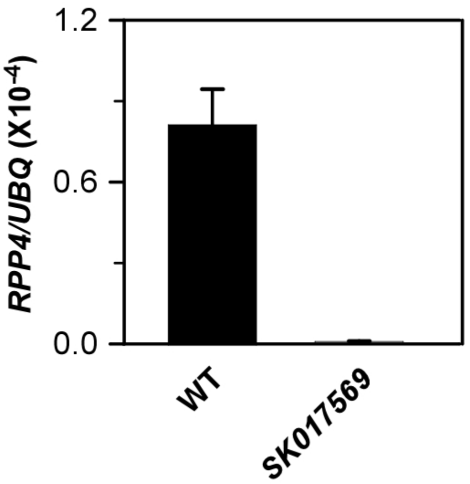
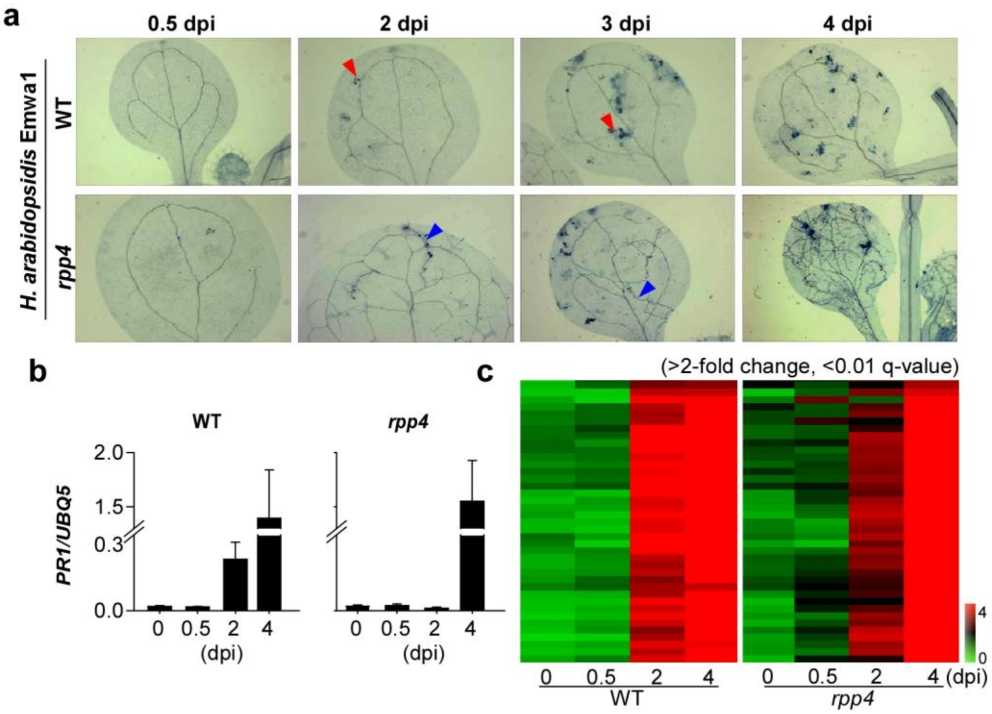
doi:10.1038/nature09766



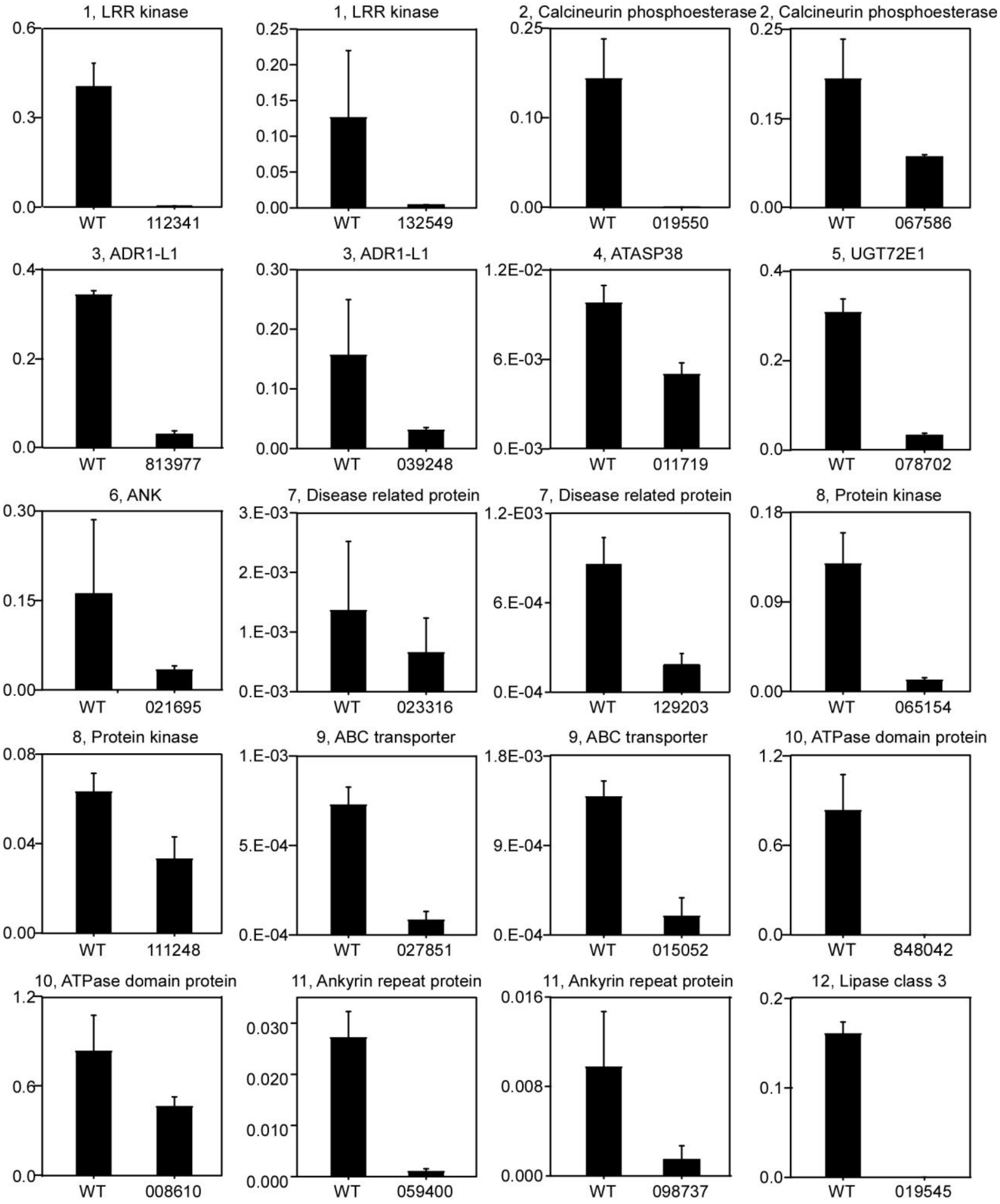
Supplementary Figure 1. The expression level of *RPP4* (At4g16860) is diminished in the *rpp4* mutant (SK017569).

