**Analysis of gene expression of selected drought-responsive genes by qRT-PCR**

Based on the results of the RNA-Seq analysis, genes responsive to the drought stress treatment were selected for validation of their expression in leaves and roots of adult plants and leaves in young plants (Supplemental Material Table S11). Actin and eIF4A (Juškyté *et al*., 2022; Hedley *et* *al*., 2010) were selected for normalization. For cDNA synthesis, 1 μg of RNA was reverse transcribed into cDNA using iScript cDNA Synthesis kit (Bio-Rad) in a 20 μL reaction following the manufacturer's instructions. Quantitative real-time PCR of selected genes was conducted with a CFX Opus 384 Real-Time PCR System (Bio-Rad). The amplification was carried out in a reaction mixture containing 5 μL iQ SYBR Green Supermix (Bio-Rad1 μL of primers (mix of forward and reverse primer,500 nM), and 4 μL cDNA (diluted 20-fold) in triplicate for each sample and gene. The PCR program started with polymerase activation at 95 °C for 3 min, followed by 39 cycles of cDNA denaturation at 95 °C for 10 s, annealing and amplification at 60 °C for 30 s, and a melt curve analysis at 65–95 °C with an increment of 0.5 °C and 5 s per step at the end. The relative gene expression and fold change (FC) were determined using the threshold cycle value (Ct) and efficiency based 2−ΔΔCT method described by Ganger et al. (2017), with a modification where log2 transformation was applied instead of log10. The reaction efficiencies were calculated using Real-time PCR Miner (Zhao & Fernald, 2005) averaged for each gene for tissue and treatment. Actin and eIF4A were employed as internal reference genes for normalization. The log2 fold changes (log2FC) were visualized in a heatmap, depicting the upregulation and downregulation of the analyzed genes. Data processing and visualization 725 were performed in R v4.2.2, utilizing the RColorBrewer v1.1-3, dplyr v1.1.4, and EnrichedHeatmap v1.28.1 packages.