

Supporting Information

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Fig. S1 Correlation between manual measurement and image-based measurement in trait of plant height and biomass.

Fig. S2 Correlation analysis for morphological and texture i-traits in two years, respectively.

Fig. S3 Coefficient of variation (CV) among 200 accessions for three sets of at seedling stage.

Fig. S4 T-test between treatment and control panels at seedling stage.

Fig. S5 Three sub-groups i-traits of 200 upland accessions.

Fig. S6 Structure analysis of 200 upland cotton accessions.

Fig. S7 GWAS results by morphological and texture i-traits.

Fig. S8 Linkage disequilibrium (LD) decay distance at whole genome level.

Fig. S9 Distribution of QTLs associated with morphological traits in 26 chromosomes in cotton.

Fig. S10 VIGS of *GhDNRs* (*TRV:GhDNRs*) in drought-resistant accession ZY168 under drought stress.

Table S1 Cotton resources information and resequencing information used in this study.

Table S2 ANOVA for morphological traits across years in 2015 and 2017.

Table S3 Correlation analysis of morphological traits over two years.

Table S4 Variants rate details.

Table S5 Information of associated loci.

Table S6 DEGs in two cotton accessions under drought stress.

Table S7 QTLs with DEGs in four i-traits.

Table S8 Date of two-year seedling experiment of cotton.

Table S9 List primers used in this study.

File S1 The image processing and i-traits extraction.

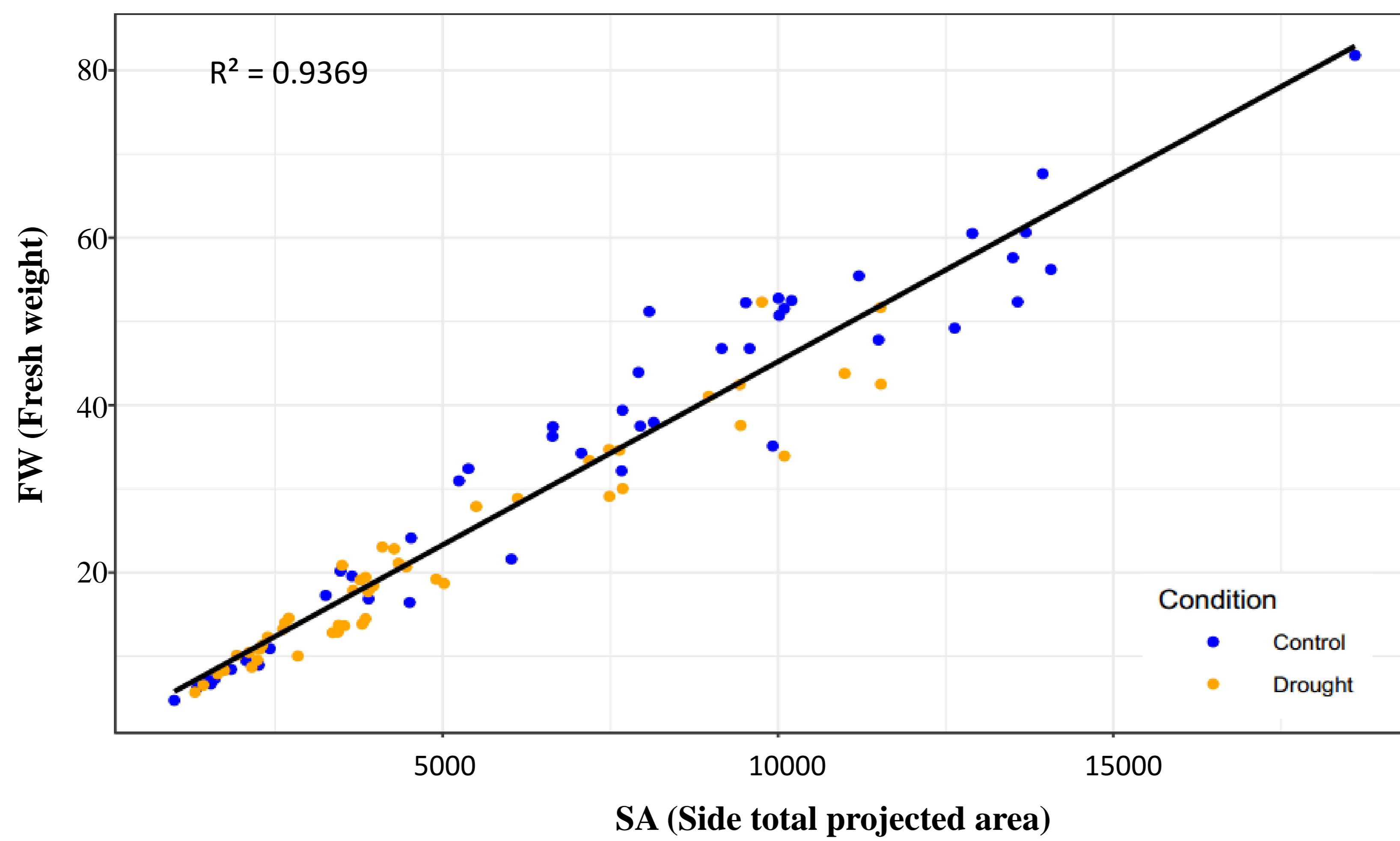
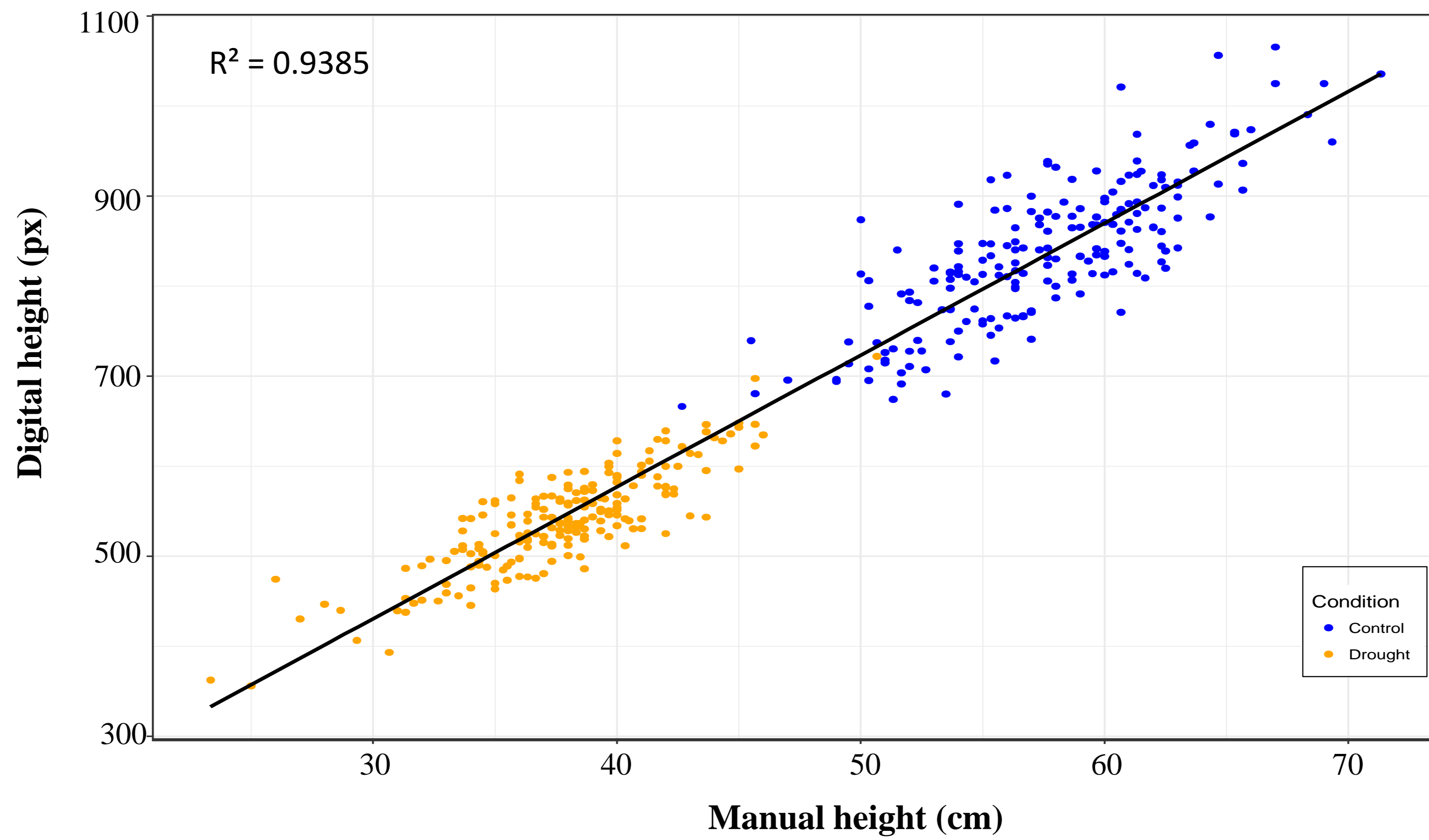


