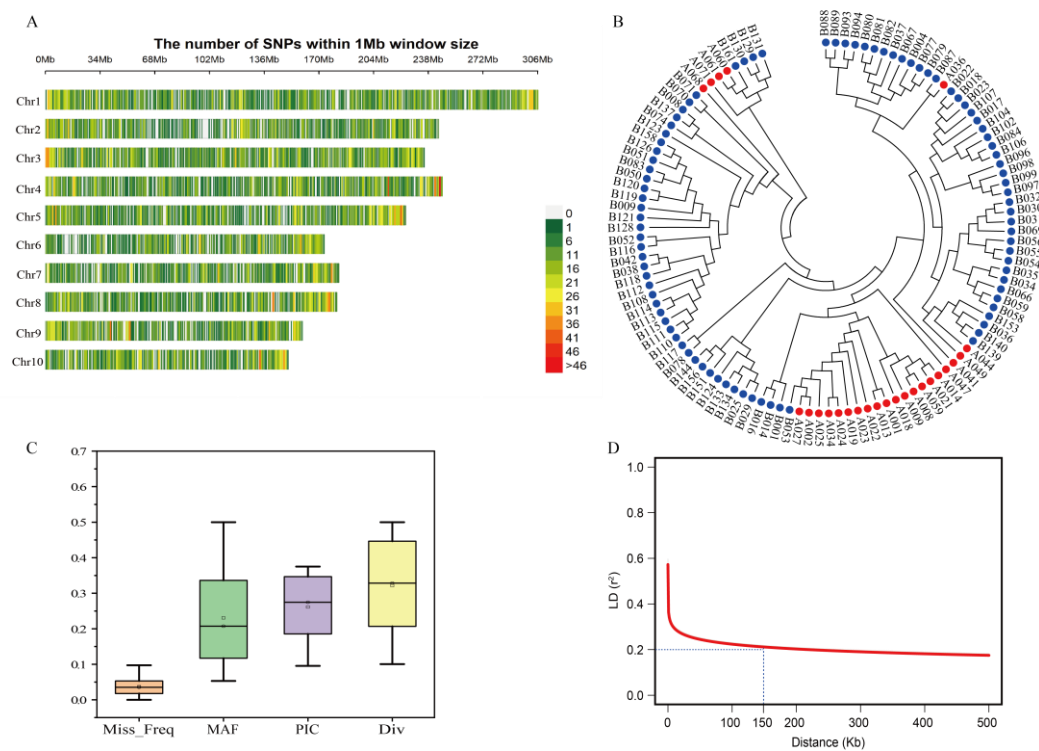
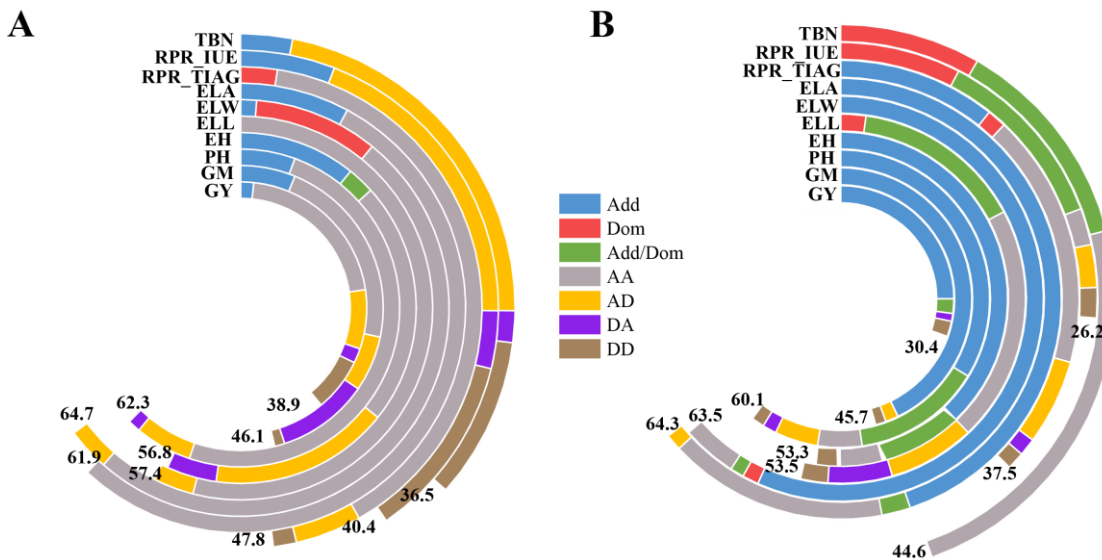


