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Genetic control of grain amino acid composition in a UK soft wheat mapping population

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Supplementary figures
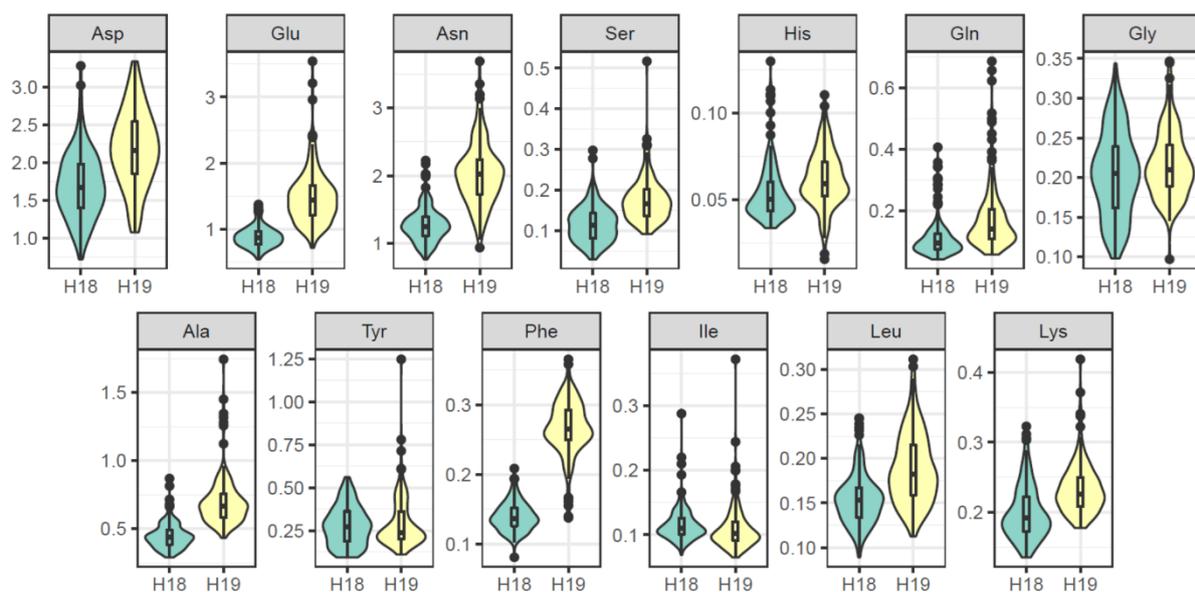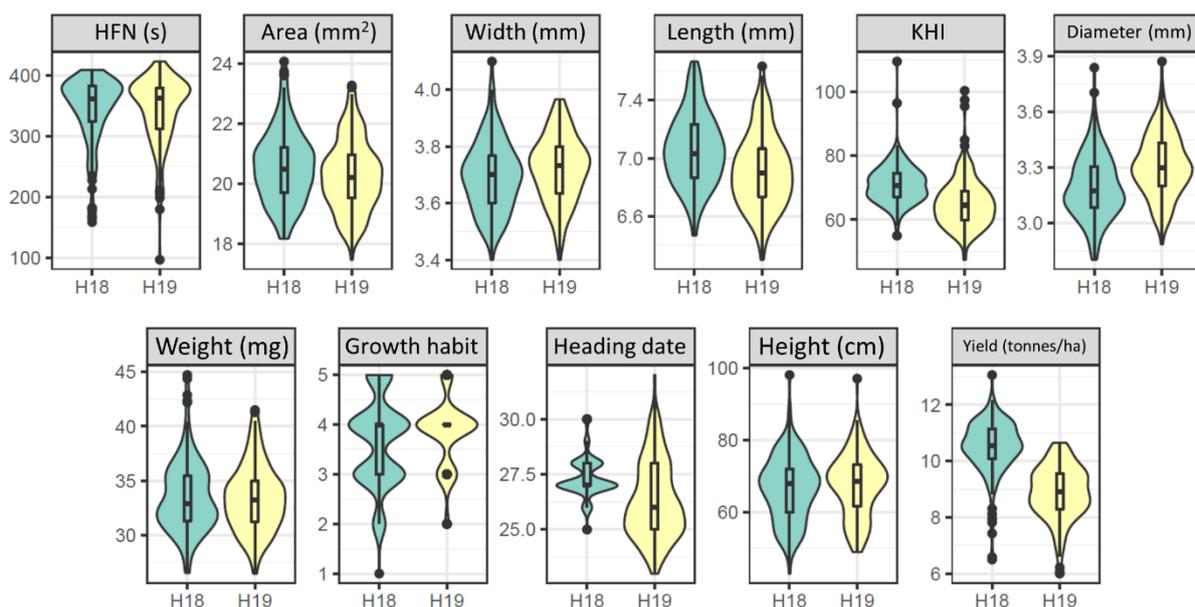
Supplementary figure 1. Trait measurements from the Claire x Robigus mapping population grown across two years (H18 and H19). a. Concentration of amino acids (mmol per kg) in wheat grain in both environments. **b.** Measurements of other quality and agronomic traits across both environments.
