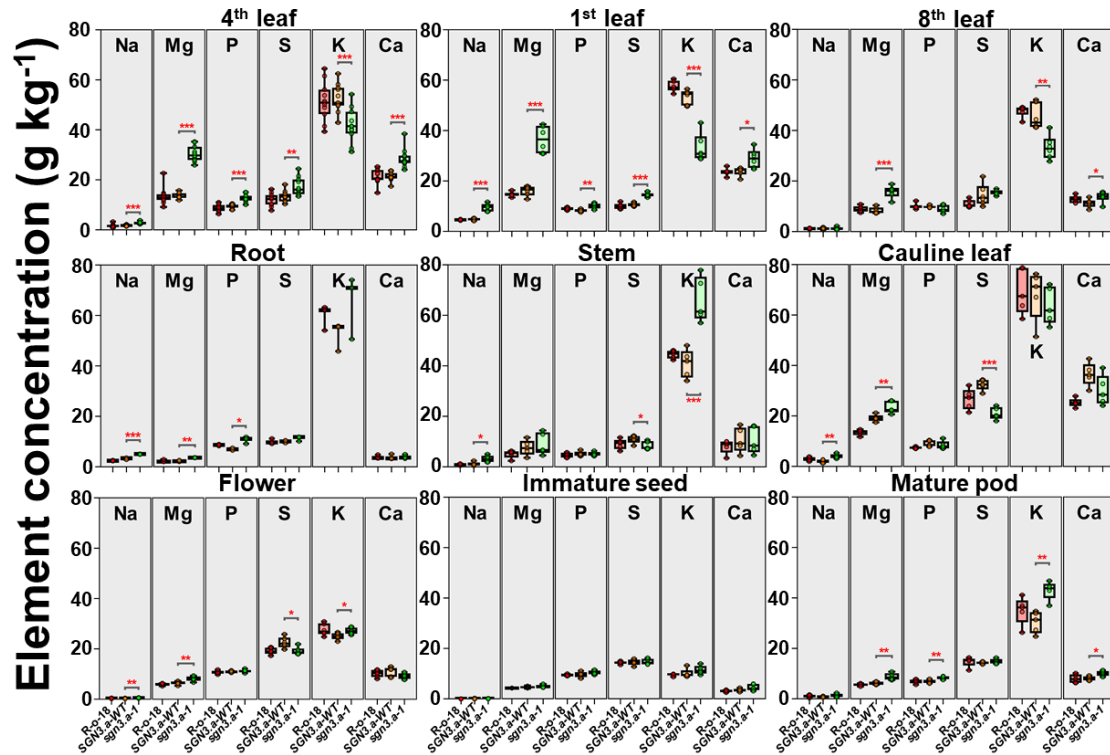
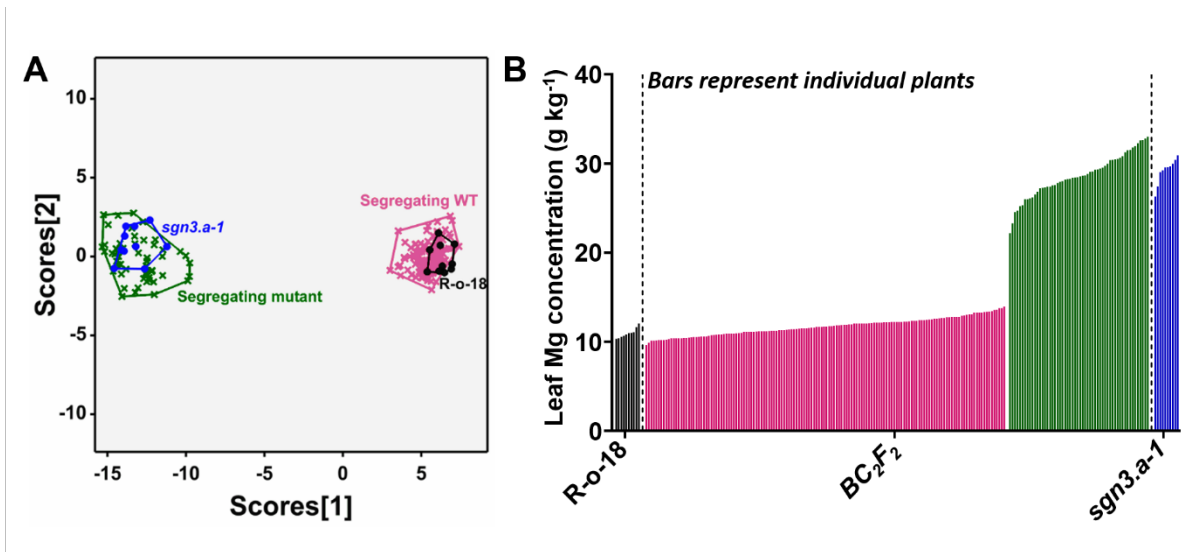


Magnesium and calcium over-accumulate in the leaves of a *schengen3* mutant of *Brassica rapa*

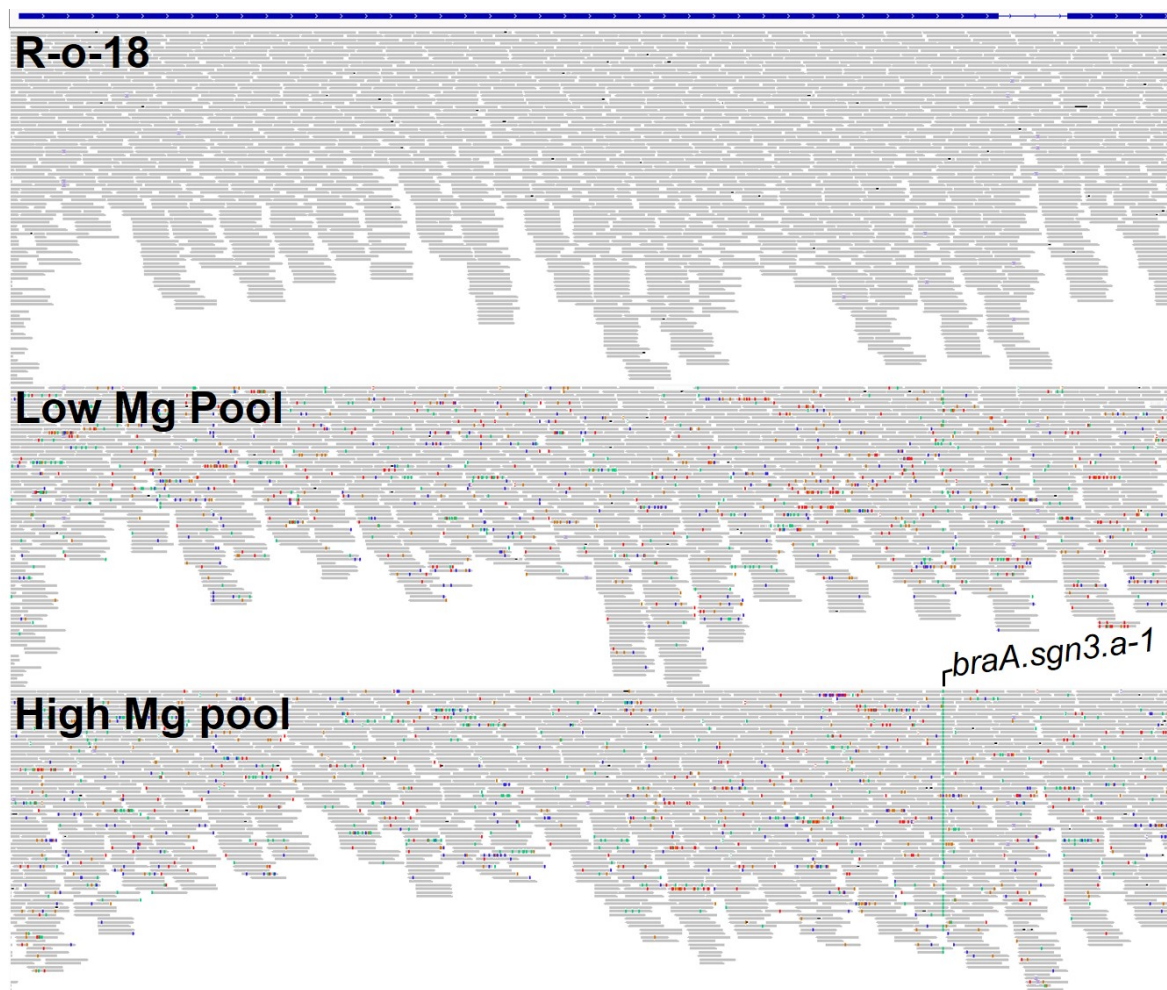
Supplemental Figures:



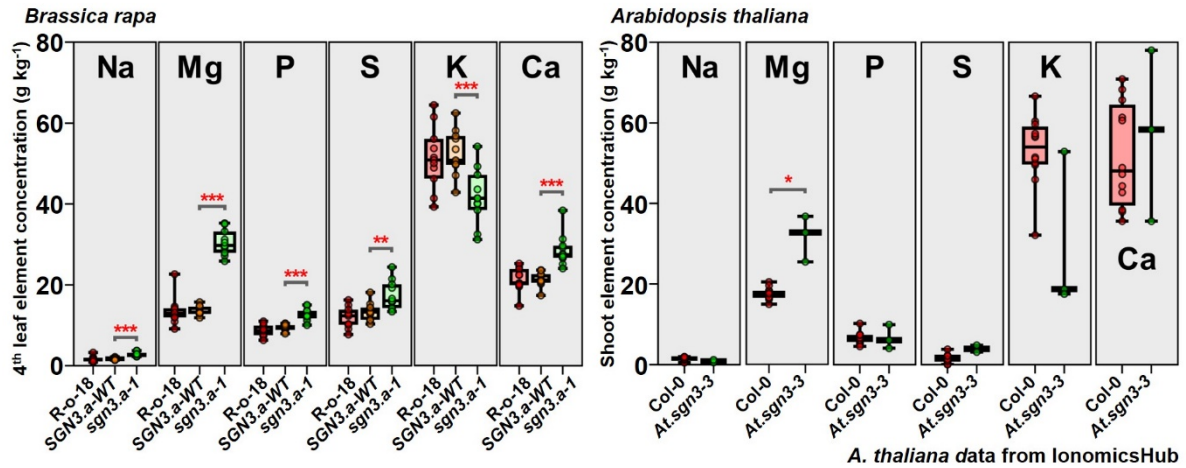
Supplemental Figure S1. Tissue specific element concentrations in BC_1F_3 generation *braA.sgn3.a-1* (*sgn3.a-1*), segregating wild-type (*SGN3.a-1*) and un-mutagenised R-o-18 in fourth leaves ($n = 11$), first leaves, eighth leaves, flowers ($n = 6$), stems, cauline leaves, immature seeds, mature pods ($n = 5$), and roots ($n = 3$). Boxes represent interquartile range with the median shown. Whiskers show entire data range, with data points shown. Stars above boxes represent differences (two-tailed T-tests) between *braA.sgn3.a-1* and *BraA.SGN3.a-WT* at $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***).



