Figure S1

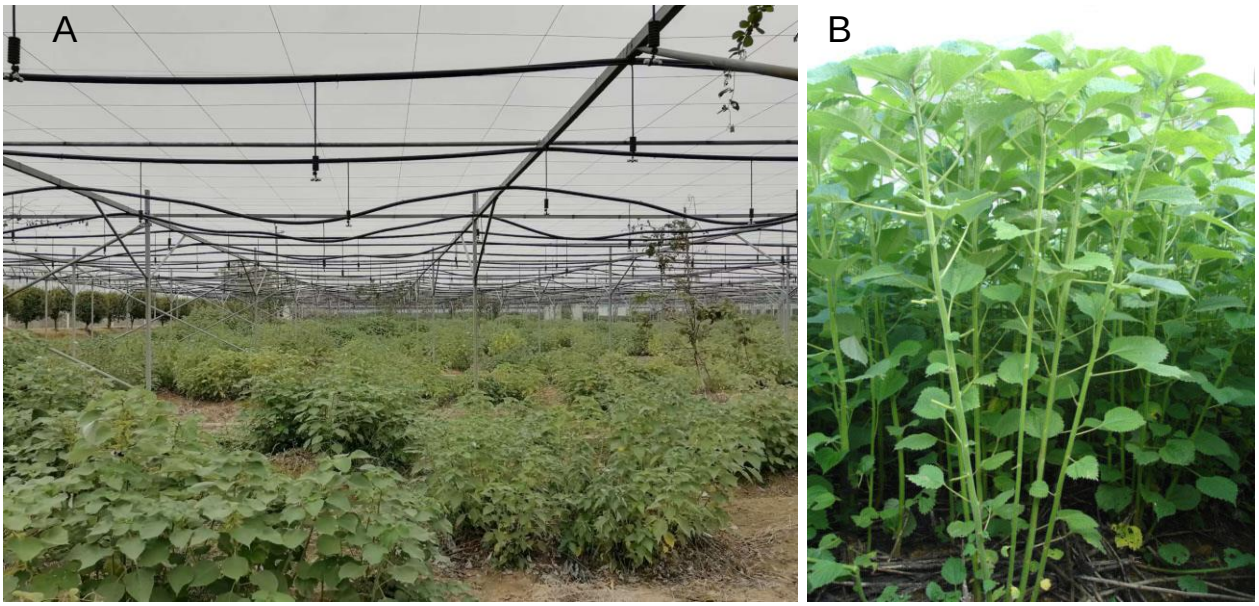
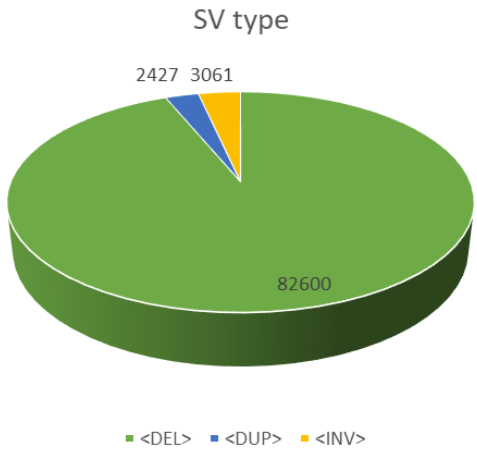


Figure S1. Photos of ramie in germplasm pool and field. (A) Patronal ramie accessions used in this study. **(B)** Presentative ramie cultivar as reference genome and one of parent planted in field.

Figure S2

A



B

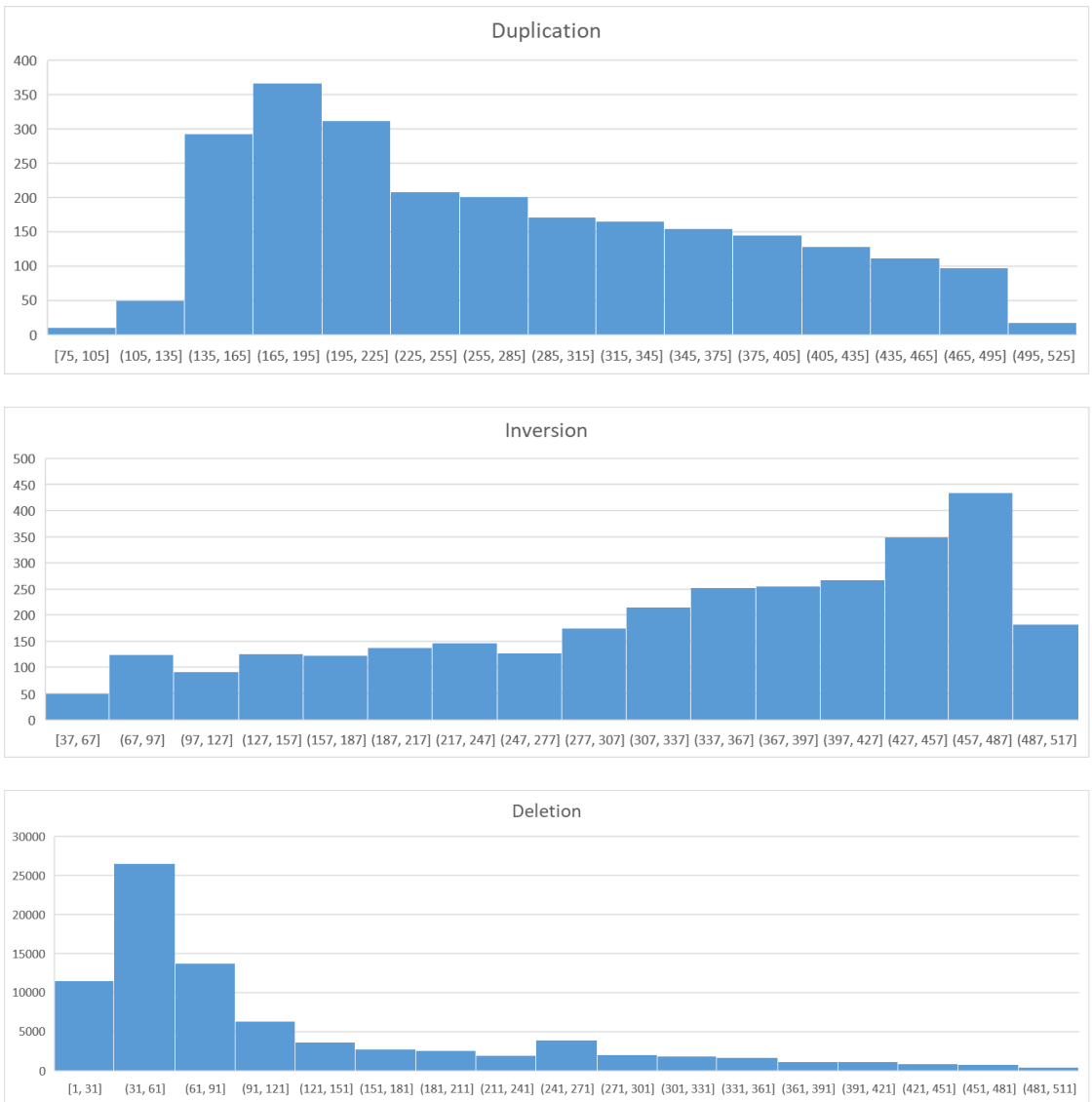


Figure S2. Statistics of structure variation (SV) in genome identified by Lumpy. (A) Ratio of three SV type. **(B)** Length distribution of three SV. DEL: deletion; DUP: duplication; INV: inversion.

