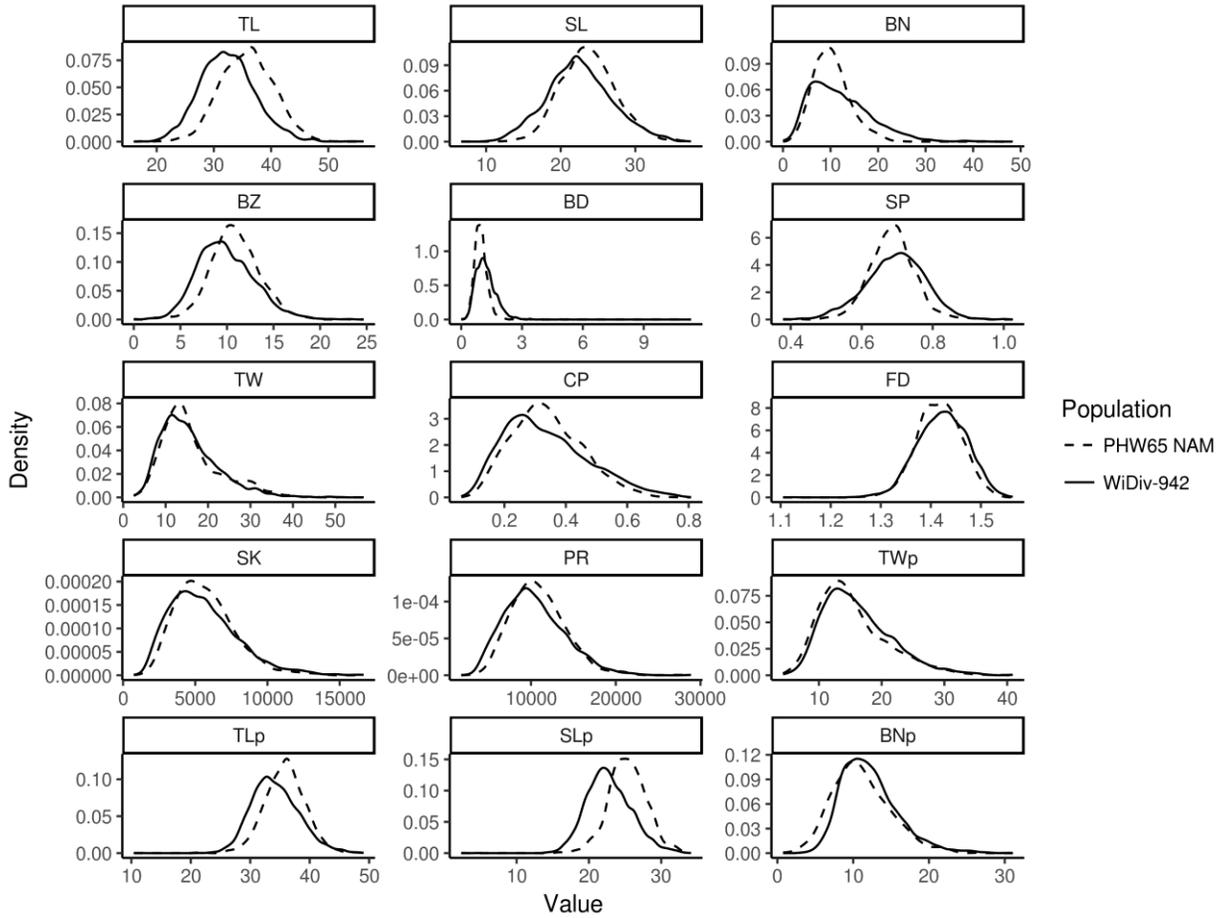


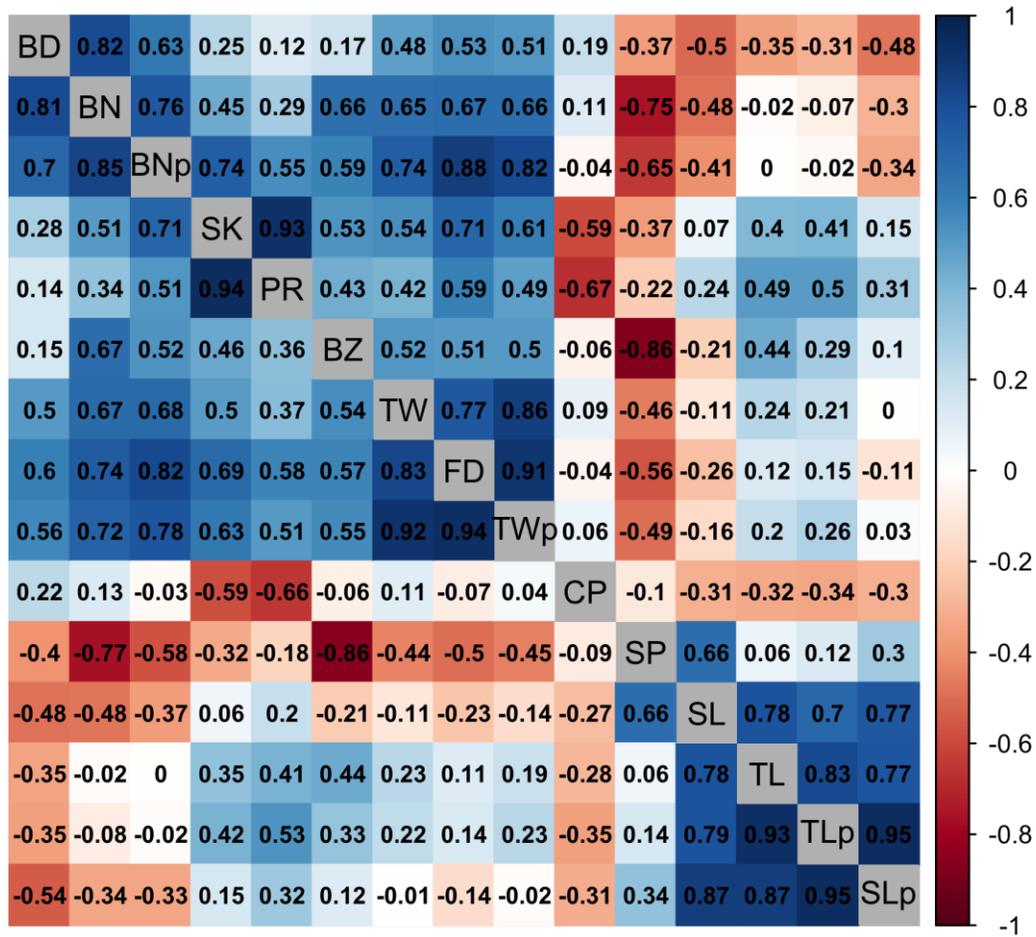
Supplemental Figures