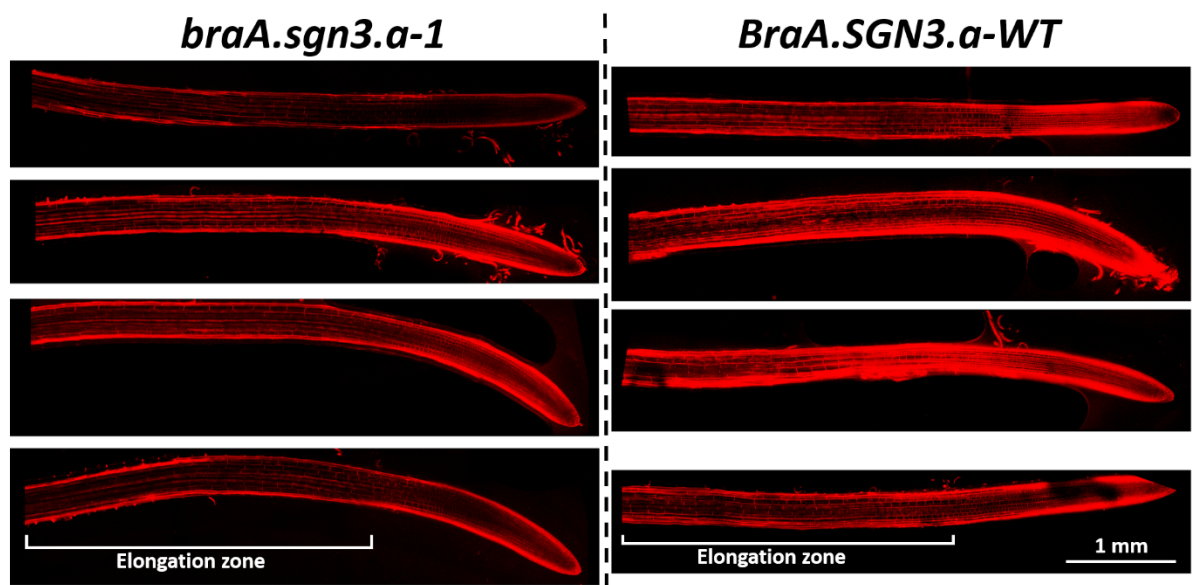
Supplemental Figure S2. A. Segregant groupings in 2D variance space as modelled through linear discriminant analysis based on leaf concentrations of Na, Mg, P, S, K and Ca. *sgn3.a-1* represents *BC₁F₄ braA.sgn3.a-1* control plants. Dots and crosses represent individual plants. Lines are group polygons enclosing all units. **B.** Plant specific magnesium (Mg) concentrations in R-o-18 wild-type control (black), *BC₁F₄ braA.sgn3.a-1* (*sgn3.a-1*) control (blue) and segregating *BC₂F₂* population (magenta = low Mg segregants, dark green = high Mg segregants, based on groupings assigned in **A.**).



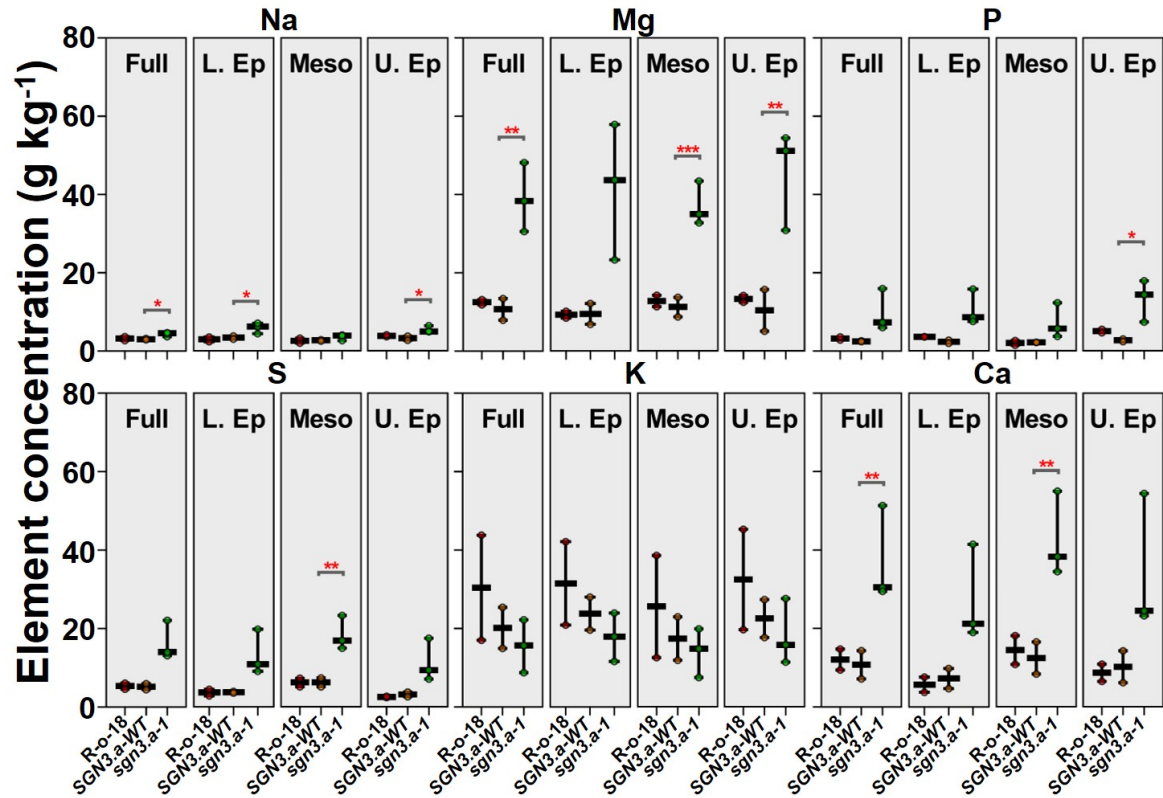
Supplemental Figure S3. Reads aligned to *BraA.SGN3.a* showing locations of SNP calls in R-o-18, Low Mg and High Mg DNA pools. Position of SNP leading to perturbed ionome in *braA.sgn3.a-1* marked.



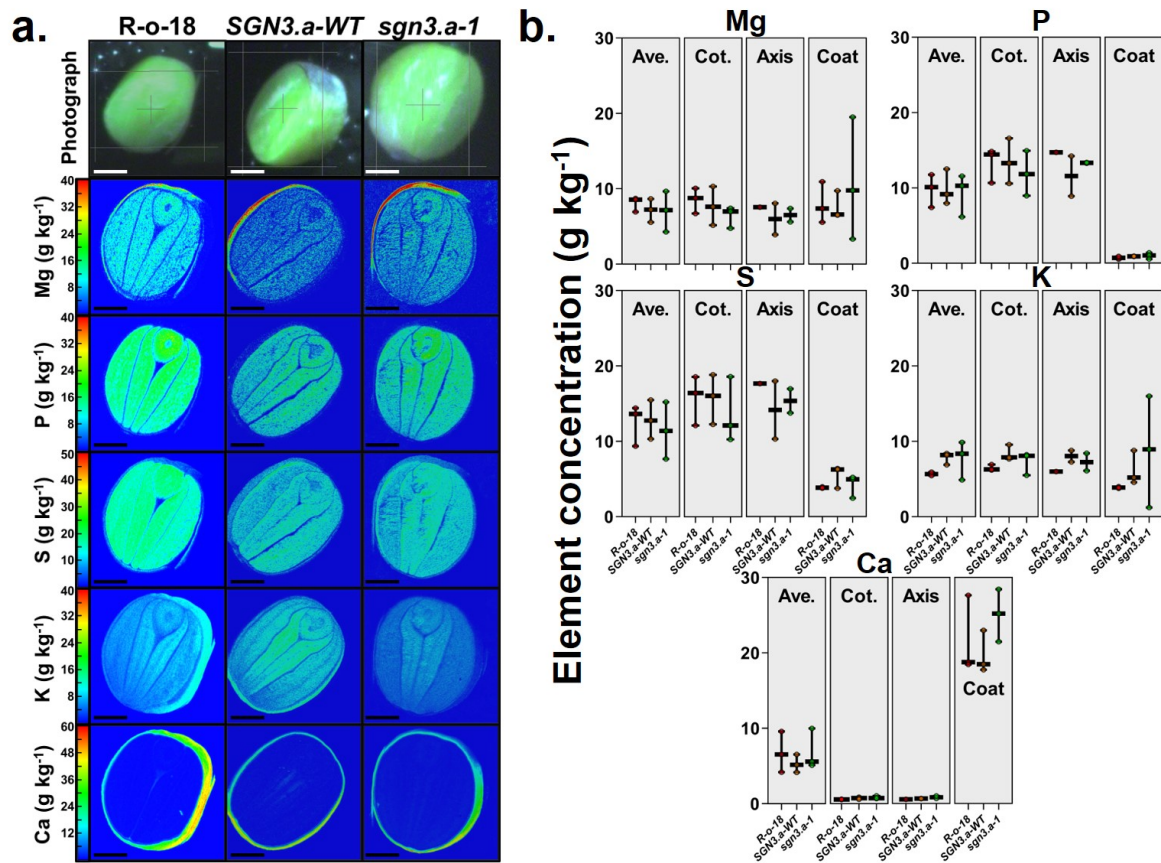
Supplemental Figure S4. Fourth leaf element concentrations in BC_1F_3 generation *Brassica rapa* mutant *braA.sgn3.a-1* (*sgn3.a-1*; $n = 12$), segregating wild-type (*SGN3.a-1*; $n = 11$) and un-mutagenised