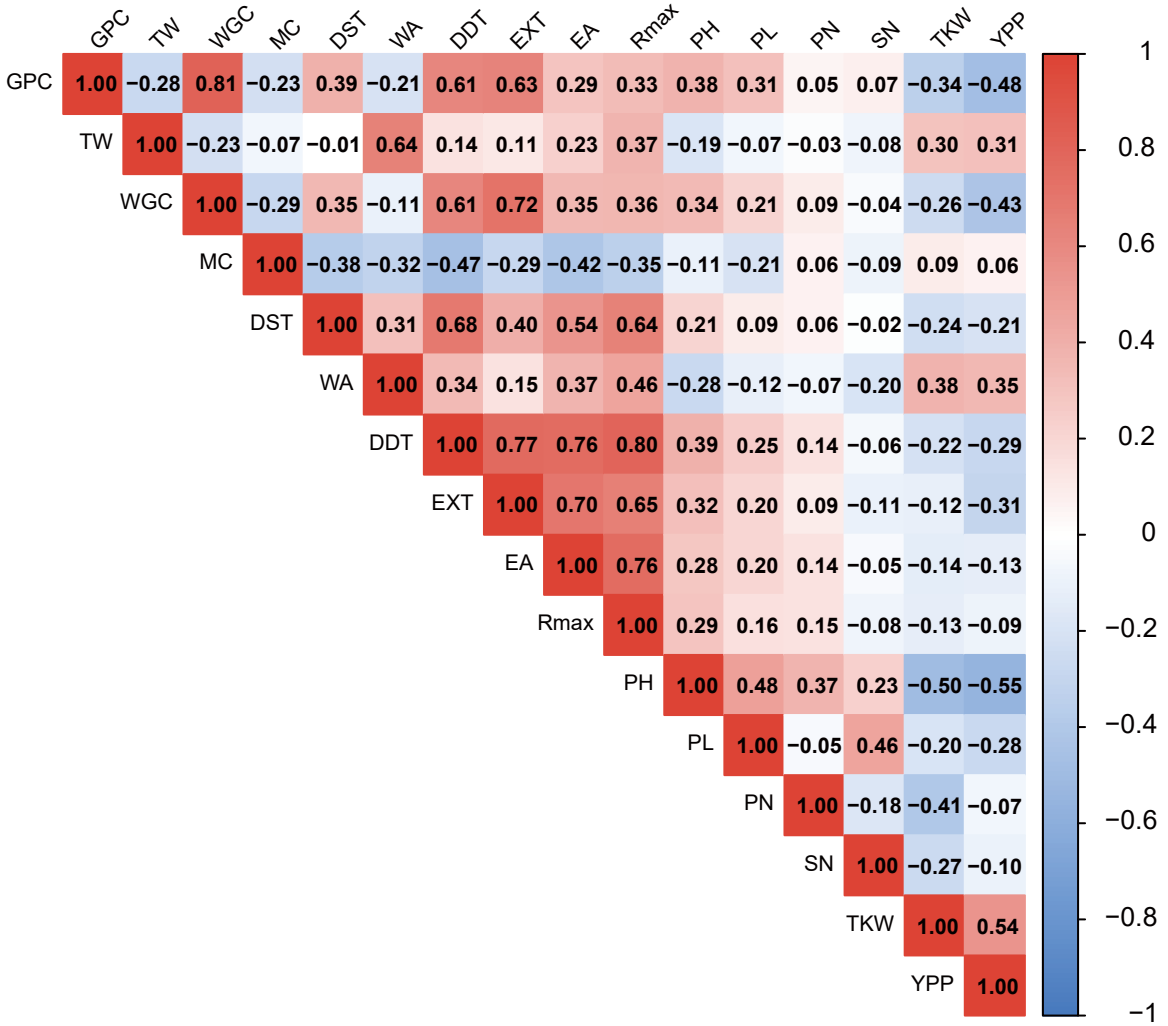


Fig S1. Phenotypic correlation matrix among sixteen traits based on BLUE values. The analysis includes ten grain quality traits: GPC (grain protein content), TW (test weight), WGC (wet gluten content), MC (moisture content), WA (water absorption), DST (dough stability time), DDT (dough development time), EXT (extensibility), EA (elastic area), Rmax (maximum resistance); and six yield-related traits: PH (plant height), PL (panicle length), PN (panicle number), SN (spikelet number), TKW (thousand-kernel weight), YPP (yield per plant).

