

Supplementary data

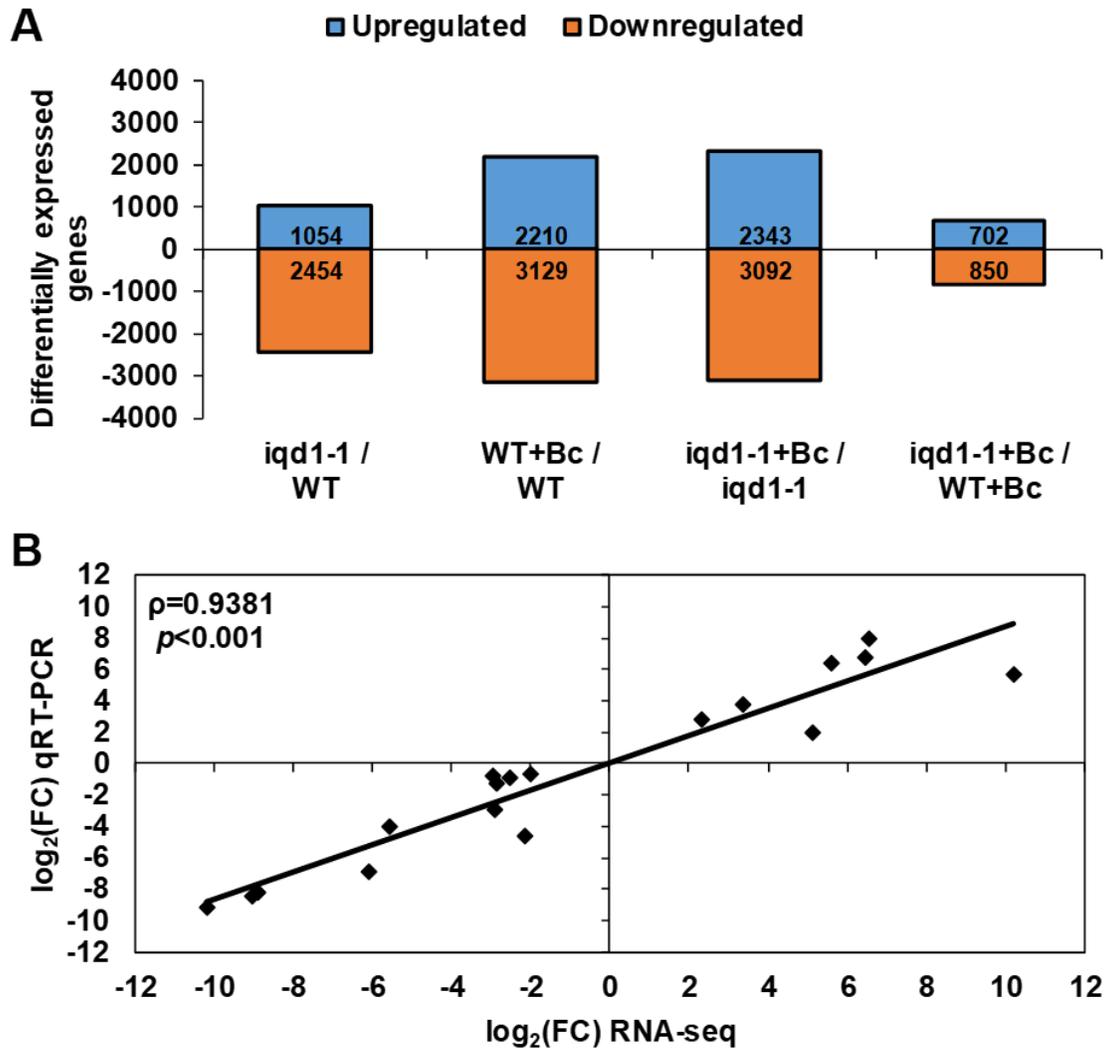


Figure S1. A. Differentially expressed *Arabidopsis thaliana* genes in mock and *B. cinerea* (Bc) infected plants. Shown are the number of upregulated and downregulated genes with more than four-fold difference between the following pairs: *iqd1-1* vs. WT, infected WT vs. WT, infected *iqd1-1* vs. *iqd1-1*, infected *iqd1-1* vs. infected WT. **B.** Correlation of qRT-PCR and RNA-Seq results. Expression ratios of 18 representative genes were determined using qRT-PCR for *iqd1-1*/WT. Each RNA-Seq value and qRT-PCR value (mean of 4 repeats) were \log_2 transformed and plotted against each other for comparison. Correlation analyses were done with Spearman's Rho test.

