

Figure S1. Schematic illustration of 3-D protein structures and the Ramachandran plot for TaELP proteins.

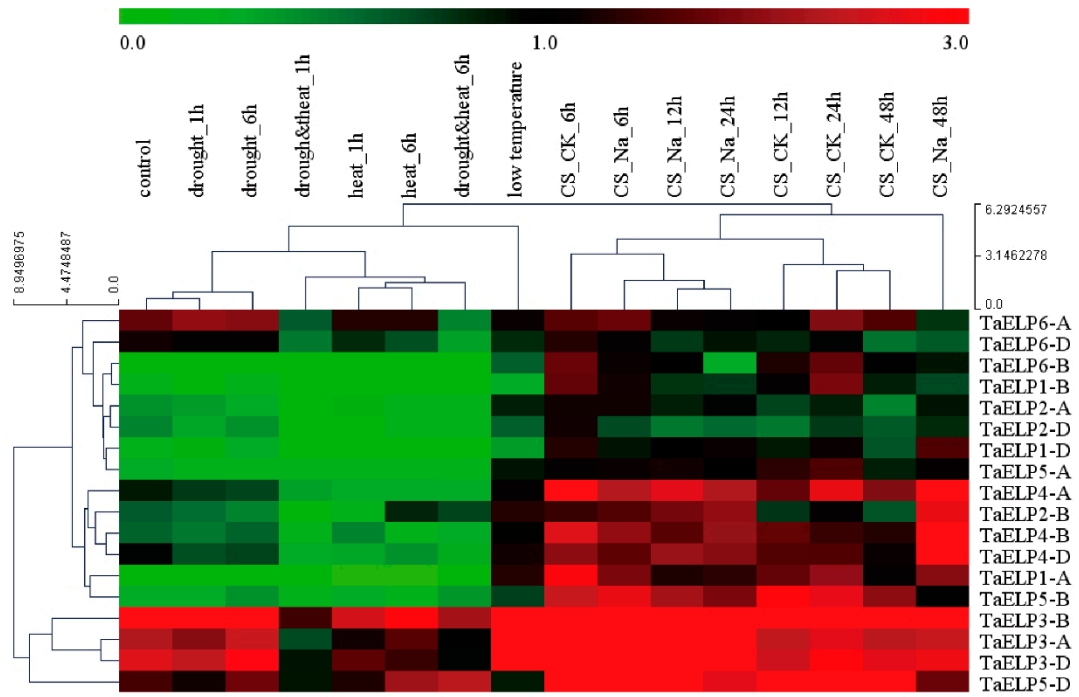


Figure S3: Heatmap representing the expression patterns of *TaELP* genes under different abiotic stress conditions. The TPM values are used directly to build the heatmap. CS: Chinese Spring Na: salt stress h: hours.

