

Supplementary Figures

Unraveling the Genetic Basis of Heat Tolerance and Yield in Bread Wheat: QTN Discovery and Its KASP-Assisted Validation

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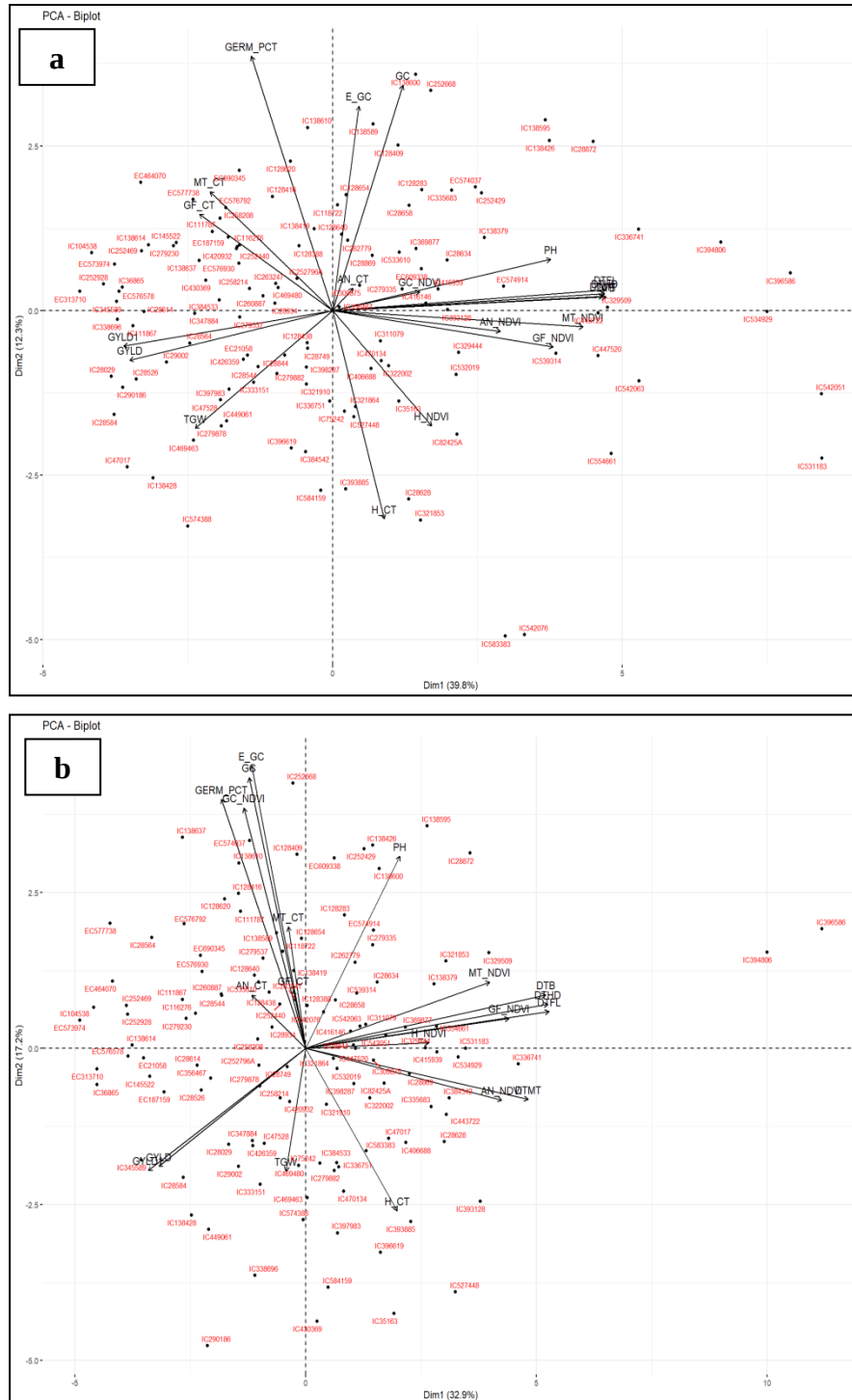