Figure S3

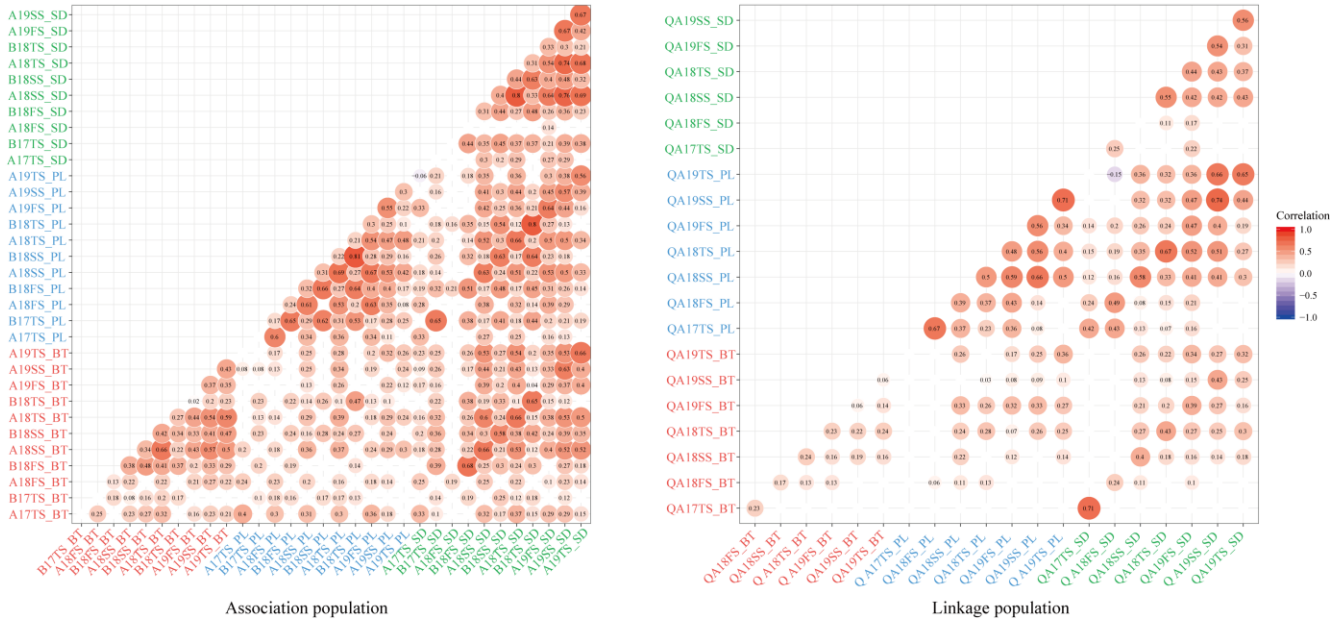
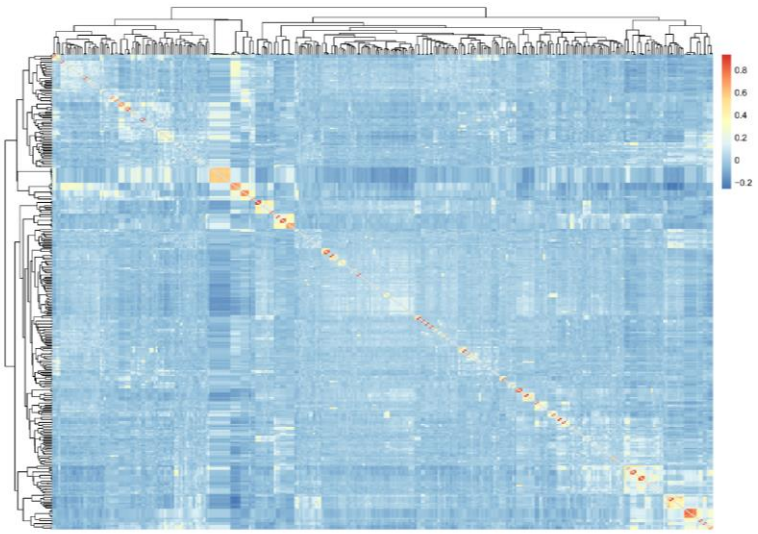


Figure S3. Correlation relationship of phenotypic data between three yield traits within population. Heatmaps of correlation coefficients between yield traits in association mapping population (left) and the linkage mapping population(right) planted in different environments. Red color of ball with marked correlation coefficient represents positive correlation and purple color indicate negative correlation. Significant correlation($p<0.05$) observed between the given traits were filtered in the picture. FD: fiber diameter; FF**:** fiber fineness; RN: ramet number; BT: bark thickness; PL: plant length; SD: stem diameter. Ramie was collected in the years from 2017 to 2018, divided into three times including FS (first season), SS (second season) and TS (third season).

Figure S4

A



B

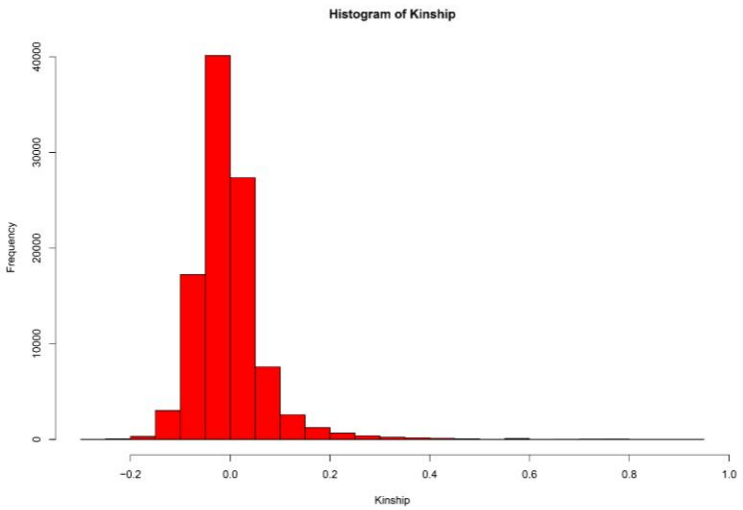
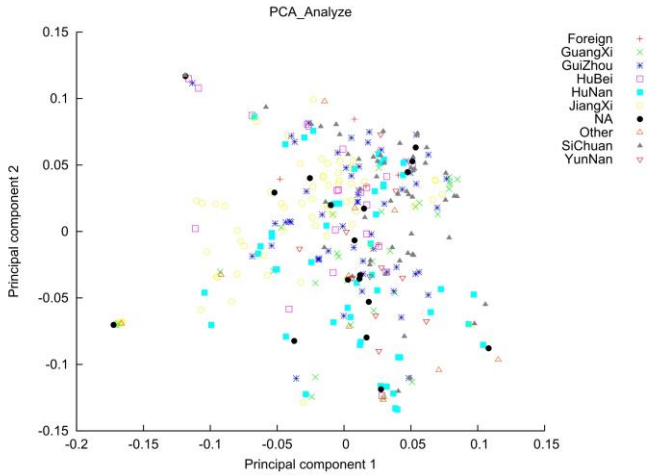


Figure S4. Kinship of individuals in association mapping population. (A) Kinship matrix of 319 accessions. **(B**) Histogram of kinship relationship.

Figure S5

A



B

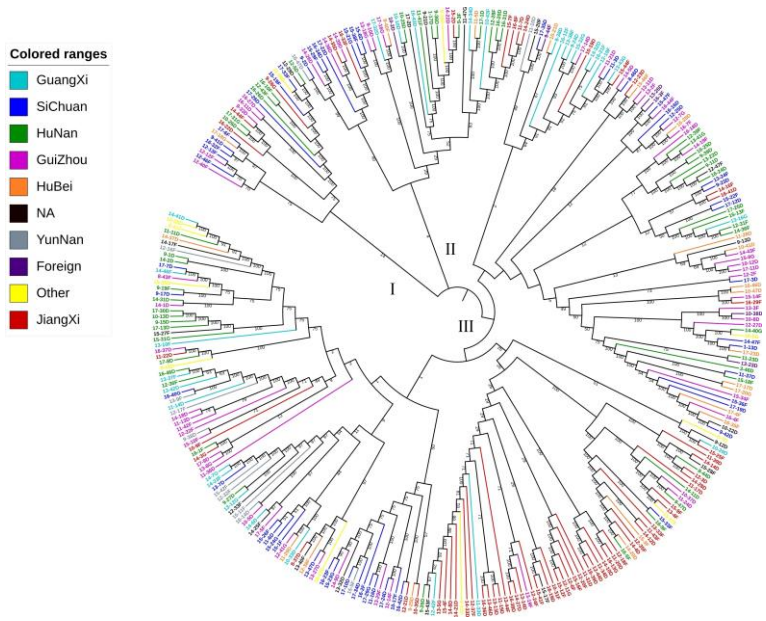


Figure S5. Correlation relationship of phenotypic data between three yield traits within population. (A) PCA analysis of 319 ramie accessions. **(B)** Phylogenetic tree of 319 accessions.

