

Figure S1. Pearson correlation coefficient and principal component analysis (PCA) of RNA-seq samples. **(A)** Pearson correlation coefficients of biological replicates. **(B)** PCA of individual biological replicates.

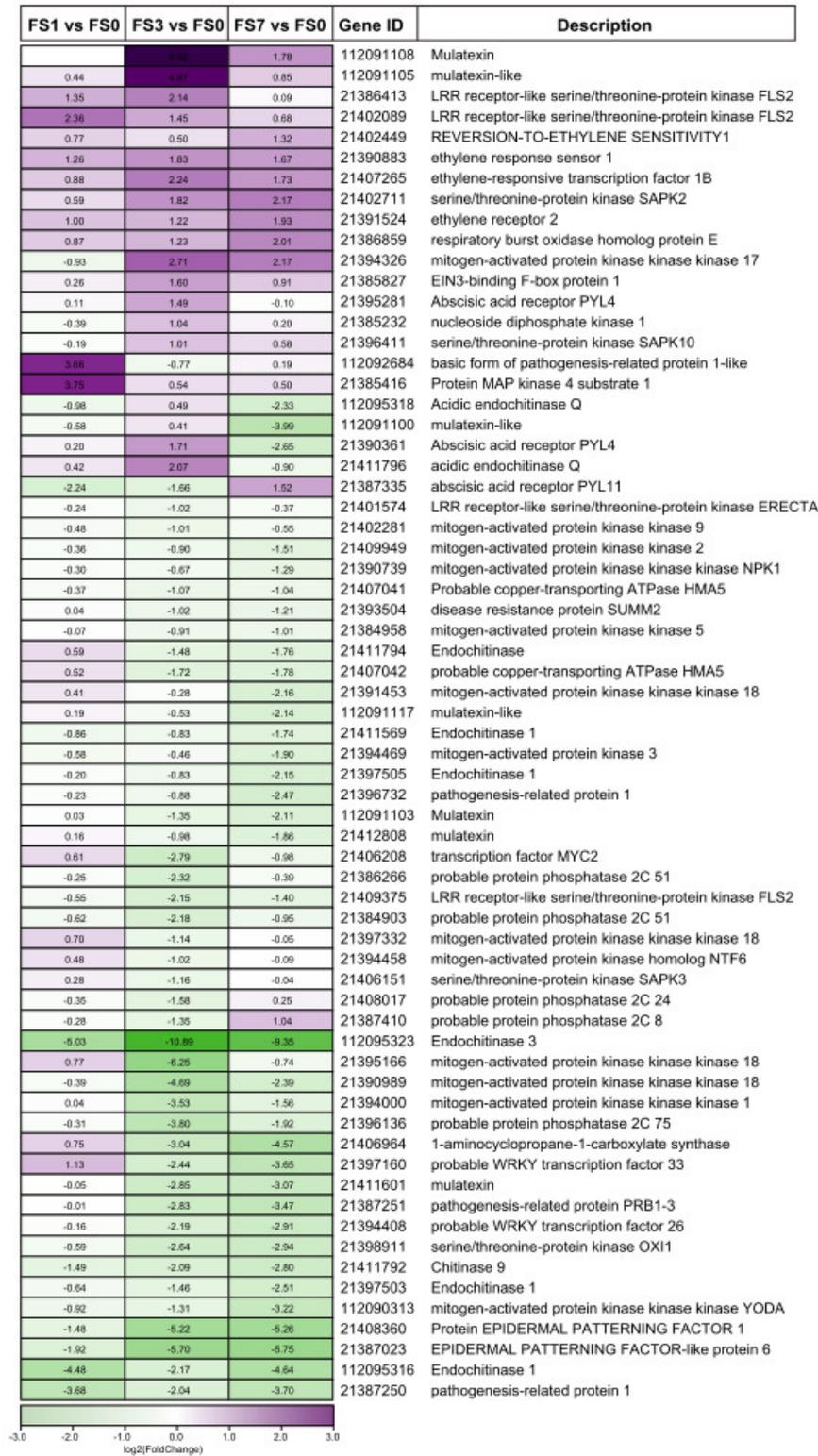


Figure S2. Heatmap of DEGs involved in MAPK signaling. The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.

