Multi-parental mapping of plant height and flowering time QTL in partially isogenic sorghum families

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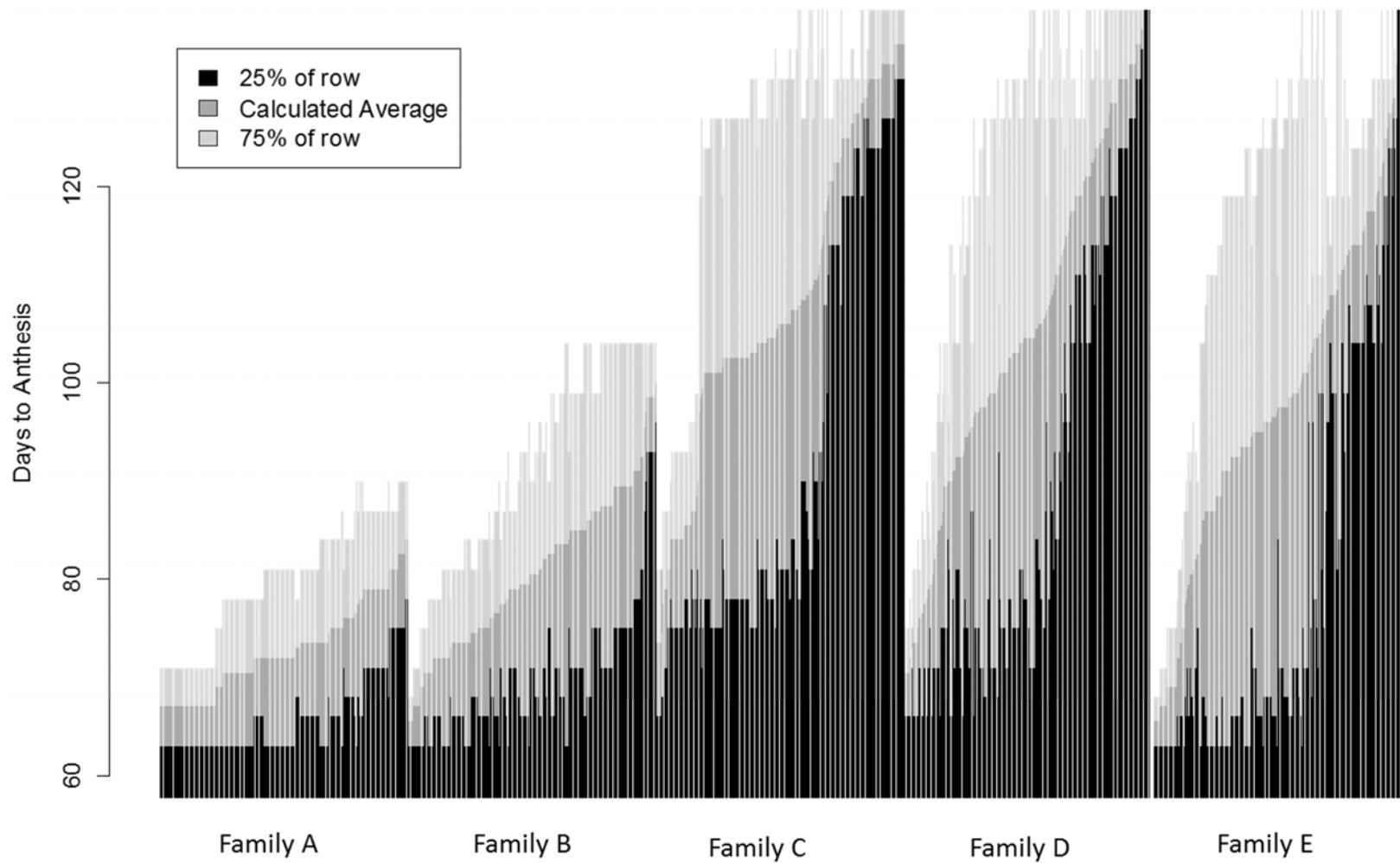
Figure S1 Raw and calculated values for days to anthesis in the temperate environment (FL-IL).