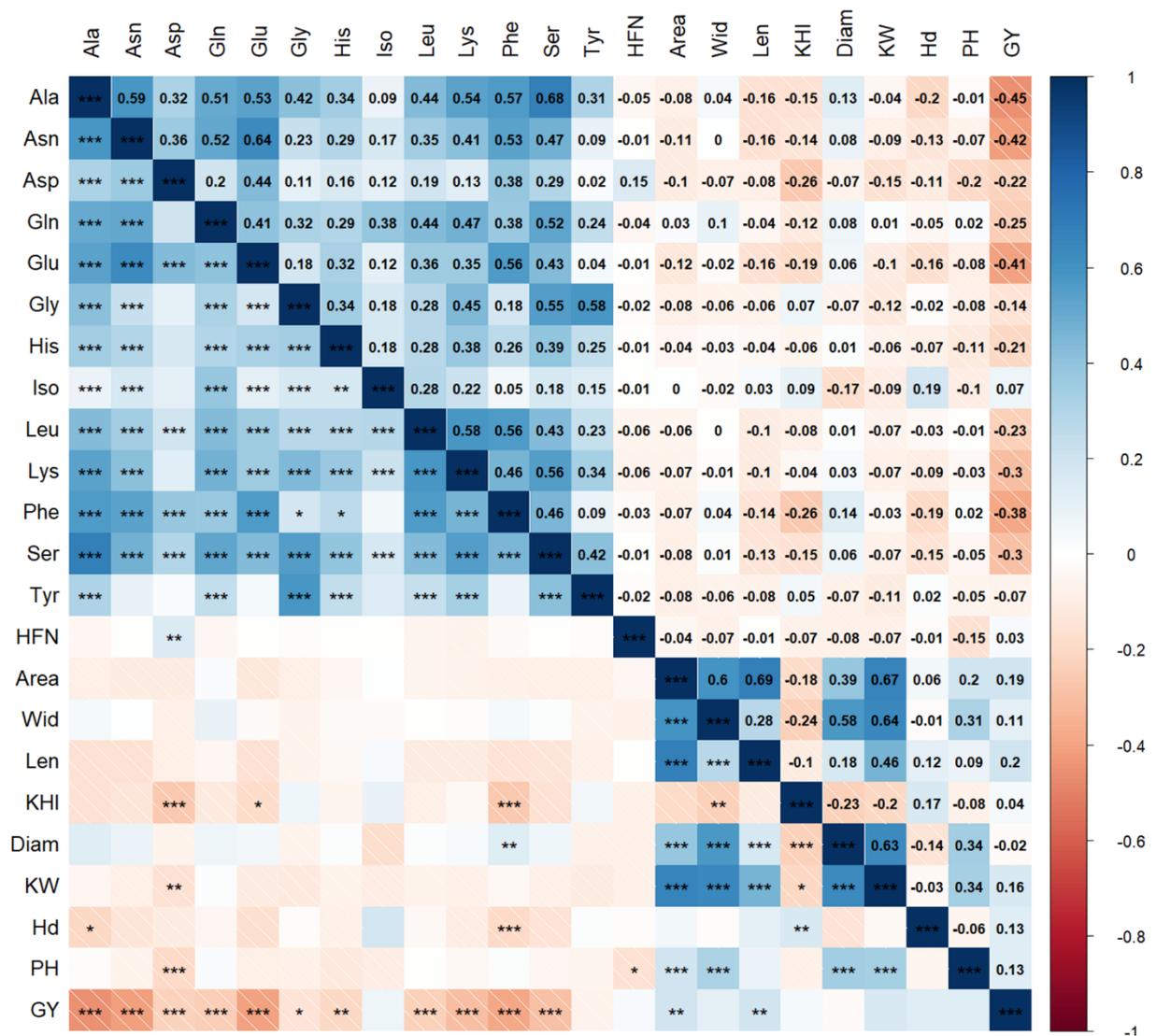
Supplementary figure 2. Correlation of traits taken from both H18 and H19 environments. Kendall correlation coefficients shown in upper right triangle and significance asterisks from adjusted p values (Bonferroni correction) shown in lower left triangle. HFN (Hagberg falling number), KHI (kernel hardness index), Diam (diameter), KW (kernel weight), Hd (heading date), PH (plant height), GY (grain yield).
