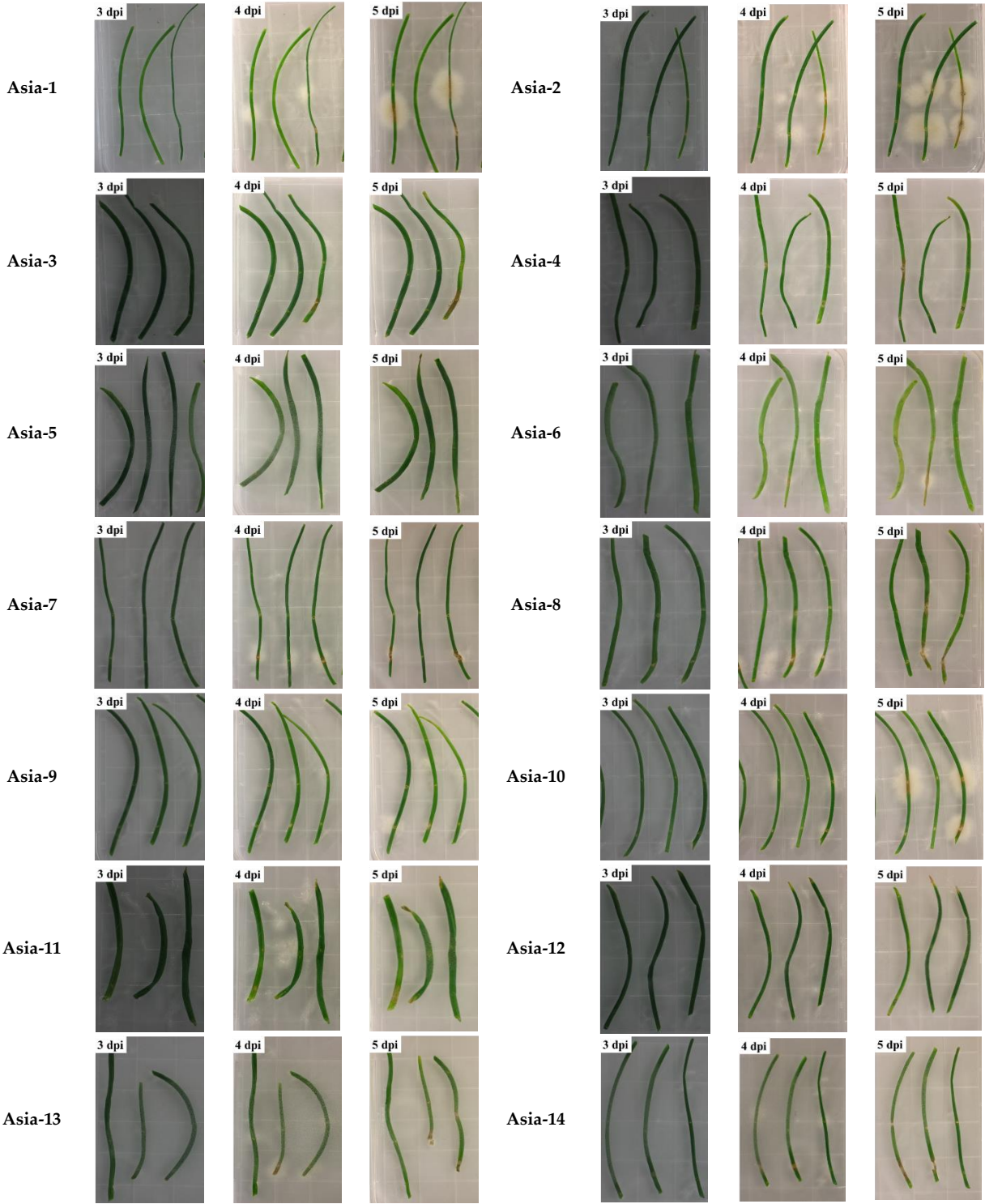
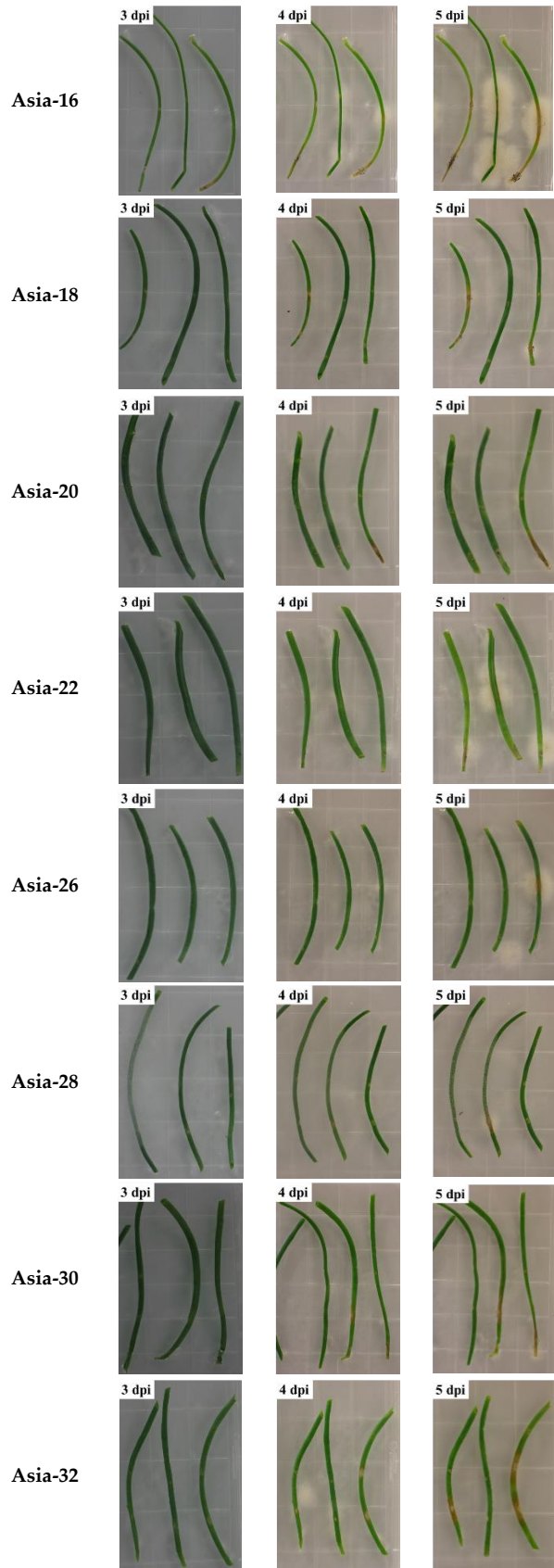
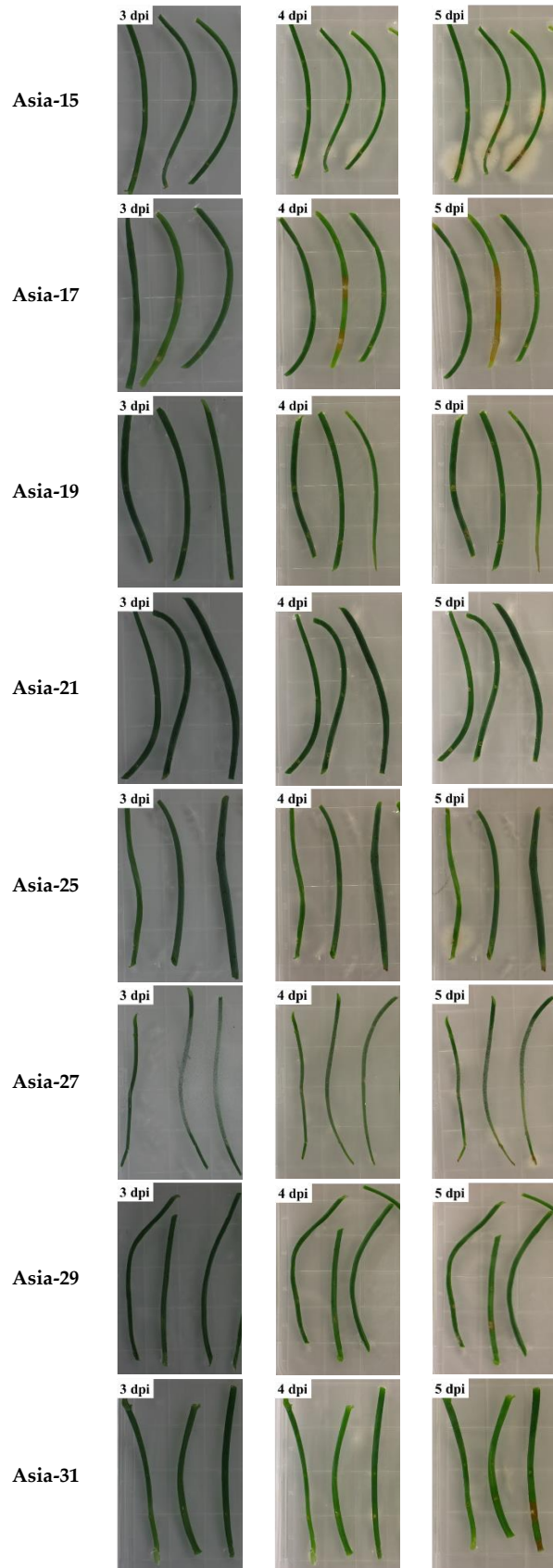
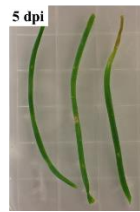


