW17379 | OQU87745 | Zm00001eb149920_P001 | 0.962 |
| PUZ47496 | Sspon.05G | KQK97579 | TKW04803 | EES10949 | Zm00001eb424280_P001 | 0.900 |
| PUZ75859 | Sspon.04G | KQL29824 | TKW39422 | EES05152 | genblast_Os02t0518600-01_Zea | |
| PUZ37393 | Sspon.01G | KQK87474 | TKV91757 | EER93588 | genblast_Os03t0710000-01_Zea | |
| PUZ60118 | Sspon.08G | KQL11581 | TKW22619 | EER89987 | Zm00001eb386130_P001 | 0.970 |
| PUZ57374 | Sspon.03G | KQL03820 | TKW12708 | EES00519 | Zm00001eb128420_P001 | 0.948 |

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| PUZ74613 | Sspon.07G | KQL29471 | TKW38907 | EES15678 | Zm00001eb406610_P001 | 0.817 |
| PUZ42053 | Sspon.01G | KQK91820 | TKV97277 | EER95213 | Zm00001eb399300_P001 | 0.905 |
| PUZ36155 | Sspon.01G | KQK86255 | TKV90280 | EER93123 | Zm00001eb211030_P001 | 0.941 |
| PUZ59904 | Sspon.08G | KQL11376 | TKW22338 | OQU76719 | Zm00001eb388040_P001 | 0.984 |

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| PUZ62068 | Sspon.08G | KQL09625 | TKW20064 | EER89250 | Zm00001eb375830_P002 | 0.950 |
| PUZ56975 | Sspon.03G | KQL03423 | TKW12183 | EES02873 | Zm00001eb130530_P001 | 0.902 |

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| PUZ49065 | Sspon.07G | KQK99079 | TKW06771 | KXG27202 | Zm00001eb069530_P001 | 0.908 |
| PUZ37099 | Sspon.01G | KQK87177 | TKV91439 | EER93483 | Zm00001eb056720_P001 | 0.962 |

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| PUZ62252 | Sspon.08G | KQL09248 | TKW19602 | EER87829 | Zm00001eb377280_P002 | 0.924 |
| PUZ41590 | genblast_C | KQK91382 | TKV96742 | EER95055 | Zm00001eb378810_P001 | 0.964 |
| PUZ36540 | Sspon.02G | KQK86617 | TKV90765 | EER99960 | Zm00001eb111900_P001 | 0.986 |
| genblast_C | Sspon.08G | genblast_C | TKW19348 | KXG19162 | Zm00001eb269290_P001 | 0.964 |
| PUZ74471 | genblast_C | KQL28321 | TKW37516 | KXG29692 | Zm00001eb206130_P001 | 0.978 |

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| PUZ59607 | Sspon.08GKQL11060 | TKW21943 | OQU76834 | Zm00001eb389700_P001 | 0.929 |
| PUZ71942 | Sspon.02GKQL25689 | TKW34620 | EER97179 | Zm00001eb104660_P002 | 0.986 |
| PUZ41483 | Sspon.03GKQK92738 | TKV98375 | OQU88032 | Zm00001eb144720_P001 | 0.985 |
| PUZ72781 | Sspon.02GKQL26519 | TKW35635 | EER99633 | Zm00001eb108400_P003 | 0.953 |
| PUZ37425 | Sspon.01GKQK87520 | TKV91816 | EER93598 | Zm00001eb054400_P001 | 0.922 |
| PUZ52746 | Sspon.06GKQL03035 | TKW24788 | KXG21007 | genblast_Os08t0177800-00_Zea | |

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| PUZ65409 | Sspon.07GKQL14903 | TKW26565 | EES19739 | Zm00001eb291480_P001 | 0.874 |
| PUZ62805 | Sspon.02GKQL23137 | TKV98926 | EER99933 | genblast_Os08t0299200-01_Zea | |
| PUZ77705 | Sspon.04GKQL31577 | TKW41676 | EES05496 | Zm00001eb255410_P001 | 0.927 |
| PUZ71614 | genblast_CKQL25395 | TKW34223 | EER99217 | Zm00001eb319000_P001 | 0.967 |
| genblast_C | genblast_CKQL13163 | TKW24372 | EES17638 | Zm00001eb265280_P001 | 0.969 |

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| PUZ60036 | Sspon.04GKQL11507 | TKW22515 | EER90017 | Zm00001eb386270_P001 | 0.966 |
| PUZ54336 | Sspon.08GKQL07376 | TKW17293 | EES18245 | Zm00001eb375450_P001 | 0.941 |
| PUZ63342 | Sspon.07GKQL13692 | TKW25094 | EES15875 | Zm00001eb133760_P001 | 0.951 |
| PUZ69432 | genblast_CKQL23394 | TKW31717 | EER96297 | Zm00001eb306130_P001 | 0.945 |
| PUZ59838 | Sspon.04GKQL11298 | TKW22221 | EER90082 | Zm00001eb275510_P004 | 0.946 |
| PUZ76805 | Sspon.04GKQL30717 | TKW40616 | EES05817 | Zm00001eb248870_P003 | 1.002 |

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| PUZ37997 | Sspon.01GKQK88099 | TKV92533 | KXG38035 | Zm00001eb219170_P001 | 0.968 |

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| PUZ77517 | Sspon.04G | genblast_CTKW41488 | EES07292 | Zm00001eb253970_P001 | 0.974 |

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| PUZ73055 | Sspon.02GKQL26795 | TKW36021 | EER97593 | Zm00001eb328320_P002 | 0.990 |
| PUZ45508 | Sspon.06GKQK95387 | TKW01787 | OQU83839 | Zm00001eb166820_P001 | 0.880 |
| PUZ41412 | genblast_CKQK91207 | TKV96533 | OQU86260 | Zm00001eb336210_P001 | 0.943 |
| PUZ56360 | genblast_CKQL05420 | TKW14798 | EES00854 | Zm00001eb162990_P001 | 0.958 |
| PUZ38991 | genblast_CKQK89224 | TKV94027 | EER91599 | Zm00001eb222930_P001 | 0.964 |
| PUZ48254 | Sspon.05GKQK98316 | TKW05726 | EES11201 | Zm00001eb075030_P001 | 0.964 |
| PUZ67473 | Sspon.02GKQL16582 | TKW28726 | EES17213 | Zm00001eb028670_P002 | 0.977 |

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| PUZ73467 | Sspon.02G | KQL27192 | TKW36532 | OQU90483 | Zm00001eb111610_P001 | 0.912 |
| PUZ61430 | Sspon.08G | KQL10005 | TKW20560 | EER89468 | Zm00001eb279570_P001 | 0.981 |
| PUZ57221 | genblast_C | KQL03627 | TKW12447 | EES02793 | Zm00001eb317280_P001 | 0.827 |
| PUZ40714 | genblast_C | KQK90456 | TKV95599 | EER92141 | Zm00001eb019720_P005 | 0.940 |
| PUZ42581 | genblast_C | KQK92325 | TKV97908 | EER92760 | Zm00001eb005780_P001 | 0.975 |
| PUZ49020 | Sspon.05G | KQK99034 | TKW06725 | EES11380 | Zm00001eb071730_P001 | 0.973 |
| genblast_C | Sspon.02G | KQL24370 | genblast_C | KXG35570 | Zm00001eb311870_P002 | 0.912 |
| PUZ64142 | Sspon.07G | KQK99281 | TKW07032 | EES19073 | Zm00001eb356360_P005 | 0.951 |

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| PUZ42598 | Sspon.01G | KQK92343 | TKV97936 | KXG40075 | Zm00001eb005600_P001 | 0.972 |

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| PUZ56404 | Sspon.02G | KQL05361 | TKW14738 | EER96506 | Zm00001eb308830_P002 | 0.961 |

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| PUZ77141 | Sspon.04G | KQL31010 | TKW40988 | KXG30977 | Zm00001eb251130_P001 | 0.972 |
| PUZ37350 | Sspon.01G | KQK87433 | TKV91728 | EER93571 | Zm00001eb055060_P001 | 0.971 |
| PUZ73465 | Sspon.02G | KQL27194 | TKW36536 | EER99921 | Zm00001eb330760_P001 | 0.960 |
| PUZ55988 | Sspon.02G | genblast_C | TKW32698 | KXG35436 | Zm00001eb309960_P001 | 0.985 |

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|---|---|---|---|---|---|---|
| PUZ36623 | genblast_C | KQK86694 | TKV90862 | EER93302 | Zm00001eb213060_P001 | 0.967 |
| PUZ66170 | Sspon.07G | KQL15663 | TKW27536 | EES19469 | genblast_Os05t0389500-01_Zea | |
| PUZ43575 | genblast_C | KQK99770 | TKW07653 | KXG22854 | Zm00001eb405250_P001 | 0.929 |
| PUZ77939 | Sspon.04G | KQL31802 | TKW41914 | EES07640 | Zm00001eb193030_P001 | 0.927 |
| PUZ36634 | Sspon.01G | KQK86711 | TKV90879 | KXG37375 | Zm00001eb060470_P001 | 0.925 |
| PUZ76986 | Sspon.04G | KQL30881 | TKW40829 | KXG31039 | Zm00001eb187000_P001 | 0.958 |
| PUZ47884 | genblast_C | KQK97959 | TKW05276 | EES11079 | Zm00001eb078120_P002 | 0.996 |

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|---|---|---|---|---|---|---|
| genblast_C | Sspon.04G | KQL29242 | TKW38643 | EES04954 | Zm00001eb237060_P001 | 0.985 |
| PUZ68089 | Sspon.02G | KQL17449 | TKW29896 | EES16459 | Zm00001eb134010_P002 | 0.969 |
| PUZ36208 | Sspon.01G | KQK86344 | TKV90383 | KXG37195 | Zm00001eb063640_P001 | 0.918 |
| PUZ73111 | Sspon.02G | KQL26857 | TKW36093 | OQU90336 | Zm00001eb110010_P001 | 0.983 |
| PUZ41666 | Sspon.01G | KQK91454 | TKV96829 | EER92464 | Zm00001eb012570_P001 | 0.972 |
| PUZ78302 | Sspon.04G | KQL32164 | TKW42325 | EES07775 | Zm00001eb191110_P003 | 0.932 |
| PUZ57356 | Sspon.03G | KQL03802 | TKW12692 | EES00527 | Zm00001eb348930_P003 | 0.969 |
| PUZ37517 | genblast_C | KQK87626 | TKV91935 | EER91052 | Zm00001eb053650_P003 | 0.973 |
| PUZ74040 | Sspon.04G | KQL28761 | TKW38030 | EES04511 | Zm00001eb232190_P002 | 0.968 |
| PUZ70259 | genblast_C | KQL23792 | TKW32203 | EES16382 | Zm00001eb308210_P003 | 0.955 |

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| PUZ46345 | Sspon.05G | KQK96376 | TKW03176 | OQU8115 | Zm00001eb088260_P001 | 0.864 |
| PUZ59590 | Sspon.08G | KQL11043 | TKW21922 | EER90182 | Zm00001eb274380_P001 | 0.941 |
| PUZ51057 | genblast_C | genblast_C | TKW09745 | OQU8749 | Zm00001eb038720_P004 | 0.917 |
| PUZ65130 | Sspon.07G | KQL14691 | TKW26290 | OQU7832 | Zm00001eb293720_P001 | 0.942 |
| PUZ37882 | Sspon.01G | KQK88010 | TKV92390 | KXG37970 | Zm00001eb050930_P002 | 0.959 |
| PUZ77913 | genblast_C | KQL31767 | TKW41871 | EES05889 | Zm00001eb256920_P001 | 0.969 |
| PUZ58817 | Sspon.03G | genblast_Z | TKW11997 | EES00012 | Zm00001eb119290_P001 | 0.919 |
| PUZ44585 | Sspon.05G | genblast_C | TKW00255 | EES08350 | Zm00001eb169160_P001 | 0.958 |
| PUZ76629 | Sspon.04G | KQL30561 | TKW40406 | EES05452 | Zm00001eb247580_P001 | 0.950 |
| PUZ54573 | Sspon.03G | KQL07168 | TKW17017 | KXG33464 | genblast_Os01t0771100-01_Ze | |
| PUZ59612 | Sspon.08G | KQL11064 | TKW21947 | OQU7682 | Zm00001eb274430_P001 | 0.971 |
| PUZ58321 | Sspon.03G | KQL04666 | TKW13779 | EES02363 | Zm00001eb122440_P001 | 0.986 |
| PUZ74951 | Sspon.04G | KQL29121 | TKW38505 | OQU8479 | Zm00001eb203460_P002 | 0.947 |
| PUZ71776 | Sspon.02G | genblast_C | TKW34392 | genblast_C | Zm00001eb319860_P001 | 0.949 |
| PUZ49366 | Sspon.05G | KQL12941 | TKW24080 | KXG27359 | genblast_Os09t0255000-01Zm | |
| PUZ49757 | Sspon.06G | KQL00164 | TKW08052 | KXG24171 | Zm00001eb174480_P001 | 0.982 |
| PUZ61032 | Sspon.08G | KQL10366 | TKW21048 | EER88272 | Zm00001eb281080_P002 | 0.975 |
| PUZ77066 | Sspon.04G | KQL30951 | TKW40906 | EES05729 | Zm00001eb250680_P001 | 0.955 |
| PUZ63891 | Sspon.07G | KQL13229 | TKW24478 | EES17660 | Zm00001eb417220_P001 | 0.922 |
| PUZ74408 | Sspon.04G | KQL28400 | TKW03986 | EES04654 | Zm00001eb234470_P001 | 0.943 |
| PUZ38515 | Sspon.01G | KQK88598 | TKV93211 | KXG38283 | Zm00001eb045210_P002 | 0.973 |
| PUZ58447 | Sspon.03G | KQL04788 | TKW13935 | EES00142 | Zm00001eb337530_P002 | 0.939 |

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| PUZ37512 | Sspon.01G | KQK87616 | TKV91928 | EER91050 | Zm00001eb053700_P001 | 0.970 |
| PUZ48520 | genblast_C | KQK98513 | TKW06048 | EES12690 | Zm00001eb073650_P001 | 0.980 |
| PUZ77949 | Sspon.04G | KQL31816 | TKW41932 | EES07645 | Zm00001eb192920_P001 | 0.986 |
| PUZ62508 | Sspon.04G | KQL27785 | genblast_Z | KXG29986 | Zm00001eb237720_P001 | 0.969 |
| PUZ48988 | Sspon.02G | KQL24347 | TKW32977 | KXG35557 | Zm00001eb311790_P001 | 0.968 |
| PUZ67343 | Sspon.02G | KQL16703 | TKW28889 | EES16100 | Zm00001eb410420_P001 | 0.929 |
| PUZ59488 | genblast_C | KQL11990 | TKW23153 | EER90219 | Zm00001eb224620_P001 | 0.980 |
| PUZ47867 | genblast_C | KQK97939 | TKW05253 | EES11073 | Zm00001eb078220_P001 | 0.984 |
| PUZ36925 | Sspon.01G | KQK86990 | TKV91231 | EER90849 | Zm00001eb214380_P001 | 0.973 |
| PUZ61546 | genblast_C | KQL10112 | TKW20698 | EER89506 | Zm00001eb371840_P001 | 0.918 |
| PUZ56544 | genblast_C | KQK94571 | TKW01927 | genblast_C | genblast_Os08t0331900-01_Zea | |
| PUZ48547 | Sspon.05G | KQK98544 | TKW06084 | EES12695 | Zm00001eb428550_P002 | 0.960 |
| PUZ71055 | Sspon.02G | KQL24851 | TKW33557 | OQU89631 | Zm00001eb101050_P001 | 0.926 |
| PUZ54042 | genblast_C | KQL07659 | TKW17638 | KXG33669 | genblast_Os01t0840200-01_Zea | |
| PUZ66245 | genblast_C | KQL15735 | genblast_C | OQU77891 | Zm00001eb285110_P001 | 0.953 |
| PUZ50962 | Sspon.08G | KQL01166 | TKW09481 | EER89590 | Zm00001eb380300_P001 | 0.983 |
| PUZ68873 | Sspon.02G | KQL22933 | TKW31048 | KXG34639 | Zm00001eb302880_P001 | 0.966 |
| PUZ63493 | Sspon.07G | genblast_C | TKW24909 | EES19248 | Zm00001eb350510_P002 | 1.000 |
| PUZ38278 | Sspon.01G | KQK88361 | TKV92892 | KXG38182 | Zm00001eb220240_P001 | 0.983 |
| PUZ41391 | Sspon.01G | KQK91191 | TKV96510 | KXG39527 | Zm00001eb014740_P001 | 0.969 |

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| PUZ59720 | Sspon.08G | KQL11160 | TKW22060 | EER88745 | Zm00001eb388810_P001 | 0.993 |
| PUZ70969 | Sspon.02G | KQL24767 | TKW33465 | EER96841 | Zm00001eb100450_P004 | 0.970 |
| PUZ47761 | Sspon.05G | KQK97847 | TKW05127 | EES12421 | Zm00001eb425520_P001 | 0.986 |
| PUZ76648 | Sspon.04G | KQL30573 | TKW40424 | OQU85345 | Zm00001eb247690_P001 | 0.954 |
| PUZ77747 | genblast_C | KQL31614 | TKW41713 | KXG31158 | Zm00001eb255680_P002 | 0.964 |
| PUZ48121 | Sspon.05G | KQK98187 | TKW05562 | EES11150 | Zm00001eb076700_P001 | 0.969 |
| PUZ41710 | Sspon.01G | KQK91591 | TKV96961 | EER92486 | Zm00001eb012160_P001 | 0.988 |
| PUZ71629 | genblast_C | KQL25409 | TKW34237 | EER99225 | Zm00001eb319240_P003 | 0.999 |
| PUZ54262 | Sspon.03G | KQL07444 | TKW17383 | EES03790 | Zm00001eb149890_P002 | 0.966 |
| PUZ43227 | Sspon.01G | KQK93005 | TKV98661 | OQU93403 | Zm00001eb404110_P001 | 0.957 |
| PUZ77985 | Sspon.04G | KQL31854 | TKW41973 | EES07653 | Zm00001eb257420_P001 | 0.945 |
| PUZ73724 | Sspon.07G | KQL29091 | TKW38473 | OQU78628 | Zm00001eb353990_P001 | 0.906 |
| PUZ55710 | Sspon.03G | KQL05985 | genblast_Z | EES01117 | Zm00001eb358800_P002 | 0.883 |
| PUZ55566 | Sspon.03G | KQL06125 | TKW15716 | genblast_C | Zm00001eb158210_P002 | 0.964 |
| PUZ41920 | Sspon.01G | KQK91679 | TKV97083 | KXG39770 | Zm00001eb010680_P001 | 0.991 |
| PUZ37476 | Sspon.01G | KQK87578 | TKV91891 | EER93613 | Zm00001eb054020_P001 | 0.967 |

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| PUZ58148 | Sspon.03G | KQL04503 | TKW13554 | OQU86274 | Zm00001eb123660_P001 | 0.975 |
| PUZ55387 | Sspon.03G | KQL06384 | TKW16008 | KXG33099 | Zm00001eb157010_P001 | 0.955 |
| PUZ65888 | Sspon.03G | KQL15381 | TKW27153 | KXG22055 | Zm00001eb288540_P005 | 0.963 |
| PUZ45059 | Sspon.06G | KQK94791 | TKW01004 | EES08586 | Zm00001eb198100_P001 | 0.949 |
| PUZ49442 | genblast_C | KQL12990 | TKW24162 | EES13066 | Zm00001eb066800_P001 | 0.949 |
| PUZ58726 | Sspon.03G | KQL13515 | TKW24883 | KXG31537 | Zm00001eb338880_P001 | 0.871 |
| PUZ38523 | Sspon.01G | KQK88600 | TKV93218 | EER91455 | Zm00001eb220990_P001 | 0.974 |
| PUZ44508 | Sspon.05G | KQK94336 | TKW00359 | EES08386 | Zm00001eb168670_P001 | 0.981 |
| PUZ40700 | Sspon.01G | KQK90440 | TKV95578 | EER94698 | genblast_Os03t0411600-00_Ze | |

