

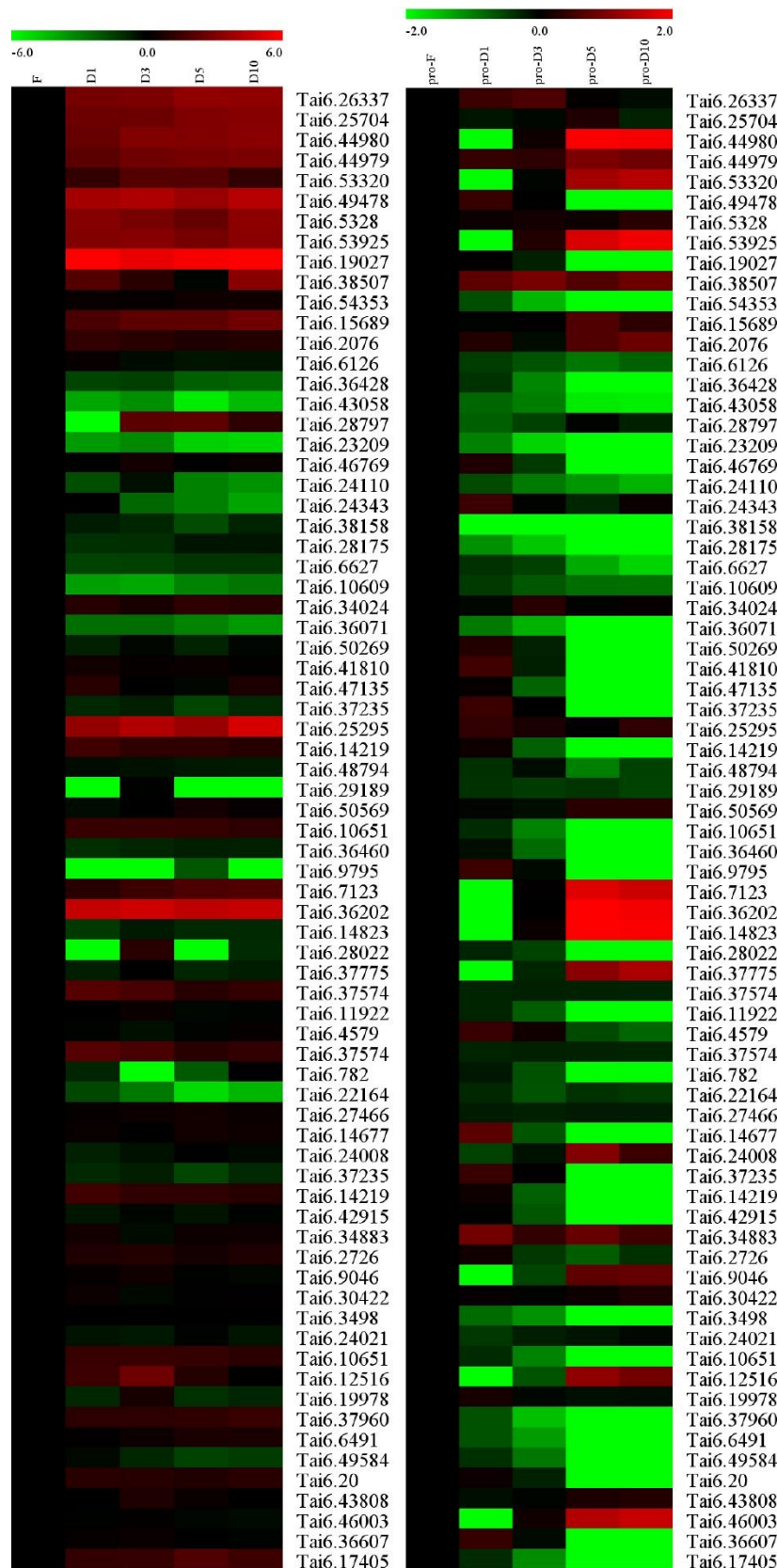


Fig. S6. mRNA (A) and protein (B) expression analysis of related genes detected in fibrous roots (F) and storage roots of D1, D3, D5 and D10 stages. Log₂-transformed fold-change data were used for producing the heatmaps by MeV4.9. The expression levels of fibrous roots (F) were set to 1. The color scales at top indicate the relative expression. Red and green shading indicates the relative high or low expression levels, respectively.