



Supplementary Figure 1 The GO and KEGG pathway analyses of the differentially expressed mRNAs. (A) The secondary classification histogram, showed the biological process, cellular component and molecular function of differentially expressed mRNAs. (B), (C), (D) showed the BP, CC and MF of the top 10 GO terms of the gene enrichment, respectively. (E) The top 10 KEGG enriched pathways of the differentially expressed mRNAs. The horizontal axis and the vertical axis indicate the enrichment score and pathways, respectively.

