

Figure S1. Venn diagram of genes differentially expressed in resistant and susceptible banana (*Musa* spp. AAA) cultivars before and after pathogen attack. **(A)** Up-regulated genes; **(B)** Down-regulated genes. BX: “Baxijiao”, highly susceptible to *Fusarium oxysporum* f.sp *cubense* tropical race 4; YK: “Yueyoukang 1”, highly resistant to *Fusarium oxysporum* f.sp *cubense* race 4. CK: the control; T: treatment with pathogen.

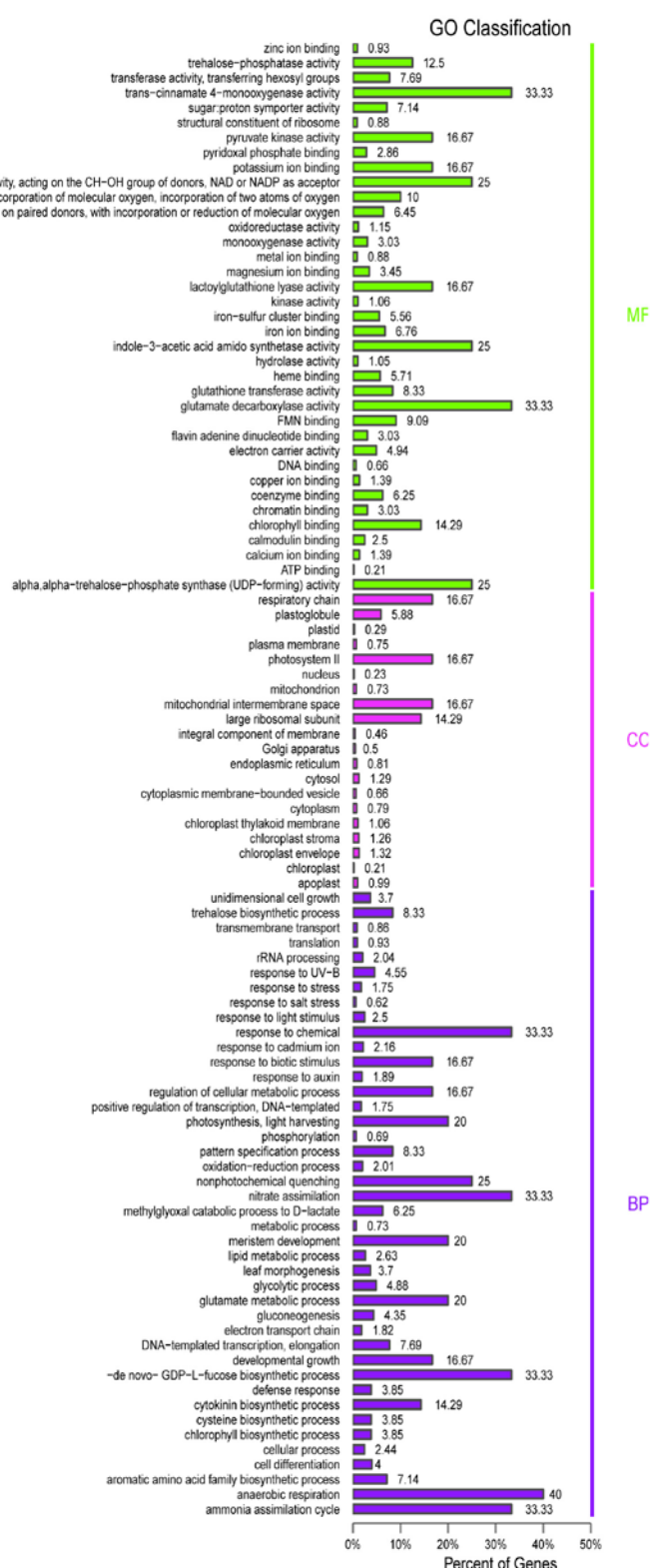


Figure S2. Gene ontology annotations enriched in the susceptible banana cultivar (*Musa* spp. AAA cv. Baxijiao) after infection with *Fusarium oxysporum* f. sp. *Cubense*. BP: biological process; CC: cellular compartment; MF: molecular function.