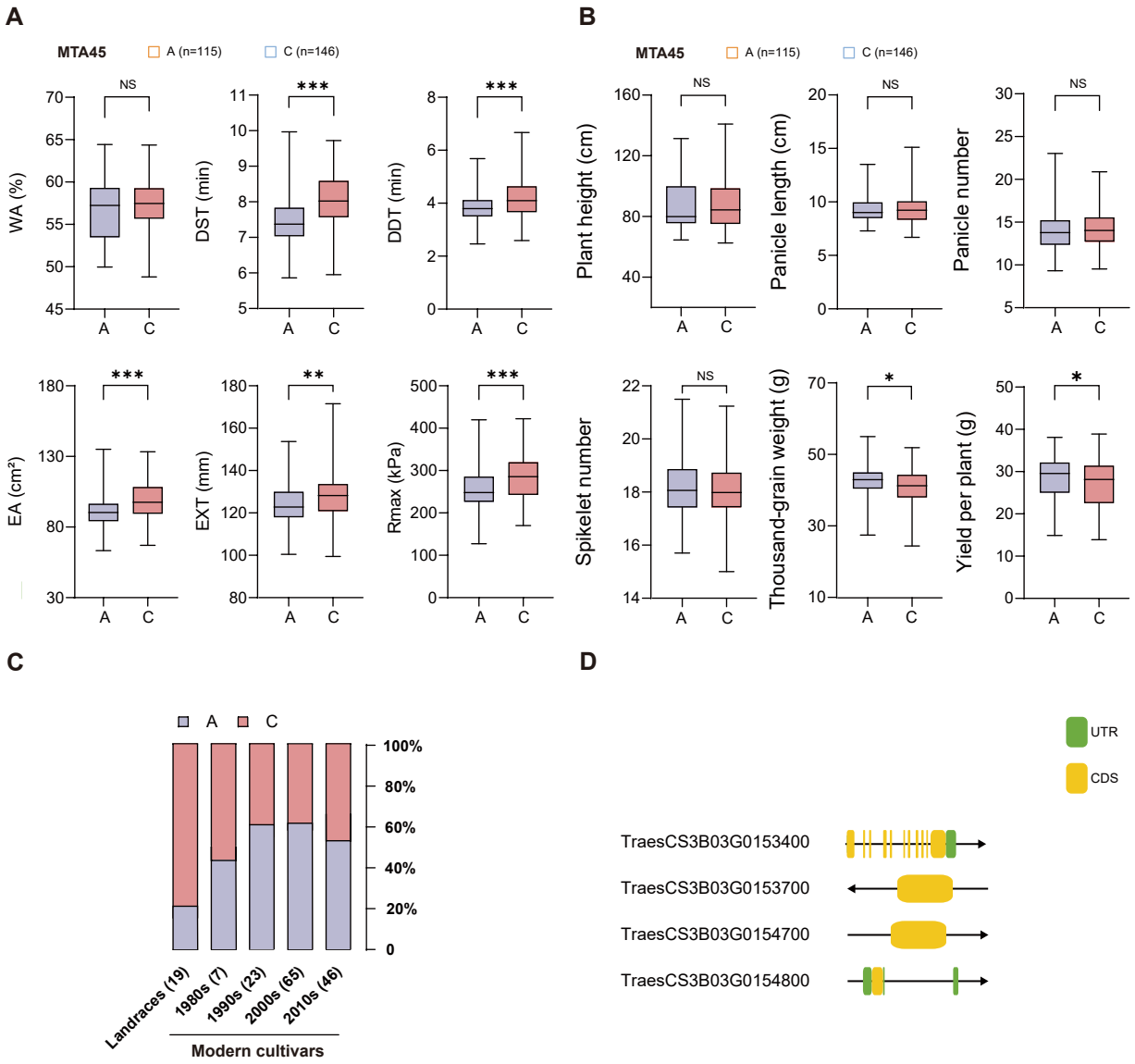


Fig S3. Genetic effects and candidate gene analyses of the MTA45 on Chromosome 3B associated with DST.

