

Supplementary information

Phylogeny and expression pattern analysis of TCP transcription factors in
cassava seedlings exposed to cold and/or drought stress

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Figure S1. Phylogenetic relationships of TCP transcription factors built with the minimal evolution method. A total of 36 *MeTCPs* from cassava, 24 *AtTCPs* from Arabidopsis and 22 *OsTCPs* from rice were used to construct the Minimum-Evolution tree by MEGA 6.0 with 1000 bootstrap based on the full length sequences of *TCPs*.

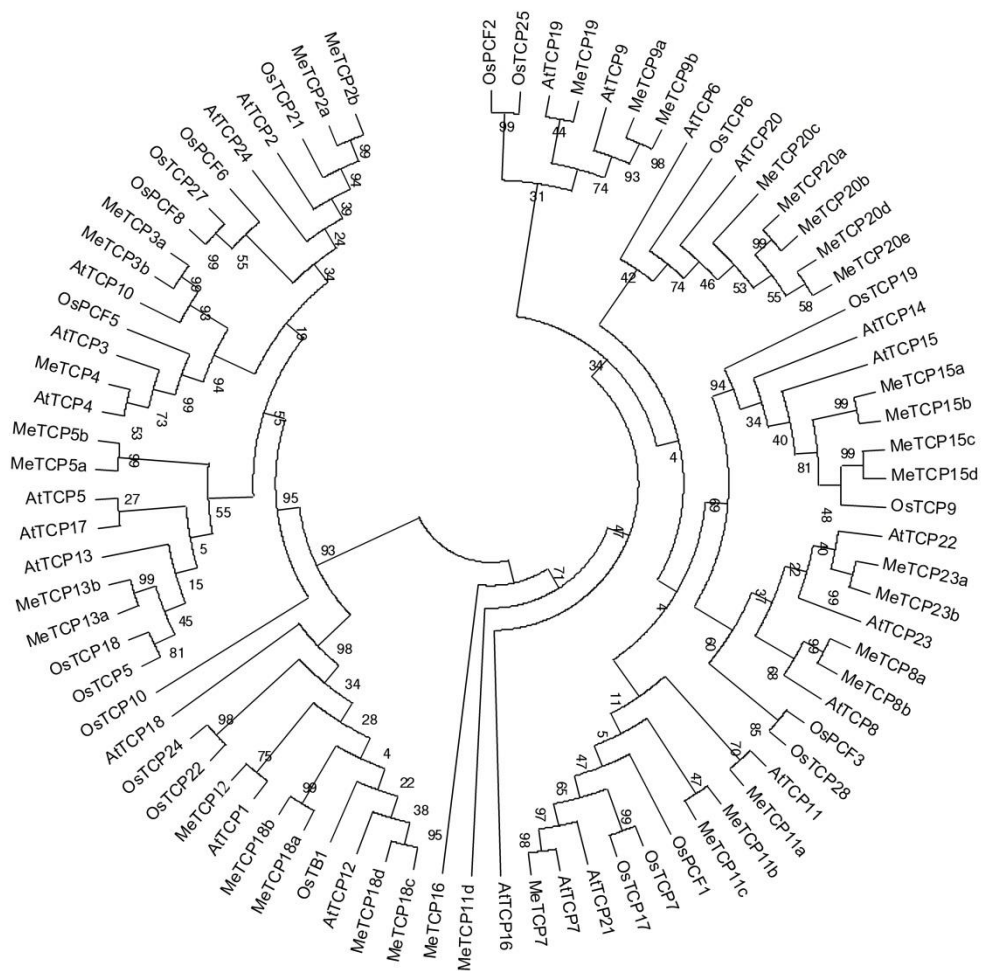


Figure S2. Protein motifs of MeTCPs identified by MEME.