The mRNA was extracted to analyze the expression level of *RPP4* using quantitative PCR (qPCR). Gene expression was normalized against constitutively expressed *UBQ5*. Error bars represent SD (n = 3). WT, wild-type.



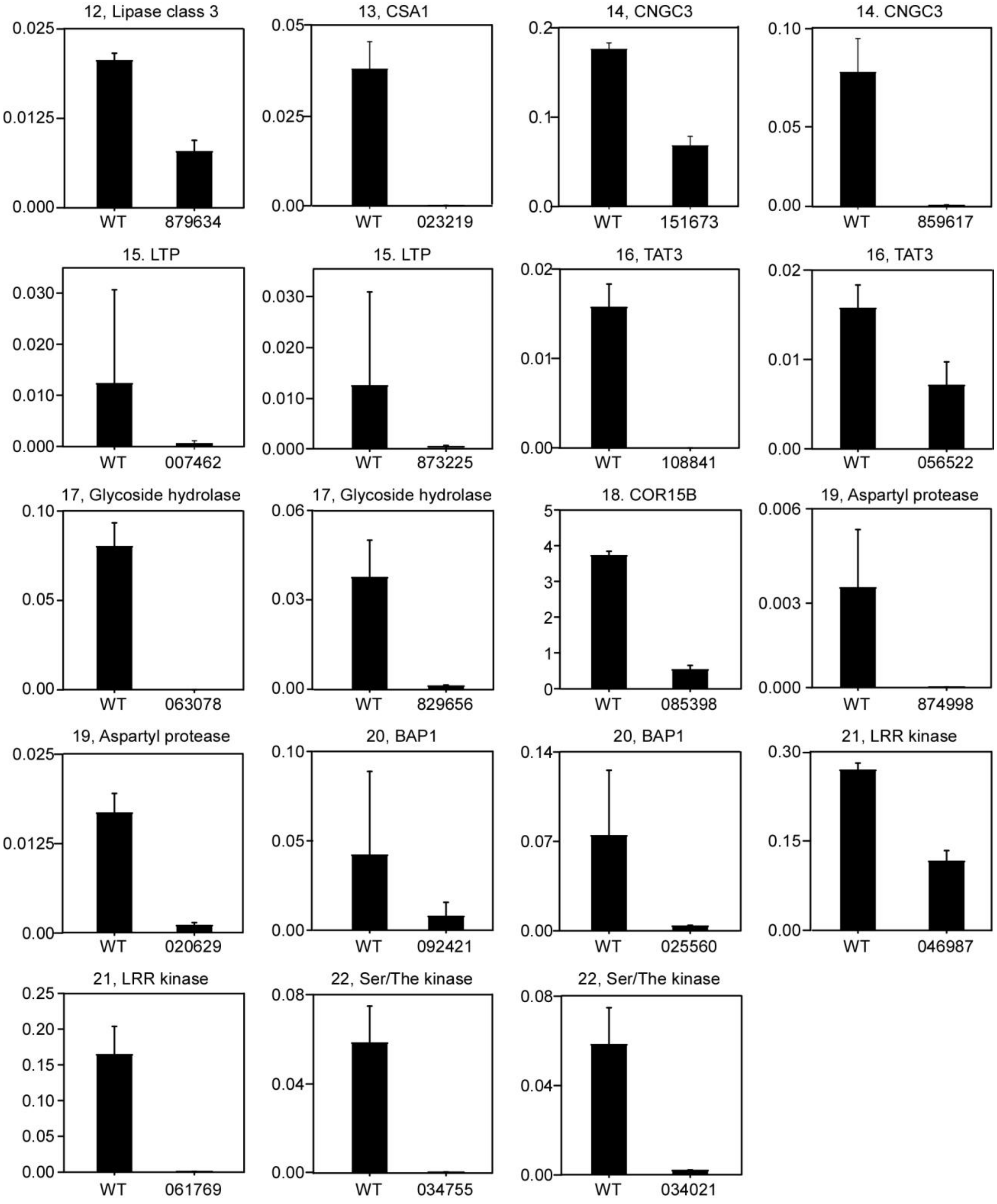
Supplementary Figure 2. Identification of RPP4-regulated genes through expression profiling.

a, *In planta* growth of *Hpa* Emwa1 and plant responses were examined under a microscope following lactophenol trypan blue (LTB) staining. Red arrows indicate HR cell death and blue arrows point at hyphae. dpi, days post inoculation. **b,** Expression levels of the marker gene *PR1* were measured using qPCR and normalized with *UBQ5*. Error bars represent SD (n = 3 biological replicates). **c,** Expression profiles of candidate genes that were significantly induced (q-values < 0.01) more than 2-fold in WT at 2 dpi.


1, LRR kinase
0.6
0.3
0.0
WT
112341
1, LRR kinase
0.25
0.20
0.15
0.10
0.05
0.00
WT
132549
2, Calcineurin phosphoesterase
0.25
0.10
0.00
WT
019550
2, Calcineurin phosphoesterase
0.25
0.15
0.00
WT
067586
3, ADR1-L1
0.4
0.2
0.0
WT
813977
3, ADR1-L1
0.30
0.20
0.10
0.00
WT
039248
4, ATASP38
1.2E-02
6.E-03
0.E-03
WT
011719
5, UGT72E1
0.4
0.2
0.0
WT
078702
6, ANK
0.30
0.15
0.00
WT
021695
7, Disease related protein
3.E-03
2.E-03
1.E-03
0.E-03
WT
023316
7, Disease related protein
1.2-E03
6.E-04
0.E-04
WT
129203
8, Protein kinase
0.18
0.09
0.00
WT
065154
8, Protein kinase
0.08
0.04
0.00
WT
111248
9, ABC transporter
1.E-03
5.E-04
0.E-04
WT
027851
9, ABC transporter
1.8E-03
9.E-04
0.E-04
WT
015052
10, ATPase domain protein
1.2
0.6
0.0
WT
848042
10, ATPase domain protein
1.2
0.6
0.0
WT
008610
11, Ankyrin repeat protein
0.030
0.020
0.010
0.000
WT
059400
11, Ankyrin repeat protein
0.016
0.008
0.000
WT
098737
12, Lipase class 3
0.2
0.1
0.0
WT
019545