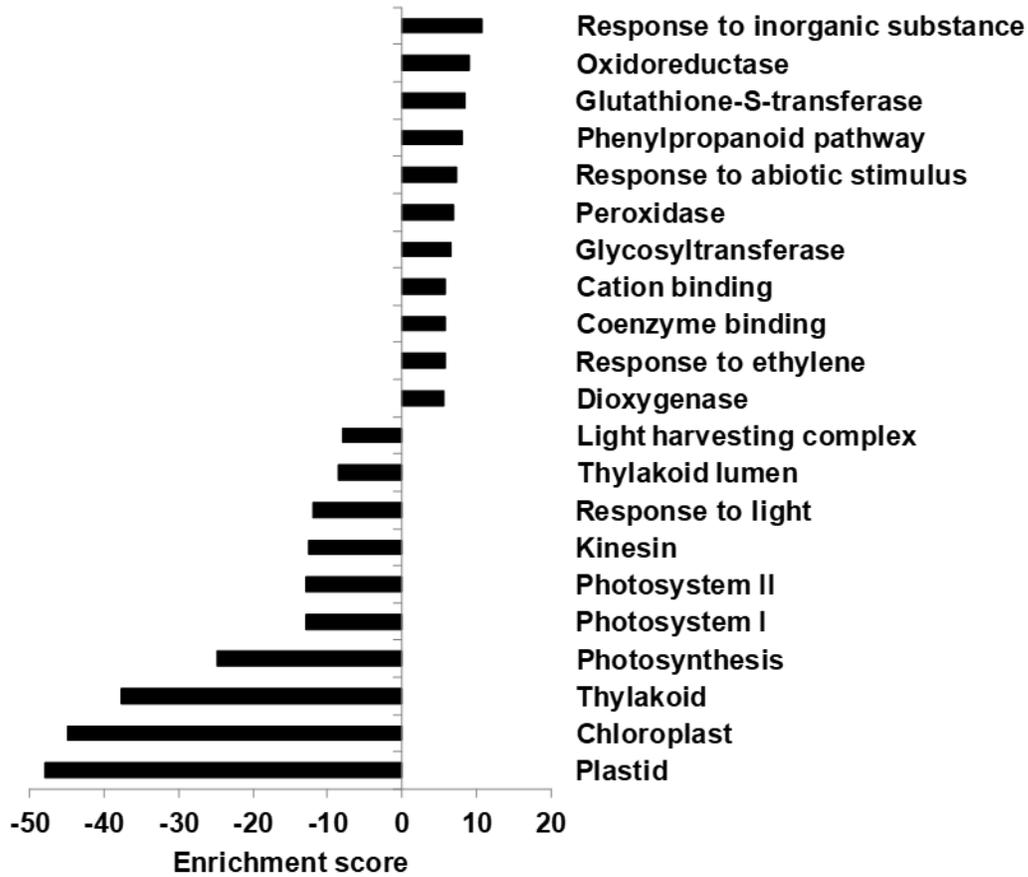


Figure S2. Differentially expressed clusters in infected vs. mock inoculated WT plants. Enriched annotation terms of functional-related genes were grouped into clusters using the DAVID bioinformatics resources website. Positive enrichment scores denote upregulated clusters in infected WT while negative values denote upregulated clusters in mock treated WT plants.