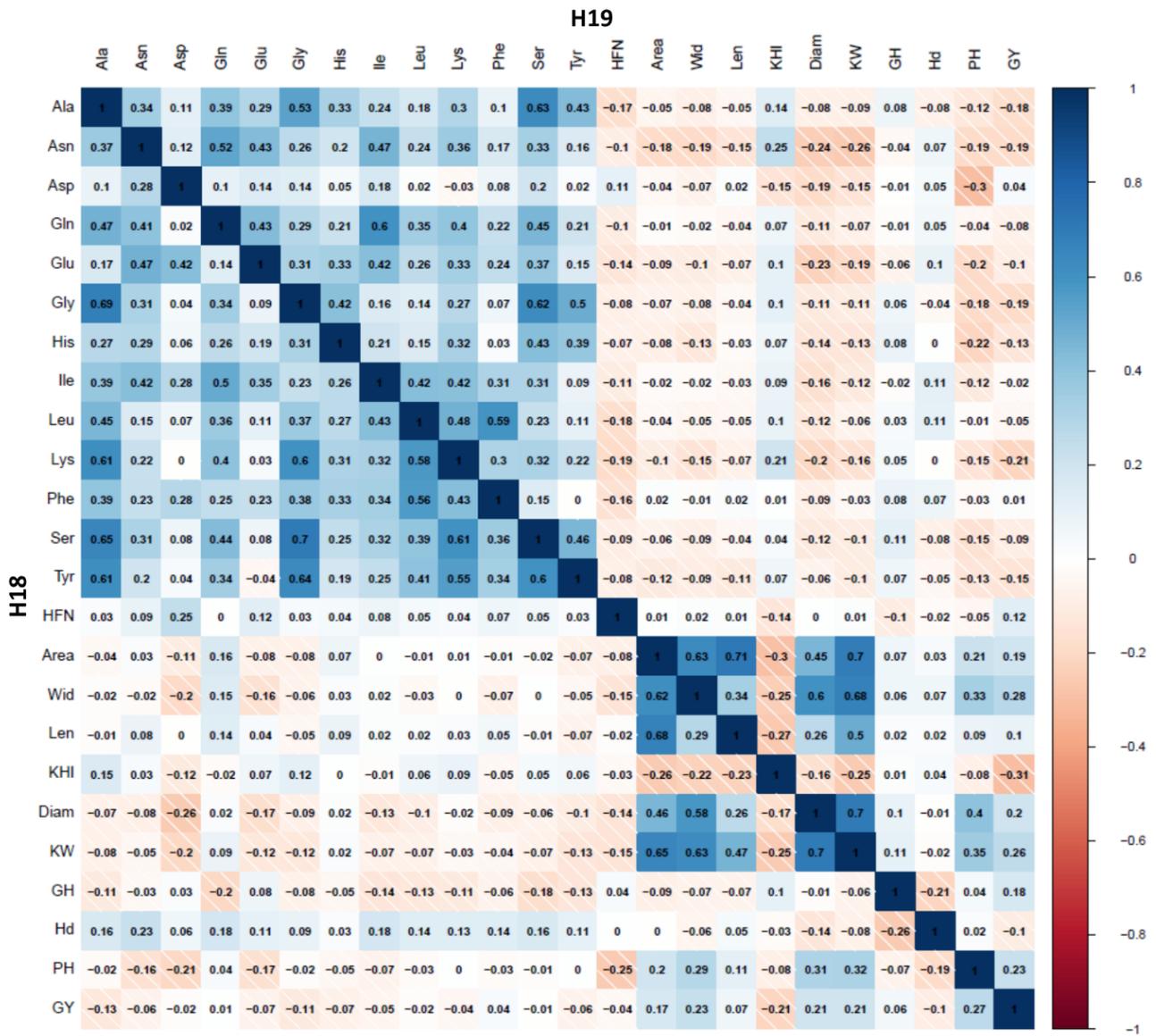
Supplementary figure 3. Kendall correlation coefficients between traits within each environment. H18 is the bottom left triangle, H19 is the upper right triangle.