Fig. S1 Correlation between manual measurement and image-based measurement in trait of plant height and biomass. Blue and yellow dots stand for plants under control and drought condition, respectively.

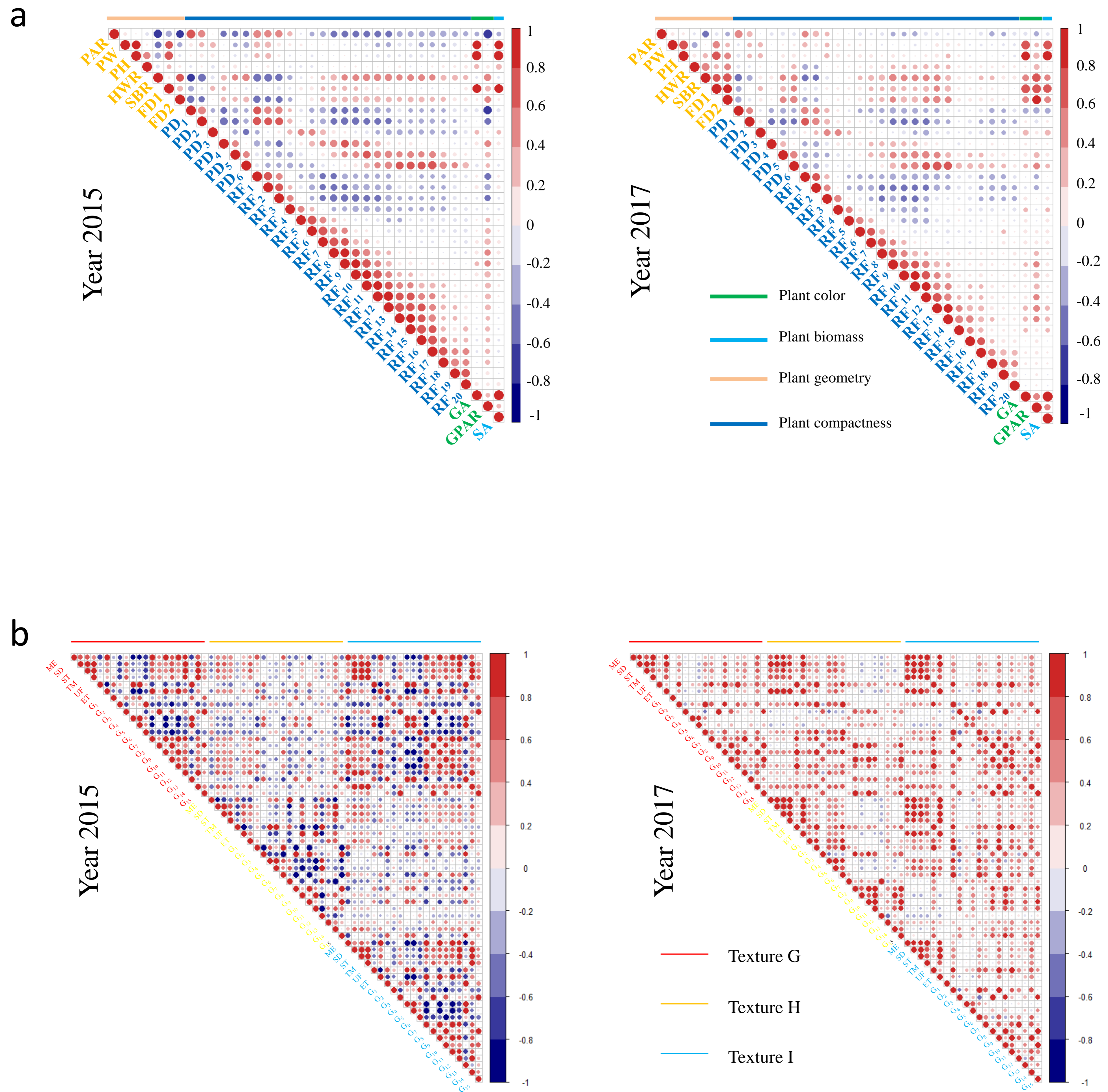


Fig. S2 Correlation analysis for morphological and texture i-traits in two years, respectively. **a** The correlation between morphological i-traits in year of 2015 and 2017. Morphological i-traits are divided in four categories: the green stands for plant color, light blue stands for plant biomass, yellow stands for plant geometry and dark blue stands for plant compactness. **b** The correlation between texture i-traits in year of 2015 and 2017. Texture i-traits are divided in three categories: the red stands for green (G), the yellow stands for hue (H), and blue stands for intensity (I). G_{1-15} was the abbreviation of $GGCM_{1-15}$.

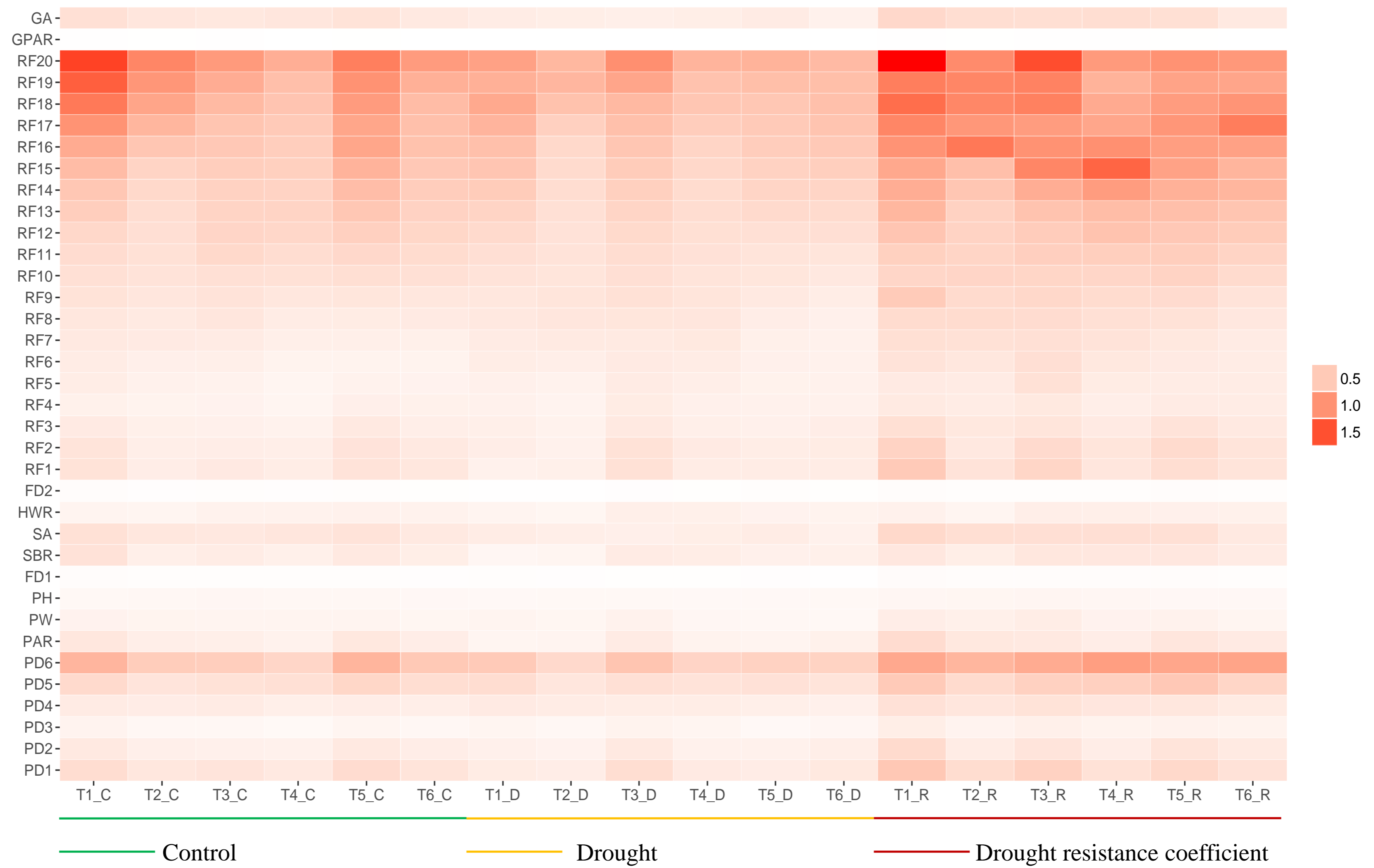


Fig. S3 Coefficient of variation (CV) among 200 accessions for three sets of data with control (suffix with _C), drought (suffix with _D) and drought coefficient (suffix with _R) at 6 early growth stages.