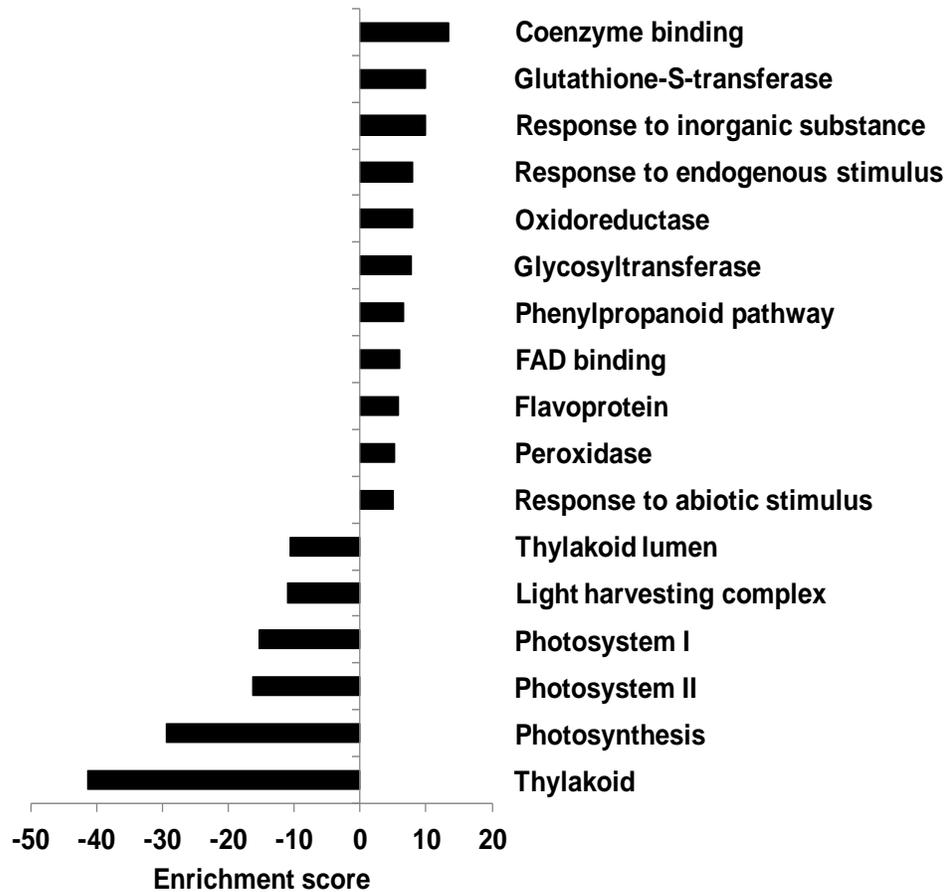


Figure S3. Differentially expressed clusters in infected vs. mock inoculated *iqd1-1* plants. Enriched annotation terms of functional-related genes were grouped into clusters using the DAVID bioinformatics resources website. Positive enrichment scores denote upregulated clusters in infected *iqd1-1* while negative values denote upregulated clusters in mock treated *iqd1-1* plants.