Figure S6

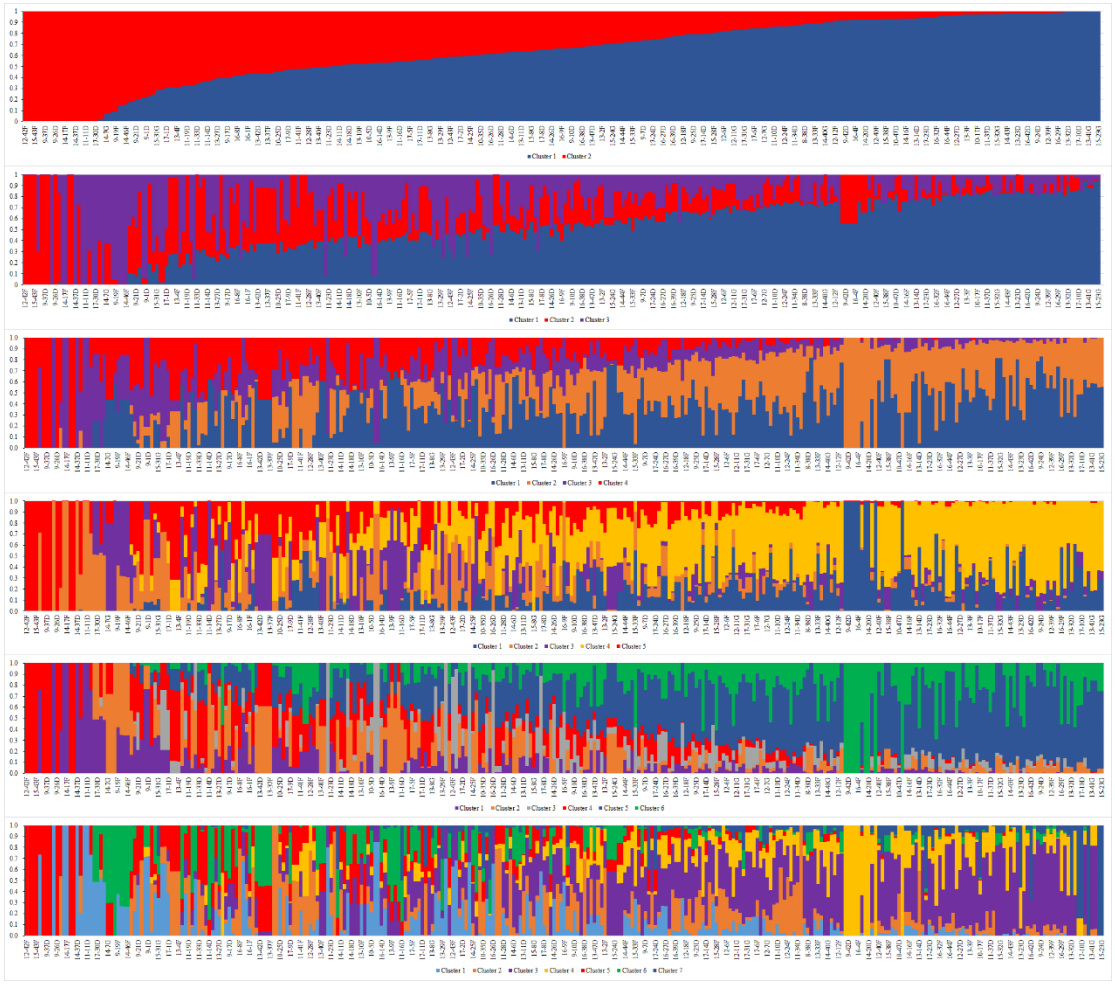


Figure S6. Population structure inferred by FRAPPE software. From up to down was K=2 (top) to 7 (bottom). The y axis quantifies cluster membership, and the x axis represents the different accessions.

Figure S7

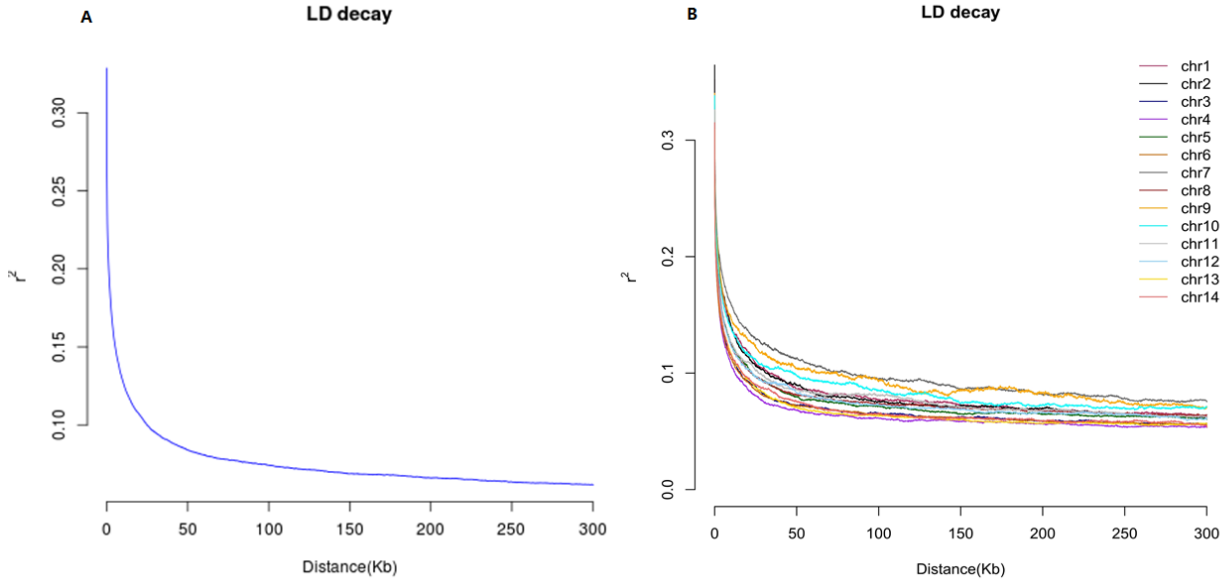
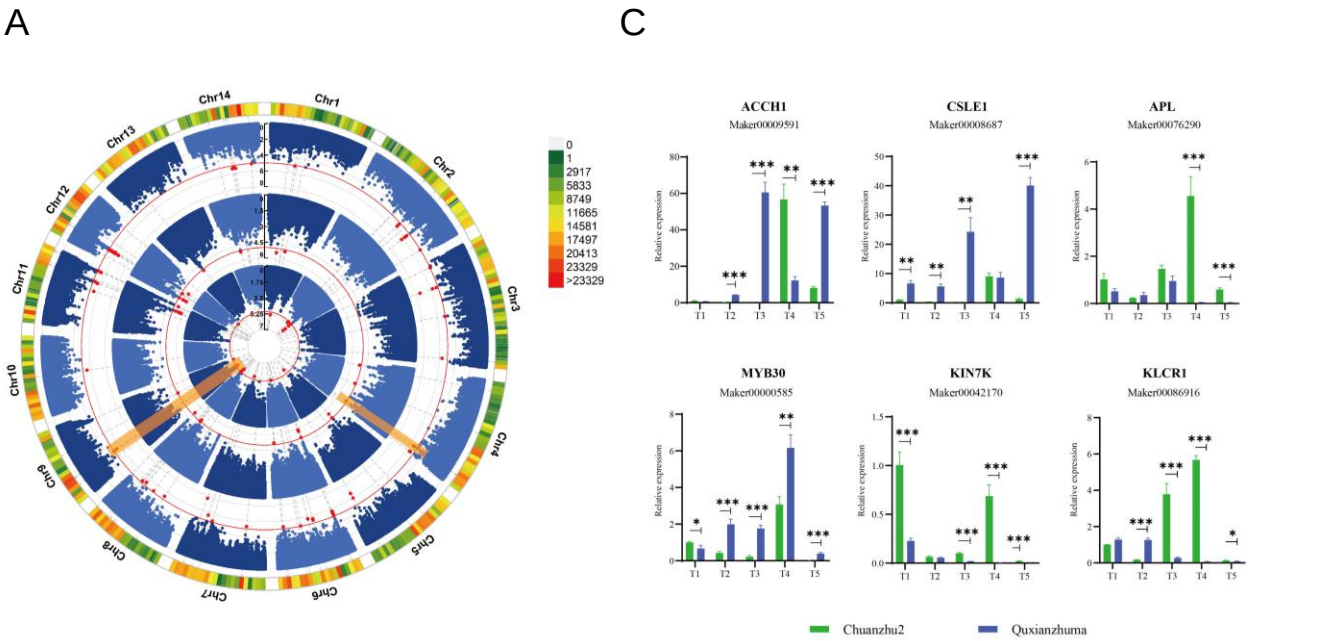


Figure S7. LD decay curve of whole genome (left) and LD decay curve of each chromosome (right).

Figure S8



B

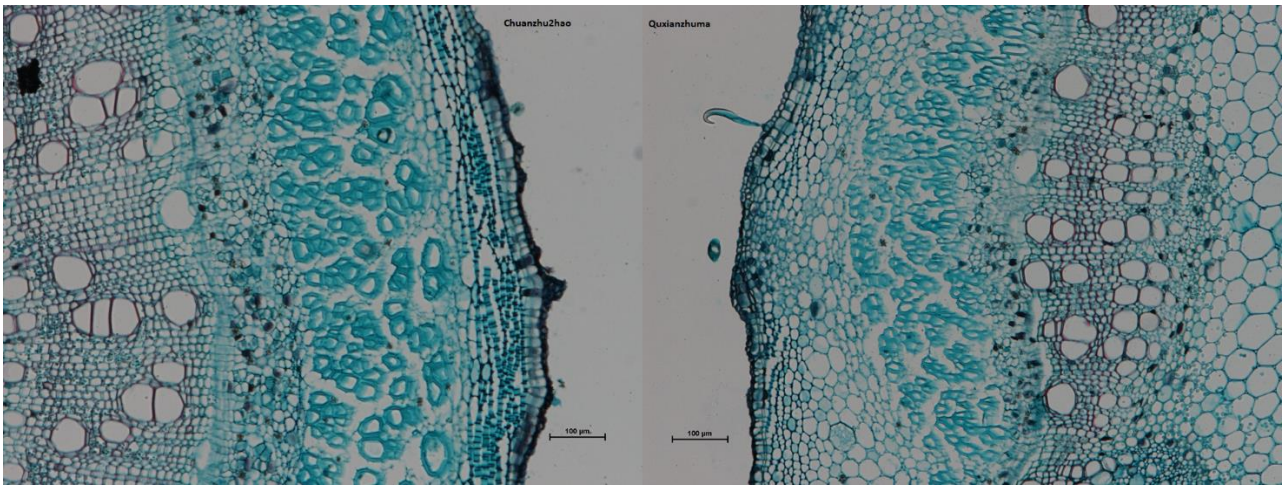


Figure S8. GWAS analysis and candidate genes associated with fiber fineness. (A) GWAS results of fiber fineness on three environments. P was set at 1×10^{-5}. **(B)** Paraffin section of two compared accessions, Chuangzhu2 (left) and Quxianzhuma (right). Scale: 100 μm. **(C)** qRT-PCR results of six candidate genes in two representative accessions. Significance marks '*', '**' and '***' indicated the t-test *P* lower than 0.01, 0.001 and 0.0001, respectively.