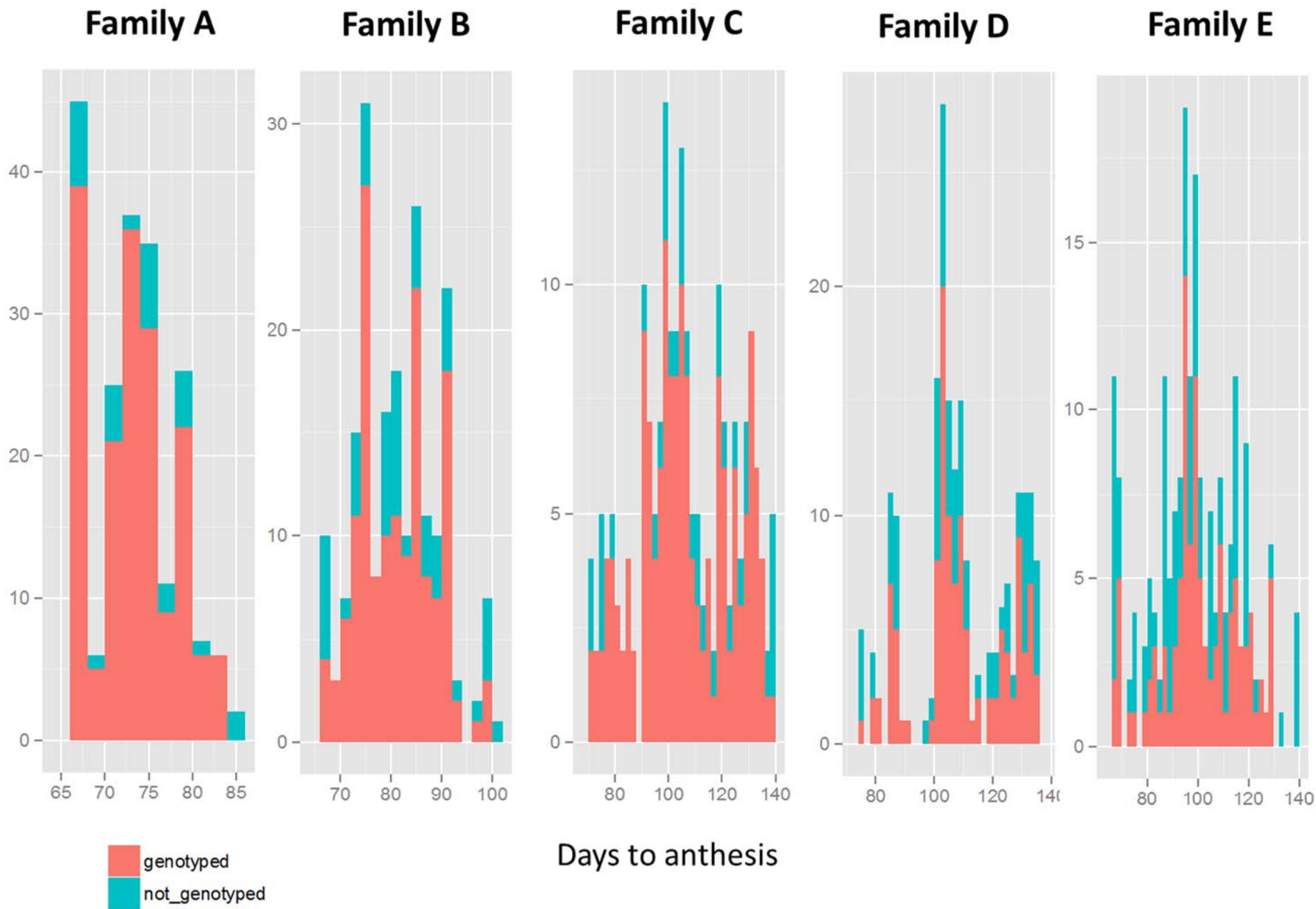
Figure S2 Temperate flowering time (FL-IL) distributions of lines with and without genotype data in each family.
