

SUPPLEMENTARY FIGURES:

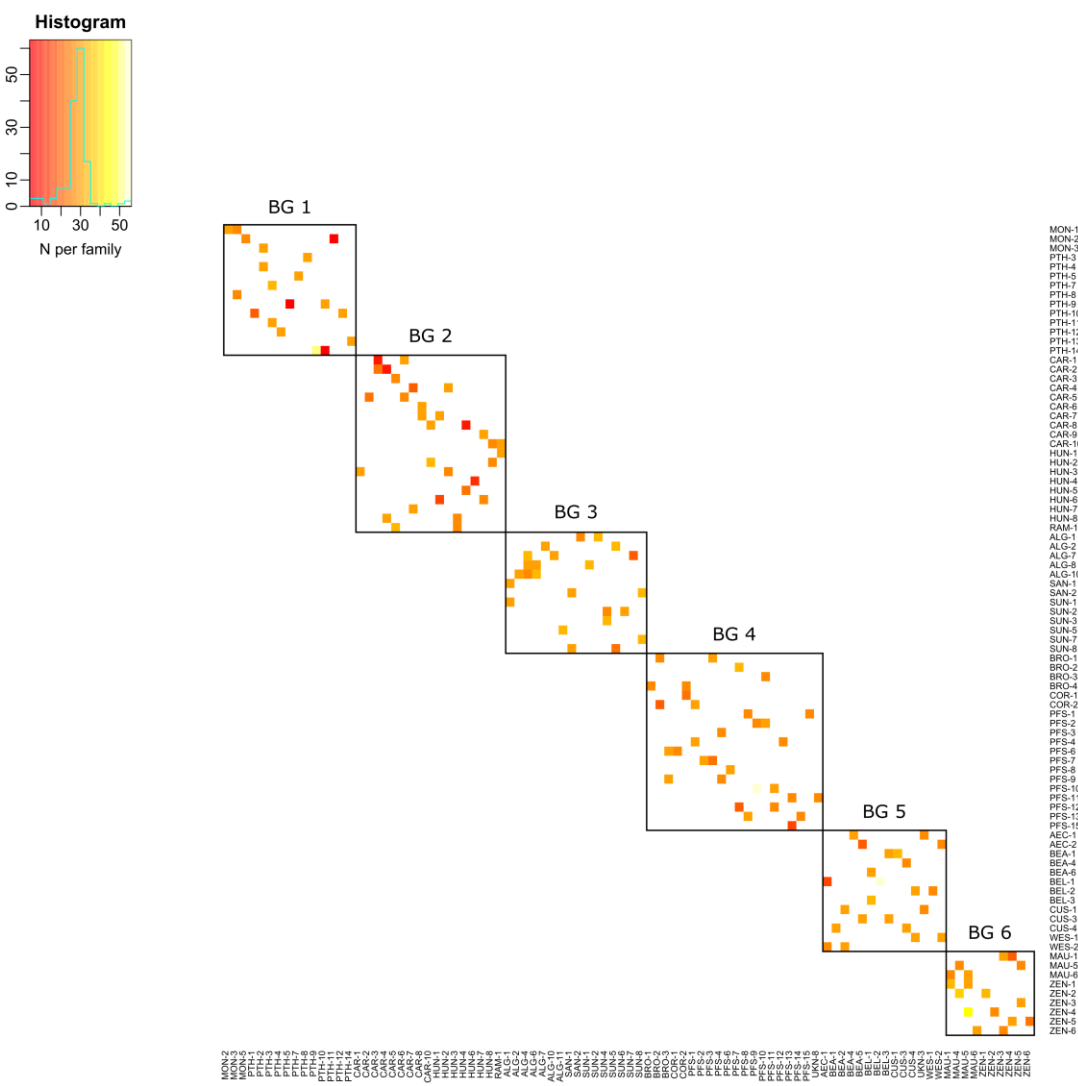


Figure S1. Partial diallel mating design for the six breeding groups (BGs, black rectangles) and the 4,066 trees used for analyses. Mothers and fathers are on the x and y axes, respectively. Each colored square represent a full-sib family and the colors indicate the number of trees sampled per full-sib family (top left color key with histogram). Dataset 1 included BGs 1, 2, 5 and 6, and dataset 2 included BGs 3 and 4.

