

Figure S1. Differentially expressed genes enriched in GO analysis. GO analysis of mRNA were performed with the R language version 3.4.4 cluster Profiler. It was conducted to determine the functional roles of these differentially expressed genes. The differentially expressed genes enriched in GO terms were associated with ‘protein binding’, ‘regulation of biological process’ and ‘response to stimulus’ (the -log10 value were 36.2, 38.6 and 38.5, respectively). The experiments were repeated 3 times.