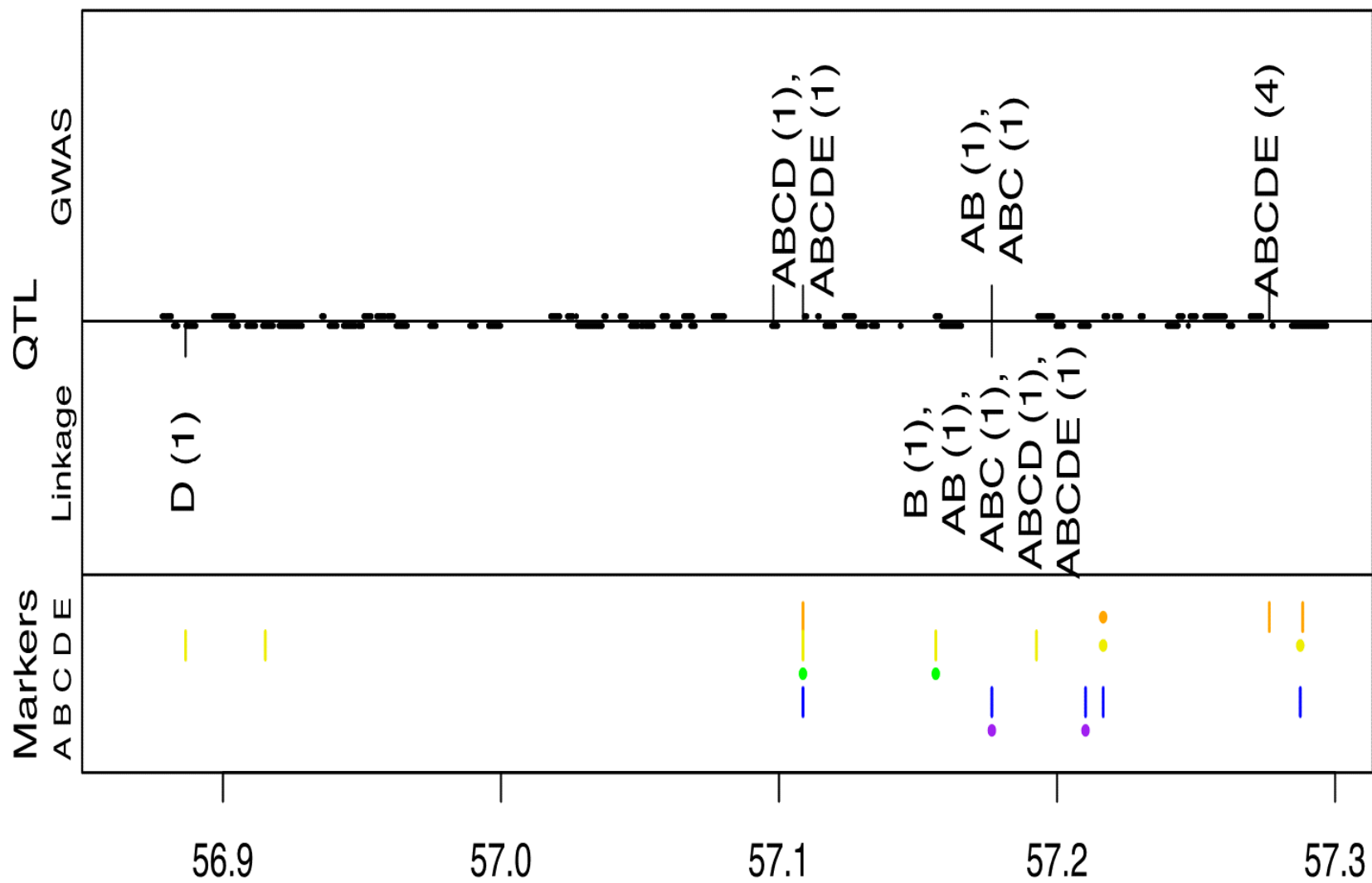
Figure S3 QTL for tropical plant height (HT-MX) in the *Dw1* region of sorghum chromosome 9. Information in the top, middle, and bottom panels is the same as in Figure 4.