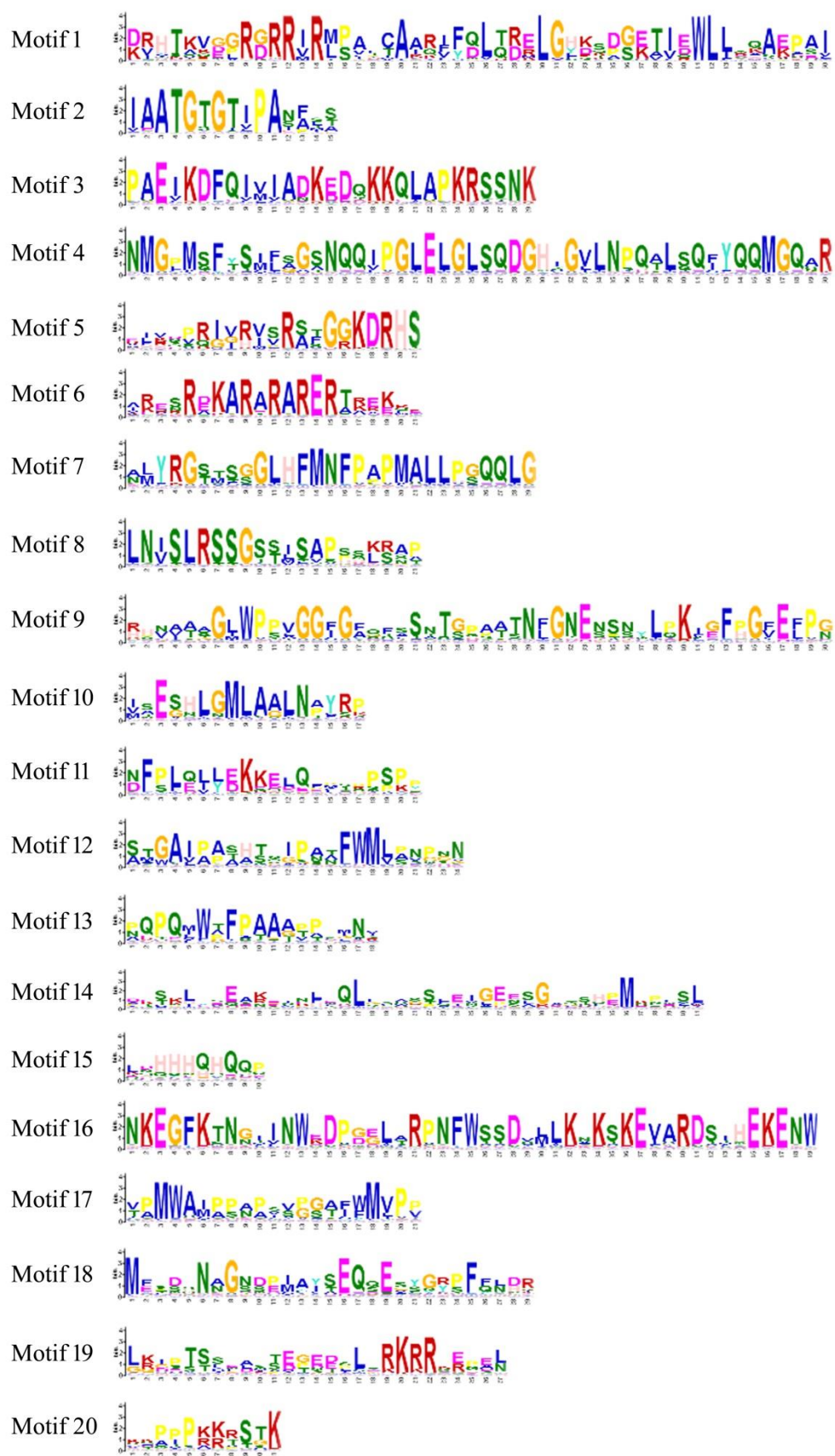


Figure S3. Scatterplot showing the correlation of TCP expressional value (z-score) between Arabidopsis and Cassava homologous genes (Part 1). R indicates root, L indicates leaf, A indicates apex, and S indicates stem, respectively. r indicates pearson correlation coefficient.

