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*.

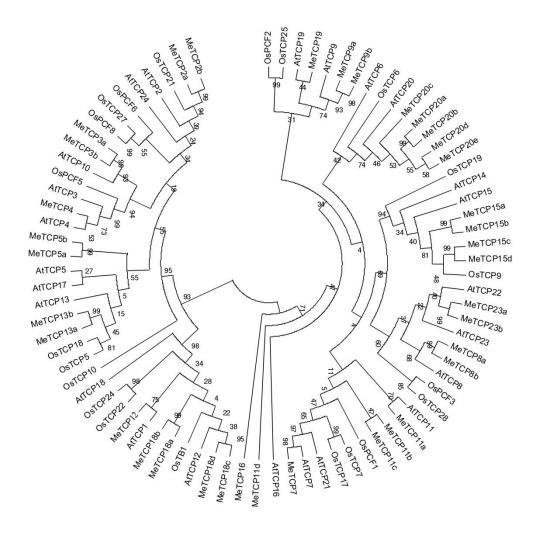


Figure S2. Protein motifs of MeTCPs identified by MEME.

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PRHIKYEGRORRURUSA CAARUFBLIBE GUKEDGETUEWLLEARDAL
Motif 1
Motif 2
Motif 3 PAEJKDFQJ&JADKED9KKQLAPKRSSNK
Motif 4 NMG-MsF-SufsGsNQQJPGLFLGLSQDGH.GVLNPQALsQFYQQMGQ-R
Motif 5 RELEASE BLARYS REGEROR S
Motif 6
Motif 7 PRINTPAPMALLPSQQLG
Motif 8 LNUSLRSSGSSLSACESEE
Motif 9 SECONDENSE LEKTER FEGE EERS NISE OF INE GNE WAS LEKTER FEGE EERS
Motif 10
Motif 11
Motif 12 SIGAL ASILLES EMLESS
Motif 13
Motif 14
Motif 15 Manual Que
Motif 16 NKEGFKING, INW DESEL RENFWSSD LLK KSKEYARDS, LEKENW
Motif 17
Motif 18 MERINOGURENA SEQUES SECTIONS
Motif 19
Motif 20
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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.

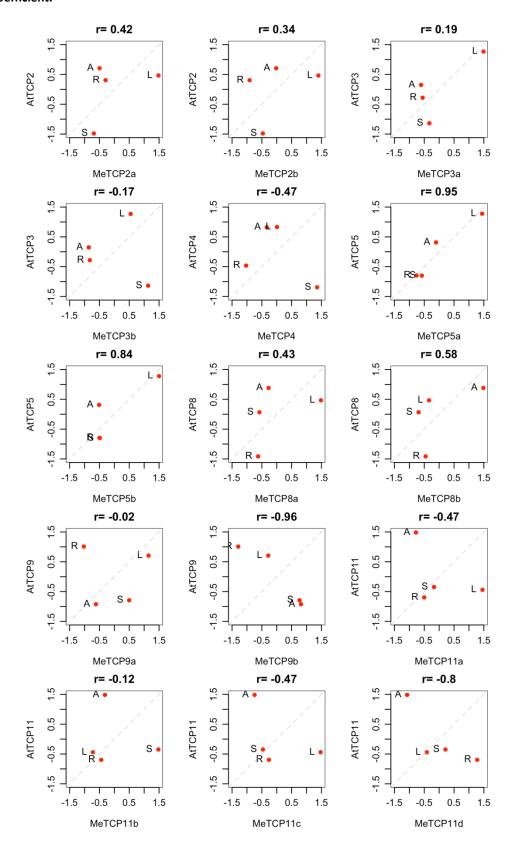


Figure S4. Scatterplot showing the correlation of TCP expressional value (z-score) between Arabidopsis and Cassava homologous genes (Part 2). R indicates root,L indicates leaf, A indicates apex, and S indicates stem, respectively. r indicates pearson correlation coefficient.

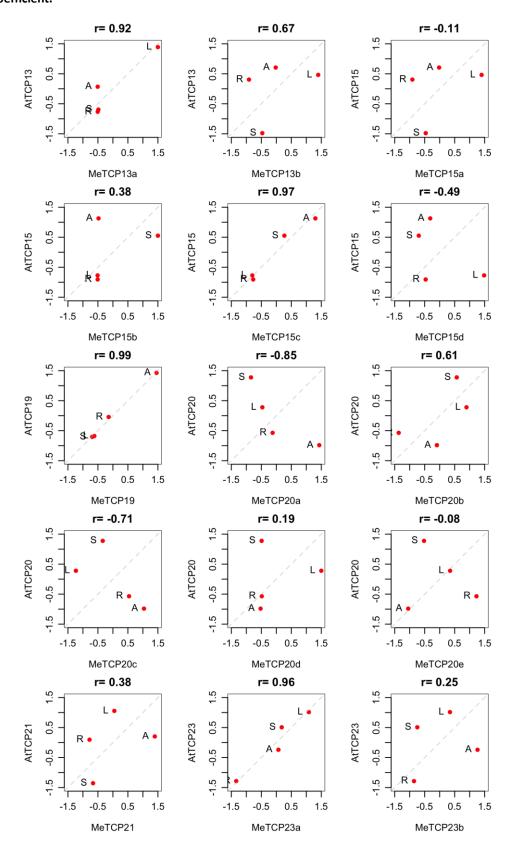


Figure S5. Motifs identified in the promoter of MeTCPs by MEME.

