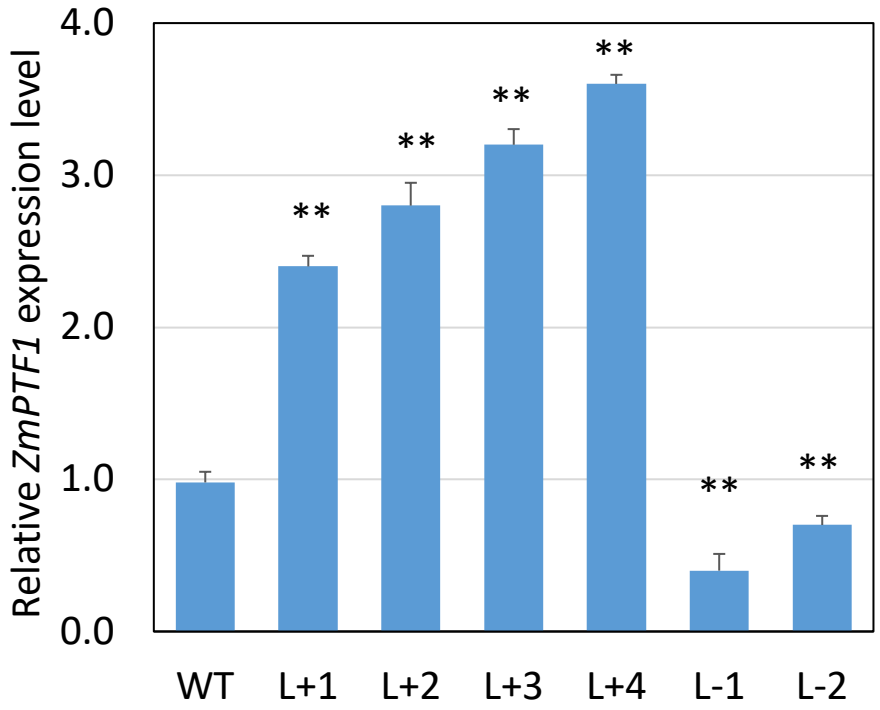

Figure S1 Real-time RT-PCR analysis of *ZmPTF1* expression in the roots of the maize transgenic lines used in this paper

L+1, L+2, L+3 and L+4 are the *ZmPTF1* overexpression lines, L-1 and L-2 are the antisense lines, WT is the wild type control DH4866. The roots from different lines were collected from the 3-leaf stage maize plants cultured in the nutrient solution. The value of the WT was taken as one fold. The values are the means ± sd; three biological replicates were used for real-time RT-PCR. The asterisks indicate significant differences between the transgenic and WT lines at the **0.01 level according to *t*-tests.