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| PUZ59151 | Sspon.08G | KQL12172 | TKW23375 | EER88945 | Zm00001eb272560_P001 | 0.975 |
| PUZ59940 | Sspon.08G | KQL11419 | TKW22402 | EER88648 | Zm00001eb388290_P001 | 0.969 |
| PUZ36544 | Sspon.01G | KQK86621 | TKV90768 | EER90722 | Zm00001eb212760_P001 | 0.997 |
| PUZ36625 | Sspon.01G | KQK86700 | TKV90868 | KXG37374 | Zm00001eb213090_P001 | 0.877 |
| PUZ49569 | Sspon.05G | KQL12727 | TKW23827 | EES13120 | Zm00001eb433970_P001 | 0.962 |

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| PUZ50273 | Sspon.06G | KQL00664 | TKW08773 | EES13415 | Zm00001eb415250_P001 | 0.935 |

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| PUZ76617 | Sspon.01G | KQL30547 | TKW40392 | EES07164 | Zm00001eb185040_P001 | 0.951 |

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| PUZ52104 | Sspon.06G | KQL02389 | TKW11051 | EES14287 | Zm00001eb199660_P001 | 0.913 |
| PUZ72166 | Sspon.02G | KQL25915 | TKW34886 | EER97263 | genblast_Os07t0564100-01_Ze |  |
| PUZ55656 | Sspon.03G | KQL06038 | TKW15574 | EES03332 | Zm00001eb359100_P001 | 0.924 |
| PUZ59811 | Sspon.08G | KQL11268 | TKW22175 | EER88703 | Zm00001eb387160_P001 | 0.967 |
| PUZ48025 | Sspon.05G | KQK98105 | TKW05462 | EES11118 | genblast_Os04t0517500-01_Ze |  |
| PUZ77623 | Sspon.04G | KQL31510 | TKW41580 | EES05527 | Zm00001eb254910_P004 | 0.963 |
| PUZ54929 | Sspon.03G | KQL06829 | TKW16579 | EES01411 | Zm00001eb361960_P001 | 0.986 |
| PUZ69746 | Sspon.07G | KQL28045 | TKW37166 | EER92101 | Zm00001eb393310_P001 | 0.977 |
| PUZ54885 | genblast_C | KQL06881 | TKW16643 | OQU8749 | Zm00001eb153900_P001 | 0.944 |
| PUZ36751 | Sspon.01G | KQK86819 | TKV91017 | KXG37436 | Zm00001eb213570_P002 | 0.939 |
| PUZ77532 | Sspon.04G | KQL31420 | TKW41469 | KXG30803 | Zm00001eb190390_P001 | 0.971 |
| PUZ36279 | Sspon.01G | KQK86379 | TKV90420 | KXG37228 | Zm00001eb063170_P001 | 1.000 |
| PUZ65334 | Sspon.07G | KQL14854 | TKW26499 | EES19766 | Zm00001eb291900_P001 | 0.909 |
| PUZ42334 | Sspon.01G | KQK92101 | TKV97624 | EER92688 | Zm00001eb007820_P003 | 0.942 |
| PUZ73401 | Sspon.02G | KQL27113 | TKW36410 | EER97704 | Zm00001eb330310_P001 | 0.976 |
| PUZ54379 | Sspon.03G | KQL07332 | TKW17241 | KXG33551 | Zm00001eb150810_P001 | 0.961 |
| PUZ36803 | genblast_C | KQK86875 | TKV91067 | genblast_C | Zm00001eb059190_P001 | 0.966 |
| PUZ37704 | Sspon.01G | KQK87849 | TKV92193 | KXG37899 | Zm00001eb052670_P001 | 0.900 |
| PUZ42094 | Sspon.01G | KQK91859 | TKV97337 | EER92613 | Zm00001eb009370_P002 | 0.962 |
| PUZ72959 | Sspon.02G | KQL26716 | TKW35892 | OQU9027 | Zm00001eb327760_P001 | 0.865 |
| PUZ65413 | Sspon.07G | KQL14908 | TKW26574 | EES19738 | Zm00001eb291420_P001 | 0.938 |
| PUZ77404 | Sspon.04G | KQL31270 | TKW41312 | EES05613 | Zm00001eb253070_P001 | 0.908 |

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| PUZ71467 | genblast_C | KQL25234 | TKW34028 | OQU89754 | genblast_Os09t0508250-00_Ze | |
| PUZ46409 | Sspon.05G | genblast_C | TKW03247 | EES11923 | Zm00001eb087050_P001 | 0.977 |

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| PUZ48689 | Sspon.05G | KQK94165 | TKW00114 | OQU82230 | Zm00001eb072230_P001 | 0.911 |
| genblast_C | genblast_C | genblast_C | TKW41038 | EER99673 | Zm00001eb251360_P001 | 0.975 |
| PUZ66333 | Sspon.07G | KQL15813 | TKW27732 | KXG21836 | Zm00001eb285520_P003 | 0.925 |
| PUZ57417 | Sspon.03G | KQL03852 | TKW12747 | EES00508 | Zm00001eb127860_P004 | 0.962 |
| PUZ61540 | Sspon.04G | KQL10102 | TKW20692 | EES07284 | Zm00001eb254150_P001 | 0.855 |
| PUZ36556 | genblast_C | KQK86631 | TKV90783 | EER93278 | Zm00001eb061120_P001 | 0.981 |
| PUZ36933 | Sspon.01G | KQK87003 | TKV91245 | KXG37500 | Zm00001eb058000_P001 | 0.980 |
| PUZ67212 | Sspon.02G | genblast_C | TKW29108 | EES16016 | genblast_Os12t0502200-01_Ze | |
| PUZ60444 | Sspon.08G | KQL10854 | TKW21703 | EER88444 | Zm00001eb383310_P001 | 0.957 |
| PUZ41657 | genblast_C | genblast_C | TKV96816 | EER92461 | Zm00001eb012660_P001 | 0.904 |
| PUZ43331 | Sspon.01G | KQK93108 | TKV98786 | KXG40437 | Zm00001eb000170_P003 | 0.936 |
| PUZ71869 | Sspon.02G | genblast_C | genblast_C | OQU89905 | Zm00001eb320750_P001 | 0.950 |
| PUZ73731 | Sspon.06G | KQK87000 | TKV91240 | EER88460 | Zm00001eb261690_P002 | 0.950 |
| PUZ46188 | Sspon.03G | KQK96334 | TKW03132 | EES10416 | Zm00001eb211510_P001 | 0.939 |
| PUZ70686 | Sspon.02G | KQL24472 | TKW33106 | KXG35621 | Zm00001eb312490_P001 | 0.948 |
| PUZ67278 | Sspon.02G | genblast_C | TKW28994 | KXG23576 | Zm00001eb410890_P002 | 0.939 |
| PUZ64542 | Sspon.07G | KQL14069 | TKW25578 | EES20033 | genblast_Os05t0587400-01_Ze | |

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| PUZ72486 | genblast_C | KQL26244 | TKW35299 | EER99532 | Zm00001eb106890_P001 | 0.972 |
| PUZ59596 | Sspon.08G | KQL11045 | TKW21926 | EER90179 | Zm00001eb389820_P001 | 0.955 |
| PUZ67228 | genblast_C | KQL16828 | TKW29081 | EES16032 | Zm00001eb138070_P002 | 0.857 |
| PUZ41385 | Sspon.01G | KQK91184 | TKV96503 | OQU92711 | Zm00001eb014810_P001 | 0.948 |

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| PUZ74733 | Sspon.04G | KQL28114 | TKW37240 | EES06527 | Zm00001eb205110_P001 | 0.938 |
| PUZ65878 | Sspon.07G | KQL15371 | TKW27133 | KXG22057 | Zm00001eb348860_P001 | 0.960 |

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| PUZ39908 | Sspon.01G | KQK89744 | TKV94704 | EER94425 | Zm00001eb025030_P001 | 0.987 |
| PUZ37410 | genblast_C | KQK87506 | TKV91795 | EER93591 | genblast_Os03t0708000-01_Ze | |
| PUZ57022 | Sspon.03G | KQL03448 | TKW12222 | EES00643 | Zm00001eb339970_P001 | 0.980 |
| PUZ65506 | Sspon.07G | KQL15004 | TKW26711 | EES19702 | Zm00001eb290750_P001 | 0.959 |
| PUZ52203 | genblast_C | KQL02456 | TKW11146 | KXG25625 | Zm00001eb035320_P001 | 0.921 |
| PUZ72256 | Sspon.02G | KQL26020 | TKW35018 | KXG36348 | genblast_Os07t0517800-00_Ze | |
| PUZ38384 | Sspon.05G | genblast_C | TKV93013 | EES12776 | Zm00001eb430090_P001 | 0.965 |
| PUZ65756 | genblast_C | KQL15269 | TKW27019 | EES18309 | Zm00001eb289000_P001 | 0.962 |
| PUZ38112 | Sspon.01G | KQK88197 | TKV92702 | EER93872 | Zm00001eb049190_P001 | 0.960 |
| genblast_C | Sspon.02G | KQK85914 | TKW29940 | KXG34242 | Zm00001eb118400_P001 | 0.974 |
| PUZ41492 | Sspon.01G | KQK91290 | TKV96641 | EER95020 | Zm00001eb396820_P002 | 0.963 |
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| PUZ60861 | Sspon.08G | KQL10272 | TKW20917 | EER89594 | Zm00001eb380390_P001 | 0.927 |
| PUZ70843 | genblast_C | KQL24652 | TKW33336 | EER98970 | Zm00001eb314050_P001 | 0.970 |
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| PUZ77090 | Sspon.02G | KQL30968 | TKW40935 | EES05721 | Zm00001eb321290_P001 | 0.839 |
| PUZ40931 | Sspon.01G | KQK90721 | TKV95893 | EER92214 | Zm00001eb018120_P001 | 0.959 |
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| PUZ47472 | Sspon.05G | KQK97557 | TKW04778 | EES12286 | Zm00001eb424030_P001 | 0.992 |
| PUZ41565 | Sspon.01G | KQK91353 | TKV96716 | OQU92781 | Zm00001eb013150_P002 | 0.929 |
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| PUZ75308 | Sspon.02G | KQL29342 | TKW38761 | KXG34441 | Zm00001eb240650_P001 | 0.958 |
| PUZ55548 | Sspon.03G | genblast_C | TKW15733 | EES03365 | genblast_Os01t0654400-01_Ze | |
| PUZ62527 | Sspon.08G | KQL08960 | TKW19229 | EER89058 | Zm00001eb379130_P001 | 0.988 |
| PUZ59670 | Sspon.08G | KQL11111 | TKW22004 | KXG20524 | Zm00001eb274760_P001 | 0.977 |

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| PUZ56725 | Sspon.03GKQL05117 | TKW14386 | OQU86843 | Zm00001eb131620_P001 | 0.979 |
| PUZ54316 | genblast_CKQL07388 | TKW17308 | KXG33576 | Zm00001eb150400_P003 | 0.942 |
| PUZ36324 | Sspon.01GKQK86424 | TKV90483 | OQU90715 | Zm00001eb211680_P001 | 0.950 |
| PUZ77338 | Sspon.04GKQL31213 | TKW41225 | KXG30887 | Zm00001eb188950_P002 | 0.947 |
| PUZ64705 | Sspon.03GKQL14225 | TKW25778 | OQU78453 | Zm00001eb344210_P003 | 0.889 |
| PUZ53448 | Sspon.03GKQL08177 | TKW18306 | EES01913 | Zm00001eb365590_P001 | 0.970 |
| PUZ59853 | Sspon.08GKQL11315 | TKW22248 | OQU76745 | Zm00001eb275570_P001 | 0.943 |

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| PUZ36329 | Sspon.01GKQK86428 | TKV90491 | EER90623 | Zm00001eb211690_P001 | 0.952 |
| PUZ58631 | Sspon.03GKQL04939 | TKW14127 | EES00074 | Zm00001eb120150_P003 | 0.792 |
| PUZ70270 | Sspon.02GKQL24069 | TKW32560 | EER96535 | Zm00001eb309530_P001 | 0.940 |
| PUZ76516 | Sspon.04GKQL30453 | TKW40256 | EES05411 | Zm00001eb246860_P001 | 0.982 |
| PUZ73435 | Sspon.02GKQL27074 | TKW36363 | KXG36887 | Zm00001eb110980_P001 | 0.973 |
| PUZ40733 | genblast_CKQK90471 | TKV95616 | EER92151 | Zm00001eb019590_P001 | 0.975 |
| PUZ46410 | Sspon.05GKQL15546 | TKW27390 | OQU81553 | genblast_Os09t0133000-01Zm0 |  |
| PUZ37920 | genblast_CKQK88044 | TKV92443 | EER93785 | Zm00001eb051200_P003 | 0.930 |
| PUZ62042 | Sspon.08GKQL09602 | TKW20039 | EER89264 | Zm00001eb375600_P001 | 0.930 |
| PUZ36066 | Sspon.01GKQK86173 | TKV90181 | EER90514 | Zm00001eb210770_P001 | 0.983 |
| PUZ40182 | Sspon.01GKQK89971 | TKV94994 | EER91946 | Zm00001eb023450_P001 | 0.981 |
| PUZ38897 | Sspon.01GKQK88924 | TKV93657 | EER91565 | Zm00001eb047240_P002 | 0.951 |
| PUZ40332 | Sspon.07GKQK90130 | TKV95173 | KXG22919 | Zm00001eb405990_P001 | 0.960 |
| PUZ63381 | Sspon.07GKQL13634 | TKW25034 | KXG23363 | Zm00001eb133570_P001 | 0.966 |
| PUZ62905 | Sspon.05GKQK93523 | TKV99198 | EES09238 | Zm00001eb093130_P001 | 0.948 |
| PUZ60389 | genblast_CKQL10898 | TKW21756 | EER89876 | genblast_Os06t0538900-01_Zea |  |
| PUZ67581 | Sspon.02GKQL16916 | TKW29195 | KXG23787 | Zm00001eb029550_P001 | 0.973 |
| PUZ63794 | Sspon.07GKQL13138 | TKW24350 | EES17631 | Zm00001eb265510_P001 | 0.987 |
| PUZ73581 | Sspon.02GKQL27298 | TKW36675 | KXG37036 | Zm00001eb331570_P002 | 0.964 |

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| PUZ43314 | genblast_C | KQK93098 | TKV98771 | EER93042 | Zm00001eb404520_P001 | 0.973 |
| PUZ58200 | Sspon.03G | KQL04551 | TKW13618 | KXG31784 | Zm00001eb123280_P003 | 0.815 |
| PUZ43449 | Sspon.07G | KQK93367 | TKW07517 | KXG22935 | Zm00001eb163880_P001 | 0.932 |
| PUZ61777 | Sspon.08G | KQL09898 | TKW20415 | EER89389 | Zm00001eb373760_P001 | 0.949 |
| PUZ78146 | Sspon.06G | KQL32013 | TKW42150 | KXG24512 | Zm00001eb172140_P002 | 0.927 |
| PUZ54638 | Sspon.03G | KQL07112 | TKW16951 | KXG33438 | Zm00001eb370310_P002 | 0.951 |
| PUZ76089 | Sspon.04G | genblast_C | TKW39717 | KXG30414 | Zm00001eb243640_P003 | 0.968 |
| PUZ73984 | Sspon.04G | KQL28820 | TKW38114 | KXG29425 | Zm00001eb231770_P001 | 0.978 |
| PUZ46935 | genblast_C | KQK97052 | TKW04115 | EES12063 | Zm00001eb084710_P001 | 0.941 |
| PUZ47955 | Sspon.05G | KQK98032 | TKW05369 | OQU81941 | Zm00001eb077380_P001 | 0.959 |
| PUZ42130 | genblast_C | KQK91908 | TKV97385 | EER92625 | Zm00001eb008970_P001 | 0.970 |
| PUZ57880 | Sspon.03G | KQL04251 | TKW13251 | EES02550 | Zm00001eb335220_P001 | 0.985 |
| PUZ72305 | Sspon.08G | KQK99593 | TKW07436 | EER88837 | Zm00001eb194600_P001 | 0.950 |
| PUZ60866 | Sspon.08G | KQK85757 | TKW21456 | EER88430 | Zm00001eb281490_P001 | 0.899 |
| PUZ63396 | Sspon.08G | KQL13615 | TKW25015 | OQU76903 | Zm00001eb225370_P001 | 0.958 |
| PUZ37610 | Sspon.01G | KQK87739 | TKV92074 | OQU91204 | Zm00001eb217400_P001 | 0.894 |
| PUZ42009 | Sspon.01G | KQK91775 | TKV97218 | EER95200 | Zm00001eb010040_P003 | 0.990 |
| PUZ77491 | Sspon.04G | KQL31464 | TKW41531 | KXG30786 | Zm00001eb254190_P001 | 0.968 |
| PUZ36132 | Sspon.01G | genblast_C | TKV90244 | EER93113 | Zm00001eb112030_P001 | 0.923 |
| PUZ77788 | Sspon.08G | KQL31663 | TKW41764 | EES07583 | Zm00001eb373350_P001 | 0.913 |
| genblast_C | Sspon.04G | KQK98520 | TKW06057 | EES11285 | Zm00001eb073590_P001 | 0.980 |
| PUZ68761 | Sspon.02G | KQL22800 | TKW30897 | OQU88602 | Zm00001eb116580_P004 | 0.968 |

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|---|---|---|---|---|---|---|
| PUZ54185 | Sspon.03G | KQL07524 | TKW17483 | OQU87769 | Zm00001eb149360_P002 | 0.908 |
| PUZ53074 | Sspon.03G | KQL08542 | genblast_Z | OQU88172 | Zm00001eb363330_P001 | 0.943 |
| PUZ60728 | Sspon.08G | KQL10259 | TKW20900 | KXG19770 | Zm00001eb280420_P004 | 0.939 |
| PUZ42673 | Sspon.01G | KQK92413 | TKV98010 | EER95445 | Zm00001eb005190_P002 | 0.979 |
| PUZ64684 | Sspon.07G | KQL14212 | TKW25760 | KXG22577 | Zm00001eb296520_P005 | 0.891 |
| PUZ62471 | genblast_C | KQL09021 | TKW19311 | EER87737 | Zm00001eb177740_P002 | 0.906 |

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| PUZ42640 | Sspon.01G | KQK92390 | TKV97990 | EER95435 | Zm00001eb005320_P002 | 0.953 |
| PUZ48115 | Sspon.04G | KQK98177 | TKW05553 | EES12539 | Zm00001eb076740_P001 | 0.850 |

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| PUZ61611 | Sspon.08G | KQL10175 | TKW20790 | OQU76182 | Zm00001eb280730_P003 | 0.963 |
| PUZ35971 | Sspon.01G | KQK86074 | TKV90051 | EER93055 | Zm00001eb210350_P003 | 0.798 |
| PUZ61262 | genblast_C | genblast_C | TKW21351 | EER89755 | Zm00001eb278180_P001 | 0.942 |
| PUZ42624 | Sspon.01G | KQK92377 | TKV97973 | OQU93151 | Zm00001eb402270_P001 | 0.965 |
| PUZ53704 | Sspon.03G | KQL07960 | TKW18002 | EES01849 | Zm00001eb145950_P001 | 0.993 |
| PUZ70783 | genblast_C | KQL24566 | TKW33241 | OQU89525 | Zm00001eb313540_P005 | 0.935 |
| PUZ61462 | Sspon.01G | genblast_C | TKW20602 | OQU93323 | Zm00001eb403530_P001 | 0.967 |

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| PUZ42150 | Sspon.01G | KQK91927 | TKV97413 | EER95261 | Zm00001eb008830_P002 | 0.950 |

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| PUZ72890 | Sspon.02GKQL26630 | TKW35782 | KXG36678 | Zm00001eb109110_P003 | 0.953 |
| PUZ69179 | Sspon.01GKQK86515 | TKV90618 | OQU90772 | Zm00001eb212350_P001 | 0.906 |
| PUZ63011 | Sspon.05GKQK99636 | TKW07483 | KXG22985 | Zm00001eb406930_P001 | 0.970 |
| PUZ73420 | genblast_CKQL27091 | TKW36383 | EER99879 | Zm00001eb330160_P001 | 0.952 |