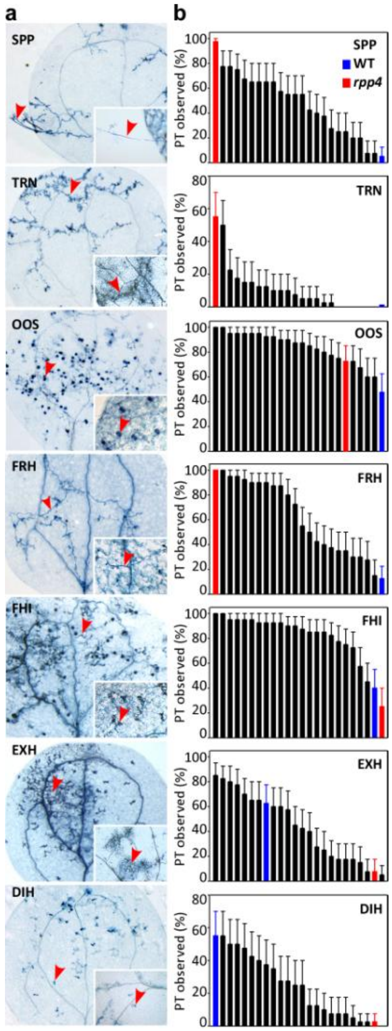
Supplementary Figure 3-1. T-DNA insertion diminished the expression of candidate genes as measured by qPCR.

Gene expression levels were normalized against *UBQ5*. Error bars represent SD (n = 3 biological replicates). Full numbers for the T-DNA insertion mutant lines are shown in Supplementary Table 1. Primers used in this analysis are shown in Supplementary Table 2.


12, Lipase class 3
0.025
0.0125
0.000
WT
879634
13, CSA1
0.05
0.025
0.00
WT
023219
14, CNGC3
0.2
0.1
0.0
WT
151673
14. CNGC3
0.10
0.05
0.00
WT
859617
15. LTP
0.030
0.020
0.010
0.000
WT
007462
15. LTP
0.030
0.020
0.010
0.000
WT
873225
16, TAT3
0.02
0.01
0.00
WT
108841
16, TAT3
0.02
0.01
0.00
WT
056522
17, Glycoside hydrolase
0.10
0.05
0.00
WT
063078
17, Glycoside hydrolase
0.06
0.03
0.00
WT
829656
18. COR15B
5
4
3
2
1
0
WT
085398
19, Aspartyl protease
0.006
0.003
0.000
WT
874998
19, Aspartyl protease
0.025
0.0125
0.00
WT
020629
20, BAP1
0.10
0.05
0.00
WT
092421
20, BAP1
0.14
0.07
0.00
WT
025560
21, LRR kinase
0.30
0.15
0.00
WT
046987
21, LRR kinase
0.25
0.20
0.15
0.10
0.05
0.00
WT
061769
22, Ser/The kinase
0.08
0.04
0.00
WT
034755
22, Ser/The kinase
0.08
0.04
0.00
WT
034021

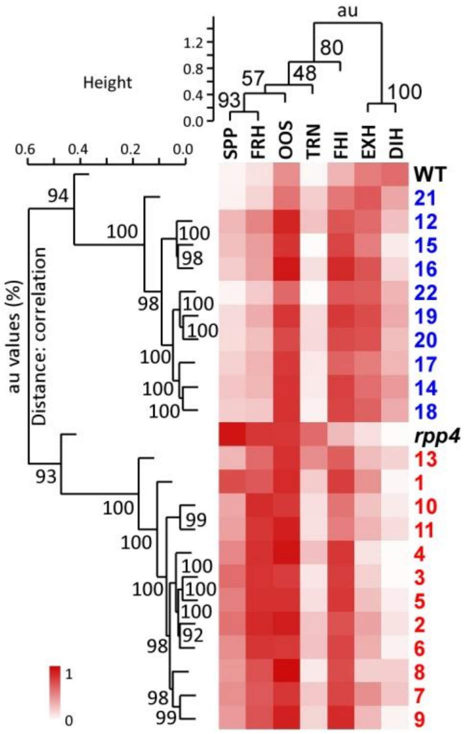
Supplementary Figure 3-2. T-DNA insertion diminished the expression of candidate genes as measured by qPCR.

Gene expression levels were normalized against *UBQ5*. Error bars represent SD (n = 3 biological replicates). Full numbers for the T-DNA insertion mutant lines are shown in Supplementary Table 1. Primers used in this analysis are shown in Supplementary Table 2.



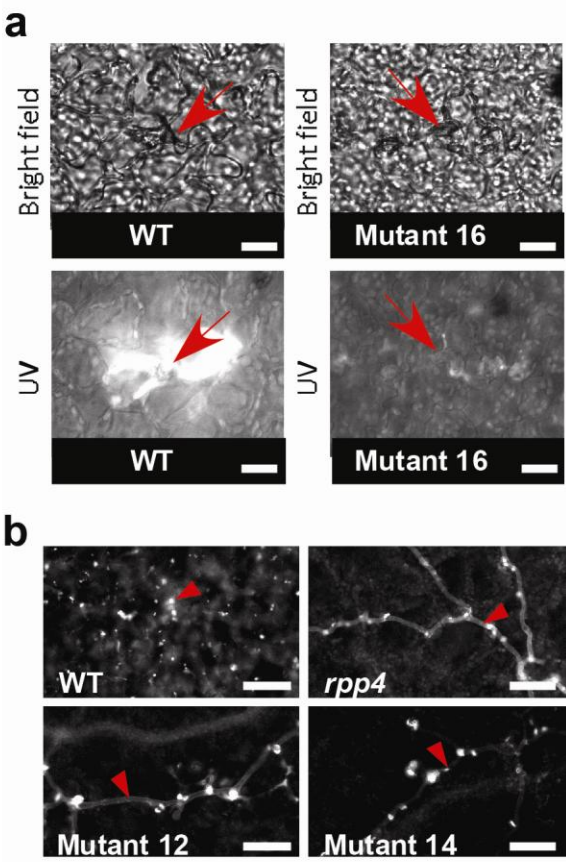
Supplementary Figure 4. Characterization of mutants in RPP4-mediated resistance against *Hpa* Emwa1.

a, The seven phenotypes scored in WT, *rpp4*, and 22 mutants 7 dpi with *Hpa* Emwa1. SPP, Sporangiophore; TRN, Trailing necrosis; OOS, Oospore; FRH, Free hypha; FHI, Free hyphal intermediate; EXH, Expanding HR; DIH, Discrete HR. **b,** Bar graphs showing distributions of phenotype (PT) scores (% of occurrence in 40 leaves/genotype) of the mutants (black bars) compared with WT (blue bar) and *rpp4* (red bar). Mutants are ranked from the highest to the lowest with no correspondence from panel to panel. The error bars, 95% confidence intervals based on binomial distribution.