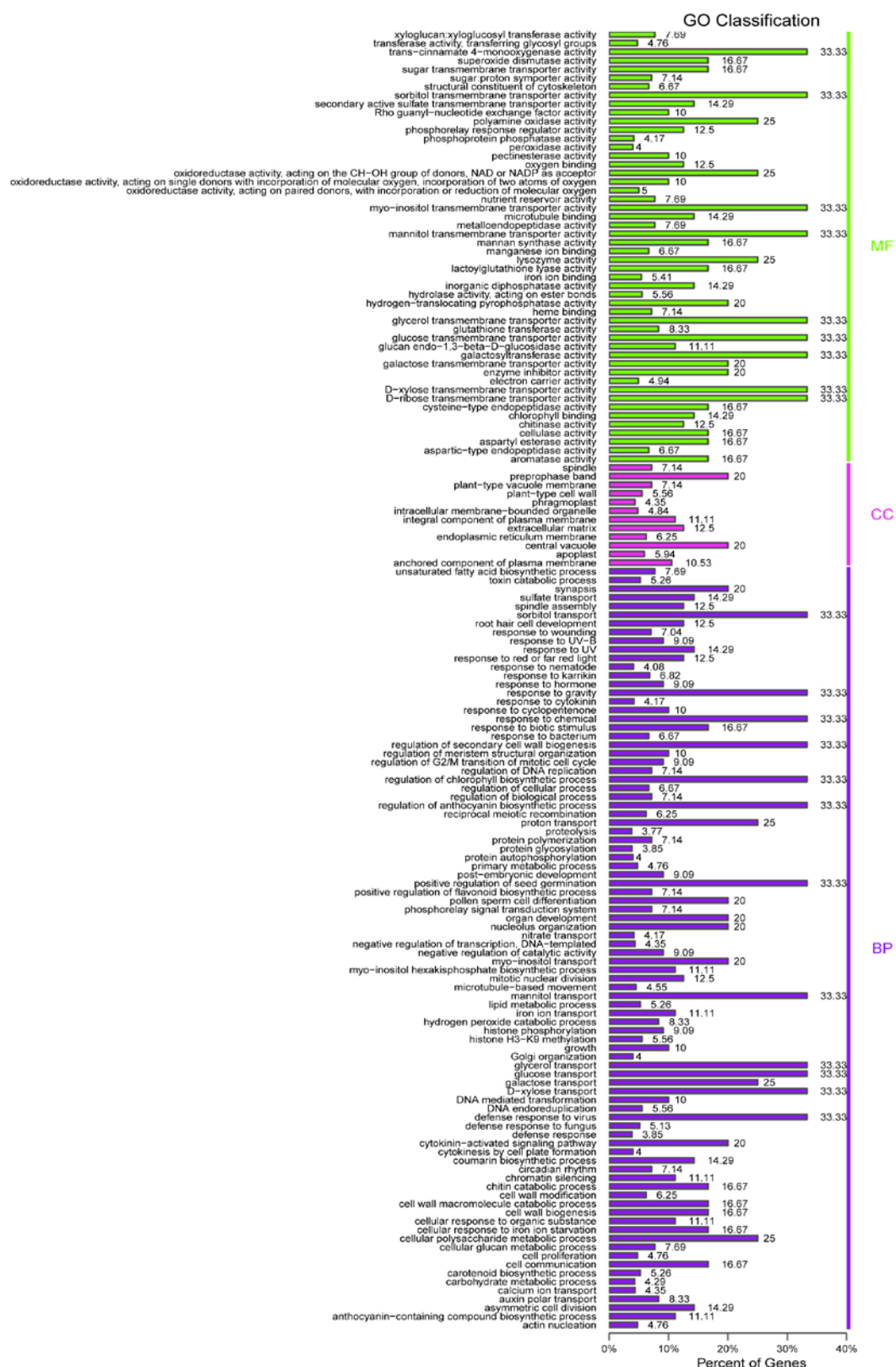


Figure S3. Gene ontology annotations present between the susceptible (*Musa* spp. AAA cv. Baxijiao) and resistant (*Musa* spp. AAA cv. Yueyoukang 1) banana cultivars. BP: biological process; CC: cellular compartment; MF: molecular function.