Fig S1. Principal component analysis (PCA) of 126 genotypes of bread wheat (a) Timely sown conditions (b) Late sown conditions

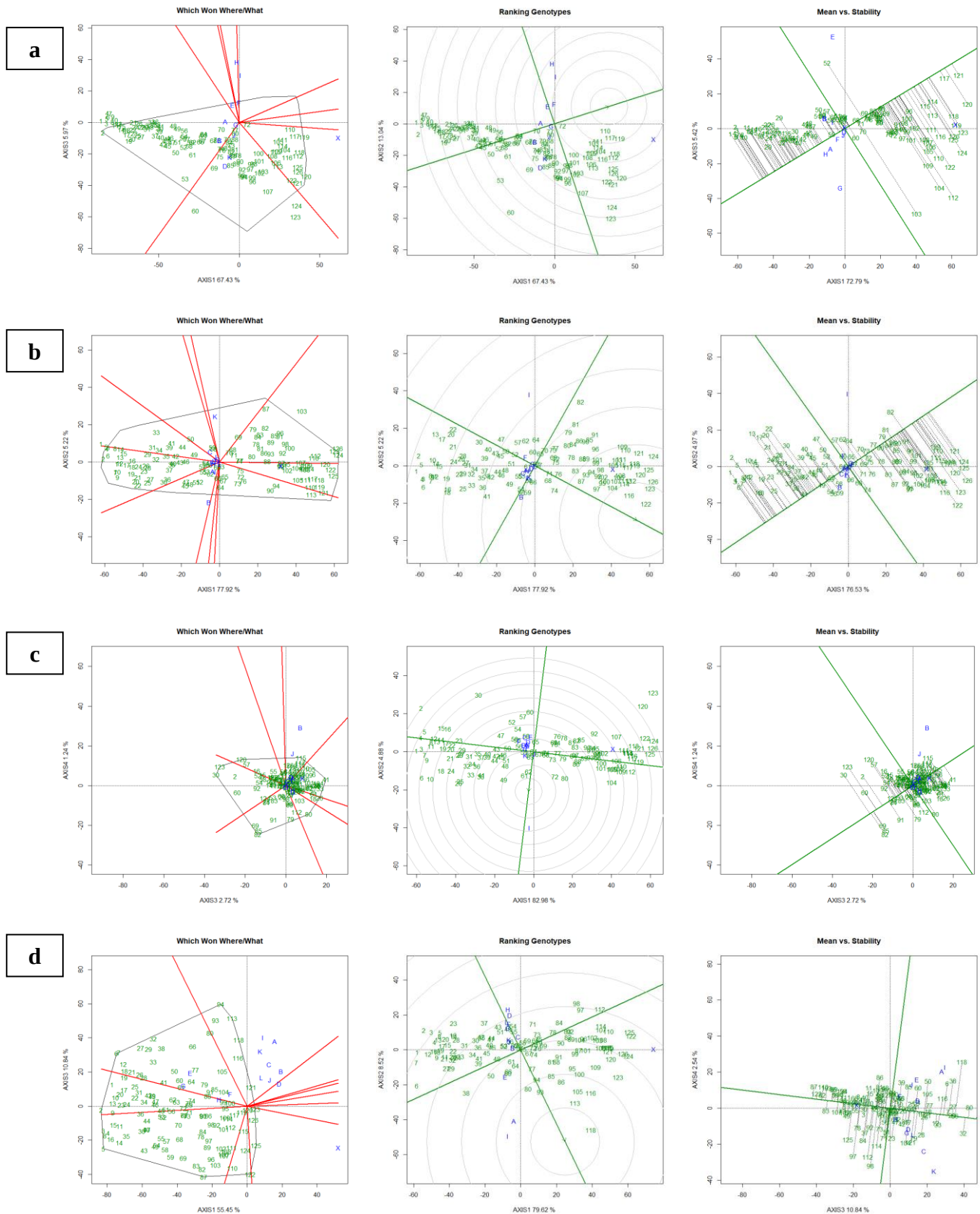


Fig. S2. Which-won-where', 'raking genotypes' and 'mean vs. stability' view of the GGE biplot of (a) GERM_PCT (b) E_GC (c) GC and (d) DTB of 126 diverse wheat genotypes evaluated in twelve environments during season 2020-21 and 2021-22.

