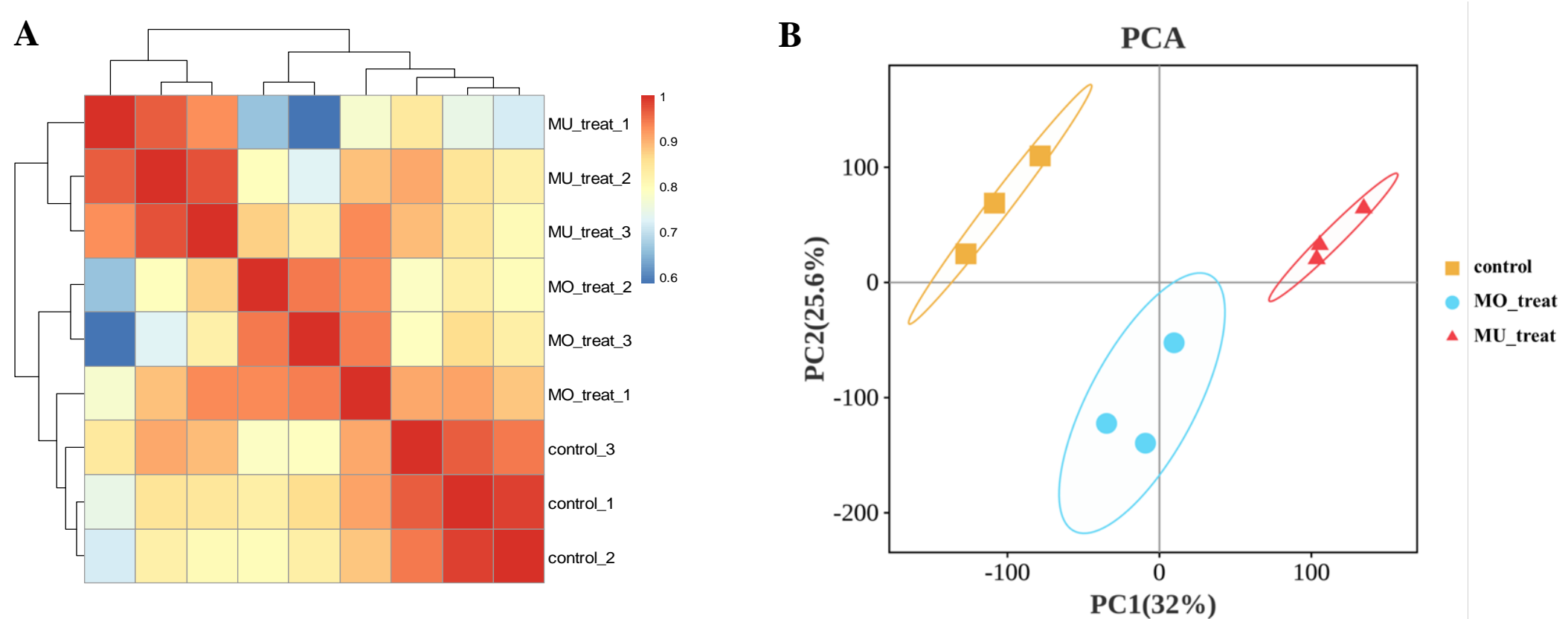
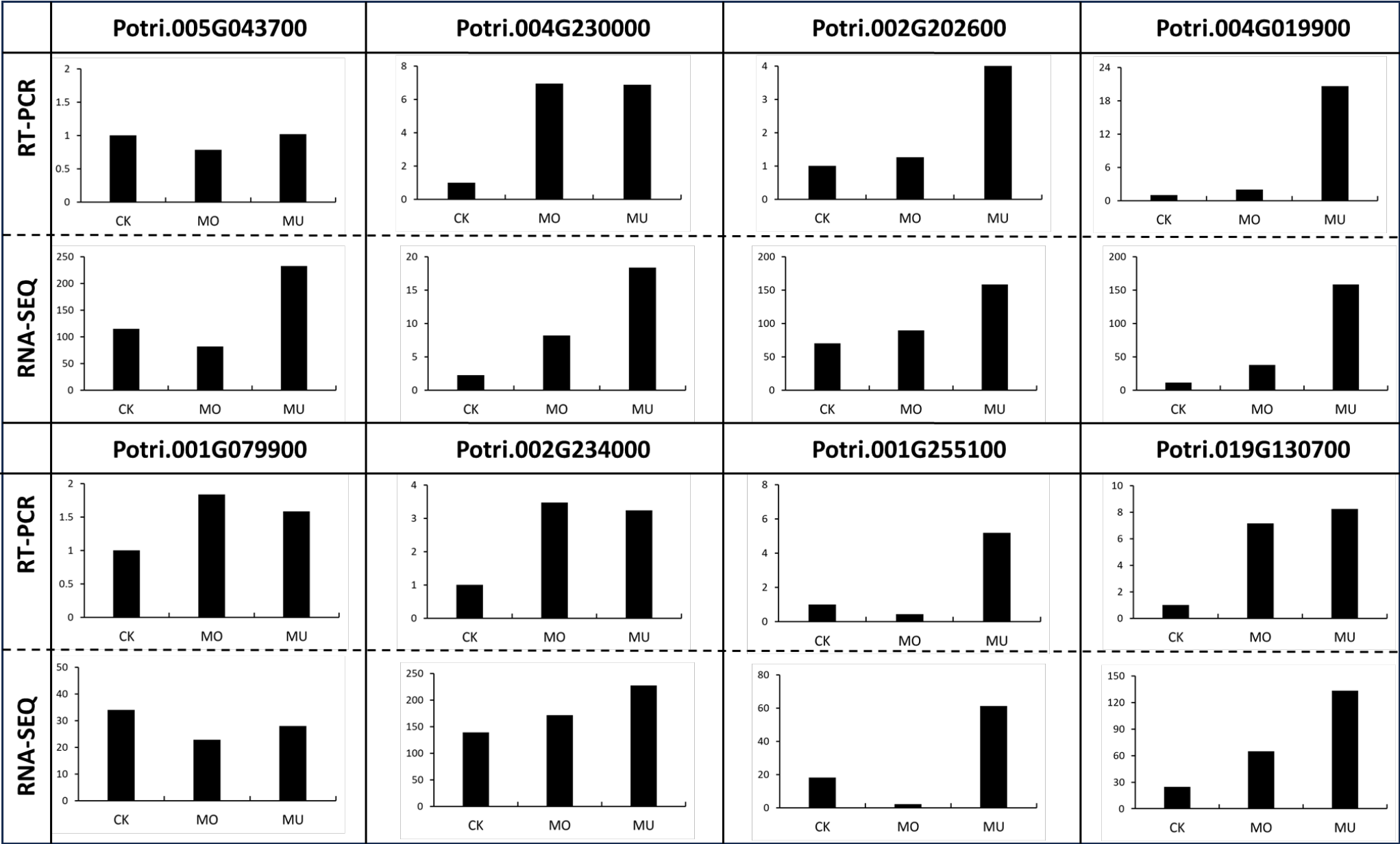


