**Supplementary Figure 1.** Plot of different number of subpopulations (K) from 1 to 20 versus cross validation error (CV error). The cross validation procedure as implemented in ADMIXTURE was used to initially find the optimum number of subpopulations (K) by minimizing the cross validation error. Multiple runs of ADMIXTURE were conducted at different values of K ranging from 1 to 20.

**Supplementary Figure 2.** Population structure within the diversity panel assessed using principal component analysis (a) and ADMIXTURE (b). (a) PC1 and PC2 explained 6% and 5% variance respectively. (b) Each vertical bar corresponds to an inbred line, where lines are arranged horizontally according to *a priori* information on subpopulation. Vertical bars are colored according to subpopulation membership.

**Supplementary Figure 3.** Haplotype block analysis showing regions with significant SNPs on Chromosome 1, 2 and 5. Haplotype block analysis was conducted on each genomic region with significant SNPs to assess local LD decay rate. Haplotype analysis was performed with software Haploview. Standard color scheme was used in which bright red color indicates D’ =1 and LOD ≥ 2, blue color indicates D’ =1 and LOD < 2, white indicates D’ <1 and LOD < 2, and shades of pink/red indicates D’ <1 and LOD ≥ 2. D prime values are shown in boxes, empty boxes indicate D prime equals to 1. (a) Chromosome 1 region, had seven haplotype blocks with block 2 having maximum length of 4 kilo base pairs (kb). (b) Largest haplotype blocks were found on chromosome 2 region with maximum length of 79 kb. (c) Chromosome 5 region had 2 haplotype blocks with largest block length of 12 kb.

**Supplementary Table 1**. Treatments applied to the samples for the RNA-seq experiment.

**Supplementary Table 2**. Significant Gene Ontology terms found using AgriGO server for the genes of second module.

**Supplementary Table 3**. Gene annotations for genes of second module. All gene annotations for Zea mays were downloaded from gramene.org (Gramene FTP site) and compared to the list of genes of second module.