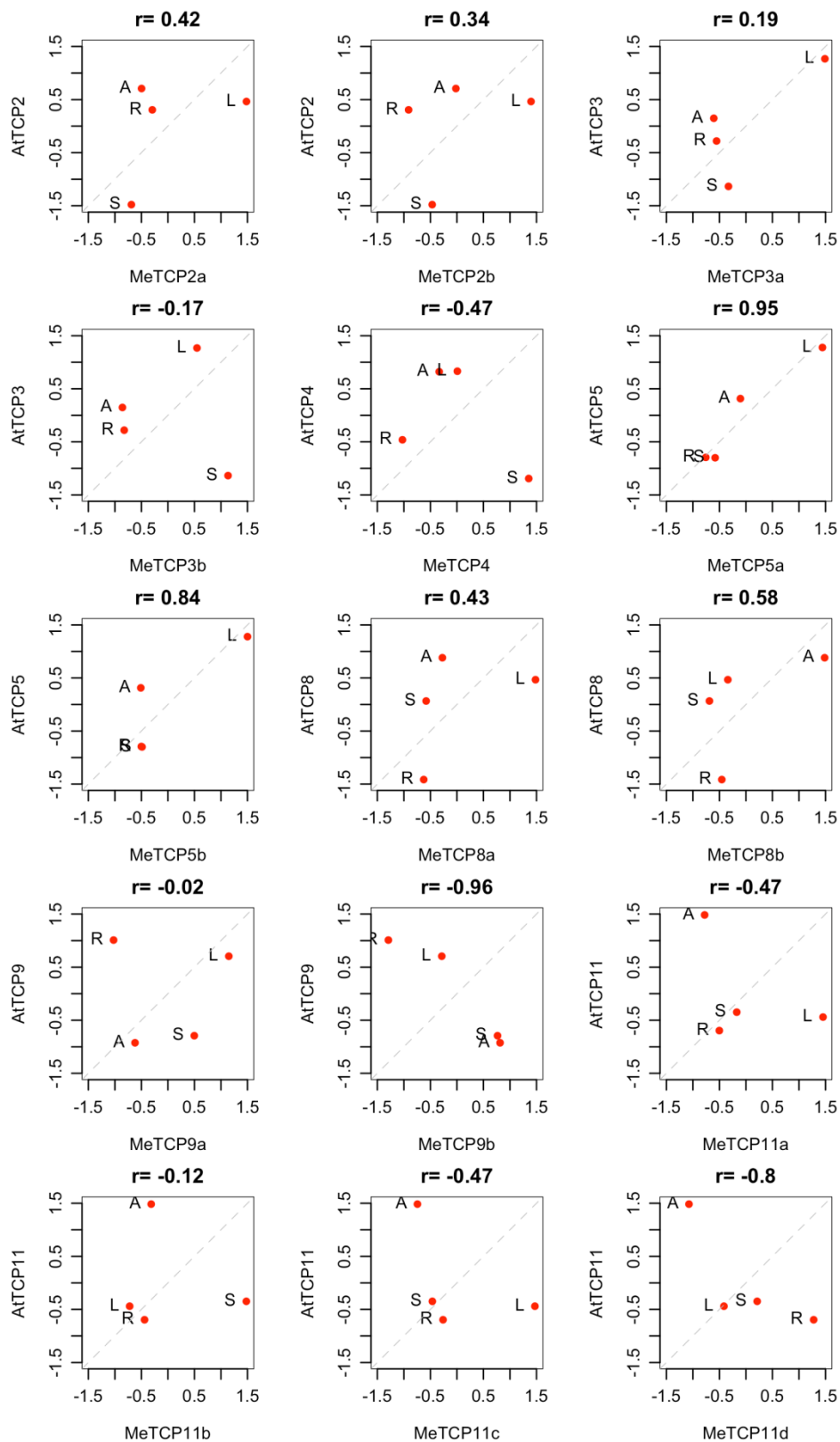


Figure S4. Scatterplot showing the correlation of TCP expressional value (z-score) between Arabidopsis and Cassava homologous genes (Part 2). R indicates root, L indicates leaf, A indicates apex, and S indicates stem, respectively. r indicates pearson correlation coefficient.