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| PUZ59676 | Sspon.08GKQL11117 | TKW22010 | KXG20531 | Zm00001eb274840_P001 | 0.960 |
| PUZ77753 | genblast_CKQL31622 | TKW41719 | KXG31161 | Zm00001eb255700_P001 | 0.939 |
| PUZ42950 | Sspon.01GKQK92673 | TKV98317 | EER95549 | Zm00001eb402740_P001 | 0.992 |
| PUZ72291 | Sspon.02GKQL26054 | TKW35069 | EER97318 | Zm00001eb106230_P001 | 0.984 |

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| PUZ48603 | Sspon.05GKQK98616 | TKW06166 | EES11318 | Zm00001eb072890_P001 | 0.991 |
| PUZ72147 | genblast_CKQL25888 | TKW34860 | OQU88311 | Zm00001eb118200_P001 | 0.963 |
| PUZ72585 | genblast_CKQL26345 | TKW35447 | OQU90135 | Zm00001eb325020_P001 | 0.961 |
| PUZ41347 | Sspon.01GKQK91136 | TKV96443 | genblast_C | Zm00001eb015140_P001 | 0.991 |
| PUZ71533 | Sspon.02GKQL25307 | TKW34110 | EER97044 | Zm00001eb318390_P001 | 0.971 |

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| PUZ56451 | genblast_C | genblast_C | genblast_C | KXG23158 | Zm00001eb138660_P001 | 0.925 |
| PUZ62227 | Sspon.08GKQL09271 | TKW19628 | EER89188 | Zm00001eb377130_P001 | 0.962 |

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| PUZ64550 | Sspon.01GKQL14077 | TKW25595 | EES18781 | Zm00001eb297590_P001 | 0.895 |

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| PUZ44056 | Sspon.05G | KQK93963 | TKV99820 | KXG28001 | Zm00001eb168910_P001 | 0.965 |
| PUZ38422 | Sspon.01G | KQK88488 | TKV93075 | EER91672 | Zm00001eb142300_P003 | 0.865 |

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|---|---|---|---|---|---|---|
| PUZ48815 | genblast_C | KQK98823 | TKW06426 | OQU82274 | Zm00001eb071370_P001 | 0.846 |
| PUZ59410 | Sspon.08G | KQL11925 | TKW23062 | EER88839 | Zm00001eb225520_P001 | 0.970 |

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| PUZ43666 | Sspon.05G | KQK99850 | TKW07748 | OQU82855 | Zm00001eb196530_P002 | 0.917 |
| PUZ43156 | Sspon.01G | KQK92913 | TKV98565 | OQU93371 | Zm00001eb001360_P004 | 0.977 |

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| PUZ57275 | Sspon.03G | KQL03770 | TKW12651 | KXG32253 | Zm00001eb332870_P001 | 0.965 |
| PUZ62413 | Sspon.08G | KQL09085 | TKW19390 | EER87755 | Zm00001eb378600_P003 | 0.952 |
| PUZ57545 | genblast_C | KQL03967 | TKW12867 | KXG32159 | Zm00001eb127200_P002 | 0.919 |
| PUZ57434 | Sspon.03G | KQL03874 | TKW12783 | EES00506 | Zm00001eb127750_P001 | 0.969 |
| PUZ42061 | Sspon.01G | KQK91832 | TKV97292 | EER95216 | Zm00001eb009580_P002 | 0.989 |

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| PUZ38808 | Sspon.01G | KQK88852 | TKV93556 | KXG38421 | Zm00001eb046690_P001 | 0.963 |
| genblast_C | Sspon.01G | KQK92729 | TKV98369 | EER95568 | genblast_Os03t0132200-01_Ze | |

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| PUZ77663 | Sspon.04G | KQL31542 | TKW41628 | EES05517 | Zm00001eb194240_P001 | 0.897 |
| PUZ62701 | Sspon.05G | KQK93397 | TKV99063 | EES07869 | Zm00001eb195160_P001 | 0.948 |
| PUZ71147 | Sspon.02G | KQL24921 | TKW33638 | EER99049 | Zm00001eb101380_P001 | 0.954 |
| PUZ48224 | Sspon.05G | KQK98290 | TKW05689 | EES11192 | Zm00001eb075370_P001 | 0.926 |
| PUZ73113 | genblast_C | KQL26860 | TKW36094 | EER97616 | Zm00001eb110000_P001 | 0.988 |

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| PUZ67085 | Sspon.02G | KQL16418 | TKW28516 | EES15957 | Zm00001eb408920_P001 | 0.970 |
| PUZ65716 | Sspon.07G | KQL15229 | TKW26975 | EES19631 | Zm00001eb289450_P001 | 0.960 |
| PUZ44106 | Sspon.05G | KQK94032 | TKV99904 | EES09509 | Zm00001eb112540_P001 | 0.953 |
| PUZ51519 | Sspon.06G | KQL01869 | TKW10369 | EES15014 | Zm00001eb179330_P004 | 0.977 |
| PUZ48525 | Sspon.04G | KQK98519 | TKW06054 | EES11284 | genblast_Os04t0571300-01_Ze | |
| PUZ70355 | Sspon.02G | KQL24158 | TKW32701 | EER96579 | Zm00001eb098250_P003 | 0.965 |
| PUZ39698 | genblast_C | KQK89531 | TKV94429 | EER94358 | Zm00001eb026400_P006 | 0.975 |

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| PUZ64099 | Sspon.07G | KQK99254 | TKW06997 | EES17741 | Zm00001eb282750_P001 | 0.981 |
| PUZ71500 | Sspon.02G | genblast_C | TKW34079 | EER97032 | Zm00001eb318170_P001 | 0.940 |
| PUZ40910 | Sspon.01G | KQK90665 | TKV95865 | KXG39277 | Zm00001eb018350_P001 | 0.962 |
| PUZ65979 | genblast_C | KQL15466 | TKW27266 | EES19530 | Zm00001eb288130_P001 | 0.961 |
| PUZ75022 | Sspon.04G | KQL27837 | TKW36908 | EES06857 | Zm00001eb241660_P001 | 0.865 |

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| PUZ46270 | Sspon.05G | KQK96485 | TKW03332 | OQU81217 | Zm00001eb419550_P002 | 0.966 |
| PUZ53279 | Sspon.03G | KQL08337 | TKW18512 | EES04112 | Zm00001eb143290_P001 | 0.990 |

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| PUZ69107 | Sspon.02G | KQL23035 | TKW31210 | EER96087 | Zm00001eb303620_P001 | 0.955 |
| PUZ69811 | Sspon.02G | KQL23735 | TKW32127 | EER98563 | Zm00001eb307090_P001 | 0.954 |
| PUZ57330 | Sspon.03G | KQL03753 | TKW12629 | KXG32228 | Zm00001eb333190_P001 | 0.978 |
| PUZ59277 | Sspon.08G | KQL11797 | TKW22891 | EER88890 | Zm00001eb226660_P001 | 0.963 |

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| PUZ37297 | Sspon.01G | KQK87383 | TKV91671 | OQU91090 | Zm00001eb055460_P001 | 0.989 |
| genblast_C | genblast_C | genblast_C | TKW30002 | OQU88302 | Zm00001eb298410_P001 | 0.931 |
| PUZ77317 | genblast_Z | KQL31189 | TKW41204 | EES07375 | Zm00001eb252440_P001 | 0.977 |

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| PUZ58337 | genblast_C | KQL04677 | TKW13796 | OQU86203 | Zm00001eb122270_P001 | 0.966 |

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| PUZ77681 | Sspon.04G | KQL31556 | TKW41648 | EES05513 | Zm00001eb255240_P001 | 0.988 |
| PUZ66642 | Sspon.05G | KQL16168 | TKW28156 | EES15935 | Zm00001eb408530_P001 | 0.940 |
| PUZ73836 | Sspon.04G | KQL28929 | TKW38262 | EES06208 | Zm00001eb208580_P004 | 0.946 |
| PUZ36041 | genblast_C | KQK86141 | TKV90133 | KXG37111 | Zm00001eb064660_P001 | 0.874 |
| PUZ76048 | Sspon.04G | KQL29984 | TKW39665 | OQU85098 | Zm00001eb243460_P001 | 0.968 |
| PUZ65451 | Sspon.07G | KQL14933 | TKW26611 | EES19721 | Zm00001eb291260_P001 | 0.984 |
| PUZ76361 | Sspon.04G | KQL30291 | TKW40063 | EES05363 | Zm00001eb183690_P001 | 0.934 |
| PUZ52259 | Sspon.06G | KQL02517 | TKW11224 | KXG25602 | Zm00001eb174620_P001 | 0.987 |
| PUZ62940 | Sspon.05G | KQK93572 | TKW07781 | OQU82868 | Zm00001eb092850_P002 | 0.896 |
| PUZ77290 | Sspon.04G | KQL31164 | TKW41172 | EES05647 | Zm00001eb188550_P001 | 0.983 |
| PUZ65666 | Sspon.07G | genblast_C | TKW26909 | EES18348 | Zm00001eb351300_P002 | 0.965 |
| PUZ36760 | Sspon.01G | KQK86826 | TKV91024 | OQU90894 | Zm00001eb059610_P002 | 0.958 |
| PUZ62956 | Sspon.07G | KQK99885 | TKW07807 | EES16636 | genblast_Os11t0150400-01Zm0 | |
| PUZ54050 | Sspon.03G | KQL07650 | TKW17628 | EES01728 | Zm00001eb148530_P001 | 0.966 |
| PUZ64801 | Sspon.03G | KQL14334 | TKW25899 | EES19942 | Zm00001eb295750_P001 | 0.950 |
| PUZ59101 | Sspon.08G | KQL12228 | TKW23440 | KXG20884 | Zm00001eb228040_P001 | 0.990 |
| PUZ37257 | Sspon.01G | KQK87354 | TKV91639 | EER90960 | Zm00001eb055750_P001 | 0.963 |

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| PUZ59681 | Sspon.08G | KQL11120 | TKW22020 | EER88761 | Zm00001eb389400_P001 | 0.907 |
| PUZ57914 | Sspon.03G | KQL04279 | genblast_C | EES00362 | Zm00001eb125100_P001 | 0.929 |
| PUZ38396 | Sspon.01G | KQK88456 | TKV93030 | EER91414 | Zm00001eb044170_P001 | 0.952 |

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| PUZ36759 | Sspon.01G | KQK86824 | TKV91022 | OQU90893 | Zm00001eb213580_P001 | 0.860 |
| PUZ41126 | Sspon.01G | KQK90918 | TKV96153 | KXG39399 | Zm00001eb016610_P001 | 0.933 |
| PUZ38982 | Sspon.01G | KQK89234 | TKV94038 | EER94226 | Zm00001eb047810_P001 | 0.915 |
| PUZ39640 | genblast_C | KQK89406 | TKV94270 | KXG38664 | Zm00001eb026840_P001 | 0.973 |
| PUZ58615 | Sspon.03G | KQL04932 | TKW14118 | EES00077 | Zm00001eb120200_P001 | 0.952 |
| PUZ53355 | genblast_C | KQL08264 | TKW18416 | OQU88089 | Zm00001eb365020_P002 | 0.967 |
| PUZ47422 | Sspon.05G | KQK97511 | TKW04714 | KXG26434 | Zm00001eb081210_P001 | 0.988 |
| PUZ41917 | Sspon.01G | KQK91676 | TKV97080 | EER95171 | Zm00001eb010710_P001 | 0.977 |
| PUZ41048 | Sspon.01G | KQK90832 | TKV96035 | OQU92576 | Zm00001eb394510_P001 | 0.979 |

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| PUZ54370 | Sspon.03G | KQL07340 | TKW17247 | EES01606 | Zm00001eb150730_P001 | 0.961 |
| PUZ62328 | genblast_C | KQL09160 | TKW19493 | EER89141 | Zm00001eb377910_P002 | 0.938 |
| PUZ50179 | Sspon.06G | KQL00746 | TKW08888 | EES14570 | Zm00001eb172580_P002 | 0.977 |
| PUZ73069 | Sspon.02G | KQL26804 | TKW36031 | EER97596 | Zm00001eb328370_P002 | 1.003 |
| PUZ62254 | genblast_Z | KQL09238 | TKW19591 | EER87825 | Zm00001eb377290_P001 | 0.941 |
| PUZ73523 | genblast_C | KQL27246 | TKW36602 | EER99937 | Zm00001eb331180_P002 | 0.968 |
| PUZ77171 | Sspon.04G | KQL31037 | TKW41023 | KXG30968 | Zm00001eb251310_P003 | 0.996 |
| PUZ57985 | genblast_C | KQL04344 | TKW13371 | KXG31918 | Zm00001eb335690_P001 | 0.916 |
| PUZ45122 | Sspon.06G | KQK94849 | TKW01078 | OQU83599 | Zm00001eb197740_P001 | 0.975 |
| PUZ49139 | Sspon.05G | KQK99150 | TKW06865 | EES11521 | Zm00001eb431840_P001 | 0.960 |
| PUZ67337 | Sspon.02G | KQL16708 | TKW28903 | EES16093 | Zm00001eb410450_P001 | 0.992 |
| PUZ68014 | Sspon.02G | KQL17367 | TKW29779 | EES17465 | Zm00001eb032640_P005 | 0.945 |
| PUZ70425 | Sspon.02G | KQL24223 | TKW32790 | genblast_C | Zm00001eb310530_P003 | 0.982 |
| PUZ46101 | Sspon.05G | KQK96224 | TKW02972 | genblast_Z | genblast_Zm00001eb089410_P0 | |
| PUZ67665 | Sspon.02G | KQL16989 | TKW29314 | EES16259 | Zm00001eb030410_P001 | 0.952 |
| PUZ40930 | Sspon.01G | KQK90720 | TKV95891 | EER94791 | Zm00001eb394080_P002 | 0.921 |
| PUZ76351 | genblast_C | KQL30273 | TKW40046 | OQU85237 | Zm00001eb183600_P001 | 0.985 |
| PUZ66002 | Sspon.07G | KQL15490 | TKW27311 | OQU78006 | Zm00001eb288010_P001 | 0.953 |
| PUZ77426 | genblast_C | KQL31292 | TKW41343 | KXG30855 | Zm00001eb189050_P001 | 0.906 |
| PUZ76107 | Sspon.04G | KQL30026 | TKW39724 | EES06963 | Zm00001eb182020_P001 | 0.873 |

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| PUZ39274 | Sspon.01G | KQK89257 | TKV94065 | OQU91909 | Zm00001eb027800_P002 | 0.947 |
| PUZ48641 | Sspon.05G | KQK98656 | TKW06207 | KXG27004 | Zm00001eb428290_P001 | 0.975 |
| PUZ36697 | Sspon.01G | genblast_C | TKV90970 | KXG37408 | Zm00001eb059960_P001 | 0.884 |
| PUZ74588 | Sspon.04G | KQL28221 | TKW37392 | OQU84595 | Zm00001eb235630_P002 | 0.987 |
| PUZ42533 | Sspon.01G | KQK92288 | TKV97842 | EER95391 | Zm00001eb401720_P001 | 0.978 |
| PUZ59906 | Sspon.08G | KQL11375 | TKW22340 | EER90058 | Zm00001eb388030_P001 | 0.961 |
| PUZ73568 | Sspon.02G | KQK91277 | TKW36662 | OQU90552 | Zm00001eb111920_P001 | 0.953 |

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| PUZ48553 | Sspon.05G | KQK98547 | TKW06089 | OQU82188 | Zm00001eb073420_P001 | 0.981 |
| PUZ62058 | genblast_C | KQL09616 | TKW20052 | EER87912 | Zm00001eb375710_P004 | 0.949 |
| PUZ41845 | Sspon.01G | KQK91614 | TKV96992 | EER95156 | Zm00001eb398250_P001 | 0.942 |
| PUZ56820 | genblast_C | KQL05234 | TKW14528 | EES03952 | Zm00001eb366640_P001 | 0.989 |
| PUZ52597 | Sspon.06G | KQL02872 | TKW11654 | KXG25431 | Zm00001eb202800_P002 | 0.981 |
| PUZ59687 | Sspon.08G | KQL11127 | genblast_C | OQU76806 | Zm00001eb274870_P001 | 0.942 |
| PUZ48452 | Sspon.05G | KQK98462 | TKW05961 | KXG26900 | Zm00001eb073980_P001 | 0.974 |
| PUZ47067 | Sspon.05G | KQK97189 | TKW04299 | OQU81520 | Zm00001eb421950_P001 | 0.924 |
| PUZ49624 | genblast_C | KQL12667 | TKW23736 | KXG27497 | Zm00001eb076150_P001 | 0.918 |
| PUZ54670 | genblast_C | KQL07082 | TKW16909 | EES13213 | Zm00001eb260040_P001 | 0.970 |
| PUZ69215 | Sspon.02G | KQL23207 | TKW31461 | EER96209 | Zm00001eb304770_P004 | 0.976 |
| PUZ56272 | Sspon.03G | KQL05497 | TKW14907 | EES00895 | Zm00001eb162550_P001 | 0.942 |
| PUZ40781 | Sspon.01G | KQK90532 | TKV95713 | OQU92452 | Zm00001eb392730_P001 | 0.970 |
| PUZ70413 | Sspon.02G | genblast_C | TKW32776 | EER98776 | Zm00001eb098430_P004 | 0.964 |
| PUZ37120 | Sspon.01G | KQK87200 | TKV91465 | KXG37605 | Zm00001eb056520_P003 | 0.975 |
| PUZ41203 | Sspon.01G | KQK90989 | TKV96236 | KXG39424 | Zm00001eb016110_P003 | 0.968 |

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|---|---|---|---|---|---|---|
| PUZ73460 | genblast_C | KQL27189 | TKW36526 | KXG36949 | Zm00001eb330720_P003 | 0.968 |
| PUZ54926 | Sspon.03G | KQL06833 | TKW16584 | EES01417 | Zm00001eb361970_P001 | 0.982 |
| PUZ74751 | Sspon.04G | KQL28048 | TKW37167 | EES04782 | Zm00001eb239700_P002 | 0.860 |

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| PUZ73483 | Sspon.01G | KQL27218 | TKW36571 | KXG36971 | Zm00001eb330890_P001 | 0.967 |
| PUZ52144 | Sspon.06G | KQL02422 | TKW11099 | OQU80945 | Zm00001eb034890_P001 | 0.946 |
| PUZ49447 | genblast_C | KQL12849 | TKW23973 | EES11631 | Zm00001eb066780_P001 | 0.945 |

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| PUZ40206 | Sspon.01G | KQK89998 | TKV95023 | EER91963 | Zm00001eb391600_P005 | 0.963 |

-1.2 1
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a_mays_1 0.897 0.0 1
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0.4 1
a_mays_1 0.807 -1.0 1
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a_mays_6 0.739 -2.1 1
0.3 1

-0.1 1
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a_mays_5 0.832 -0.7 1
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a_mays_5 0.809 -0.1 1

0.3 1
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a_mays_2 0.790 -1.8 1
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 0.6 1
 -0.3 1
a_mays_6 0.967 0.5 1
 0.7 1
 0.1 1
 0.5 1
 -0.4 1
 0.4 1

 0.3 1
 0.1 1








 -0.1 1
 -1.6 1
 0.6 1
 0.6 1
 0.5 1
 -0.3 1
 0.6 1
 -0.5 1



 0.6 1

a_mays_10 0.804 -0.9 1
 0.5 1







 0.4 1
```

| | |
|---|---|
| −1.1 | 2 |
| −0.3 | 1 |
| −0.4 | 1 |
| 0.3 | 1 |

| | |
|---|---|
| 0.6 | 1 |
| 0.5 | 1 |
| −0.2 | 1 |
| −3.6 | 1 |
| −1.2 | 1 |
| 0.6 | 1 |
| 0.0 | 1 |
| 0.8 | 1 |
| 0.5 | 1 |
| 0.5 | 1 |
| −0.7 | 1 |

| | |
|---|---|
| 0.3 | 1 |

0.8 1
−0.8 1
−0.4 1
0.6 1
0.2 1

0.3 1
−1.1 1
0.5 1
0.3 2
0.5 1
−0.1 1
−0.8 1
−0.8 1
1.3 1

0.4 1
0.3 1
0.6 1

0.0 1
0.7 1

1.2 1
0.2 1

0.6 1
0.2 1
0.1 1
0.4 1
−2.1 1
0.5 1

0.4 1
0.8 1

0.7 1
0.9 1
−0.1 1
0.1 1
0.5 1