A Haplotype analysis of MTA45 for six quality traits: WA, DST, DDT, EXT, EA, and Rmax. **B** Haplotype analysis of MTA45 for yield-related traits: plant height, panicle length, panicle number, spikelet number, thousand-grain weight, and yield per plant. **C** Changes in allele frequencies of MTA45 throughout wheat breeding history in China. **D** Genomic structure of the candidate gene at the MTA45 locus.

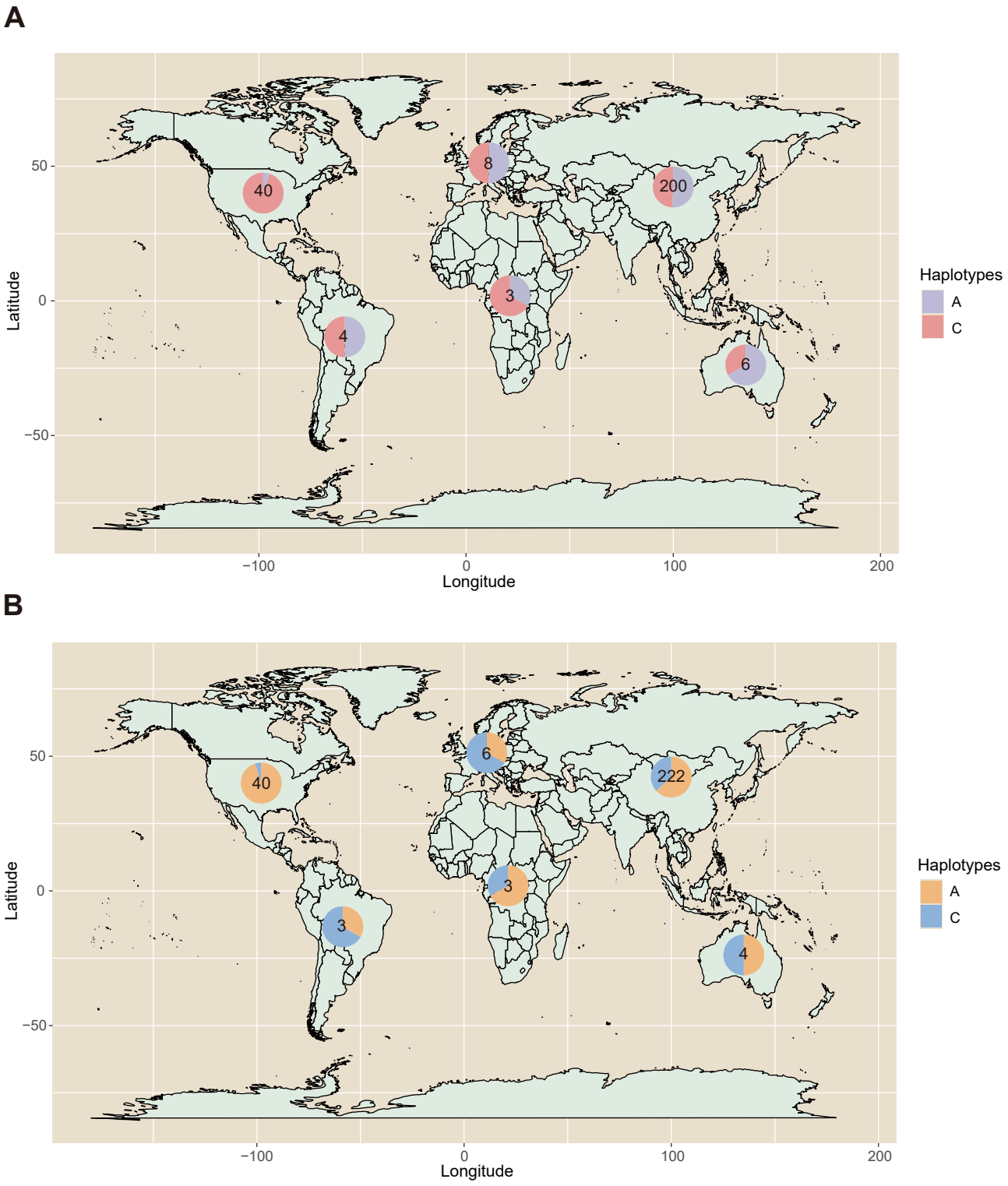
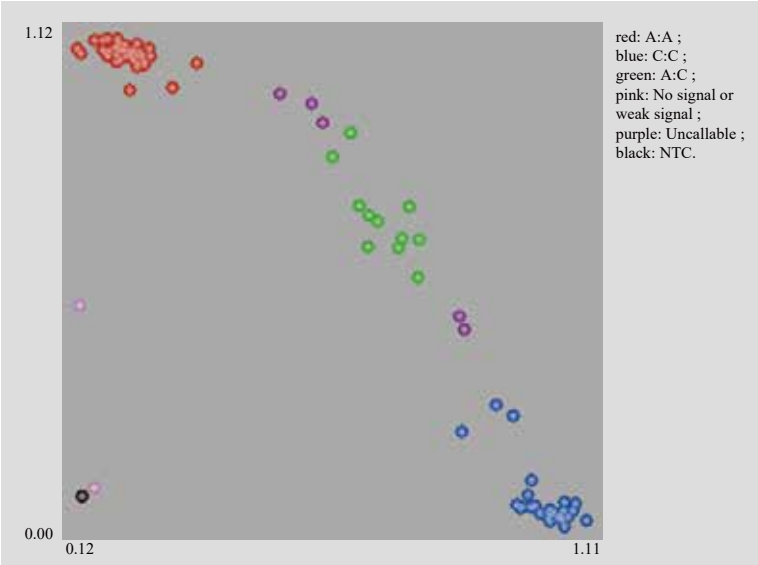