Supplementary materials

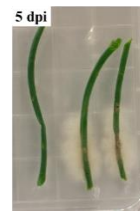




Asia-33



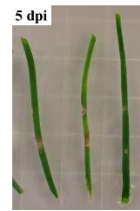
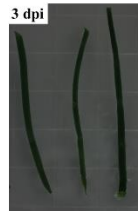
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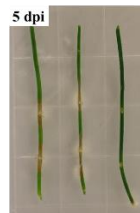
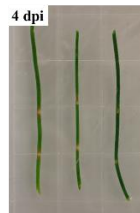
Asia-35



Asia-36



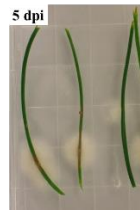
Asia-37



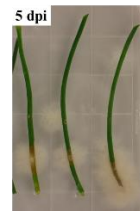
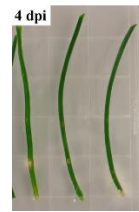
Asia-38



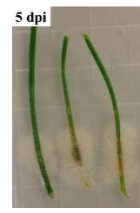
Asia-39



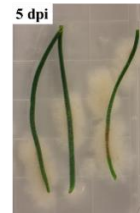
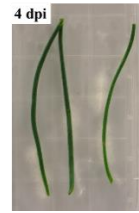
Asia-40



Asia-41



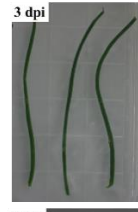
Asia-42



Asia-43



Asia-44



Asia-45



Asia-46



Asia-47



Asia-48



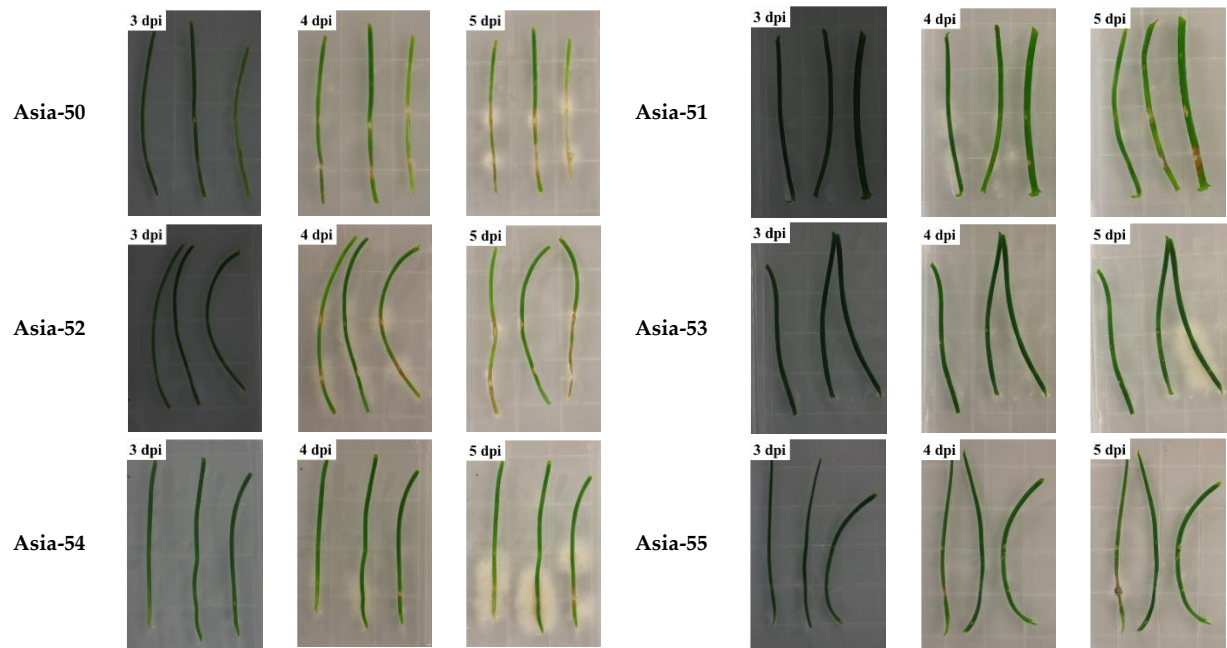
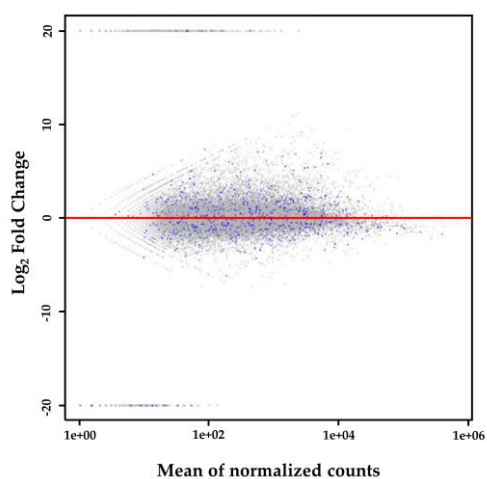
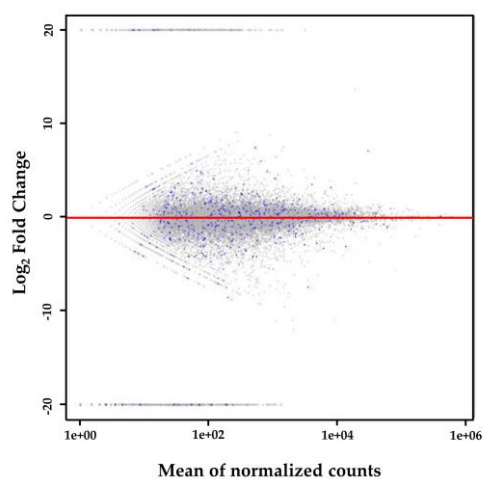