```
a_mays_4 0.753 -1.3 1
3 0.8 1











3 0.3 1
9 0.8 1
5 0.5 1



5 -0.1 1
















3 0.2 1
2 0.1 1
2 0.5 1
0 0.7 1
5 -0.4 1
```

–0.2 1

0.6 1

0.6 1
0.5 1
0.4 1

0.2 1

–2.6 1
0.5 1
–0.1 1
0.4 1
0.2 1

0.4 1

0.4 1
0.3 1
–0.2 1
0.8 1
0.2 1
0.5 1

0.3 1
0.7 1
0.0 1
0.2 1
0.1 1
0.5 1

0.3 1
a_mays_9 0.946 0.6 1
-0.4 1
0.6 1
-0.2 1

0.6 1
-0.0 1
0.4 1
-1.7 1
0.4 1
0.4 1

0.9 1
0.5 1
-2.3 1
0.9 1
-0.7 1
0.5 1
-0.4 1

0.5 1
0.7 1
0.3 1
0.3 1
0.2 1
0.8 1
-0.1 1
-1.6 2
0.2 1
0.2 1
-1.0 1
0.4 1
0.9 1

0.8 1
0.5 1

0.3 1
0.6 1
−0.5 1
0.7 1

0.5 1
−0.6 1
0.1 1
0.8 1
0.4 1
0.4 1
−1.4 1
−0.1 1
0.4 1
−1.4 1
−0.5 1

0.4 1

0.8 1
0.0 1
−0.1 1

0.0 1
0.2 1
0.8 1

−1.3 1
0.6 1

```
 0.8 1
 -0.3 1
 0.3 1
a_mays_8 0.883 -0.4 1
 0.5 1
 0.0 1
 0.7 1


 -0.5 1
 0.3 1
 0.7 1
 -0.7 1
 -2.0 1
 -1.4 1
001_Zea_mays_1 0.731 -2.3 1
 -0.5 1
a_mays_3 0.731 -3.2 1
 0.0 1




 0.3 1




 0.5 1
 -0.1 1
 -1.9 1
 0.3 1
 0.4 1
 0.1 1
 0.2 1
0001eb087630_P001_Zea_mays_2 0.895
 1.0 1
 0.2 1
 0.1 1


 0.3 1
 0.1 1
 0.4 1
```

```
0.7 1
0.2 1
-1.1 1
0.4 1
0.4 1
-1.2 1
-1.5 1
1.2 1
-0.3 1
-0.7 2
0.3 1
00001eb007790_P001_Zea_mays_1 0.730 -
0.2 1
0.6 1
0.2 1
0.5 1
a_mays_4 0.863 -0.9 1


0.8 1
a_mays_4 0.962 0.4 1
a_mays_3 0.777 -1.5 2
-1.6 1
0.7 1
a_mays_1 0.882 -0.1 1
0.9 1
0.0 1



0.1 1
0.5 1
```

0.6 1
-0.0 1

0.1 1

0.7 1
0.8 1

-0.9 1
0.6 1
0.8 1
0.3 1
0.0 1

0.7 1
-1.0 1

-0.1 1
0.6 1
a_mays_10 0.893 -1.2 1
-0.8 1

0.3 1
0.7 1
0.8 1
-0.0 1

0.7 1
0.8 1
0.5 1

0.3 1

0.6 1
0.3 1
0.1 1
0.3 1
0.6 1
0.4 1
0.2 1
0.1 1
0.6 1
0.3 1
0.7 1
0.2 1
0.6 1

-1.7 1
0.4 1
0.3 1
-0.5 1
-1.2 2

a_mays_5 0.727 -2.4 1

0.1 1
0.3 1

−1.6 2
1.0 1
−0.1 1
0.6 1
0.3 1
0.5 1
0.8 1
0.4 1

−0.8 1
−2.0 2

0.4 1
0.4 1
0.7 1

0.5 1
0.4 1
0.6 1
0.3 1
0.5 1
0.4 1

−0.3 1
0.7 1
0.3 1
0.5 1

0.2 1

0.1 1

-0.1 1
0.2 1
0.2 1

-0.0 2
0.3 1
0.6 1
a_mays_9 0.951 0.3 1
0.4 1

0.6 1
0.5 1
1.3 1

0.4 1
0.5 1

-0.9 1
0.6 1
0.1 1
-0.3 1
0.5 1
0.2 1
0.8 1
0.7 1
0.4 1
0.4 1
0.8 1
0.4 1

0.2 1
-3.4 1
0.4 1
0.7 1

a_mays_5 0.725 -3.2 1

0.6 1
0.2 1
0.3 1
0.3 1
0.3 1
0.6 1
0.4 1
-0.8 1
0.5 1
0.1 1
0.7 1
0.4 1

0.7 1
0.4 1
-1.7 1
-0.6 1
0.8 1

0.5 1
0.4 1
-0.4 1
0.3 1
a_mays_5 0.826 -0.6 1
0.4 1

-0.8 1
a_mays_1 0.724 -2.4 1

-0.2 2
-2.9 1
-0.6 1
0.8 1
0.4 1
-0.7 1
0.2 1
0.5 1
0.3 1
0.3 1
-0.6 1
0.3 1

0.7 1
0.1 1
a_mays_3 0.829 -0.5 2

4 0.1 1
4 -1.9 3
2 0.7 1
2 -0.1 1
7 0.6 1
9 0.1 1

5 0.8 1
2 0.4 1
0 0.1 1

9 0.3 1
2 0.3 1
4 0.4 1
2 0.3 1
7 1.1 1
3 0.3 1
0 0.1 1
5 -0.1 1
3 0.2 1
0 1.1 1
3 0.2 1
5 -0.4 1
3 -0.5 1
7 0.4 1
5 0.3 1
3 0.4 1
3 0.3 1
a_mays_10 0.856 -0.7 1
7 0.3 1
9 0.5 1
0 0.5 1
1 0.5 1
2 0.2 1
a_mays_2 0.908 -0.5 1
9 0.2 1
0 0.3 1

2 -0.1 1
7 -0.4 1

```
2 -1.4 1
4 0.2 1
a_mays_1 0.951 0.4 1
0 -0.3 1
a_mays_10 0.722 -3.4 1
6 0.3 1
2 0.6 1
1 0.2 1
0 0.7 1
3 0.6 1
1 -0.6 1
2 0.2 1
4 -0.3 1
2 0.6 1



2 0.7 1
0 0.5 1
3 -0.0 1
7 0.2 1
2 0.6 1
4 0.8 1
00001eb135350_P001_Zea_mays_3 0.854 -
2 1.3 1
7 0.4 1
7 -0.4 1
1 0.6 1


9 -1.3 1
1 0.3 1



1 -1.1 1


3 -0.2 1
9 -1.2 2
9 -1.4 1
3 0.4 1
```

0.1 1

−0.4 1
0.3 1
0.6 1
−0.9 1
0.5 1
0.6 1
−3.0 1
0.5 1
0.3 1
0.6 1
−1.9 2
0.4 1
0.6 1

0.4 1
−0.4 1
0.6 1
0.3 1
0.7 1

0.5 1
0.6 1

−0.7 1
−0.0 1
−0.8 1
0.0 1

-0.0 1
0.8 1
0.8 1
0.5 1
0.3 1
0.5 1

0.6 1
0.6 1
0.6 1
0.1 1
0.8 1
0.5 1
0.5 1
0.8 1
0.3 1
0.2 1
-0.6 1

-0.5 2

a_mays_1 0.738 -2.4 1

0.0 1
a_mays_3 0.767 -2.1 1
0.2 1
0.7 1
-2.0 1
-0.2 1
a_mays_9 0.835 -1.0 1

0.3 1
-2.6 1
0.2 1

0.1 1

-1.4 1
0001eb053050_P002_Zea_mays_1 0.718 -
0.3 1
0.6 2
0.4 1
a_mays_10 0.717 -3.0 1
0.3 1
-1.5 1
1.0 1
-1.4 1

0.4 1
0001eb057130_P001_Zea_mays_1 0.717 -
-1.1 1
0.4 1
0.3 1
0.3 1

0.5 1
0.8 1

-0.6 1
a_mays_2 0.878 0.0 1

–0.4 1
0.3 1
0.3 1
0.3 1
0.5 1
0.7 1

0.6 1
0.7 1
0.7 1
0.7 1
0.5 1
–0.2 1
0.4 1
0.3 1
0.4 1
0.4 1
–1.4 1
–0.0 1

0.5 1

0.2 1
–1.3 1
0.6 1
0.8 1
–0.7 1
–0.0 1
0.9 1
0.5 1
0.1 1
0.5 1
0.4 1
–2.4 1
0.6 1

0.4 1
-0.3 1

0.8 1
0.2 1
-1.2 1
0.1 1
-1.0 1
0.7 1

0.3 1
0.4 1
-1.0 1
0.0 1
-0.3 1
0.6 1
-0.6 1
-0.0 1
0.0 1

-0.4 1
0.4 1
-0.1 1
0.2 1
0.6 1
0.5 1
0.6 1
0.6 1

-0.1 1

-0.0 1
0.5 1
-1.7 1
-0.1 1

```
a_mays_4 0.834 -1.1 1
 0.6 1
 -0.3 1
 0.6 1





 0.4 1

 0.3 1
 0.3 1
 0.5 1
 0.2 1




 0.6 1
 0.7 1

 0.4 1
 0.6 1




 -2.0 2
 0.4 1



 -1.4 1
 -2.3 1
 0.2 1
 0.5 1
 -0.4 2
 0.2 1




 0.6 1
 0.5 1
 -0.4 1
 -0.3 2
 0.3 1
```

0.5 1

0.8 1
1.1 1
−0.4 1
0.2 1
0.4 1
0.8 1
0.5 1
0.6 1
0.5 1
−1.9 1
0.7 1

0.2 1

0.5 1
0.8 1
0.4 1
−0.7 2

0.3 1

0.2 1

a_mays_8 0.712 -1.5 1
-0.5 1
-1.0 1
0.4 1
0.0 1
0.7 1
1.0 1
0.9 1
-0.9 1
0.5 1

0.3 1
-0.6 2

0.0 1
0.3 1
-1.8 1
0.3 1

-0.7 1
0.4 1
-0.5 1
0.5 1

0.4 1

0.7 1
0.8 1
−1.7 1

−0.7 1
0.6 1
0.8 1
1.0 1
0.6 1
−0.0 1
0.1 1
0.3 1
−0.3 1
0.8 1
−2.0 2
−0.0 1

0.3 1
0.5 1

−0.6 2
0.7 1

```
-0.1 1
0.6 1
-0.2 1

-1.1 1
0.3 1
0.4 1
0.1 1
-0.0 1

0.6 1
0.9 1
0.9 1
0.3 1
0.5 1
-0.2 2
0.7 1
1.0 1
0.4 1
0.2 1
-0.4 1
0.1 1

0.0 1
0.1 1
a_mays_1 0.925 0.3 1
0.3 1

0.4 1

-0.5 1
0.3 1
1.3 1
```

0.2 1
0.7 1
0.9 1
0.1 1
1.4 1
0.5 1
−0.0 1

−0.8 1
0.5 1
0.4 1
−0.5 1
0.1 1

−0.3 1
0.3 1

0.5 1
0.4 1
0.2 1
0.5 1
0.2 1
−0.2 1
0.2 1
1.0 1
0.8 1
0.3 1
−0.4 1

−0.5 1
0.5 1

0.4 1

-1.7 1

0.6 1
a_mays_1 0.760 -1.6 1
0.4 1
0.4 1

0.1 2
0.4 1

-0.3 1
a_mays_5 0.904 -0.2 1
0.7 1
0.2 1
0.9 1
-2.5 1
0.5 1

0.3 1
0.3 1
-0.4 1
0.6 1
-0.0 1

-0.4 1

-0.9 2
0.5 1
a_mays_7 0.849 -0.3 1
-1.6 1

0.4 1
–0.2 1

–1.9 1

–1.0 1
–0.2 1
0.4 1

1.0 1
0.8 1

0.5 1
–0.1 1
0.3 1
–0.2 1
a_mays_10 0.949 –0.0 1
–0.2 1
0.3 1

-0.6 1
-0.1 1
0.4 1
-2.3 1
-0.3 1

0.5 1
0.2 1
-0.3 1
0.3 1
a_mays_2 0.812 0.4 2
0.4 1
1.3 1
0.6 1

0.3 1
-0.5 1

a_mays_8 0.704 -1.6 1

-1.6 1
-1.0 1
0.2 1
0001eb032920_P001_Zea_mays_5 0.704 -

0.8 1
a_mays_3 0.934 0.2 1
0.4 1

0.2 1
0.4 1

-2.1 1

0.8 1

0.7 1

```
0.2 1
0.6 1
0.3 1
0.3 1
a_mays_6 0.802 -1.4 1
0.5 1
-2.2 1
0.3 1
0.3 1
-0.5 1
0.5 1
001_Zea_mays_8 0.899 -0.1 2
0.2 1
1.0 1
0.6 1
0.7 1
0.3 1


0.4 1
-0.2 1
0.4 1
-0.7 1


0.3 1
0.7 1
0.5 1

-0.1 1
0.7 1
0.5 1
0.5 1
0.7 1
0.6 1
-0.2 1

0.2 1
a_mays_3 0.937 1.6 1
0.2 1
```

0.5 1
-0.8 1
0.5 1
0.5 1

0.6 1

0.6 1
-1.9 1
0.1 1
0.6 1

0.4 1
0.2 1

-0.6 1
0.3 1

0.0 1
-0.1 1

0.2 1

1.2 1
0.4 1
-0.8 1
0.4 1
0.2 1
-2.3 2
0.2 1
0.4 1
0.1 1

0.2 1
0.4 1
-0.6 1
0.5 1
-0.2 1
0.2 1
0.1 1

0.9 1
0.0 1

| | |
|---|---|
| 0.3 | 1 |
| −0.7 | 1 |
| 0.4 | 1 |
| 0.8 | 1 |
| 0.6 | 1 |
| 1.6 | 1 |
| −0.3 | 2 |

| | |
|---|---|
| −1.1 | 2 |
| 0.1 | 1 |
| −0.2 | 1 |
| 0.6 | 1 |
| 0.1 | 1 |
| 0.5 | 1 |
| −1.4 | 1 |
| 0.4 | 1 |

0.8 1
0.1 1
-0.0 1
-2.2 1
0.6 1
-1.4 2

-0.9 1

0.7 1
0.7 1
-0.0 1
0.5 1
0.3 1

0.5 1
1.1 1
0.4 1
-0.0 1
0.2 1

a_mays_8 0.698 -2.8 1
0.4 1
0.0 1
0.2 1
0.3 1
0.3 1

```
 -0.9 1
 0.5 1
a_mays_3 0.698 -2.5 1



 0.4 1
 1.0 1


 0.2 1
 0.7 1




 0.4 1






 -0.4 1
 0.2 1
 0.3 1


 0.8 1
 0.5 1
 -0.6 1
a_mays_6 0.823 0.0 1
a_mays_3 0.966 0.3 1
 0.0 1
 0.3 1






 -0.1 1
 0.5 1


 0.4 1
 0.5 1
```

```
-0.4 1
0.4 1
0.8 1
0.1 1


0.7 1
-0.4 1
a_mays_1 0.697 -3.2 1




0.0 1
0.6 1
0.1 1
0.8 1
0.2 1
0.2 1
0.4 1
0.8 1






0.3 1






0.3 1
0.8 1
-0.2 1
0.4 1
0.3 1
0.1 1




0.6 1
0.7 1
-0.1 1

0.2 1
```

```
-0.5 1
1.1 1
0.5 1
0.5 1
-0.6 1


0.5 1
-0.5 1
0.0 1
0.7 1


0.3 1
0.7 1
0.3 1
-0.4 1
0.2 2
-1.6 1


0.5 1
0.8 1
0.4 1
0.1 1
0.1 1
0.6 1
0.7 1
0.5 1
0.5 1
0.5 1
0.7 1
a_mays_10 0.922 0.2 1
0.5 1
0.3 1
0.3 1
0.4 1
0.4 1
0001eb124380_P001_Zea_mays_8 0.887 1
0.4 1
0.2 1
0.7 1
0.5 1
-0.0 1
```

| | |
|---|---|
| 0.1 | 1 |
| 0.5 | 1 |
| 0.1 | 1 |
| 0.5 | 1 |
| 0.6 | 1 |
| 0.6 | 1 |
| 0.0 | 1 |
| 0.2 | 1 |
| −0.1 | 1 |
| −0.3 | 1 |
| 0.5 | 1 |
| −0.3 | 2 |
| −1.0 | 1 |
| 0.6 | 1 |
| 0.2 | 1 |
| −0.9 | 1 |
| 0.5 | 1 |
| −1.5 | 1 |
| 1.1 | 1 |
| 0.2 | 1 |
| 0.2 | 1 |
| 0.2 | 1 |
| 0.6 | 1 |
| 0.8 | 1 |
| 0.1 | 1 |
| −0.2 | 1 |
| −0.1 | 1 |

0.0 1
0.5 1

0.6 1
0.4 1
0.5 1
-2.2 1

0.3 1
0.8 1
-0.5 1
0.4 1
0.6 1
-1.0 1
-0.2 1
0.1 1

-0.1 1

0.5 1
0.1 1
0.5 1
-1.3 1
a_mays_3 0.828 -0.7 1

-0.1 1
0.1 1
0.7 1

```
a_mays_1 0.887 -0.1 1
 -0.8 1
 0.8 1
 0.9 1
 0.4 1
 -2.0 1
 0.2 1
 -2.1 2
 0.5 1
 -0.2 1
 -1.1 1
 0.7 1
 -0.1 1
 -0.6 1
 0.4 1
 -0.4 2
 -0.7 1
 -0.2 1



 0.5 1
 -0.3 1
 0.3 1
a_mays_7 0.955 0.8 1
 0.1 1
 0.4 1
 0.4 1
 0.6 1
 0.7 1
 0.4 1
 -0.6 1
 0.5 1
 0.2 1
a_mays_9 0.920 0.8 1
 0.1 1





 -0.8 1
 0.2 1
 0.7 1
 0.1 1




a_mays_3 0.861 -0.6 1
```

-0.5 1
0.1 1
0.9 1

0.4 1

0.4 1
0.4 1
a_mays_2 0.688 -2.4 1
0.6 1
0.3 1
0.4 1
-0.6 1

-0.5 1
-0.1 1
-0.0 1
a_mays_7 0.861 -0.6 2

0.2 1
0.4 1
0.7 1
-0.4 1
0.2 1
0.1 1
0.5 1

0.7 1
-0.8 1
0.6 1

0.5 1
0.3 1
0.2 1

-0.8 1
0.8 1

0.3 1

0.6 1
-0.2 1
0.2 1
0.2 1
0.5 1
0.6 1
-0.5 1
-0.1 1

-1.4 1

0.3 1
-0.0 1

0.6 1
0.6 1
-0.4 1
0.1 1

0.9 1
-0.4 1

1.1 1
0.7 1
-2.0 1
0.7 1
-0.5 1

0.6 1
-1.1 2
0.7 1

2 0.2 1

2 0.5 1
3 0.3 1
5 0.3 1
a_mays_3 0.685 -3.4 1
5 0.4 1
7 0.4 1

7 -1.4 1
3 0.5 1
7 0.5 1
2 0.3 1
3 0.2 1
5 0.6 1
9 0.3 1
5 -2.3 1
2 0.7 1
1 0.3 1

5 0.3 1
4 0.2 1

4 0.5 1
2 0.1 1

-0.0 1
0.1 1
-0.9 1
0.8 1
-1.8 1
0.2 1

0.5 1
0.3 1
0.4 1
0.3 1
-0.5 2

0.3 1
0.3 1
-0.4 1
0.5 1
-0.5 1
-0.3 1
0.3 1
-0.5 1
0.5 1
-0.0 1
-0.6 1
0.3 1

-1.5 4

0.6 1

-2.4 1
1.2 1
-0.6 1
0.4 1

0.1 1
0.3 1
0.4 1

0.2 1
0.3 1
-1.3 1

-0.2 1
0.5 1
0.4 1
0.8 1

1.0 1

a_mays_1 0.922 0.3 1
-0.1 1
0.6 1
0.6 1
-1.6 1
a_mays_4 0.734 -1.9 1

