

Figure S1. Phenotypes of J11 and Z2 after 20 days inoculation with *V.dahliae*.

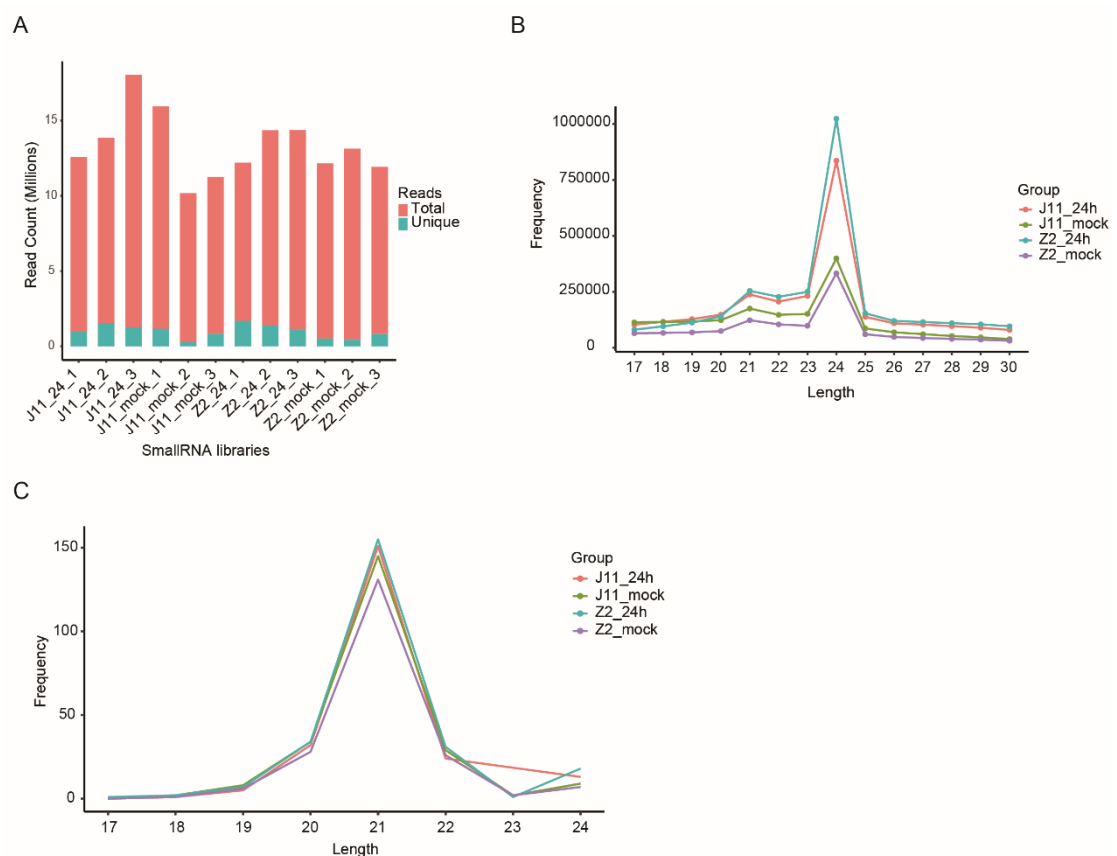


Figure S2. Cotton small RNA reads distributions. **(A).** Pre-processed reads distribution of small RNA libraries. **(B).** Length distributions of unique small RNAs in J11 and Z2. **(C).** The frequency distribution of miRNAs in J11 and Z2.