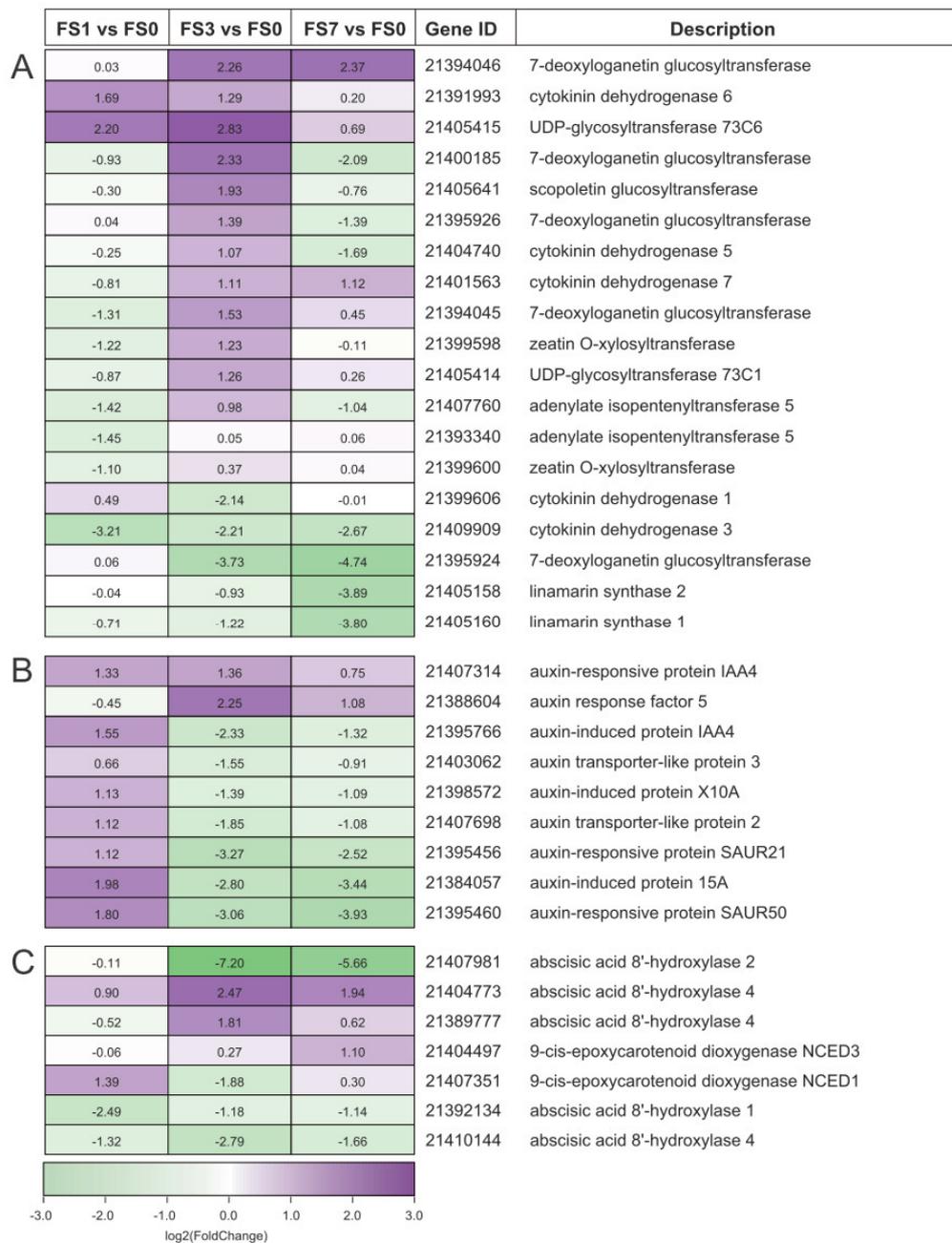


Figure S3. Heatmap of DEGs involved in zeatin (A), auxin (B), and ABA (C) signaling. The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.