Supplemental Figure 1: Trait distributions



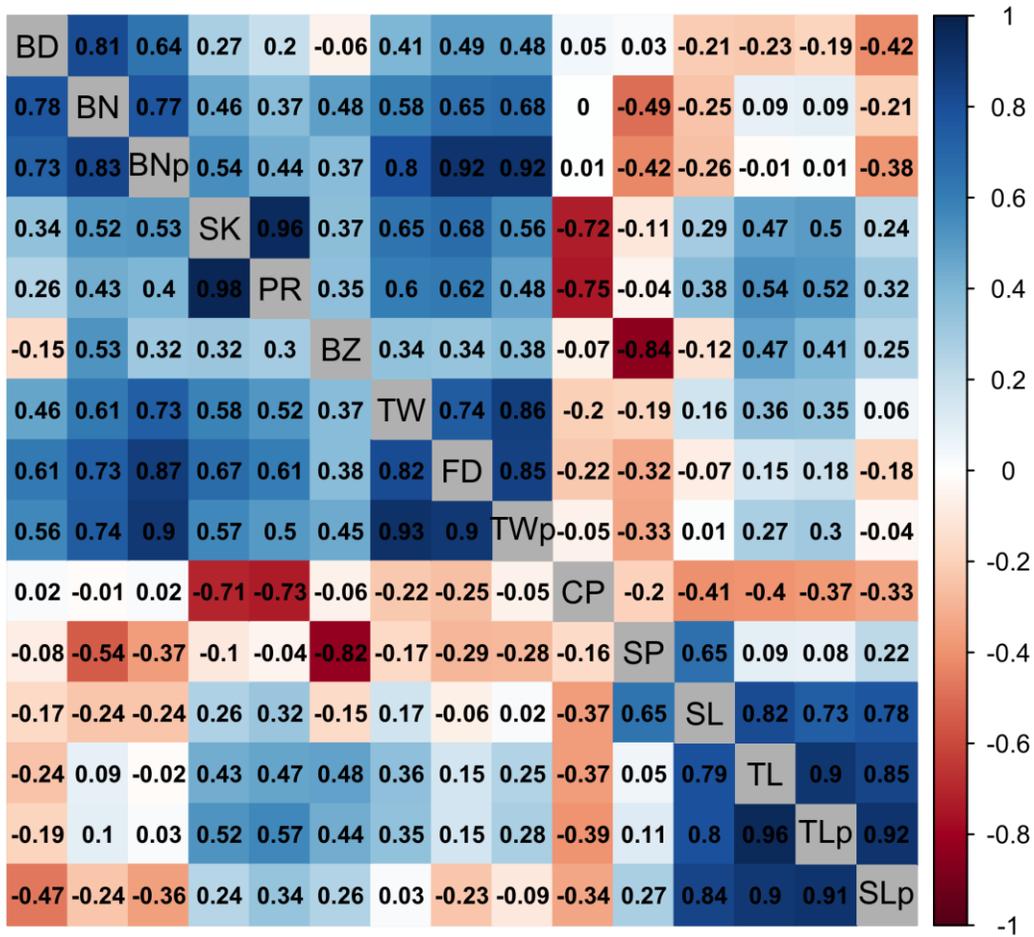
Distributions of all raw phenotypic values for the WiDiv-942 (solid) and PHW65 NAM (dashed).