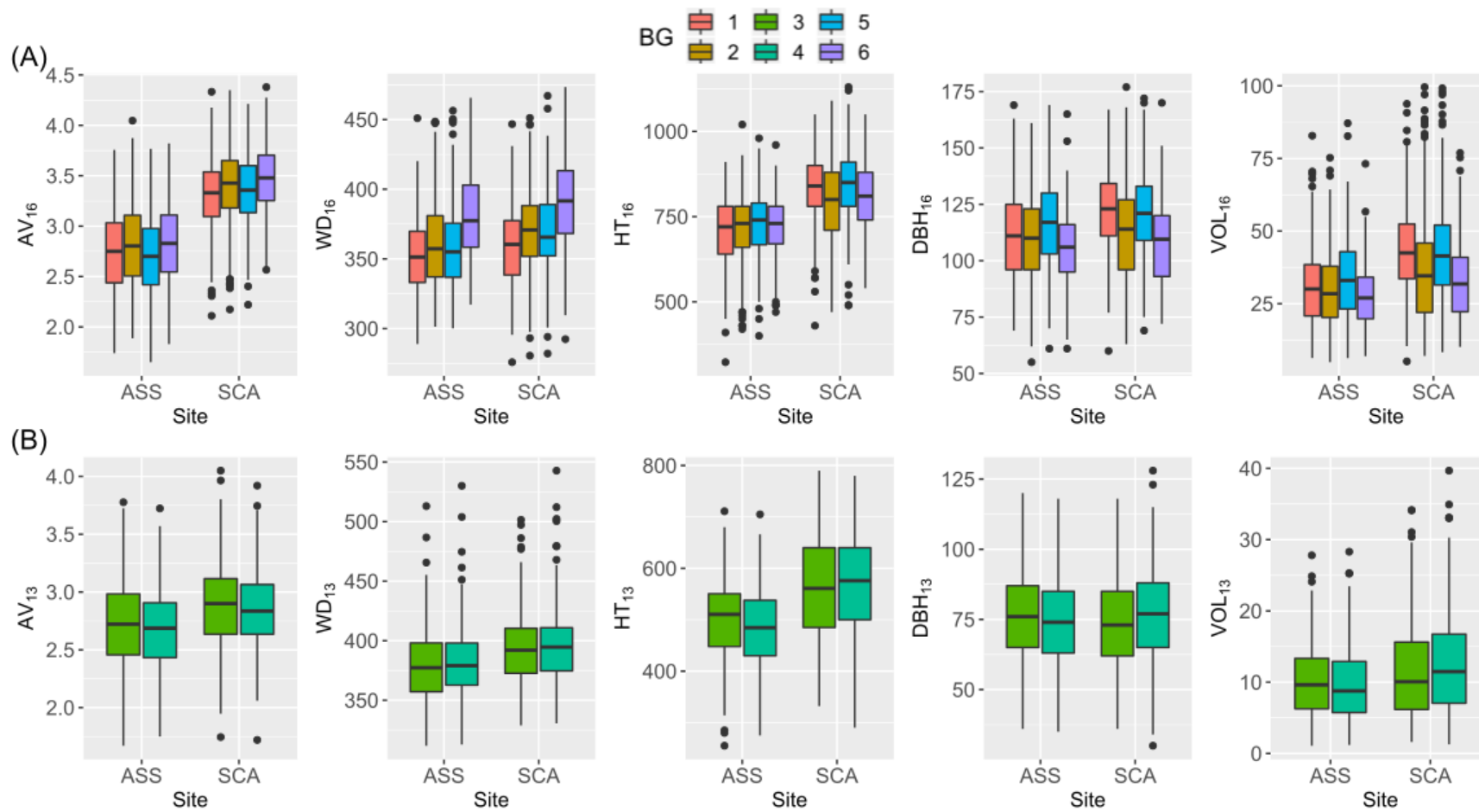


Figure S2. Boxplots of phenotypes for (A) dataset 1, that is breeding groups (BGs) 1, 2, 5, and 6; and for (B) dataset 2, that is BGs 3 and 4. Trees for BGs 1, 2, 5 and 6 were 16 years old, whereas those of BGs 3 and 4 were 13 years old. The phenotypes are grouped by sites Asselin (ASS) and St. Casimir (SCA) on the x-axis, and are colored by BG. See Table 2 for a description of traits.

