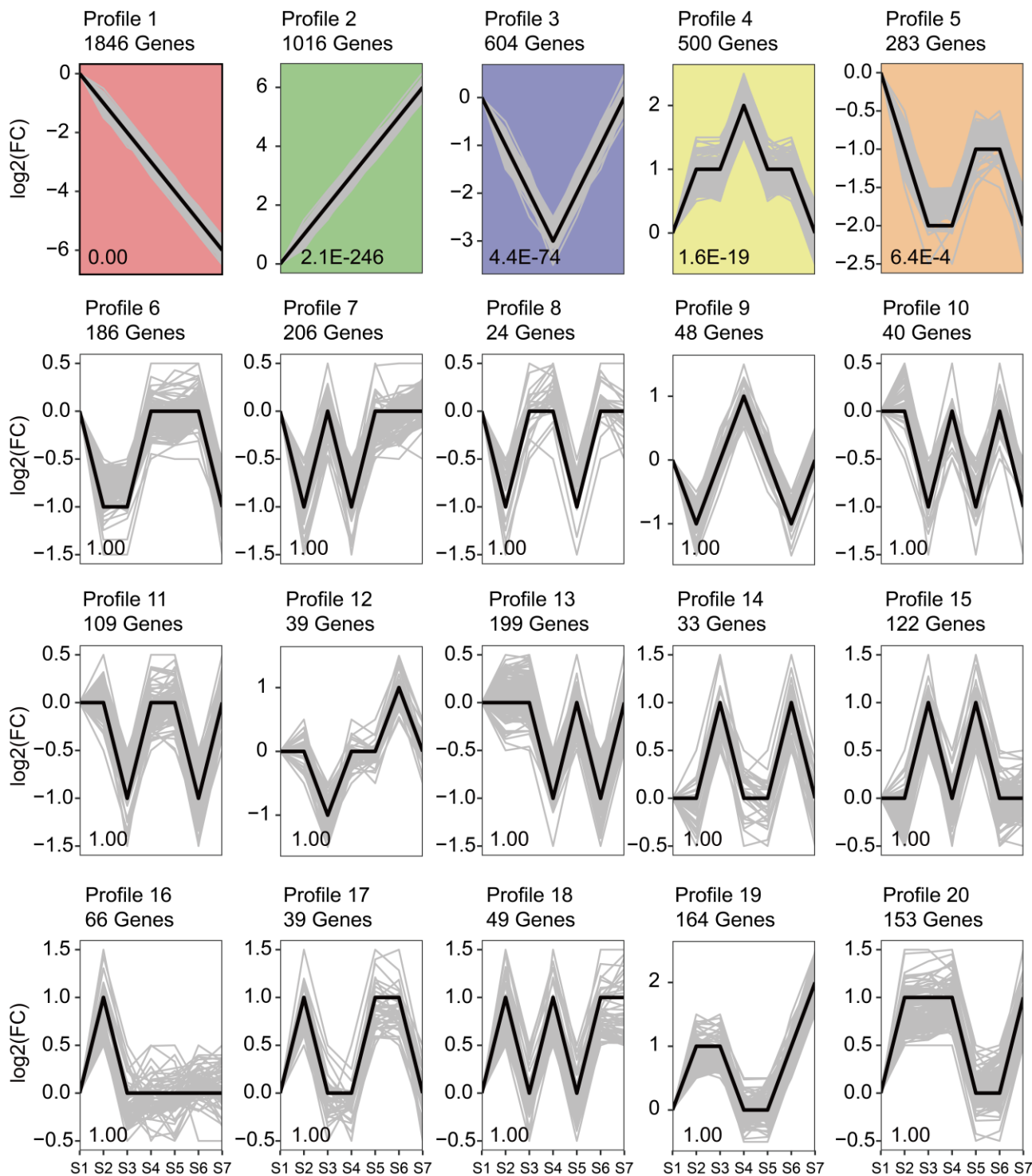
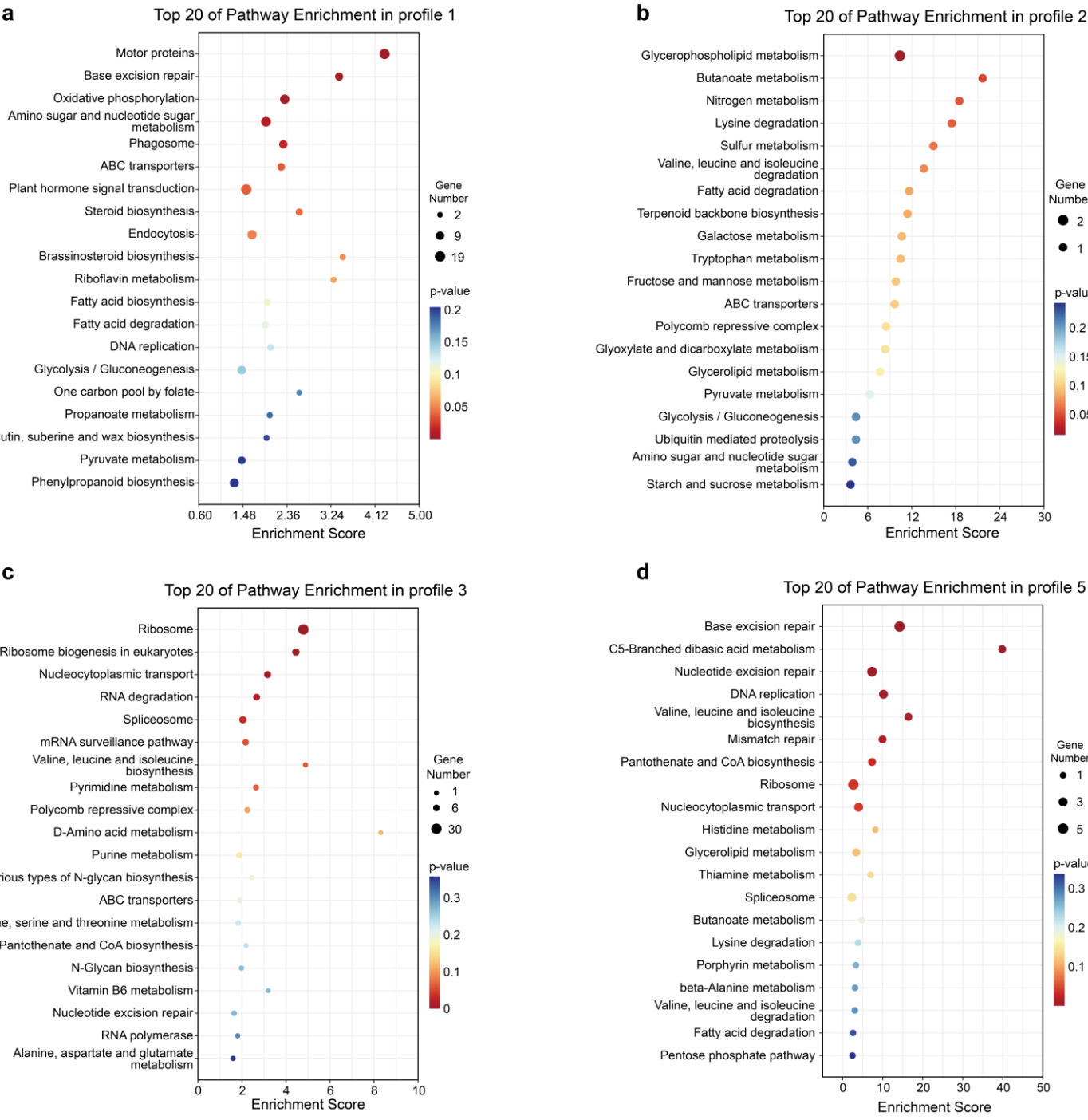
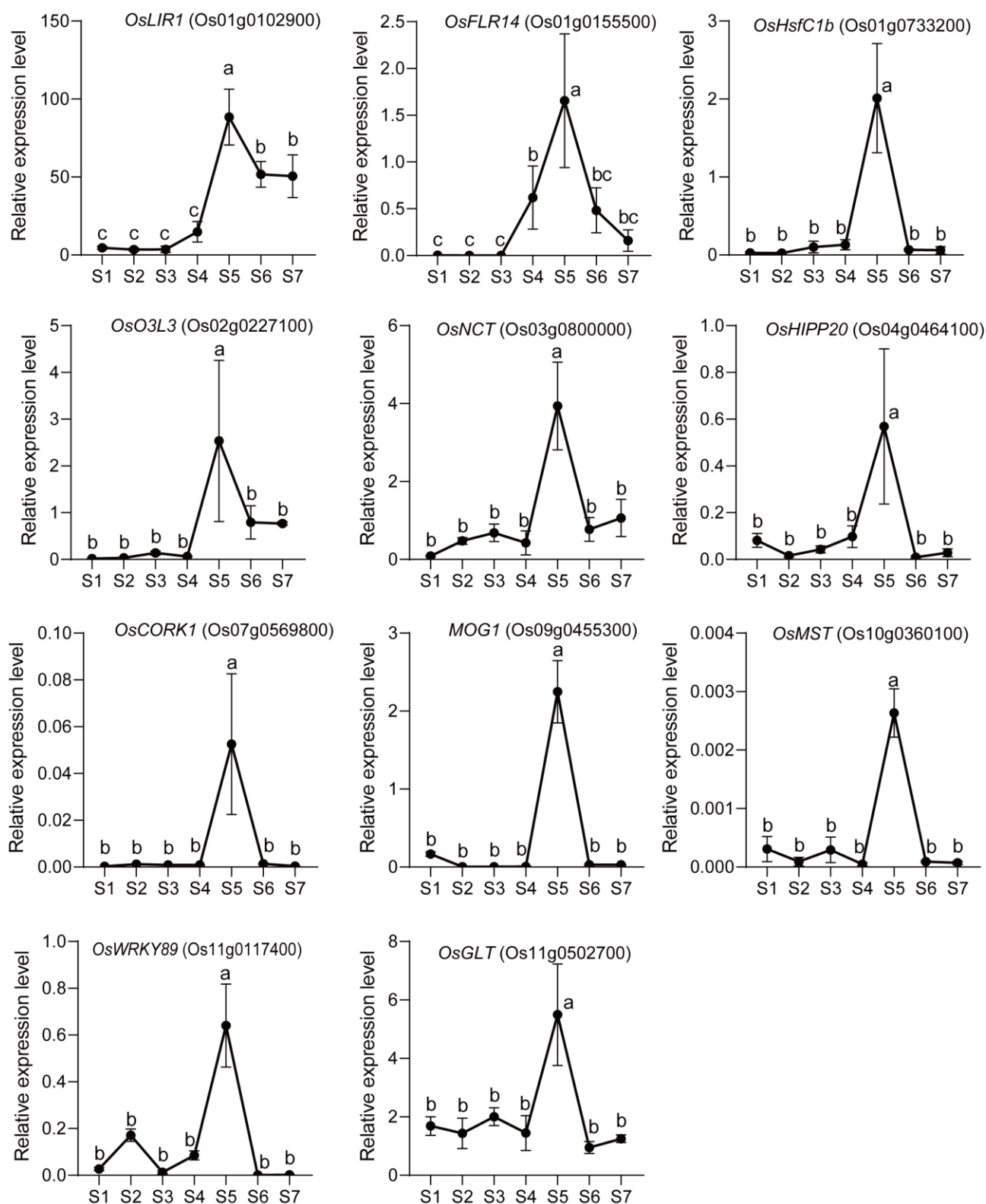




Supplemental figure S1. Short Time-series Expression Miner (STEM) analysis of genes in node I at seven reproductive growth stages. 20 profiles were identified and five significant profiles in color background were shown in Fig. 2. *p*-value were represented below each profile and gene numbers in each profile were showed on the top. Each gray line represents a gene, and the bold black line represents dynamic expression patterns.



Supplemental figure S2. KEGG pathway enrichment analysis of genes in 4 profiles in Fig. 2. KEGG enrichment analysis of DEGs in the profile 1 (a), profile 2 (b), profile 3 (c), and profile 5 (d). The top 20 GO terms or KEGG pathway with lowest p -value were shown.



Supplemental figure S3. qRT-PCR Verification of the expression pattern of selected genes that are highly activated at the S5 stage in the node I. The relative expression levels were determined by qRT-PCR and presented as $2^{-\Delta Ct}$ using the rice *Actin* gene as internal reference gene. Different letters indicate significant differences of gene expression levels among different stage at $P \leq 0.05$ with three biological replicates (Tukey's multiple comparisons test).