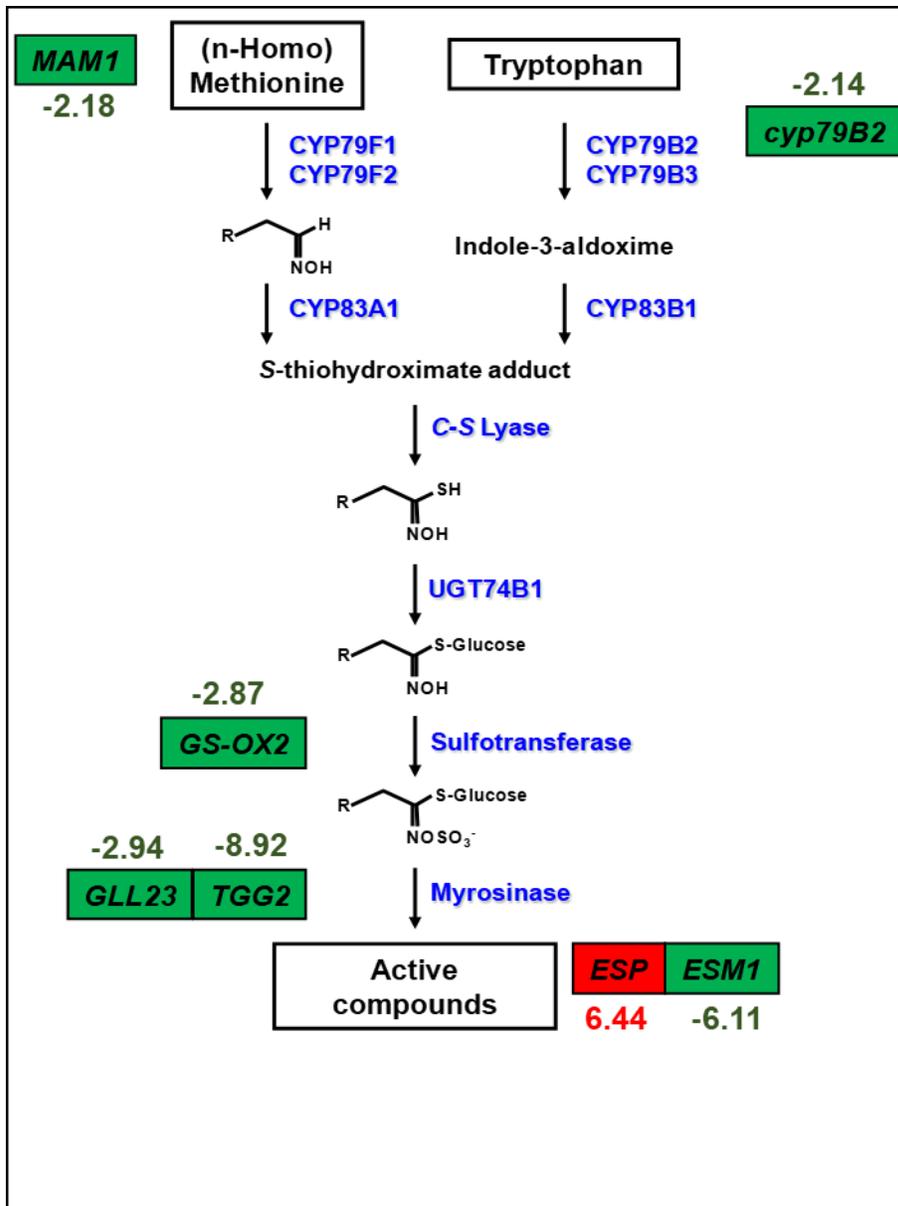


Figure S4. Differentially expressed GS related genes in *iqd1-1* compared to WT. Schematic overview of important genes involved in glucosinolate biosynthesis. Upregulated genes in *iqd1-1* are in red boxes and downregulated genes are in green boxes (numbers represent fold change).