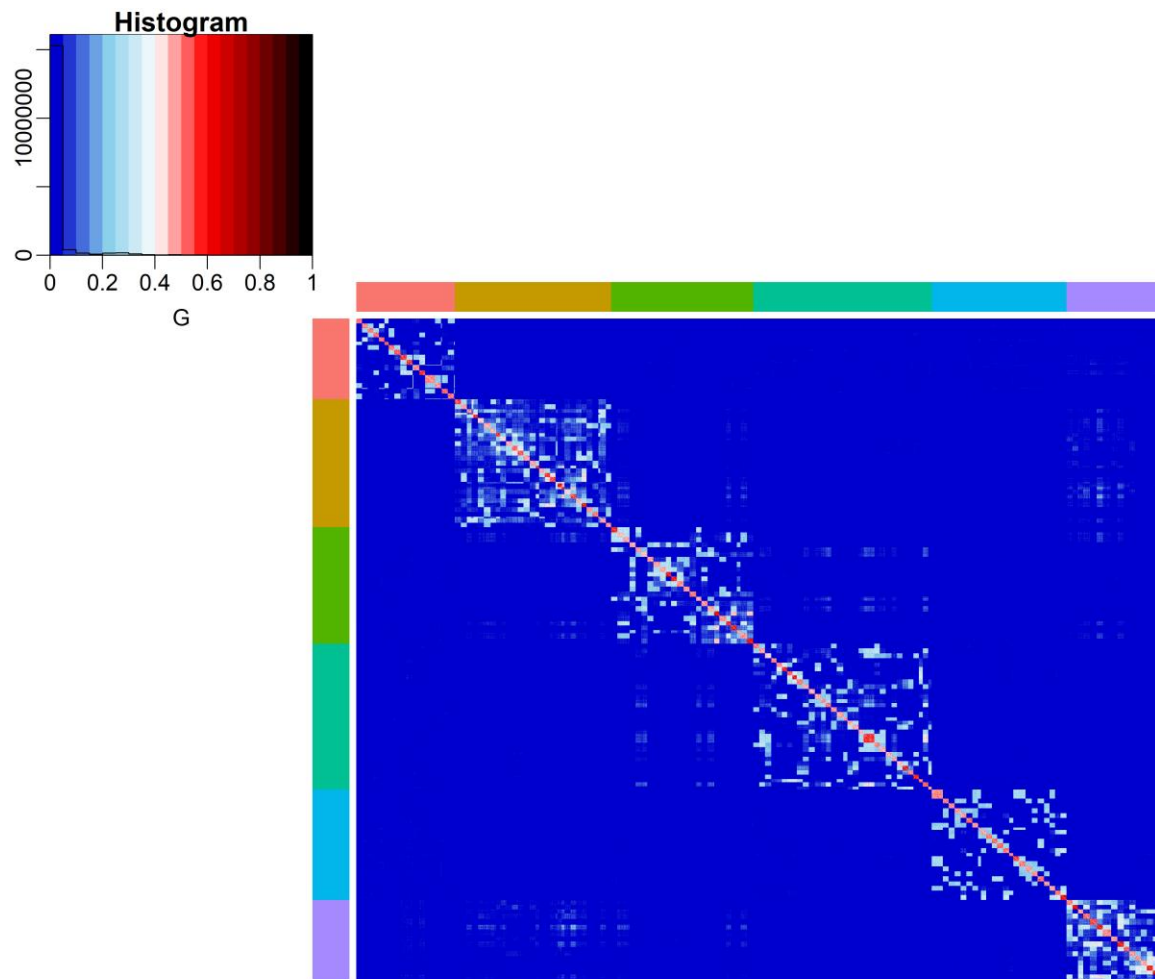


Figure S3. Realized genomic additive relationship matrix (\mathbf{G}_a). The histogram on the top left represents the color key for the values of \mathbf{G}_a . The side colors on the x and y-axes represent the six breeding groups (BGs) in order 1, 2, 3, 4, 5, and 6 from top to bottom. Dataset 1 included the BGs 1, 2, 5 and 6, and dataset 2 included the BGs 3 and 4. The values of \mathbf{G}_a vary around 0.5 between full-sibs, around 0.25 between half-sibs, and around 0 for unrelated trees. The mean additive genomic relationship within full-sib families was 0.511 with a standard deviation of 0.072.