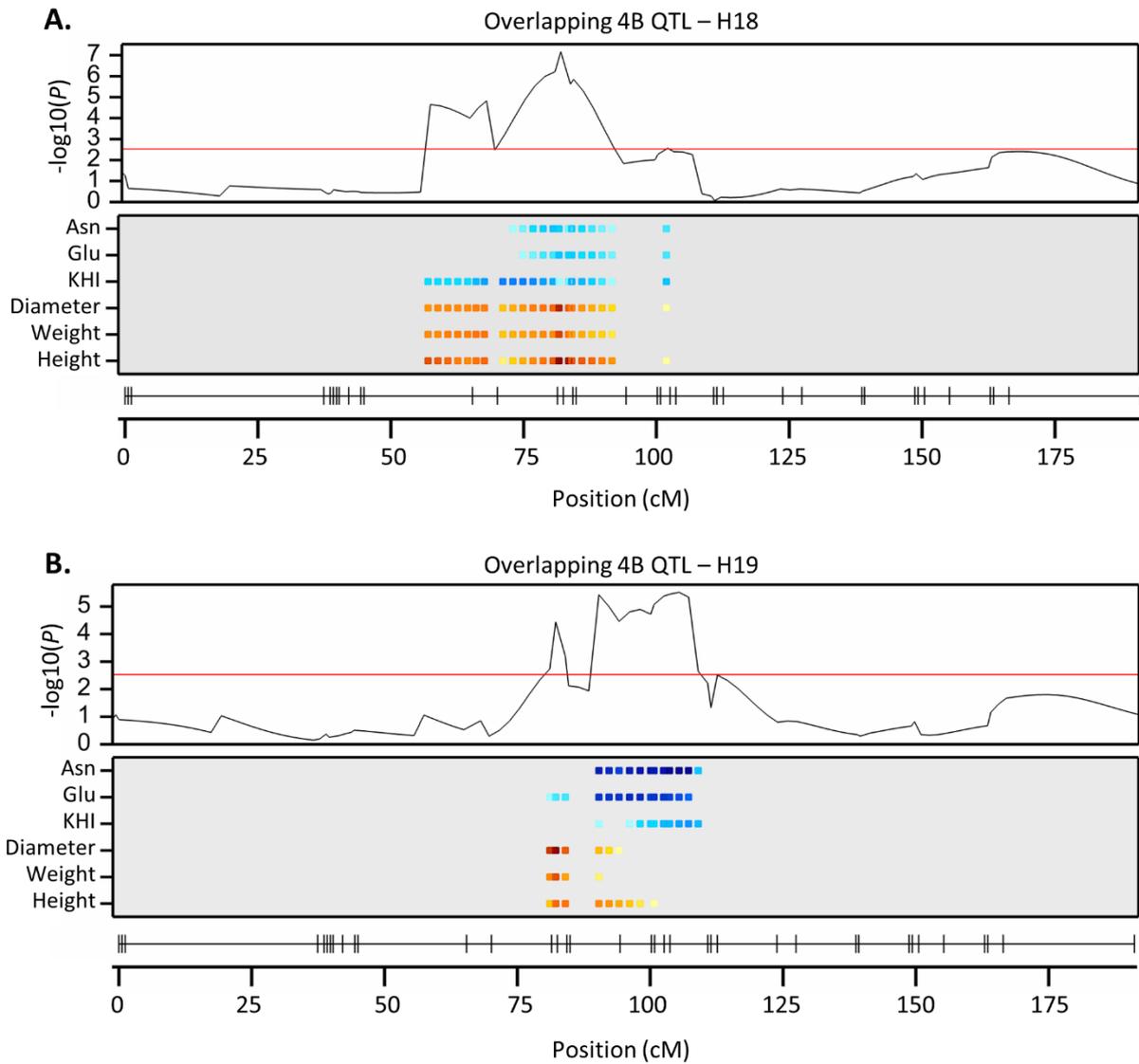
Supplementary figure 4. Multi-trait analysis of the asparagine QTL on 4B in the Claire x Robigus mapping population. Blue indicates Robigus additive allele whilst red indicates Claire additive allele. The darkness of colour corresponds to the magnitude of the effect.