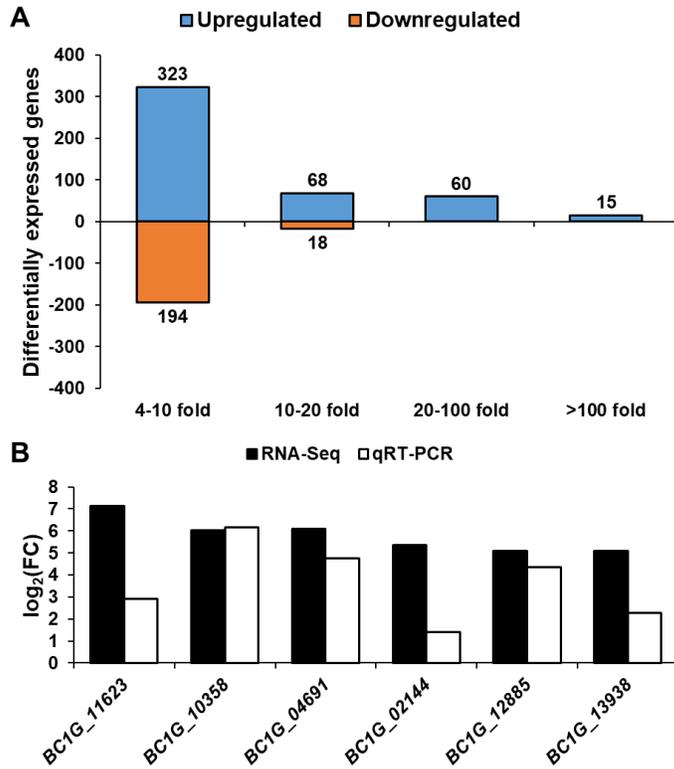


Figure S5. A. Differentially expressed *Botrytis cinerea* genes when infecting *iqd1-1* compared to WT. Shown are the number of upregulated (positive values) and downregulated (negative values) genes with more than four-fold difference between *B. cinerea* infecting *iqd1-1* as compared to infecting WT. **B.** qRT-PCR validation of RNA-Seq results. Comparison of *B. cinerea* candidate genes expression levels after infection of *iqd1-1* plants vs. WT.

Table S1. Reads of each dataset and mapping results

Read type	Ws-0	<i>iqd1-1</i>
Total reads	45,881,751	47,458,716
Mapped reads*	6,359,210 (13.86%)	3,659,067 (7.71%)
Uniquely mapped reads*	3,129,135 (6.82%)	2,477,345 (5.22%)
Multiple mapped reads*	3,230,075 (7.04%)	1,181,722 (2.49%)
Unmapped reads*	39,522,541 (86.14%)	43,799,649 (92.29%)
Uniquely counted reads**	2,488,753 (79.535%)	1,955,746 (78.945%)
Multiple counted reads**	125 (0.004%)	74 (0.003%)
Uncounted reads**	640,257 (20.461%)	521,525 (21.052%)

Table S2. Summary of mapped and counted reads of RNA from *B. cinerea* and mock infected tissues.

Read type	WT	<i>lqd1-1</i>	WT+Bc	<i>lqd1-1</i> +Bc
Total reads	49,778,547	31,852,780	45,881,751	47,458,716
Mapped reads*	48,275,235 (96.98%)	29,779,164 (93.49%)	40,527,351 (88.33%)	42,480,297 (89.51%)
Uniquely mapped reads*	44,541,844 (89.48%)	26,335,879 (82.88%)	26,207,656 (57.12%)	35,043,516 (73.84%)
Multiple mapped reads*	3,733,391 (7.50%)	3,443,285 (10.81%)	14,319,695 (31.21%)	7,436,781 (15.67%)
Unmapped reads*	1,503,312 (3.02%)	2,073,616 (6.51%)	5,354,400 (11.67%)	4,978,419 (10.49%)
Uniquely counted reads**	43,129,103 (96.828%)	25,238,861 (95.835%)	24,014,417 (91.631%)	33,296,296 (95.014%)
Multiple counted reads**	636,503 (1.429%)	433,225 (1.645%)	357,735 (1.365%)	556,491 (1.586%)
Uncounted reads**	778,591 (1.746%)	664,718 (2.524%)	1,837,157 (7.010%)	1,190,779 (3.398%)