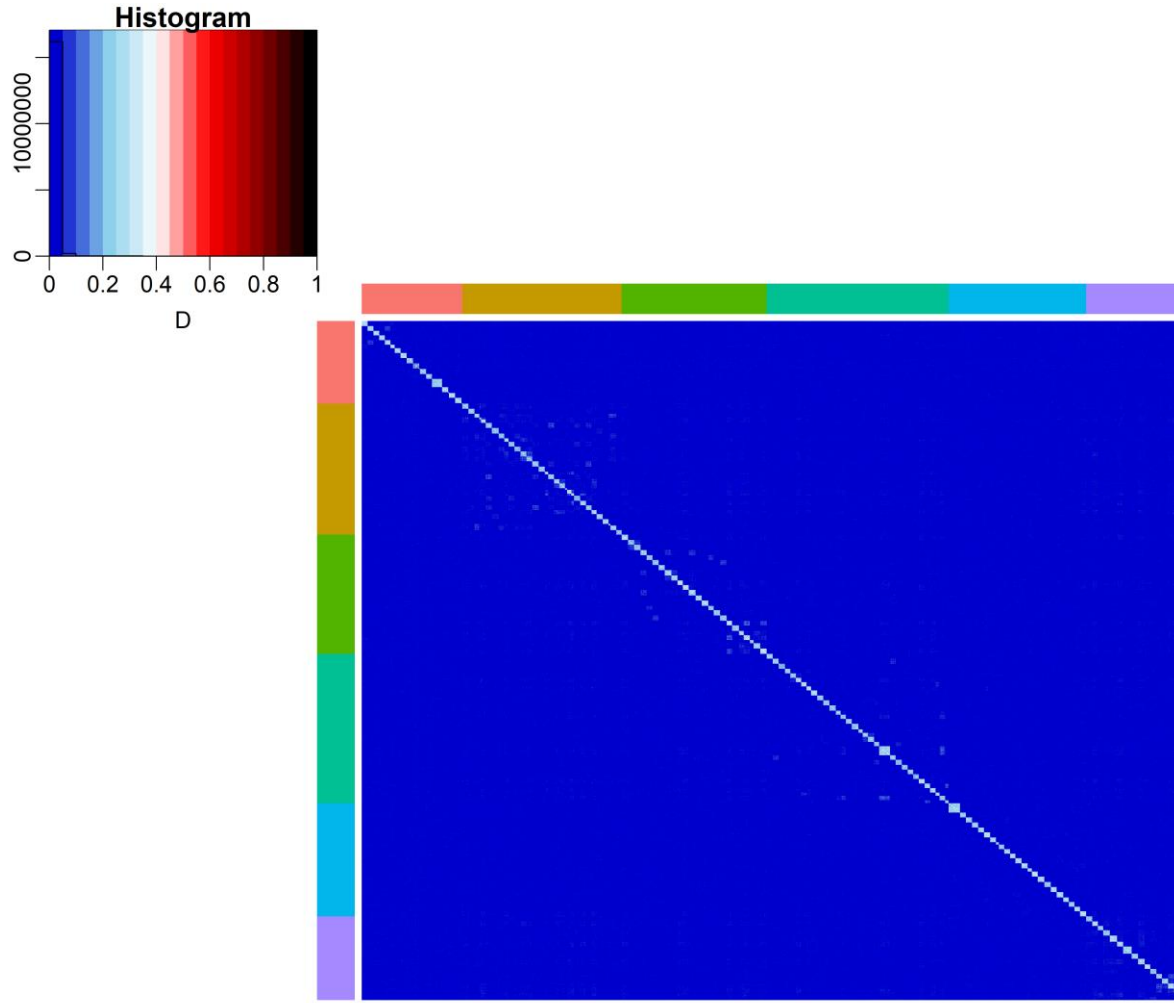


Figure S4. Realized genomic dominance relationship matrix (\mathbf{G}_d). The histogram on the top left represents the color key for the values of \mathbf{G}_d . The side colors on the x and y-axes represent the six breeding groups (BGs) in order 1, 2, 3, 4, 5, and 6 from top to bottom. Dataset 1 included the BGs 1, 2, 5 and 6, and dataset 2 included the BGs 3 and 4. The values of \mathbf{G}_d vary around 0.25 between full-sibs, and around zero otherwise. The mean dominance genomic relationship within full-sib families was 0.251 with a standard deviation of 0.067.