Fig. S4 Global distribution of haplotypes associated with MTA45 and MTA81 across six continents.
A MTA 45 haplotype distribution by continent. **B** MTA 81 haplotype distribution by continent. The pie chart shows haplotype distribution percentages, and the numbers above the chart represent the number of varieties.

A



B

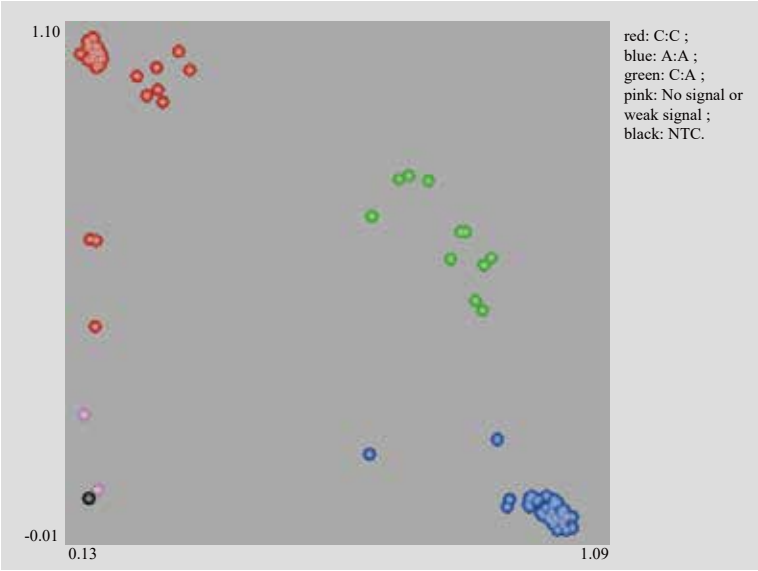


Fig. S5 KASP genotyping of quality trait loci.
A MTA45 allelic distribution **B** MTA81 allelic distribution