Figure S1

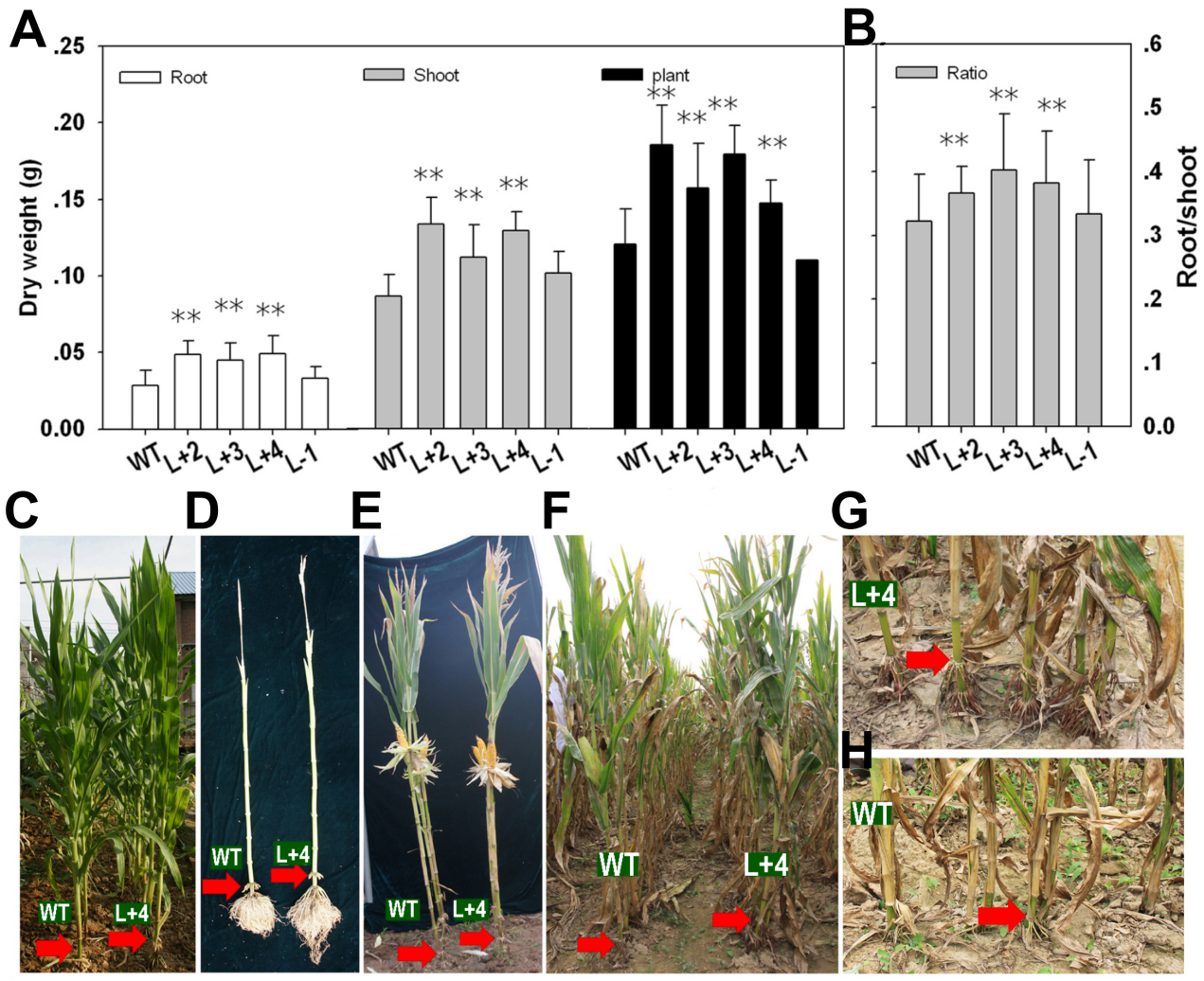

Figure S2 Biomass and morphological analysis of the *ZmPTF1* overexpression and antisense lines and the WT plants

A Biomass analysis of seedlings of the *ZmPTF1* overexpression and antisense lines and WT grown in nutrient solution. B The root/shoot ratio of seedlings of the *ZmPTF1* overexpression and antisense lines and WT grown in nutrient solution. The asterisks indicate significant differences between the transgenic and WT lines at the **0.01 level according to *t*-tests, six biological replicates were used for the experiment. C~H Morphology of the seedlings of the *ZmPTF1* overexpression line and WT grown in the field. The red rows showed the brace roots of maize.