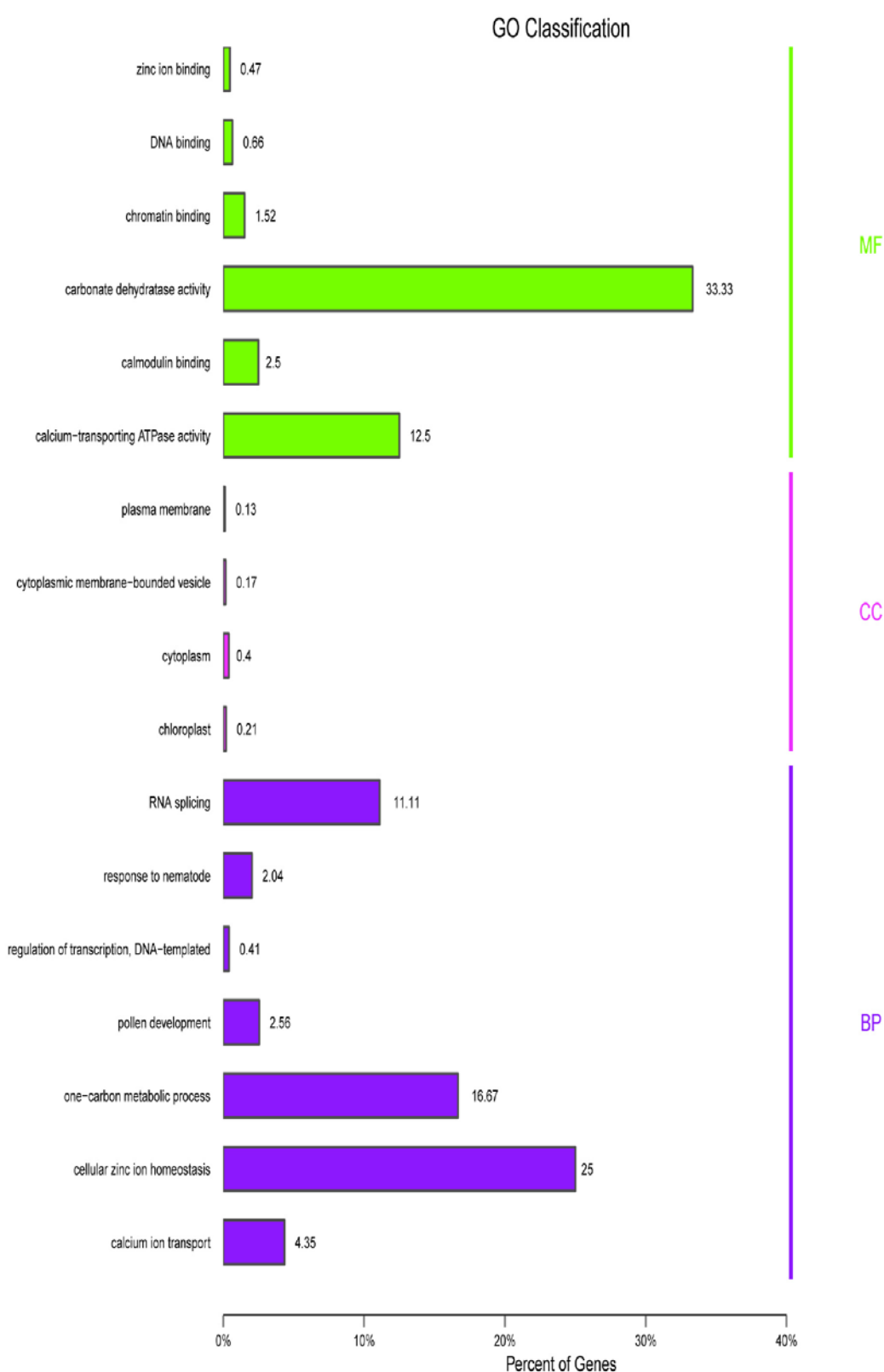


Figure S4. Gene ontology annotations enriched in the resistant banana cultivar (*Musa* spp. AAA cv. Yueyoukang 1) after infection with *Fusarium oxysporum* f. sp. *Cubense*. BP: biological process; CC: cellular compartment; MF: molecular function.