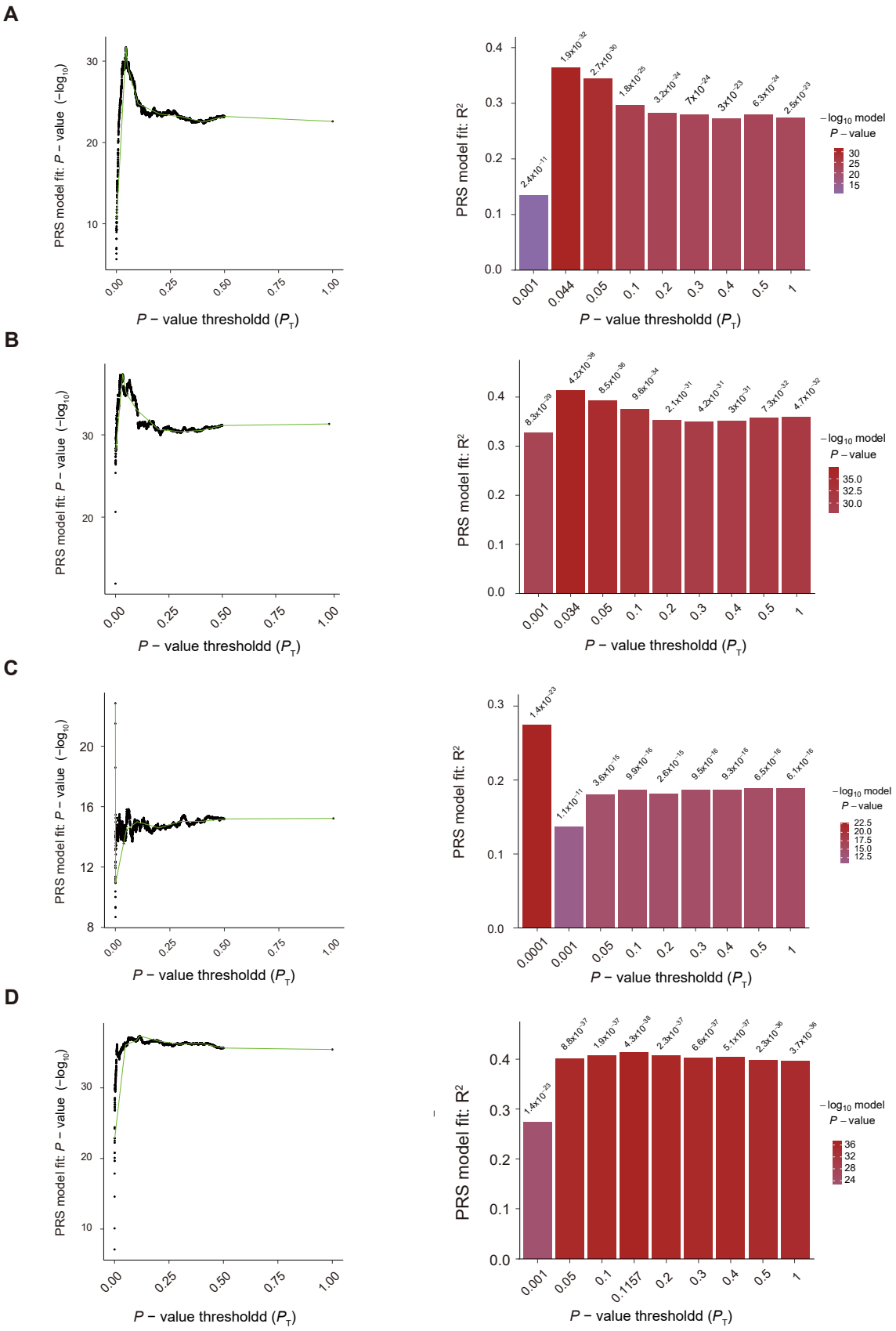


Fig S6. Distribution and trends of polygenic scores for four grain quality traits.
A GPC **B** TW **C** WGC **D** MC
Line plot: Trend of model significance across P-value thresholds.
Bar plot: Model performance showing variance explained (bar height) and statistical significance (color intensity) at different thresholds.