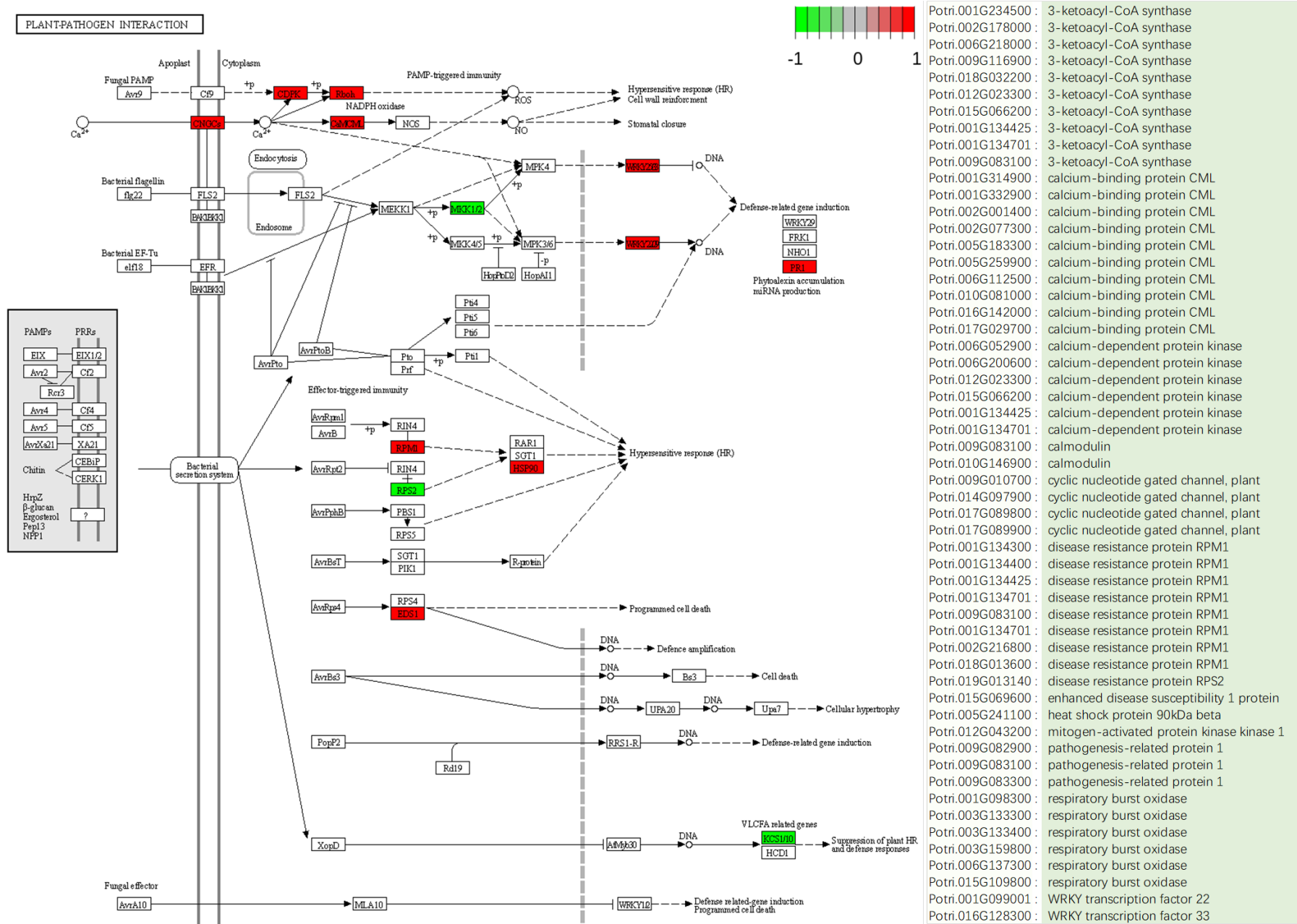
Supplementary Figure S1. Correlation among RNA-seq samples. **(A)** heat map of the Pearson correlation of sequenced samples based on the expression data of all genes. **(B)** principal component analysis (PCA) of RNA-seq samples based on the expression data of all genes.