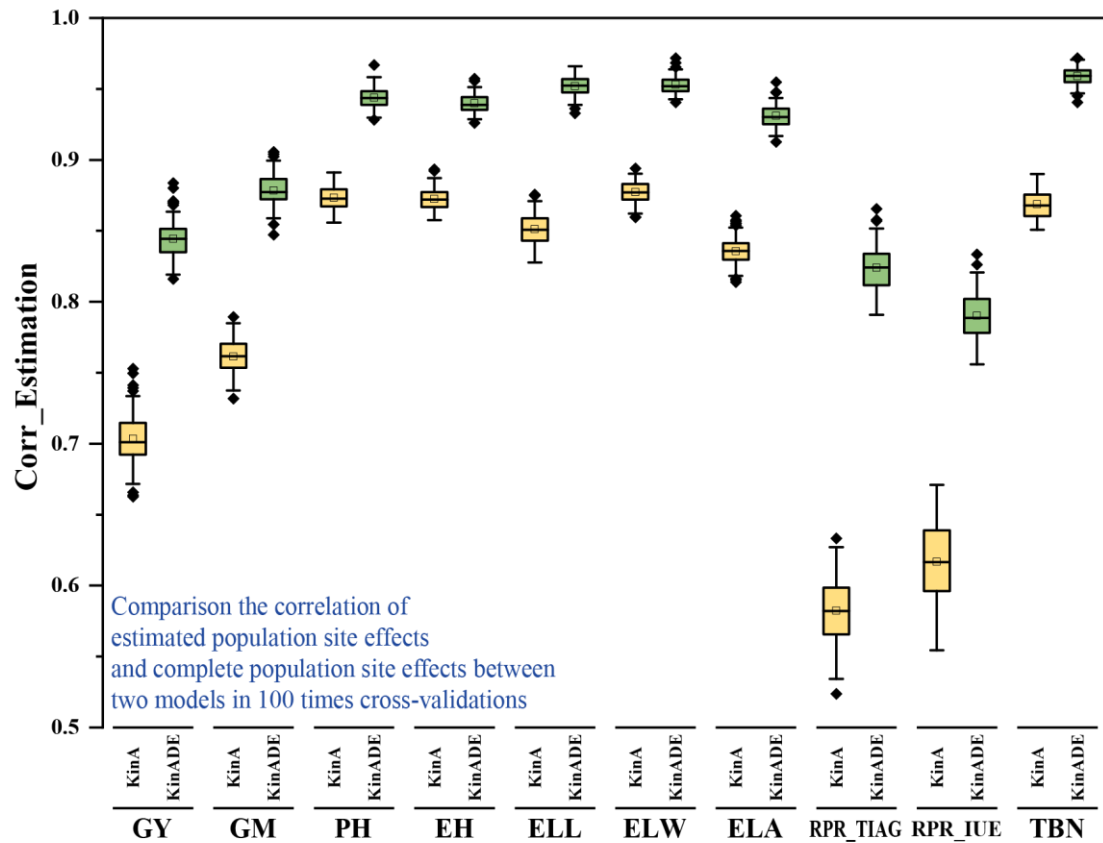
Supplementary Figures



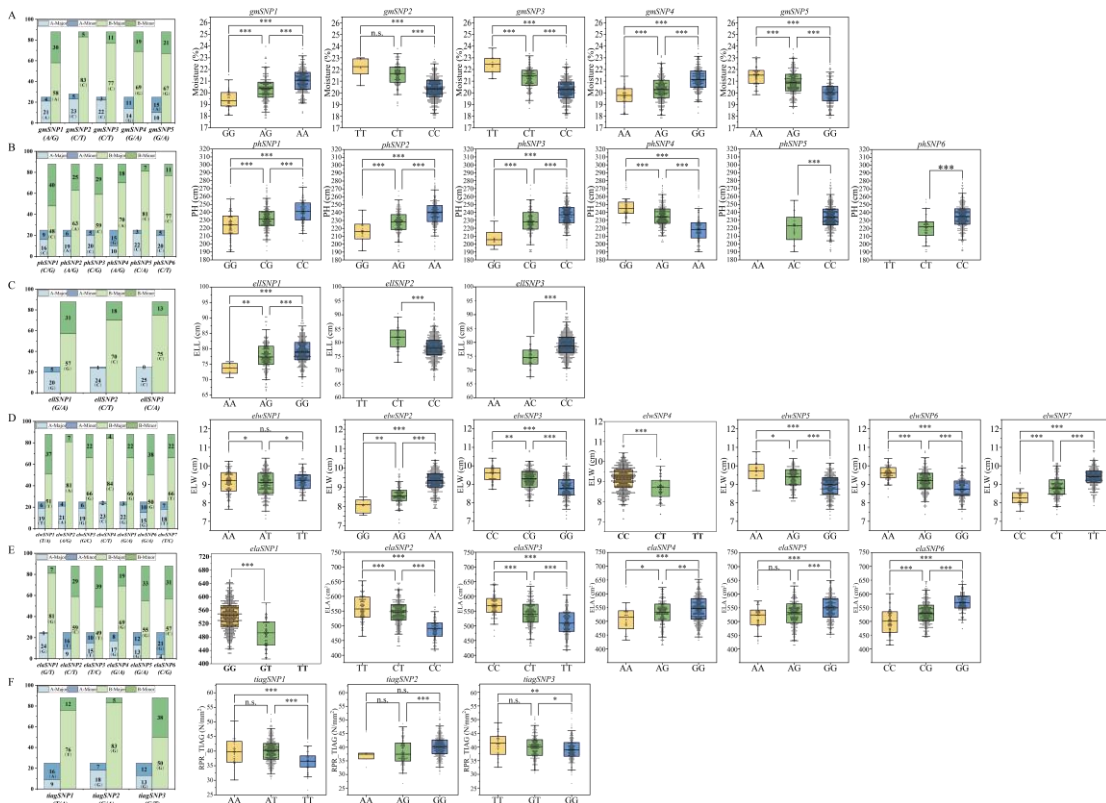
**Figure S1. Genetic profile of 113 inbred lines using 19,461 SNPs.** (A) Density distribution of SNPs across different Chromosomes; (B) Neighbor joining tree based on the genetic distances among 113 lines genotyped by 19,461 SNP markers.; (C) Descriptive statistical indicators of the 19,461 SNPs in the 113 parental materials; (D) Linkage disequilibrium (LD) decay in the parental population.



**Figure S2. Phenotypic variation explained in ten traits by positive QTNs detected from models KinA (A) and KinADE (B).** Add: Additive effect, Dom: dominance effect, AA: epistatic effect of Additive-by-Additive, AD: epistatic effect of Additive-by-dominance, DA: epistatic effect of dominance -by- Additive, DD: epistatic effect of dominance-by-dominance.

