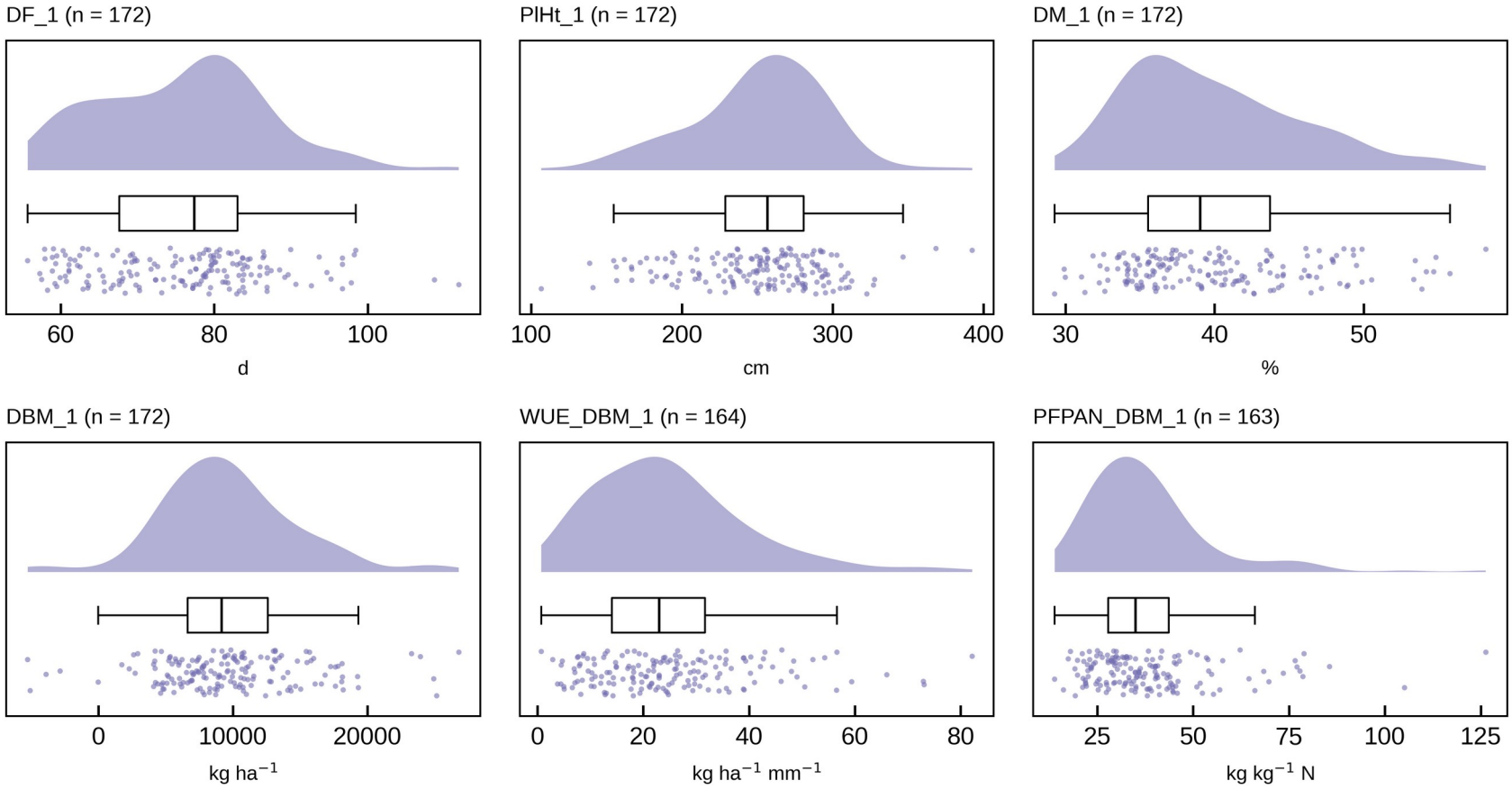


Fig. S1 Phenotypic distribution of agronomic and RUE traits in Combination 1 (IT21 + IND22 + IND23), shown as raincloud plots.