Table S3. *Arabidopsis thaliana* homozygous mutants verification primers

Mutant	Primer name	Sequence
<i>IQD1^{oxp}</i>	H30 For	CGGAGGCGGAGAAAAGTTATTG
	H30 Rev	CACAGGCAAAGCATTACACGAC
<i>NahG</i>	NahG1 f	CTGCCGCTACTCCCATATCCA
	NahG1 r	TCGGCTTCGGCTCGCTAC
<i>npr1-1</i>	npr1-1 f	AGGCACTTGACTCGGATGAT
	npr1-1 r	ATGCACTTGACACCTTTTTC
<i>aos</i>	Salk_017756 LP	CGAGAAATTAACGGAGCTTCC
(Salk_017756)	Salk_017756 RP	CTAACCGGAGGCTACCGTATC
<i>coi1</i>	Salk_095916 LP	TCACCGACCTTACAGATACC
(Salk_095916)	Salk_095916 RP	TGGTTCAAGATTGATTCCGAG
<i>jar1-1</i>	jar1-1 f	CAGTGTGTGTGTTTTTATGATCATAAGCT
	jar1-1 r	CAAATTTAAACTATACCTGTTTCTGAAGG
<i>ein2-1</i>	ein2-1 f	CCAGAGGAAAGAGAGTTGGATGTAAGTACTCTACCG CT
	ein2-1 r	CGCCATCTTTGTTTCAACAATCAGATCC
<i>eto1-1</i>	eto1-1 f	GCAACACAACCTTGACCTCTT
	eto1-1 r	GGGAGAATCCCTCAGAAAGG
<i>pad3-1</i>	pad3-1 f	CAAAGACATCGGGATGGCAC
	pad3-1 r	AGCCTTTAGCAC AAGATCCACG
<i>cyp79B2</i>	cyp79B2 F	CTCGTTCAAGAATCCGACATCC
	cyp79B2 R	TCTCCGGTTTAAAGCAAAGTGG
<i>cyp79B3</i>	cyp79B3 F	AAGGCAATCCACCAATATCCG
	cyp79B3 R	TCGTGGTCAACATGCTTTATGC

Table S4. LC-MS/MS conditions

Time (minutes)	Solvent A (%), Water + 0.1% acetic acid	Solvent B (%), Methanol
0	80	20
1	80	20
12	4	96
20	4	96
20.1	80	20
25	80	20
Additional parameters		
Column temperature (°C)		40
Injection volume (µl)		5
Flow rate (ml/min)		0.25

Table S5. MRM parameters.

Compound	Fragmentor voltage (V)	Collision energy (eV)	MRM transitions
Abscisic acid	80	10	263→219
		10	263→204
Abscisic acid D6	80	10	269→225
		10	269→159
Jasmonic acid	80	10	209→59
Jasmonic acid D5	80	10	213→61
Salicylic acid	80	15	137→93
		15	137→65
Salicylic acid D4	80	15	141→97