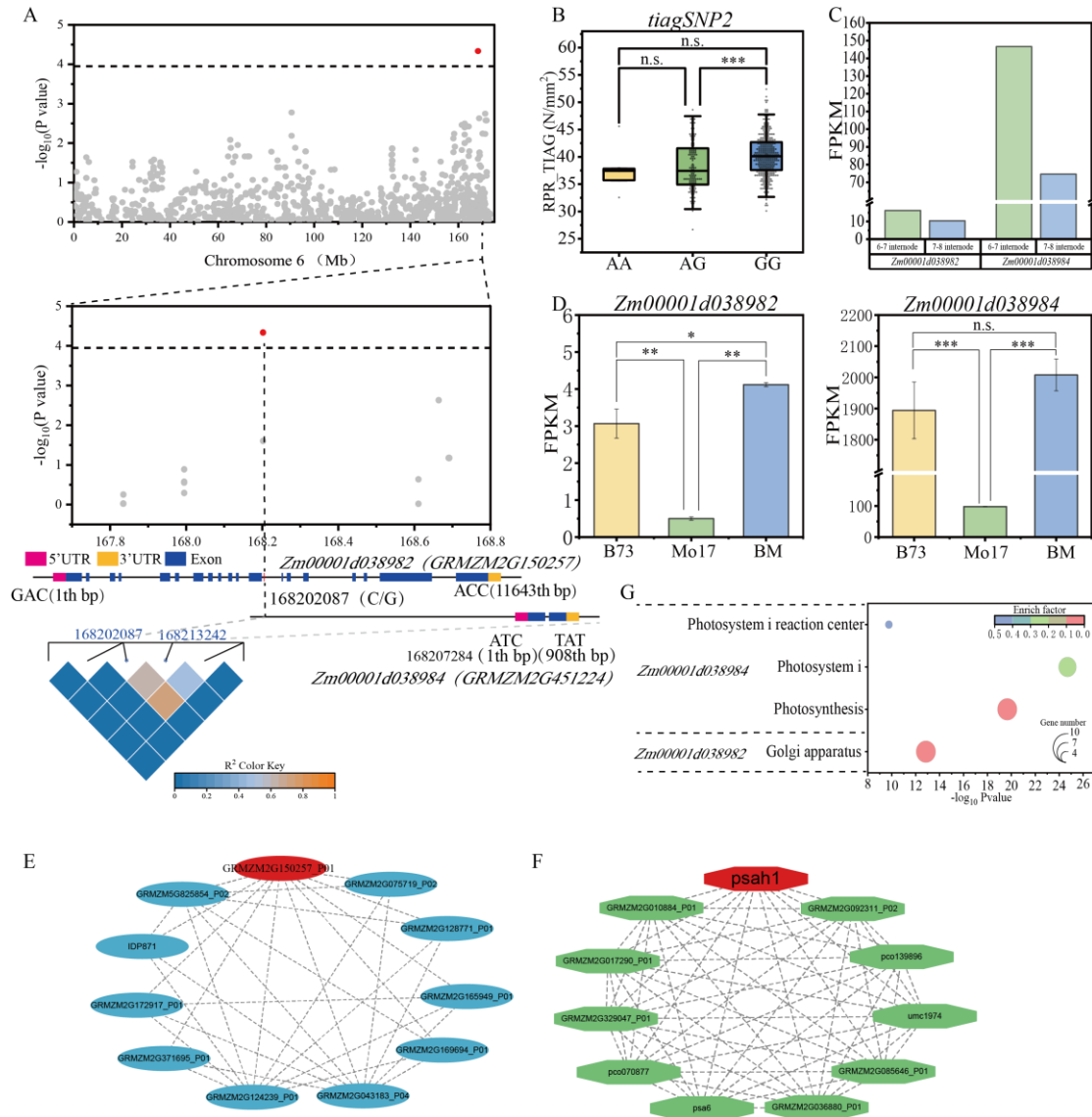


**Figure S3.** Comparison of estimates of the PVE for ten traits between Model KinA and KinADE based on cross validation.

