



**Figure 6. The core genes are involved in biotic and abiotic stress responses.**

(A) The bar plot shows that among the 321 core genes, the number of genes that were differentially regulated in rice treated with *Magnaporthe oryzae* (GSE83219), *Ustilagoideae virens* (GSE39049), *Xanthomonas oryzae* (GSE36272) or drought (GSE57950) in polished transcriptome data sets. (B) Hierarchical clustering of the 321 core genes based on the  $\log_2$ -fold change with various treatments as in (A). (C) Similarity comparison among the data sets as in (A) based on the  $\log_2$ -fold change of the 321 core genes.