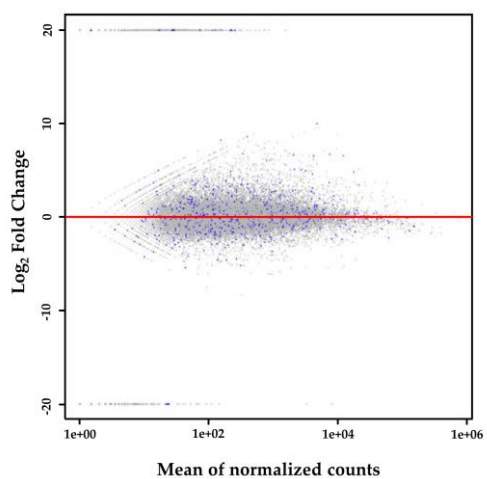
Figure S1. *In vitro* inoculation for screening gray mold resistant and susceptible onion lines using detached onion leaves and conidia of *B. squamosa*. A representative image of lesion appearance in inoculated leaves were taken at 3 – 5 days post inoculation (dpi).



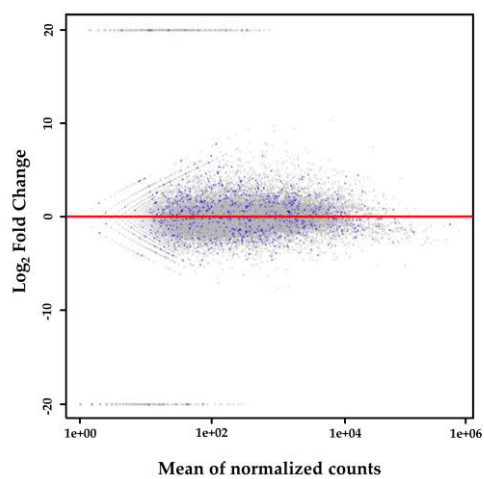
Asia-23 0 hpi vs 4 hpi



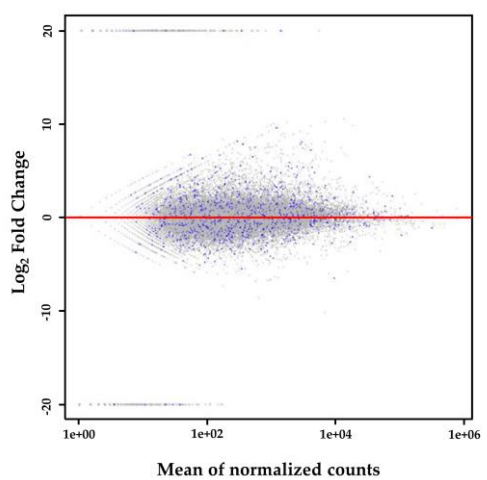
Asia-24 0 hpi vs 4 hpi



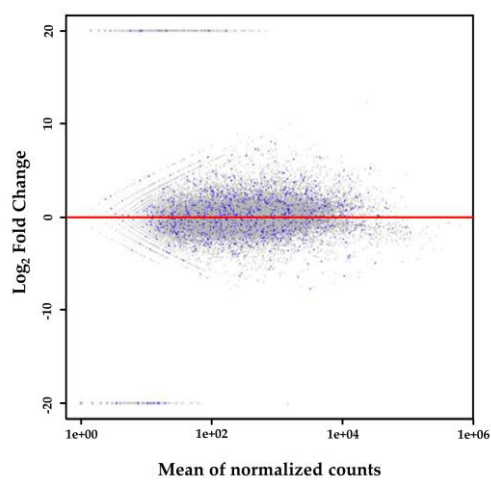
Asia-23 0 hpi vs 8 hpi



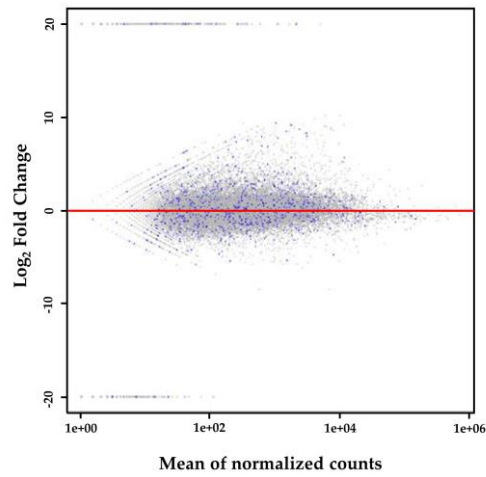
Asia-24 0 hpi vs 8 hpi



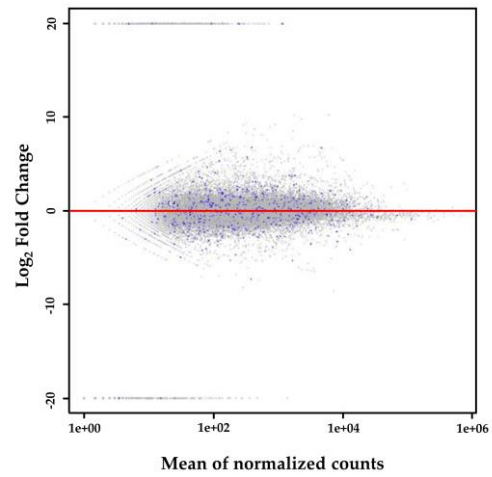