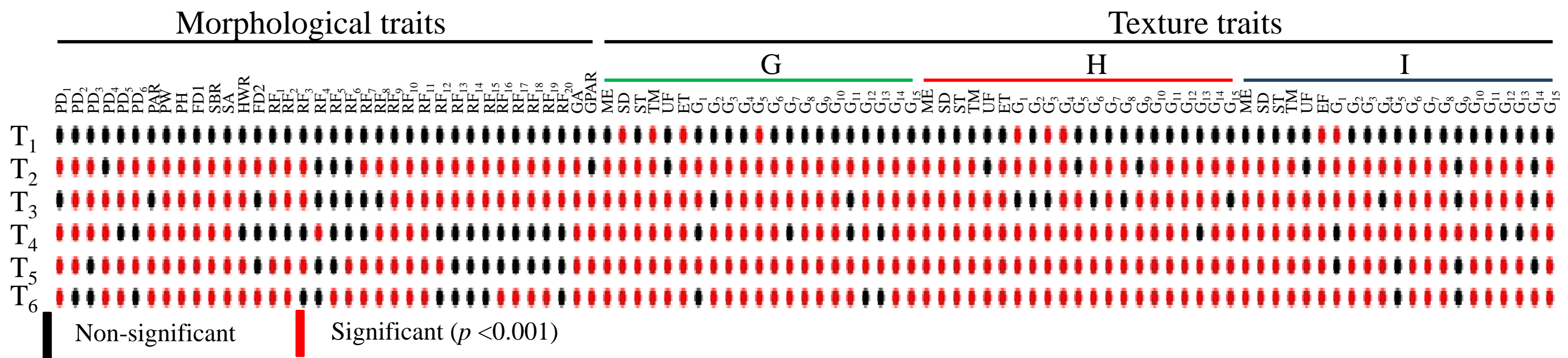


Fig. S4 T-test between treatment and control panels at seedling stage. The red bar indicates significant difference and black bar indicates non-significant difference between control and drought condition. G₁₋₁₅ was the abbreviation of GGCM₁₋₁₅.

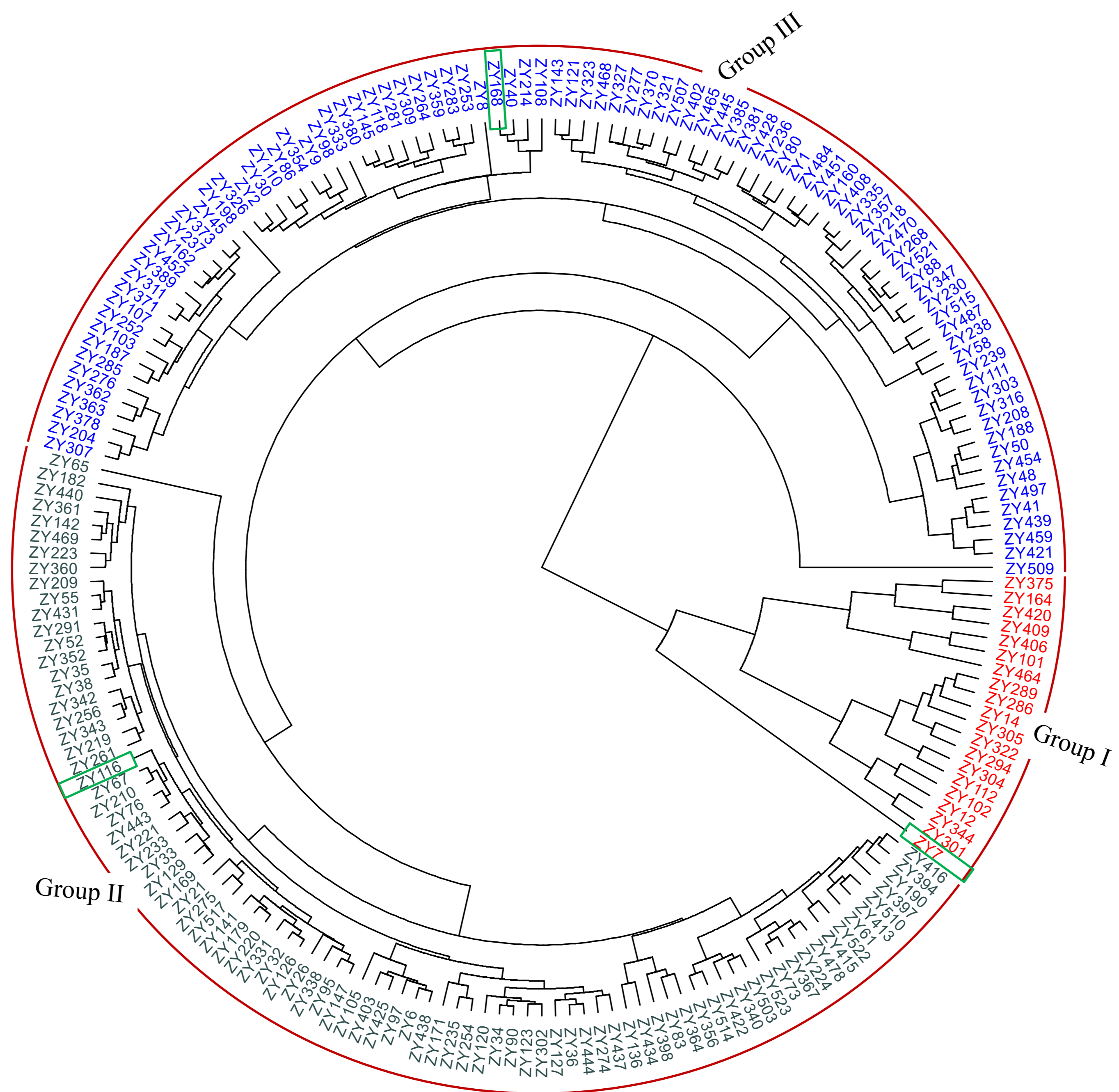
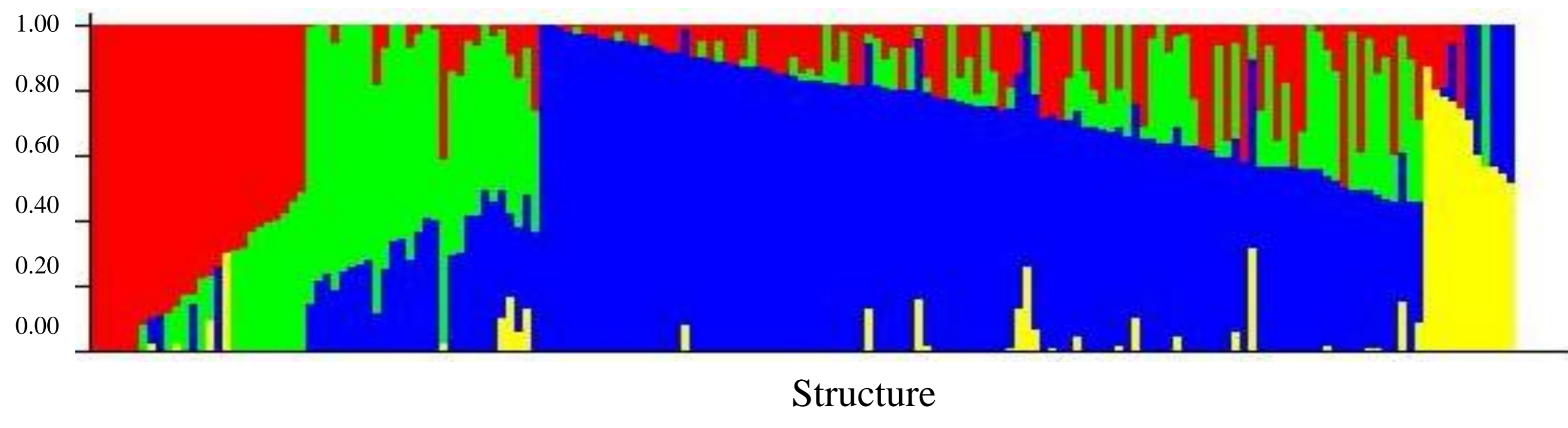