Supplemental Figure 2: Phenotypic and genotypic correlations in the WiDiv-942



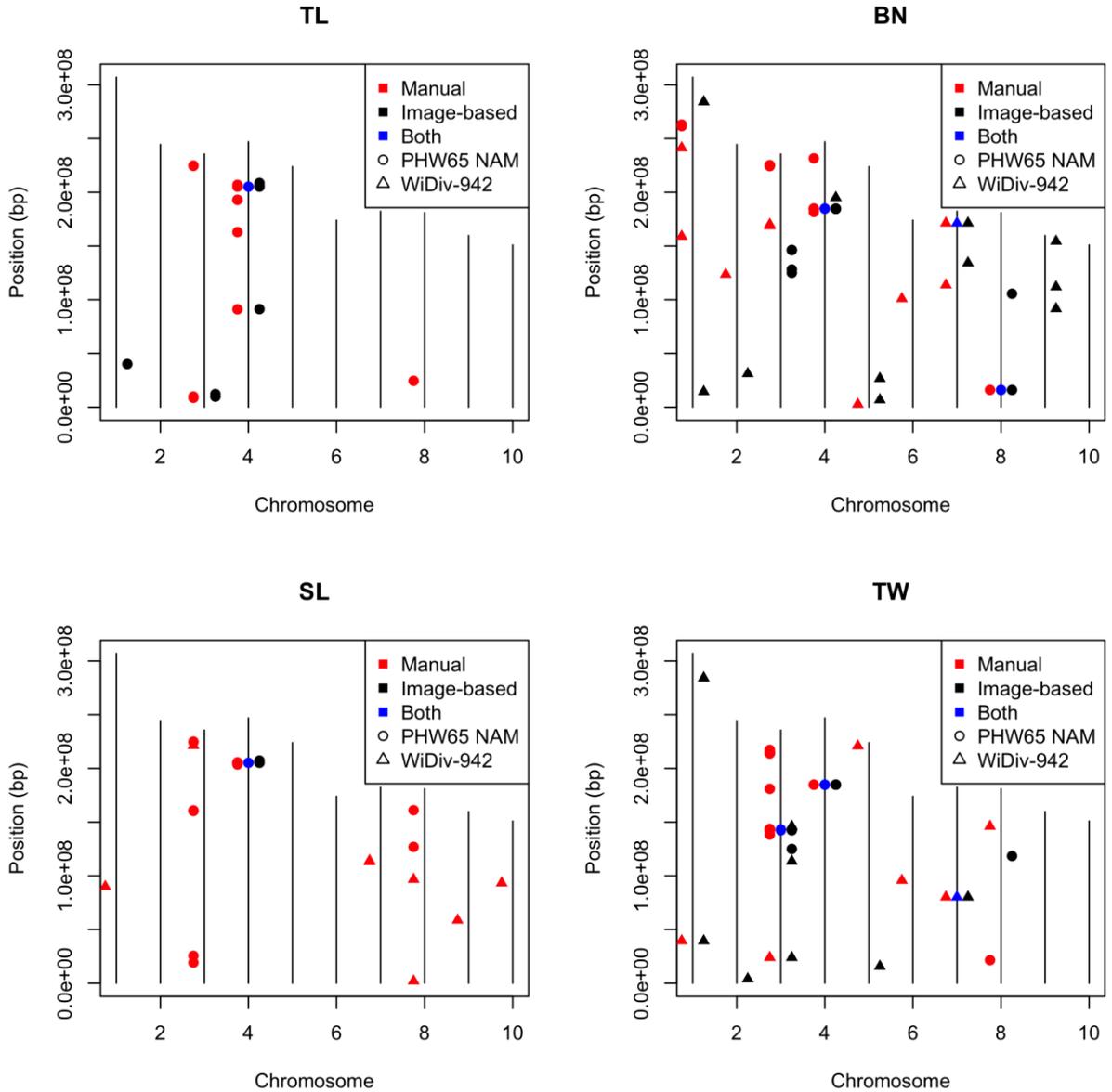
Phenotypic (top triangle) and genotypic (lower triangle) correlations between all traits in the WiDiv-942. Correlations were calculated using only data from a single location, including only individuals that were phenotyped for all traits in that location (n = 693).