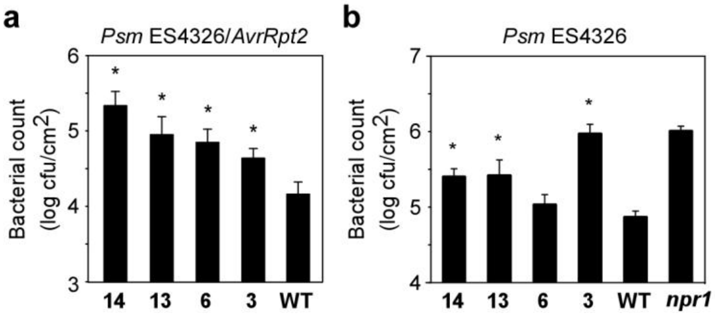
Supplementary Figure 5. Phenotypic clustering analysis using data from 3 biological replicates.

Hierarchical clustering performed using the mean phenotype scores of the three biological replicates with bootstrap (100,000 times) showed that mutants were divided into 2 groups similar to Fig. 1b (Mutants were coloured according to Fig. 1b). Distance was measured by the standard correlation coefficient (average linkage; scale 0-1).



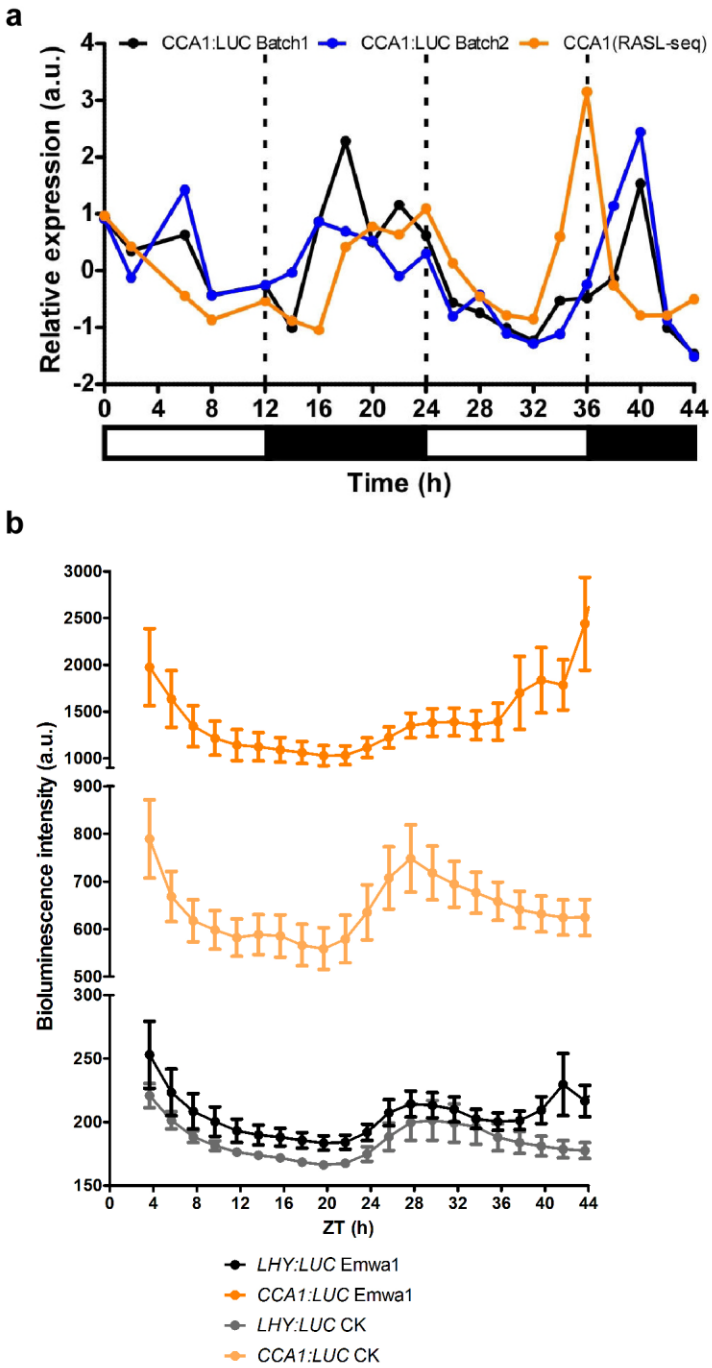
Supplementary Figure 6. Defects in *R* gene-mediated resistance in Group 2 mutants.

a, Phenolic compound accumulation at 7 dpi with *Hpa* Emwa1. Arrows point at sites of spore penetration. **b,** Callose deposition 7 dpi with *Hpa* Emwa1. Red arrows indicate callose produced by plants (WT) and along the hyphae of the pathogen (mutants).



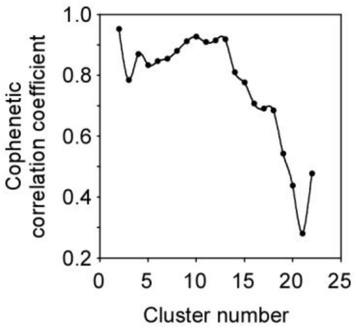
Supplementary Figure 7. Some of the mutants compromised in RPP4-mediated resistance against *Hpa* Emwa1 are also defective in immune responses against *Pseudomonas*.

a, Mutants 2, 6, 8 and 12 are compromised in RPS2-mediated resistance against *Psm* ES4326/*AvrRpt2*. Error bars represent 95% confidence interval (n = 8). cfu, colony-forming unit. This experiment was performed three times with similar results. Asterisks indicate p-values < 0.01. **b,** Mutants 2, 8, and 12 showed enhanced susceptibility to *Psm* ES4326.


a
CCA1:LUC Batch1
CCA1:LUC Batch2
CCA1(RASL-seq)
Relative expression (a.u.)
4
3
2
1
0
-1
-2
0
4
8
12
16
20
24
28
32
36
40
44
Time (h)
b
Bioluminescence intensity (a.u.)
3000
2500
2000
1500
1000
900
800
700
600
500
300
250
200
150
0
4
8
12
16
20
24
28
32
36
40
44
ZT (h)
LHY:LUC Emwa1
CCA1:LUC Emwa1
LHY:LUC CK
CCA1:LUC CK

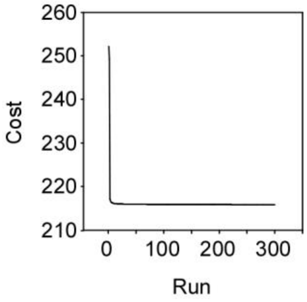
Supplementary Figure 8. Luciferase-based diurnal and free running tests.

a, Luciferase measurement of *CCA1:LUC* under the conditions used for the RASL-seq experiment (Fig. 3c, Col CK). Two biological replicates were included. The white bars, the day; black bar, the night. **b,** Free running test of *CCA1:LUC* and *LHY:LUC* expression with/without *Hpa* Emwa1 treatment. CK, control; Emwa1, *Hpa* Emwa1 treated; ZT, zeitgeber time. Error bars represent SEM (n=18). This experiment has been repeated three times with similar results.