Asia-23 0 hpi vs 16 hpi



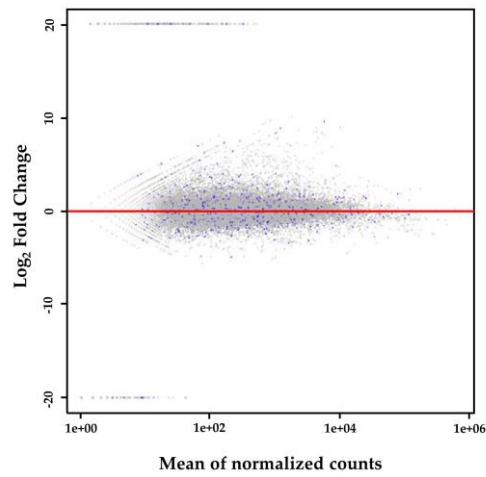
Asia-24 0 hpi vs 16 hpi



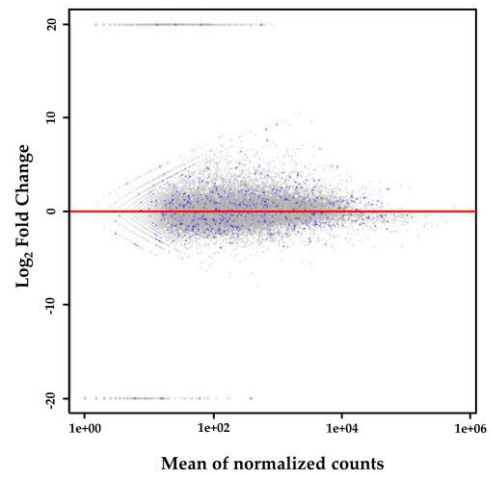
Asia-23 0 hpi vs 24 hpi



Asia-24 0 hpi vs 24 hpi

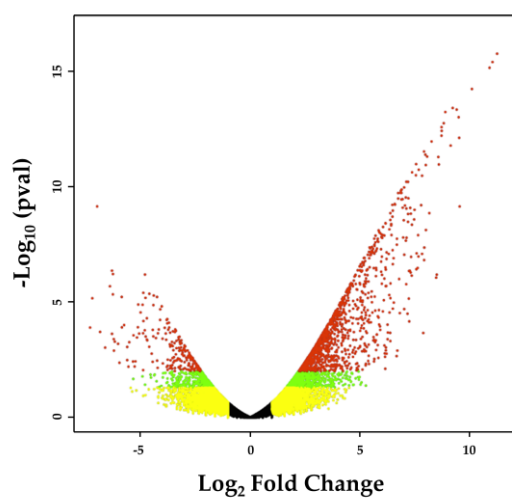


Asia-23 0 hpi vs 32 hpi

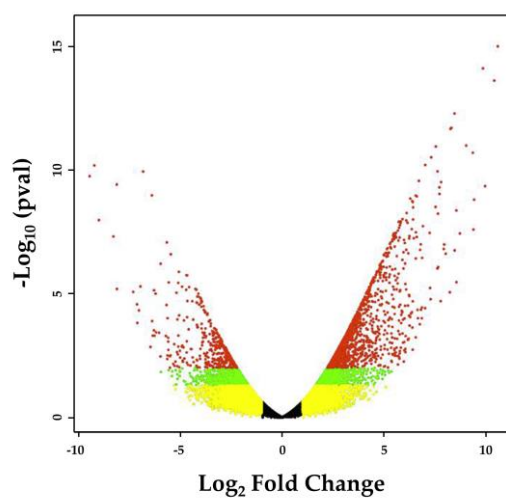


Asia-24 0 hpi vs 32 hpi

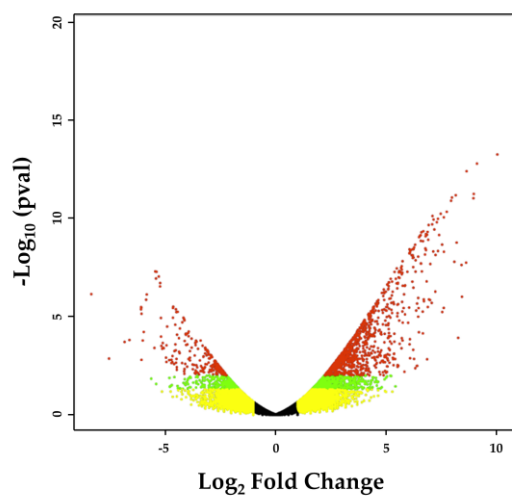
Figure S2. Differentially expressed gene (DEG) results expressed as MA plot. In the MA plot, transcripts of significantly upregulated or downregulated genes in each comparative analysis ($p < 0.01$) are indicated with blue dots. hpi: hours post inoculation.