```
 0.5 1
 -0.1 1

 0.3 1
 0.4 1
 0.2 1
 -0.6 1
 0.2 1
 0.0 1
 0.4 1
0001eb344380_P001_Zea_mays_10 0.887

 -1.2 1
 0.6 1
 0.1 1
 -0.8 1
 0.7 1
 0.6 1
 0.6 1
a_mays_7 0.935 0.3 1
 0.3 1
 0.4 1
 0.3 1
 -1.5 1

 0.4 1

 0.4 1
 0.6 1
a_mays_1 0.754 -1.9 2
a_mays_7 0.869 -0.4 1
 0.3 1
 0.3 1
```

```
-1.5 1
0.9 1
0.4 1
0.3 1


a_mays_9 0.680 -2.4 1
0.2 1
0.5 1
0.3 1
0.1 1
0.6 1
0.2 1
-0.1 1
0.5 1



0.4 1




0.7 1








1.1 1
-0.5 1
0.0 1





0.4 1
-0.8 1



0.5 1




0.2 1
```

```
 0.2 1
a_mays_7 0.868 0.0 1
 -0.1 1
 0.9 1


 0.5 1
 0.5 1
 -0.6 1
 -0.1 1


 0.3 1
a_mays_8 0.691 -2.2 1


 0.1 1
 -0.5 1
 -0.2 1
 0.3 1
 0.1 1
 0.1 1

a_mays_10 0.944 0.1 1
a_mays_1 0.902 -0.2 1


 0.5 1
 0.3 2
 0.3 1
 0.8 1
 1.2 2
```

```
 1.3 1
 0.7 1
a_mays_4 0.677 -2.8 1
 0.7 1
 0.2 1
 0.5 1
 0.9 1
 0.5 1
 -0.5 1
 0.5 1
 0.7 1
 0.5 1
 -0.3 1


 0.5 1


 0.7 1


 0.1 1
 0.3 1
 0.4 1
 0.8 1
 0.3 1
```

0.5 1
0.7 1

0.4 1
0.6 1

0.7 1
0.6 1
0.9 1
0.2 2
0.4 1

–0.0 1

0.3 1
-0.2 1
0.6 1
0.6 1
-1.0 1
-2.7 2
0.6 1
0.3 1
-2.3 1
0.5 1
0.9 1
0.5 1

0.1 1
0.4 1

a_mays_3 0.799 -1.1 1
-1.0 2
0.4 1
0.6 1
0.6 1
0.5 1
-0.6 1
-1.2 1

0.4 1

-0.5 1
0.2 2
0.2 1
-2.4 1
0.2 1
0.8 1
0.6 1
0.5 1

0.8 1
0.5 1
0.6 1

-0.7 1
a_mays_7 0.968 0.6 1
0.1 1

0.5 1
0.3 1
0.3 1
a_mays_1 0.674 -2.2 2

0.9 3
-0.7 1
0.0 1
0.8 1
0.5 1
0.5 1
-0.5 1

-0.0 1
0.5 1
0.5 1
0.8 1

0.2 1

0.4 1
0.2 1
0.0 1

-0.4 1

0.3 1

0.4 1
0.4 1
a_mays_7 0.781 -1.0 1
0.5 1

```
0.6 1
0.7 1
0.7 1

0.3 1
0.4 2
0.5 1
0.4 1
a_mays_10 0.869 0.2 1
0.6 1
-0.3 1
0.5 1
0.3 1
-0.1 1
0.5 1
0.8 1
0.0 1
0.4 1
0.5 1
-0.1 1
0.1 1
0.4 1
-2.5 1
0.9 1
-0.2 2
0001eb157020_P001_Zea_mays_5 0.866
-0.1 1
-0.2 1
```

0.3 1

0.3 1

0.0 1

0.4 1
0.2 1
0.2 1
0.4 1
-0.1 1

0.3 1
0.6 1

```
 0.8 1

 0.7 1
 0.3 1
001_Zea_mays_1 0.920 0.4 1
 -0.2 1
 0.6 1
 0.4 1




 0.7 1
 0.8 1
 0.4 1
 -1.9 1
 -0.5 1



 0.3 1
 -0.1 1
 0.2 1
 -0.6 1




 1.0 1
 0.1 1
 0.7 1
 0.0 1
 0.6 1
 0.7 1






 0.1 1
 0.3 1
 0.3 1
 0.6 1
 -2.4 1
 0.2 1
 0.3 1
 0.3 1
 0.7 1
```

0.0 1
0.4 1
-1.0 1
0.5 1

0.1 1
0.5 1
-0.1 2

0.2 1
0.4 1
0.3 1
0.4 1
a_mays_3 0.859 0.1 1
-0.2 1

0.1 1

0.5 1

-0.1 1

-0.2 1
-0.4 1
1.1 1

-0.6 1
0.4 1

0.4 1
0.6 1
0.3 1
-0.1 1
a_mays_1 1.000 0.5 1
0.5 1
0.6 1
-1.6 1
a_mays_4 0.838 0.1 1
0.5 1
-0.3 1
0.4 1
0.2 1
0.7 1

0.9 1
a_mays_6 0.804 -3.0 1
0.8 1
-0.4 1

1.1 1

0.1 1

0.1 1
0.6 1
–0.3 1
–0.1 1
0.8 1
0.3 1

0.1 1
0.3 1
0.7 1
0.0 1

0.3 1
-2.4 1
0.5 1
0.6 1

0.5 1

-1.4 2
-1.1 2
0.5 1

-0.1 2
0.8 1
0.6 1

0.2 1
0.4 1
0.8 1
0.6 1

0.5 1

0.4 1
a_mays_1 0.850 -0.1 1

0.4 1
0.8 1

-0.1 1

0.6 1
0.2 1

0.3 1
-0.1 1
0.4 1

0.4 1

0.4 1
0.6 1
0.5 1
0.4 1
0.8 1

0.5 1
0.6 1

-0.0 1
-0.1 1
0.5 1
0.3 1
0.3 1

-3.1 1
0.6 1
-0.4 1
0.5 1
-0.4 1
-0.7 1
0.5 1

-0.5 1

0.1 1
0.3 1
-0.1 1
-0.0 1
0.5 1
0.5 1
-0.2 1

0.3 1
0.4 1

0.8 1

0.5 1
0.3 1
1.0 1
-1.2 1
-1.4 1
0.0 1
-2.6 1
a_mays_5 0.677 -2.0 1
0.1 1
-1.5 2
0.4 1

0.5 1
0.8 1
-1.2 1

0.2 1
0001eb406020_P001_Zea_mays_1 0.725 -
0.4 1
0.5 1

0.6 1
0.5 1
−0.0 1
0.8 1
−0.3 1
0.4 1
1.0 1
0.3 1
0.4 1

0.5 1
0.3 1
0.3 1
0.4 1

0.3 1
−0.9 1
0.5 1
0.3 1
−0.9 1
0.4 1
0.4 1
0.5 1
−1.6 1
0.7 1

−0.1 1

−0.8 1

2 0.3 1

4 −0.0 1
9 −1.9 2
00001eb116530_P001_Zea_mays_2 0.659 -
3 0.9 1

3 0.3 1

0 0.5 1
9 0.3 1
2 0.5 1
4 0.6 1
1 −0.7 1
4 −0.4 1
3 −0.0 1
5 −1.8 1
9 −0.8 2

0.9 1
-0.7 1
-0.4 1
0.8 1

-0.0 1
0.4 1
-1.2 1
-0.1 1
0.2 1

00001eb170300_P001_Zea_mays_6 0.758 -

0.7 1
0.1 1

0.2 1
0.5 1
0.5 1
0.1 1
0.1 1
0.2 1
0.4 1

0.5 1
0.1 1
0.2 1
0.6 1
-1.4 1
0.2 1
0.4 1
0.7 1

0.2 1
-0.8 1
-0.0 1
0001eb370820_P001_Zea_mays_5 0.656 -

-1.2 2

0.4 1
0.3 1
0.5 1

0.1 1
0.8 1
-0.2 2
0.6 1

-0.1 1
0.1 1
-2.4 1

0.2 1
0.8 1

a_mays_2 0.655 -3.7 1
-0.2 1
0.4 1

0.3 1

0.5 1
0.1 1
0.3 1
0.3 1
a_mays_3 0.661 -1.8 1

-1.4 1

a_mays_10 0.655 -3.7 2

0.2 1
-0.4 1
0.1 1
-0.7 2

0.4 1
-0.1 1
-0.1 1

```
 0.3 1




 0.4 1
 -2.5 1
 -1.9 1
 0.3 1
 -2.3 1
 -0.3 1
 0.3 1
 0.4 1
 1.1 1


a_mays_9 0.654 -3.7 2
 -0.5 1
 0.3 1
 0.0 1
 0.5 1
 -0.6 1












 0.6 1


 0.8 1
 0.4 1
 0.7 1








 0.3 1
a_mays_2 0.950 0.9 1
```

0.3 1
0.1 1
0.4 1
0.0 1
-1.8 1

a_mays_3 0.736 -1.4 1
0.2 1
0.2 1
-0.1 1

0.3 1
0.1 1

-2.6 2
-0.2 1

-0.2 1

-0.5 1
0.4 1
a_mays_6 0.652 -2.5 3
0.5 1

0.5 1

1.0 1
a_mays_4 0.652 -3.2 1

0.7 1
-1.2 1

-0.2 1
-0.8 1
-0.9 1
0.2 1
-0.1 1
a_mays_9 0.968 0.4 1
-1.1 2
-1.8 2
0.1 1
0.7 1
0.2 1
0.4 1
0.5 1
0.5 1
0.0 1

0.3 1
0.8 1
0.6 1
-0.1 1

1.2 1

0.7 1
a_mays_6 0.848 -0.7 1

0.1 1

-0.4 1
0.0 1
-3.0 1
0.3 1
0.4 1

0.5 1
a_mays_10 0.741 -0.8 1
0.3 1

a_mays_8 0.962 0.5 1
0.5 1
-2.0 1
0.6 1
-2.3 1
-0.9 1
0.7 1
0.7 1

0.7 1
-1.7 1
-2.1 1
-1.9 1
-0.3 1
00001eb161230_P001_Zea_mays_3 0.775 -
-0.7 1
0.9 1

1.1 1
−0.6 1
−0.4 1
0.1 1
0.4 1
1.2 1
−1.6 1
0.6 1
−0.8 1
−0.2 1
0.2 1

−0.5 1
−0.7 1
0.4 1
−0.3 1
−1.9 1

−2.1 1
0.4 1
0.5 1

0.1 1
0.8 1
0.9 1
−0.7 1
0.4 1
−0.0 1
−0.2 1
−0.8 1
−1.7 2
−0.7 1
0.1 1
1.2 1
0.6 1

−2.6 1

```
-0.4 2
-0.1 1
0.3 1

0.5 1
0.7 1
0.8 1
a_mays_5 0.789 -1.3 1
-0.0 1
0.1 1
0.1 1

0.3 1
-1.4 1
-0.4 1
0.2 1

-0.2 1

0.6 1

-0.9 1
0.5 1
-1.2 1

-1.0 1
-1.2 1
-1.5 1
-0.4 1

-1.1 1
0.8 1
-0.2 1
0.1 1
-1.3 1
-0.7 1
-0.6 1
-1.3 1
-2.9 1
```

0.6 1
-1.8 1
-1.3 1
-1.7 1
0.3 1
-0.4 1
0.0 1
0.1 1
0.2 1
1.3 1
-0.3 1
0.9 1
-0.2 1
-1.7 1
-0.2 1
0.9 1
0.0 1
0.7 1
1.0 1
0.7 1
-1.6 1
-1.8 2
0.6 1
-1.2 1
-0.6 1

0.7 1
-0.9 1

0.3 1
a_mays_3 0.853 -0.8 1
-0.2 1

−0.5 1
1.2 1
0.5 1
−0.1 1
0.1 1
−0.1 1

−1.7 1
−0.6 1
0.5 1
−0.2 1
−2.2 1
0.9 1
0.3 1

0.9 1
−1.2 1
0.4 1
−0.1 1
−0.9 1
1.0 1

0.0 1

−1.5 1
0.1 1

0.2 1

-1.0 1
-0.5 1
0.7 1
0.6 1
-1.4 1
0.6 1
0.2 1

0.4 1
-0.9 1
0.7 1

0.5 1
-0.5 1
a_mays_4 0.938 -0.2 1
0.0 1
0.1 2
0.1 1
0.7 1
0.3 1
-1.4 1
a_mays_6 0.772 -1.5 2
0.0 1

-0.6 1
0.9 1
-0.9 1
0.8 1
-0.1 1
a_mays_5 0.935 -0.1 1
-0.6 1

0.2 1
-0.1 1

0.2 1

-1.1 1
-0.8 1
-2.1 1
-0.3 1
-0.5 1
-0.7 1
-1.7 1
-0.6 1
-1.2 1
1.3 1
-1.1 1
0.1 1
-0.6 1

0.2 1
0.3 1
0.2 1
-1.3 1

| | |
|---|---|
| −1.5 | 1 |
| 0.9 | 1 |
| −0.2 | 1 |
| 1.5 | 1 |
| −1.1 | 1 |
| 0.5 | 1 |
| −0.3 | 1 |
| −0.7 | 1 |
| −0.2 | 1 |

| | |
|---|---|
| 0.4 | 1 |
| −1.1 | 1 |

| | |
|---|---|
| −1.0 | 1 |
| −0.3 | 1 |
| 0.6 | 1 |

| | |
|---|---|
| −1.0 | 1 |
| −0.2 | 1 |
| −0.1 | 1 |
| 0.6 | 1 |
| −1.0 | 1 |

| | |
|---|---|
| −1.2 | 2 |
| 0.1 | 1 |
| 0.6 | 1 |
| −0.6 | 1 |
| −1.3 | 1 |
| 0.6 | 1 |
| −0.8 | 1 |

0.4 1
-0.2 1
-2.1 1
-0.3 1

0.0 1
0.1 1
0.2 1
-1.1 1
a_mays_3 0.800 -2.1 1

0.7 1
-1.5 1
-0.6 1
0.3 1
a_mays_4 0.990 0.6 1
-0.1 1
0.9 1

0.0 1

0.8 1

-0.0 2

0.1 1
0.4 1
-2.4 1
-0.8 1

-1.5 1
0.4 1
0.6 1
0.2 1
0.4 1

0.1 1
-0.4 1

0.2 1
0.2 1

0.7 1

-0.4 1
-0.9 1
0.1 1

-0.3 1

0.9 1
-3.3 1
-0.2 1

```
0.1 1
0.2 1
0.7 1


a_mays_6 0.879 0.1 1
0.6 1
-0.4 1
-0.6 1
0.9 1
-1.9 1

0.3 1
-0.4 1
0.7 1
0.6 1
0.4 1
0.3 1
-1.4 1


0.8 1
0.5 1
0.1 1
0.1 1
0.5 1
-0.6 1
-2.7 1
0.1 1
-0.6 1
-2.2 1


-0.8 1
-1.0 1
0.7 1
0.4 1
0.1 1
-0.8 1
```

0.2 1
0.1 1
-0.0 1

-0.1 1
-0.2 1

-1.4 1
0.1 1
-0.1 1

0.5 1

0.2 1
0.2 1

0.7 1
0.4 1
-1.1 1
0.5 1
1.0 1
-0.6 1
0.6 1
0.2 1
-0.5 1
0.2 1
0.8 1
0.4 2

0.4 1

-0.3 1
-1.5 2
0.1 1
-1.1 1
-1.3 1
-1.6 1
0.4 1

-2.2 1
0001eb000370_P001_Zea_mays_1 0.955 -
0.3 1
0.1 1

-3.1 1
0.8 1
-0.2 1
0.3 1
-2.7 1
0.5 1
0.1 1
0.5 1
0.6 1
1.1 1
0.1 1
0.7 1

-2.6 1
a_mays_5 0.807 -1.1 1
0.4 1
-1.1 1
0.5 1
-0.5 1
-0.5 1
1.2 1

-0.1 1

0.3 1
-0.6 1
-1.3 1
-0.3 1
-0.6 1
-0.0 1
-0.3 1
0.3 1
0.1 1
-0.9 1
1.7 1
-1.4 1

0.0 1
-0.5 1
-0.0 1

-0.1 1
-0.1 1

0.3 1
0.2 1
-0.1 1
a_mays_10 0.949 -0.4 1
0.4 1
-0.2 1
0.2 1

-0.9 1
a_mays_2 0.904 -0.1 1

0.1 1
1.1 1
-1.3 1
0.7 1

-0.7 1

0.4 1
-0.1 1
0.5 1

-0.5 2
0.8 1
-1.8 1
-0.0 1
-1.5 1
0.2 1

0.1 1
−1.3 1

−0.8 1
0.0 1
−0.6 1
0.1 1
0.4 1

−0.8 1

−0.4 1
−1.5 1
0.2 1
−1.6 1
0.2 1

−0.0 1
1.2 1
0.2 1
0.8 1
−0.4 1

-0.5 1
-0.3 1
-0.2 1
0.2 1
0.0 1
a_mays_4 0.803 -2.9 1
-0.1 1
-0.3 1

0.3 1
0.9 1
0.1 1
-0.4 1
0.9 1
-0.0 1
-0.9 1
-0.2 1
-0.0 1

-1.3 1

0.2 1
-0.5 2
1.1 1

-0.3 1
0.9 1
-0.6 1
-1.6 1
0.2 1
0.4 1
-0.4 1
0.2 1
0.2 1

−0.2 1
0.1 1
0.8 1
−0.6 1
0.1 1
0.5 1
0.6 1
0.6 1
−0.2 1
−1.4 1
−1.0 2

0.3 1
0.3 1

a_mays_5 0.928 0.2 1
0.1 1
1.5 1
0.7 1
−0.8 1
0.6 1
0.2 1
0.5 1
0.6 1
−1.6 1
−0.6 1
−0.3 1
−1.9 1

−0.8 1
−2.0 1
0.3 2
0.9 1
0.3 1

-0.4 1

0.4 1

0.7 1
-0.1 2
a_mays_5 0.903 -1.6 1
0.5 1
-2.5 1
0.2 1
0.3 1

-0.9 1
1.0 1
0.2 1
0.3 1

0.3 1
-1.9 1

-0.5 1
-0.7 1

0.4 1

0.0 1

0.8 1
-1.7 1
-1.8 1
0.3 1

0.3 1
0.4 1

0.8 1
0.5 1
−0.6 1

−0.0 1
1.1 1
0.4 1
0.9 1
0.2 1
0.4 1
−2.2 1
1.0 1

0.2 1
−0.0 1
−0.1 1
0.3 1
0.7 1
−0.0 1
−0.0 1

-1.4 1
0.8 1

-1.0 1
0.6 1
-1.0 1
-1.2 1

-0.1 1
0.3 1
-0.2 1
-0.4 1
0.5 1

0.7 1
-0.7 1
0.7 1

-1.1 1
-1.2 1
-1.5 1
-1.2 1
0.2 1

-1.4 1
-0.3 1
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-0.3 1
-0.7 1
-0.1 1
-2.3 1
-0.3 1
1.0 1
-0.1 1
-1.4 1
0.3 1
-1.7 1
0.5 1

0.4 1
0.3 1

0.9 1

0.1 1
0.9 1

0.5 1
-1.1 1
-0.8 1
-0.6 1
0.1 1
0.9 1

-0.9 1
0.5 1

0.7 1
-0.3 1
0.1 2

-0.6 1
0.1 1
0.2 1
0.2 1
-3.3 1
-1.2 1

1 0.8 1

5 -0.1 1
1 -1.3 1
3 -0.1 1
5 0.5 1
5 0.4 1
5 -0.1 1
001_Zea_mays_5 0.857 -0.7 1

9 0.2 1

4 0.6 1
9 0.5 1
2 -2.3 1
3 0.2 1
5 0.7 1

a_mays_2 0.924 -1.4 1

3 -0.3 1
3 0.9 1
7 -0.8 1

1 0.5 1

3 0.3 1
1 0.4 1
3 0.7 1

3 0.7 1
001_Zea_mays_1 0.848 -0.4 1
1 0.4 1

a_mays_9 0.951 -0.7 1
3 0.7 1
9 -1.4 1
1 -1.1 1
0 0.4 1
2 -1.0 1
5 1.0 1
2 0.6 1
3 1.2 1
3 0.6 1

3 0.3 1
5 0.3 1
3 0.2 1
00001eb299670_P002_Zea_mays_7 0.800 -
4 -0.4 1
9 -1.0 1

3 -0.3 1

4 -0.1 1
4 0.4 1

0 -1.5 1
2 -2.5 1
4 0.0 1
a_mays_5 0.925 0.0 1
3 -0.3 1
9 1.2 1

5 -0.1 1

a_mays_6 0.937 -0.2 1

1 -0.8 1
3 -0.3 1
4 -0.7 1
5 -0.7 1
5 -1.7 1

5 0.0 1
0 0.4 1
a_mays_10 0.932 -1.7 1
3 0.2 1
7 -1.4 1
2 -0.2 1
1 0.9 1
3 -1.1 1
1 0.1 1

-1.0 1

-0.1 1
0.1 1
0.6 1

-0.8 1
0.2 1
0.7 1

0.5 1

0.1 1
-0.2 1
0.9 1

-0.2 1
-1.9 1
-1.6 1
0.2 1

a_mays_4 0.968 0.5 1

-1.8 1
-0.7 1
-0.2 1

-3.0 1

-0.4 1
0.2 1
-0.6 1

0.2 1
0.2 1
0.7 1
0001eb042590_P001_Zea_mays_1 0.831 -
-0.8 1
0.2 1

-1.3 1
0.3 1

| | |
|---|---|
| -1.8 | 1 |
| -0.1 | 1 |
| -0.3 | 1 |

| | |
|---|---|
| 0.0 | 1 |
| 0.8 | 1 |
| -1.0 | 1 |
| 0.5 | 1 |
| 0.1 | 1 |
| 0.8 | 1 |
| 0.0 | 1 |
| 0.6 | 1 |
| 0.7 | 1 |
| -0.3 | 1 |
| 0.6 | 1 |

| | |
|---|---|
| -0.2 | 1 |

| | |
|---|---|
| 0.4 | 1 |
| 0.6 | 1 |
| 0.7 | 1 |
| 0.3 | 1 |
| 0.7 | 1 |

0.0 1
−0.6 1
0.2 1

−0.5 1
0.7 1

0.3 1
−1.9 1
0.6 1
−1.3 1
−0.1 1
0.9 1

0.7 1

−0.8 1

0.3 1
0.1 1
0.5 1
0.2 1
0.7 1
−0.5 1
0.8 1
0.9 1
0.3 1
1.1 1
−0.4 1
0.2 1

0.2 1
0.6 1
0.1 1
0.6 1
0.2 1
0.1 1

0.4 1
-0.4 1
0.3 1
-0.5 1
0.6 1
-0.0 1
0.7 1
0.6 1
-0.2 1
0.7 1
1.2 1
1.1 1
0.6 1
0.7 1
-0.0 1
0.8 1

-0.7 1
0.9 1
a_mays_9 0.855 -2.1 1
-0.4 1

-0.5 1
-0.3 1

-0.8 1
0.5 1
-0.4 1
0.3 1

-0.9 1
-0.3 1
-0.3 1
0.3 1
-0.6 1
0.5 1
0.7 1

-0.5 1

-1.9 1
0.7 1
1.1 1

a_mays_2 0.877 -0.8 2
-0.5 1
0.4 1
0.5 1
-0.9 1
-0.7 1
0.4 1
0.0 1

0.6 1
-0.6 1
1.1 1
0.3 1
1.0 1
-0.3 1
0.5 1
0.7 1
0.2 1
0.2 1

-1.2 1
a_mays_3 0.962 -1.2 1
-0.0 1

-1.1 1
-0.4 1
-0.1 1
-0.1 1
-0.9 1
-0.9 1
-0.9 1
-0.3 1

0.4 1
0.7 1
0.6 1
1.3 1
0.2 1
-0.3 1

0.2 1

0.3 1
-0.1 1

0.5 1
-0.3 1
0.0 1
-0.3 1

0.1 1
-0.1 1

0.4 1
-0.4 1
-0.6 1
-0.1 1

-0.5 1
-1.9 1
-0.6 1
-0.5 1
-0.4 1
-1.7 1
0.3 1
0.5 1
-0.9 1
0.3 1