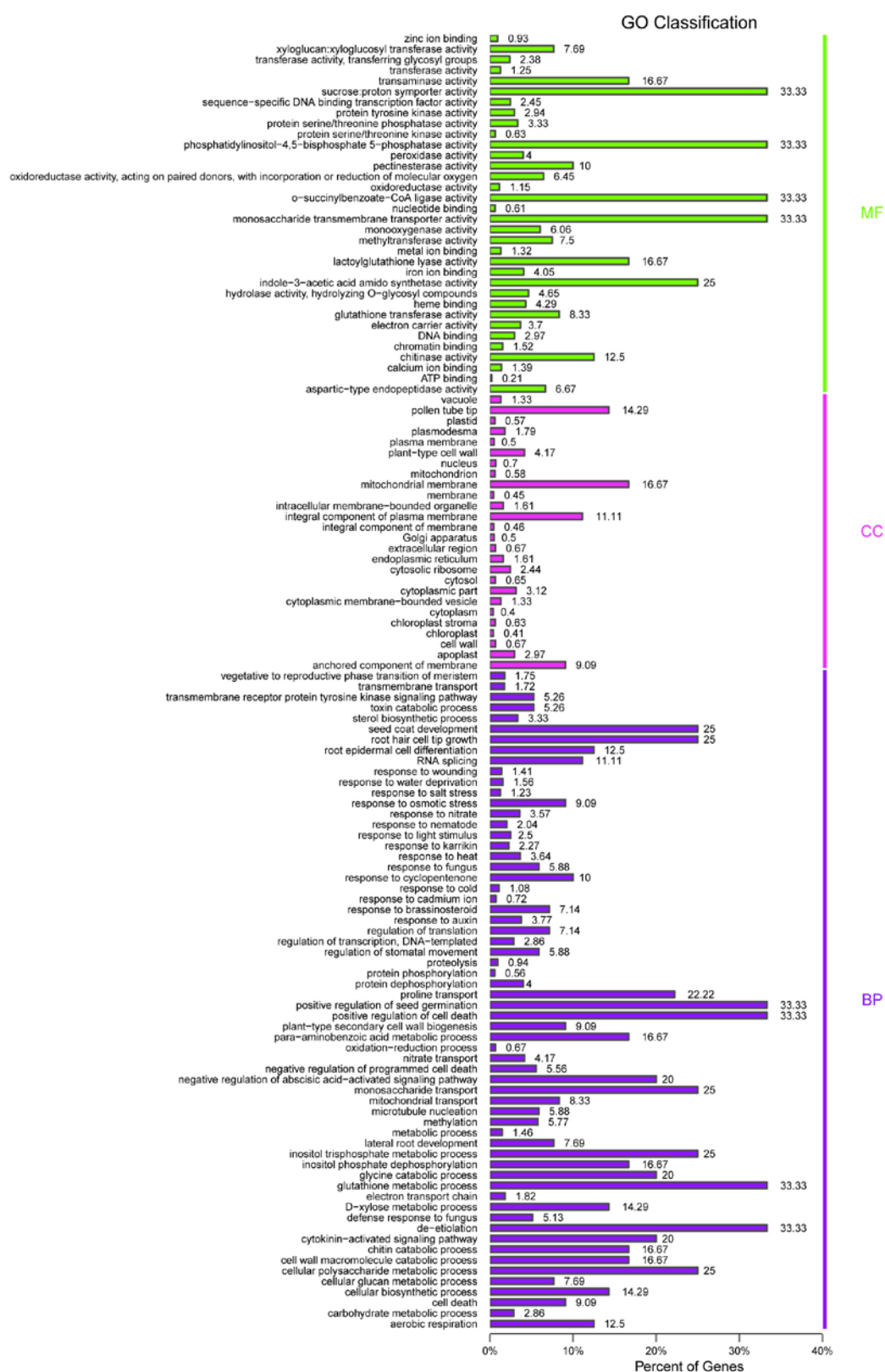


Figure S5. Gene ontology annotations present between the susceptible (*Musa* spp. AAA cv. Baxijiao) and resistant (*Musa* spp. AAA cv. Yueyoukang 1) banana cultivars after infection with *Fusarium oxysporum* f. sp. *Cubense*. BP: biological process; CC: cellular compartment; MF: molecular function.

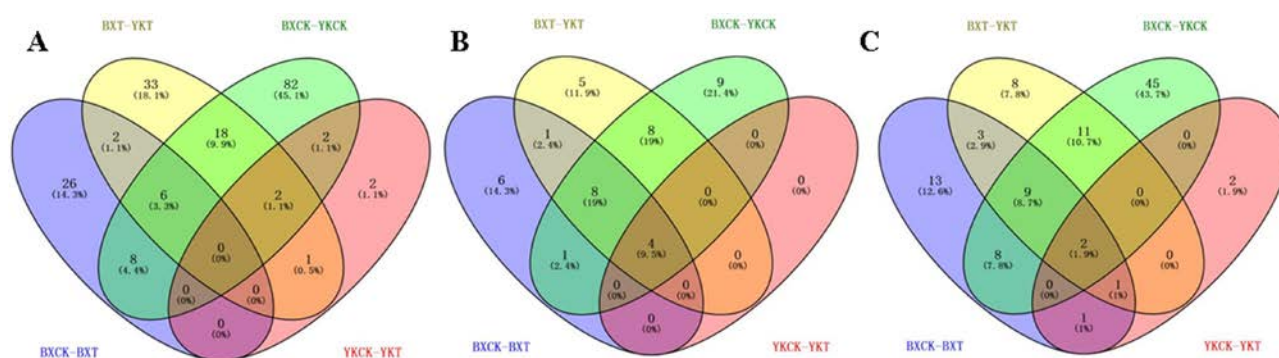


Figure S6. The Venn diagram of GO annotation items in resistant and susceptible banana (*Musa* spp. AAA) cultivars before and after pathogen attack. **(A)** Biological process; **(B)** Cellular compartment; **(C)** Molecular function. BX: “Baxijiao”, highly susceptible to *Fusarium oxysporum* f.sp *cubense* race 4; YK: “Yueyoukang 1”, highly resistant to *Fusarium oxysporum* f.sp *cubense* race 4. CK: the control; T: treatment with pathogen.