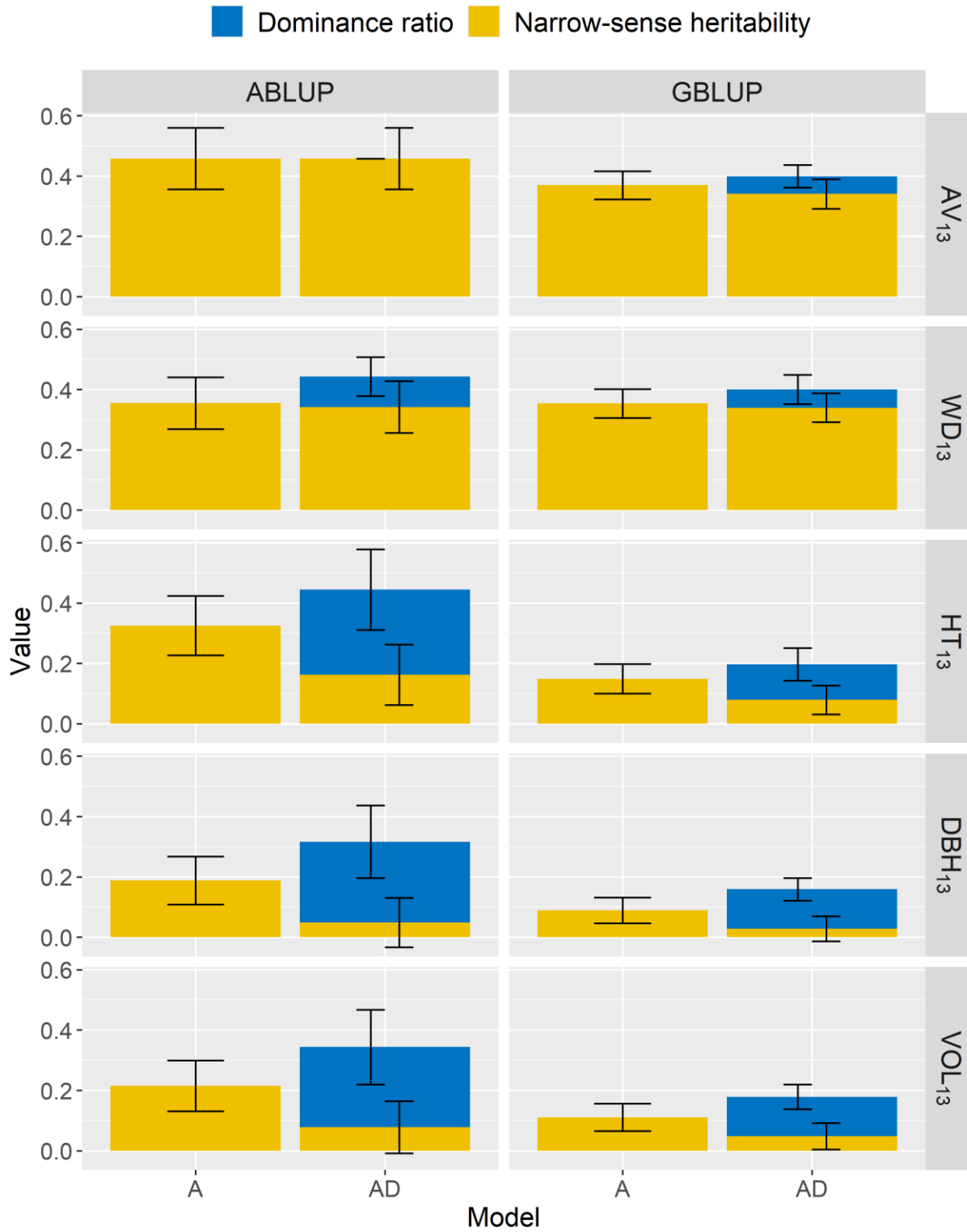


Figure S5. For the complete **dataset 2**, across-site narrow-sense heritabilities (\hat{h}_{ind}^2) and dominance ratios (\hat{d}_{ind}^2) estimated using additive (A) or additive-dominance (AD) models, with ABLUP or GBLUP. The broad-sense heritabilities (\hat{H}_{ind}^2) are estimated as the sum of \hat{h}_{ind}^2 and \hat{d}_{ind}^2 . The error bars represent the approximated standard errors of estimates calculated using the delta method. See Table 2 for a description of traits.