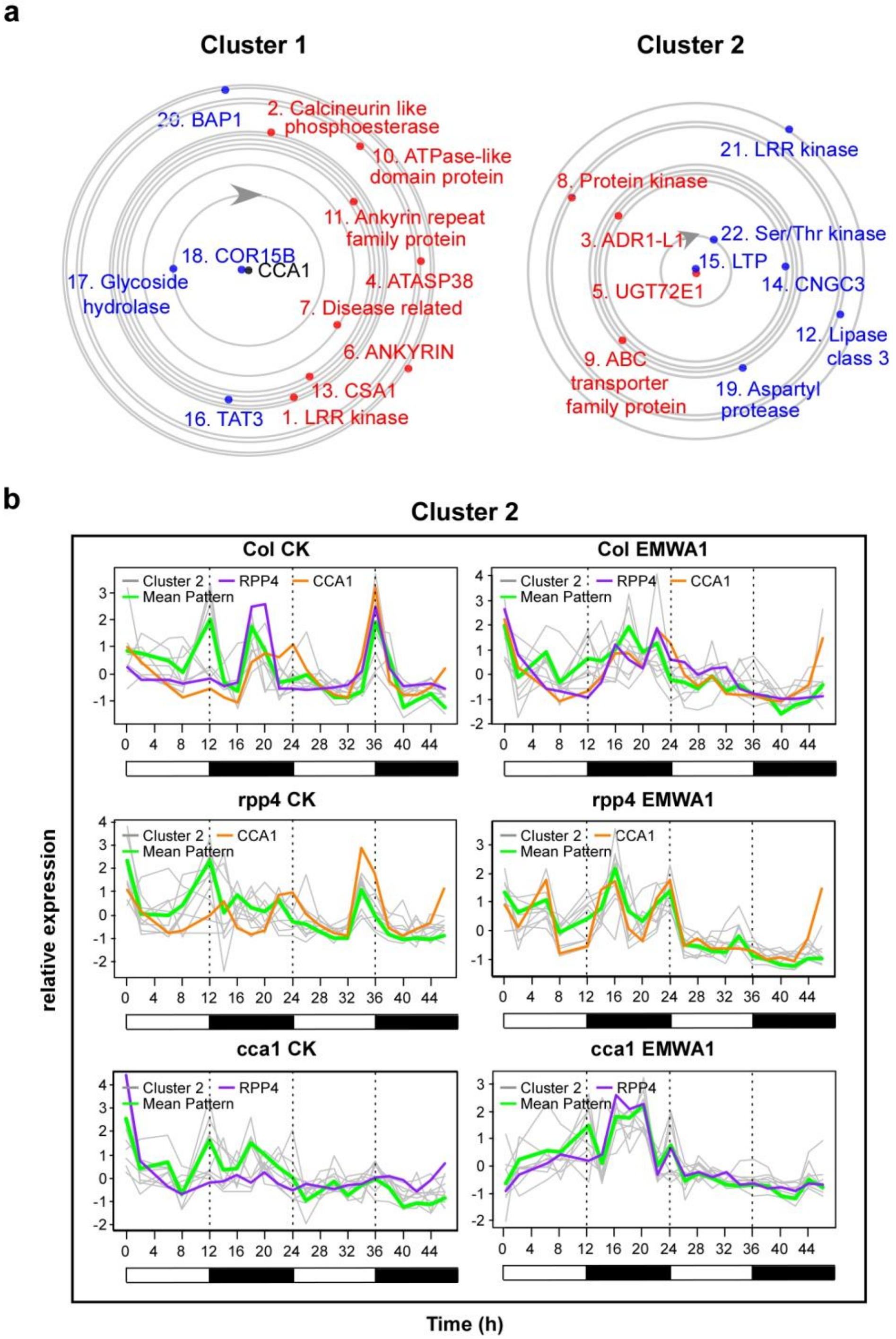
Supplementary Figure 9. Determination of the cluster number used in nonnegative matrix factorization (NMF).

A range of cluster numbers from 2 to 22 were implemented in NMF with 300 runs (10,000 iterations/run) and the corresponding cophenetic correlation coefficients were calculated. When cluster number equalled 2, the highest cophenetic correlation coefficient was achieved.



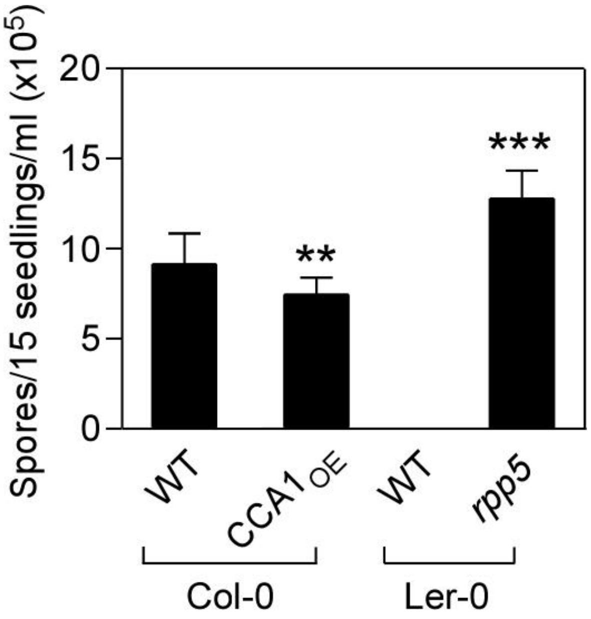
Supplementary Figure 10. Convergence of NMF.

300 runs (10,000 iterations/run) were performed using 2 clusters and the corresponding costs were calculated for each run. The NMF algorithm converged with fewer than 50 runs.


a
Cluster 1
20. BAP1
2. Calcineurin like phosphoesterase
10. ATPase-like domain protein
11. Ankyrin repeat family protein
18. COR15B
CCA1
17. Glycoside hydrolase
4. ATASP38
7. Disease related
6. ANKYRIN
13. CSA1
16. TAT3
1. LRR kinase
Cluster 2
21. LRR kinase
8. Protein kinase
22. Ser/Thr kinase
3. ADR1-L1
15. LTP
14. CNGC3
5. UGT72E1
12. Lipase class 3
9. ABC transporter family protein
19. Aspartyl protease
b
Cluster 2
Col CK
Col EMWA1
rpp4 CK
rpp4 EMWA1
cca1 CK
cca1 EMWA1
Cluster 2
RPP4
CCA1
Mean Pattern
relative expression
0 4 8 12 16 20 24 28 32 36 40 44
Time (h)

Supplementary Figure 11. Membership distance for Cluster 1 and Cluster 2 genes determined by their expression patterns.

a, The two expression clusters overlap with the phenotypic grouping (as in Fig. 1b; Group 1 genes in red and Group 2 in blue). For each gene, its membership distance in the expression cluster is represented by the radius of the circle. The calculation is detailed in Methods. **b,** Time-course expression of the NMF Cluster 2 genes with/without *Hpa* Emwa1 infection. The white bars, the day; black bar, the night. CK, control; EMWA1, *Hpa* Emwa1 inoculated.