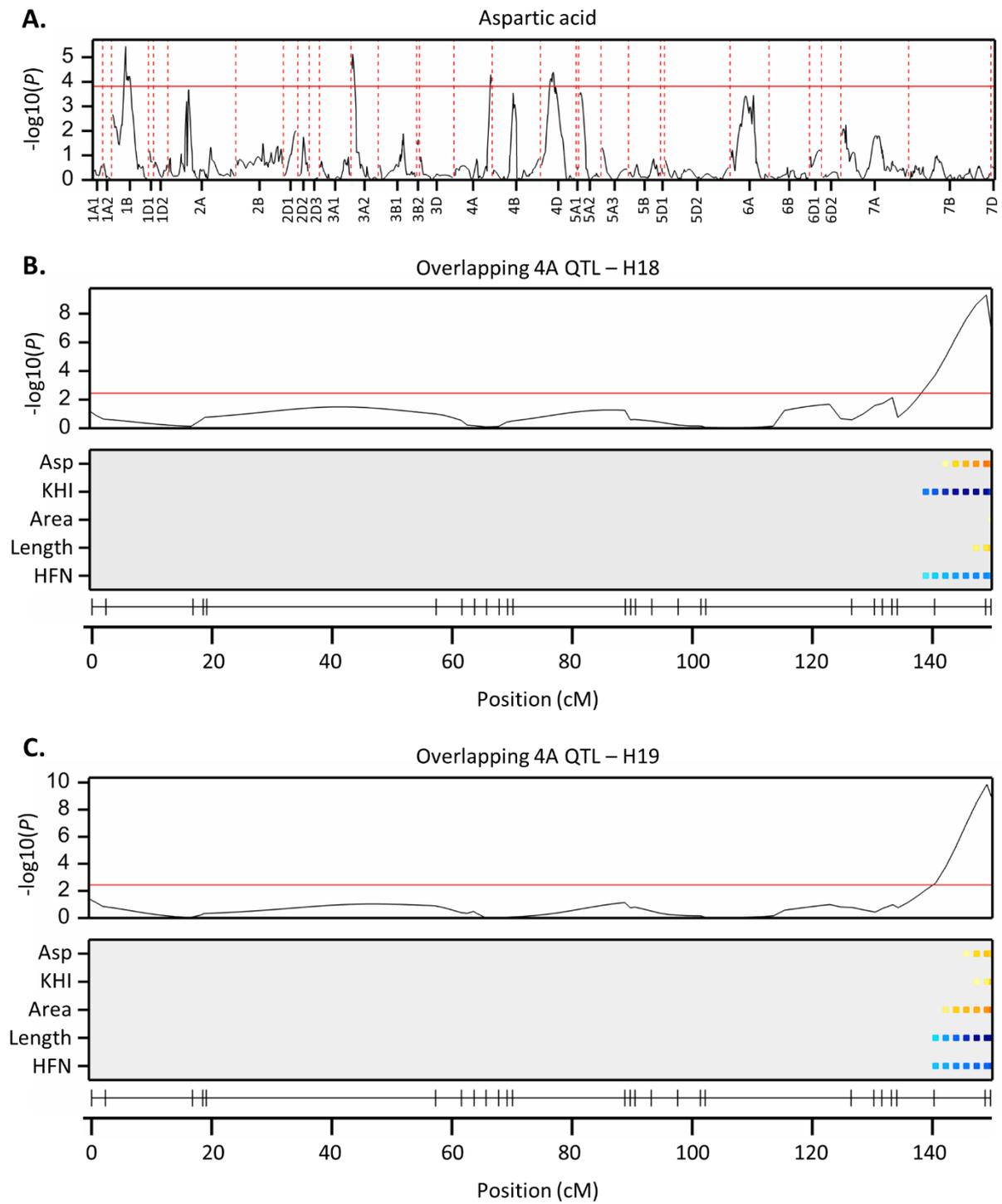
Supplementary figure 5. Multi-environment and multi-trait linkage analysis of aspartic acid QTL in the Claire x Robigus mapping population.