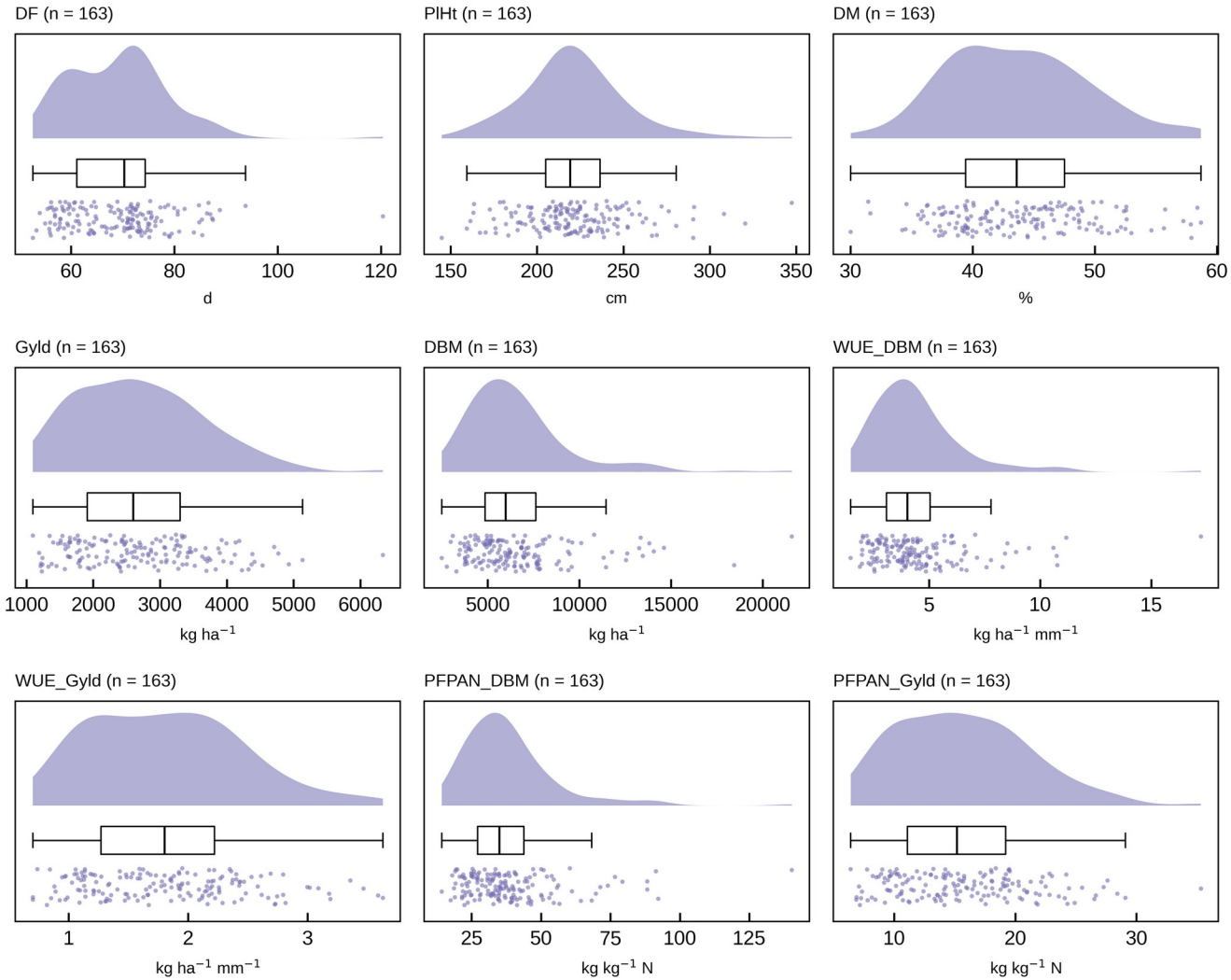


Fig. S2 Phenotypic distribution of agronomic and RUE traits in Combination 2 (IND22 + IND23), shown as raincloud plots.