Fig. S5 Three sub-groups i-traits of 200 upland accessions. Group I in red stands for sensitive to drought, group II in gray stands for relative tolerant accessions, group III in blue stands for tolerant accessions and labels in the green wire frame are three representative accessions.

a



b

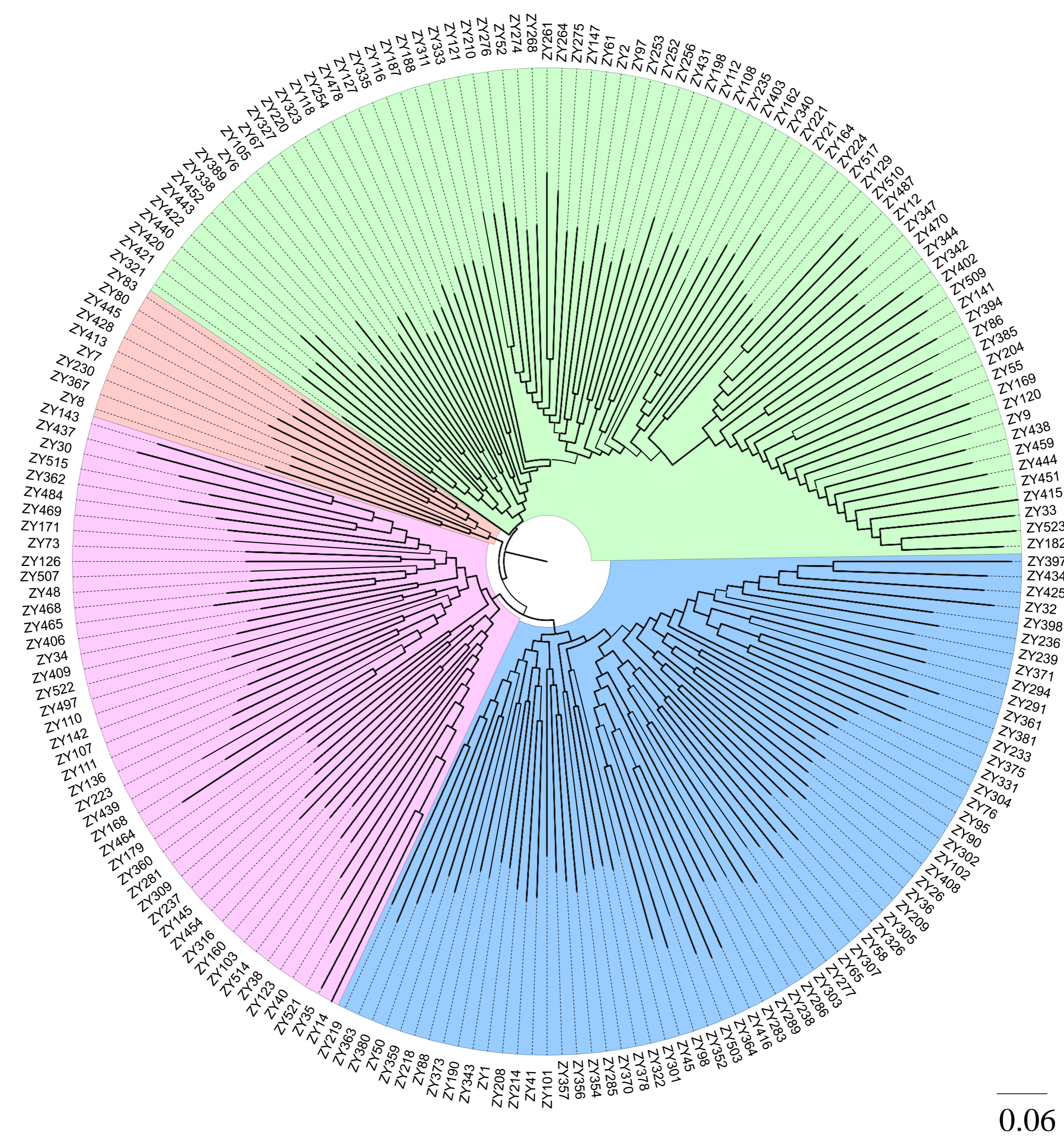


Fig. S6 Structure analysis of 200 upland cotton accessions.