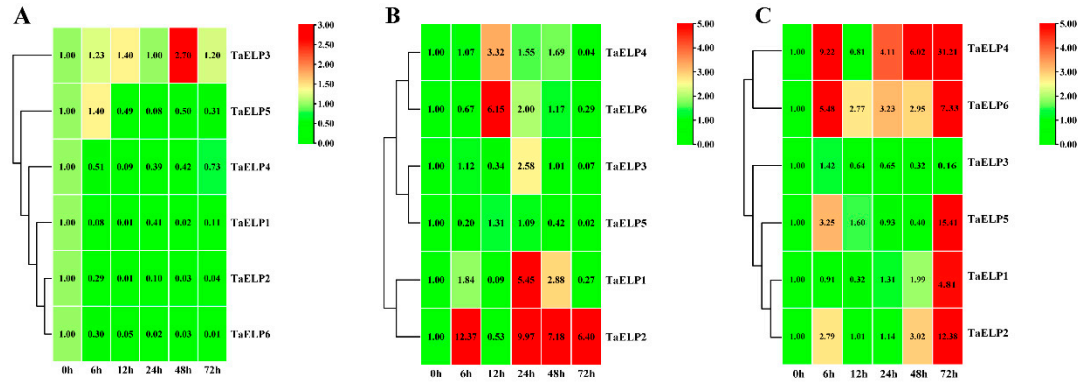


Figure S4. Relative transcript profiles of *TaELPs* in response to (A) Indole-3-acetic acid (IAA), (B) salicylic acids (SA), (C) abscisic acid (ABA). The relative transcripts of all genes were analyzed using qRT-PCR. The relative transcript levels of *TaELPs* were measured using the comparative threshold ($2^{-\Delta\Delta CT}$) method. Data normalized with the transcripts of wheat elongation factor, *TaEF-1 α* . The 0 h post-treatment (A, B, C) was used as a control and standardized with 1. Red and green colors denote strong and weak transcription of *TaELPs*, respectively. The heat map was generated with TBtools and the tree was constructed with the average linkage clustering method.

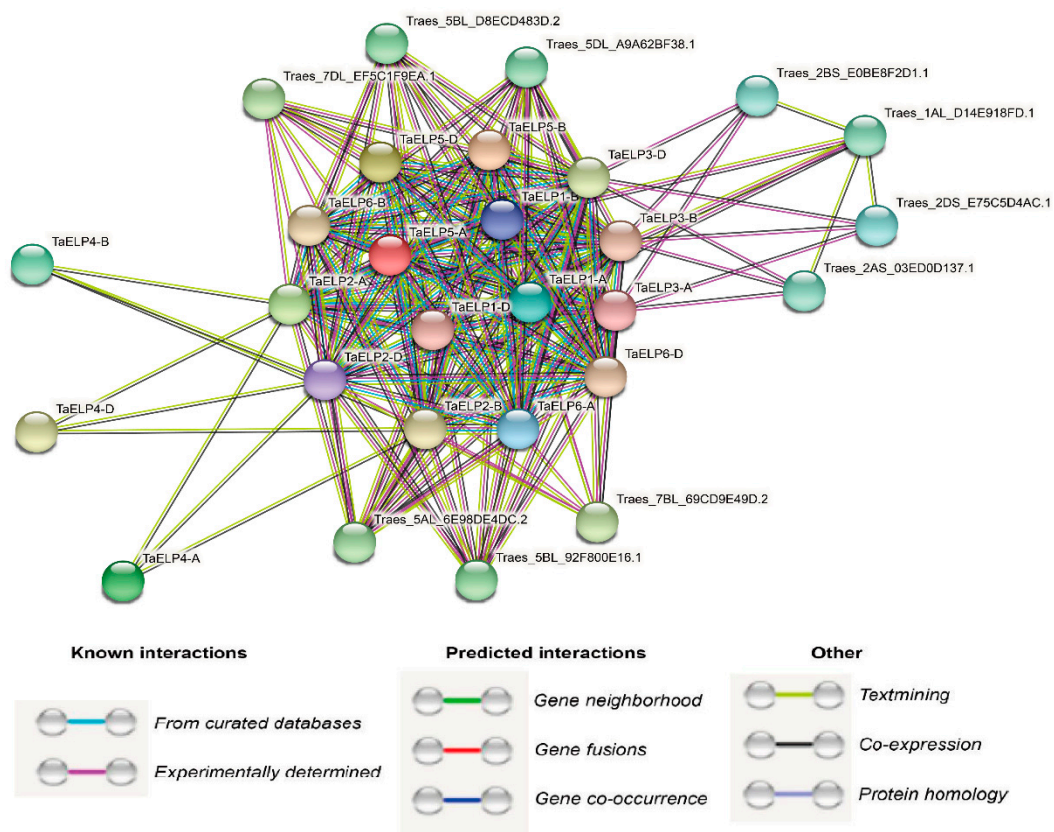


Figure S5. Protein-protein interaction analysis of TaELP proteins. Protein-protein interaction network generated by STRINGV9.1. Each node represents a protein and each edge represents an interaction, colored by evidence type.