



Figure 7. characterization of transcription factors and *cis*-regulatory motifs in differentially regulated genes in rice in responses to *M. oryzae*. (A) Hierarchical clustering of the total 313 transcription factors (TFs) that were differentially regulated in both Nipponbare (Nip) and Hui1586 in response to *M. oryzae* infection. The rows of collapse represent the average value of genes in the indicated groups in each column/condition. (B) Enrichment of the TF families of the 205 TFs (Cluster I in (A)) compared to their ratio in each family in the rice genome. (C) Overrepresentation of known TF DNA binding motifs within the 500-bp promoter of the 321 core genes. Rows indicate motifs of corresponding TF families and are colored according to the P-value for enrichment. (D) Sequence logo depiction of the key overrepresented TF DNA binding motifs in the 500-bp promoter of the 321 core genes.