Figure S2

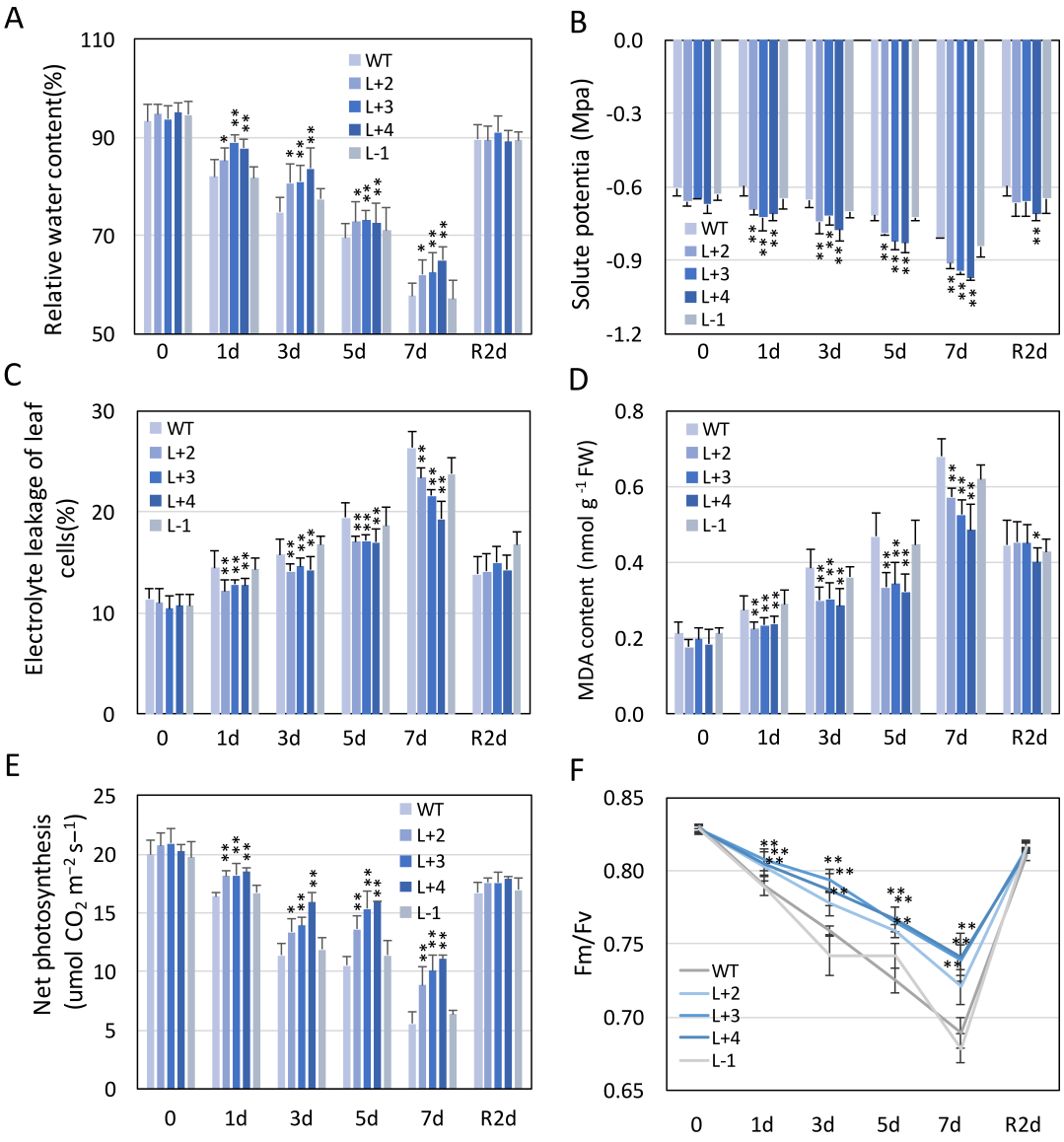

Figure S3 Effects of drought stress on the physiological parameters of the *ZmPTF1* overexpression and antisense lines and the WT plants

Physiological parameters of the WT and the *ZmPTF1* transgenic plants subjected to drought stress A Relative water content, B Soluble sugar content, C Electrolyte leakage of leaves, D MDA content, E Net photosynthetic rate and F Fv/Fm. The plants used were same as described in Figure 5E to G. The ear leaves at the pre-flowing stage were used to determine the physiological parameters at 0, 1, 3, 5, 7 days of drought stress treatment and 2 days re-watered (R2d). L+2, L+3 and L+4 are the *ZmPTF1* overexpression lines, L-1 is the antisense line, WT is the wild type control DH4866. The values are means ± sd, at least three biological replicates were used for the experiment. The asterisks indicate significant differences between the transgenic and WT lines at the *0.05 or **0.01 level according to *t*-tests.