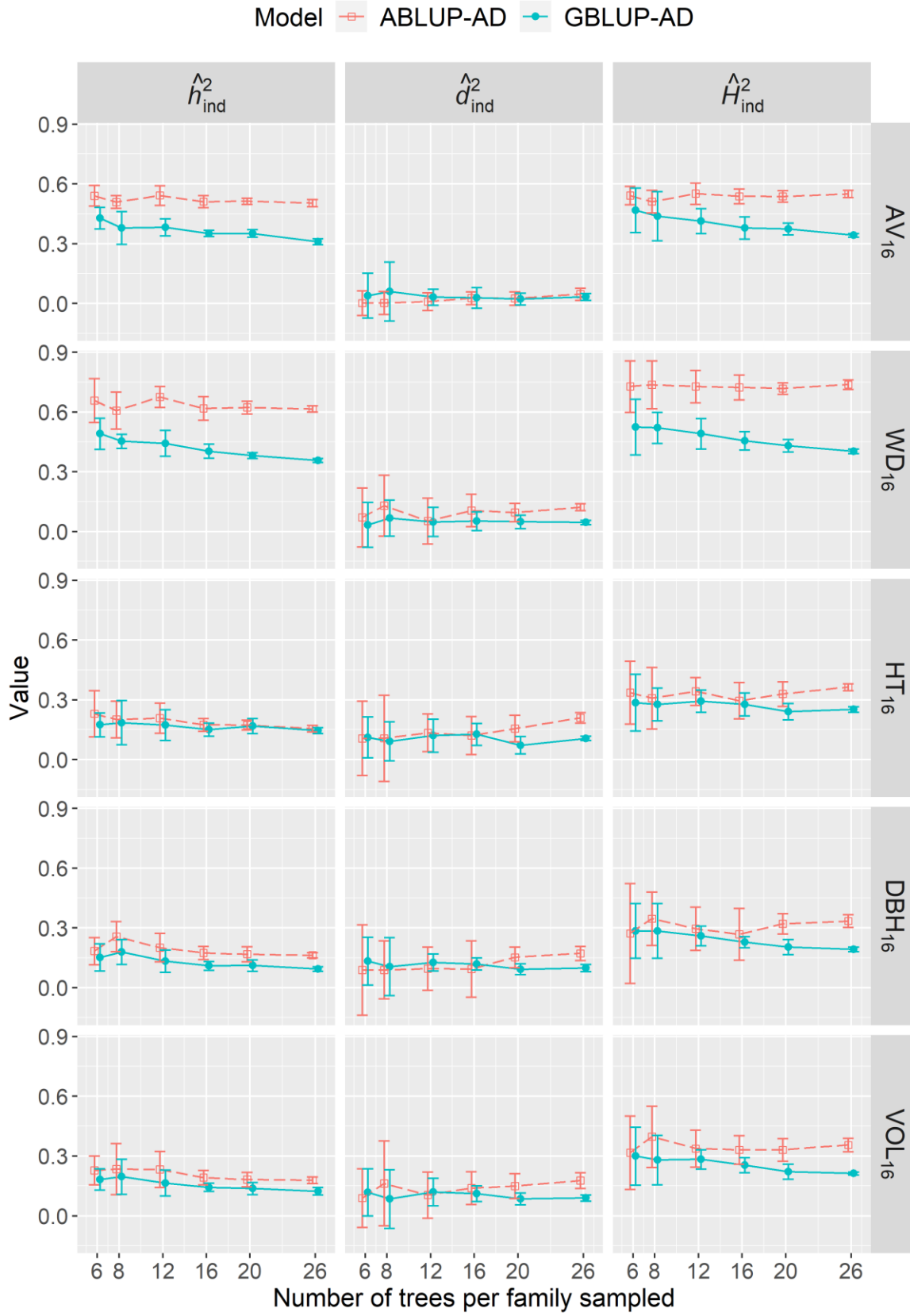


Figure S6. For **dataset 1**, across-site narrow-sense heritabilities (\hat{h}_{ind}^2), dominance ratios (\hat{d}_{ind}^2), and broad-sense heritabilities (\hat{H}_{ind}^2) estimated when varying the number of trees per family sampled using the ABLUP-AD and GBLUP-AD additive-dominance models. The error bars represent the standard deviation of estimates across the 10 replications for each level of number of trees per family sampled. See Table 2 for a description of traits.

