**Test Files**

**File 1. | Soy775 accession panel.** List of accessions.

**File 2. | AccuTool output for *pdh1* CM correspondence to pod shattering susceptible and resistant phenotypes.** *Pdh1* associated region (2.32M bp).

**File 3. | AccuTool output for *w1* CM correspondence to purple and white flower color phenotypes.** *W1* associated region.

**File 4. | Distribution of pod shattering phenotypes in Soy775 accuracy panel.** Shattering susceptible (coded as 1), shattering resistant (coded as 2) and missing data (NA).

**File 5. |** **Distribution of flower color phenotypes in Soy775 accuracy panel.** White flower color (coded as 2) and purple (coded as 1) and missing data (NA).

**File 6. |** **Distribution of stem termination phenotypes in Soy775 accuracy panel.** Determinate (coded as 2) and indeterminate (coded as 1) and missing data (NA).

**File 7. | GWAS 1 with pod shattering phenotypes on the GRIN collection of accessions genotyped by low density SoySNP50K bead chip.** GWAS input file for AccuTool.

**File 8. | Inverse GWAS with *pdh1* CM as phenotype with the SoySNP50K marker subset from the AccuTool Soy775 accession panel.** GWAS input file for AccuTool.

**File 9. | GWAS 1 with white or purple flower color phenotype on soybean USB15x(302) data set accessions genotyped by low density SoySNP50K bead chip.** GWAS input file for AccuTool.

**File 10. | Inverse GWAS with the *w1* CM synthetic phenotype on Soy775 accession panel data set genotyped by low density SoySNP50K bead chip.** GWAS input file for AccuTool.

**File 11. | Inverse GWAS with the *w1* CM synthetic phenotype on USB15x(302) data set with all WGS positions as genotype.** GWAS input file for AccuTool.

**File 12. | GWAS 1 with determinate and indeterminate stem termination phenotypes on the soybean GRIN collection of accessions genotyped by low density SoySNP50K bead chip.** GWAS input file for AccuTool.

**File 13. | GWAS 2 with the *Dt1* haplotype tagging variant ss715635425 as a synthetic phenotype on USB15x(302) data set with all WGS positions as genotype.** GWAS input file for AccuTool.