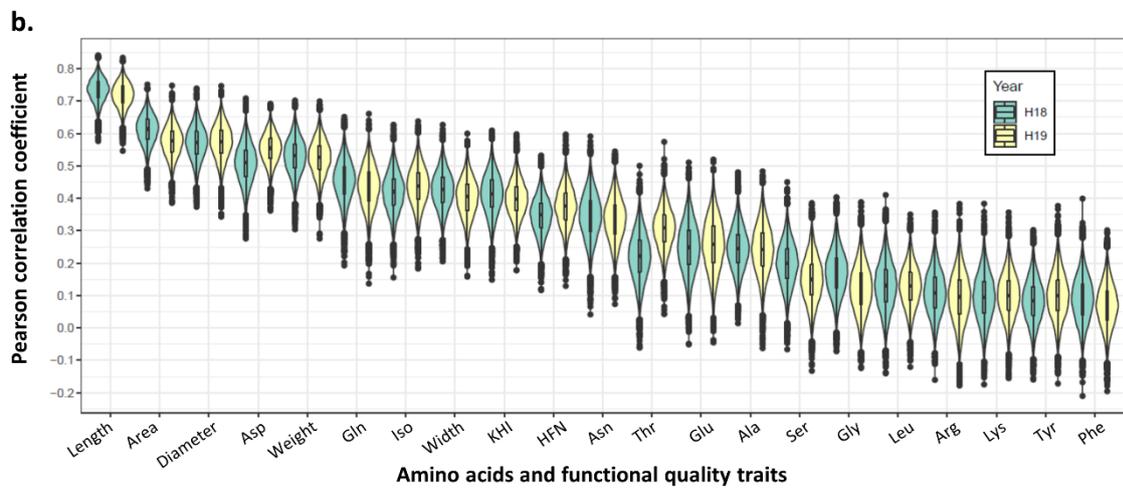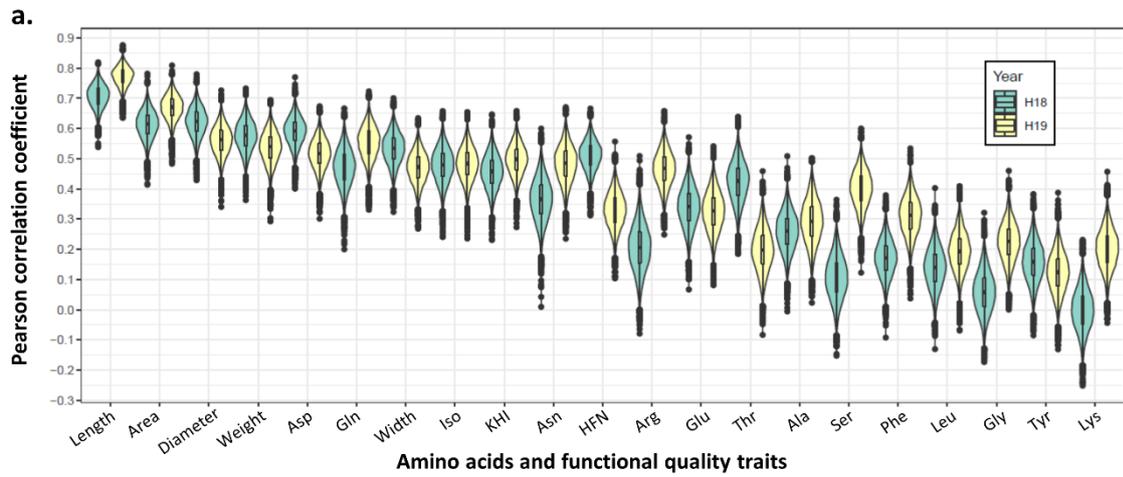
Supplementary figure 6. Accuracy of genomic selection for each trait measured in the mapping population using within (a.) and between (b.) year prediction.