



**Figure 2. Overview of transcriptome data and differentially expressed genes (DEGs) in the rice response to blast fungus.** (A) Principal component analysis of the time-series transcriptome data in Nipponbare (Nip) and Hui1586 treated with the blast isolate Guy11 (M.o) or H<sub>2</sub>O. (B) Hierarchical clustering of the samples for the normalized FPKM (fragments per kilobase of transcript per million mapped reads) values of all detectable genes. (C) The numbers of up- and downregulated genes by *M. oryzae* in Nipponbare or Hui1586 compared with the mock treatment are shown. (D) Venn diagram of total DEGs in Nipponbare compared with Hui1586.