

Supplementary file

Identification and application of exogenous dsRNA confers plant protection against *Sclerotinia sclerotiorum* and *Botrytis cinerea*

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Table S1. Mapping summary for all biological replicates of *in-vitro* and *in-planta* samples. Raw RNA-sequencing reads trimmed using Trimmomatic 0.33 and aligned to the *S. sclerotiorum* genome using TopHat v2.1.0.

	in-vitro (1)	in-vitro (2)	in-vitro (3)	ZY821 24hpi (1)	ZY821 24hpi (2)	ZY821 24hpi (3)	Westar 24hpi (1)	Westar 24hpi (2)	Westar 24hpi (3)
Trimmed reads	6537111	6339049	11826235	31473436	44428372	20453088	40287633	37020385	52025758
Mapped reads	5388394	5216455	10273216	6282525	6724081	3061161	7810054	6478810	8125640
% Mapped	82.4	82.3	86.9	20	15.1	15	19.4	17.5	15.6

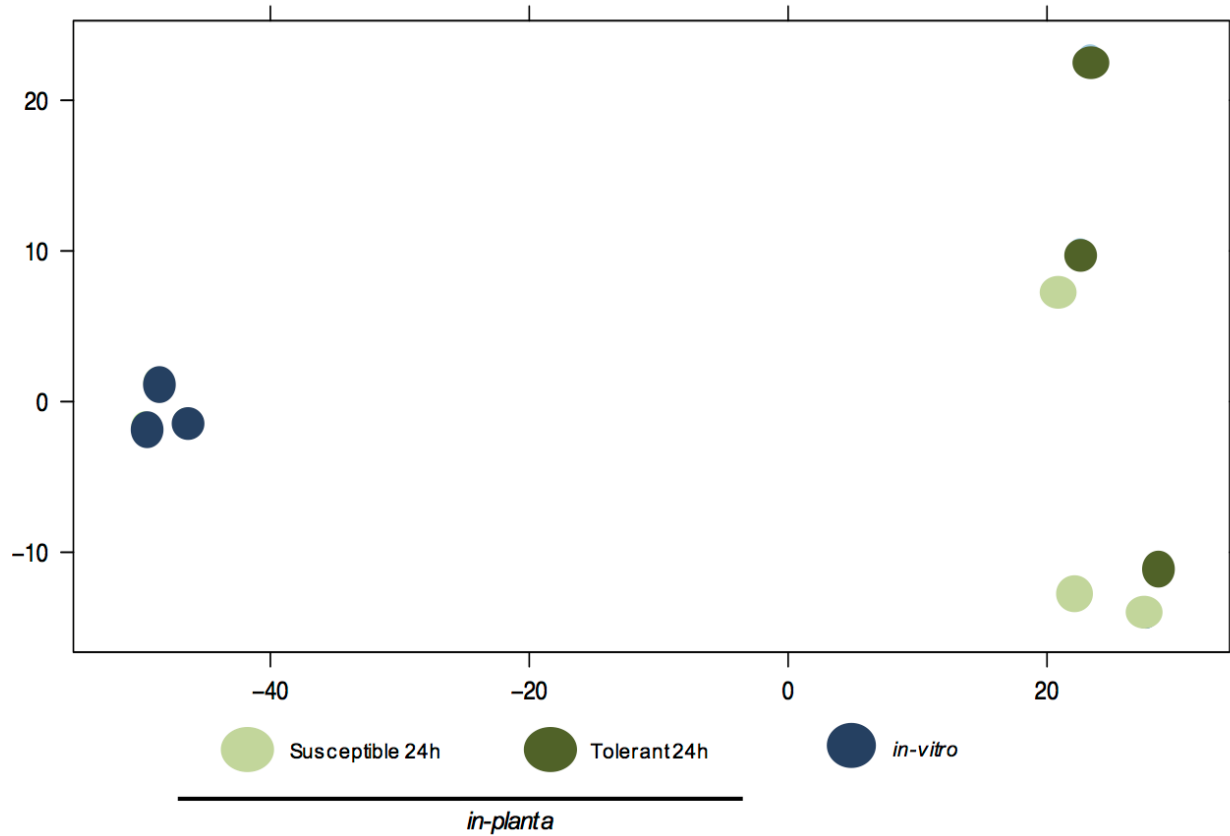


Figure S1. Principle component analysis plot of *in-planta* and *in-vitro* grown *S. sclerotiorum* based on FPKM transcript expression.