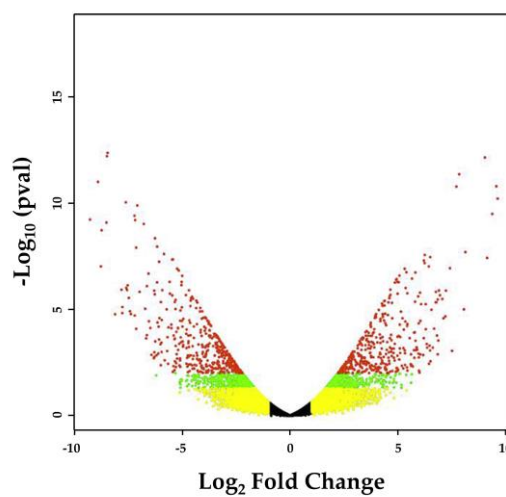
Asia-23 0 hpi vs 4 hpi



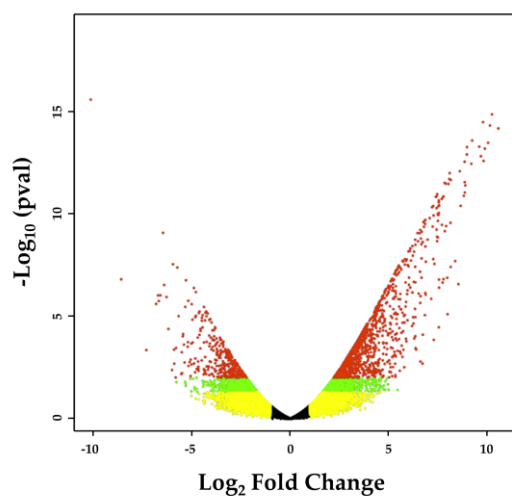
Asia-24 0 hpi vs 4 hpi



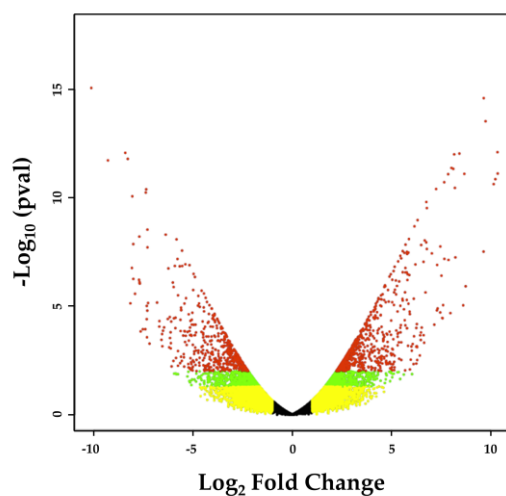
Asia-23 0 hpi vs 8 hpi



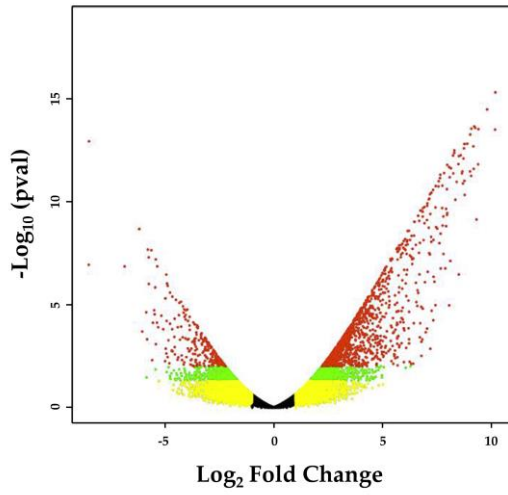
Asia-24 0 hpi vs 8 hpi



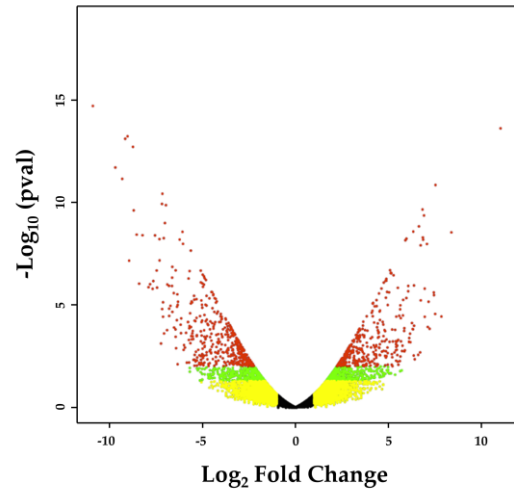
Asia-23 0 hpi vs 16 hpi



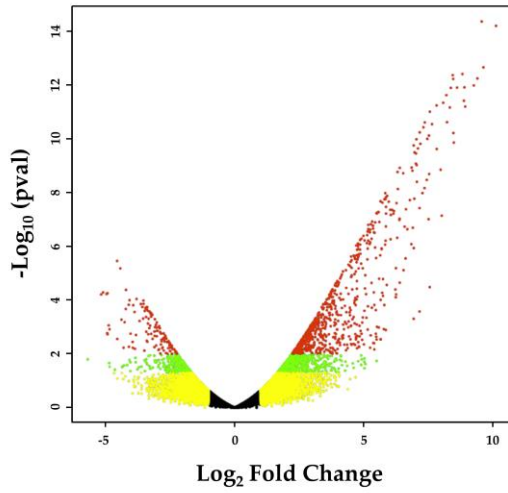
Asia-24 0 hpi vs 16 hpi



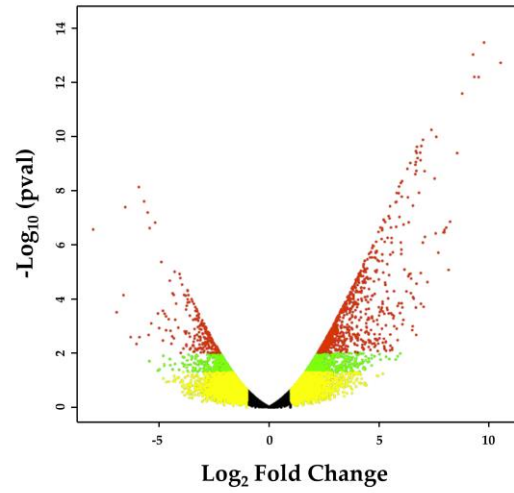
Asia-23 0 hpi vs 24 hpi



Asia-24 0 hpi vs 24 hpi



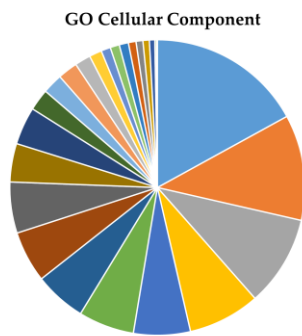
Asia-23 0 hpi vs 32 hpi



Asia-24 0 hpi vs 32 hpi

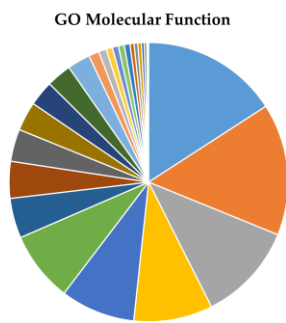
Figure S3. Differentially expressed gene (DEG) results expressed as Volcano plot. The Volcano plots were displayed in different colors according to each analysis option in the DEG analysis: $FDR < 0.01$, $2 < |\log_2 \text{fold change}|$ (red), $0.01 < FDR < 0.05$, $2 < |\log_2 \text{fold change}|$ (green), $0.05 < FDR$, $2 < |\log_2 \text{fold change}|$ (yellow), and $FDR < 0.05$, $|\log_2 \text{fold change}| < 2$ (black). hpi: hours post inoculation.

(A)



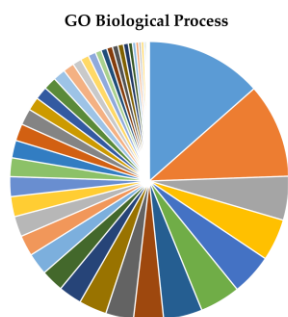
Functional category	Gene count
nucleus	1772
chloroplast	1204
cytoplasm	1034
other intracellular components	822
plasma membrane	648
mitochondrion	636
cytosol	591
plastid	585
other membranes	582
other cellular components	438
extracellular region	430
vacuole	246
Golgi apparatus	230
endoplasmic reticulum	226
thylakoid	181
unknown cellular components	143
nucleolus	108
nucleoplasm	105
cell wall	105
peroxisome	87
endosome	78
cytoskeleton	73
ribosome	62
nuclear envelope	19
lysosome	10

(B)



Functional category	Gene count
protein binding	1170
catalytic activity	1127
unknown molecular functions	842
transferase activity	674
other binding	638
hydrolase activity	601
RNA binding	341
DNA binding	315
transporter activity	276
kinase activity	248
nucleic acid binding	216
DNA-binding transcription factor activity	214
nucleotide binding	195
enzyme regulator activity	89
structural molecule activity	66
nuclease activity	54
chromatin binding	52
other molecular functions	50
lipid binding	49
carbohydrate binding	35
transcription regulator activity	31
translation factor activity, RNA binding	31
signaling receptor activity	24
motor activity	21
signaling receptor binding	10
translation regulator activity	5
oxygen binding	1

(C)