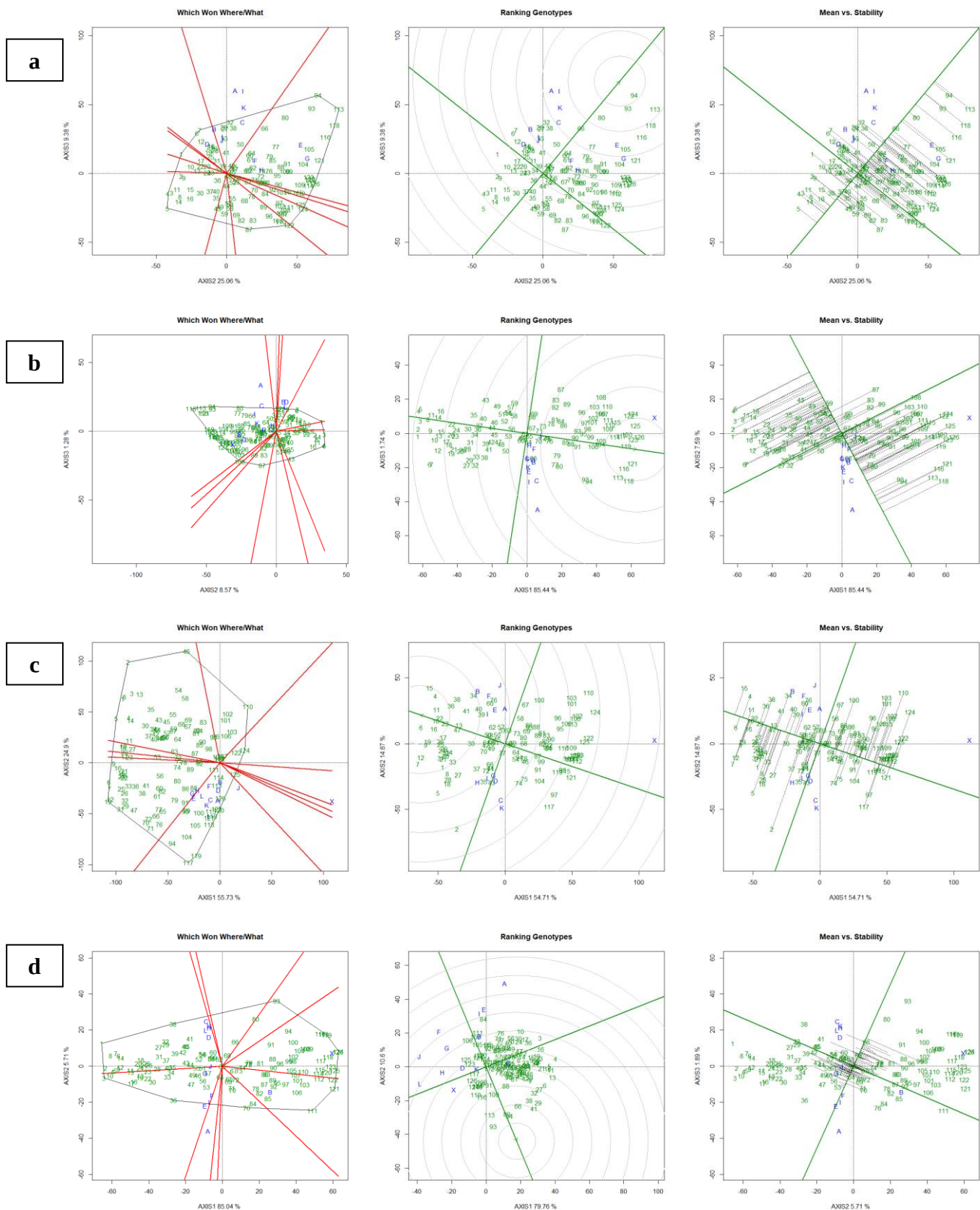


Fig. S3. Which-won-where', 'raking genotypes' and 'mean vs. stability' view of the GGE biplot of (a) DTHD (b) DTMT (c) PH and (d) TGW of 126 diverse wheat genotypes evaluated in twelve environments during season 2020-21 and 2021-22.

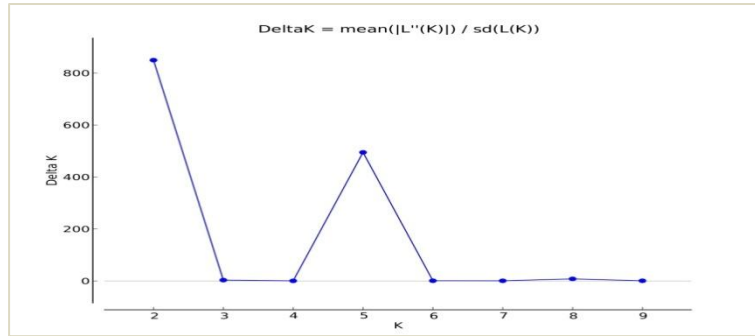


Fig S4. Structure and kinship analysis, estimated ΔK values for a given K , the ΔK showed steep declined with a clear peak value at $K=2$

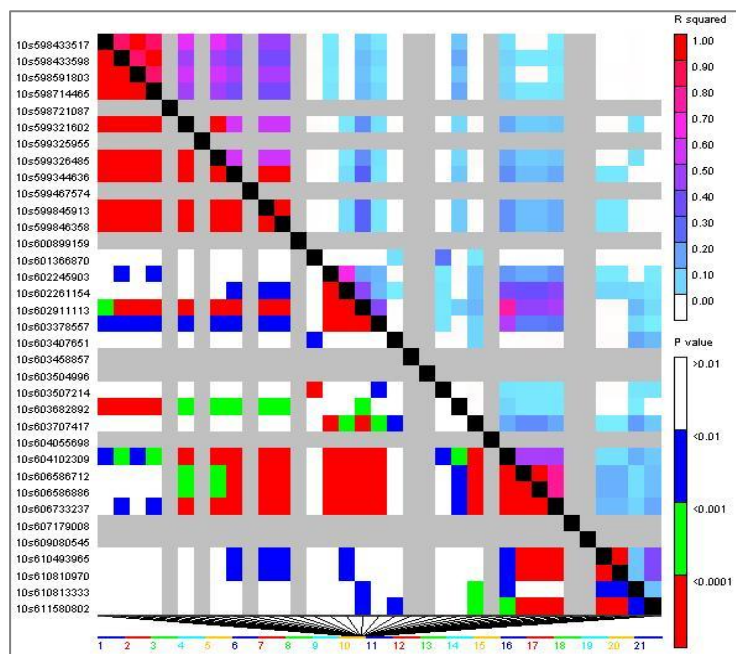


Fig.S5.Linkage disequilibrium matrix: Pair-wise LD values of polymorphic sites displaying r^2 above the diagonal and the corresponding p-values from rapid 1000 shuffle permutation test below the diagonal. Each cell represent the comparison of two pairs of marker sites with the color codes for the presence of significant LD. Colored bar code for the significance threshold levels in both diagonals is shown on right side of the figure. Large red blocks of haplotypes along the diagonal of triangle plot indicate the higher level of LD between the two loci the blocks