Figure S9

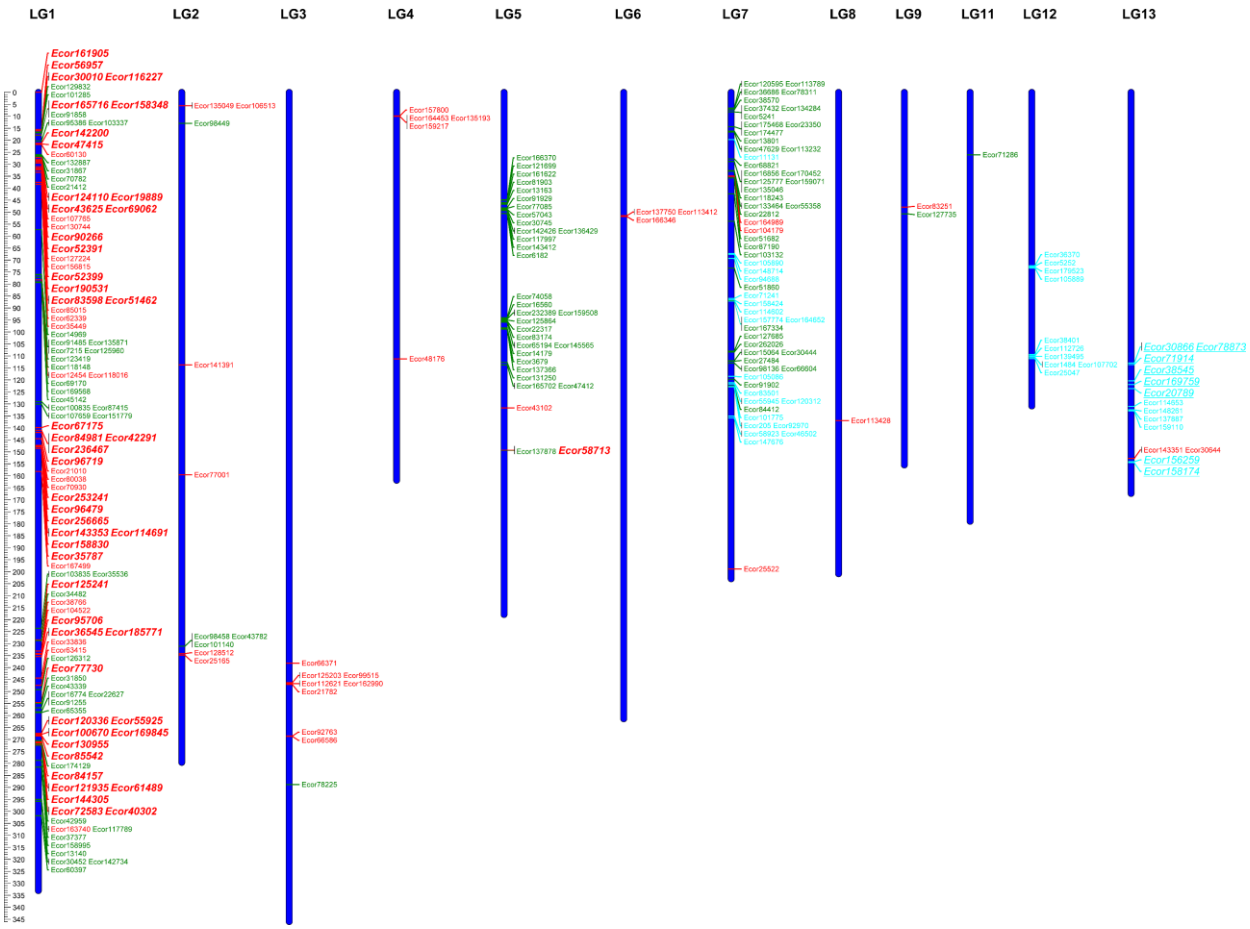


Figure S9. Linkage mapping of loci for three yield traits. Total 288 loci were showed on the 12 linkage groups (LG). Red color marks PL loci, green color representing SD loci and blue representing BT loci. Loci with red capital font indicates pleiotropic loci for PL &SD. Those pleiotropic loci for BT & SD were painted blue and underlined.

Figure S10

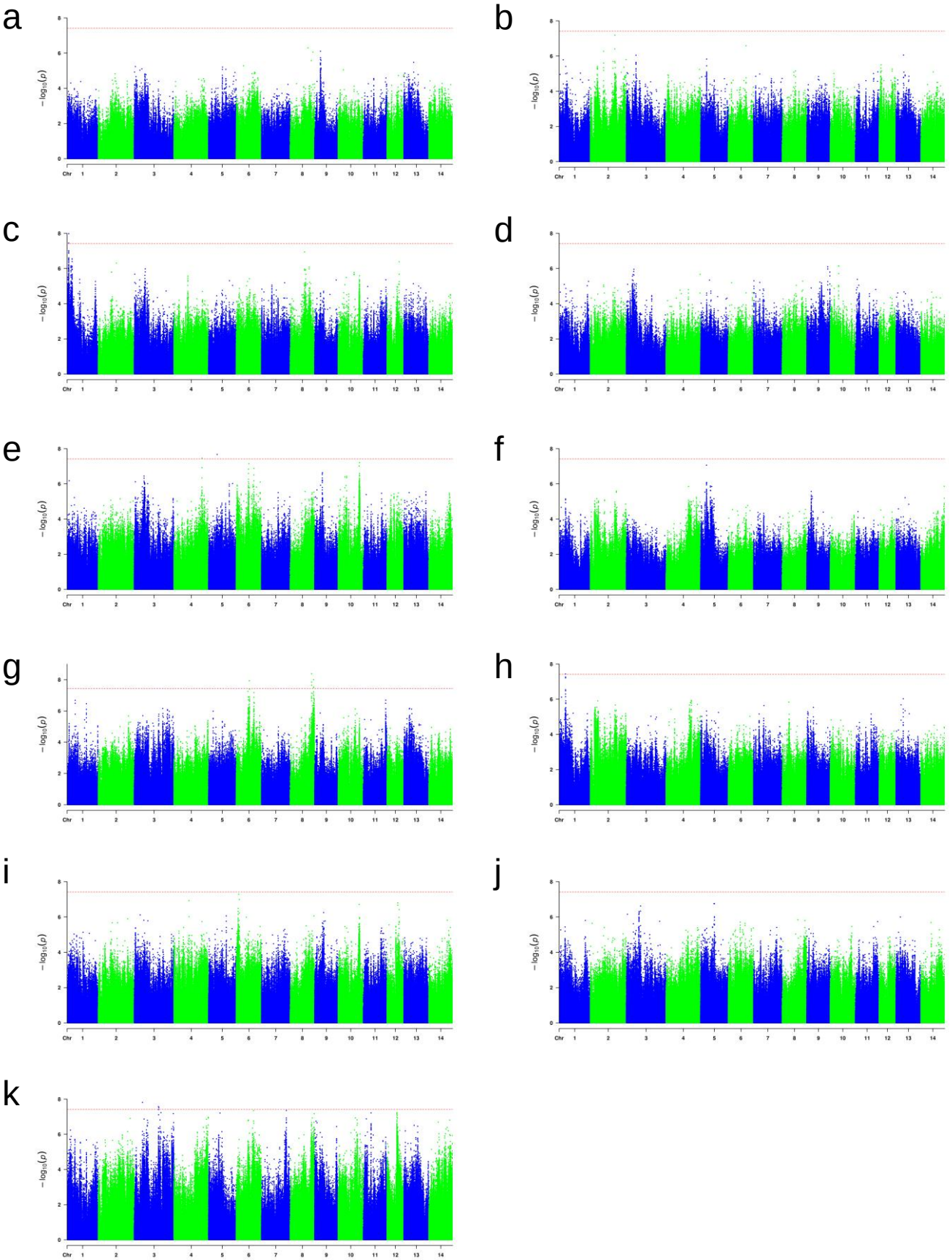


Figure S10. Manhattan plots of SNP -GWAS analysis on plant length. a-f indicated GWAS results on the environments of A17TS, B17TS, A18FS, B18FS, A18SS, B18SS, A18TS, B18TS, A19FS, A19SS and A19TS.