Supplementary Figure 12. Enhanced disease resistance to *Hpa* Noco2 observed in the CCA1$_{OE}$ transgenic line based on sporangiospore count 7 dpi.

Error bars, SD (n = 3, One-way ANOVA and Bonferroni's Multiple Comparison Test); **, p-values < 0.01, *** p-values < 0.001. This experiment has been repeated twice with similar results.

#	AGI	Description	Mutant lines	Insertion	*Hpa**						*P. syringae* ES4326		elf18	
					Emwa1			Hiks1	Cala2	Noco2	*AvrRpt2*	Vir	Callose	FW/RL
					Infection	Callose	Phenolic							
1	AT1G35710	LRR-kinase	SK112341	300-UTR5	S	+/-	NT	R	R	EDS	R	NT	+	Ins
1A			SK132549	300-UTR5	S	NT	NT	R	R	EDS	R	NT	+	Ins
2	AT1G13750	Calcineurin-like phosphoesterase	SK019550	Exon	S	+/-	NT	R	R	EDS	R	NT	+	
2A			SK067586	Exon	S	NT	NT	R	R	EDS	R	NT	+	
3	AT4G33300	ADR1-like 1 (ADR1-L1)	CS813977	Exon	S	+/-	NT	R	R	EDS	S	EDS	+	
3A			SK039248	300-UTR5	S	NT	NT	R	R	EDS	S	EDS	+	
4	AT5G02190	Aspartic protease 38 (ATASP38)	SK011719	300-UTR3	S	+/-	NT	R	R	EDS	R	NT	+	
5	AT3G50740	UDP-glucosyl transferase 72E1 (UGT72E1)	SK078702	Exon	S	+/-	NT	R	R	EDS	R	NT	+	
6	AT5G54610	Ankyrin (ANK)	SK021695	300-UTR3	S	+/-	NT	R	R	EDS	S	EDS	+	
7	AT5G45440	Disease resistance protein-related	SK023316	Exon	S	+/-	NT	R	R	EDS	R	NT	+	
7A			SK129203	300-UTR5	S	NT	NT	R	R	EDS	R	NT	+	
8	AT1G16260	Protein kinase family protein	SK065154	300-UTR5	S	+/-	+	R	R	EDS	R	NT	+	
8A			SK111248	300-UTR3	S	NT	NT	R	R	EDS	R	NT	+	
9	AT5G52860	ABC transporter family protein	SK027851	300-UTR3	S	+/-	NT	R	R	EDS	R	NT	+	
9A			SK015052	300-Exon	S	NT	NT	R	R	EDS	R	NT	+	
10	AT4G36290	ATPase-like domain containing protein	CS848042	Intron	S	+/-	NT	R	R	EDS	R	NT	+	
10A			SK008610	300-UTR5	S	+/-	NT	R	R	EDS	R	NT	+	
11	AT1G10340	Ankyrin repeat family protein	SK059400	Exon	S	+	NT	R	R	EDS	R	NT	+	
11A			SK098737	300-UTR5	S	NT	NT	R	R	EDS	R	NT	+	
12	AT3G48080	Lipase class 3 family protein	SK019545	Exon	S	-	NT	R	R	EDS	R	NT	+	
12A			CS879634	Exon	S	-	+	R	R	EDS	R	NT	+	
13	AT5G17880	Constitutive shade-avoidance 1 (CSA1)	SK023219	Exon	S	+/-	NT	R	R	EDS	S	EDS	+	

13	AT5G17880	Constitutive shade-avoidance 1 (CSA1)	SK023219	Exon	S	+/-	NT	R	R	EDS	S	EDS	+	
14	AT2G46430	Cyclic nucleotide gated channel 3 (CNGC3)	SK151673	Exon	S	-	+	R	R	EDS	S	EDS	+	
14A			CS859617	Exon	S	NT	NT	R	R	EDS	S	EDS	+	
15	AT3G22600	Lipid transfer protein family (LTP)	SK007462	300-UTR5	S	+/-	+	R	R	EDS	R	NT	+	
15A			CS873225	Intron	S	NT	NT	R	R	EDS	R	NT	+	
16	AT2G24850	Tyrosine aminotransferase (TAT3)	SK108841	Exon	S	+/-	-	R	R	EDS	R	NT	+	
16A			SK056522	Intron	S	NT	-	R	R	EDS	R	NT	+	
17	AT3G54440	Glycoside hydrolase	SK063078	Exon	S	NT	+	R	R	S	R	NT	+	
17A			CS829656	Exon	S	NT	NT	R	R	S	R	NT	+	
18	AT2G42530	Cold-responsive protein (COR15B)	SK085398	300-UTR3	S	+/-	+	R	R	EDS	R	NT	+	
19	AT3G51330	Aspartyl protease family protein	CS874998	Intron	S	NT	NT	R	R	S	R	NT	+	
19A			SK020629	Exon	S	+/-	+	R	R	S	R	NT	+	
20	AT3G61190	BON association protein 1 (BAP1)	SK092421	Exon	S	+/-	+	R	R	EDS	R	NT	+	
20A			SK025560	Exon	S	NT	NT	R	R	EDS	R	NT	+	
21	AT4G08850	LRR-kinase	SK046987	Exon	S	+	+	R	R	S	R	NT	+	
21A			SK061769	Exon	S	NT	NT	R	R	S	R	NT	+	
22	AT1G66880	Ser/Thr protein kinase family protein	SK034755	Exon	S	NT	NT	R	R	S	R	NT	+	
22A			SK034021	Exon	S	+/-	+	R	R	S	R	NT	+	
	AT4G16860	RPP4	SK017569	Intron	S	-	-	R	R	S	R	S	+	
	WT	WT	Col-0		R	+	+	R	R	S	R	S	+	

Supplementary Table 1. A list of all mutant alleles and their phenotypes.