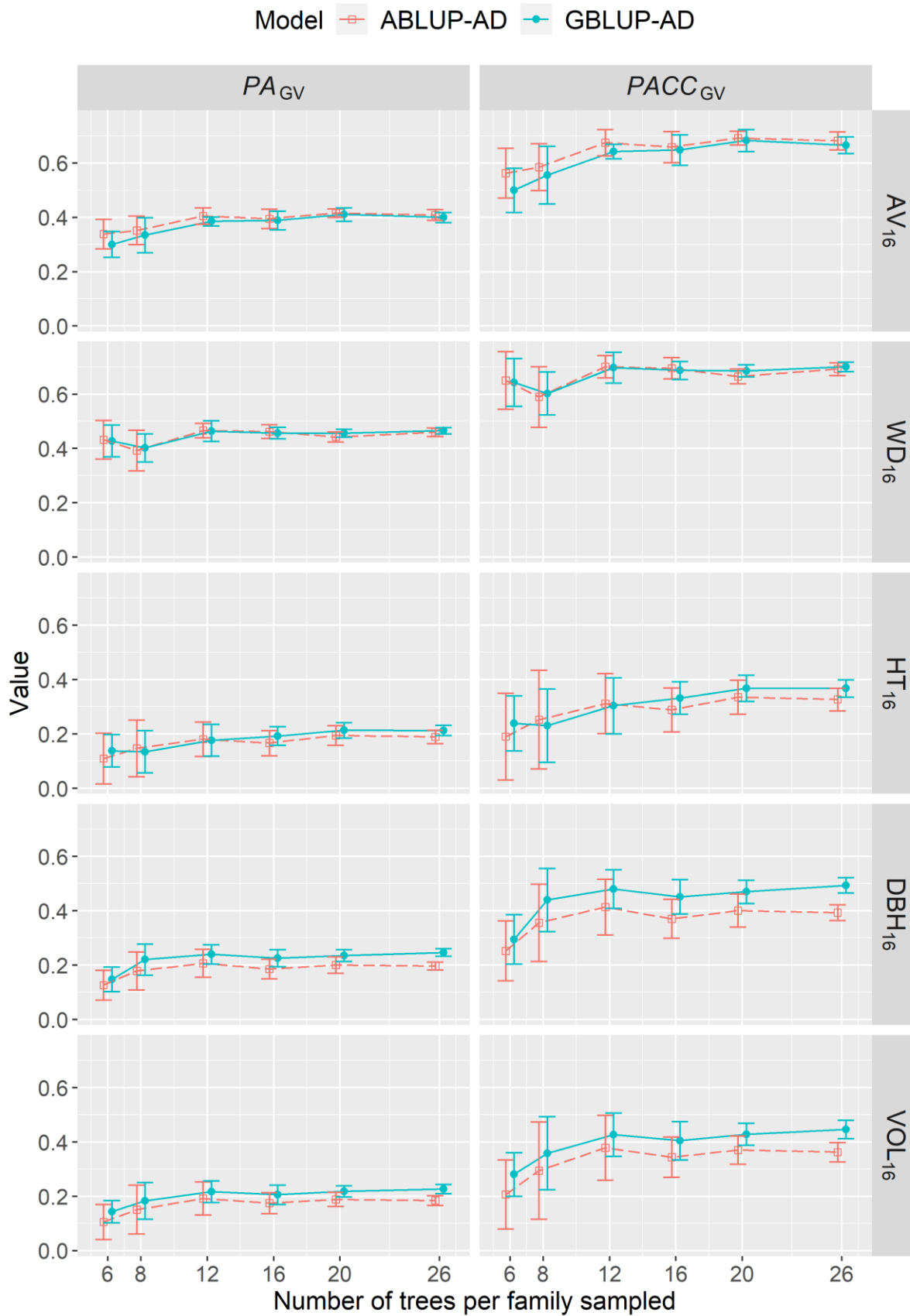


Figure S7. For **dataset 1**, Predictive ability (PA_{GV}) and prediction accuracy of genetic values ($PACC_{GV}$) estimated using CV2 and when varying the number of trees per family sampled using the ABLUP-AD and GBLUP-AD additive-dominance models. The error bars represent the standard deviation of estimates across the 10 replications for each level of number of trees per family sampled. See Table 2 for a description of traits.