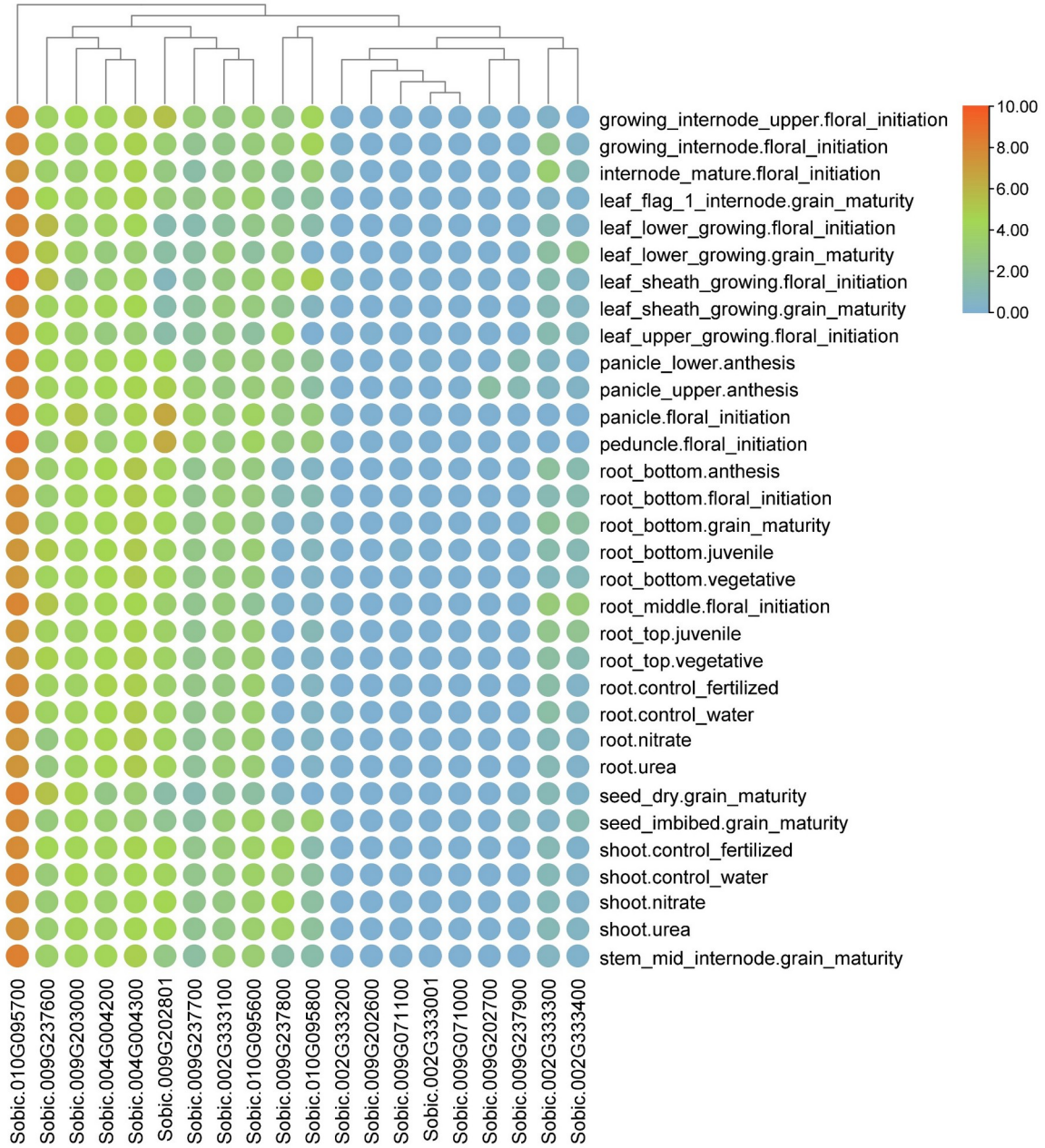


Fig. S3 Expression of the candidate genes associated with WUE_DBM_1 across 33 tissues and developmental stages.

