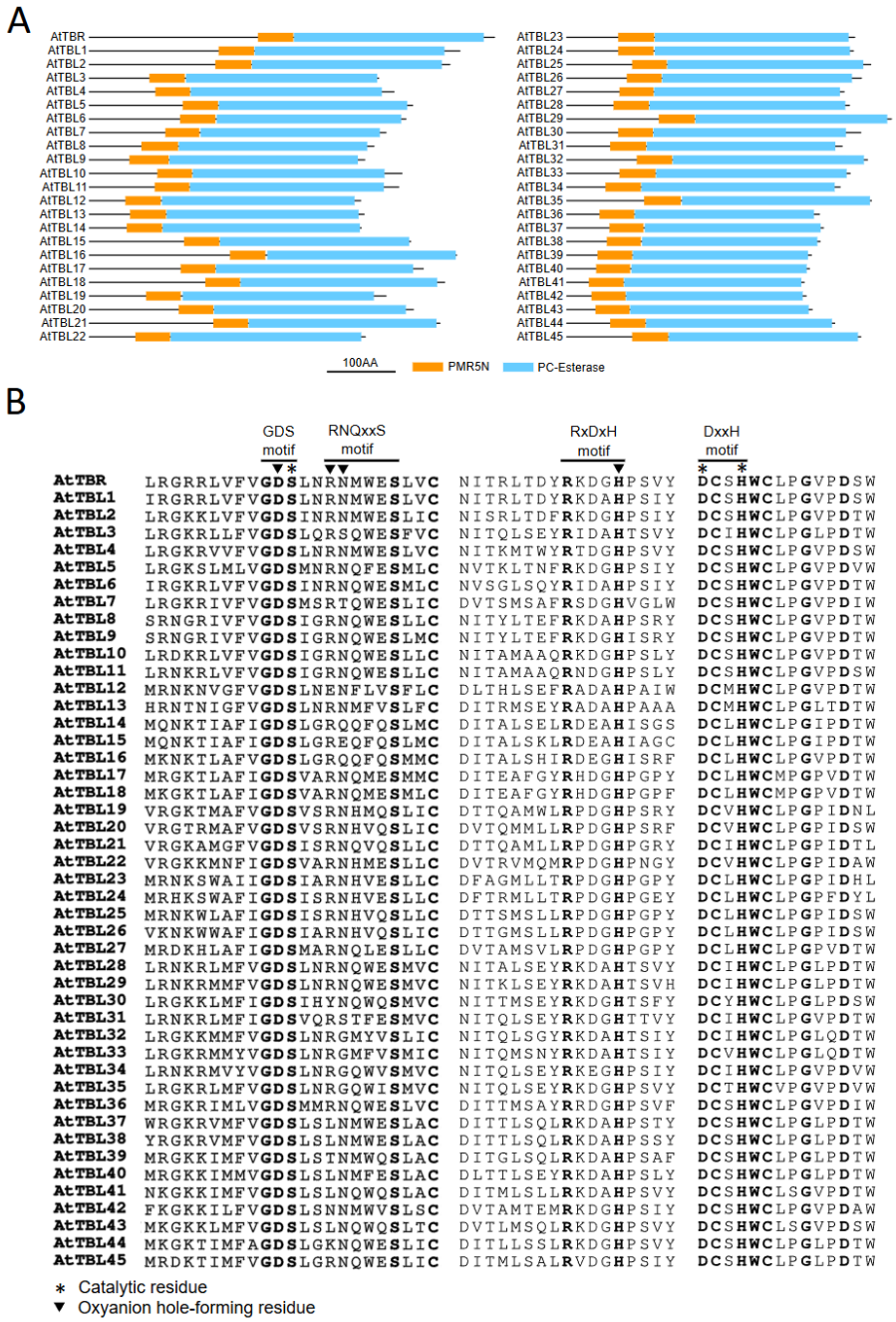


Figure S1 Protein domain prediction and alignment analysis of AtTBL proteins. **(A)** Predicted conserved protein domains of AtTBL proteins. The black lines represent the length of each protein sequence, and the conserved protein kinase domains are depicted with colored boxes. blue boxes represent PC-Esterase domain and orange boxes represent PMR5N domain. **(B)** Multiple sequence alignment analysis of AtTBL proteins, Catalytic residues of AtTBL proteins are marked by "*".

