Table S1. RT-qPCR, PagPIP2;10 CDS and selected primers used in this study.

Gene name/ ID	Forword primer	Reverse primer
qRT-PCR		
PagPIP2;10/Potri.012g085700	CCACCGATCCTAAGCGGAAC	ATGCCAGTTCCAGTGATGGG
PagPIP2;10 /CDS	ATGAGTAGTGAAGAGAGAAACAT	AGTCTGCCCACAACCGAGA
Selected preimer		
35S/NOS	GAAGTTCATTTCATTTGGAGAGA	ATTGCCAAATGTTTGAACGATC

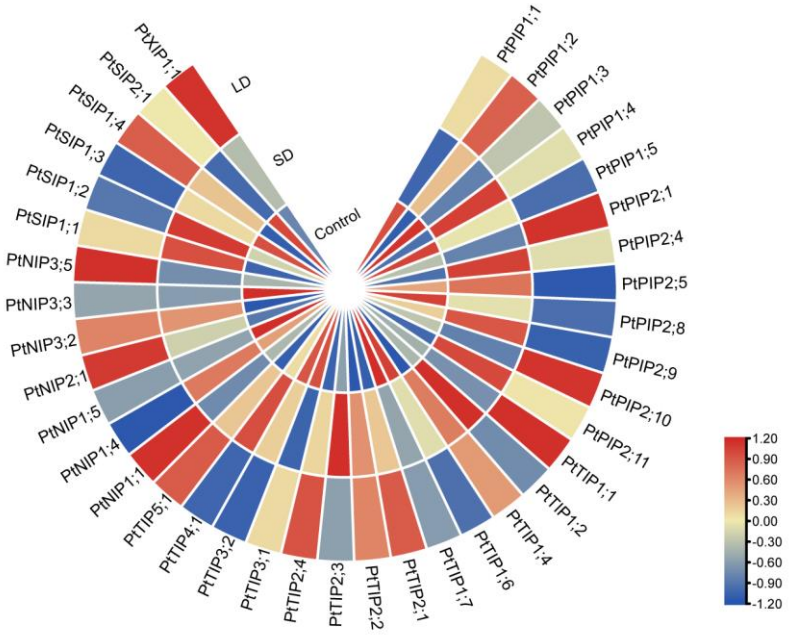

Figure S1. Expression analysis of *AQPs* family genes in poplar under drought stress. LD, long drought; SD, short drought.

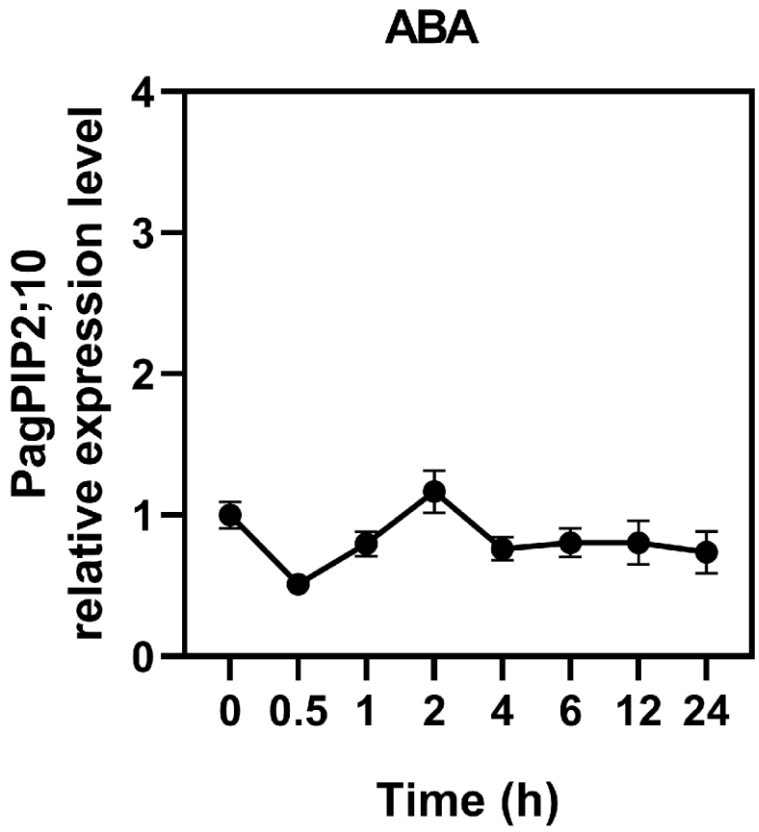

Figure S2. Expression level of *PagPIP2;10* after treatment of ABA.