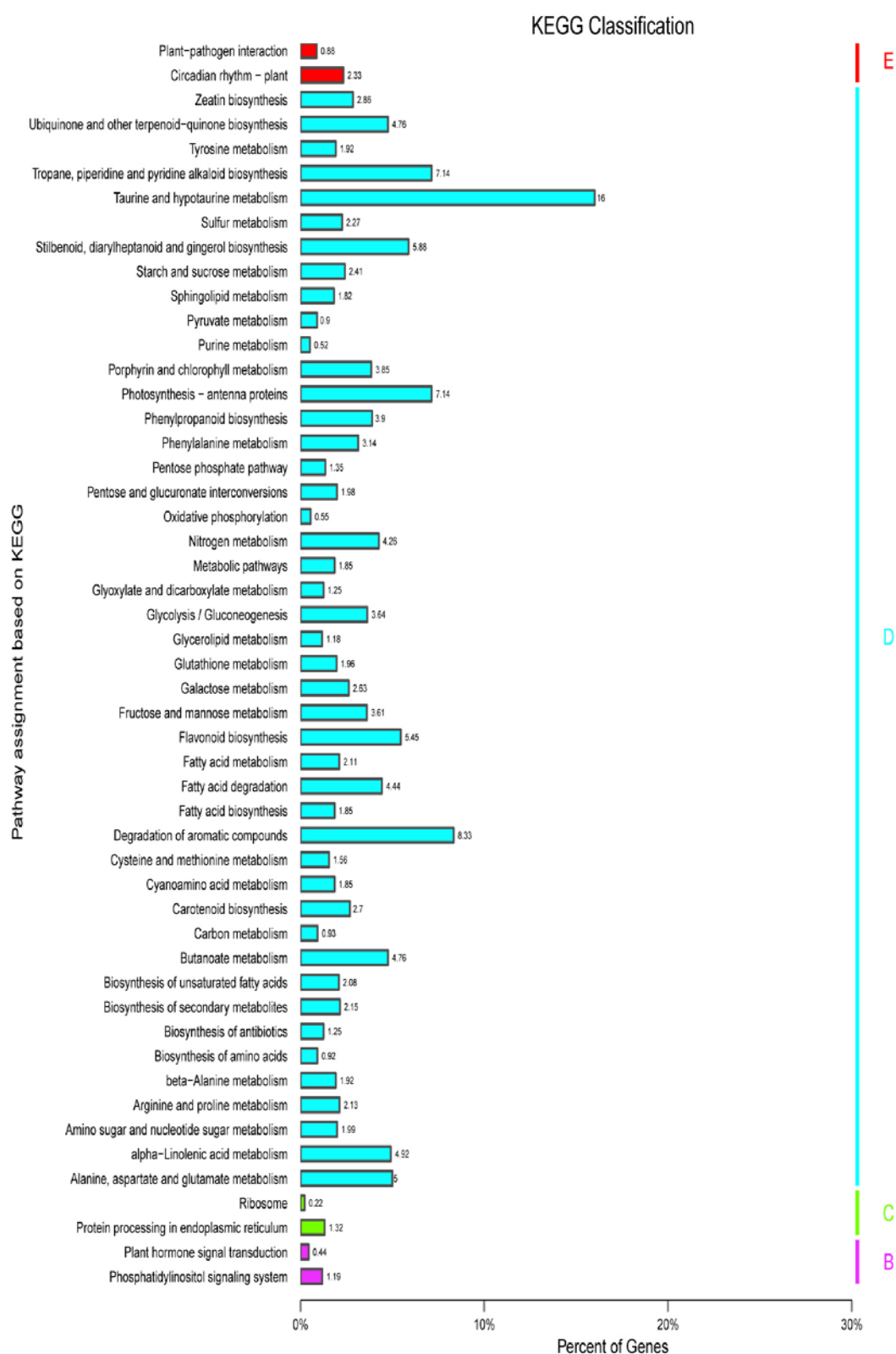


Figure S7. Kyoto encyclopedia of genes and genomes (KEGG) pathways enriched in the susceptible banana cultivar (*Musa* spp. AAA cv. Baxijiao) after infection with *Fusarium oxysporum* f. sp. *Cubense*. **B:** Environmental information processing; **C:** Genetic information processing; **D:** Metabolism; **E:** Organismal systems.