```
-1.8 1
-0.1 1
0.8 1



-1.6 1
-1.4 1
-0.1 1
0.1 1
0.3 1
-0.1 1
0.4 1
0.6 1
0.0 1
-0.3 1
0.0 1
0.2 1
-1.6 1

0.2 1
a_mays_3 0.794 -2.5 3
0.4 1
0.8 1
001_Zea_mays_5 0.805 -1.3 2
-0.0 1
-1.9 1
0.2 1
-1.1 1
-0.5 1


0.1 1
a_mays_5 0.997 0.2 1
0.4 1

-0.6 3
0.4 1
0.8 1
0.3 1
```

–0.0 1
–0.1 1
–0.2 1
–0.8 1
0.2 1
0.6 1

–0.2 1
0.1 1
0.3 2

0.5 1
0.1 1
–0.2 1
–0.1 1
–2.1 1
–2.7 1

−0.2 1
−0.6 1
−0.5 1
−1.1 1
1.0 1

−1.2 6

0.1 1
0.8 1
−0.0 1
−0.1 1
−1.0 1
0.3 1

0.4 1
0.4 1
−0.0 1
0.5 1

−2.1 1
−1.0 2
0.3 1
0.7 1
−0.0 1
0.3 1
0.5 1
−1.5 1
0.2 1

−0.2 1

−1.1 1
−1.7 1
0.4 1
0.1 1
0.5 1
0.1 1

−0.5 1
−0.2 1

0.3 1
0.9 1
0.9 1
0.8 1
−0.3 1

−0.4 1

-1.4 1
1.3 1
-0.2 1
0.5 1
0.4 1
0.7 1
0.1 1
0.8 1
0.0 1
0.2 1

-0.9 1
1.2 1
-1.1 1
-0.2 1
-0.1 1
0.7 1
0.7 1
-1.6 1
-0.3 1
1.0 1
-0.2 1
0.3 1

-0.4 1
-0.0 1

0001eb321830_P001_Zea_mays_7 0.923 -
-0.3 1
0.7 1
0.3 1

-0.9 1
0.3 1

```
-2.0 1
0.3 1
0.0 1
0.7 1
0.5 1
0.4 1
0.1 1

-0.2 1


0.3 1

0.1 1
-2.5 1







-0.4 1
-0.9 1



-1.1 1
0.5 1
-3.4 1
a_mays_1 0.911 -1.5 1



0.7 1
1.2 1
0.0 1
001_Zea_mays_6 0.879 -0.2 1
-1.9 1
0.4 1
-0.8 1
0.7 1
-0.1 1




-1.2 1
-0.6 1
```

```
0.5 1
0.8 1





0.3 1
a_mays_9 0.952 -0.5 1
0.3 1
0.2 1
0.0 1
-2.6 1

0.1 1
-0.0 1





-2.0 1
0.6 3
0.3 1





0.7 1








-2.0 1





0.8 1
0.9 1
0.9 1
-0.4 1
0.0 1
0.0 1
```

1.1 1

0.4 1
0.2 1
0.4 1
−0.7 1
0.4 1

−0.4 2
−0.8 1
−0.7 1
−0.1 1
0.3 1
−0.6 1

−1.0 1
0.3 1

−2.3 1
0.3 1
−0.8 1
0.6 1
−2.1 1
−0.5 1

0.3 1
0.3 1
0.6 1
−1.3 1
−0.2 1

1.4 1
−0.1 1

−0.6 1

−1.3 1
−0.4 1
0.1 1
−2.0 1
0.8 1

0.5 1
0.6 1
−0.8 1

0.6 1

0.7 1
−1.3 1
−0.3 1

0.2 1

0.5 1
-1.1 1
-0.1 1

-0.1 1

a_mays_3 0.885 -0.8 1
-0.9 1
-0.2 1
-0.3 1
0.1 1

0.9 1

a_mays_8 0.907 -2.4 1

a_mays_6 0.864 -3.6 1
0.6 1
0.5 1
0.4 1
-2.2 1
-0.2 1
-1.9 1
-0.1 1
-1.7 1
0.4 1
0.5 1

0.6 1
-0.5 1
-0.5 1
1.0 1
0.2 1
0.2 1

a_mays_1 0.920 -0.5 1
0.2 1
a_mays_1 0.875 -0.2 1
0.3 1

0.4 1
-0.3 1
-0.3 1
-1.2 1
-2.1 2
-1.0 1
-0.0 1
-0.4 1

| | |
|---|---|
| 0.7 | 1 |
| 0.1 | 1 |
| 0.1 | 1 |
| -0.3 | 1 |
| 1.0 | 1 |
| -1.2 | 1 |
| -0.2 | 1 |
| -1.1 | 1 |
| 0.6 | 1 |
| -1.1 | 1 |
| -1.1 | 1 |
| 0.3 | 1 |
| 0.2 | 1 |
| 0.3 | 1 |
| 0.6 | 1 |
| 0.4 | 1 |
| -0.3 | 1 |
| -0.4 | 1 |
| -0.3 | 1 |
| -0.5 | 1 |

```
-0.3 1
-0.4 1
-0.1 1
0.7 1
-1.1 1
-0.3 1
-0.3 1
-0.5 1

-0.3 1
-1.1 1



0.9 1

0.5 1
1.1 1
0.9 1
-1.5 1
0.6 1
-0.5 1


-1.3 1
-0.8 1



-1.9 1
-0.4 1
-0.1 1
-0.4 1


-0.2 1
0001eb090230_P001_Zea_mays_4 0.845 -
-0.3 1
-0.5 1
```

```
-0.5 1




0.4 1
1.1 1
-1.3 1
0.5 1










-1.1 1

-0.1 1
-1.7 1
0.3 1
0.6 1

0.3 1
-1.7 1
-0.3 1
-1.0 1



-0.1 1



-0.5 1


0.9 1
0.5 1
-0.9 1
-1.0 1
0001eb373710_P001_Zea_mays_9 0.920 -
0.2 1
0.0 1
0.4 1
0.3 1
0.0 1
-1.3 1
```

```
 0.4 1
 0.9 1
 0.4 1
 -0.6 1
 0.2 1
 -0.6 1
0001eb081310_P001_Zea_mays_2 0.955


 0.9 1
 0.6 1
 -0.2 1
 0.4 1
 0.3 1


 -1.4 1
 0.3 1
 0.7 1
 -0.4 1
 0.6 1
a_mays_6 0.892 -0.6 1
 0.1 1
 0.2 1
 0.5 1
 0.7 1
 -1.1 1
0001eb189280_P001_Zea_mays_4 0.993
 -0.6 2


 0.4 1
 0.6 1
a_mays_6 0.882 -0.7 1
```

–1.8 1
0.3 1
0.3 1

–1.1 1
1.2 1
0.3 1

| | |
|---|---|
| 0.7 | 1 |
| 0.5 | 1 |
| −0.1 | 1 |
| 0.1 | 1 |
| −1.1 | 2 |
| −1.7 | 1 |
| −1.6 | 1 |
| 0.4 | 1 |
| 0.6 | 1 |
| 0.7 | 1 |
| −0.6 | 1 |
| 0.2 | 1 |
| 0.0 | 1 |

| | |
|---|---|
| −0.6 | 1 |

| | |
|---|---|
| 0.3 | 1 |
| 0.8 | 1 |
| 0.1 | 1 |

| | |
|---|---|
| −1.5 | 1 |
| −1.5 | 2 |

| | |
|---|---|
| 0.3 | 1 |
| 0.5 | 1 |
| 0.3 | 1 |
| 0.6 | 1 |
| −0.3 | 1 |

−0.5 1
0.5 1
−0.1 1
0.2 1
−0.1 1

−1.0 1
−0.3 1
−0.9 1
−1.7 1
0.5 1
0.4 1
0.3 1
−1.3 1
0.1 1
−0.1 1
0.9 1
−0.7 1
−0.5 1
0.4 1
0.4 1
0.2 1
0.5 1
−1.8 1
0.3 1

−2.2 1
0.6 1
0.9 1

0.1 1

7 -0.2 1
5 -0.1 1
1 -0.2 1
3 0.0 1
1 0.5 1
0 -0.7 1
2 -0.8 1
4 0.5 1
0 -1.4 1
0 1.1 1
5 0.8 1

2 0.3 1
1 -0.9 1
9 -1.7 1
5 1.2 1
7 -0.7 1
2 0.2 1
2 -0.5 1
2 -2.7 1
3 1.1 1

7 0.1 1

00001eb015620_P001_Zea_mays_1 0.956 -

0.6 1

–1.6 1
0.8 1

–0.6 1
0.7 1

−1.2 1
−0.3 1
−0.1 1
−2.9 1
0.8 1
0.7 1
0.7 1

0.1 1
0.2 1

−0.0 1
−0.4 1
0.9 1

0.5 1

0.6 1
0.9 1

−0.0 1

0.5 1
0.2 1

0.2 1

0.8 1
−1.0 1
0.1 1
1.1 1
0.3 1
−1.3 1
−0.8 1

−0.4 1
0.2 1
0.1 1
0.0 1
0.9 1
−1.2 1

0.5 1
0.9 1
0.0 1
−0.2 1
−0.6 3

1.0 1

−0.4 1
0.1 1
−0.8 1
0.3 1
−0.1 1

0.0 1

0.4 1
0.4 1
-0.4 1
a_mays_1 0.822 -2.4 1
0.1 1
0.4 1
-1.6 1
0.1 1
0.3 1
-0.0 1
-0.7 1
0.1 1

0.8 1
-0.1 1

-0.5 1
0.5 1
0.6 1
0.3 1
0.3 1
-0.2 1
-0.0 1
0.4 1
-0.8 1
1.1 1

-0.5 1
0.6 1
-0.2 1
0.4 1

| | |
|---|---|
| -0.1 | 1 |
| -0.3 | 1 |
| 0.5 | 1 |
| 0.2 | 1 |
| 0.6 | 1 |
| 0.5 | 1 |
| 0.0 | 1 |
| 0.4 | 1 |
| 0.7 | 1 |

| | |
|---|---|
| -0.3 | 1 |
| -0.3 | 1 |

-0.4 1
0.2 1

a_mays_2 0.952 0.8 1

0.5 1
-0.5 1
0.2 1
0.7 1
0.4 1

-1.3 1
-1.0 1
0.7 1

0.3 1

-0.7 1
-0.6 1
-0.7 1
0.6 1
-0.2 1
0.9 1
0.2 1
0.6 1
0.6 1

a_mays_1 0.902 -1.1 1
-0.0 1
0.6 1
-0.1 1
0.0 1
-0.2 1
-0.1 1
-1.0 1
-1.2 1
0.6 1
-0.5 1
0.4 1
-1.1 1
0.3 1

0.1 1

-0.5 1
0.5 1
0.2 1
0.2 1
-0.3 1

−1.0 1
−1.0 1
0.2 1

−0.8 1
0.5 1
−0.6 1

−1.3 1
−0.5 1
−0.2 1
0.4 1
0.5 1
−0.8 1

0.5 1

−0.7 1

```
 0.1 1
 -0.4 1
 0.3 1
 -0.8 3
0001eb374190_P001_Zea_mays_9 0.818 -
 0.1 1
 0.6 1
 0.2 1
 -0.9 1
 0.6 1







 -0.7 1
 1.4 1
 0.4 1

 1.1 1
 -0.6 1
 -0.3 1
 0.6 1
 0.4 1





 1.0 1
 0.5 1
 0.5 1
 -0.2 1
 0.4 1
 0.5 1
 0.1 1
 0.6 1
01_Zea_mays_3 0.843 -1.9 1
 0.7 1
```

0.9 1
0.2 1
0.5 1
-0.4 1
0.5 1
0.7 1
0.5 1
-0.7 1

0.5 1

0.4 1
0.8 1
-0.1 1

-1.2 1
-1.2 1
0.6 1

0.6 1
0.2 1
0.4 1
-0.6 1
0.4 1
-0.5 1
0.7 1
0.2 1

-1.8 1
-0.6 1
0.5 1
a_mays_2 0.759 -3.0 1
-1.4 1

-0.3 1

-0.4 1

0.4 1
0.5 1
-2.2 1
-0.1 1
0.3 1

-0.5 1
-0.2 1

0.6 1
0.9 1
1.1 1
0.7 1
a_mays_1 0.815 -1.0 1
-0.4 1

-0.1 1
-0.5 1
-2.0 1

-1.0 1

-0.1 1
0.7 1

0.2 1
-0.7 1
0.6 1
-1.0 1
0.3 1
0.1 1
-2.5 1
0.6 1
-0.2 1
-0.2 1

-0.1 1
0.7 1
0.6 1
-0.2 1
0.6 1
0.4 1
0.1 1
a_mays_7 0.953 0.2 1

-0.4 1

-0.4 1
0.8 1
1.0 1
0.5 1
0.3 1
-3.0 1

-1.0 1
0.4 1
-0.1 1
a_mays_5 0.918 -0.8 1
0.3 1
0.1 1
-1.7 1

-2.1 2
-0.1 1

0.6 1

-0.0 1
0.4 1
0.2 1
0.9 1
0.7 1
0.2 1
-0.9 3
0.3 1
-1.2 1
0.1 1
0.7 1
-1.8 1
0.3 1
0.2 1
0.3 1

0.4 1
0.3 1
0.1 1
0.7 1

0.4 1

0.4 1

0.3 1
0.9 1
0.1 1
−0.1 1
−0.3 1
−0.2 1
0.7 1
0.5 1
−0.3 1
0.3 1

0.4 1
0.7 1
0.3 1
0.3 1
−1.8 1
0.5 1

0.5 1
0.4 1
−1.1 1
0.5 1
0.1 1
−2.5 1
0.8 1
0.6 1
−0.5 1

0.1 1
-0.1 1
-2.0 1
0.1 1
-0.1 1
-0.2 1
-1.3 1

0.4 1
-2.0 1
0.8 1
0.6 1
0.4 1

-1.0 1
0.2 1
-1.7 1
-0.0 1
0.0 1
0.3 1
0.6 1
0.6 1
0.1 1

0.9 1
-0.4 1
-1.5 1
-0.0 1
-1.2 1
a_mays_3 0.900 -0.1 1
-2.2 1
-0.1 1
0.4 1
-1.7 1
0.2 1
-0.4 1
-0.6 1
-2.9 2
0.6 1

| | |
|---|---|
| −1.2 | 2 |
| 0.1 | 1 |
| −0.2 | 1 |
| 0.7 | 1 |
| −0.2 | 1 |
| −0.0 | 1 |
| 0.6 | 1 |
| | |
| −1.2 | 1 |
| −0.4 | 1 |
| | |
| −0.0 | 1 |
| 0.3 | 1 |
| −0.3 | 1 |
| | |
| 1.5 | 1 |
| 0.3 | 1 |
| −0.4 | 1 |
| 1.3 | 1 |
| 0.3 | 1 |
| | |
| 0.4 | 1 |
| −2.5 | 1 |
| | |
| 0.7 | 1 |
| 0.5 | 1 |
| −0.9 | 1 |
| −1.5 | 1 |
| 0.5 | 1 |
| | |
| −1.2 | 1 |
| −0.5 | 1 |
| −0.1 | 1 |
| 0.6 | 1 |

0.7 1
0.1 1
−0.9 1
0.1 1
−0.4 1
1.0 1
−0.1 1

0.5 1
0.6 1
0.5 1
−1.6 1
0.5 1
0.6 1
0.3 1

0.5 1
−0.5 1
−1.4 1
0.7 1

2 –0.3 1
7 0.4 1
3 0.7 1
3 0.0 1

00001eb281800_P001_Zea_mays_6 0.901 -
2 –1.2 1
1 0.1 1
7 –0.1 1
9 0.2 1
2 –0.1 1

7 0.6 1

−0.5 2
0.5 1
1.0 1
0.7 1
0.5 1

−1.2 1

0.6 1
1.0 1

−0.3 1
0.6 1
−0.7 1
−0.2 1
0.8 1
−1.4 1
−2.8 2
0.6 1
−0.6 1
0.9 1
0.3 1
−0.5 1
−0.9 1
0.5 1
0.6 1
−0.1 1
−1.3 1

0.4 1

0.4 1

0.6 1

-1.9 1
-2.5 1
0.1 1

0.4 1
-0.9 1
0.4 1

-2.0 1
0.3 2
-1.1 1

0.2 1
0.9 1
0.3 1
-0.1 1
0.2 1
-2.3 1
-0.0 1
a_mays_8 0.789 -2.6 1

-0.1 1
0.7 1
-0.5 1
0.9 1

-0.5 1
-0.3 1
-0.1 1
0.2 1
0.1 1

-0.3 1
0.4 1
0.6 1
-0.5 1
-1.8 1
0.2 1
-0.2 1

a_mays_6 0.874 -0.5 1
0.8 1

0.4 1
-0.7 1
0.2 1

0.4 1

0.4 1
0.5 1
1.1 1
0.4 1
a_mays_5 0.875 -2.4 1

-1.1 1
-0.0 1
0.9 1
0.1 1

3 0.9 1
0 -1.4 1

1 0.5 1
1 0.2 1
5 0.7 1
6 0.5 1
3 0.7 1
0 -0.4 1
9 0.0 1
3 0.2 1
4 0.4 1
1 -0.6 1
5 -0.4 1
6 0.0 1

6 -1.2 4
2 0.9 1
7 -0.6 1
9 0.8 1
a_mays_7 0.969 0.9 1
4 -0.0 1
4 1.1 1

3 -0.0 1
6 0.4 1
a_mays_5 0.782 -2.4 1
3 0.7 1

