

## **Transcriptomic profile of tobacco in response to *Phytophthora nicotianae* infection**

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**Supplementary Table S1.** All genes and their gene expression data. FPKM was used to represent the expression level.

**Supplementary Table S2.** All genes and their expression fold change (FC) compared to controls. LogFC means of log-transformed value.

**Supplementary Table S3.** Annotation of 15 upregulated differentially expressed genes shared by two varieties. Annotation was from non-redundant (NR) protein database in NCBI.

**Supplementary Table S4.** Annotation of five unique upregulated differentially expressed genes for RBST. Annotation was from non-redundant (NR) protein database in NCBI.

**Supplementary Table S5.** GO enrichment for unique upregulated differentially expressed genes in HD at 12 h. *P* value was corrected with FDR.

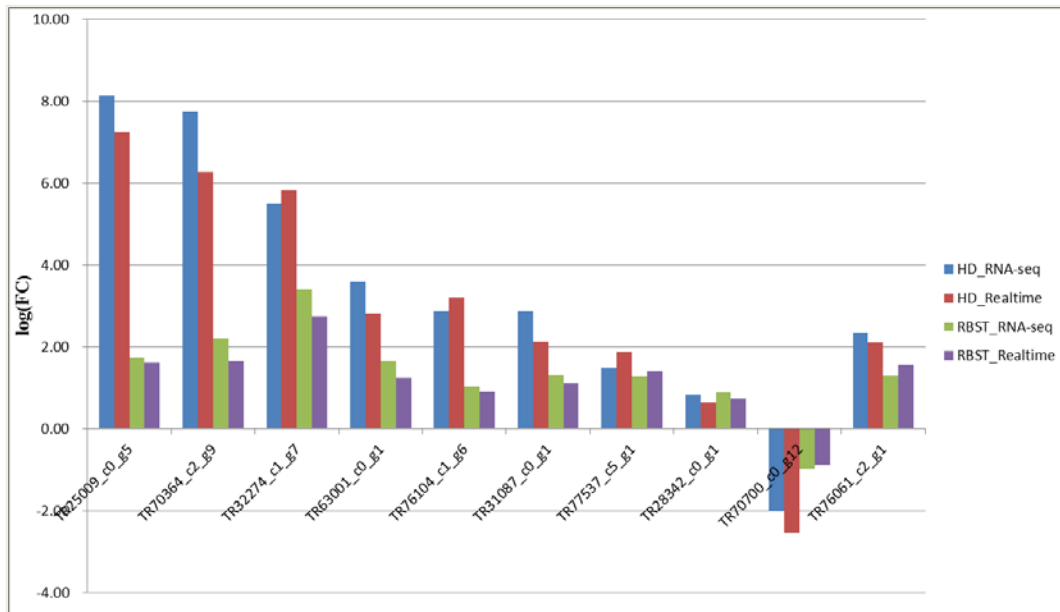
**Supplementary Table S6.** GO enrichment for unique upregulated differentially expressed genes in HD at 72 h. *P* value was corrected with FDR.

**Supplementary Table S7.** GO enrichment for unique upregulated differentially expressed genes in RBST at 12 h and 72 h. *P* value was corrected with FDR.

**Supplementary Table S8.** GO enrichment for upregulated differentially expressed genes shared by HD and RBST. *P* value was corrected with FDR.

**Supplementary Table S9.** GO enrichment for downregulated differentially expressed genes shared by HD and RBST. *P* value was corrected with FDR.

**Supplementary Table S10.** Primer sequences of ten genes for qRT-PCR validation.



**Supplementary Figure S1.** qRT-PCR validation of differentially expressed ten genes. Expression profiles of selected genes as determined by qRT-PCR and DEG. The signal intensity of each transcript was normalized using *actin* gene. The y-axis shows the normalized expression level of the transcript.

## Supplementary Materials and Methods

### Development of the tobacco breeding line RBST

Flue-cured tobacco cultivar Coker 371-Gold possesses a dominant gene, *Ph* derived from *N. plumbaginifolia*, which confers high resistance to black shank disease, caused by race 0 of the pathogen *P. nicotianae*<sup>S1</sup>. Flue-cured tobacco cultivar Coker 176 possesses a dominant gene, *N* derived from *N. glutinosa*, which confers high resistance to TMV (Tobacco mosaic virus)<sup>S2</sup>. Coker 371-Gold is hybridized with Coker 176 to produce F1. Haploid plants were produced by crossing F1 (Coker 371-Gold × Coker 176) plant to *N. africana* (pollinator) using the maternal haploid method<sup>S3</sup>. Haploid plants were chromosome doubled using the midvein culture method<sup>S4</sup> to produce the flue-cured tobacco doubled haploid (DH) breeding line RBST, which is high resistance to both black shank disease and TMV.

### Development of the flue-cured tobacco cultivar Honghuadajinyuan (HD)

The flue-cured tobacco cultivar HD was developed from a spontaneous mutant with deep red flower in a Yunnan farmer's field growing the flue-cured tobacco cultivar Gold Dollar, which is the farmer variety in USA<sup>S5</sup>. HD could produce high quality tobacco leaves, but it was susceptible

to black shank disease.

### **Supplementary References**

- S1. Johnson, E. S., Wolff, M. F., Wernsman, E. A., Atchley, W. R. & Shew, H. D. Origin of the black shank resistance gene, Ph, in tobacco cultivar Coker 371-Gold. *Plant Dis* **86**, 1080–1084 (2002).
- S2. Lewis, R. S., Milla, S. R. & Levin, J. S. Molecular and genetic characterization of *Nicotiana glutinosa* L. chromosome segments in Tobacco mosaic virus-resistant tobacco accessions. *Crop Sci* **45**, 2355–2362 (2005).
- S3. Burk, L. G., Gerstel, D. U. & Wernsman, E. A. Maternal haploids of *Nicotiana tabacum* L. from seed. *Science* **206**, 585 (1979).
- S4. Kasperbauer, M. A. & Collins, G. B. Reconstitution of diploids from leaf tissue of anther derived haploids in tobacco. *Crop Sci* **12**, 98–101 (1972).
- S5. Moon, H.S. *et al.* Changes in Genetic Diversity of U.S. Flue-Cured Tobacco Germplasm over Seven Decades of Cultivar Development. *Crop Sci* **49**, 498–508 (2009).