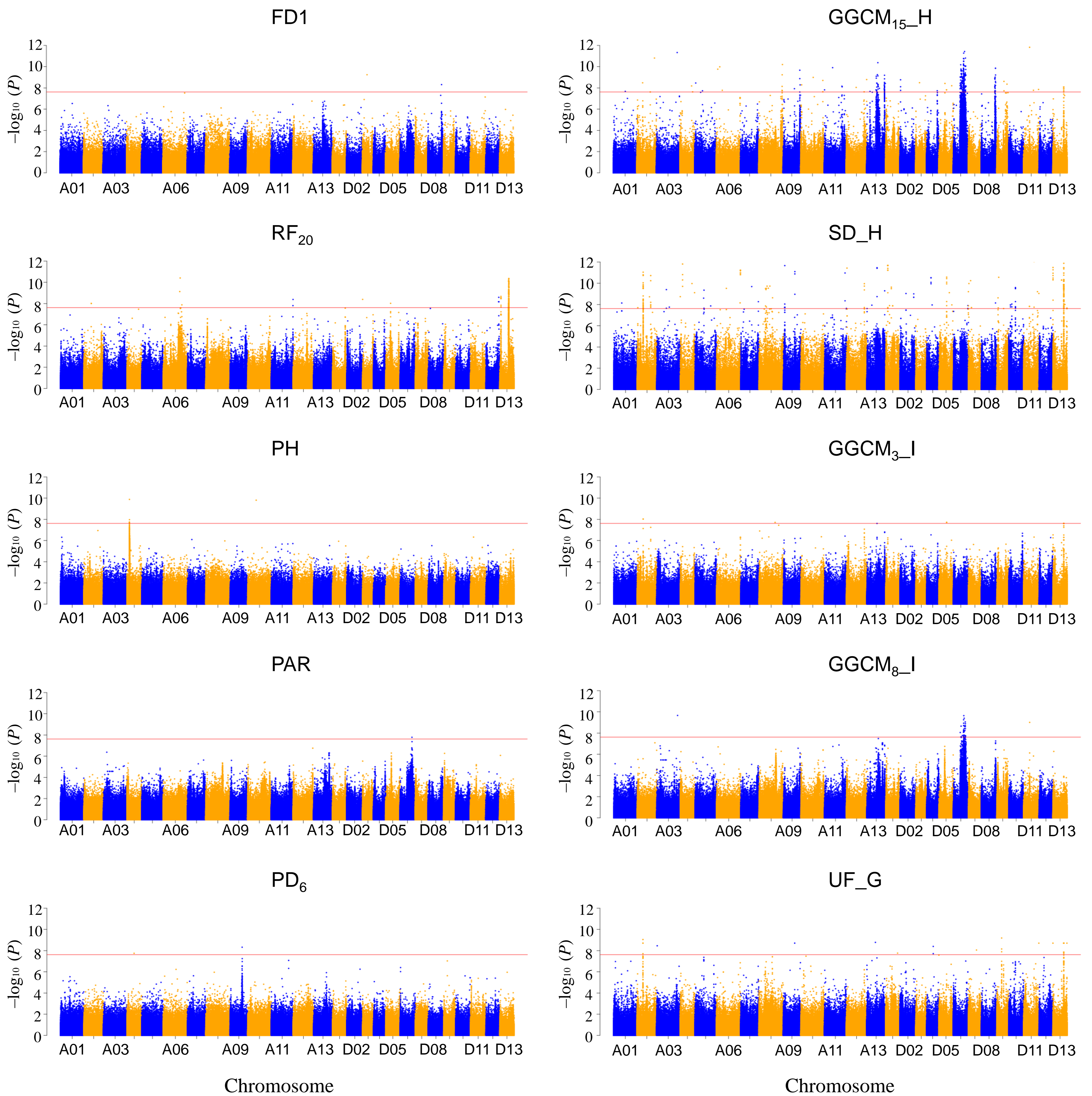


Fig. S7a GWAS results by morphological and texture i-traits.

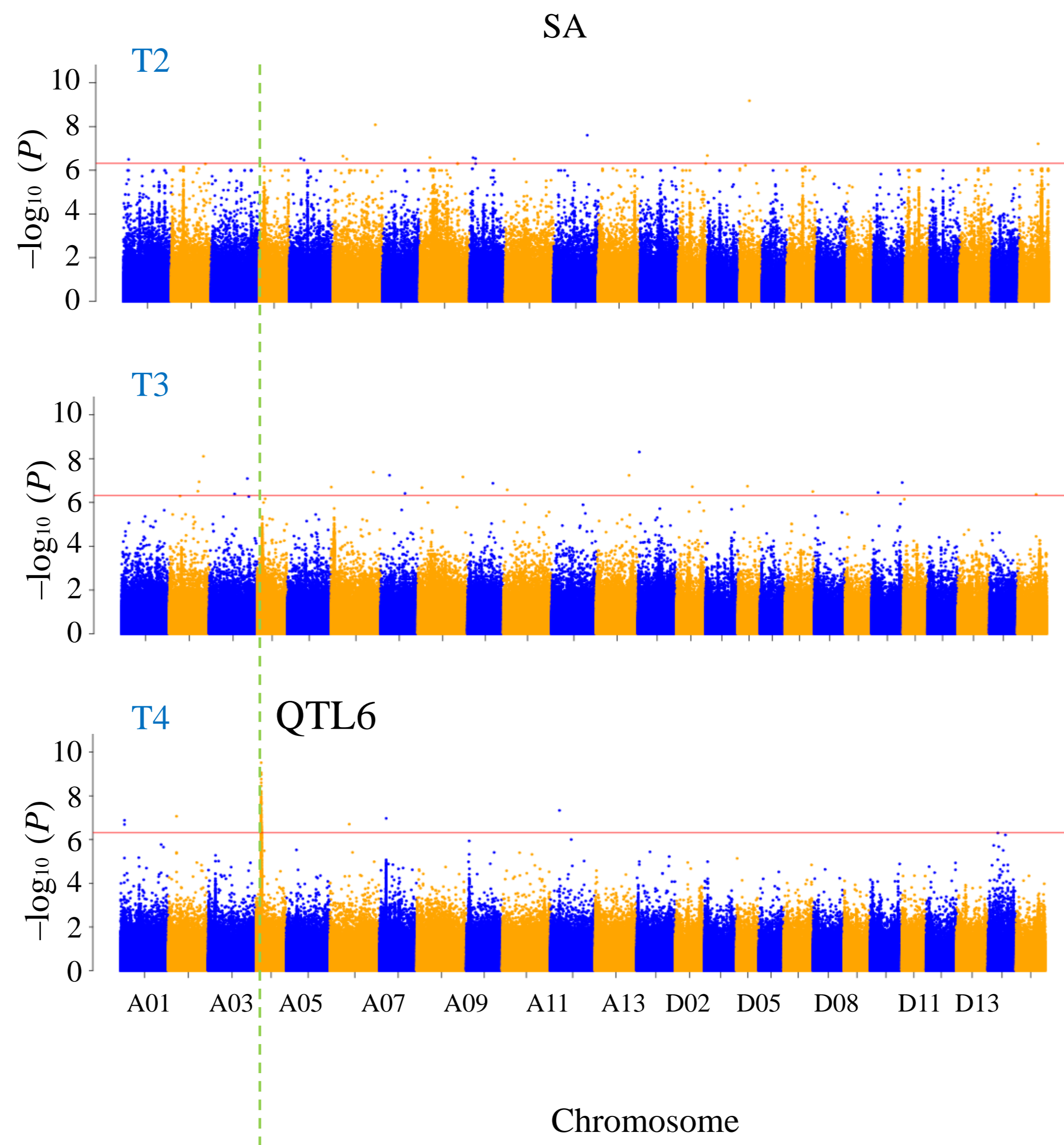


Fig. S7b Dynamic GWAS for a gradual strengthening QTL for SA at T_2 to T_4 .