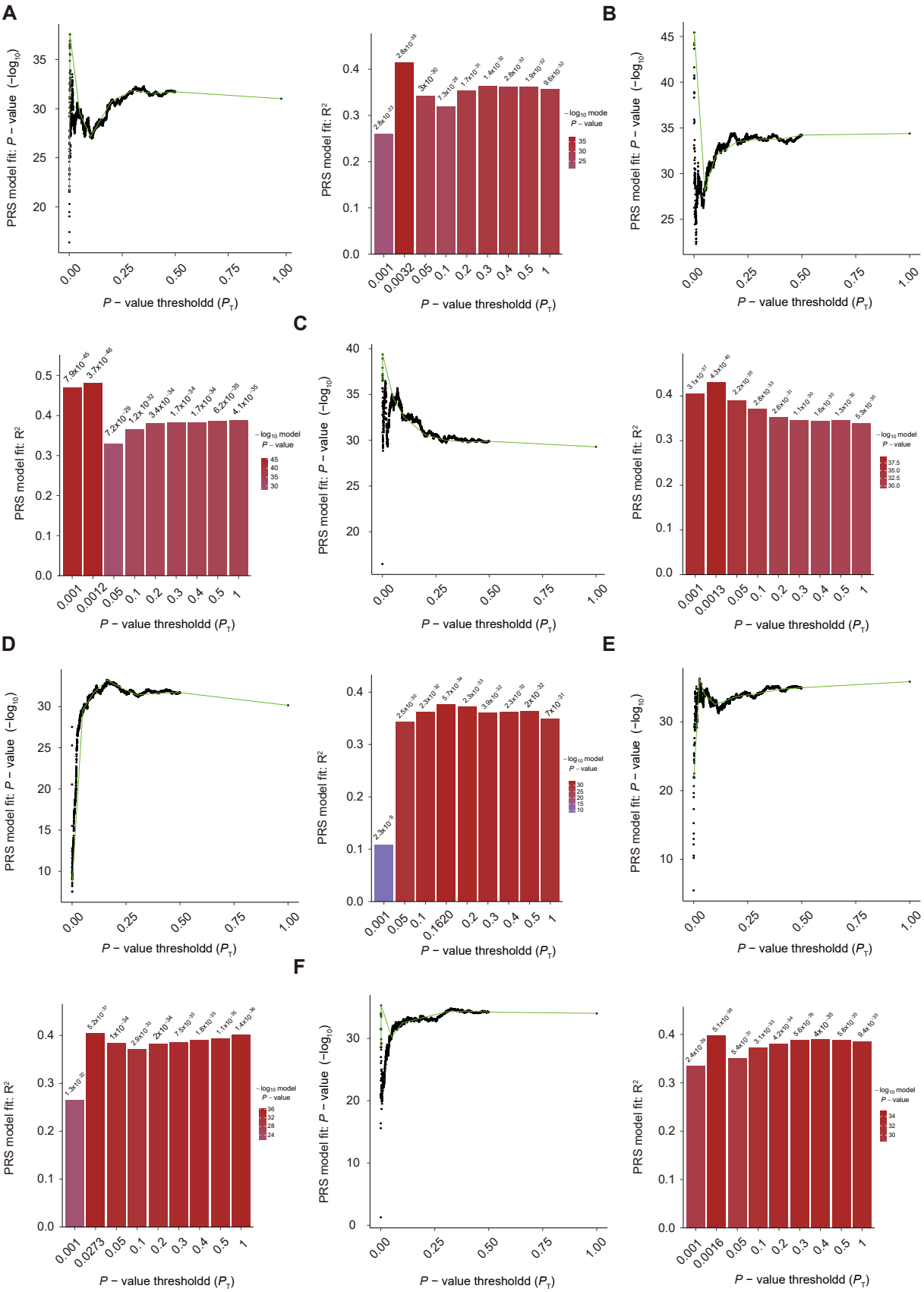


Fig S7. Distribution and trends of polygenic scores for four grain quality traits.
A WA **B** DST **C** DDT **D** EXT **E** EA **F** Rmax
Line plot: Trend of model significance across P-value thresholds.
Bar plot: Model performance showing variance explained (bar height) and statistical significance (color intensity) at different thresholds.