Table S2. Target identification pipeline guidelines for selecting targets to control phytopathogenic fungi using RNAi

Criteria	Choose	Avoid
RNA-seq dataset	Upregulated genes common amongst infection conditions	Down regulated genes in response to infection
Essential Genes	Genes of closely related species. Genes can be found in the Database of Essential Genes ¹	Essential genes from distant or unrelated relatives
Biological processes	Mitochondria, ROS response, protein modification, pathogenicity factors, transcription, splicing, protein modification, translation, cell wall modification	General growth, transcription factors, transport, electron carriers, signal transduction, pigment synthesis, carbohydrate metabolism
Expression levels	FPKM values between 1 and 500	Lowly (FPKM <1) and Highly (FPKM > 500) expressed during infection
Log2-fold change (control vs. infection)	Fold changes between -0.5 and 4	Fold changes below -0.5 and above 4
Transcript length	Above 200 nucleotides	Below 200 nucleotides
Gene location	Nuclear-encoded	Organelle-encoded
Redundancy	Single function or without homologues	Genes with multiple homologues and functionally similar roles
Regulation		Genes that are heavily regulated

(1) www.essentialgene.org ¹

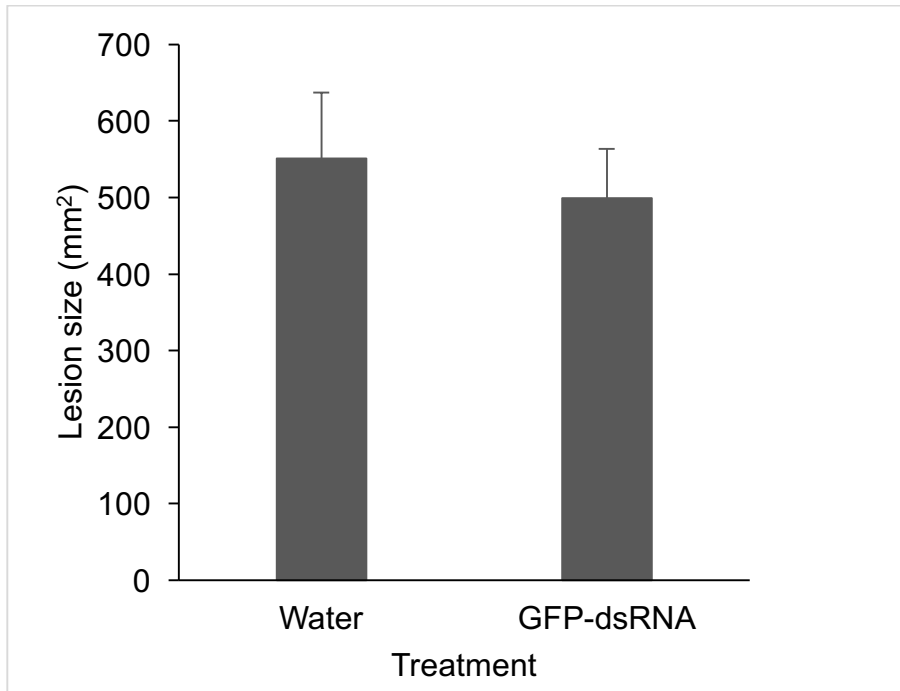


Figure S2 *Sclerotinia sclerotiorum* infection on *B. napus* leaves ($n = 10$) 2 dpi after treatment of water or GFP-dsRNA. No significant difference was observed ($p = 0.63$, student's *t*-test).

References

1. Luo, H., Lin, Y., Gao, F., Zhang, C. T. & Zhang, R. DEG 10, an update of the database of essential genes that includes both protein-coding genes and noncoding genomic elements. *Nucleic Acids Res.* **42**, 574–580 (2014).