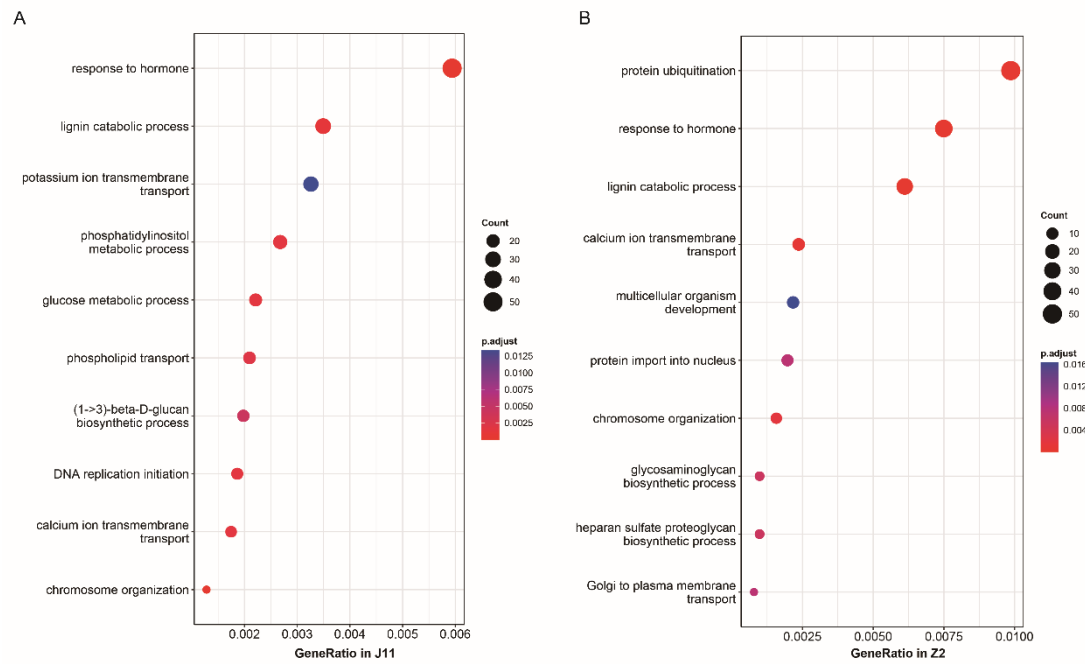
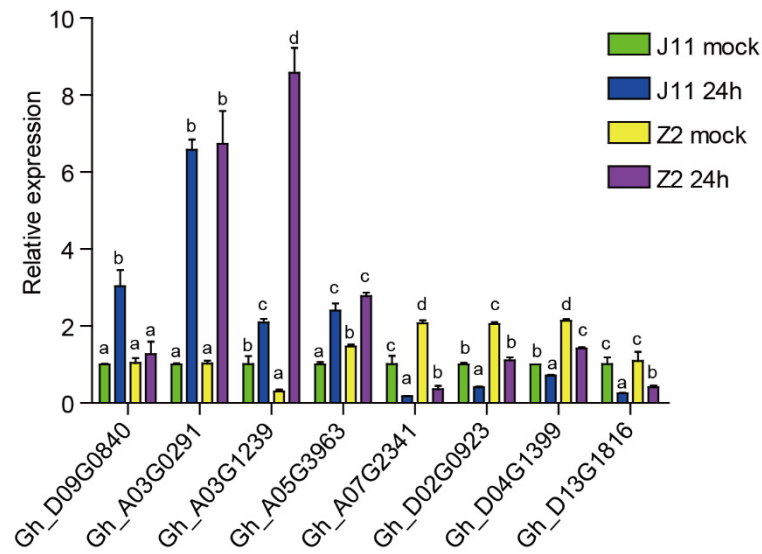


Figure S3. GO enrichment analysis of target unigenes of DEMs in J11 (A) and Z2 (B).

A



B

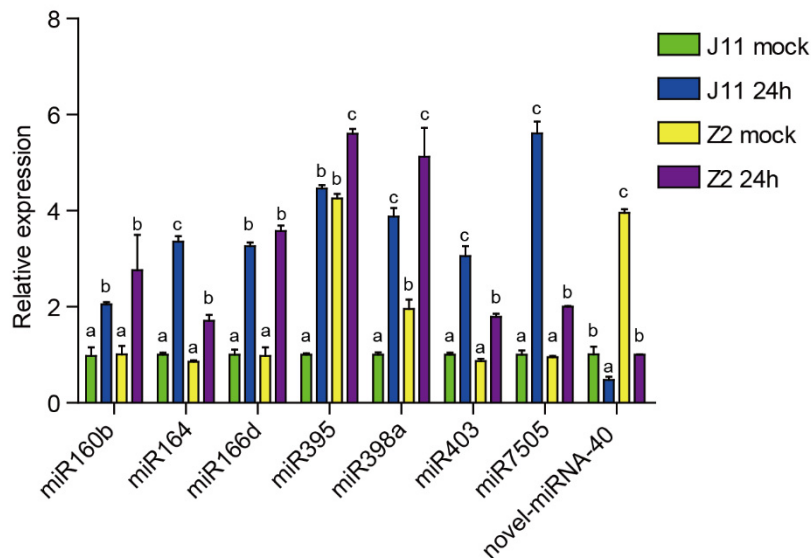


Figure S4. Quantitative real-time PCR (qRT-PCR) validation of selected unigenes and miRNAs. **(A)** qRT-PCR was performed to determine the expression levels of 8 unigenes relative to GhUBQ7. **(B)** The expression of 7 known miRNAs and 1 novel miRNA was verified by stem-loop qRT-PCR with U6 snRNA as an internal reference gene and data are means \pm SD from three biological replicates. Different letters indicate significant differences, $p < 0.05$ (ANOVA test).