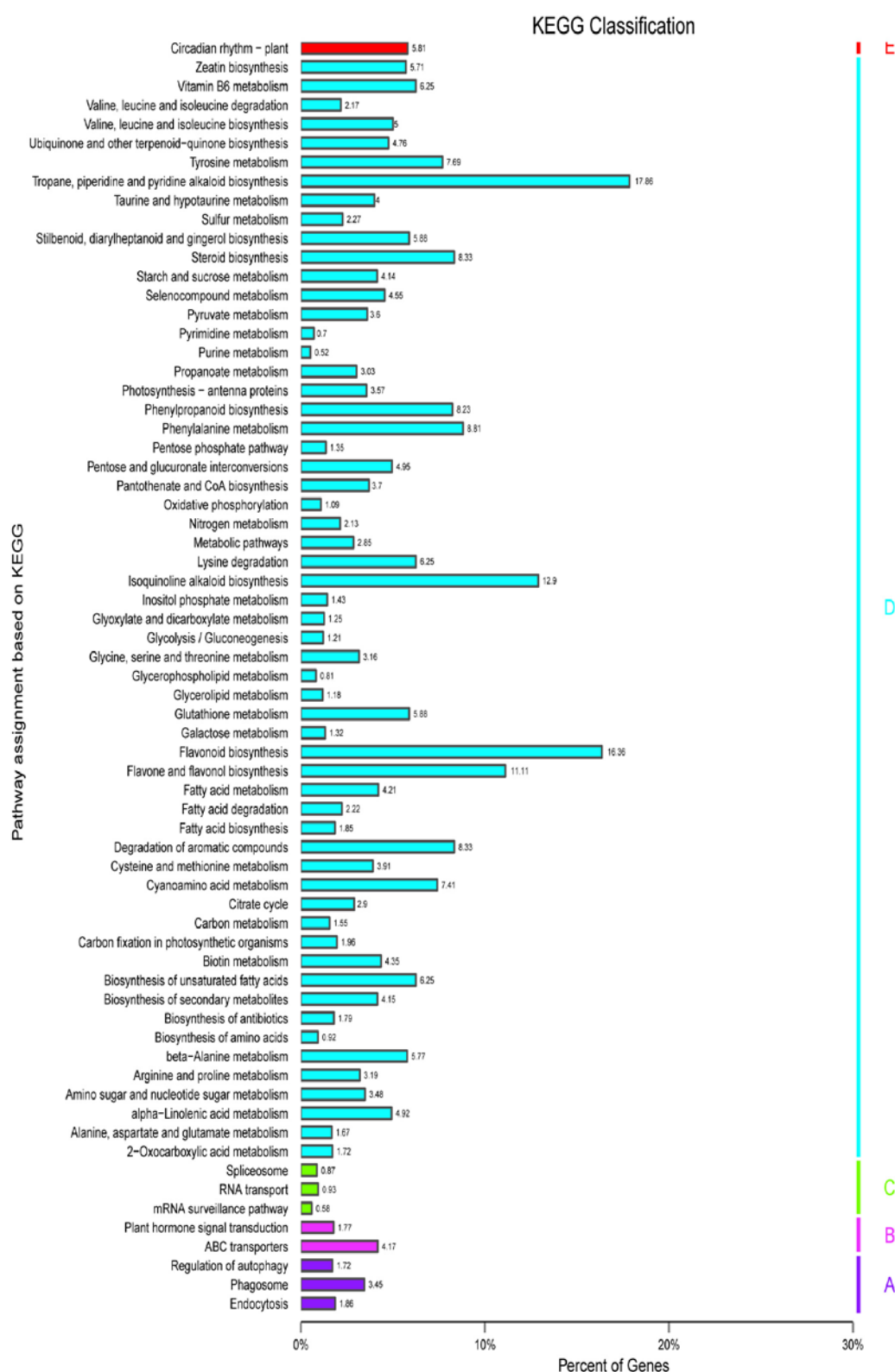


Figure S8. Kyoto encyclopedia of genes and genomes (KEGG) pathways present between the susceptible (*Musa* spp. AAA cv. Baxijiao) and resistant (*Musa* spp. AAA cv. Yueyoukang 1) banana cultivars. A: Cellular processes; B: Environmental information processing; C: Genetic information processing; D: Metabolism; E: Organismal systems.