SK, Salk line; CS, Sail line; S, susceptible; R, resistant; +, WT level of callose or phenolic deposition observed; +/-, lower than WT level of callose observed. NT, not tested; EDS, enhanced disease symptoms; Ins, insensitive. Vir, virulent; MAMP, microbial-associated molecular pattern; FW/RT, fresh weight assay and root length assay. Note (*) that the infection phenotype against *Hpa* Emwa1 was determined based on microscopic observations of the symptoms; not all alleles were quantitatively measured as in Fig. 1a.

#	Description	Mutant		Sequence
1	**LRR-kinase**	**SK112341**	**F**	**GGCTCACGCTTTATCG**
			R	**TGTCCCCGTGGTTCTA**
		SK132549	**F**	**GGCTCACGCTTTATCG**
			R	**TGTCCCCGTGGTTCTA**
2	**Calcineurin-like phosphoesterase**	**SK019550**	**F**	**CCCAACTCAGGATCGT**
			R	**ACGGTGAGCGAGGAATA**
		SK067586	**F**	**CCCAACTCAGGATCGT**
			R	**ACGGTGAGCGAGGAATA**
3	**ADR1-like 1 (ADR1-L1)**	**CS813977**	**F**	**TCTCGTGGCACTACCT**
			R	**CAACGTCGGTATCGCA**
		SK039248	**F**	**TCTCGTGGCACTACCT**
			R	**CAACGTCGGTATCGCA**
4	**Aspartic protease 38 (ATASP38)**	**SK011719**	**F**	**GTACTCAGTTTACTTTCCTGC**
			R	**GTTCTGCTGATGATGATGTC**
5	**UDP-glucosyl transferase 72E1 (UGT72E1)**	**SK078702**	**F**	**TGCAGTGCATATTTATCCG**
			R	**GCCCTCGTAATCACTCC**
6	**Ankyrin (ANK)**	**SK021695**	**F**	**AGGTGACGTAGACCTT**
			R	**AAAACCGTGTTGCCTC**
7	**Disease resistance protein-related**	**SK023316**	**F**	**ATTGTGTTTGATGATGTCC**
			R	**AGCCAACAGTCTAGCA**
		SK129203	**F**	**ACGAATGGCTAGGGAC**
			R	**CACCGTATTCTCCGACA**
8	**Protein kinase family protein**	**SK065154**	**F**	**CAGAACATCGCCCTAC**
			R	**GTGAGGCATTAGTGGTTT**
		SK111248	**F**	**CAGAACATCGCCCTAC**
			R	**GTGAGGCATTAGTGGTTT**
9	**ABC transporter family protein**	**SK015052**	**F**	**TGCCCCAAATTACATTACG**
			R	**TGGAGGCTAAGCACGA**
		SK027851	**F**	**CCGATGCTACTGCTCT**
			R	**GGCGAACATACCGAAT**
10	**ATPase-like domain-containing protein**	**CS848042**	**F**	**TTCGTACCGCTATCGAC**
			R	**CTCCCATAACACCATTGC**
		SK008610	**F**	**TTCGTACCGCTATCGAC**
			R	**CTCCCATAACACCATTGC**
11	**Ankyrin repeat family protein**	**SK059400**	**F**	**TTGGGAATTAACAGCC**
			R	**GCAACCGTATTACCTC**

		SK098737	**F**	**GCACTGTTCACGTCCT**
			R	**AGTACGGTCAACGCTC**
12	**Lipase class 3 family protein**	**SK019545**	**F**	**ACTCAATAGGCTCCGC**
			R	**CTCTGCTCCCCTCGAA**
		CS879634	**F**	**ACTCAATAGGCTCCGC**
			R	**CTCTGCTCCCCTCGAA**
13	**Constitutive shade-avoidance 1 (CSA1)**	**SK023219**	**F**	**AACTGTAAAAGTCATGCC**
			R	**CATTCCTTGGGGATGGAAC**
14	**Cyclic nucleotide gated channel 3 (CNGC3)**	**SK151673**	**F**	**AGGACATTAAACGCCATC**
			R	**ATAGGGAATTGGGAACTG**
		CS859617	**F**	**AGGACATTAAACGCCATC**
			R	**ATAGGGAATTGGGAACTG**
15	**Lipid transfer family protein (LTP)**	**SK007462**	**F**	**ATGGTCTCTGCTCAGT**
			R	**CTGGTACGGTTTTCGAT**
		CS873225	**F**	**ATGGTCTCTGCTCAGT**
			R	**CTGGTACGGTTTTCGAT**
16	**Tyrosine aminotransferase 3 (TAT3)**	**SK108841**	**F**	**AATACCGTCGCAATGG**
			R	**CTTGAACTACCCCTGTAGAT**
		SK056522	**F**	**AATACCGTCGCAATGG**
			R	**CTTGAACTACCCCTGTAGAT**
17	**Glycoside hydrolase**	**SK063078**	**F**	**GATCGAGTAGTTGGGA**
			R	**GCCAAAGGTATTGTCA**
		CS829656	**F**	**GGAGTGGAAGTCAGGT**
			R	**GTAGGTGCTCGCCAAA**
18	**Cold-responsive protein (COR15B)**	**SK085398**	**F**	**TCGTTGATATACGCCG**
			R	**CTCTTCTGCTTTACCCTC**
19	**Aspartyl protease family protein**	**SK020629**	**F**	**TAGCGCCATGTACTGC**
			R	**AGGGACTAGATTGGCTG**
		CS874998	**F**	**TGCACTACGCCAATGT**
			R	**GCTCTAAACCCTCGTCC**
20	**BON association protein 1 (BAP1)**	**SK092421**	**F**	**CTGAGATGATGGCGGT**
			R	**GCAATTGAAGTAGCAGAAACA**
		SK025560	**F**	**CTGAGATGATGGCGGT**
			R	**GCAATTGAAGTAGCAGAAACA**
21	**LRR-kinase**	**SK046987**	**F**	**TGCTGGTACTTACGGC**
			R	**AGAAAAGGCAGTGGAG**
		SK061769	**F**	**TGAAAGGTGTGGCTCAT**
			R	**GCCGTAAGTACCAGCA**

22	**Ser/Thr protein kinase family protein**	**SK034755**	**F**	**GTGGCTTCGGTACTGT**
			R	**CGGGTTGACCAGCAGA**
		SK034021	**F**	**GTGGCTTCGGTACTGT**
			R	**CGGGTTGACCAGCAGA**
	Recognition of Peronospora parasitica 4 (RPP4)	**SK017569**	**F**	**GCATTTGAAGTTGCCGAGC**
			R	**GGGCATCCAGTGAGATTGAGG**

Supplementary Table 2. Primers used in qPCR characterization of gene expression in T-DNA insertion mutants in Supplementary Fig. 3. SK, Salk line; CS, Sail line.