Supplemental Figure 3: Phenotypic and genotypic correlations in the PHW65 NAM



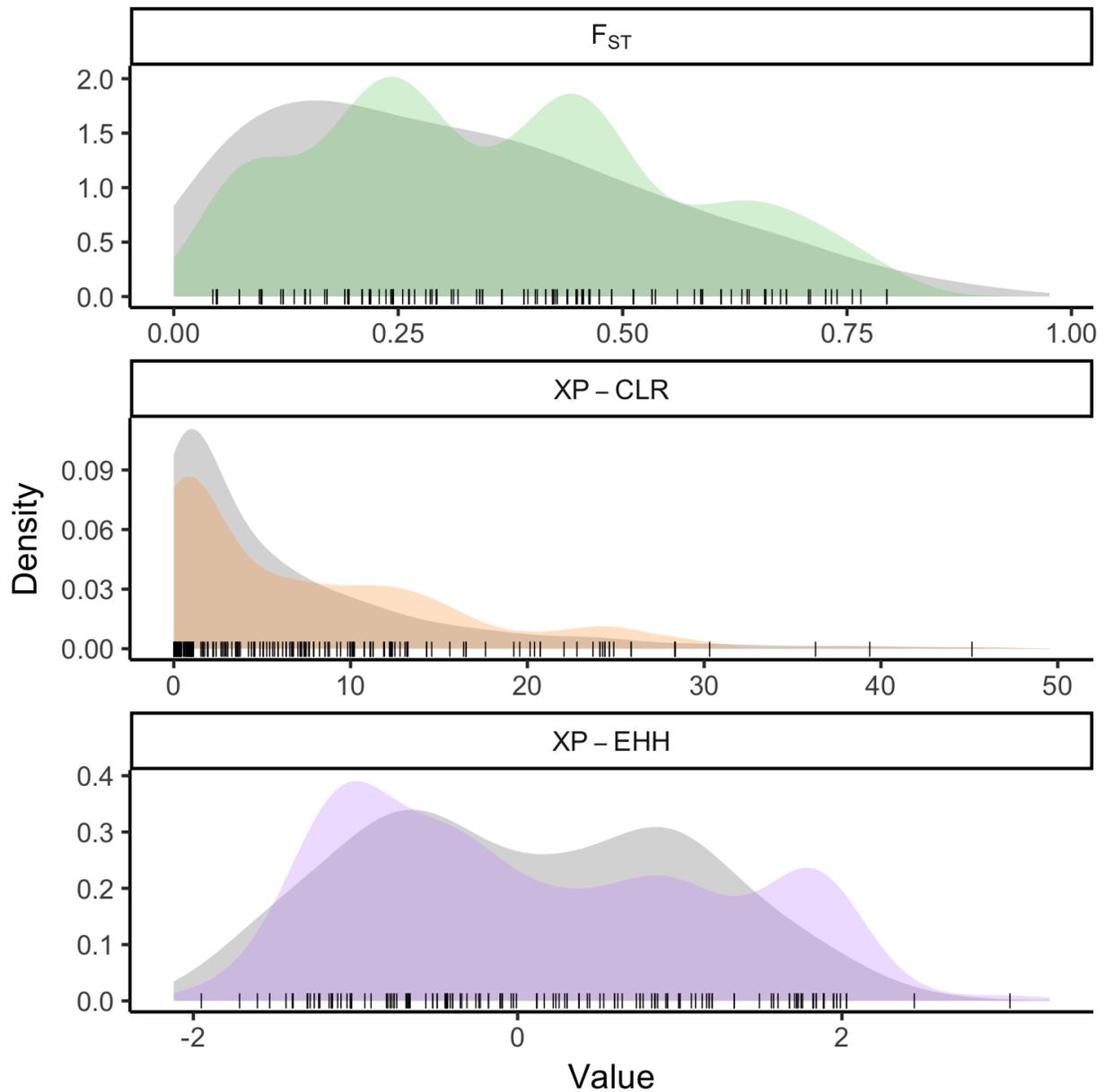
Phenotypic (top triangle) and genotypic (lower triangle) correlations between all traits in the PHW65 NAM. Correlations were calculated using only data from a single location, including only individuals that were phenotyped for all traits in that location (n = 569).

Supplemental Figure 4: Colocalization of manual and image-based GWAS hits



Tassel length (TL), spike length (SL), branch number (BN), and tassel weight (TW) were all measured manually and by image-based methods. Red and black points show locations of GWAS hits from manual and image-based traits, respectively. If both measurements identified the same exact SNP, the SNP is additionally marked by a blue point. Horizontal ticks represent known inflorescence development genes.