Table S6. *Arabidopsis thaliana* qRT-PCR primers

Gene	Primer name	Sequence
<i>ef1a</i>	Ef1a SYBR f1	TGAGCACGCTCTTCTTGCTTTCA
	Ef1a SYBR r1	GGTGGTGGCATCCATCTTGTTACA
<i>nsp4</i>	NSP4 f1	TCAAGTTTGAGTATGTCAATGGTTCTC
	NSP4 r1	CAATCTCAAACCTCTTCAAACCTCTAGCT
<i>esp</i>	ESP f1	CTACAGGAGCGAAACCTTCC
	ESP r1	GATCAGGCCATACCTCACCT
<i>cml42</i>	CML42 f1	TCGGATCTCGCCGAGGCGT
	CML42 r1	ACGCGACCATCTTGATTCCGGT
<i>erf114</i>	ERF114 f1	CAAGTTGCGCCTACTCATCA
	ERF114 r1	TTTTGGGTCTCGGATTTTCA
<i>At4G24420</i>	AT4G24420 f1	ACGCTGATGAGAAGGTGATGCT
	AT4G24420 r1	GGGAGTAGGGTTGGCCTTGA
<i>tip2-3</i>	TIP2-3 f1	TTCTATTGGATTGCTCAGTGTCTTG
	TIP2-3 r1	GGTACGCTCTTGCCATTAGTAACA
<i>At4G22490</i>	AT4G22490 f1	AGTGTGCACTGCCCTCAATG
	AT4G22490 r1	CAACGGAATCGCCTGAA
<i>sr1</i>	SR1 SYBR f2	TTTGACGCCAGGGATAGTT
	SR1 SYBR r2	GGACTGTTGATAGTTTGTCTTGTGTC
<i>iqd24</i>	IQD24 f1	TCCGCTTTTCGTGGCTACTT
	IQD24 r1	CCCTTACCAACGCTTGAA
<i>iqd31</i>	IQD31 f1	TTCAAGATCATTATTCTGATGCA
	IQD31 r1	GCCGAGCCAAGTAACCTCTAAA
<i>esm1</i>	ESM1 f1	TCGTAGGATTGCGACAGG
	ESM1 r1	CCTGAGCCTTCTGTGTGTG
<i>tgg2</i>	TGG2 f1	CCGCAAGGCCATCAAGGAGAAG
	TGG2 r1	AATCTGACGGTGTAGCCGTTGC
<i>mam1</i>	MAM1 f1	CGGCTGAAAGAGTTGGGATA
	MAM1 r1	ATGCCTTCAAATCAGCATCC
<i>fmo gs-ox2</i>	GS-OX2 f1	GCCGTGTGTTTGCAGTGGAC
	GS-OX2 r1	ATTTCCGATGACCACCACCACCTC
<i>gll23</i>	GLL23 f1	CAGACTTCCTCGCTAAATTCATGA
	GLL23 r1	CTCCACGTGAGACATTGACGTT
<i>At1G63880</i>	AT1G63880 f1	TGCATTCTAGCCAGCTCGAGTA
	AT1G63880 r1	TCCGGGAGTTGCTTCAAATT
<i>At1G66100</i>	AT1G66100 f1	TGTCTTGACATTAGTGAGTCGACATG
	AT1G66100 r1	TCAGTGACAGCATCACCTGTGTT
<i>abcc11</i>	ABCC11 f1	TTCAAGGTTGGGCATGATCTATC
	ABCC11 r1	ACCCAAGCTGGATCACCTTCT
<i>cyp705A27</i>	CYP705A27 f1	CTTATTGTGGAGCTTTTCCTTGGA
	CYP705A27 r1	TGGTTAATGAGTTCGGCCATT
<i>cyp71A24</i>	CYP71A24 f1	ATCTTGGATGTTTTGTGGGTGAT
	CYP71A24 r1	TGGTGGCATAGTAGCTCTGTCATT
<i>cyp76C6</i>	CYP76C6 f1	TCGAACACCTACTTCTCGATATGTTT
	CYP76C6 r1	TAACCTCTGCCATTGCCATTTC
<i>cyp82C2</i>	CYP82C2 f1	AATCTACCTGCCTGGCACTG
	CYP82C2 r1	GAGAAATGGCCATGTAAGG
<i>At1G66540</i>	AT1G66540 f1	GATTGATCACTTGTCTTCTTTGCA
	AT1G66540 r1	CGCAAGTATAAGAGAAAGCATGGTT
<i>cyp81K2</i>	CYP81K2 f1	GTCGCTTGCTGTTGGAGCAT
	CYP81K2 r1	ACGAGGCCCTCATGTCTATGT
<i>cyp76C5</i>	CYP76C5 f1	CACCTACTTCTCGATATGTTTCTAGCA
	CYP76C5 r1	CTCTGTCATTGCCATTCCA
<i>cyp72A11</i>	CYP72A11 f1	TCAAGACTCATGGGAGGACTTTC
	CYP72A11 r1	TGTGATTGCTCAGGATCCATT

Table S7. *Botrytis cinerea* qRT-PCR primers.

Gene	Primer name	Sequence
<i>Bcactin</i> (<i>Bc1G_08198</i>)	08198F	CCCAATCAACCCAAAGTCCAACAG
	08198R	CAAATCACGACCAGCCATGTC
<i>Bc1G_11623</i>	11623F	GTTGCATCTACCGGATCGT
	11623R	AAACACAGCACCACCATTGA
<i>Bc1G_10358</i>	10358F	GGCGAGCAAAACGCTCTAT
	10358R	GGTGAGAGGAGGAGCTTGTG
<i>Bc1G_04691</i>	04691F	CATAACCGAAAACGGCACTT
	04691R	GGCCCACTCAAAGTTATCCA
<i>Bc1G_02144</i>	02144F	GTTGATGCCACCTGGAAACT
	02144R	GGGGAGTCAAATGCGTAGAA
<i>Bc1G_12885</i>	12885F	TTCACCAAAGTCCCTCAACC
	12885R	AACCGAGGCTACCATCATTG
<i>Bc1G_13938</i>	13938F	CTCTTTTGCCTGCTTGCTG
	13938R	TCCAGGTCTCTCCACCATC