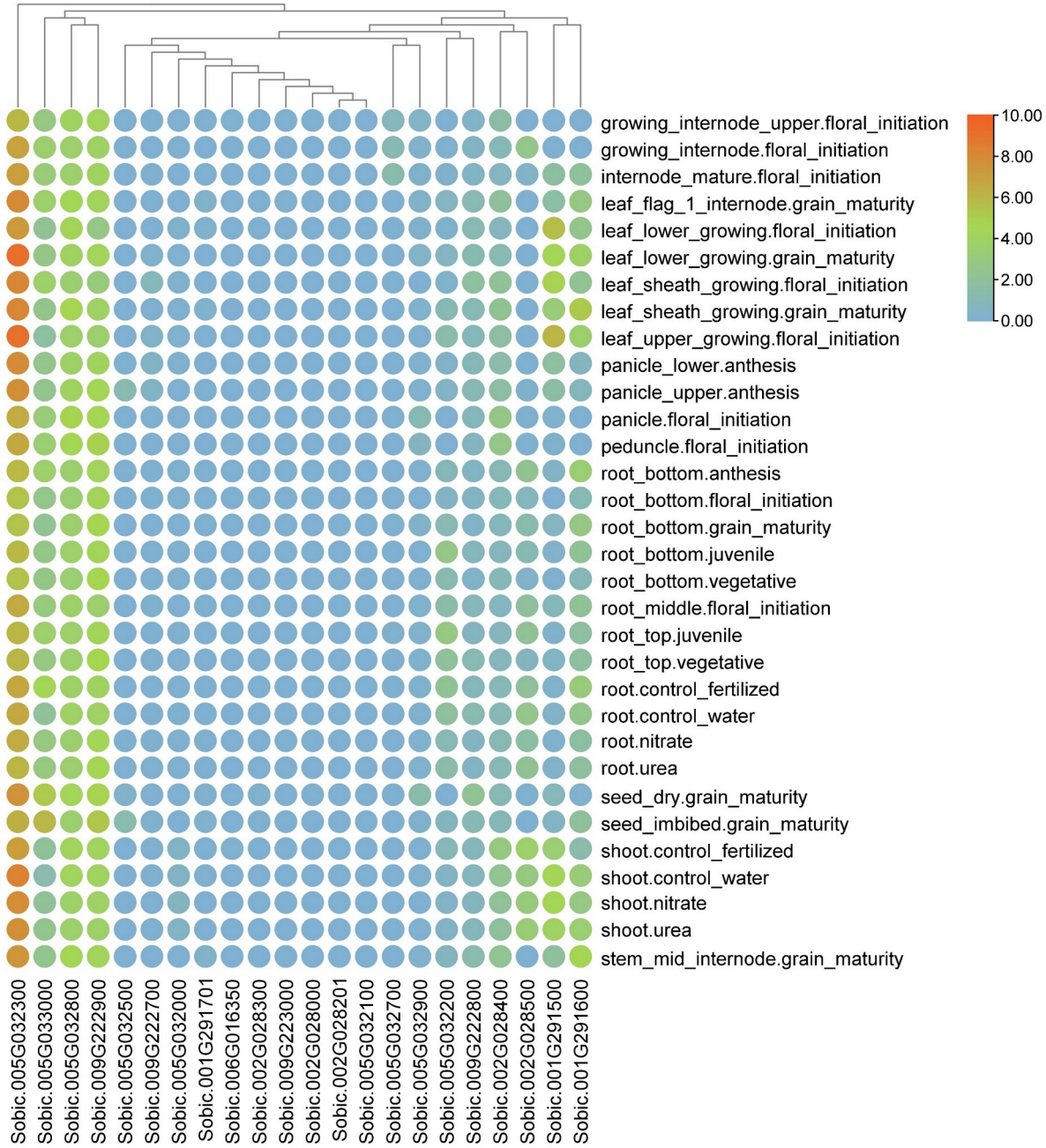


Fig. S4 Expression of the candidate genes associated with WUE_DBM across 33 tissues and developmental stages.