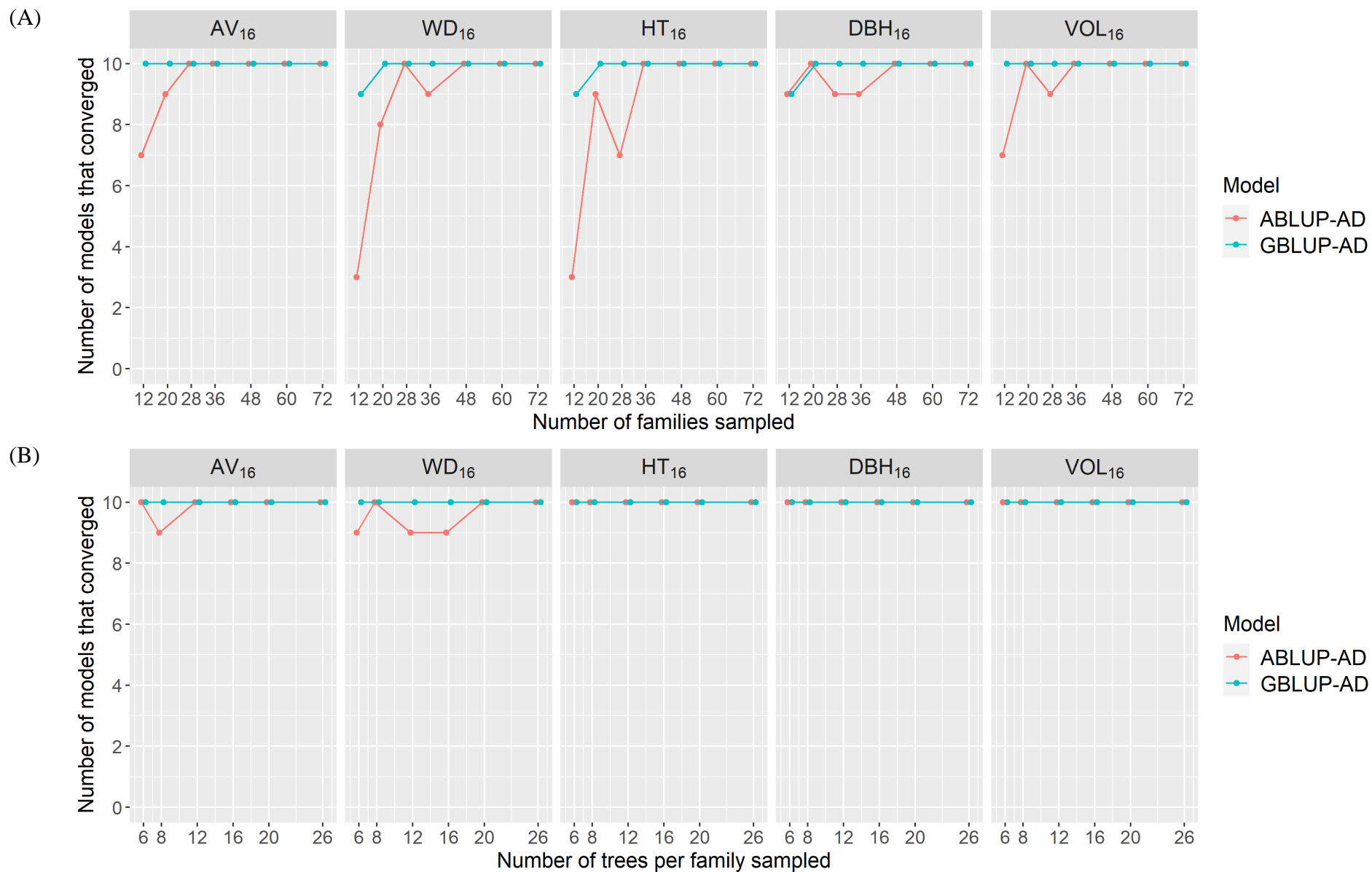


Figure S8. For **dataset 1**, number of models that converged using the ABLUP-AD and GBLUP-AD additive-dominance models when **(A)** varying the number of families sampled; and **(B)** varying the number of trees per family sampled. See Table 2 for a description of traits.