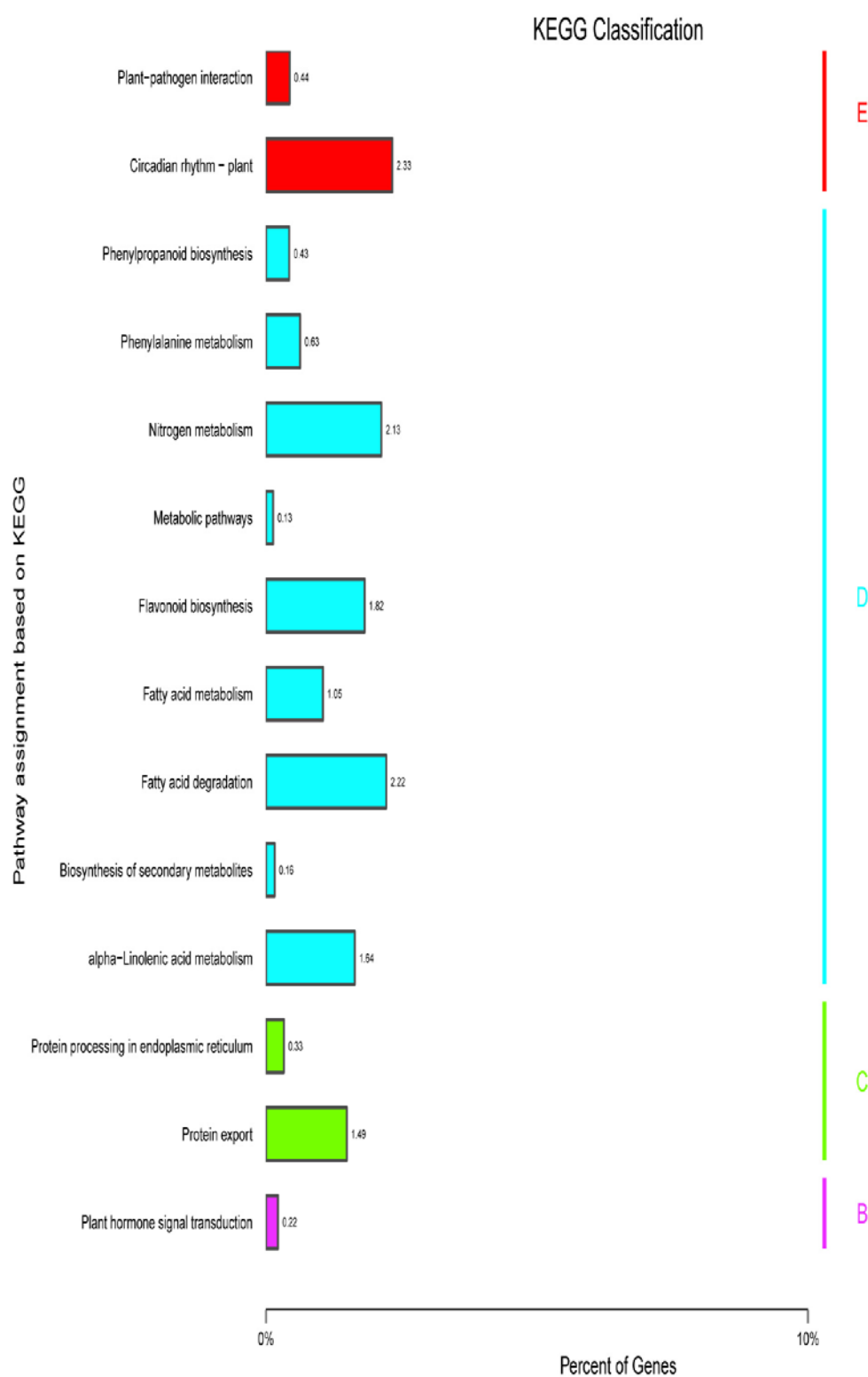


Figure S9. Kyoto encyclopedia of genes and genomes (KEGG) pathways enriched in the resistant banana cultivar (*Musa* spp. AAA cv. Yueyoukang 1) after infection with *Fusarium oxysporum* f. sp. *cubense*. B: Environmental information processing; C: Genetic information processing; D: Metabolism; E: Organismal systems