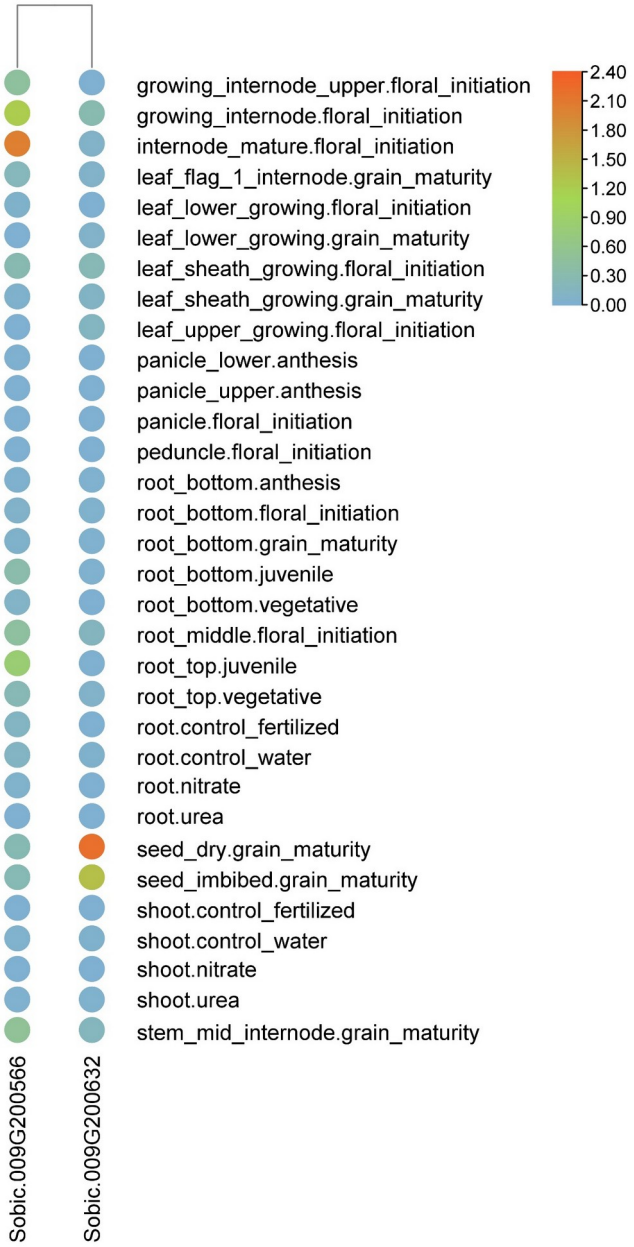


Fig. S5 Expression of the candidate genes associated with PFPAN_DBM across 33 tissues and developmental stages.

