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**Figure S1.** Phylogenetic tree of *TCP* genes in maize

The phylogenetic tree was constructed based on the sequence alignments of full-length protein sequences of 46 ZmTCP in maize. The neighbor-joining (NJ) method was implemented in MEGA 7.0 software by combining with the JTT model and the complete-deletion option, and bootstrap values from 1,000 replicates were shown at each node.



**Figure S2.** Comparison of survival rates between maize inbred lines carrying a ZmTCP42 drought tolerant or sensitive allele. The allelic grouping was based on the most significant polymorphisms in the 5′-UTR. “AA” indicates the tolerant allele, while “GG” indicates the sensitive allele. Mixed linear model in TASSEL program was applied to analyze the statistical differences of survival rate in maize seedlings.