**Figure S1.** Scree plot showing amount of genetic variation explained by the first 10 principal coordinates for the drought tolerance association panel. The amount of variation explained starts to level off at four coordinates, and therefore the first four coordinates were used as covariates in the GWAS models to help correct for potential population structure.

**Figure S2.** Bayesian clustering (fastSTRUCTURE) results for K = 2 - 10 using simple option for the association panel. Color in vertical bars represents proportion individual belongs to each K group.

**Figure S3.** Plots showing relationship of canopy wilting scores of the lines ranked across environments with **(A)** maturity group (MG), and **(B)** days to flowering (DTF).

**Table S1.** Association panel canopy wilting scores, ranking, number of beneficial alleles, and breeding values. Each environment was ranked individually, and the mean of those rankings was used to rank all of the 162 genotypes tested. Canopy wilting scores shown are the mean of all reps within each respective environment.

**Table S2.** Candidate genes and their functional annotation identified using the Glyma2.1 gene models in SoyBase (www.soybase.org) within plus or minus 10 kb of SNPs significantly associated with canopy wilting from GWAS.

**File S1.** SNP genotype data used for GWAS in HapMap format.

**File S2.** Canopy wilting score raw data.