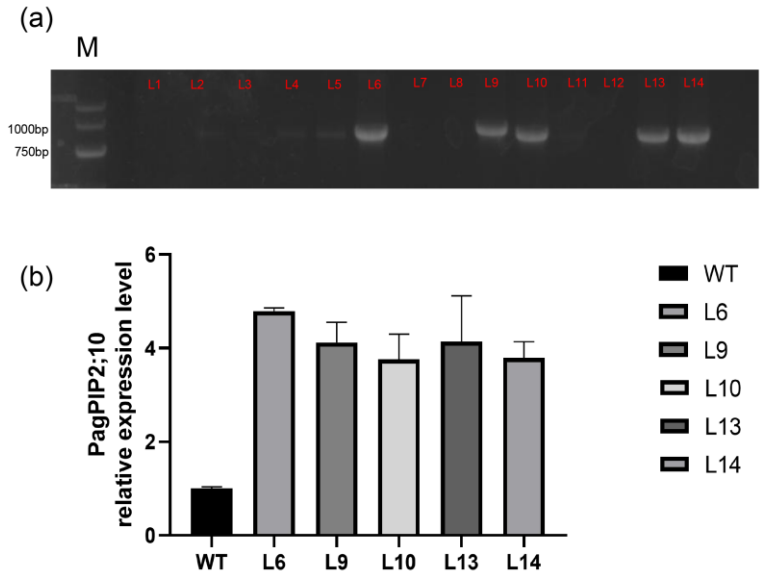

Figure S3. Selection of overexpression lines. (a) PCR analysis of plants; (b) Relative expression level of *PagPIP2;10* in selected lines by RT-qPCR.

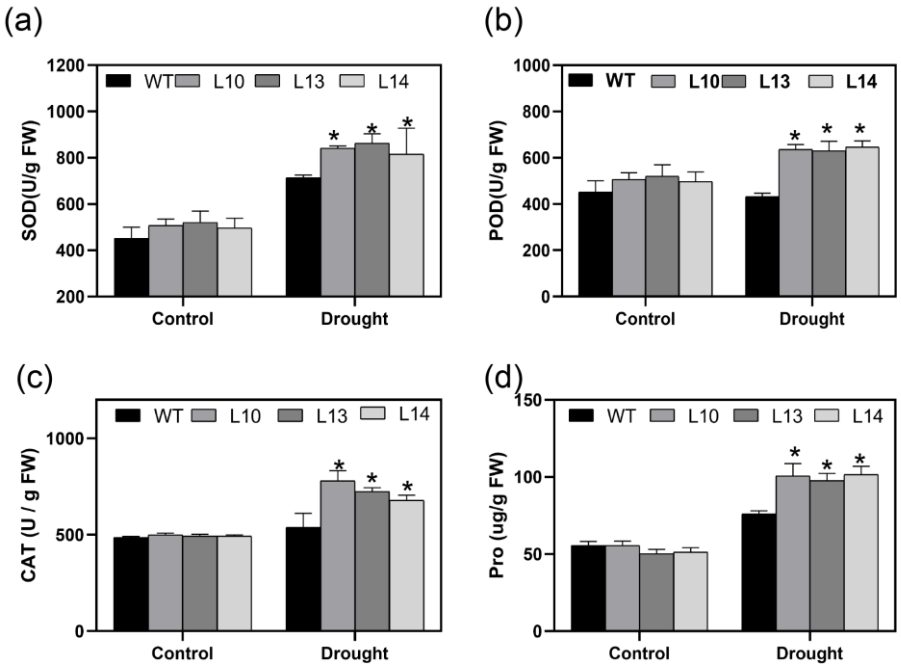

Figure S4. Activity of antioxidant enzymes in WT and overexpression lines after nine days of water deficit; (a) SOD activity; (b) POD activity; (c) CAT activity; (d) Proline content. Each treatment was performed with three biological replicates (n=3) and values are means ± SE. Data were analyzed through Student's t- test in the ANOVA program of SPSS (IBM SPSS17.0). * indicates a significant difference compared with the control (*$P<0.05$).

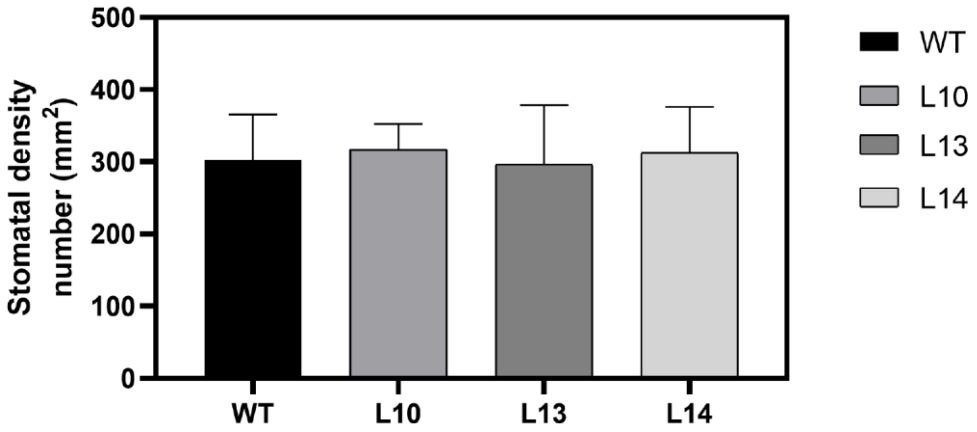

Figure S5. Stomatal density of WT and *PagPIP2;10ox* lines. Error bars are means ± SE (n = 30). Data were analyzed through the Student's t- test in the ANOVA program of SPSS (IBM SPSS17.0).