Supplementary Figure S2. Comparison of expression values measured by qRT-PCR and RNA-seq.

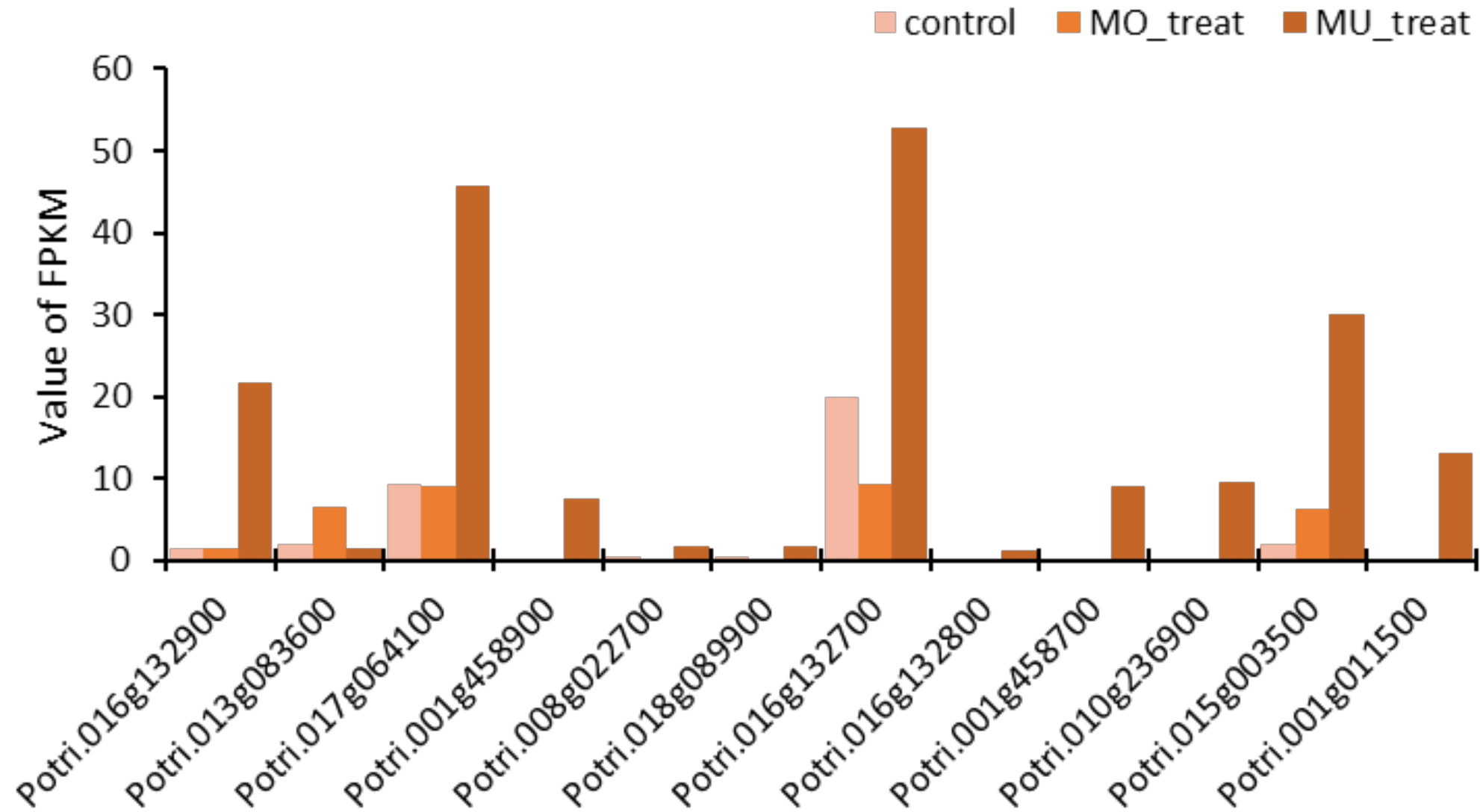


Supplementary Figure S3. Annotation and expression profiles of genes involved in plant-pathogen interaction (ko04626) enriched by the DEGs of MU_treat vs. control.



Potri.001G234500	3-ketoacyl-CoA synthase
Potri.002G178000	3-ketoacyl-CoA synthase
Potri.006G218000	3-ketoacyl-CoA synthase
Potri.009G116900	3-ketoacyl-CoA synthase
Potri.018G032200	3-ketoacyl-CoA synthase
Potri.012G023300	3-ketoacyl-CoA synthase
Potri.015G066200	3-ketoacyl-CoA synthase
Potri.001G134425	3-ketoacyl-CoA synthase
Potri.001G134701	3-ketoacyl-CoA synthase
Potri.009G083100	3-ketoacyl-CoA synthase
Potri.001G314900	calcium-binding protein CML
Potri.001G332900	calcium-binding protein CML
Potri.002G001400	calcium-binding protein CML
Potri.002G077300	calcium-binding protein CML
Potri.005G183300	calcium-binding protein CML
Potri.005G259900	calcium-binding protein CML
Potri.006G112500	calcium-binding protein CML
Potri.010G081000	calcium-binding protein CML
Potri.016G142000	calcium-binding protein CML
Potri.017G029700	calcium-binding protein CML
Potri.006G052900	calcium-dependent protein kinase
Potri.006G200600	calcium-dependent protein kinase
Potri.012G023300	calcium-dependent protein kinase
Potri.015G066200	calcium-dependent protein kinase
Potri.001G134425	calcium-dependent protein kinase
Potri.001G134701	calcium-dependent protein kinase
Potri.009G083100	calmodulin
Potri.010G146900	calmodulin
Potri.009G010700	cyclic nucleotide gated channel, plant
Potri.014G097900	cyclic nucleotide gated channel, plant
Potri.017G089800	cyclic nucleotide gated channel, plant
Potri.017G089900	cyclic nucleotide gated channel, plant
Potri.001G134300	disease resistance protein RPM1