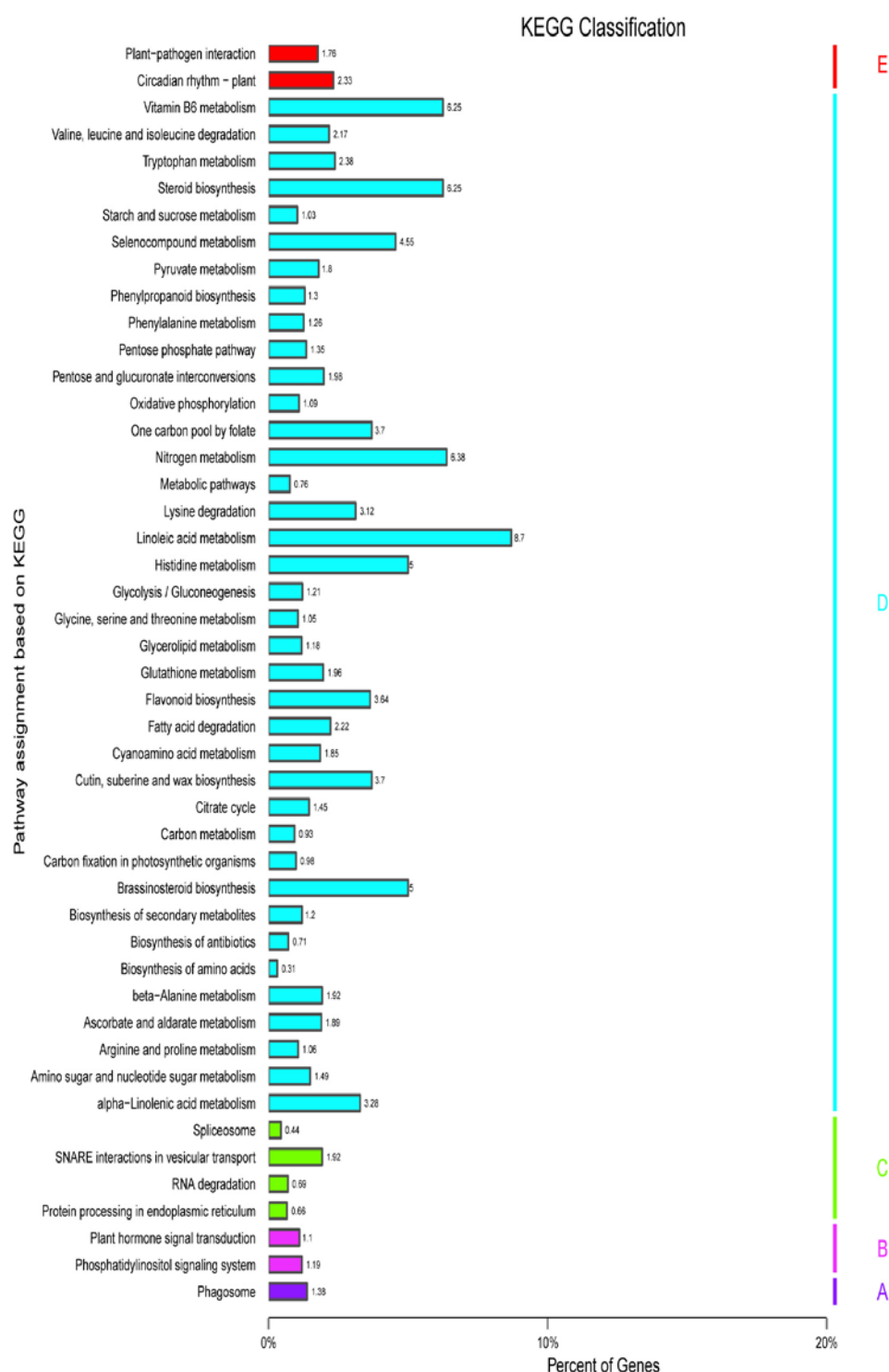


Figure S10. Kyoto encyclopedia of genes and genomes (KEGG) pathways present between the susceptible (*Musa* spp. AAA cv. Baxijiao) and resistant (*Musa* spp. AAA cv. Yueyoukang 1) banana cultivars after infection with *Fusarium oxysporum* f. sp. *cubense*. **A:** Cellular processes; **B:** Environmental information processing; **C:** Genetic information processing; **D:** Metabolism; **E:** Organismal systems

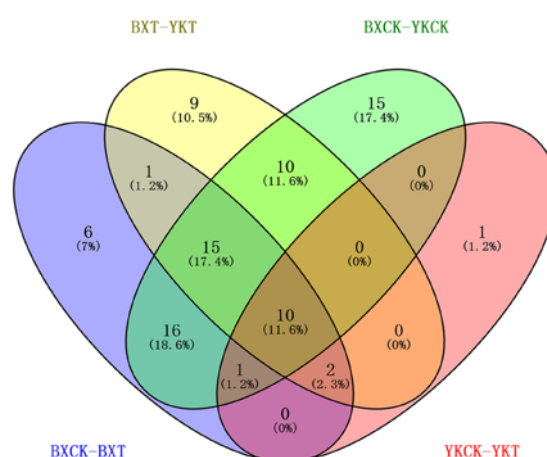


Figure S11. The Venn diagram of accumulated KEGG pathways in resistant and susceptible banana (*Musa* spp. AAA) cultivars before and after pathogen attack. BX: “Baxijiao”, highly susceptible to *Fusarium oxysporum* f.sp. *cubense* race 4; YK: “Yueyoukang 1”, highly resistant to *Fusarium oxysporum* f.sp. *cubense* race 4. CK: the control; T: treatment with pathogen.

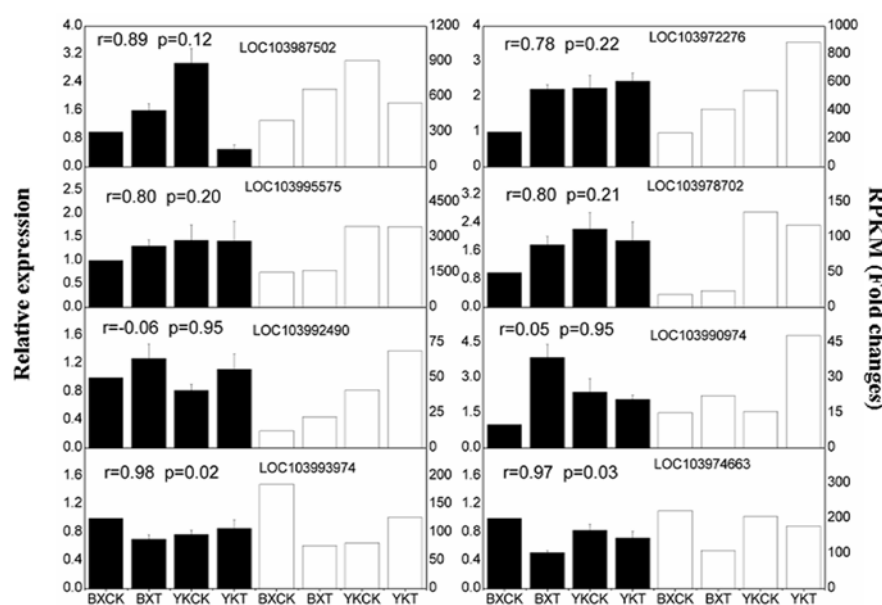


Figure S12. Validation of DGE data by *qRT-PCR*. Graphs show the relative expression of selected genes as examined by *qRT-PCR* (black columns), and their corresponding RPKM values from RNA-Seq (white columns). Error bars are standard errors. BX: “Baxijiao”, highly susceptible to *Fusarium oxysporum* f.sp. *cubense* race 4; YK: “Yueyoukang 1”, highly resistant to *Fusarium oxysporum* f.sp. *cubense* race 4. CK: the control; T: treatment with pathogen. DGE: digital gene expression; RPKM: reads per kilobase of transcript per million mapped reads.