Figure S11

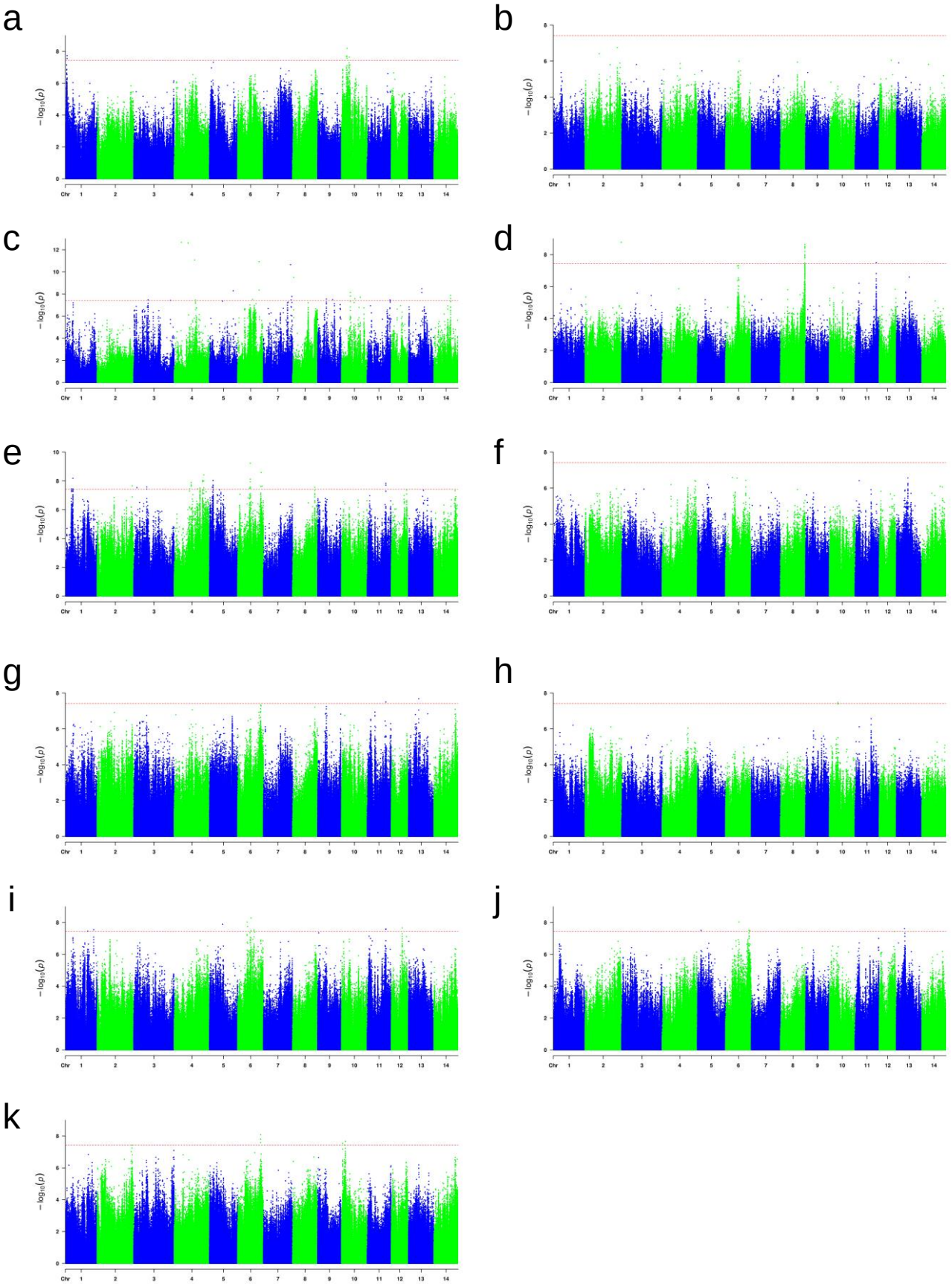


Figure S11. Manhattan plots of SNP-GWAS analysis on stem diameter. a-f indicated GWAS results on the environments of A17TS, B17TS, A18FS, B18FS, A18SS, B18SS, A18TS, B18TS, A19FS, A19SS and A19TS.

Figure S12

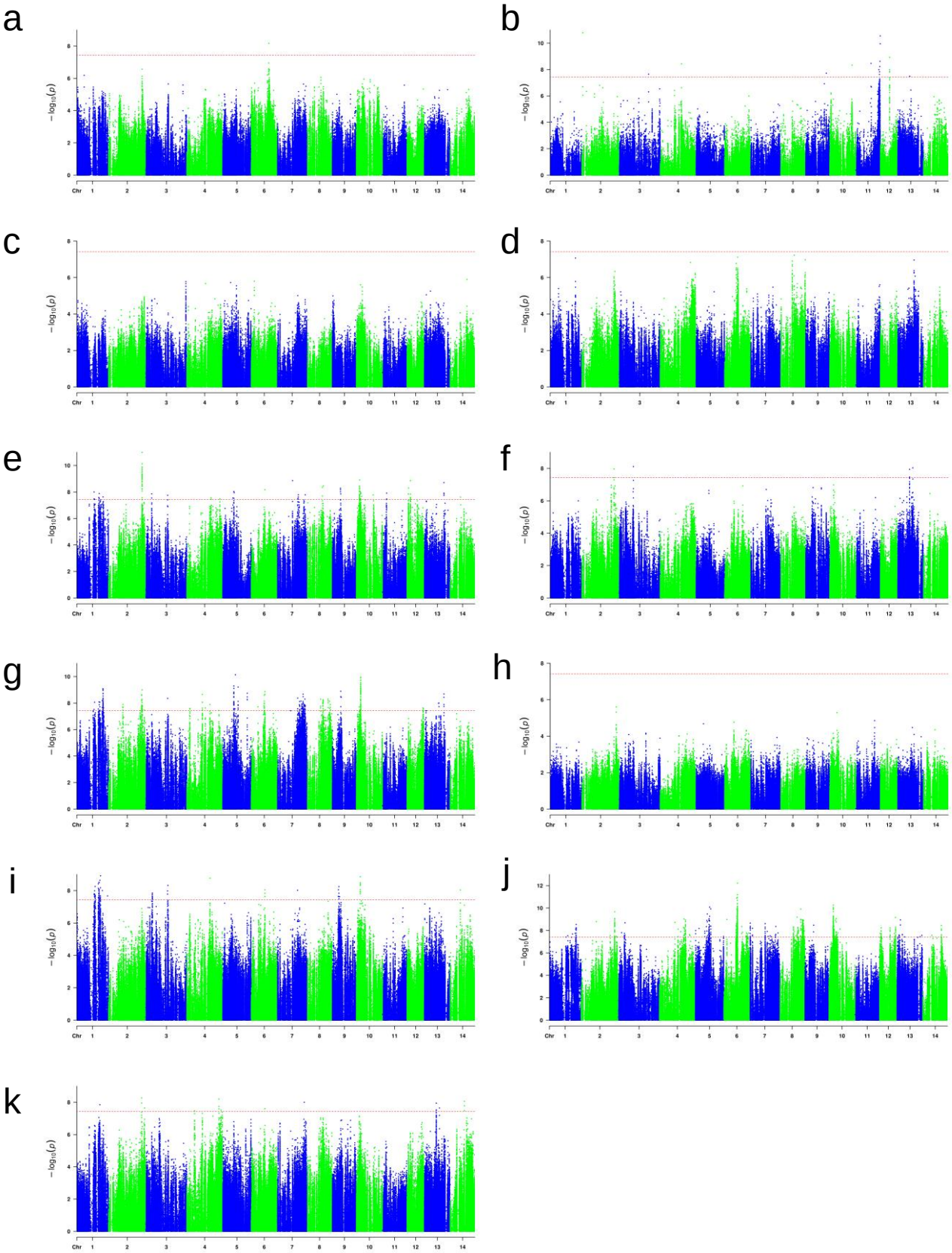


Figure S12. Manhattan plots of SNP-GWAS analysis on bark thickness. a-f indicated GWAS results on the environments of A17TS, B17TS, A18FS, B18FS, A18SS, B18SS, A18TS, B18TS, A19FS, A19SS and A19TS,