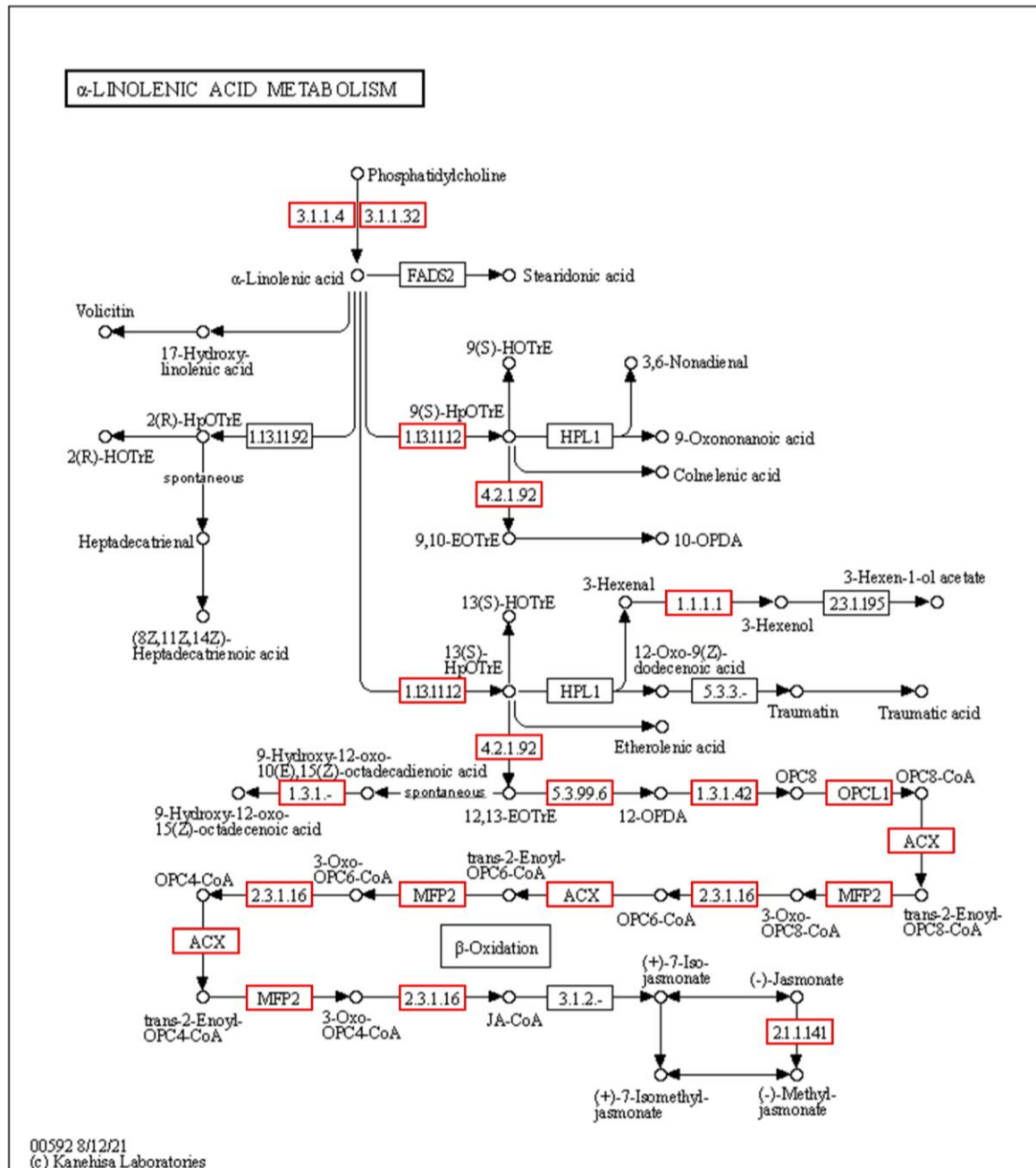


Functional category	Gene count	Functional category	Gene count
other cellular processes	2913	lipid metabolic process	320
other metabolic processes	2368	growth	310
anatomical structure development	1099	cell differentiation	276
response to stress	1048	carbohydrate metabolic process	220
biosynthetic process	1032	embryo development	209
response to chemical	1012	cell cycle	191
multicellular organism development	972	cell communication	149
nucleobase-containing compound metabolic process	750	DNA metabolic process	148
cellular component organization	696	flower development	144
reproduction	696	secondary metabolic process	140
post-embryonic development	582	cell growth	137
response to abiotic stimulus	563	translation	125
cellular protein modification process	547	generation of precursor metabolites and energy	101
response to external stimulus	520	pollination	82
catabolic process	510	photosynthesis	72
response to light stimulus	503	regulation of molecular function	66
response to endogenous stimulus	496	cellular homeostasis	62
transport	469	cell death	39
response to biotic stimulus	439	circadian rhythm	38
signal transduction	426	tropism	27
unknown biological processes	407	regulation of gene expression, epigenetic	19
other biological processes	336	cell-cell signaling	10
protein metabolic process	324	abscission	6

Figure S4. GO annotation of transcripts clustered in Cluster 4. (A) GO Cellular Component, (B) GO Molecular Function, (C) GO Biological Process.

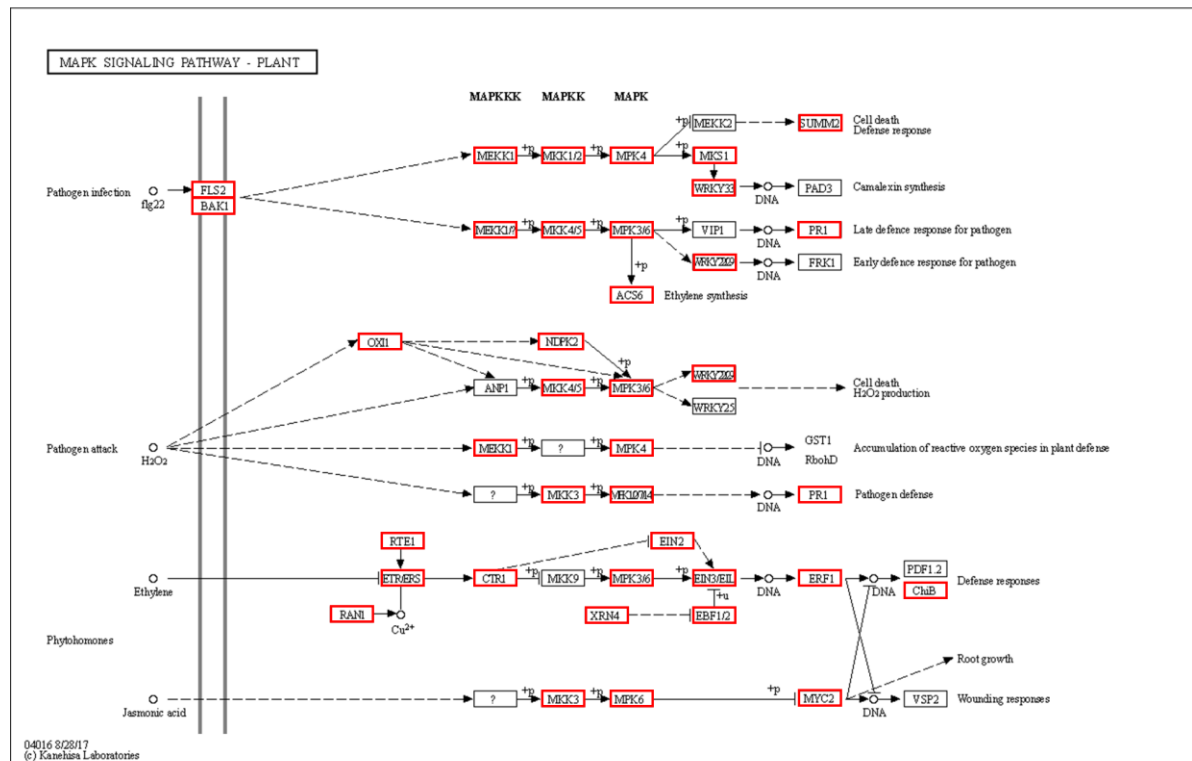
(A)

Alpha-linolenic acid metabolism pathway



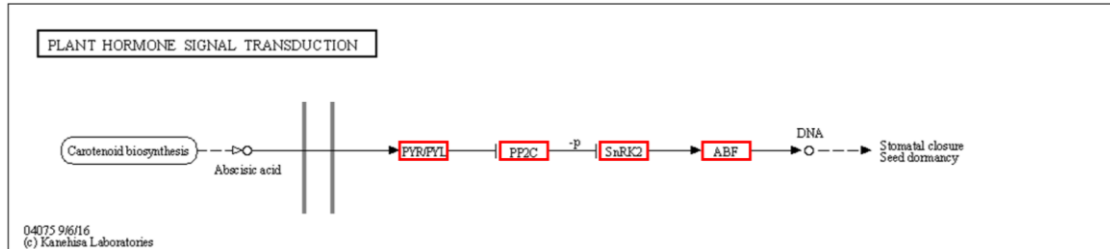
(B)

