



**Figure 3. Analysis of differentially expressed genes (DEGs) between Nipponbare and Hui1586 in the mock treatment.** (A) The numbers of DEGs between Nipponbare and Hui1586 at the indicated time points after H<sub>2</sub>O treatment. (B) Venn diagram of DEGs in (A). (C-D) KEGG pathway (C) and GO (D) enrichment analysis of 1331 DEGs in (B). The y-axis represents the negative log<sub>10</sub>-transformed Q-value (blue bars) and gene numbers (yellow dots). (E) Enrichment of the *LRR* and *NLR* genes in the 1331 DEGs compared with their ratio in the rice genome.