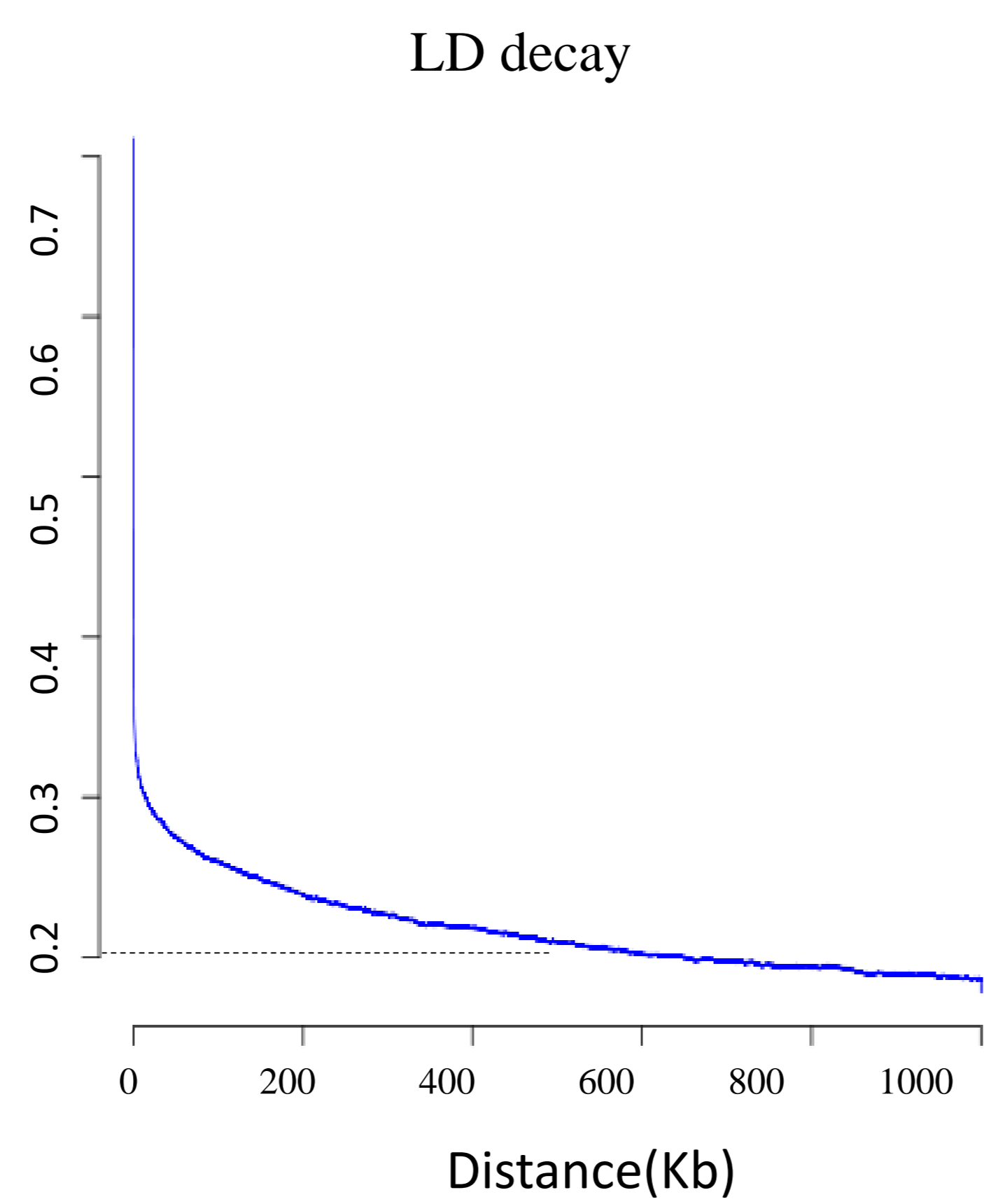


Fig. S8 linkage disequilibrium (LD) decay distance at whole genome level.