	Description	Name	Sequence
1	LRR-kinase	1G35710AD1	CTGGTGCAACGTAGCCGTAGCCTGTGGTCGTAGCATCAGC
		1G35710pA1	AATGATACGGCGACCACCGAGATCTTCATCGTGTAAGCAAACT
2	Calcineurin-like phosphoesterase family protein	1G13750AD1	CTGGTAAACCGGGCATGTTCCCTGTGGTCGTAGCATCAGC
		1G13750pA1	AATGATACGGCGACCACCGAGATTCATGACTCGTGCATACACT
3	ADR1-like 1 (ADR1-L1)	4G33300AD1	CAGTATGAATAGAGACAATCCCTGTGGTCGTAGCATCAGC
		4G33300pA1	AATGATACGGCGACCACCGAGATTTGCATTTCATTCATTTCCC
4	Aspartic protease 38 (ATASP38)	5G02190AD2	TGATGATGTCCAATCACGTACCTGTGGTCGTAGCATCAGC
		5G02190pA2	AATGATACGGCGACCACCGAGATCGATCCACATGTTCTGCTGA
5	UDP-glucosyl transferase 72E1 (UGT72E1)	3G50740AD1	TGACACGCTCCAAAAGATGCCCTGTGGTCGTAGCATCAGC
		3G50740pA1	AATGATACGGCGACCACCGAGATGGCACCACGTGCCATGCACC
6	Ankyrin (ANK)	5G54610AD2	CTCCTCTACCACGAATACGACCTGTGGTCGTAGCATCAGC
		5G54610pA2	AATGATACGGCGACCACCGAGATAAGATGCAATGGTGTCATAC
7	Disease resistance protein-related	5G45440AD1	CTTCTGAATTGGGGTTGTCGCCTGTGGTCGTAGCATCAGC
		5G45440pA1	AATGATACGGCGACCACCGAGATCAGAGGTTTAGTTTTACTCT
8	Protein kinase family protein	1G16260AD1	TTAAAATGGCTGGCCAAGTTCCTGTGGTCGTAGCATCAGC
		1G16260pA1	AATGATACGGCGACCACCGAGATTCCAGAGCTTAGAGTTCCAC
9	ABC transporter family protein	5G52860AD1	CAACACACGATAAAGTACGACCTGTGGTCGTAGCATCAGC
		5G52860pA1	AATGATACGGCGACCACCGAGATCTAAGGAGAGCAAGAAAACA
10	ATPase-like domain-containing protein	4G36290AD1	CGTCTGTTCTACTTCATTCTCCTGTGGTCGTAGCATCAGC
		4G36290pA1	AATGATACGGCGACCACCGAGATTCTTTTTCTAAGCTCTTTAC
11	Ankyrin repeat family protein	1G10340AD2	TAGTGGATCCACTTGATATGCCTGTGGTCGTAGCATCAGC
		1G10340pA2	AATGATACGGCGACCACCGAGATCAGTATAGTCCCTACGATAC
12	Lipase class 3 family protein	3G48080AD1	CATTCCAAGGTCGTCGAGAGCCTGTGGTCGTAGCATCAGC
		3G48080pA1	AATGATACGGCGACCACCGAGATCACTGTCTGGCTCTTGTGCT
13	Constitutive shade-avoidance 1 (CSA1)	5G17880AD2	CTCATCGCATCGTTTAAGCGCCTGTGGTCGTAGCATCAGC
		5G17880pA2	AATGATACGGCGACCACCGAGATAAAATCTCAGGAACACAACT
14	Cyclic nucleotide gated channel 3 (CNGC3)	2G46430AD1	CTGAACATGTGTCGGAGTTGCCTGTGGTCGTAGCATCAGC
		2G46430pA1	AATGATACGGCGACCACCGAGATGCCATTGCACTGAATAAAAC
15	Lipid transfer family protein (LTP)	3G22600AD2	CGGTATTACAGCGACTGACACCTGTGGTCGTAGCATCAGC
		3G22600pA2	AATGATACGGCGACCACCGAGATAGAACCACCACCACCACCAC
16	Tyrosine aminotransferase 3 (TAT3)	2G24850AD2	CCATAAATAAGAACAAGATTCCTGTGGTCGTAGCATCAGC
		2G24850pA2	AATGATACGGCGACCACCGAGATATTGATGTGTCAAGCTTCAA
17	Glycoside hydrolase family	3G54440AD2	CTTCCAACCTTCAATAGTCCCCTGTGGTCGTAGCATCAGC
		3G54440pA2	AATGATACGGCGACCACCGAGATATAAGGAGAACTCCTTGAAT

18	Cold-responsive protein (COR15B)	2G42530AD1	GTGGCTTCGTTGAGGTCATCCCTGTGGTCGTAGCATCAGC
		2G42530pA1	AATGATACGGCGACCACCGAGATCGAAATCAGAAGCTTTCTTT
19	Aspartyl protease family protein	3G51330AD1	AATCAGACCGTTTCCAACCCCCTGTGGTCGTAGCATCAGC
		3G51330pA1	AATGATACGGCGACCACCGAGATCAAGCTTTCATCTTCAAAAC
20	BON association protein 1 (BAP1)	3G61190AD1	CCCAAACCGGAACTCCGGTACCTGTGGTCGTAGCATCAGC
		3G61190pA1	AATGATACGGCGACCACCGAGATAAATTGGCGTTGATACAGAC
21	LRR-kinase	4G08850AD1	CTGGAGCAACATAGCCGTAACCTGTGGTCGTAGCATCAGC
		4G08850pA1	AATGATACGGCGACCACCGAGATTTTCATCGCATAAGCTAGTT
22	Ser/Thr protein kinase family protein	1G66880AD1	CTTTTATGTGGAGGAATGATCCTGTGGTCGTAGCATCAGC
		1G66880pA1	AATGATACGGCGACCACCGAGATGATGTCTCTGTGTATGATTC
	Ubiquitin 5 (UBQ5)	3G62250AD1	GAACCTTTCCAGATCCATCGCCTGTGGTCGTAGCATCAGC
		3G62250pA1	AATGATACGGCGACCACCGAGATGCACTCCTTCCTCAAACGCT
	Late elongated hypocotyl (LHY)	1G01060AD2	TTTCGTTGGTAAGGGATACTCCTGTGGTCGTAGCATCAGC
		1G01060pA2	AATGATACGGCGACCACCGAGATTCAATGTCGCCACTTACCTG
	Circadian clock associated 1 (CCA1)	2G46830AD1	CTCGTCAGACACAGACTTCCCCTGTGGTCGTAGCATCAGC
		2G46830pA1	AATGATACGGCGACCACCGAGATGCTTGGAAGGCAATTCGACC

Supplementary Table 3. Primers used in RASL-seq in Fig. 3c.