Figure S3

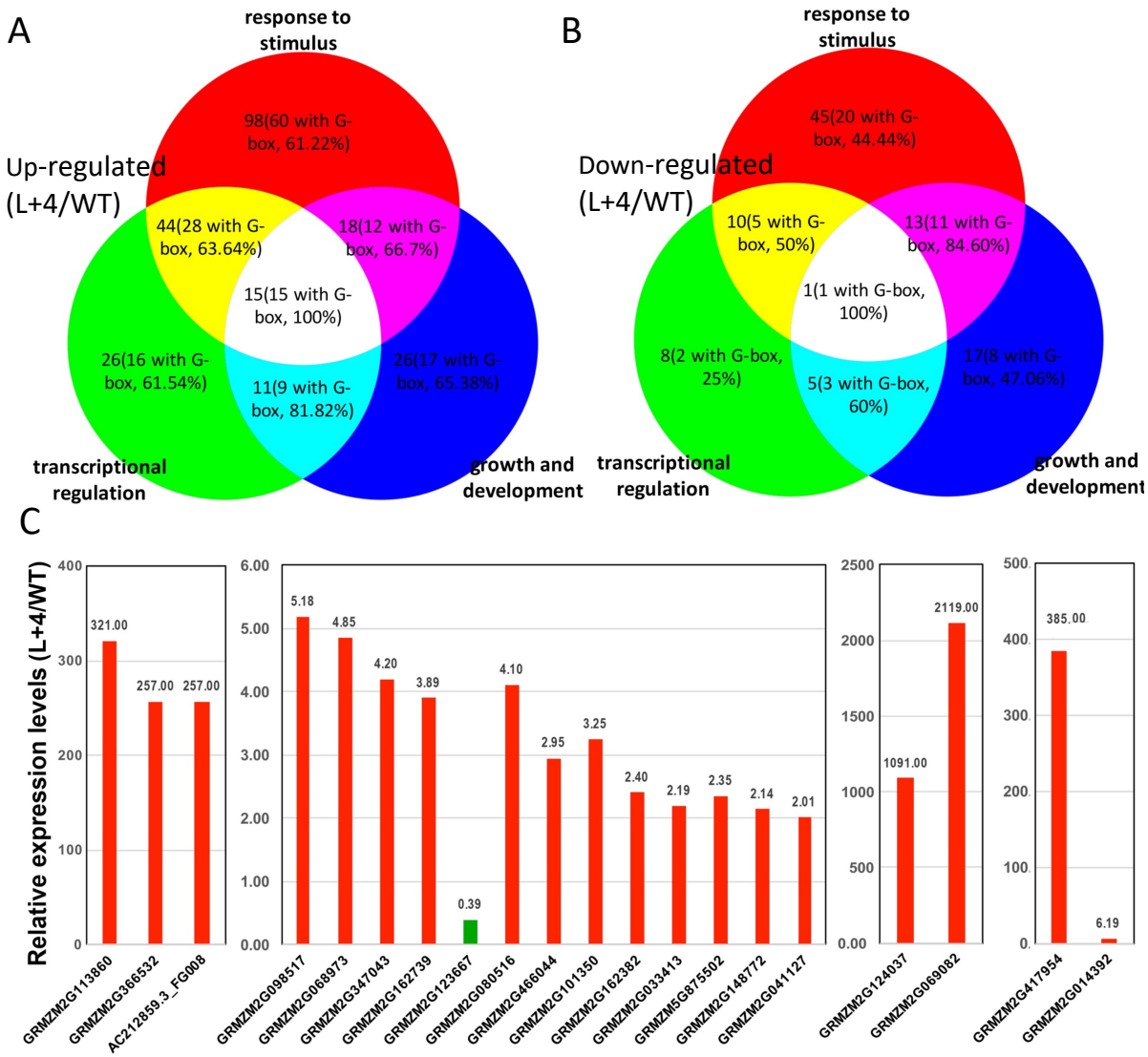

Figure S4 Overexpression of *ZmPTF1* activated stress responses and modified transcriptional regulation

A and B Analysis of the differentially expressed genes involved in the GO categories response to stimulus, growth and development and transcriptional regulation and the percentage of G-box elements in these genes. A was the up-regulated differential expressed genes and B was down-regulated differential expressed genes; C Key genes involved in stress stimuli, development and transcriptional regulation. The criterion "FDR $\leq$ 0.001 and the absolute value of log2Ratio(L+4/WT) $\geq$ 1" was used as the threshold to judge the significance of gene expression differences.