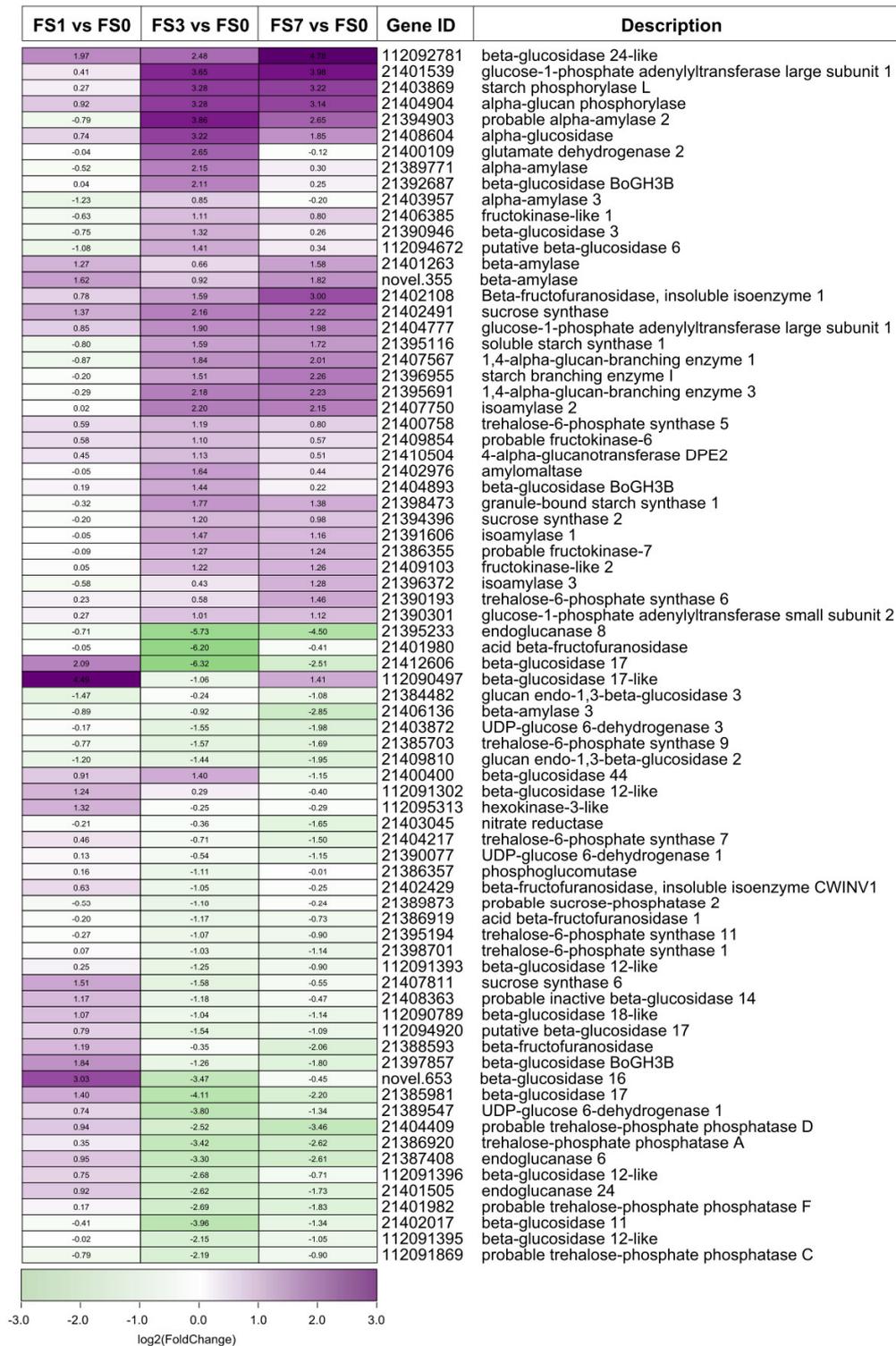


Figure S4. Heatmap of DEGs involved in starch and sucrose metabolism pathways. The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.