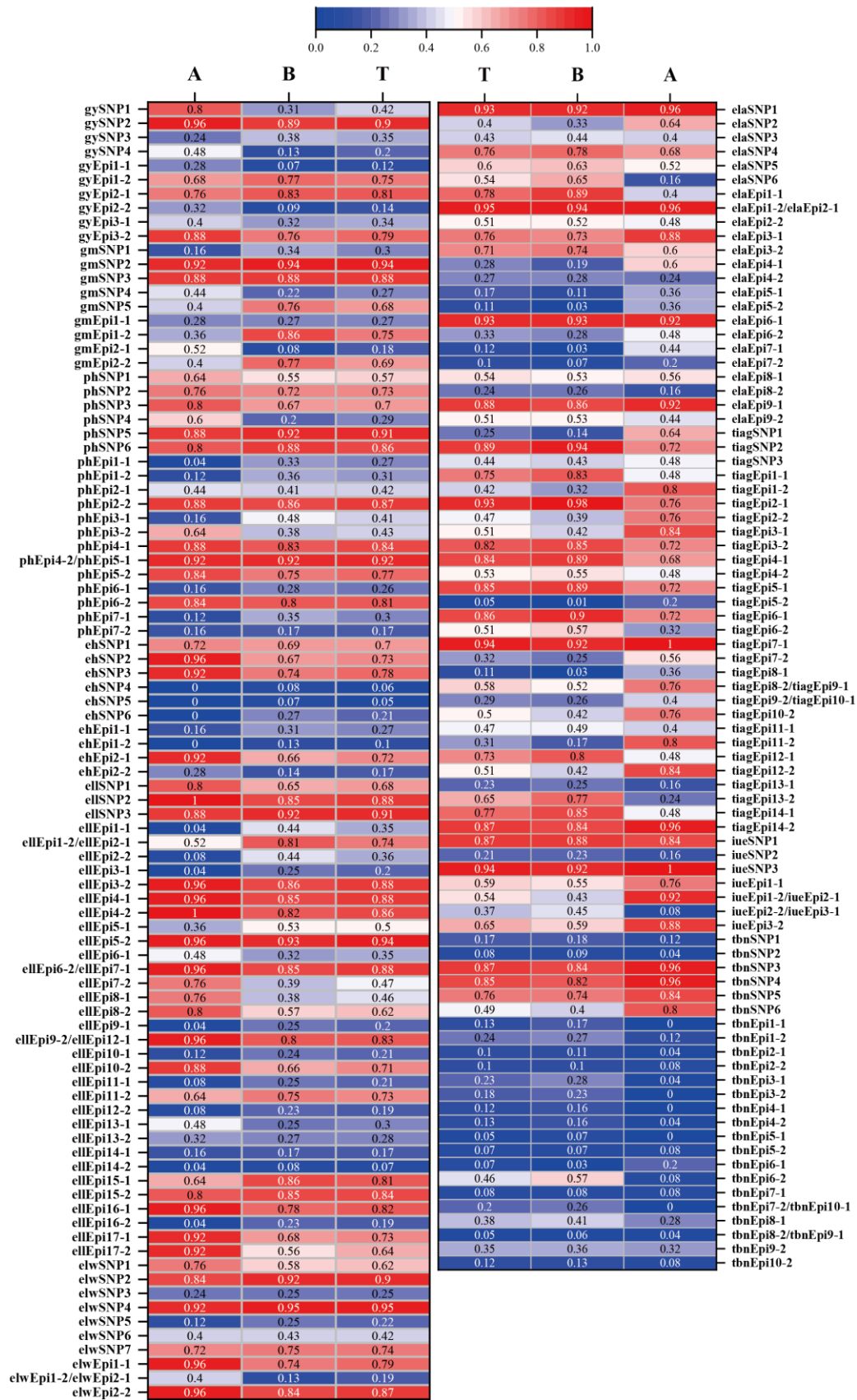


**Figure S4.** Allele frequency and phenotypic information of different genotypes of each main effect QTN for GM (A), PH (B), ELL (C), ELW (D), ELA (E) and RPR\_TIAG (F). A-

Major and A-Minor means the globe major and globe minor allele distribution within Shaan A group; B-Major and B-Minor means the globe major and globe minor allele distribution within Shaan B group. \*, \*\*, and \*\*\* means significant at  $P \leq 0.05$ ,  $P \leq 0.01$ , and  $p \leq 0.001$ , respectively.



**Figure S5. Multi-omic identification of candidate genes *Zm00001d038982* and *Zm00001d038984*.** (A) Structure and mutation sites of the RPR\_TIAG-related genes *Zm00001d038982* and *Zm00001d038984* on chromosome 6; (B) Phenotypic level of different genotypes in the hybrid population. \*\* and \*\*\* mean significance levels at 0.01 and 0.001, respectively; (C) Transcription level of gene *Zm00001d038982* and *Zm00001d038984* on 6-8 internode in B73; (D) Transcription level of gene *Zm00001d038982* and *Zm00001d038984* at seedling stage in two inbred lines and their hybrid; (E,F) Protein-protein interaction network of candidate genes *Zm00001d038982* (E) and *Zm00001d038984* (F), Red indicates the protein encoded by the candidate gene; (G) Biological functions of candidate genes and the interaction networks.



**Figure S6.** Enrichment degree of favorable genotypes of QTNs detected by model KinADE within ShaanA (A), ShaanB (B), and Total (T) population.