```
-2.9 1

0.2 1

0.2 1
0.1 1
0.2 1



-0.2 1




a_mays_5 0.864 -0.1 1
-0.4 1
-2.1 1
0.7 1


-0.8 1
-0.2 1


-0.0 1
0.4 1
0.7 1
0.3 1
-0.9 1
-1.7 1
```

0.5 1
-1.7 2

-0.3 1
0.5 1
0.9 1
-0.1 1

0.5 1
0.5 1

0.1 1
0.8 1

-0.8 1
0.1 1
-2.1 1
0.1 1
0001eb198990_P001_Zea_mays_4 0.821 -

0.6 1
0.7 1
0.4 1

-2.1 1

0.2 1
-1.0 1
0.6 1

-0.0 1
-0.2 1

-2.5 1
0.6 1
-0.8 1
0.8 1
0.6 1

1.0 1
0.3 1
-0.1 1
a_mays_5 0.868 -1.2 1

-0.9 1

0.8 1
0.5 1
0.4 1
0.6 1
0.1 1
0.5 1
-1.3 1

0.2 1

0.7 1

0.4 1
-0.1 1
-0.3 1

-0.6 1

-0.1 1
-0.6 1
0.4 1
-0.6 1
0.4 1
-0.5 1
0.5 1

0.2 1
0.2 1
-0.5 1

0.0 1
-0.4 1
-0.5 1

0.3 1
0.0 1
0.6 1

0.8 1
0.7 1
0.1 1
0.7 1
-0.3 1
a_mays_6 0.977 1.3 1
-0.1 1
a_mays_8 0.957 -0.8 1
-1.5 1
-0.3 1

0.9 1
-0.4 1
1.0 1

0.5 1
0.7 1
a_mays_2 0.762 -2.5 2
0.3 1
0.2 1

-0.7 1

0.7 1
-0.9 2

0.0 1
-1.6 1
-0.7 1

a_mays_10 0.958 -1.0 1

-1.9 1
0.7 1
-0.8 1
0.5 1

0.6 1
0.8 1
-0.5 1
0.4 1
-1.1 1
-1.0 1
-1.4 1
-1.9 1
-1.7 1
-1.7 1
0.1 1

-2.0 1
-0.8 1
0.5 1
-0.1 1

-0.3 1
-0.7 1

0.7 1
-0.2 1

-1.0 1

0.6 1
0.0 1
0.4 1

0.7 1
0.1 2

0.6 1

0.7 1
0.8 1
0.3 1
0.4 1

−1.2 1
0.9 1
0.1 1
0.5 1

−0.0 1
0.5 1

0.5 1

0.8 1
-0.1 1
0.1 1
-1.3 1
a_mays_4 0.920 0.6 1
-0.5 1
-1.0 1
0.5 1
0.1 1

1.0 1
-0.2 1

0.5 1
0.6 1
-1.9 1
0.6 1
-1.2 1
0.7 1
0.5 1
0.0 1
-0.5 1
0.8 1
-1.9 1
0.4 1
a_mays_3 0.805 -1.2 1
a_mays_3 0.938 0.3 1

```
-0.6 1
-0.9 1
0.1 1


0.0 1
0.1 1


0.4 1
-0.7 1
-0.1 1
0.3 1
0.5 1
0.8 1
0.4 1
a_mays_3 0.778 -3.2 1
-0.0 1
0.4 1
0.4 1
-1.6 1
-0.7 1
-0.1 1
0.1 1




-1.0 1
-0.5 1
0.3 1
0.1 1
0.3 1
-0.1 1
-1.8 1
0.3 1
-0.0 1
-1.6 2
0.3 1
-0.8 1
-1.3 1
0.4 1




0.5 1
0.8 1
```

```
-0.6 1
-0.0 1
0.8 1
0.9 1
0.0 1
1.0 1
0.0 1
0.3 1
1.1 1
-0.0 1
a_mays_5 0.948 0.3 1
0.4 1
a_mays_2 0.787 -1.6 1
0.3 1

0.3 1
-0.2 1
-0.9 1
-0.2 1
1.1 1
1.1 1
-0.5 1
0.2 1
0.3 1
0.4 1
-0.2 1
-0.4 1
0.2 1
0.2 1
0.8 1
0.5 1
0.1 1

-1.7 1
0.5 1
-0.1 1
0.0 1
```

0.7 1

-0.0 1
-0.0 1

0.2 1
-1.3 1
-0.0 1
1.2 1

1.4 1
0.7 1
0.3 1
0.1 1
0.4 1
0.7 1
0.5 1
-3.5 1
-0.1 1
-1.6 1
-0.1 1
0.6 1
0.2 1
-0.6 1
0.4 1

-0.7 1
-1.0 1
0.4 1
0.2 1

–1.3 1
0.0 1

0.4 1
–0.2 1
–2.8 1
1.0 1

0.8 1
-1.3 1
0.8 1

-2.4 1
-0.1 1
0.8 1
-0.7 1
0.7 1
0.3 1
0.1 2
-0.5 1
0.8 1
-1.5 1
0.5 1

-0.9 1
0.5 1
a_mays_6 0.814 -3.0 1
0.2 1

0.9 1
-0.0 1

0.3 1
-0.7 1
-0.5 2

0.3 1
-0.8 1

-0.1 1
0.1 1
0.5 1
0.0 1
-0.0 1

0.2 1
-0.0 1
0.3 1
-0.2 1
0.5 1
-2.5 1
a_mays_9 0.985 0.8 1
0.1 1
a_mays_9 0.783 -1.8 1

-0.1 1
-0.3 1
-1.0 1

0.0 1
0.6 1

0.6 1

0.1 1

0.1 1
0.5 1
0.1 1

-0.4 1
-1.1 2
-0.7 1

0.9 1
0.4 1
0.9 1
0.8 1
0.6 1

-0.1 1
0.5 1
-0.5 1
0.3 1
-0.2 1
0.7 1
1.0 1
0001eb121890_P001_Zea_mays_8 0.932
0.4 1
0.5 1
0001eb314590_P001_Zea_mays_7 0.883 -

0.8 1

-0.5 1

0.5 1
0.4 1
-0.2 1
0.6 1
0.5 1
-0.1 1
-0.8 2

0.2 1
0.4 1

0.6 1
-0.5 1

–1.1 1

0.9 1
0.7 1
0.7 1
–0.6 1
–0.3 1
0.6 1
1.0 1
–0.1 1

–0.2 1

0001eb105480_P001_Zea_mays_7 0.930

0.6 1
0.4 1
0.4 1

-0.5 1
-2.1 1
-1.3 1
0.4 1
0.1 1

0.1 1
-0.2 1
1.2 1

-1.9 1

-0.1 1
0.5 1
-0.0 1
0.2 1
-0.5 1

0.6 1
-0.7 1
0.4 1
-1.9 1

0.5 1
-0.3 1
-0.1 1
0.1 1
0.1 1
0.5 1
0.1 1

-1.2 1
-0.3 1
0.5 1
-1.4 1
-0.1 1

0.5 1
0.3 1
-0.3 1
-1.7 1
-0.1 1

1.0 1
0.2 1
-0.1 1
-1.5 1
-2.7 1
1.0 1

0.4 1

0.0 1

0.3 1

0.5 1
-1.6 1
-0.3 1
-0.2 1
0.7 1

0.8 1
-1.8 1

-0.7 1
1.0 1
0.6 1

```
a_mays_4 0.877 0.3 1
 0.0 1
 0.4 1
 -0.1 1
 -1.7 1



 0.7 1
 -0.1 1
 0.4 1
 0.4 1
 -0.1 1
 -0.4 1
 0.8 1







 0.3 1






 -2.1 1
 0.2 1
 0.5 1
 -0.2 2
 0.5 1
 0.5 1
a_mays_7 0.880 -0.3 1
 0.9 1
 0.8 1
 0.6 1
 0.5 1

a_mays_5 0.897 -1.4 1




 -0.6 1
 1.2 1
```

-0.5 1
0.5 1
0.0 1
0.6 1
0.6 1
0.3 1
0.6 1
a_mays_1 0.950 -0.1 1

0.3 1
0.6 1

-0.2 1
0.2 1
0.1 1
0.4 1

-0.1 1
1.1 1
0.6 1
0.7 1
-0.6 1
0.2 1

0.5 1

-0.4 1
0.3 1

-0.3 1
0001eb403980_P002_Zea_mays_9 0.974
0.7 1
0.9 1
-0.0 1
-1.9 1
-2.0 1
1.2 1
0.4 1
-1.6 1
-0.9 1
-0.2 1

0.8 1
-0.4 1
0.4 1
0.2 1
a_mays_9 0.919 -2.6 1
-0.9 1
-1.0 1
0.1 1
-0.6 1
-1.6 1

0.7 1

| | |
|---|---|
| 0.6 | 1 |
| | |
| 0.3 | 1 |
| 1.8 | 1 |
| 0.9 | 1 |
| | |
| −0.7 | 1 |
| 0.7 | 1 |
| | |
| 0.6 | 1 |
| −0.0 | 1 |
| −0.2 | 1 |
| −0.2 | 1 |
| 0.1 | 1 |
| 0.6 | 1 |
| 0.6 | 1 |
| | |
| 0.4 | 1 |
| | |
| 0.6 | 1 |
| 1.1 | 1 |
| | |
| 0.8 | 1 |

-0.1 1
0.4 1
0.6 1
-0.3 1

-1.9 1
0.4 1

0.2 1
-1.9 1
0.7 1
0.5 1
0.1 1
0.6 1
0.8 1
0.0 1
0.4 1
-0.5 1
-1.3 1

0.8 1
-0.1 1
-1.5 1
a_mays_4 0.868 -2.1 1
0.4 1
0.3 1
0.8 1
-2.4 1

-0.1 1
-0.1 1

-1.1 1
-0.7 1
0.0 1
-0.2 1
1.1 1
0.7 1
-0.6 1
-0.6 1

-1.3 1
-1.1 1
0.3 1
-0.1 2
0.2 1

0.6 1
1.0 1
0.2 1
-1.2 1
0.8 1
0.2 1
0.7 1
-0.3 1
0.9 1
0.1 1
0.1 1
-0.0 1

a_mays_4 0.851 -0.9 2
0.1 1
-0.6 1
-0.3 1
0.1 1

0.0 1

0.6 1

-0.5 1
0.8 1
-0.1 1
-0.1 1
1.1 1

0.3 1
0.6 1

-0.4 1
-0.5 1

-0.7 1

0.6 1

-1.9 2
-0.6 1

```
 0.7 1
 0.0 1
 -0.1 1

 -1.2 1

a_mays_2 0.909 -2.1 1
 0.2 1

 0.5 1
 -0.7 1
 -0.2 1
 0.3 1
 1.1 1

 -0.3 1
 0.9 1
```

0.6 1
0.6 1
-1.0 1
0.5 1
-0.3 1
0.7 1
0.7 1
0.4 1
1.0 1

0.8 1
0.7 1
-1.5 1
0.2 1
0.5 1
0.2 1
-0.9 1
0.5 1
-0.2 1
-0.1 1
-0.5 1
-0.8 1
-0.0 1
1.1 1
-0.4 2
0.7 1

-0.5 1
a_mays_1 0.949 0.2 1
0.3 1
0.6 1
0.9 1
-1.0 1
0.4 1

| | |
|---|---|
| 0.4 | 1 |
| 0.5 | 1 |
| 0.0 | 1 |
| −0.5 | 1 |
| −0.2 | 1 |
| 1.0 | 1 |
| 0.2 | 1 |
| 0.8 | 1 |
| 0.2 | 1 |
| 0.2 | 1 |
| −0.4 | 1 |
| 0.2 | 1 |
| −2.0 | 1 |
| 1.1 | 1 |
| −1.7 | 1 |
| −0.2 | 1 |
| 0.9 | 1 |
| −2.8 | 1 |
| 0.6 | 1 |
| −0.1 | 1 |
| 0.6 | 1 |

0.8 1
0.1 1
0.2 1

0.1 1

0.7 1
1.3 1
–1.7 2
–0.2 1
0.8 1
0.2 1
0.7 1

–0.1 1
–0.6 1
–2.3 1
–0.3 1
0.7 1
–0.6 1
1.0 1

0.9 1
–0.1 1
0.3 1
0.4 1

0.2 1
0.5 1

0.5 1
−0.6 1
0.4 1
0.7 1
−1.2 1

−0.2 1
−1.1 1
0.4 1

−0.2 1
−0.1 1
−0.2 1
0.2 1
0.1 1
−1.5 1
0.9 1
0.8 1
−0.3 1
−2.2 1
−0.1 1
0.8 1
−0.4 1

```
0.9 1


-0.1 1
-0.1 1
0.7 1
0.3 1
0.6 1
0.1 1

-0.6 1
-2.4 1
0.4 1
0.3 1
0.0 1
0.8 1



0.4 1
a_mays_10 0.917 -0.8 1



0.0 1

-0.3 1
0.2 1
-1.0 1
-0.1 1
-1.6 1




-0.6 1
```

0.1 1
1.0 1

0.5 1
0.3 1

0.6 1
0.5 1
−0.7 1

−2.8 2
0.3 1

0.9 1
0.4 1
−0.4 1
−3.3 1
−0.2 1

```
0.4 1
0.4 1
a_mays_1 0.932 0.6 1


-0.9 1


-0.3 1
0.2 1
0.1 1

-1.4 1
0.2 1
0.1 1
-0.1 1
-0.4 1
0.5 1
0.6 1
0.4 1
0.2 1
0.6 1

-0.4 1
-0.1 1
0.6 1
-0.1 1
0.4 1
-0.0 1
0.3 1
-2.7 1
-0.7 1
0.8 1
0.8 1
0.5 1
0.2 1
-1.3 1
```

0.6 1
-1.2 1

0.6 1
0.5 1
-0.1 1
1.1 1
0.3 1
0.8 1
0.6 1
0.7 1
-0.2 1
a_mays_1 0.882 -1.5 1
0.7 1
0.4 1
0.5 1
0.1 1

0.1 1
0.3 1
-3.5 1

0.7 1
0.4 1
0.1 1
0.1 1
-0.8 1
0.1 1
-0.1 1
-0.2 1
1.0 1

0.5 1
0.6 1
0.5 1
-0.3 1
0.8 1
-0.0 1
0.9 1

0.7 1
0.2 1
a_mays_2 0.955 0.1 1
0.7 1
0.1 1
1.0 1
0.6 1
0.5 1
-0.1 1
0.8 1
0.6 1
-0.6 1
-0.8 1

0.0 1
-1.1 1

-0.1 1
0.3 1
-0.4 1
0.1 1

0001eb090200_P001_Zea_mays_2 0.972

-0.1 1

-0.6 1
-0.3 1
0.6 1

-1.6 1
-0.3 1
-0.3 1
-0.0 1
-3.2 1
1.3 1
0.2 1
0.4 1

-0.2 2
0.7 1

0.4 1
0.5 1

0.5 2
0.2 1
0.1 1
0.8 1

0.6 1
1.2 1
-1.0 1
-0.6 1

-0.1 1
a_mays_4 0.799 -1.6 1
0.1 1
-1.2 1

0.5 1
-0.7 1
-0.1 1
0.6 1
0.4 1
0.9 1

0.5 1
0.6 1
0.9 1
-1.2 1
0.4 1
0.7 1
0.2 1
1.3 1
0.7 1
0.8 1
0.0 1
0.5 1

a_mays_5 0.805 -1.7 1
-2.8 1
-3.0 1

1.0 1

0.3 1

0.8 1

0.6 1
−0.9 1
0.6 1
0.2 1

−0.0 1
0.2 1
−0.8 1
0.6 1
0.6 1
0.1 1
−0.1 1

0.4 1
0.2 1
−1.1 1
−0.2 1
0.5 1

| | |
|---|---|
| −0.6 | 1 |
| 0.8 | 1 |
| 0.8 | 1 |
| 0.2 | 1 |
| −0.1 | 1 |
| 0.3 | 1 |
| −0.8 | 1 |
| 0.6 | 1 |
| 0.5 | 1 |
| 0.1 | 1 |
| −1.9 | 1 |
| 0.1 | 1 |
| 0.5 | 1 |
| −2.3 | 1 |
| 0.2 | 1 |
| 0.7 | 1 |
| 0.9 | 1 |
| −0.9 | 1 |
| 0.7 | 1 |
| 0.5 | 1 |
| 0.6 | 1 |
| 0.1 | 1 |
| −0.7 | 1 |
| 0.6 | 1 |
| −0.1 | 1 |
| 0.0 | 1 |
| −0.1 | 1 |
| 0.8 | 1 |
| −0.6 | 1 |
| −0.3 | 1 |
| −3.5 | 1 |
| 0.1 | 1 |
| 0.6 | 1 |
| −2.4 | 1 |

0.3 1
0.7 1

−0.6 1
0.9 1

−0.7 1
−0.1 1
−3.4 1
−1.1 1
0.2 1
0.8 1
0.9 1
−0.8 1
0.2 1
−0.2 1

0.6 1
−1.4 1
0.5 1
−0.7 1
−0.1 1
0.7 1
−0.3 1

0.6 1
0.2 1
0.3 1
0.2 1

−0.0 1
0.8 1
1.3 1
0.0 1
−0.1 1
0.7 1
0.2 1
−1.8 1

0.1 1
−0.1 1
−0.2 1
0.6 1
0.2 1
−0.6 1
0.7 1
0.5 1
0.3 1
−0.1 1

−1.4 1
0.5 1
−0.4 1
−0.9 1
−0.6 1

0.4 1

0.2 1

```
0.1 1
0.1 1
-0.5 1



-1.1 1
1.2 1
0.3 1
0.5 1
0.5 1
a_mays_7 0.761 -1.9 1
-0.0 1
-0.2 1
-2.2 1
-0.6 1
-0.4 1
0.3 1
0.4 1
0.8 1
1.1 1
0.5 1



-0.1 1
-0.5 1
0.6 1
-1.9 2
0.4 1
0.4 1
-0.3 1

0.1 1
-0.0 1
-0.3 1
0.4 1
0.5 1
```

–0.3 1
–0.1 1
0.5 1
0.2 1

0.6 1
0.4 1
0.7 1
0.6 1

–2.3 1
0.1 1
0.7 1

–0.9 1
–1.6 1

0.2 1
–0.8 1
–1.0 1
0.0 1
1.1 1
1.2 1
0.5 1
0.6 1

-0.3 1

-1.2 1
0.3 1
0.4 1

-1.1 1
0.2 1
-0.8 1
0.4 1
-0.3 1
0.7 1
0.1 1
-0.1 1
0.8 1

0.0 1
-0.5 1