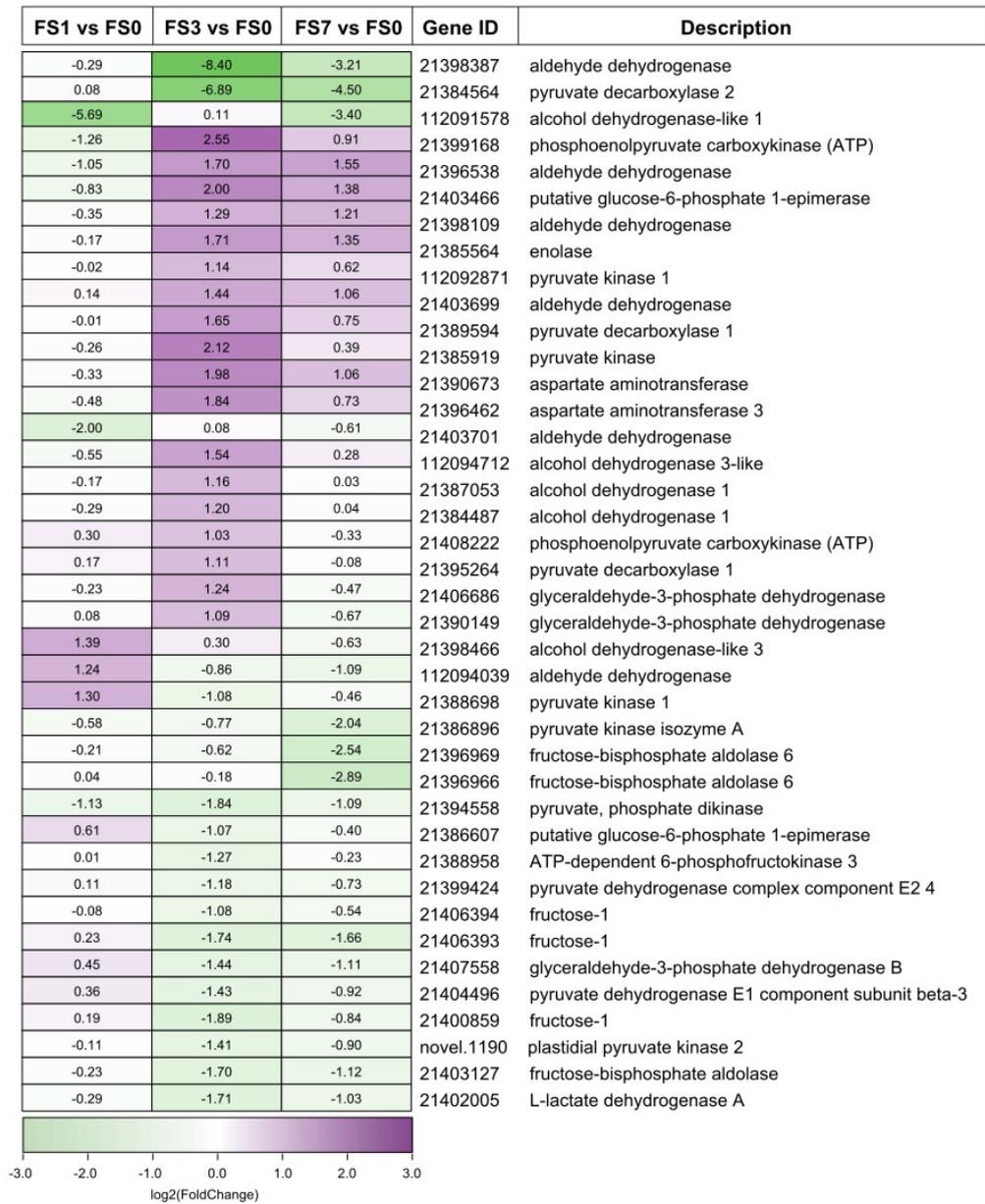


Figure S5. Heatmap of DEGs related to glycolysis/gluconeogenesis. The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.