Figure S13

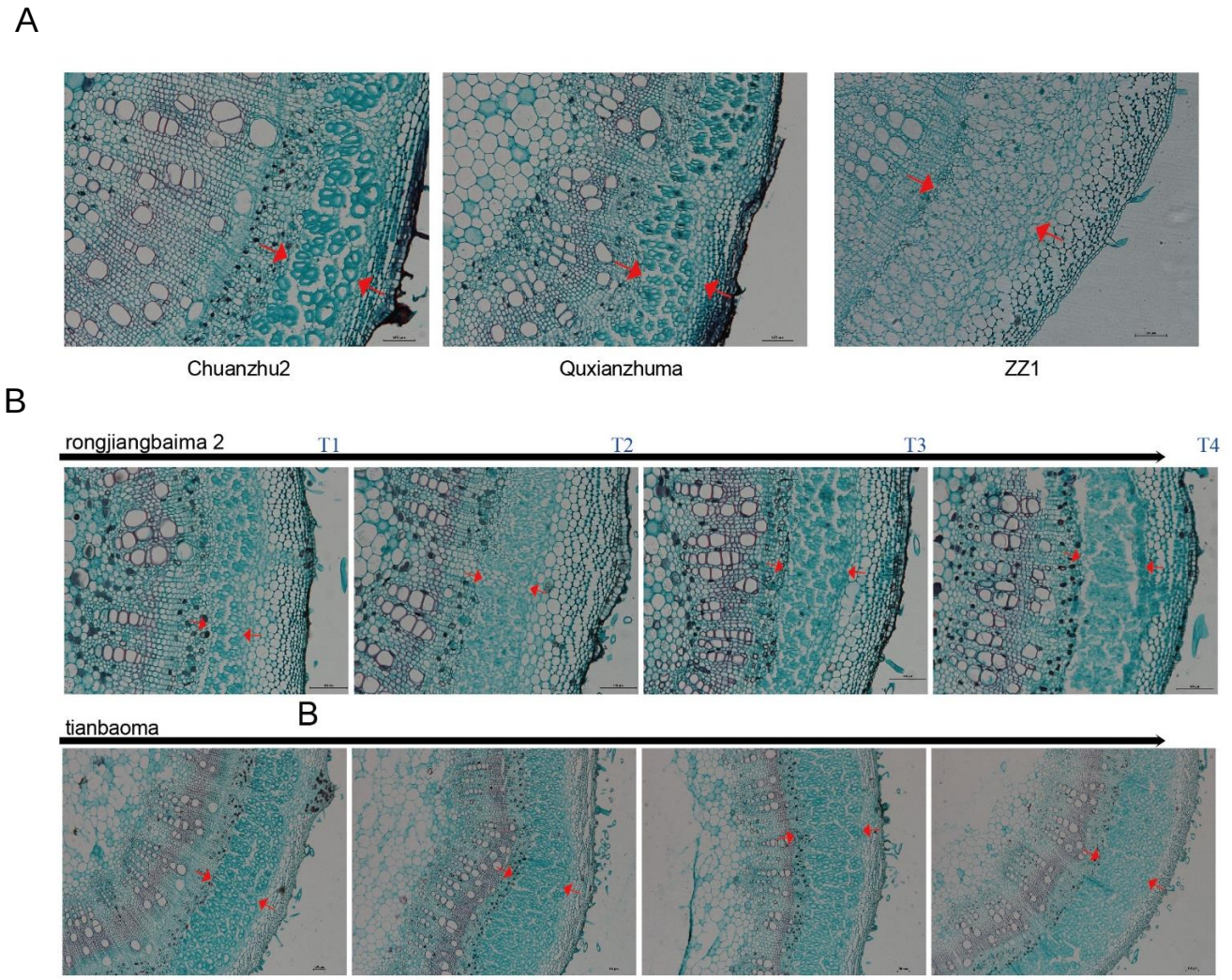


Figure S13. Morphological features of stem from five species. Red arrow indicated the region of phloem fiber. (**A**) Paraffin section of two landraces and representative cultivar Zhongzhu 1 (ZZ1). **(B)** Paraffin section of rongjiangbaima 2 (low thickness) and tianbaoma (high thickness) collected from four developmental stages.

Figure S14

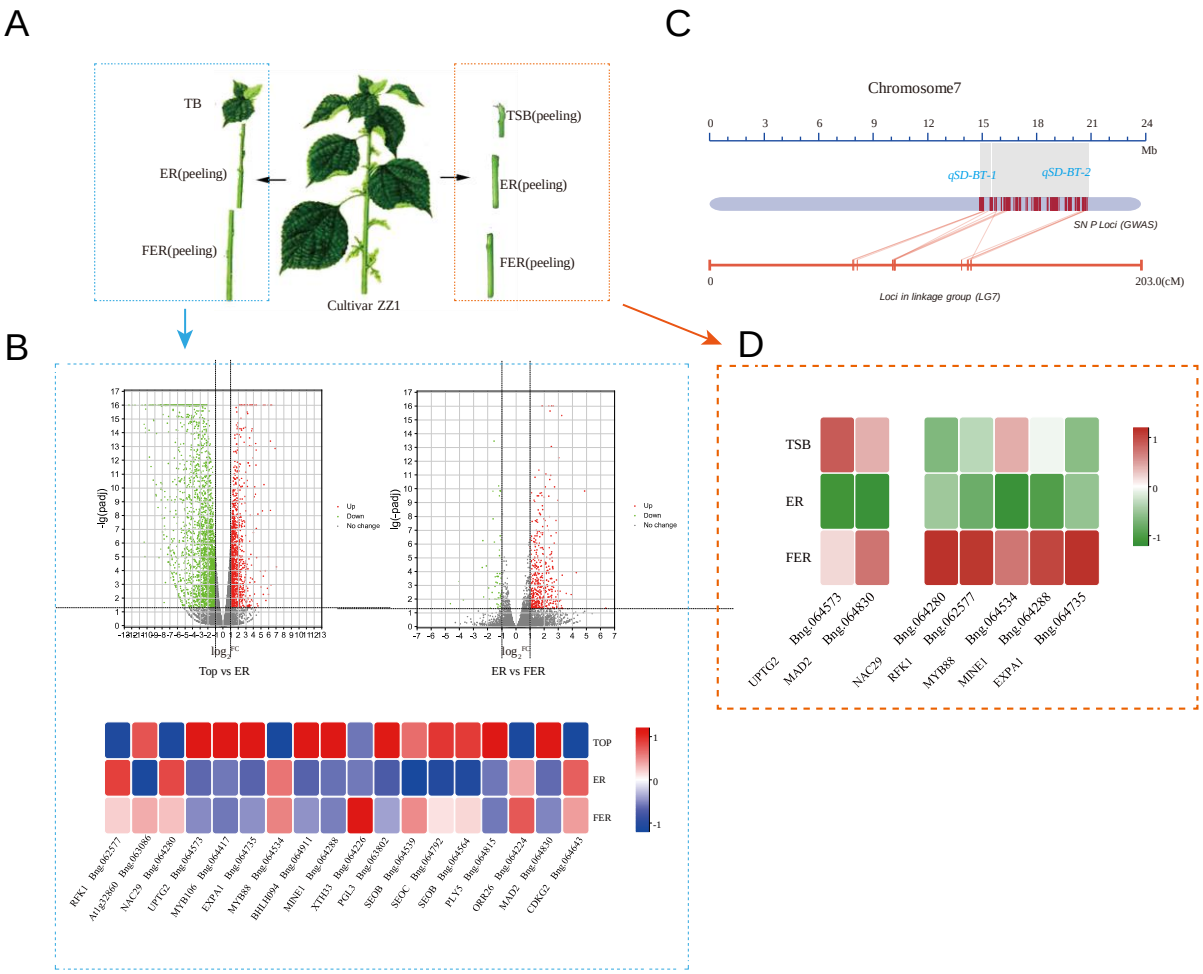


Figure S14. Expression analysis of candidate genes associated with bark thickness. (A) Schematic diagram of sampling position in cultivar Zhongzhu 1. TB: top bud; TSB: top stem bark; ER: elongating region; FER: fully elongated region. **(B)** RNA-seq results and identified DEGs of candidate genes. FPKM in heatmap was scaled at column level with the function: $\log_2$(FPKM+1). **(C)** Colocalization of two loci associated with bark thickness and stem diameter using genetic map and physical map. **(D)** qRT-PCR identification of candidate genes.