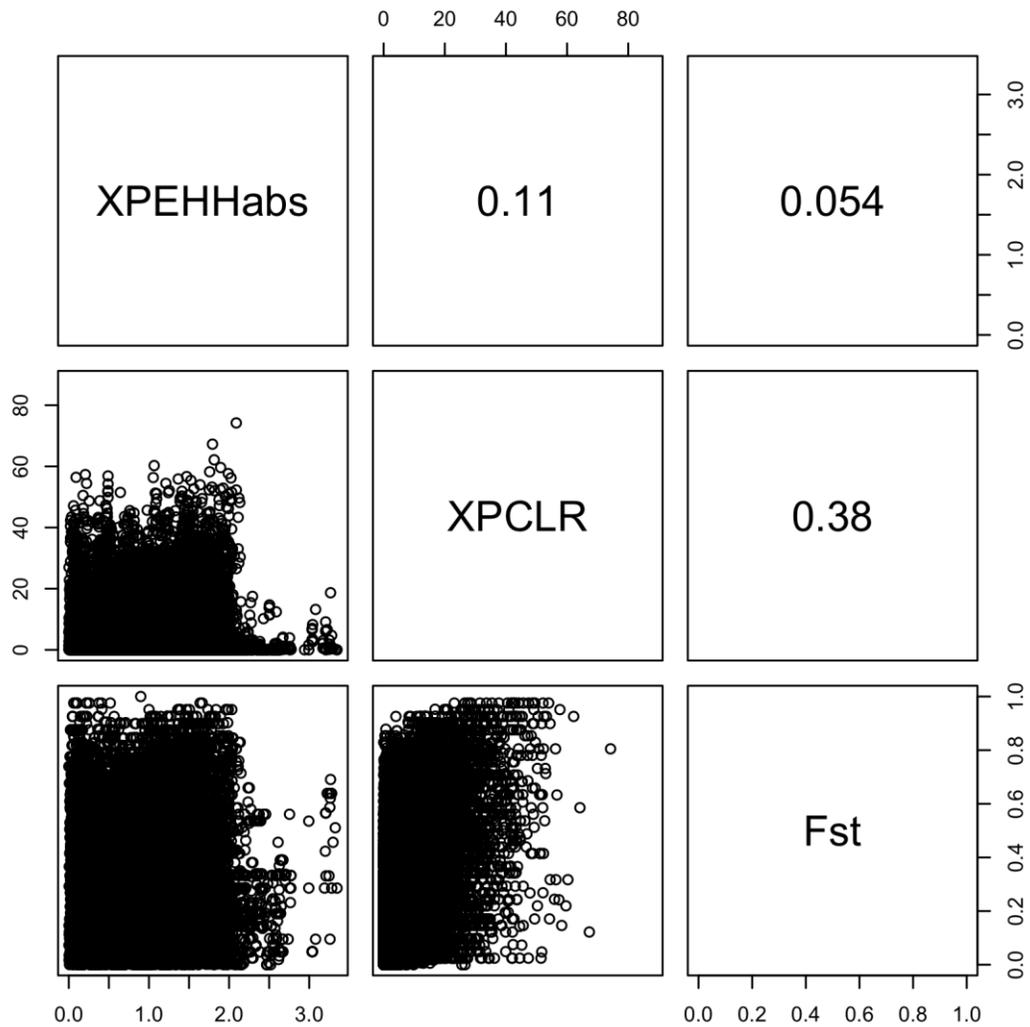
Supplemental Figure 5: Densities of selection statistics for SNPs associated with tassel morphological traits



Distributions of selection statistics for single nucleotide polymorphisms (SNPs) associated with tassel morphological traits (colored), compared to genome-wide null distributions (grey) derived by sampling windows with similar numbers of genes, recombination rate, and average allele frequencies in both the BSSSC0 and ex-PVP lines. Values of individual