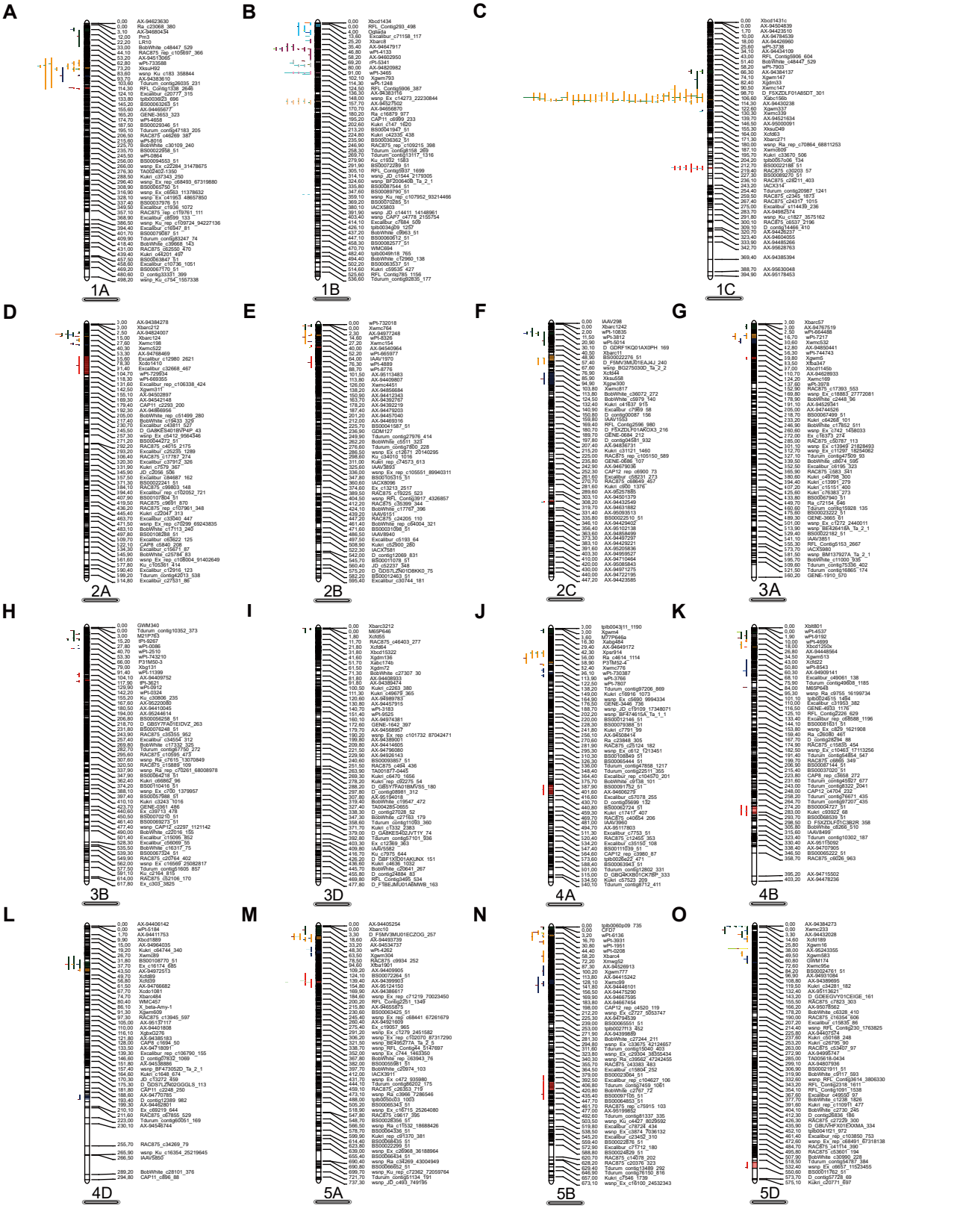


Fig S8. Consensus genetic map of QTL associated with wheat quality traits. **A–O** Chromosomes 1A–5D. The dot-to-horizontal-line scale to the left of each chromosome represents the continuous change in phenotypic variance explained by individual QTL. Vertical lines indicate QTL confidence intervals

Fig S9. Consensus genetic map of QTL associated with wheat quality traits.
P–U Chromosomes 6A–7D. The dot-to-horizontal-line scale to the left of each chromosome represents the continuous change in phenotypic variance explained by individual QTL. Vertical lines indicate QTL confidence intervals