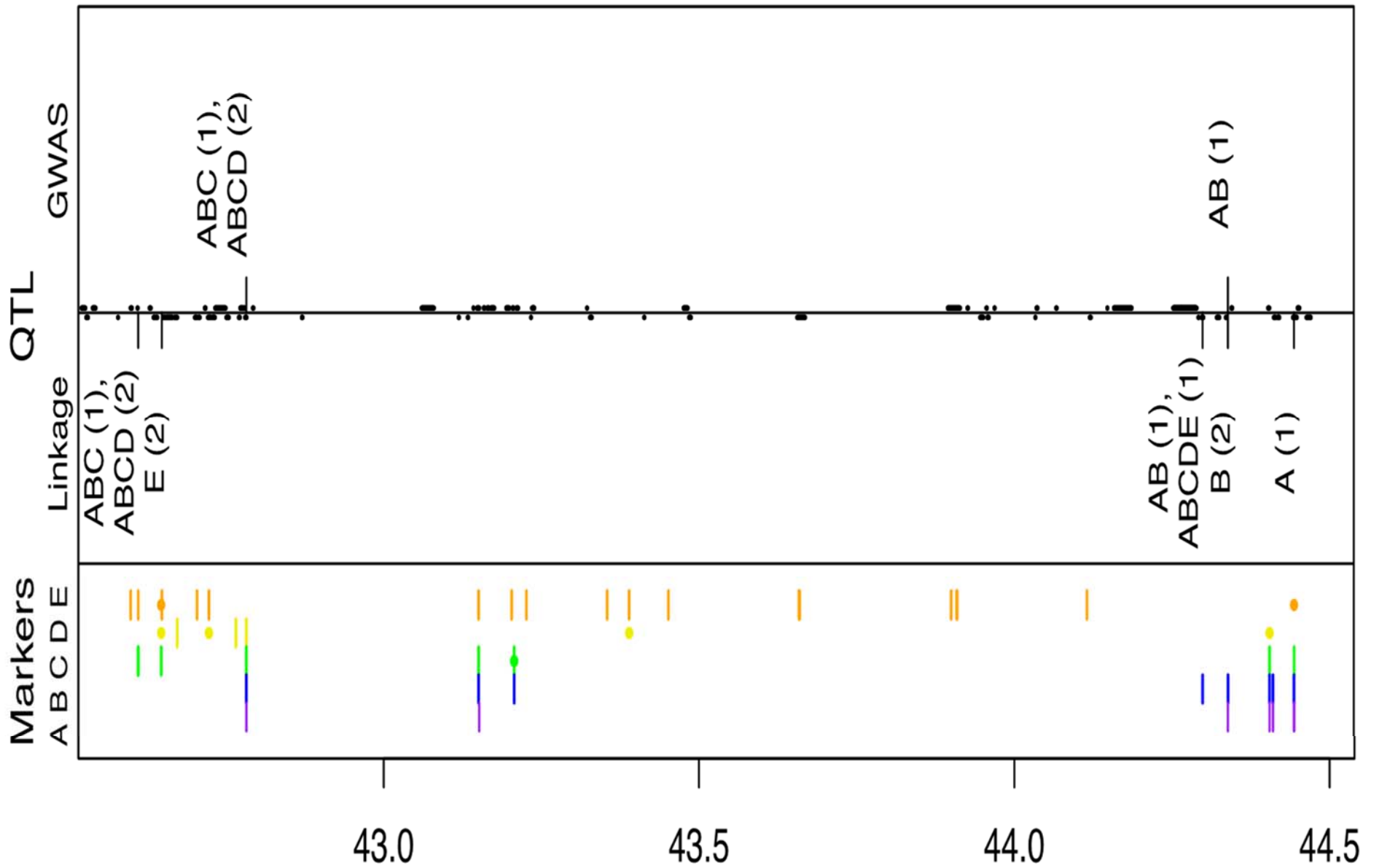
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Figure S4 QTL for temperate plant height (HT-IL) in the *Dw2* region of sorghum chromosome 6. Information in the top, middle, and bottom panels is the same as in Figure 4.
