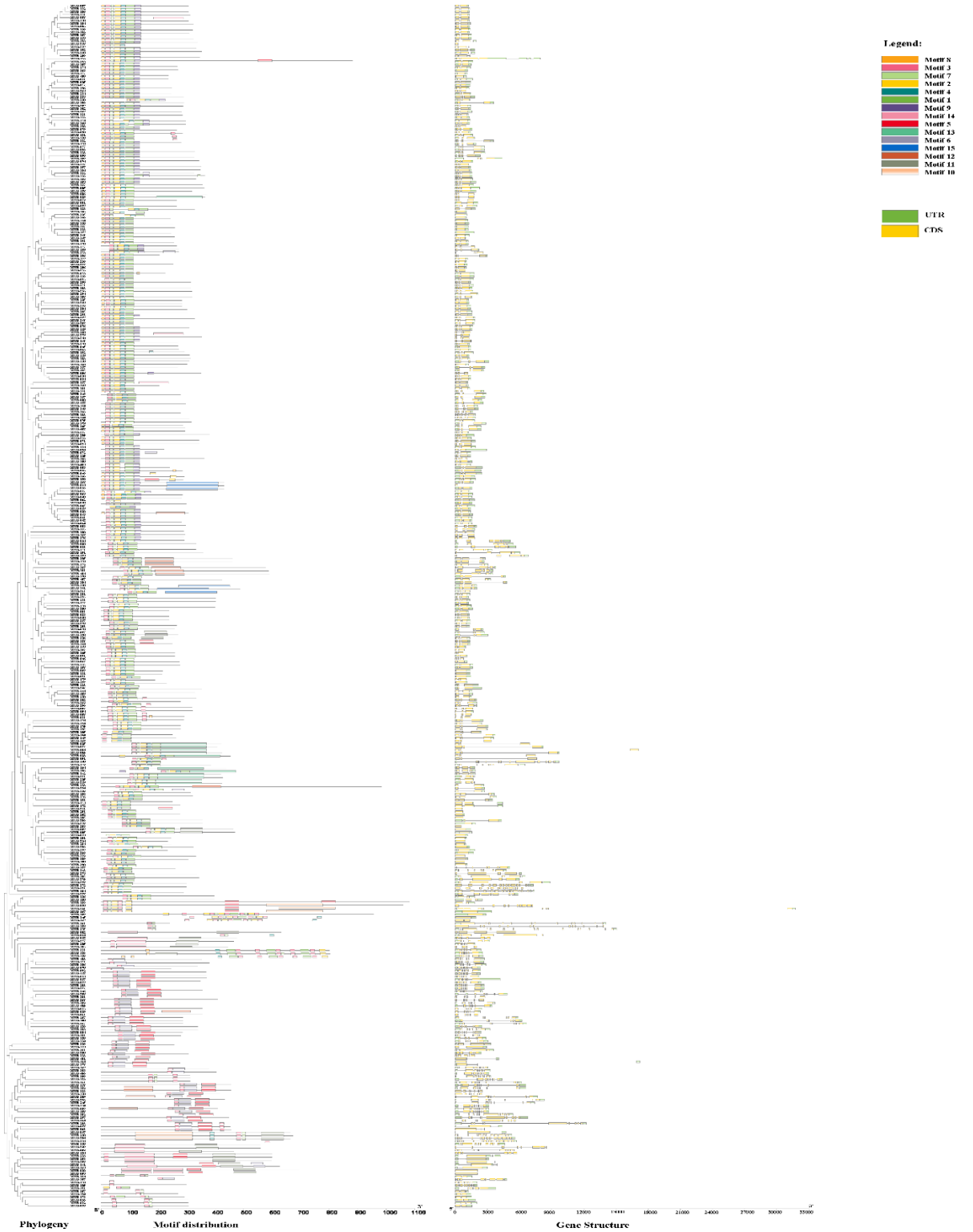
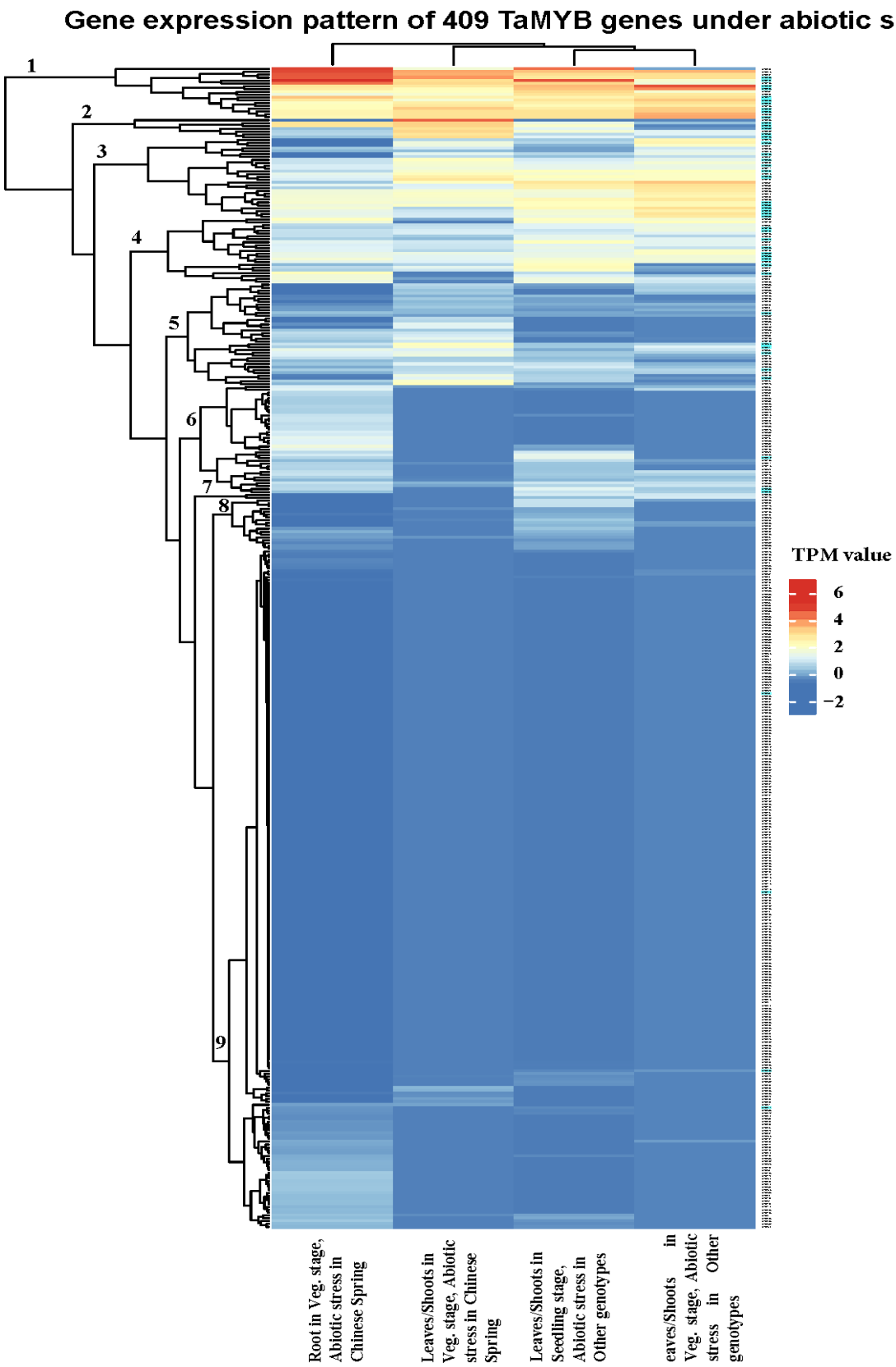
Characterization of TaMYB Transcription Factor Genes Revealed Possible Early Stage Selection for Heat Tolerance in Wheat