```
0.4 1
0.7 1
0.5 1
0001eb346830_P001_Zea_mays_3 0.980 -
1.1 1
-1.7 1
0.4 1
-1.8 1
-1.8 1
0.0 1
0.9 1
0.5 1
-1.2 1
0.4 1
-0.5 1
-0.3 1
-0.1 1
0.2 1
0.6 1
-0.8 1


0.1 1
0.3 1
-1.6 1
0.6 1
0.8 1
-0.7 1
-0.5 1
0.2 1
-1.2 1
0.4 1
-1.2 1
0.6 1
0.1 1
0.2 1
-0.8 1
```

```
a_mays_6 0.889 -0.9 1









 -0.0 1

 0.2 1
 0.5 1
 0.7 1
 0.5 1
 -0.3 1
001_Zea_mays_1 0.787 -2.0 1



 0.0 1
 0.4 1
 0.4 1
 0.3 1
 0.5 1
 0.4 1
0001eb277240_P001_Zea_mays_6 0.897 -
 0.2 1
 0.7 1
 -0.0 1
 0.8 1

 0.4 1
 0.3 1
 -1.3 1
 -0.1 1
 -0.0 1
 0.3 1
 0.1 1
 -0.2 1
 0.5 1
```

| | |
|---|---|
| 0.1 | 1 |
| 0.3 | 1 |
| 0.5 | 1 |
| -0.0 | 1 |
| 0.3 | 1 |
| -0.2 | 1 |
| 0.4 | 1 |
| -0.2 | 1 |
| -0.4 | 1 |
| 0.3 | 1 |
| | |
| 0.9 | 1 |
| -0.0 | 1 |
| 0.2 | 1 |
| -1.1 | 1 |
| | |
| 0.6 | 1 |
| | |
| -0.9 | 1 |
| | |
| 0.7 | 1 |
| 0.6 | 1 |
| -0.9 | 1 |
| 0.5 | 1 |
| | |
| 0.0 | 1 |
| -2.9 | 2 |

0.7 1
–1.4 1
0.4 1
0.5 1
0.1 1
0.2 1

0.2 1
–1.2 1
–0.0 1
0.6 1
–0.6 1
0.2 1
–0.1 1
–1.1 1
0.3 1
0.1 1
0.1 1
0.3 1
0.7 1
–0.3 1
0.7 1
1.1 1
0.7 1
0.5 1
–0.6 1
0.9 1
–0.6 1
–0.5 1
0.6 1
0.0 1
0.5 1
0.5 1

–1.0 1
0.2 1
0.6 1
–2.4 1
0.2 1
0.5 1
–0.9 1

–0.4 1

-0.5 1
-1.5 1
-0.2 1
-0.8 1
0.8 1
0.1 1
-0.1 1

-2.1 1
0.5 1
-0.2 1
a_mays_2 0.952 -1.4 1

-0.1 1

a_mays_2 0.919 -0.5 1
-0.4 1

a_mays_1 0.878 -0.1 2
-0.5 1
0.2 1
-0.2 1
0.3 1
-0.4 1
-0.5 1
-2.1 1
a_mays_1 0.889 -1.3 1
0.5 1
a_mays_4 0.928 -0.4 1

0.7 1
-0.1 1
-2.7 1
-0.1 1
1.2 1
0.1 1
0.4 1
-2.3 1
0.6 1
0.0 1
0.9 1
0.2 1
0.6 1
0.4 1
0.2 1
-0.1 1

-0.6 1

0.3 1
a_mays_3 0.859 -1.5 1
-1.2 1
-0.4 1
0.1 1
0.3 1
0.4 1

-0.7 1
0.6 1
0.1 1
1.6 1
0.7 1
-0.2 1
-0.1 1
-0.3 2
0.5 1

0.2 1

0.5 1
-0.4 1

0.5 1
0.1 1
0.3 1

1.3 1

-0.1 1

0.8 1
-1.9 1

-2.7 1
-0.7 1
0.2 1
-1.5 1

0.7 1
-0.1 1
-0.7 1
1.2 1

0.5 1
0.0 1

-0.7 1
-0.0 1
0.8 1
0.4 1
-0.1 1
0.5 1
0.6 1
0.3 1
1.0 1
0.2 1

0.7 1
0.8 1
0.8 1

0.4 1

0.7 1
a_mays_2 0.896 -1.5 1

0.4 1

0.4 1
0.4 1
0.4 1
0.4 1
−0.5 1
0.5 1

0.6 1
−2.4 1
0.7 1
0.3 1
0.2 1
0.4 1
0.4 1
0.3 1
0.4 1
0.6 1

0.3 1

0.2 1
0.9 1
1.0 1
0.5 1
0.8 1
−1.1 1

−0.3 1
0.7 1
−0.0 1

0.3 1
0.6 1
-0.0 1
0.3 1

a_mays_1 0.969 0.3 1
0.2 1

-1.0 1
0.7 1
a_mays_10 0.929 -0.5 1
0.0 1
-0.3 1
1.0 1

-1.9 1

0.1 1
-0.0 1
-0.4 1

-0.4 1
0.5 1

0.7 1
0.6 1
-1.1 1
0.7 1
0001eb146600_P001_Zea_mays_3 0.935 -
-0.1 1
0.1 1

-2.9 1
-1.7 1

-0.7 1
0.6 1
0.5 1

```
 -0.2 1
a_mays_5 0.759 -3.0 1
 -0.5 1



 -0.9 1

 1.1 1

 0.3 1
 0.6 1
 0.4 1
 1.1 1
 -0.7 1




 -1.0 1
 0.3 1
 -2.4 1
 0.0 1
```

−1.4 1

−0.6 1

0.3 1
0.9 1
−0.7 1
0.6 1
0.4 1
−2.3 1

0.6 1
0.8 1
0.5 1

−0.2 1
0.3 1

```
 0.1 1
 0.7 1
 0.3 1
 0.4 1
 -1.3 2






 0.3 1





a_mays_8 0.862 -0.5 1
 -0.0 1
 0.9 1

 0.5 1

 -1.2 1
 0.6 1
 0.9 1
 -0.2 1
 0.3 1
 -0.5 1
 0.5 1


 0.6 1




 0.6 1
 0.4 1
 -0.8 1
 0.2 1







 0.4 1
 0.0 1




 0.6 1
```

0.1 1
-2.0 1
0.2 1
-1.5 1
0.5 1
-1.2 1
-1.4 1

0.8 1
0.8 1
-0.2 1

0.4 1
0.2 1
0.1 1
a_mays_2 0.945 0.6 1
0.8 1
0.5 1

-0.3 1
a_mays_10 0.866 -0.9 2
-2.1 1
0.2 1
-2.1 1
-0.6 1
0.6 1
0.3 1

-0.3 1
0.5 1

0.5 1

0001eb135610_P001_Zea_mays_1 0.963 -
0.2 1
-0.3 1

-1.5 1

0.2 1
0.1 1
1.0 1
0.6 1
0.7 1
-0.3 1
0.2 1

1.0 1
-1.1 1
0.5 1
0.2 1

-0.8 1
0.3 1
-0.1 1
0.4 1

```
 0.5 1




 0.5 1
0001eb119580_P002_Zea_mays_3 0.895
 0.6 1
 -0.1 1
 0.5 1

 -1.1 1
 0.1 1

 -1.1 1
 -0.5 1
 0.1 1
 0.5 1
 -1.1 1
 1.0 1
a_mays_3 0.748 -3.4 1
 -0.0 1
a_mays_9 0.850 -1.7 1
 0.7 1
 0.1 1
 -0.1 1
 0.2 1
 0.3 1
 0.4 1
 -0.5 1
 0.7 1
 0.5 1
 0.7 1
 0.5 1
 -1.0 1
 0.0 1
```

−0.8 1
0.1 1

0.3 1
−0.4 1

−2.0 1
0.8 1

0.2 1
0.1 1
0.2 1
0.3 1
0.4 1
−0.0 1
−0.3 1
0.5 1
0.3 1

−0.2 1
−0.0 1
0.1 1
0.2 1

0.3 1
-1.2 1
-0.7 1
0.5 1
-1.0 2
-0.6 1

0001eb116650_P001_Zea_mays_6 0.831 -
1.4 1
-0.7 1

1.1 1
0.4 1
-0.9 1
0.6 1

0.3 1
0.0 1
0.6 1
0.3 1
-0.6 1
0.5 1
-0.8 1
0.2 1
-0.9 1
-0.2 1
-0.9 1

3 0.5 1
2 -1.9 1
3 0.6 1
4 -0.9 1
0 -0.5 1

9 -1.7 1
001_Zea_mays_3 0.885 -0.6 1
9 0.2 1
9 0.4 1

6 -0.9 1

0 0.2 1
6 -0.2 1
6 0.3 1
3 0.0 1
2 -0.7 1
3 0.7 1
2 -1.8 1
3 0.1 1
3 0.1 1
4 0.4 1
0 -0.4 1
3 0.7 1

–1.7 1
0.2 1
–1.1 1
–0.7 1
0.2 1
0.4 1
0.1 1

–0.0 1
–1.3 1

0.5 1
0.5 1
0.4 1
0.6 1

```
 0.4 1





 0.1 1
 -2.8 1
 0.4 1
 -0.6 1
 -0.0 1
 0.5 1
 0.7 1
 0.7 1











 0.1 1
 0.2 1
003_Zea_mays_4 0.853 -0.5 1
 -0.6 1
 0.5 1
 -1.8 1
 -0.2 1
 -0.2 1



 -0.2 1
 -0.8 1
a_mays_1 0.927 -0.6 1
 1.2 1
 -0.3 1
 -0.3 1


a_mays_5 0.825 -2.7 1
 -0.5 1
 0.6 1
```

```
-0.8 1
a_mays_5 0.772 -2.1 1
0.2 1
-0.0 1
-0.4 1
0.1 1
-1.9 1



-1.4 1
0.3 1
-1.6 1
-0.0 1
0.0 1
-0.9 1
0.5 1
0.5 1
0.7 1
-0.5 1
-0.2 1
0.8 1
0.1 1
0.8 1
0.9 1
0.5 1


0.9 1
0.9 1



-1.1 1
0.4 1
-0.7 1
1.0 1


1.1 1
0.9 1
```

0.8 1

0.5 1
0.4 1
-2.0 1
a_mays_1 0.949 -0.9 1
0.0 1

-1.6 1
-0.2 1
-0.6 1
-0.2 1
-1.1 1
0.3 1
0.1 1
0.6 1
0.2 1

-0.2 1
-0.5 1

0.4 1

0.5 1
a_mays_2 0.906 0.0 1
-0.3 1
-2.5 1

0.7 1

0.4 1
0.4 1
0.7 1

-0.9 1
-0.1 1
-0.8 1

-0.3 1
0.7 1

0.2 1
0.4 1
1.3 1
-0.0 1

0.7 1
0.4 1
-1.8 1

1.3 1

-1.7 1

-1.8 1
-0.7 1
0.4 1
0.8 1
0.3 1
0.5 1

−0.1 1
−1.2 1
−0.4 1
0.3 1
−0.2 1
0.3 1
0.8 1
0.4 1
−1.5 1

−1.1 1
0.1 1

−0.9 1
−0.1 1
−2.3 1

0.2 1

0.6 1
0.8 1
−1.3 2
1.1 1
−0.0 1

0.9 1
-0.3 1
-0.1 1
0.9 1
0.1 1
-0.2 1

0.0 1
0.9 1
0.1 1
0.2 1
0.4 1
-0.1 1
-0.8 1
-0.1 1

-0.6 1

0.8 1

0.1 1

-2.9 1
0.9 1
0.0 1
0.4 1
-0.7 1
0.6 1
0.9 1

-1.1 1
0.3 1
0.8 1
-0.7 1
-0.8 1
-1.5 1
-0.5 1
0.8 1
-0.7 1
-2.0 1
0.3 1
0.5 1
0.4 1
-2.8 1
0.7 1

-0.6 1
0.5 1
-0.9 1
-1.2 1
-1.1 1
0.7 1

-0.4 1

-0.3 1
-1.6 1
-0.3 1
-1.3 1
-3.1 3
a_mays_3 0.876 -3.1 2

-0.3 1
-2.1 1
-2.8 1

0.3 1
-0.8 1
0.3 1
-1.8 1
-1.4 1
0.2 1
0.7 1
-0.2 1

0.4 1
0.4 1
0.3 1
0.9 1
-0.8 1
0.4 1
0.2 1
0.5 1
0.0 1
0.3 1
0.5 1
0.6 1

-0.5 1

0.9 1
0.3 1
0.5 1
0.4 1
−0.3 1

0.3 1
−0.0 1
−0.9 1
0.4 1

0.1 1
0.1 1

0.5 1
1.0 1

−0.7 1
−0.8 1
−0.2 1
0.5 1
−0.2 1
0.6 1
0.1 1

```
0.8 1
0.4 1
-0.2 1
-1.4 1
0.5 1

-0.2 1
0.5 1
0.5 1
0.7 1

0.2 1
-0.6 1
a_mays_2 0.935 -1.8 1
a_mays_1 0.933 0.7 1
-0.1 1
0.0 1

-0.9 1
0.4 1
0.0 1
0.9 1

-0.0 1
-1.2 1

-0.1 1
0.8 1

-0.2 1
0.1 1
0.6 1
0.5 1
0.0 1
```

```
0.1 1
0.3 1
0.5 1
-0.0 1
0.5 1
a_mays_4 0.895 -0.1 1



-0.5 1
a_mays_7 0.763 -3.4 1
-1.2 1
0.5 1
0.8 1



0.6 1
-0.3 1
0.3 1
0.3 1
0.2 1
1.4 1


-0.0 1


0.1 1


0.7 1
-2.6 1
0.6 1
0.6 1
-0.1 1
1.0 1
-0.8 1
```

2 -0.0 1
1 0.5 1
7 -2.3 1
0 -0.1 1
5 0.2 1
8 0.3 1
2 0.9 1
1 -0.7 1

2 0.1 1

1 0.4 1

2 0.4 1
1 0.6 1
0 -0.6 1
5 0.4 1

7 0.4 1
a_mays_6 0.967 0.5 1
9 -0.8 1
7 -1.4 1
5 0.8 1
8 -0.1 1
6 0.7 1

5 0.4 1
9 0.5 1
8 0.8 1
8 0.4 1
2 0.5 1
2 0.8 1
9 0.2 1
8 0.6 1
8 0.3 1
5 0.1 1

0.1 1
-2.0 1
-0.3 1
0.5 1
-0.1 1
0.2 1
-0.0 1
0.4 1

-0.2 1
a_mays_3 0.909 -1.0 1
0.7 1
1.0 1

-0.2 1

-0.3 1
0001eb067250_P001_Zea_mays_2 0.870 -
-0.7 1

-0.0 1
0.4 1
-2.0 1
0.4 1

0.1 1

-0.3 1

0.5 1

0.1 1
0.4 1
0.6 1
0.8 1
0.7 1

-0.2 1
0.4 1
0.0 1
-1.4 1
a_mays_8 0.869 -0.2 1
0.7 1
0.4 1
a_mays_3 0.955 -0.4 1

-0.3 1
0.4 1

0.4 1
0.7 1
0.8 1

0.9 1

0.9 1
0.5 1
0.5 1
-1.1 1
-0.3 1
0.4 1
0.4 1
0.8 1
0.4 1
0.8 1
0.0 1
-0.2 1
-1.4 1
0.2 1
0.6 1
0.7 1

0.8 1
0.2 1
0.6 1
0.5 1
0.8 1
-1.0 1
0.1 1
0.5 1
a_mays_9 0.942 0.2 1

0.6 1
0.8 1
1.2 1
-1.5 1
0.4 1

0.1 1

0.6 1

-0.6 1
a_mays_2 0.866 -0.6 1

-0.9 1
0.9 1
a_mays_5 0.851 -2.9 1
0.1 1
0.5 1
0.8 1

-0.5 1
0.2 1
0.3 1
1.1 1
0.2 1
-0.0 1

0.6 1

1.1 1
-0.6 1

0.6 1
-0.6 1
-2.2 1
0.8 1
-1.1 1

```
a_mays_7 0.908 -0.5 1
 0.5 1



 -0.4 1
 0.5 1
 -1.4 1
 0.5 1
 -1.0 1
 0.4 1
 0.5 1
a_mays_3 0.802 -1.5 1
 -0.4 1
 -1.2 1
 0.8 1
 0.9 1
 -0.2 1
 0.6 1
 0.0 1
 -0.7 1
a_mays_4 0.928 -0.0 1






 0.2 1
 -0.0 1
 -1.6 1
 -0.5 1







 -0.2 1
 0.5 1
```

0.6 1
a_mays_1 0.963 0.8 1
0.7 1
-0.9 1
0.1 1
a_mays_7 0.799 -1.8 1
0.4 1
0.1 1
0.4 1
0.8 1
0.3 1

0.9 1
-0.1 1

-0.2 1
-0.4 1

0.4 1
-1.2 1

-0.0 1
a_mays_3 0.938 0.5 1
0.4 1
0.8 1

0.3 1
0.4 1
-0.4 1
0.5 1
-0.6 1
0.1 1
0.3 1

0.3 1
-2.3 1
1.1 1
1.1 1
0.5 1
0.6 1
0001eb083370_P001_Zea_mays_2 0.966 -
-2.4 1
-1.8 1
0.9 1
0.3 1
0.2 1
-0.6 1
0.5 1
1.0 1
a_mays_6 0.947 0.3 1
0.2 1
-0.0 1
0.6 1

0.8 1
-2.0 1
0.2 1
0.4 1
-1.0 1
0.3 1
0.9 1
0.6 1
0.7 1
0.6 1
0.4 1
0.7 1
0.1 1
-0.3 1
0.9 1
-0.1 1
1.3 1
0.8 1
-0.8 1
-1.6 1
1.1 1
0.1 1

-0.1 1
0.3 1
0.4 1
0.3 1
-0.0 1
-1.4 1

0.1 1
-2.6 1

0.6 1
-1.3 2
0.5 1
0.2 1
0.6 1
-1.1 1
0.3 1

0.5 1

0.7 1
-0.7 1
0.6 1
-0.2 1

-0.1 1
-0.7 1
0.5 1
0.6 1

0.1 1
-0.2 1
0.0 1
0.5 1
-0.4 1

-0.1 1
0.6 1

-1.1 1

0.1 1
-0.2 1

-0.6 1
-0.5 1

-0.9 1
0.6 1

0.5 1
0.7 1
-0.4 1
0.2 1
-0.0 1

0.2 1
a_mays_1 0.927 -1.7 1

-0.8 2
0.6 1
-0.8 1
0.3 1
0.5 1

1.1 1
0.2 1
0.1 1
0.8 1
a_mays_2 0.960 0.1 1
0.2 1
-0.1 1

0.8 1
0.1 1
-0.4 1
-2.0 1
-3.0 1

-1.2 1
1.3 1

1.3 1
-1.2 1
1.3 1
0.2 1

0.4 1
0.6 1
0.3 1

0.3 1

0.1 1
-0.4 1
-0.6 1
-0.5 1
0.9 1
0.1 1
-0.1 1
0.8 1
-0.3 1
0.1 1
0.5 1
-0.2 1
0001eb406570_P002_Zea_mays_10 0.940
-0.2 1
0.2 1
0.6 1
0.4 1

-0.0 1
0.3 1
0.4 1

-2.2 1
-0.6 1
0.0 1
0.7 1
-1.0 1
0.0 1
0.8 1
0.1 1
0.1 1

-0.0 1
0.7 1
-0.3 1
0.3 1
-2.2 1
0.7 1
0.6 1
-0.0 1
0.7 1
0.5 1
1.6 1
-0.4 1
0.9 1
001_Zea_mays_10 0.931 0.3 1
-0.2 1
-1.4 1
0.4 1
-0.2 1
-0.1 1
0.0 1

0.2 1
1.0 1
-0.9 1
0.9 1
0.3 1
0.5 1
0.5 1

0.8 1
-0.2 1
0.2 1
0.5 1
0.8 1
-0.0 1
0.6 1

-0.8 1
-1.1 1
0.1 1
0.0 1
-0.7 1
0.5 1
0.1 1
0.6 1
0.3 1

0.6 1
0.6 1
-1.4 1

0.4 1
0.5 1
0.1 1

-0.4 1