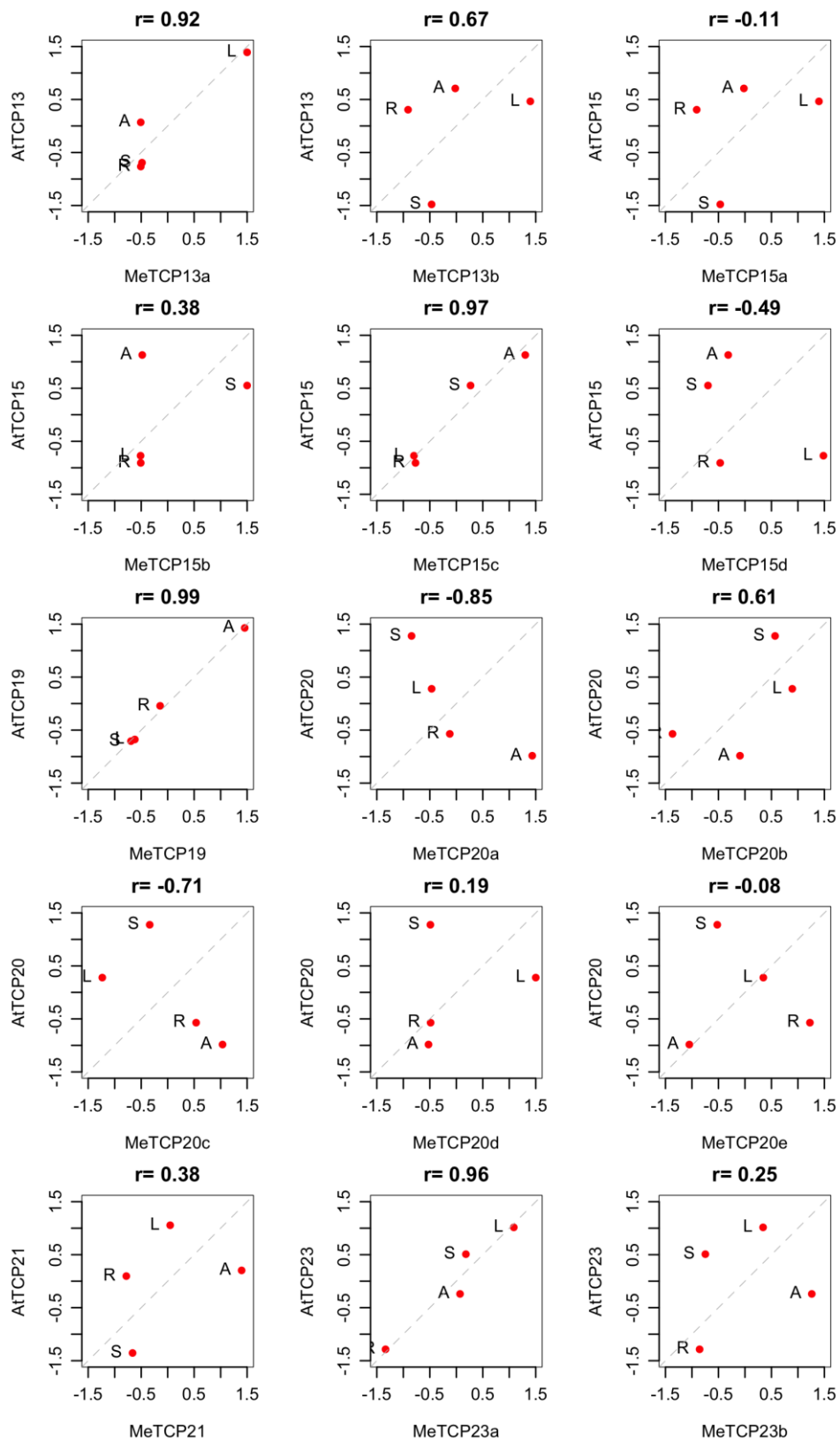


Figure S5. Motifs identified in the promoter of *MeTCPs* by MEME.