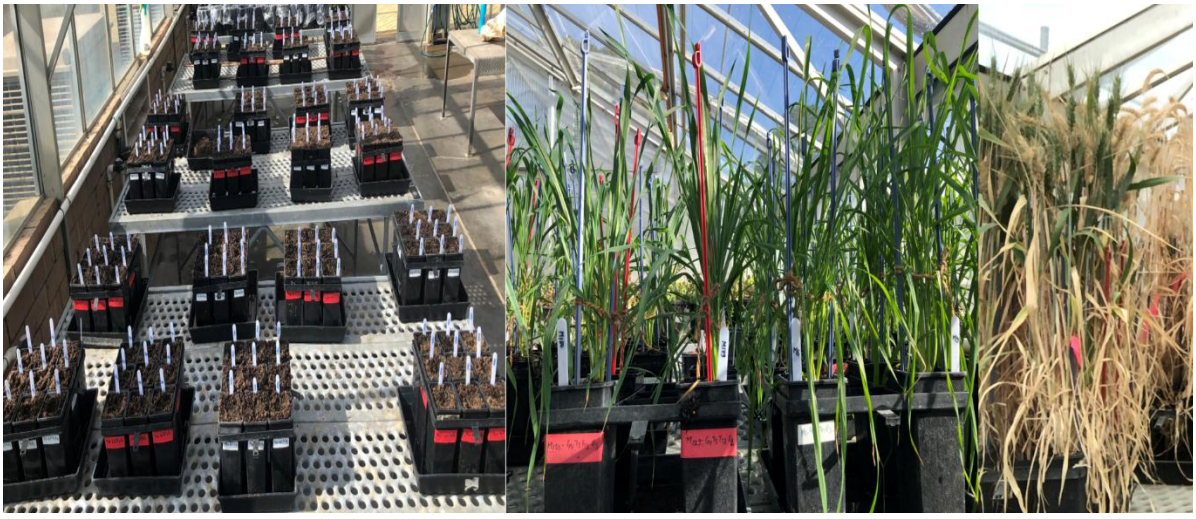
Supplementary Fig. 1 Phylogenetic grouping, distribution of conserved motifs, and gene structure of 409 TaMYB family TF genes. The phylogenetic tree was constructed using MEGAX with bootstrap values of 1000 repeats, motif composition analysed using online MEME tool and gene structure analyzed using GSDS online server. In the motif graph, the coloured blocks represent the position of motifs in corresponding proteins coding TF genes, block fonts indicates the length of motifs and grey lines connecting the coloured bocks represents non-conserved sequences. In the gene structure graph, the yellow blocks are exons, green blocks are UTRs and grey lines are introns. The relative position of each motif, exon, intron, and UTR can be determined with the help of scale displayed just below the corresponding graph.



Supplementary Fig. 2 The expression pattern profiling of 409 TaMYB TF genes under abiotic stress using publicly available transcriptome data. The intensity of colour shows the level of gene expression, where blue colour shows the least expressed genes, and the red colour shows the highest expressed genes. The genes are clustered into nine clusters based on their expression values forming a bigger cluster (cluster 9) of relatively lowest expressed genes (62.1%) and a smaller cluster (cluster 1) of highest expressed genes (4.4%) under abiotic stress.



Supplementary Fig. 3 Diagram illustrating the effect of heat stress on seedling root depth in all three genotypes (a) Perenrjori, (b) Brazil 32 and (c) Yitpi.



Supplementary Fig. 4 Glass house experiments showing the three different stages of wheat growth (a) sowing, (b) vegetative growth, and (c) reproductive growth approaching physiological maturity.