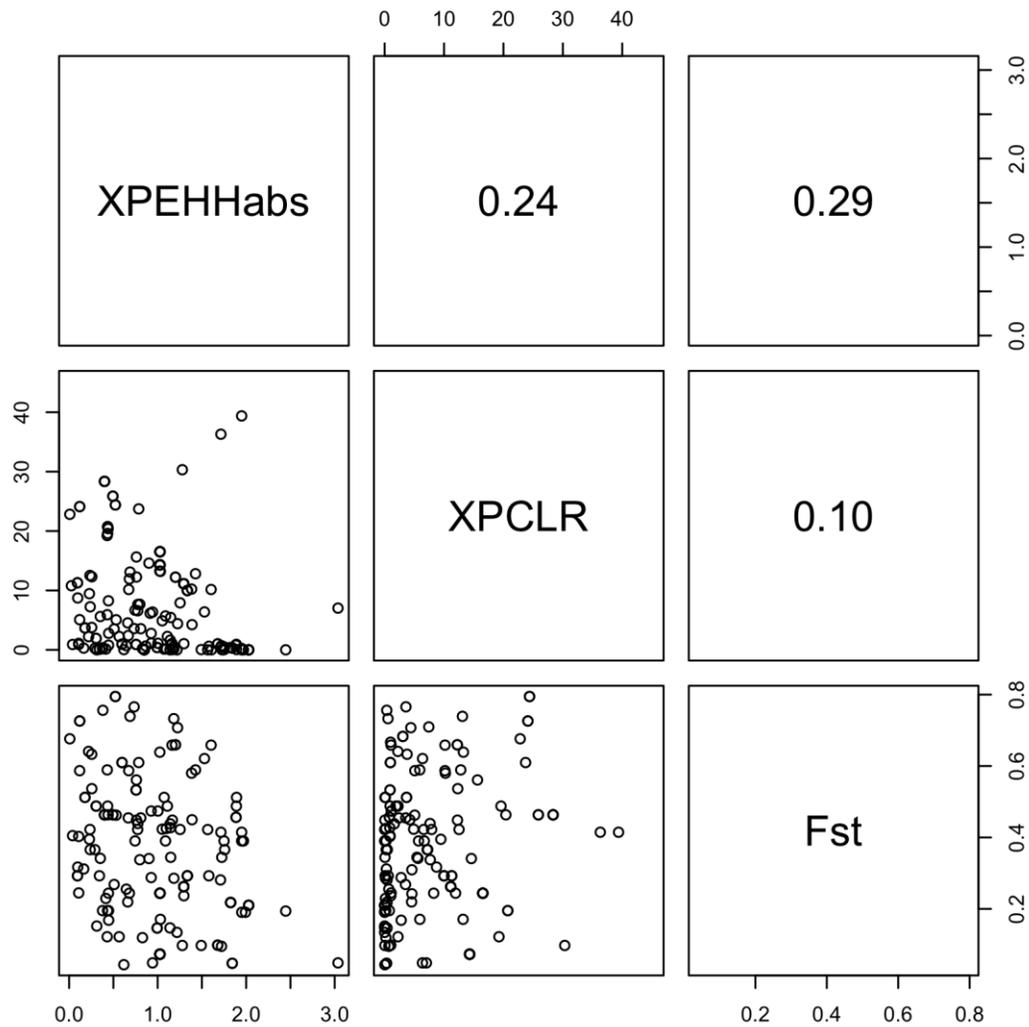
SNPs associated with tassel traits are represented by points along the bottom of each plot. The XP-CLR plot was truncated at 50 for better visualization. All three statistics were conducted between 41 BSSSC0-derived inbreds and 21 ex-PVP inbreds directly derived from BSSS lines.

Supplemental Figure 6: Genome-wide relationships between selection statistics



Comparison of XP-EHH, XPCLR, and F_{ST} XP-EHH, XPCLR, and F_{ST} values for all windows shows little systematic relationship between statistics. Upper triangle represents the absolute value of Pearson's correlation coefficient. XPEHHabs represents the absolute value of XP-EHH.

Supplemental Figure 7: Relationships between selection statistics at GWAS hits



Comparison of XP-EHH, XPCLR, and F_{ST} XP-EHH, XPCLR, and F_{ST} values for all windows containing SNPs significantly associated with morphological traits shows little systematic relationship between statistics. Upper triangle represents the absolute value of Pearson's correlation coefficient. XPEHHabs represents the absolute value of XP-EHH.