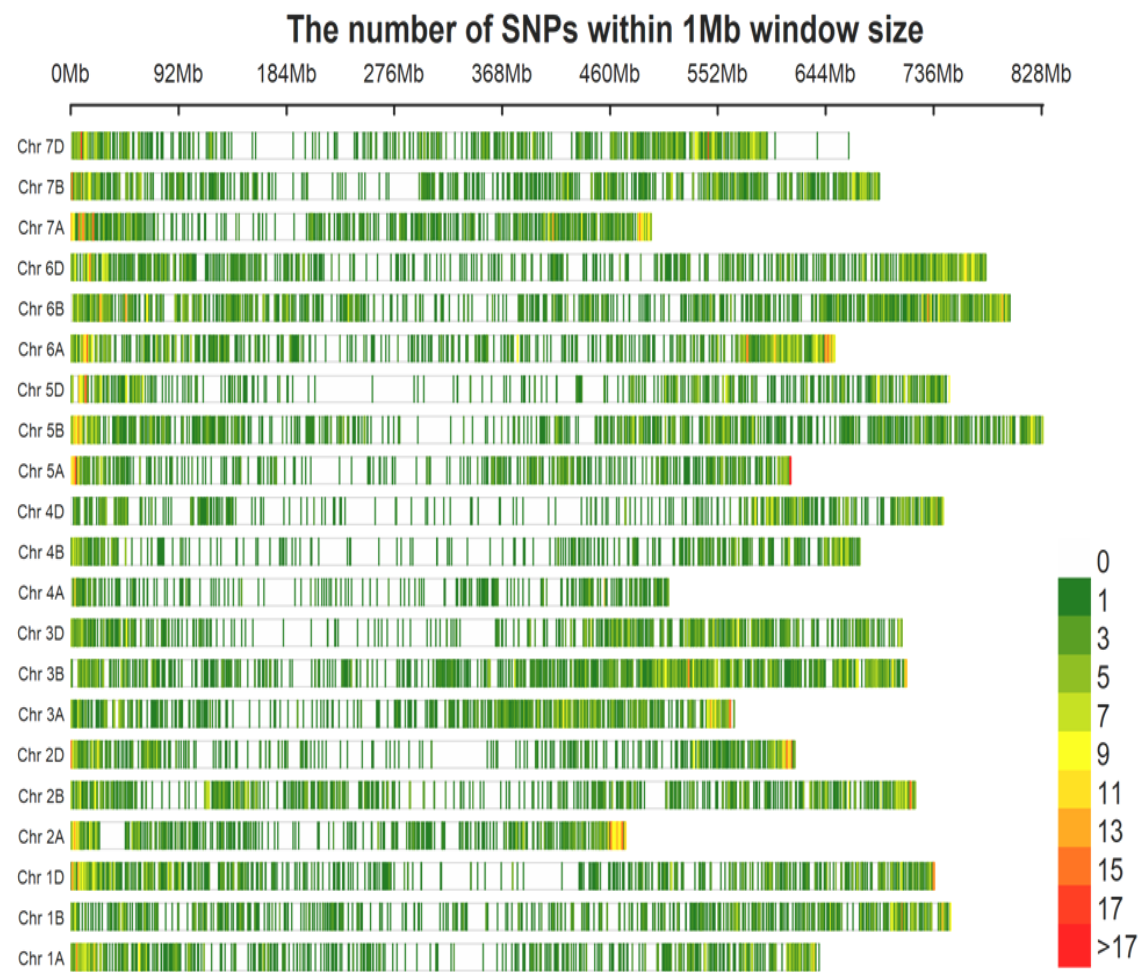


Fig.S6. Marker density map showing distribution of SNP markers within 1 Mb window size across twenty one chromosomes of *T.aestivum*.