R-o-18 ($n = 11$), compared with *Arabidopsis thaliana* *sgn3-3* T-DNA insertion mutant (SALK_043282; *At.sgn3-3*; $n = 3$) and wild-type Col-0 ($n = 12$). *A. thaliana* data taken from *Arabidopsis* database at IonomicsHub (www.ionomicshub.org/arabidopsis/). Boxes represent interquartile range with the median shown. Whiskers show entire data range, with data points shown. Stars above boxes represent differences (two-tailed T-tests) between *braA.sgn3.a-1* and *BraA.SGN3.a-WT* or differences between Col-0 and *At.sgn3-3* at $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***).



Supplementary Figure S5. Confocal images of 5 day old (post-sowing) root tips of *braA.sgn3.a-1* and *BraA.SGN3.a-WT* plants stained with propidium iodide (PI). Scale bar represents 1 mm. Approximate location of root elongation zone indicated. Note black rectangular boxes around root images digitally placed to aid visualisation.



Supplemental Figure S6. Tissue specific element concentrations in BC_1F_5 generation *Brassica rapa* mutant *braA.sgn3.a-1* (*sgn3.a-1*; $n = 3$), segregating wild-type (*SGN3.a-1*; $n = 2$) and un-mutagenised R-o-18 ($n = 2$) as quantified by micro-particle induced X-ray emission (micro-PIXE). Full = average whole-leaf concentrations, L. Ep = lower epidermis, Meso = mesophyll and U. Ep = upper epidermis concentrations. Median value plotted in each panel where whiskers represent range with data points shown. Stars above boxes represent differences (two-tailed T-tests) between *braA.sgn3.a-1* and all wild-types at $p < 0.05$ (*), $p < 0.01$ (**), and $p < 0.001$ (***).



Supplemental Figure S7. A. Quantified spatial distribution of magnesium (Mg), phosphorus (P), sulphur (S), potassium (K) and calcium (Ca) in seeds of R-o-18, *BraA.SGN3.a-WT* (*SGN3.a-WT*) and *braA.sgn3.a-1* (*sgn3.a-1*) as analysed by micro-particle induced X-ray emission (micro-PIXE). Scale bars = 500 μm . **B.** Concentrations of the above elements in seed cotyledons (Cot.), embryonic axes (Axis), seed coats (Coat) and an average of all three (Ave.) in three replicates each of R-o-18, *BraA.SGN3.a-WT* (*SGN3.a-WT*) and *braA.sgn3.a-1* (*sgn3.a-1*). Median value plotted in each panel where whiskers represent range with data points shown ($n = 3$).