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

Higgins RH*§, Thurber CS§, Assaranurak I*2, and Brown PJ*§

*Department of Crop Sciences, University of Illinois, Urbana, IL, USA 61801
§Energy Biosciences Institute, University of Illinois, Urbana, IL, USA 61801

1 Current address: Department of Agronomy, Iowa State University, Ames, IA 50011
2 Current address: Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14850

Corresponding author: Patrick J Brown, 1408 IGB, 1206 W Gregory Drive, Urbana IL, 61801; (217)-333-8182; pjb34@illinois.edu

DOI: 10.1534/g3.114.013318
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 DwI region of sorghum chromosome 9. Information in the top, middle, and bottom panels is the same as in Figure 4.
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.
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.