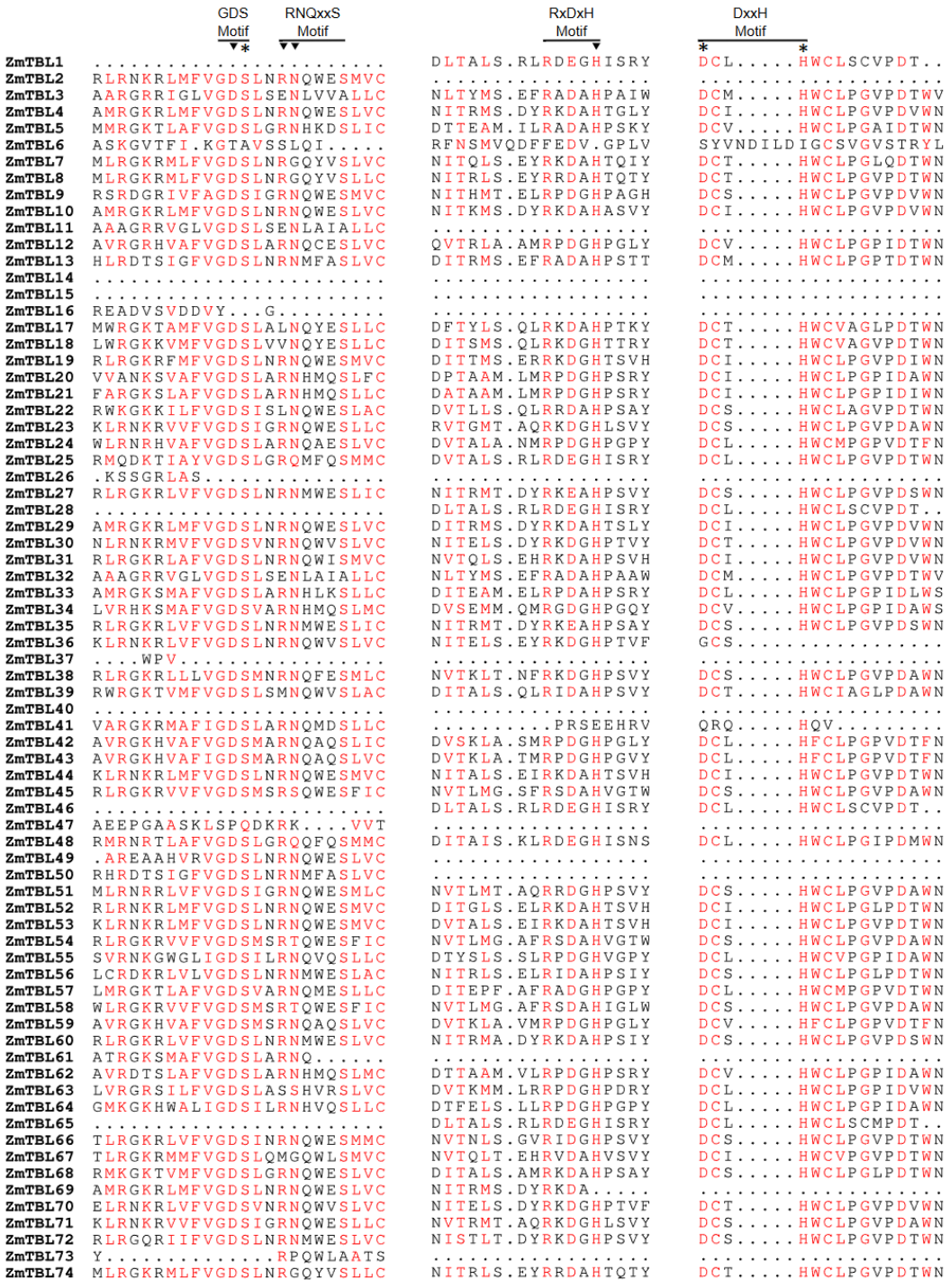


Figure S2 Multiple sequence alignment analysis of maize TBL proteins. Catalytic residues of ZmTBL proteins are marked by "*".