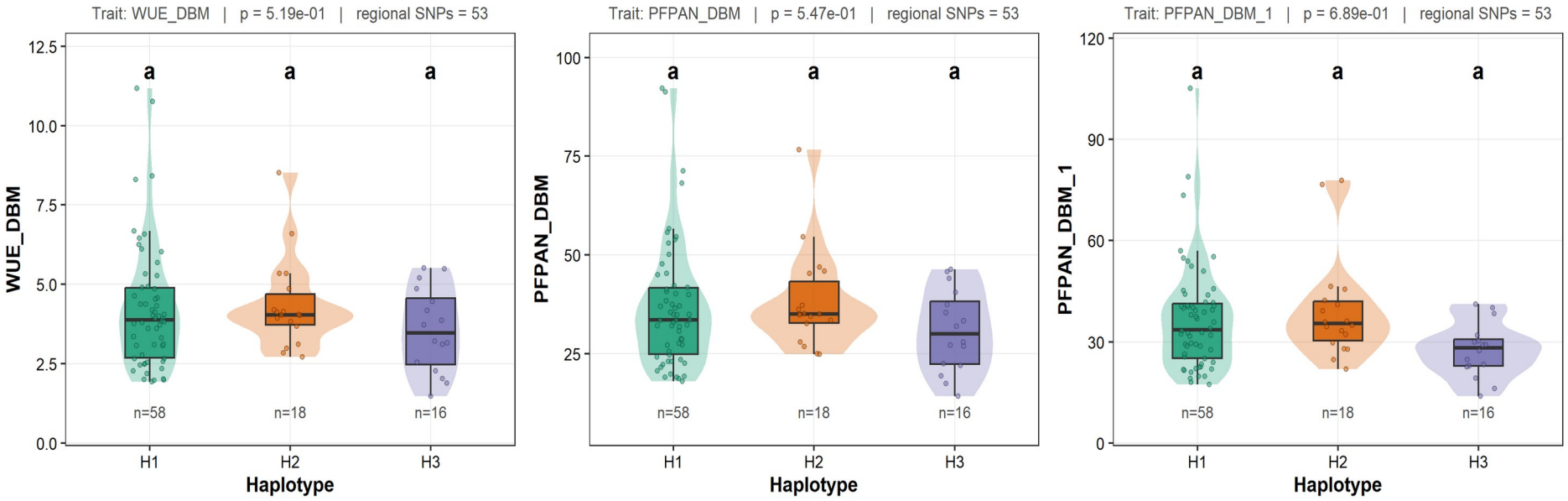


Fig. S6 Haplotype distribution at the chromosome 9 locus S09_55037491 for the three traits with significant single-SNP associations: (A) WUE_DBM, (B) PFPAN_DBM and (C) PFPAN_DBM_1. Despite the large single-SNP effect (PVE = 54.5–73.9%; Table 4), no haplotype–trait association was significant at this locus (all p > 0.5), indicating that the association signal is carried by the focal SNP rather than by the surrounding haplotype block. Each panel reports the haplotype-level p-value and the number of carriers per haplotype (n) from the model Y = HapID + PC1 + PC2 + PC3.

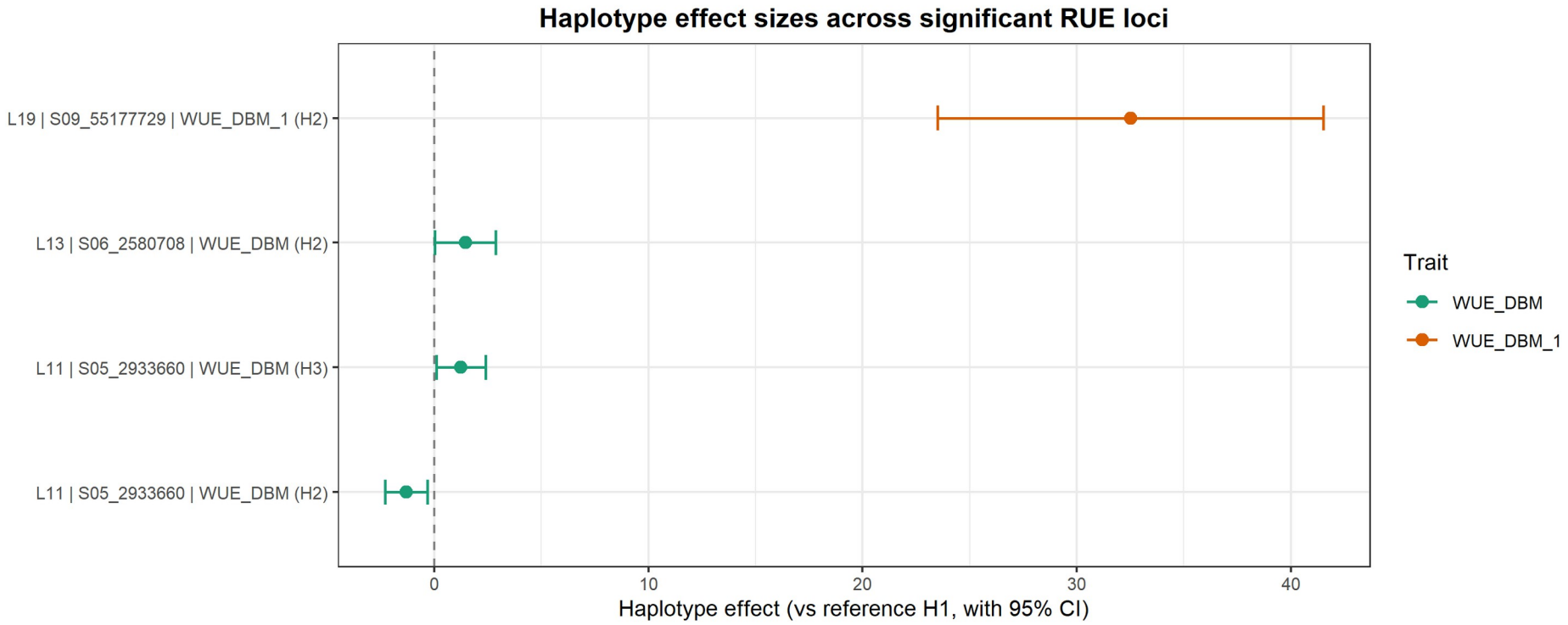


Fig. S7 Forest plot of haplotype effect sizes (relative to the reference haplotype H1, with 95% confidence intervals) for the four haplotypes nominally significant at $p < 0.05$. Effects are expressed in trait-specific units; colours indicate the trait (WUE_DBM, WUE_DBM_1).