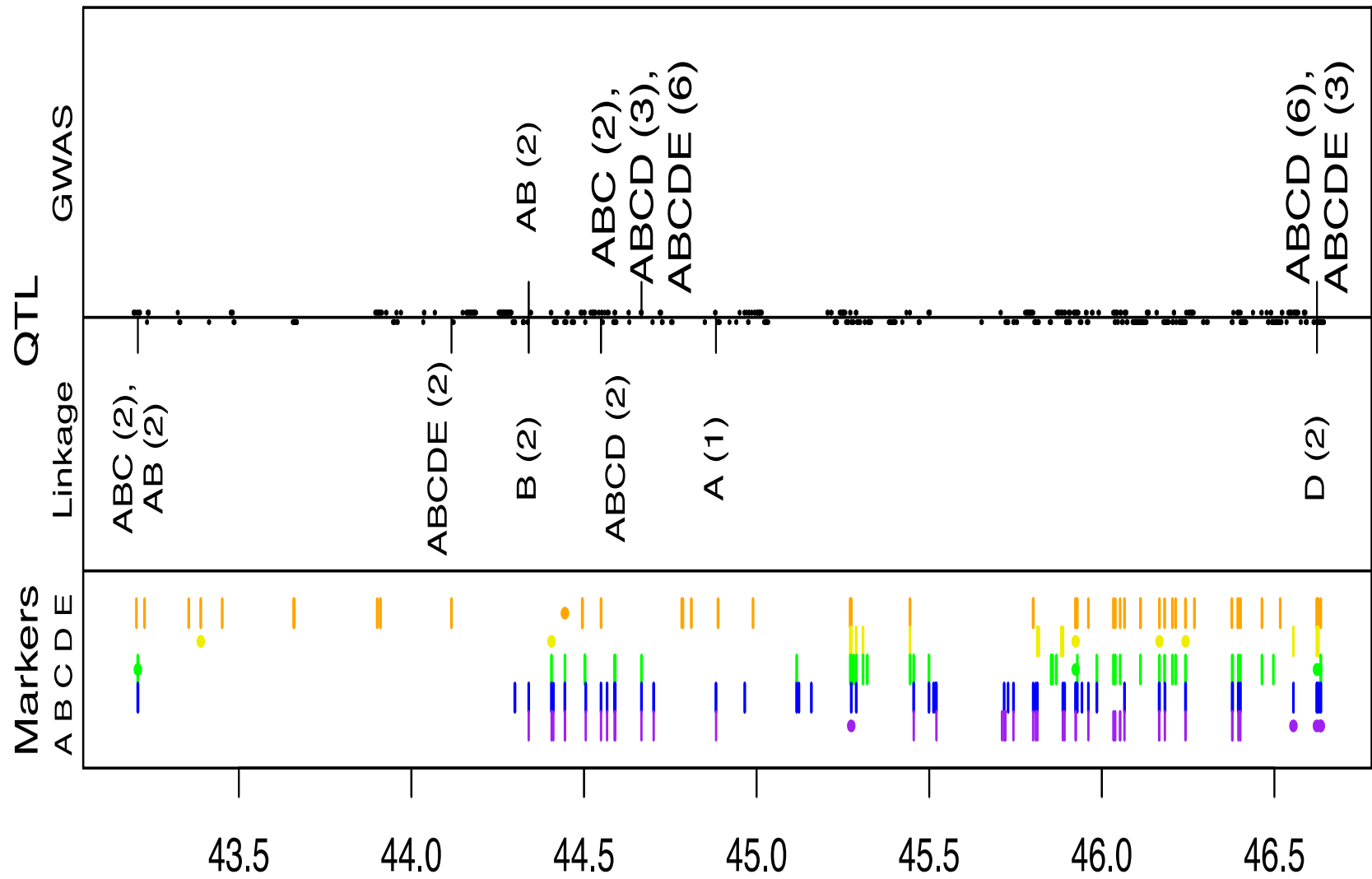
Figure S5 QTL for tropical plant height (HT-MX) in the *Dw2* region of sorghum chromosome 6. Information in the top, middle, and bottom panels is the same as in Figure 4.

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Tables S1-S5

Available for download as Excel files at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013318/-/DC1

Table S1   Segregation of 9139 SNPs across families A-E. Marker segregation by family: 0 = fixed for reference allele, 1 = segregating; 2 = fixed for alternate allele.

Table S2   Raw and modeled phenotypes. Raw phenotypic data ("_raw") and phenotypic values used for QTL analysis ("_out"). For FL-IL, days at which each row reached 25% and 75% anthesis are also shown.

Table S3   Phenotypic variance components. REML estimates of variance components for each phenotype, obtained using the lmer() function in R

Table S4   QTL models. Markers and p-values for each step in each QTL model.

Table S5   Raw genotypes. Genotypes used for QTL analysis. 0= fixed for reference allele; 1=heterozygous; 2= fixed for alternate allele; NA = missing.