MAPK signaling pathway

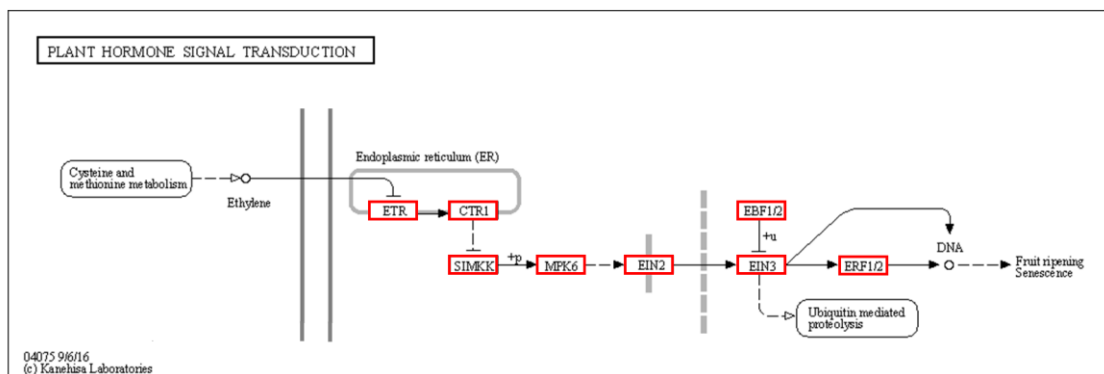


(C)

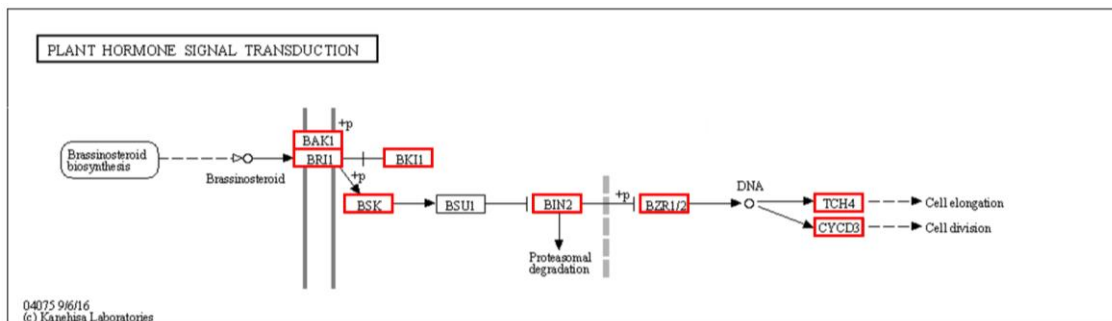
Plant hormone signal transduction – Carotenoid biosynthesis pathway



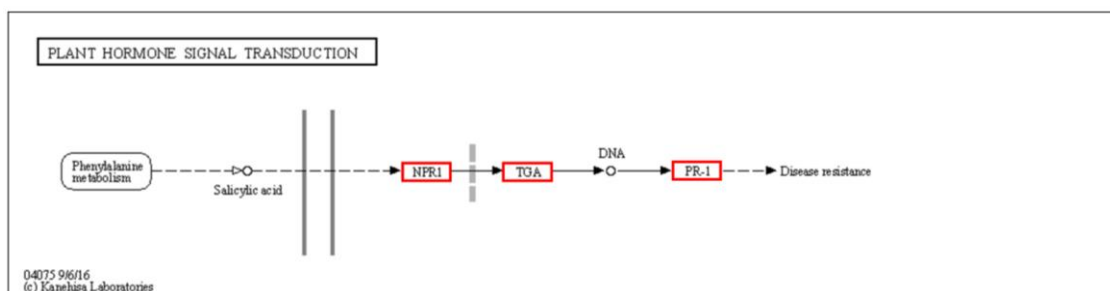
Plant hormone signal transduction – Cysteine and methionine metabolism



Plant hormone signal transduction – Brassinosteroid biosynthesis



Plant hormone signal transduction – Phenylalanine metabolism



(D)

Plant – Pathogen interaction

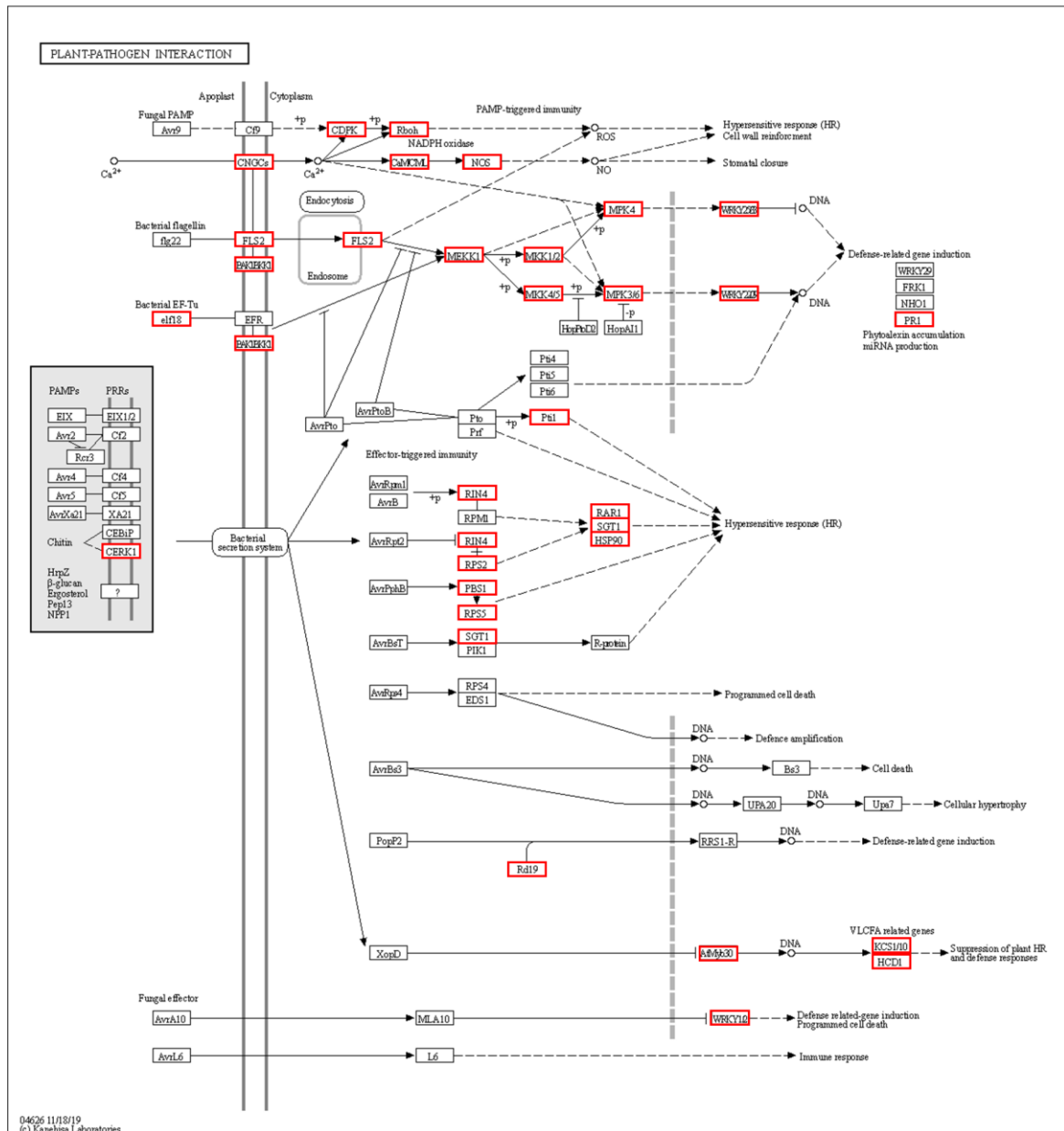


Figure S5. Results of KEGG pathway analysis considered to be related to gray mold resistance. (A) Alpha-linolenic acid metabolism, (B) MAPK signaling pathway, (C) Plant hormone signal transduction-Carotenoid biosynthesis pathway; Plant hormone signal transduction-Cysteine and methionine metabolism; Plant hormone signal transduction-Brassicosteroid biosynthesis; Plant hormone signal transduction-Phenylalanine metabolism, (D) Plant-pathogen interaction. The genes matched with onion transcripts were displayed red box.

