



**Figure 4. Pathway enrichment of DEGs in the rice response to blast fungus.** (A) Venn diagram of DEGs induced by *M. oryzae* in Nipponbare and Hui1586 compared with mock treatment within 48 hpi. Up- and downregulated DEGs are indicated by upward and downward pointing arrows, respectively. (B) Hierarchical clustering of all the DEGs at 12 hpi based on the  $\log_2$  fold change in transcript levels in Nipponbare (Nip) and Hui1586 (Hui) with *M. oryzae* treatment relative to the mock treatment. (C) KEGG pathway and GO enrichment analysis of 3398 upregulated DEGs at 12 h in (A). The y-axis represents the negative  $\log_{10}$ -transformed Q-value and gene numbers. (D) The enrichment of ribosome- and rRNA-related genes in the 3398 DEGs in (C) compared with its ratio in the rice genome. (E) Hierarchical clustering of ribosome- and rRNA-related genes in the 3398 DEGs in (C) based on the  $\log_2$  fold change as in (B).