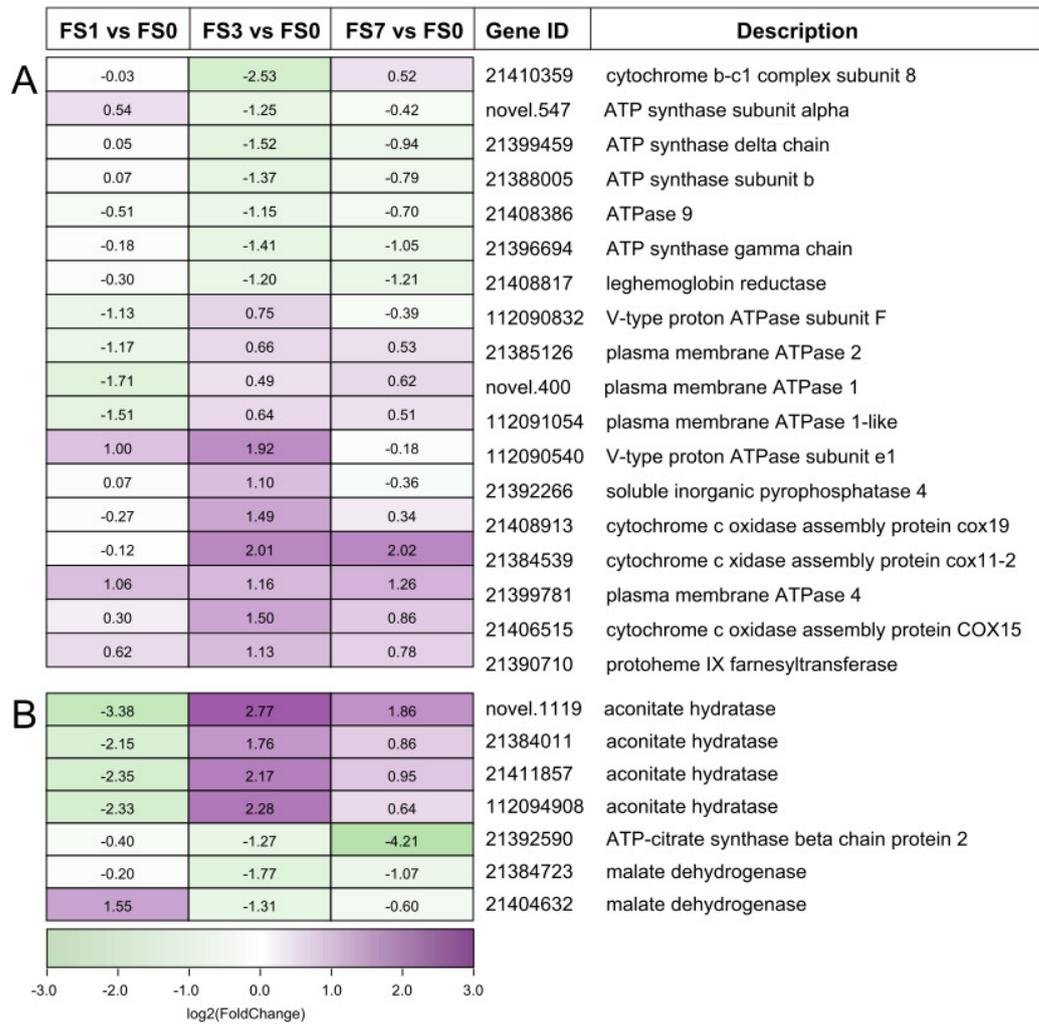


Figure S6. Expression profiles of DEGs related to oxidative phosphorylation (A) and the TCA cycle (B). The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.