Table S1. Primer sets for confirmation of selected gene sequences

Gene	Primer name	Orientation	Nucleotide sequences (5' to 3')
<i>JAR1</i>	1st exon	Forward	TGT TTT CCG CAG ACC TTT TGA A
	(Include start codon)	Reverse	TGG CTT CCC TTT TGT AGT ACC A
	2nd exon	Forward	AGC TGC CTT CAG TCA TCA CAA
		Reverse	CAC TAC ACT TGT GAC ATG TTC CG
	3rd exon	Forward	TCT ACG AGA AGG GGT AGC TGT
	(Include stop codon)	Reverse	AGA ATA CGA ACA AAC CTG CAC C
<i>COI1</i>	1st exon	Forward	TGC CGC TAG TAT AAT GTT GAG CT
	(Include start codon)	Reverse	ACT TGT ATC AGC TGC CCA GT
	2nd exon	Forward	GGA GGA GGC GGA AGT GTT TT
		Reverse	GCT CTG CTC CTC CCC TAA CA
	3rd exon	Forward	AGA GAT GTT TGC GTG CGA GT
	(Include stop codon)	Reverse	ACA AAA CCA GCC AAG CAA ATT TTT A
<i>MYC2</i>	1st exon	Forward	CTC GAC GCA CTA ACC GGA G
	(Include start codon)	Reverse	TGC TAA AAC AAC GCT CGA TCA
	2nd exon	Forward	CCT TCT CCT TCT ACC TCA TTT CCT C
	(Include stop codon)	Reverse	CAT ATC TAA AAG TCC GTC TTC TCC G

Table S2. Primer sets for high-resolution melting (HRM) analysis.

Primer name	Orientation	Nucleotide sequences (5' to 3')
<i>JAR1</i>	Forward	GCT GAG TAT TTG CAA AAT TTG GGT C
	Reverse	TGT CAA TGG AGT TCC GGT CAG
<i>COI1</i>	Forward	GGC GGC GAT TTC CTA CGT TA
	Reverse	CCT GCA TAG CCT CCC CAA TC
<i>MYC2</i>	Forward	CAA CCA GGA ATC CCT CCA GC
	Reverse	GAC TGC CAG AAG ATG GCG TA

Table S3. Statistics of sequence raw data.

Sample ID	Total read bases	Total reads	Q30 ^a (%)
Asia_23_0 hpi	5,159,368,052	51,082,852	93.96
Asia_23_4 hpi	5,397,686,642	53,442,442	93.99
Asia_23_8 hpi	5,410,303,966	53,567,366	94.85
Asia_23_16 hpi	5,459,818,004	54,057,604	93.19
Asia_23_24 hpi	5,427,496,792	53,737,592	94.04
Asia_23_32 hpi	5,164,047,382	51,129,182	93.58
Asia_24_0 hpi	5,343,300,768	52,903,968	95.06
Asia_24_4 hpi	5,301,659,276	52,491,676	93.99
Asia_24_8 hpi	5,356,953,342	53,039,142	93.92
Asia_24_16 hpi	5,322,845,642	52,701,442	94.17
Asia_24_24 hpi	5,252,278,962	52,002,762	93.94
Asia_24_32 hpi	5,122,853,118	50,721,318	94.36

^a Ratio of bases that have phred quality score greater than or equal to 30.

Table S4. Pre-processing results of onion RNA sequence raw data.

Sample ID	Raw Data		Trimmed Data	
	Total Reads	Total read bases (bp)	Total Reads	Total read bases (bp)
Asia-23_0_hpi	53,442,442	5,397,686,642	48,159,176	4,846,678,416
Asia-23_4_hpi	53,567,366	5,410,303,966	49,467,140	4,979,339,740
Asia-23_8_hpi	54,057,604	5,459,818,004	47,964,876	4,824,642,022
Asia-23_16_hpi	53,737,592	5,427,496,792	49,021,478	4,932,839,546
Asia-23_24_hpi	51,129,182	5,164,047,382	45,008,816	4,529,201,024
Asia-23_32_hpi	51,947,444	5,246,691,844	46,223,388	4,651,745,224
Asia-24_0_hpi	52,903,968	5,343,300,768	48,938,402	4,927,956,063
Asia-24_4_hpi	52,491,676	5,301,659,276	47,029,632	4,732,586,446
Asia-24_8_hpi	53,039,142	5,356,953,342	47,633,440	4,793,750,309
Asia-24_16_hpi	52,701,442	5,322,845,642	47,396,334	4,770,861,379
Asia-24_24_hpi	52,002,762	5,252,278,962	46,667,746	4,696,488,290
Asia-24_32_hpi	50,721,318	5,122,853,118	45,931,580	4,623,373,129

Table S5. Results of mapping and alignment to reference data of pre-processed RNA sequence data.

Sample	Progressed reads	Mapped reads	Mapping rate ^a (%)
Asia-23_0_hpi	48,159,176	40,345,980	83.80%
Asia-23_4_hpi	49,467,140	36,736,709	74.30%
Asia-23_8_hpi	47,964,876	37,878,527	79.00%
Asia-23_16_hpi	49,021,478	40,383,170	82.40%
Asia-23_24_hpi	45,008,816	38,654,847	85.90%
Asia-23_32_hpi	46,223,388	39,394,150	85.20%
Asia-24_0_hpi	48,938,402	40,505,969	82.80%
Asia-24_4_hpi	47,029,632	37,595,701	79.90%
Asia-24_8_hpi	47,633,440	36,243,746	76.10%
Asia-24_16_hpi	47,396,334	37,886,277	79.90%
Asia-24_24_hpi	46,667,746	38,889,514	83.30%
Asia-24_32_hpi	45,931,580	38,286,473	83.40%

^a Mapping rate: (Mapped reads / Progressed reads) × 100

Table S6. DEG comparison at each hour post inoculation (hpi) within the resistant and susceptible sample groups.

DEG group	Upregulated genes	Downregulated genes	Total
Asia_23_0 hpi vs Asia_23_4 hpi	770	90	860
Asia_23_0 hpi vs Asia_23_8 hpi	535	73	608
Asia_23_0 hpi vs Asia_23_16 hpi	677	136	813
Asia_23_0 hpi vs Asia_23_24 hpi	673	101	774
Asia_23_0 hpi vs Asia_23_32 hpi	317	37	354
Asia_24_0 hpi vs Asia_24_4 hpi	670	166	836
Asia_24_0 hpi vs Asia_24_8 hpi	476	131	607
Asia_24_0 hpi vs Asia_24_16 hpi	761	300	1061
Asia_24_0 hpi vs Asia_24_24 hpi	340	112	452
Asia_24_0 hpi vs Asia_24_32 hpi	406	58	464