Figure S15

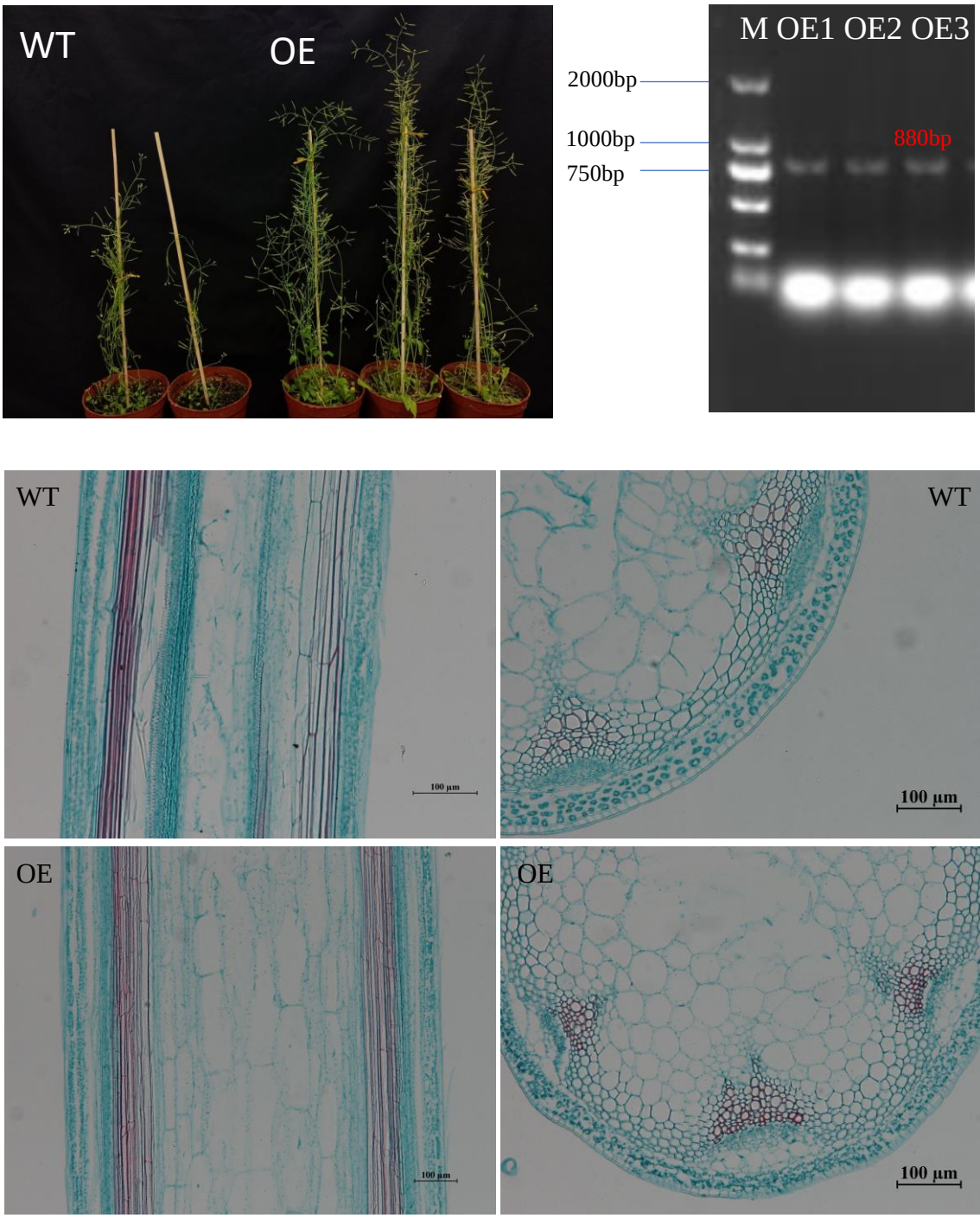


Figure S15. Morphological features of stem from wild and transgenic Arabidopsis. WT: wild type of *Arabidopsis thaliana*; OE: overexpressed gene line.

Figure S16

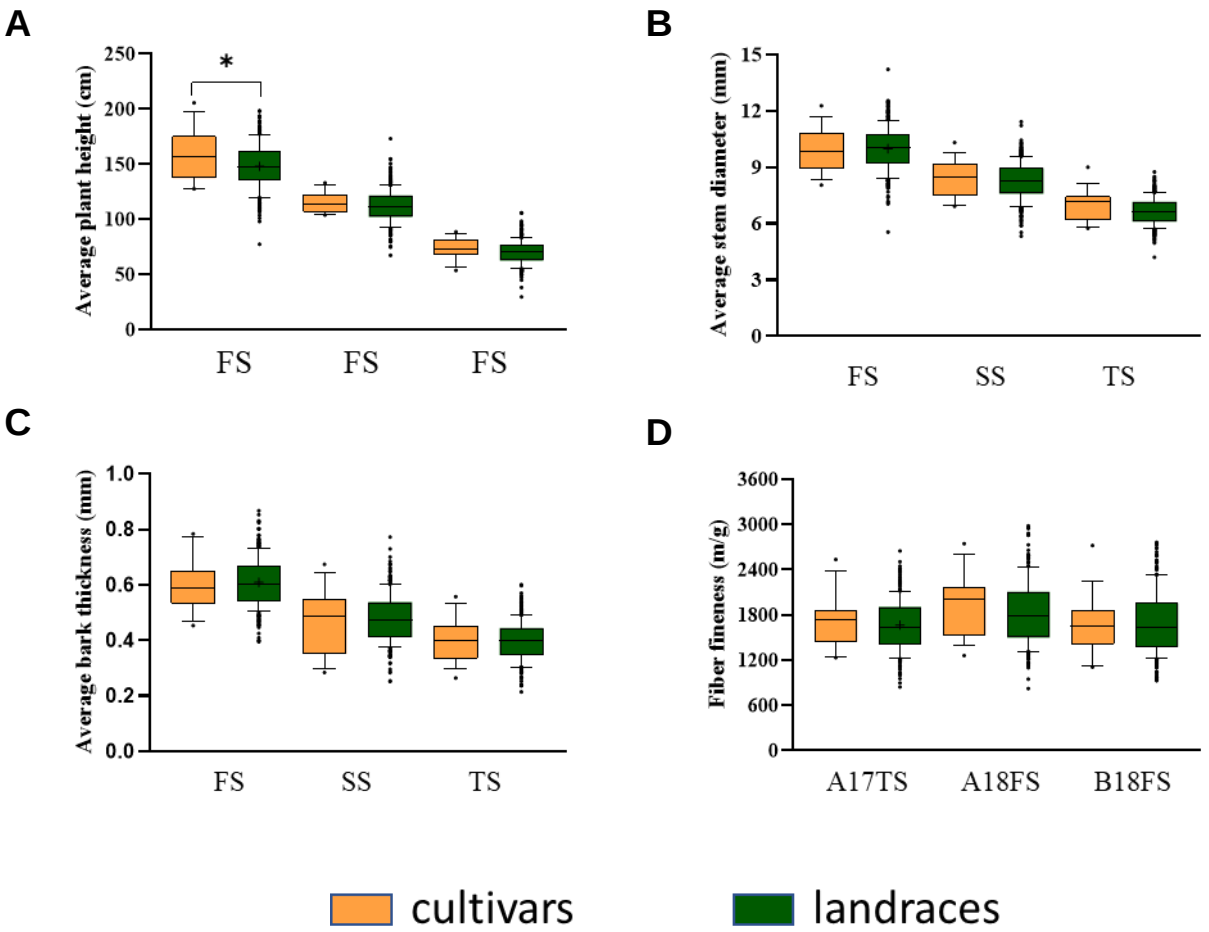


Figure S16. Properties evaluations between cultivars and landraces. (A-D) exhibited the comparison of average value of plant height, stem diameter, bark thickness and fiber fineness. '*' indicated the significance lower than 0.05.