Potri.001G134400	disease resistance protein RPM1
Potri.001G134425	disease resistance protein RPM1
Potri.001G134701	disease resistance protein RPM1
Potri.009G083100	disease resistance protein RPM1
Potri.001G134701	disease resistance protein RPM1
Potri.002G216800	disease resistance protein RPM1
Potri.018G013600	disease resistance protein RPM1
Potri.019G013140	disease resistance protein RPS2
Potri.015G069600	enhanced disease susceptibility 1 protein
Potri.005G241100	heat shock protein 90kDa beta
Potri.012G043200	mitogen-activated protein kinase kinase 1
Potri.009G082900	pathogenesis-related protein 1
Potri.009G083100	pathogenesis-related protein 1
Potri.009G083300	pathogenesis-related protein 1
Potri.001G098300	respiratory burst oxidase
Potri.003G133300	respiratory burst oxidase
Potri.003G133400	respiratory burst oxidase
Potri.003G159800	respiratory burst oxidase
Potri.006G137300	respiratory burst oxidase
Potri.015G109800	respiratory burst oxidase
Potri.001G099001	WRKY transcription factor 22
Potri.016G128300	WRKY transcription factor 33

Supplementary Figure S4. The expression level of genes belonged to the module “Peroxidases” in Mapman analysis.



Supplementary Figure S5. The enriched GO terms (biological process) analyzed by the DEGs of MO_treat vs. MU_treat and NL895-H vs. NL895-W. **(A)** the GO terms enriched by DEGs of NL895-H vs. NL895-W, NL895 is a poplar clone containing high resistance to weak active strain of *Marssonina brunnea* f. sp. *multigermtubi* (W) and showed certain susceptible to high active strain (H) (Chen. C *et al*, 2015. “A comprehensive analysis of the transcriptomes of *Marssonina brunnea* and infected poplar leaves to capture vital events in host-pathogen interactions”). **(B)** the GO terms enriched by DEGs of MO_treat vs. MU_treat in this study.

