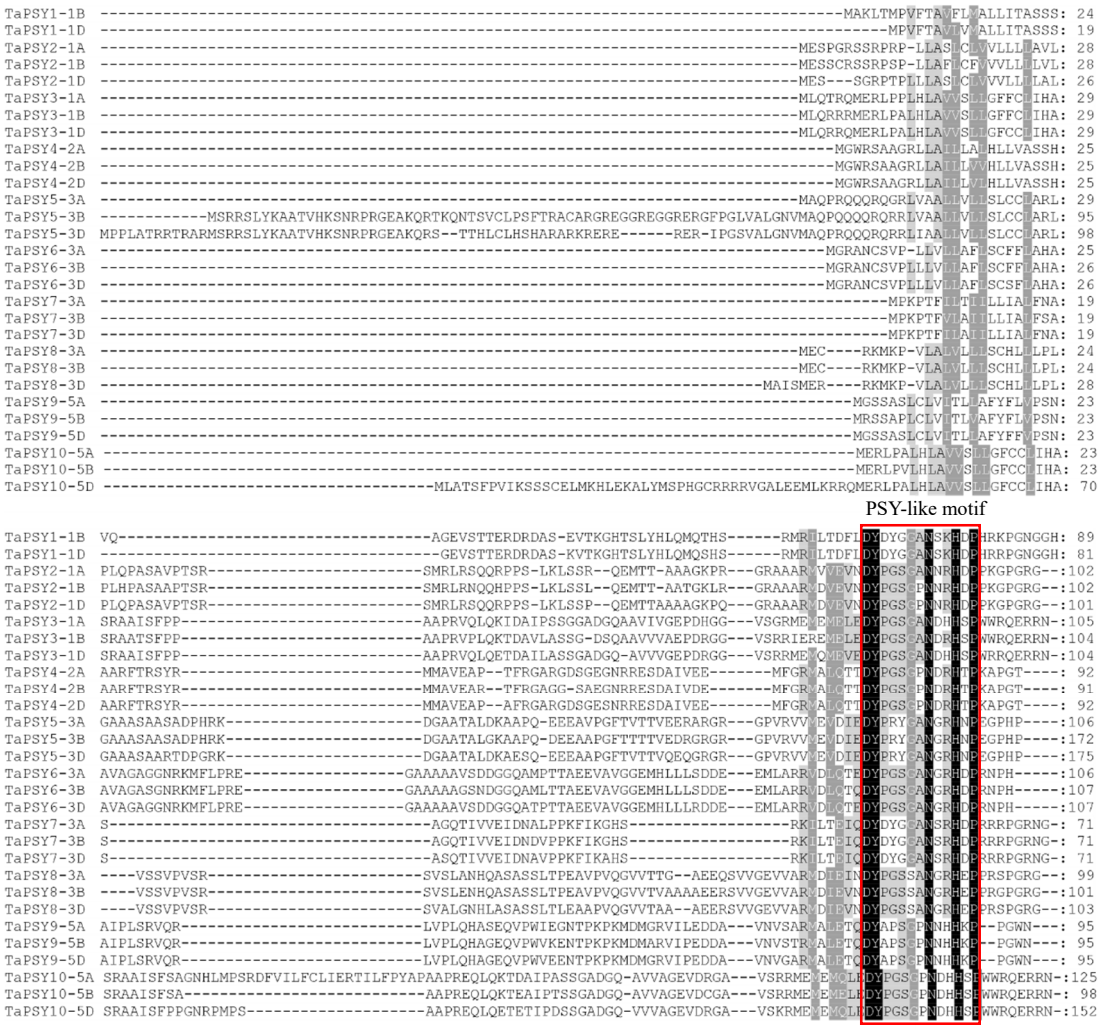

Figure S1. Alignment of predicted TaPSYs amino acid sequences with a signature PSY-like motif in the C-terminal region.