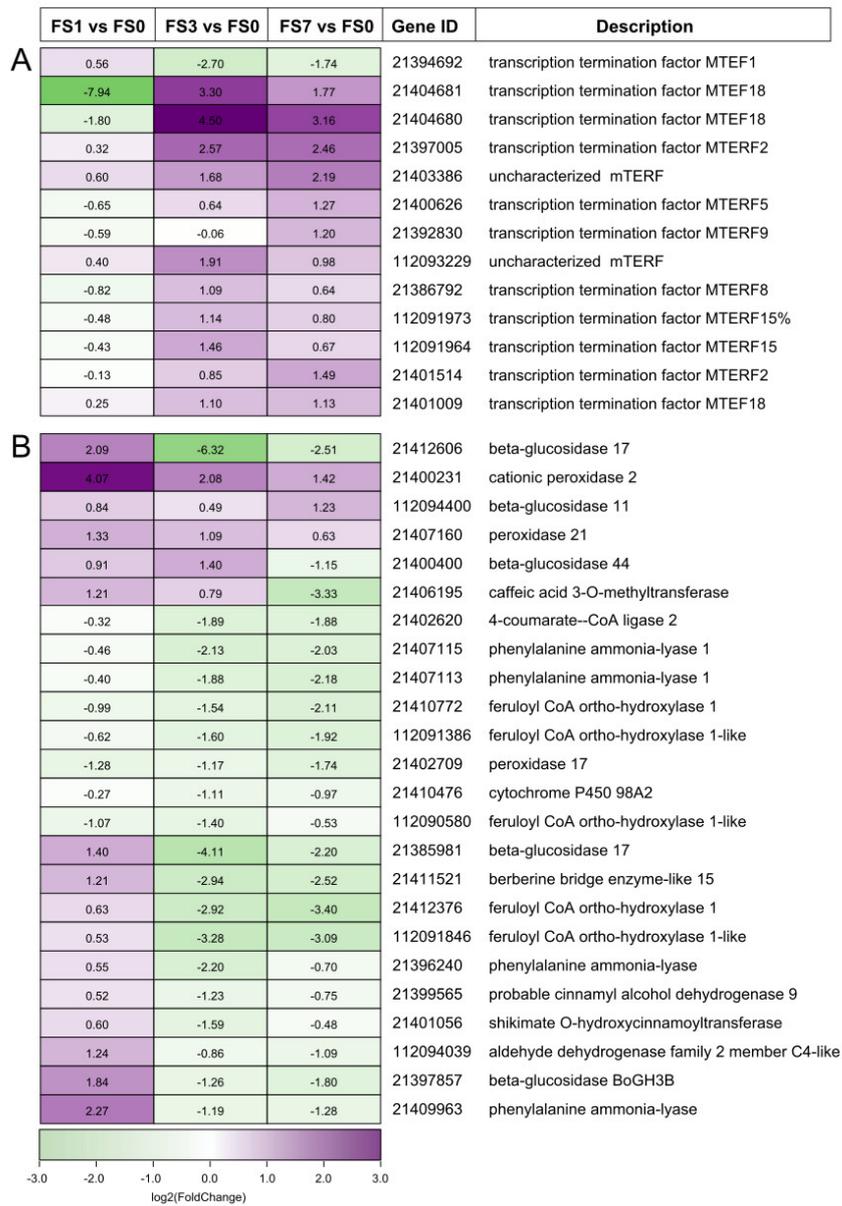


Figure S7. Expression profiles of DEGs related to mitochondrial function (A) and phenylpropanoid biosynthesis (B). The numbers in the heatmap indicate the Log₂(fold change). FS0, FS1, FS3, and FS7 indicate 0 d, 1 d, 3 d, and 7 d after submergence, respectively.