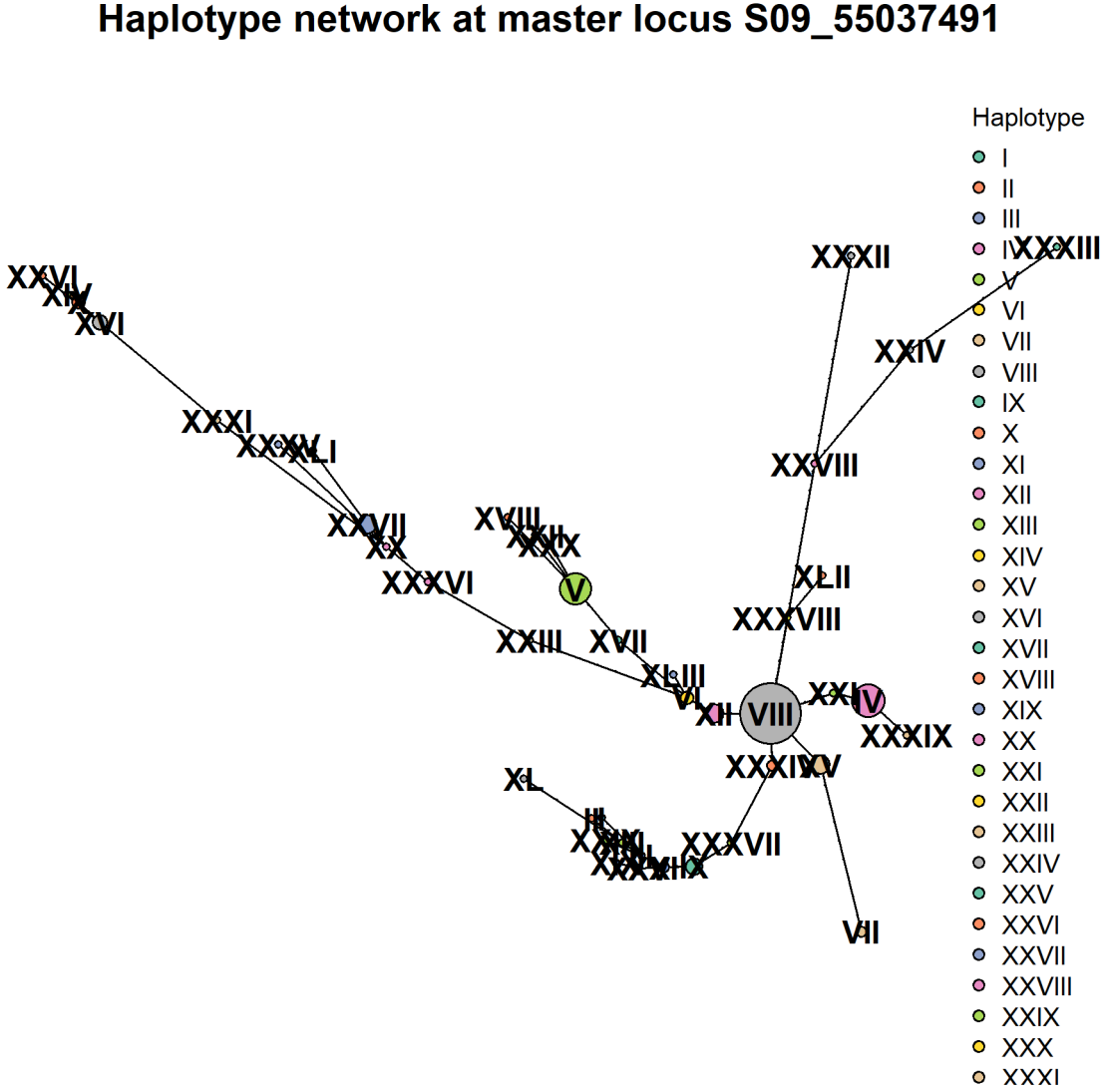


Fig. S8 Median-joining haplotype network (pegas) for the 27.6 kb LD window centred on the chromosome 9 locus S09_55037491. Circles represent unique haplotypes, with area proportional to the number of carriers in the panel; branches show the inferred mutational steps between haplotypes.