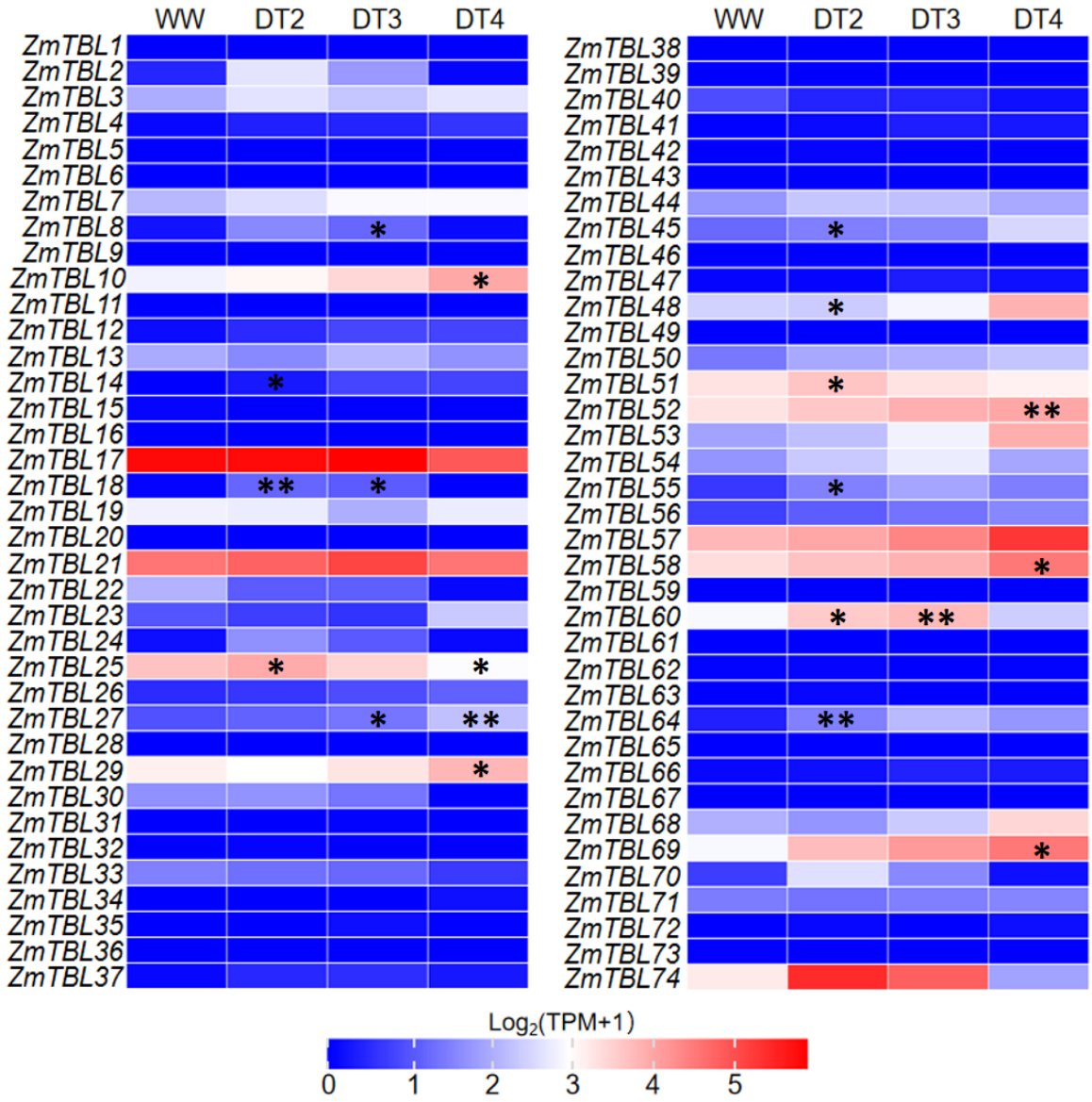


Figure S3 Expression analysis of *ZmTBLs* under drought stress. The genes were labeled on the left and the drought stress treatments were displayed at the top of each column. The TPM values of the *ZmTBLs* were used to draw a heat map by using HEMI. Statistical significance was determined by Student's t test: "*" $P < 0.05$ and "**" $P < 0.01$.