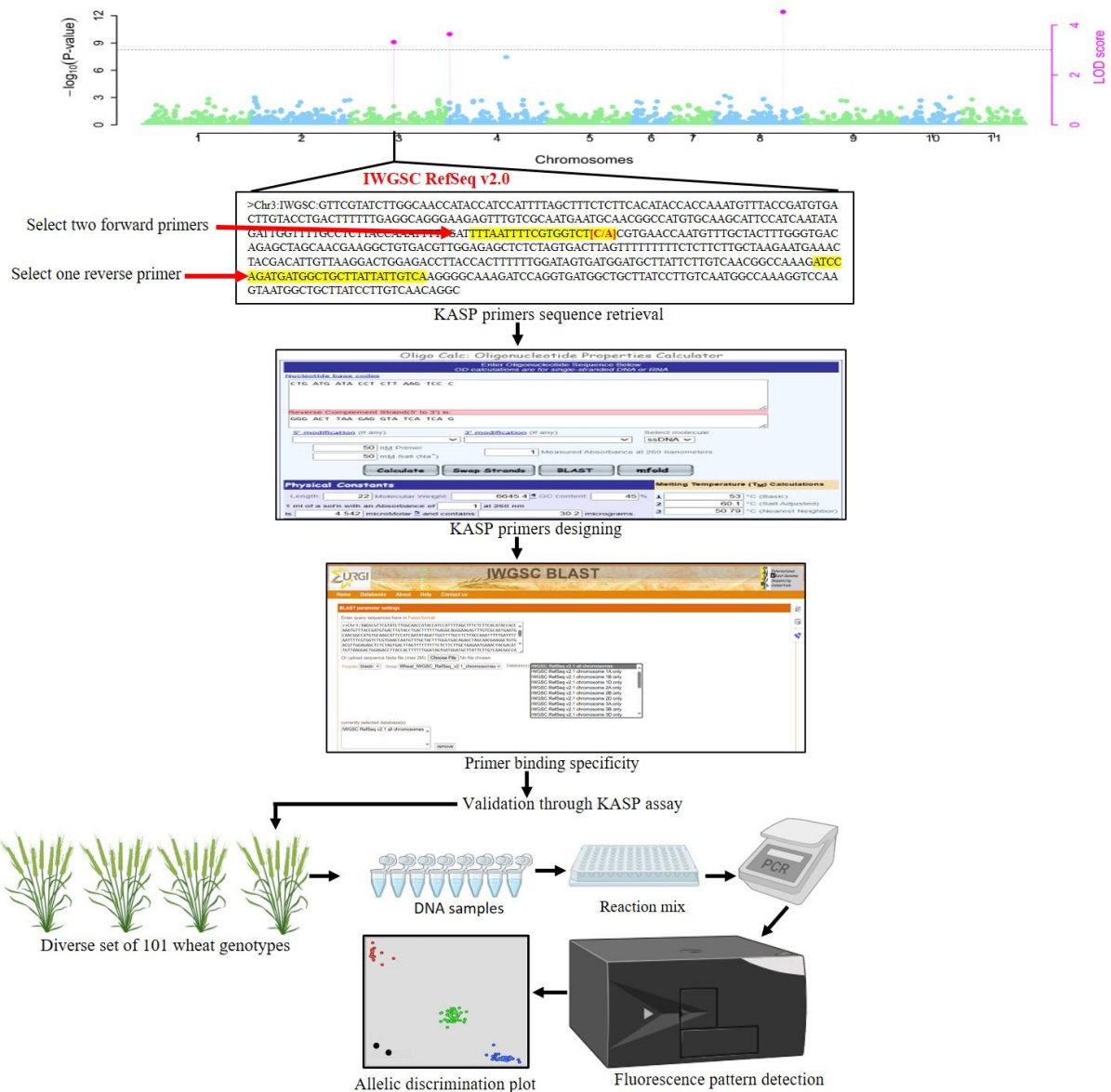


Fig S7. Systematic representation of the workflow used to validate identified QTNs associated with the yield related traits in bread wheat under heat stress through KASP assay.