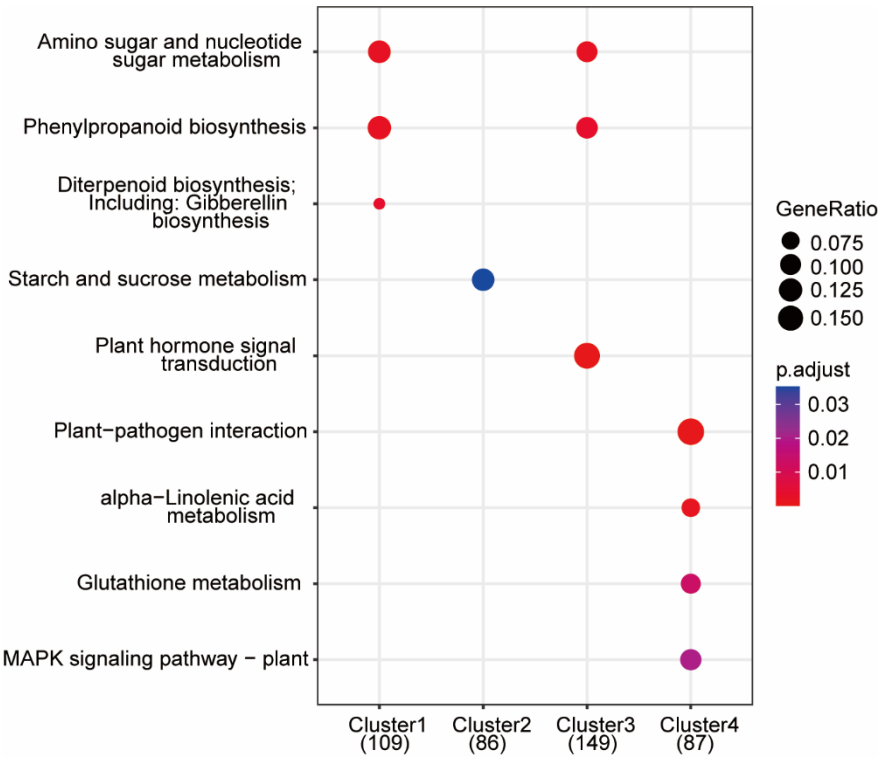


Figure S1. KEGG analysis of consistently differentially expressed genes.

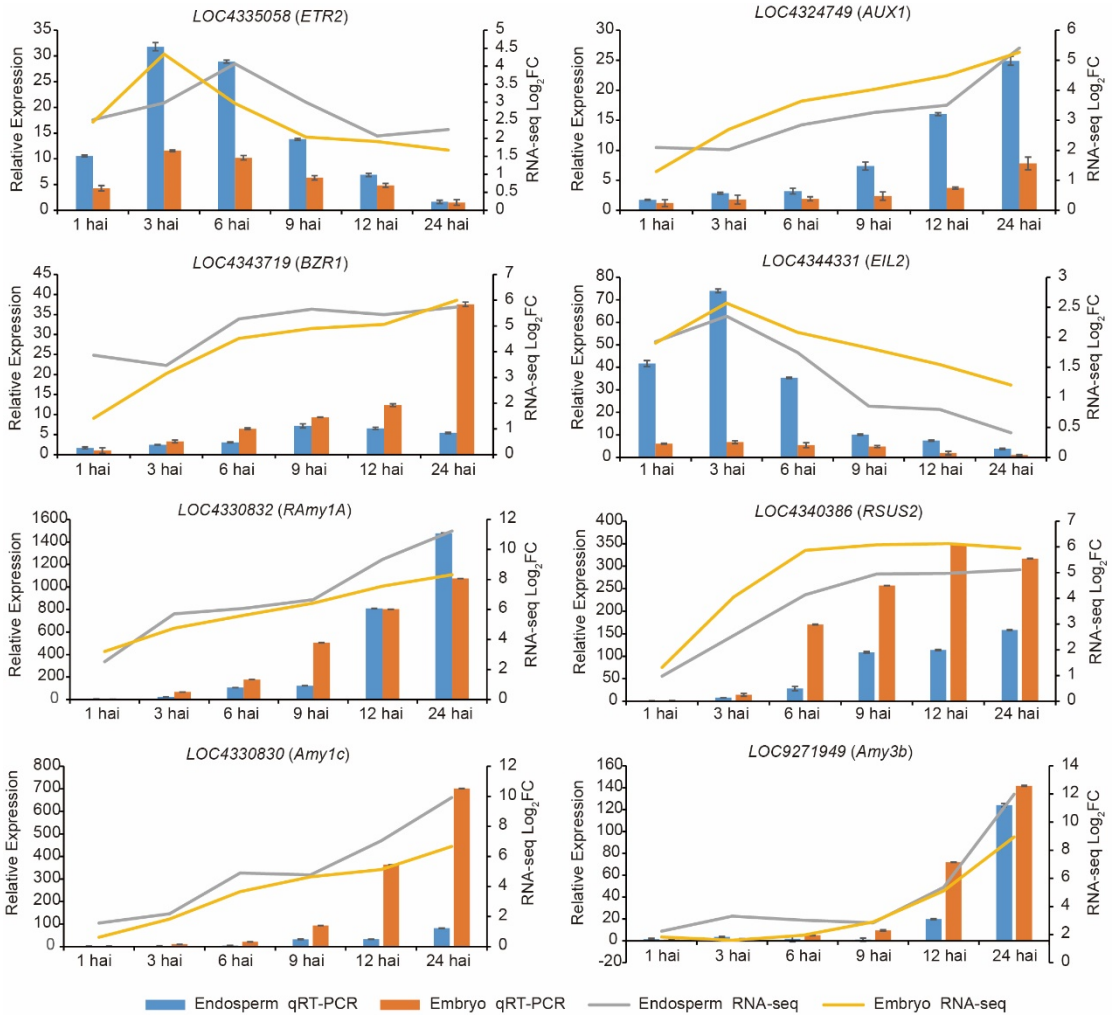


Figure S2. Quantitative RT-PCR validation of 8 DEGs. Expression of DEGs was normalized to the endogenous control *UBQ10* gene. The histogram represents qRT-PCR data of genes expression, with blue represents endosperm and orange represents embryo. The line chart represents Log_2 fold change expression of the DEGs from RNA-seq data, with grey represents endosperm and yellow represents embryo. Three biological replicates of each sample were used for qRT-PCR analysis. Error bars represent the standard deviation of relative expression level from three biological replicates.