Figure S4

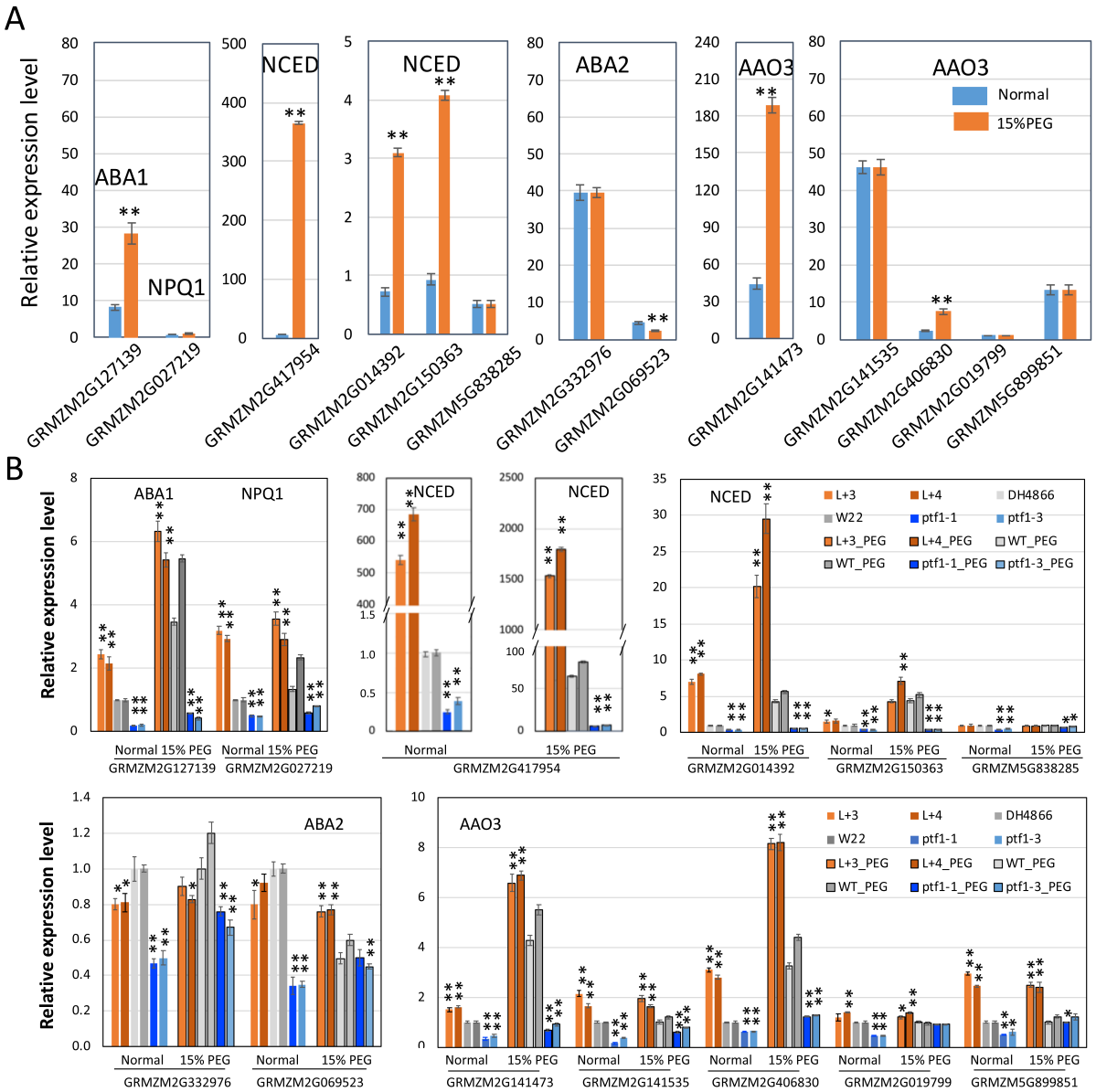

Figure S5 Expression levels of the key genes involved in ABA biosynthesis in the roots of different lines under normal and 15% PEG8000 treatment conditions

A Expression levels of the key genes involved in ABA biosynthesis in the roots of WT line (DH4866) under normal and 15% PEG8000 treatment conditions. The plants cultured in a normal nutrient solution for 11 days and then transplanted into nutrient solutions with and without 15% PEG8000 for another 24 h, the roots were used for gene expression analysis. The levels of the gene transcripts were calculated using the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001) with maize *Actin1* (NM_001155179.1) as an internal control, and the level of 1/32 *Actin1* was set as 1-fold (Li *et al.*, 2018). The values are the means ± sd; three biological replicates were used for real-time RT-PCR. B Expression levels of the key genes involved in ABA biosynthesis in the roots of

different lines by using real-time RT-PCR. the *ZmPTF1* overexpression lines, WT DH4866 plants, *ZmPTF1* Mu insertion lines and WT W22 under normal and 15% PEG8000 treatment conditions The levels of the gene transcripts were calculated using the $2^{-\Delta\Delta Ct}$ method (Livak and Schmittgen, 2001) with maize *Actin1* (NM_001155179.1) as an internal control, and the levels of WT under normal conditions (DH4866 and W22) were set as 1-fold. L+3 and L+4 are the *ZmPTF1* overexpression lines in the DH4866 background. *ptf1-1* and *ptf1-3* are the *ZmPTF1* Mu insertion lines in the W22 background. The values are the means ± sd; three biological replicates were used for real-time RT-PCR. The asterisks indicate significant differences between the *ZmPTF1* transgenic, Mu insertion lines and their corresponding wild-type control at the *0.05 or **0.01 level according to *t*-tests.

Figure S5