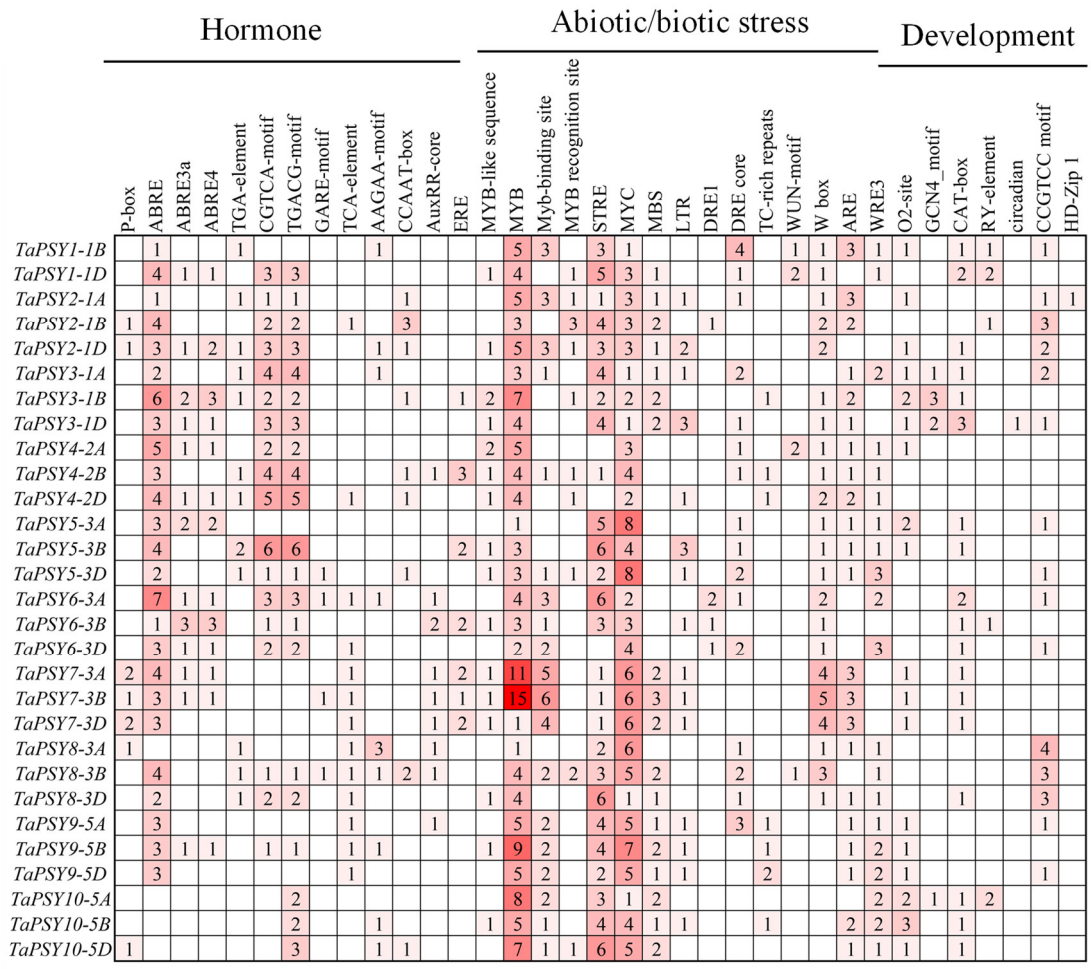

Figure S2. Prediction of cis-acting regulatory elements in the *TaPSY* gene promoters.

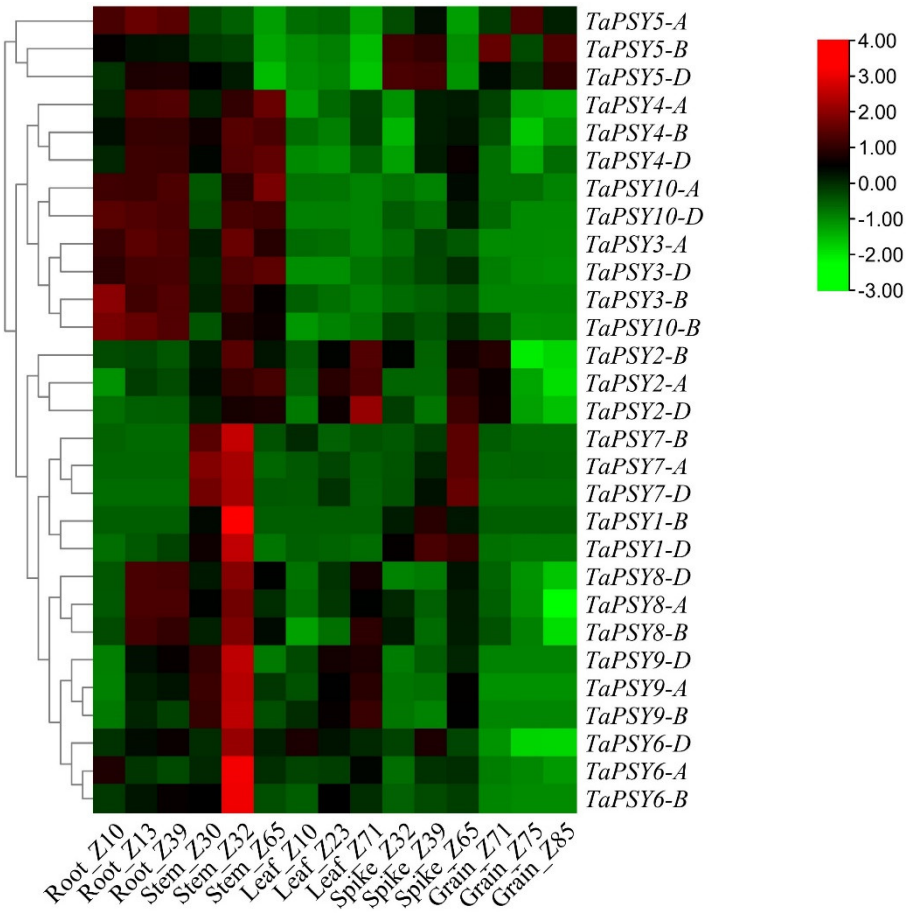

Figure S3. Heatmap of *TaPSY* gene expression patterns in five different tissues at three different developmental stages. The RNA-sequence data was obtained from leaves, stems, roots, spikes, and grains at developmental stages. For each tissue, three biological replicates were used. The color gradient (red/black /green) indicates the gene expression level (from high to low).

