Figure S2: Genome-wide associations for preflag leaf height using RIG-generated variants called from reduced representation data. Of the 733 sorghum germplasm samples used to generate the Population Reference Variant Resource as part of the RIG workflow, 171 of the lines had been previously phenotyped by Brown et al. (2008). After producing a recalibrated, sensitive variant resource with the RIG workflow, missing genotypes were filled in using Beagle v4 release 1274 (Browning and Browning 2007). Variants were pre-processed (minor allele frequency > 5%) and converted to PLINK binary format using PLINK v1.90-1 (Purcell and Chang 2014). The 171 phenotypes from Brown et al. (2008) were normalized using an Empirical Normal Quantile Transformation (ENQT) (Peng et al. 2007). Using GCTA v1.24.3, a genomic relationship matrix was generated and associations were calculated using GCTA’s mixed linear model implementation (Yang et al. 2011). As shown in Supplemental Table S3, this analysis reproduced known QTL at the sorghum dwarfing loci Dw1, Dw2, and Dw3 on chromosomes 9, 6, and 7, respectively (Morris et al. 2013; Higgins et al. 2014).