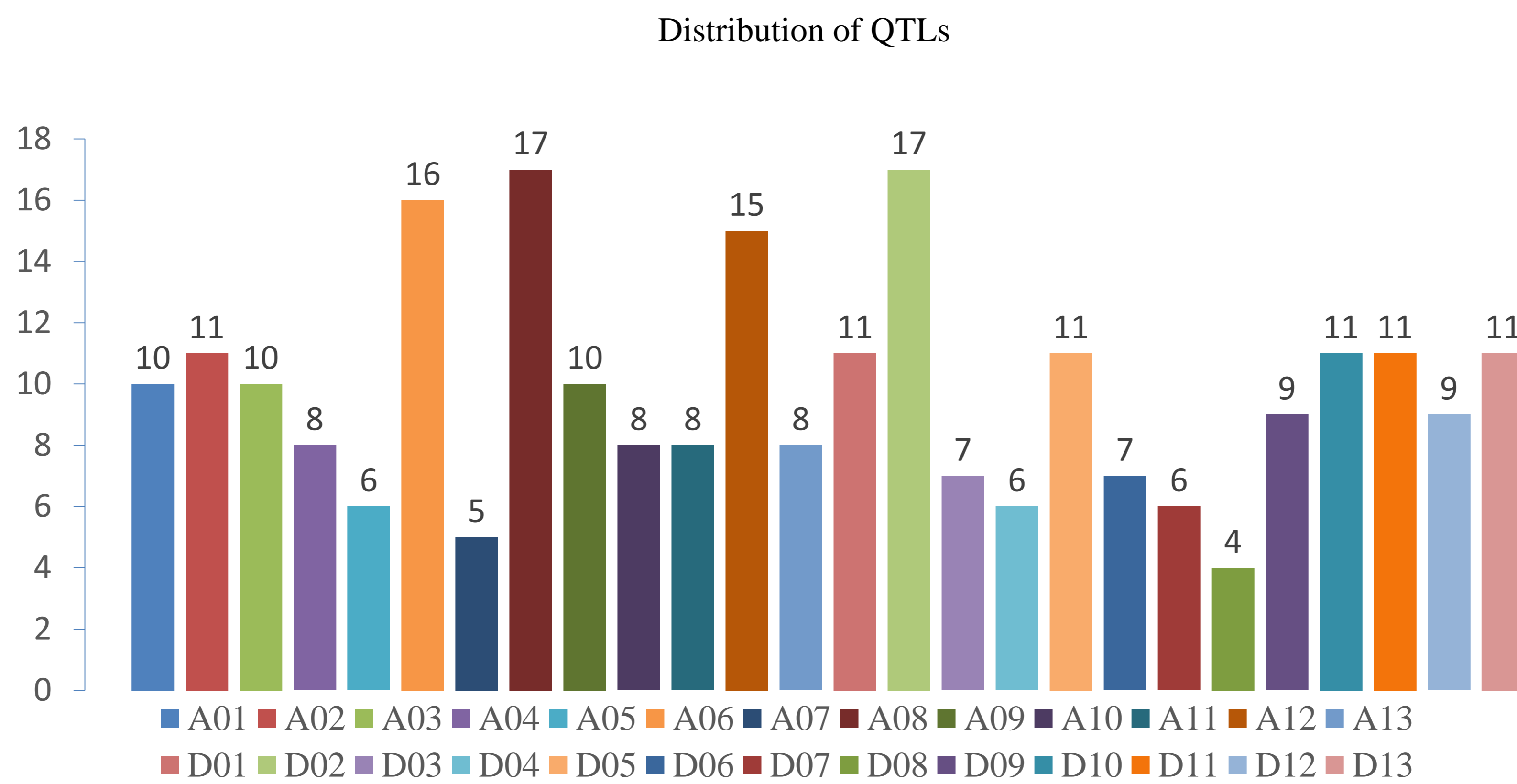


Fig. S9 Distribution of QTLs associated with morphological traits in 26 chromosomes in cotton.

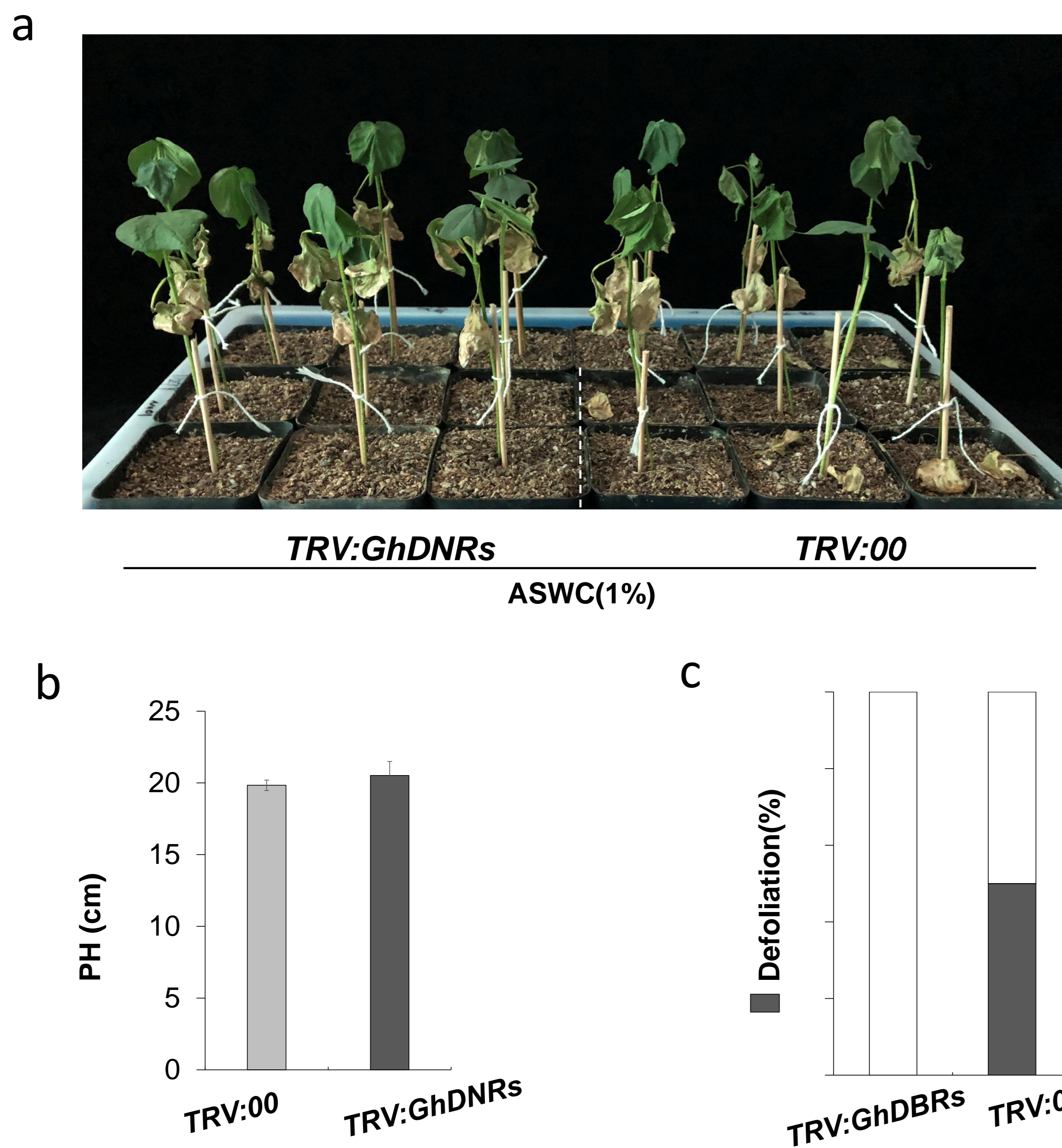


Fig. S10 VIGS of GhDNRs (TRV:GhDNRs) in drought-resistant accession ZY168 under drought stress.