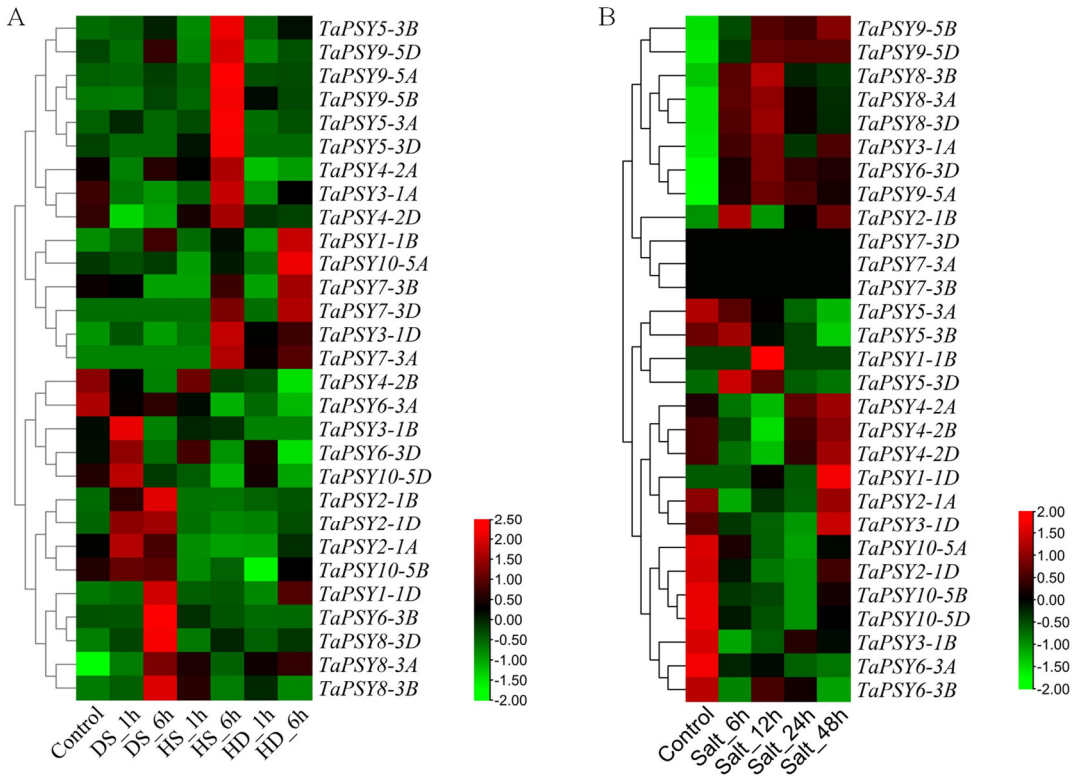

Figure S4. Expression patterns of *TaPSY* genes under drought and salt treatments. The heat maps generated by TBtools show the cluster map of *TaPSY* genes under drought (**A**) and salt (**B**) treatments. Values are created using log2-transformed transcripts per million (TPM) expression values.

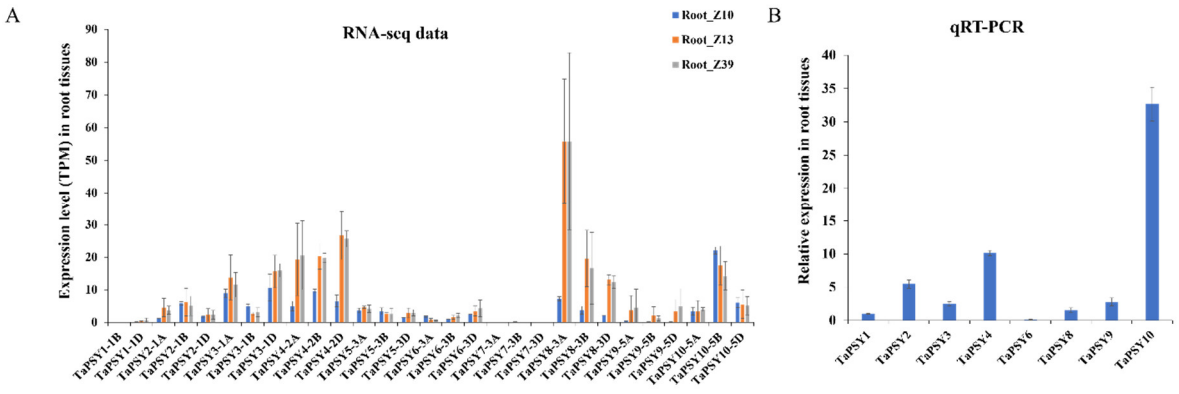

Figure S5. Gene expression of *TaPSYs* in root tissues. (**A**) The expression patterns of *TaPSY* genes in root tissue at different developmental stages using RNAseq data. (**B**) qRT-PCR analysis of selected *TaPSY* genes in root tissues at the seedling stage.