Figure S1 Symptoms of rust on B. striata; A, B. leaves infected with urediospore (A. back; B. front); C. plants infected with urediospore; D, E. leaves infected with teleutospore (D. back; E. front); F. plants infected with teleutospore.

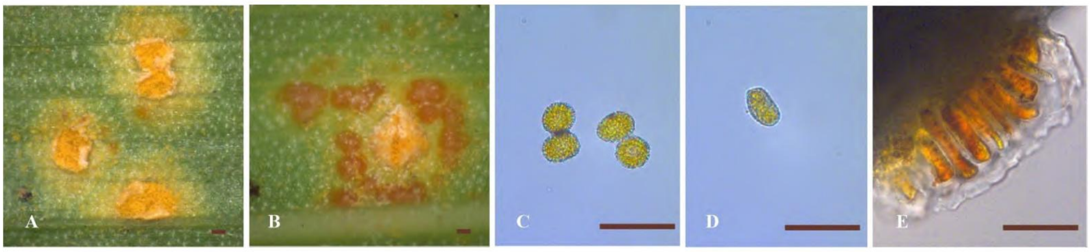

Figure S2 Morphological characteristics of rust pathogen; A,B. uredinium; C,D. urediospore; E. teleutospore; scale bar: A,B=0.1mm; C-E=50um.

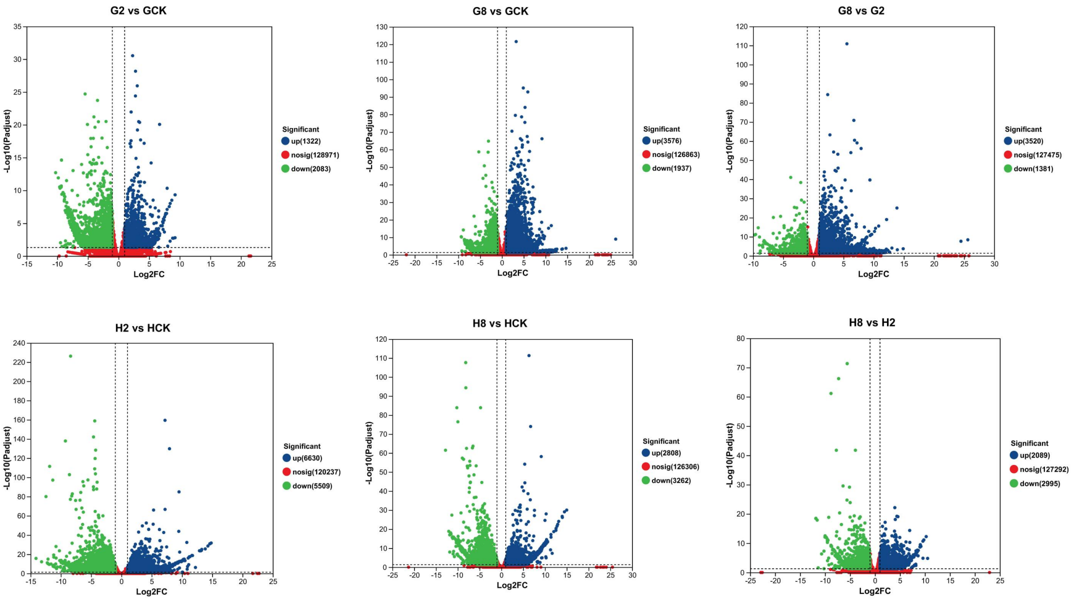

Figure S2. Number of differentially expressed genes (DEGs) between different groups.GCK, G2 and G8 represent samples on 0, 2 and 8 dpi in susceptible material; HCK, H2 and H8 represent samples on 0, 2 and 8 dpi in resistant material.

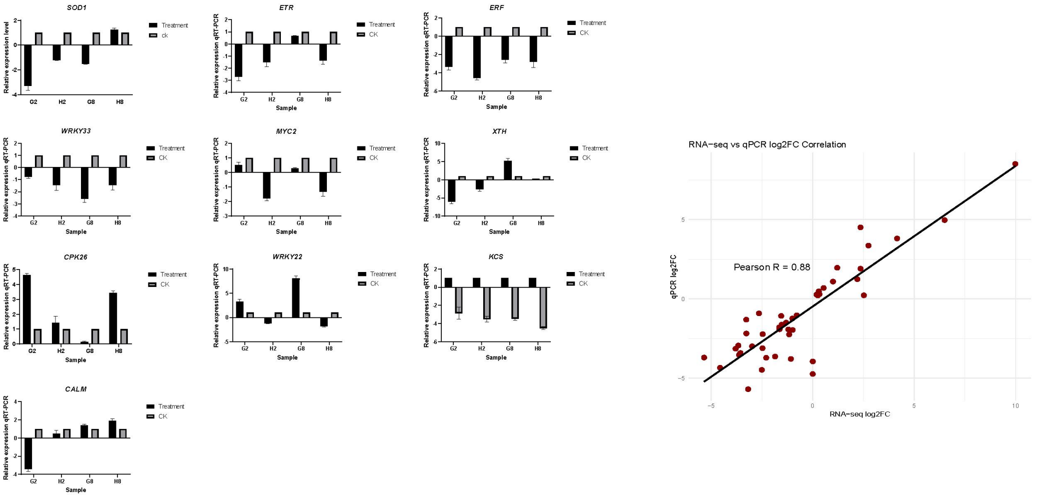

Figure S3. Validation of RNA-seq results by qPCR; a, qPCR results of 10 candidate genes; b, correlation of $\log_2$fold-changes for 10 candidate genes between RNA-seq (TPM normalized) and qPCR. The strong positive correlation (r= 0.88, p <0.01) confirms the reliability of transcriptome data.