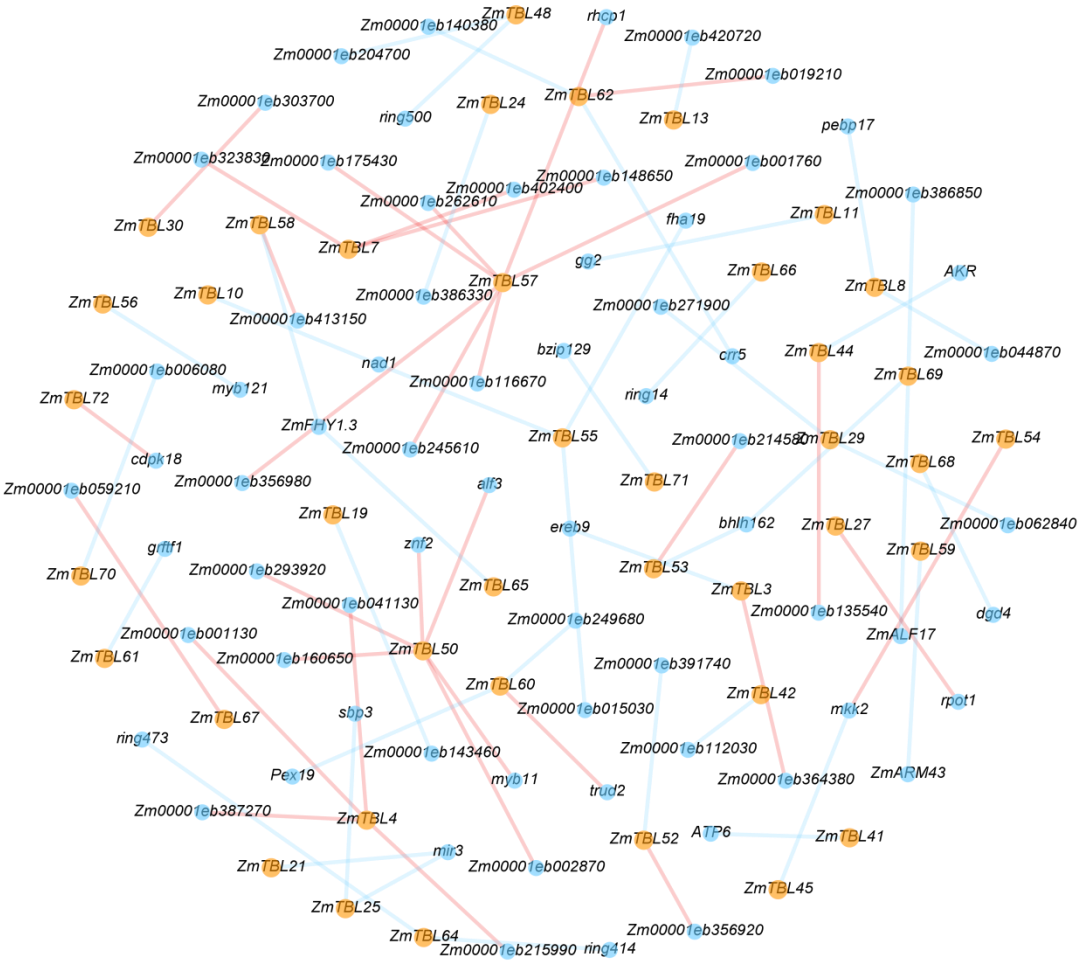


Figure S4. Interacting proteins of ZmTBLs. Interaction Protein-ZmTBL pairs are shown in blue and red line, respectively, corresponding to low confidence and high confidence.

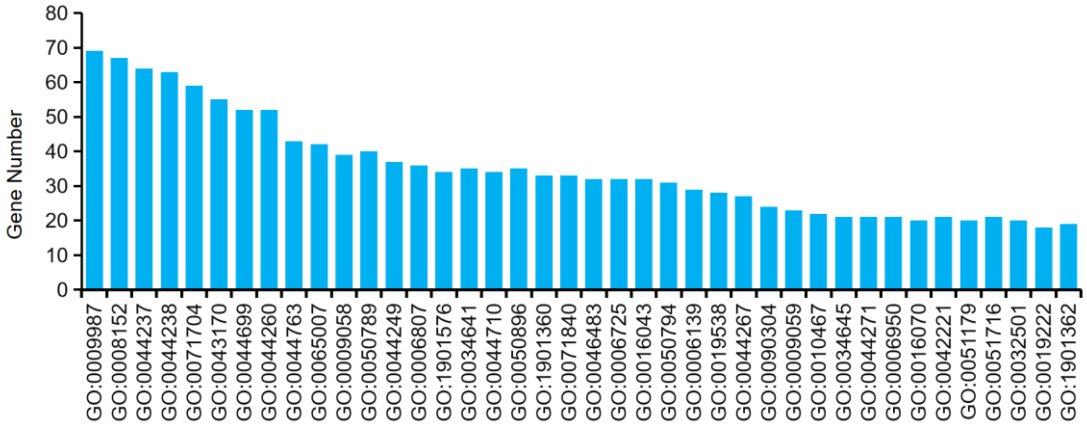


Figure S5. GO annotation of ZmTBL interaction protein coding genes.