Figure S17

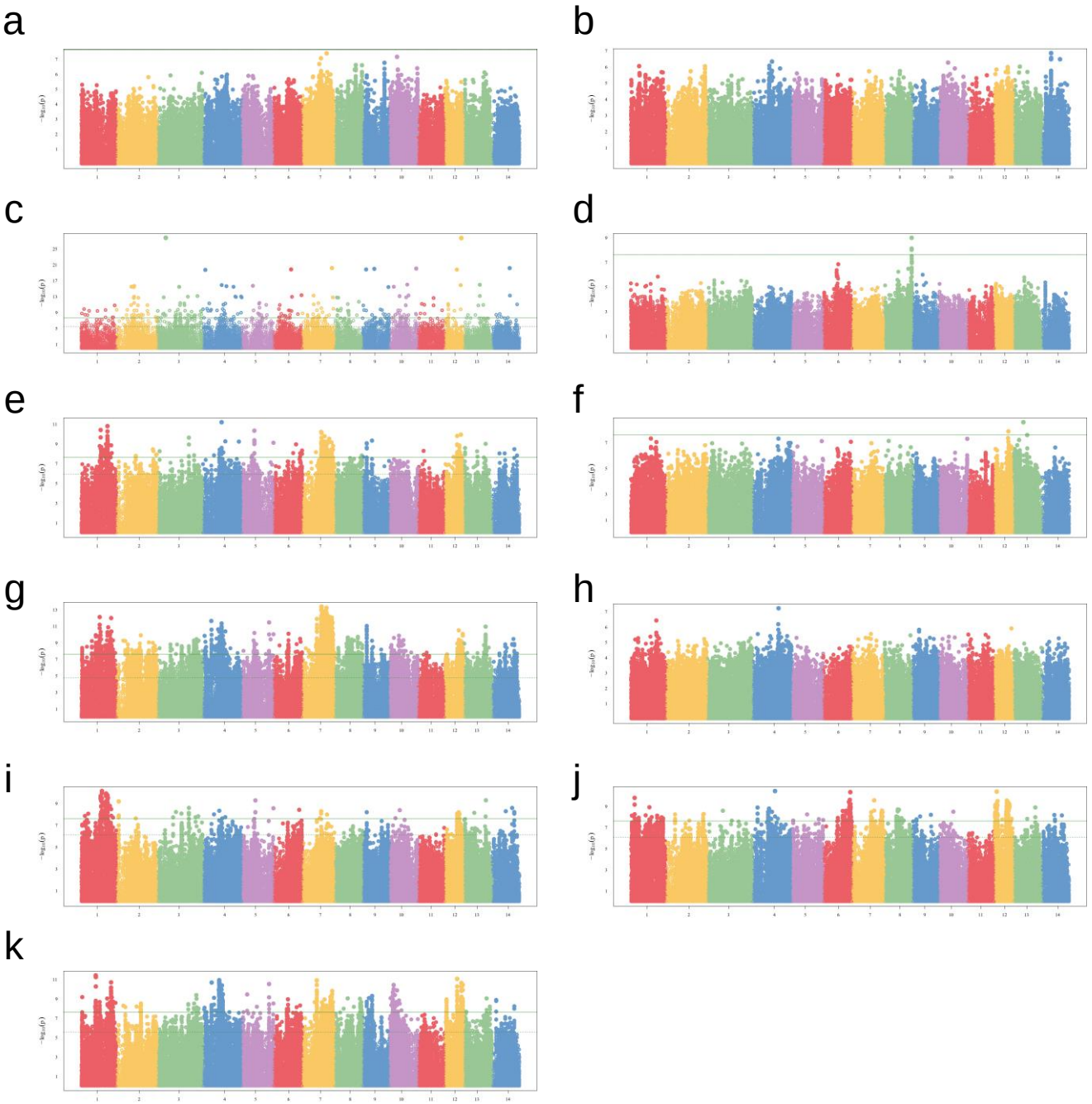


Figure S17. Manhattan plots of Indel-GWAS analysis on stem diameter. a-f indicated GWAS results on the environments of A17TS, B17TS, A18FS, B18FS, A18SS, B18SS, A18TS, B18TS, A19FS, A19SS and A19TS.

Figure S18

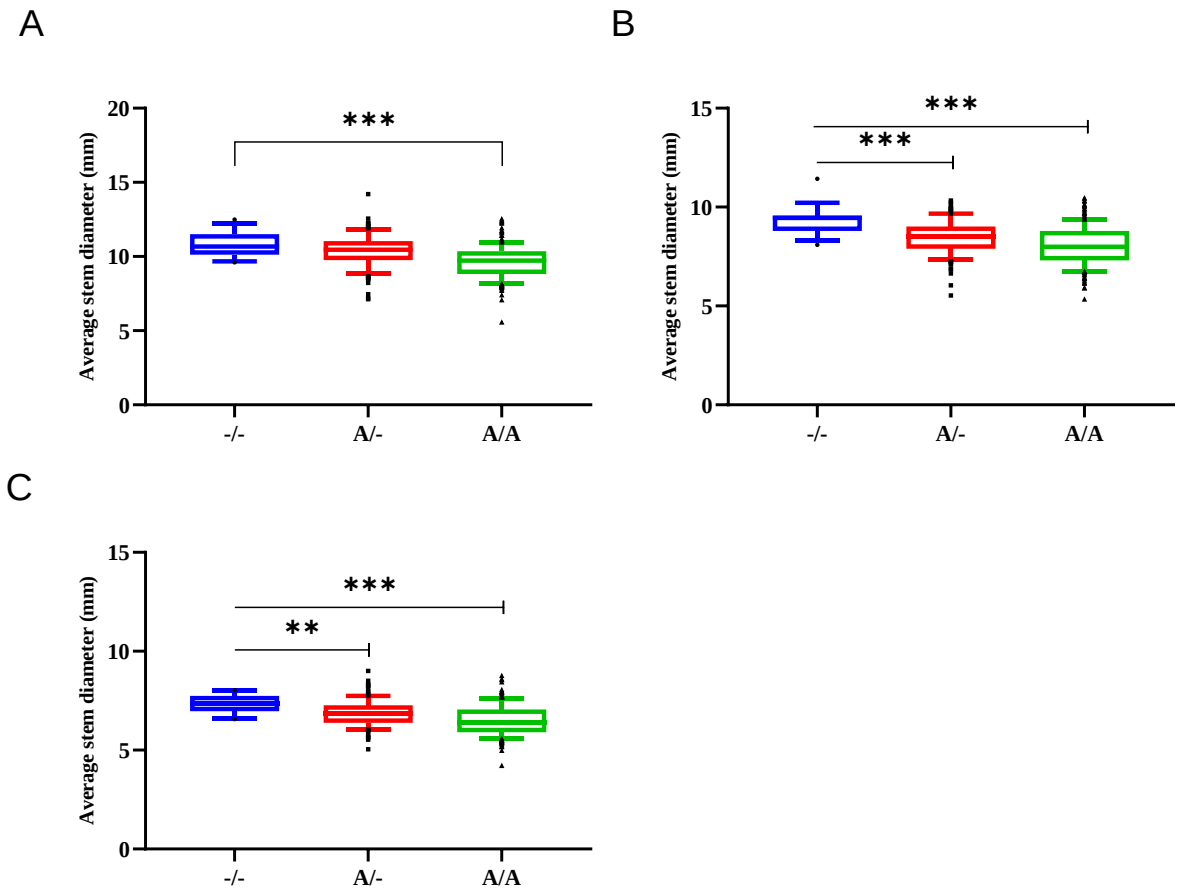


Figure S18. Genotype of Indels in *VIT1* gene associated with stem diameter. (A-C) indicated the t-test results of haplotypes in FS, SS and TS. '* *': P < 0.01, '***':P < 0.001.

Figure S19

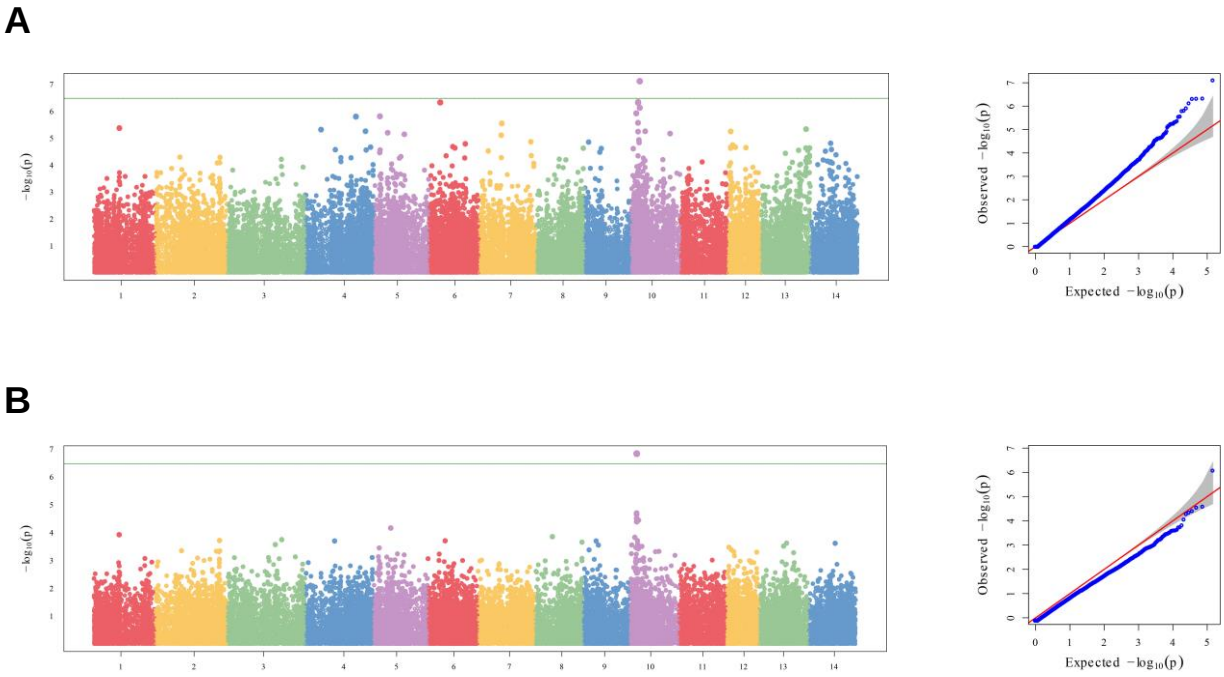


Figure S19. Manhattan plots and QQ-plots of SVs-GWAS analysis on bark thickness. (A) GWAS analysis results on bark thickness (A18SS) using general liner model (CLM) model. **(B)** GWAS results on bark thickness (A18SS) using mixed liner model (MLM) model. The threshold in Manhattan plots were set as 4.76×10^{-8} by default plotting parameter in GAPIT.