Supporting Legends

Supplemental Figure S1. Amino acid sequence alignment of RxLR24 effector homologs. Identical amino acids are highlighted in black and similar residues are shown as grey boxes. Sequences encoding signal peptides (SP) are not included. RxLR and dEER motifs are marked with asterisks. Sequence accessions: *P. brassicae* RxLR24 (MG489826), *P. infestans* RxLR24 (XP002997548/ PITG 18405), *P. parasitica* RxLR24 (XP008915662), *P. sojae* RxLR24 (XP009516297) and *P. nicotianae* RxLR24 (KUF87794).

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Supplemental Figure S4. High magnification pictures of GFP-RxLR24 positive vesicles. RxLR24 positive vesicles observed under confocal microscope in the cells of transgenic

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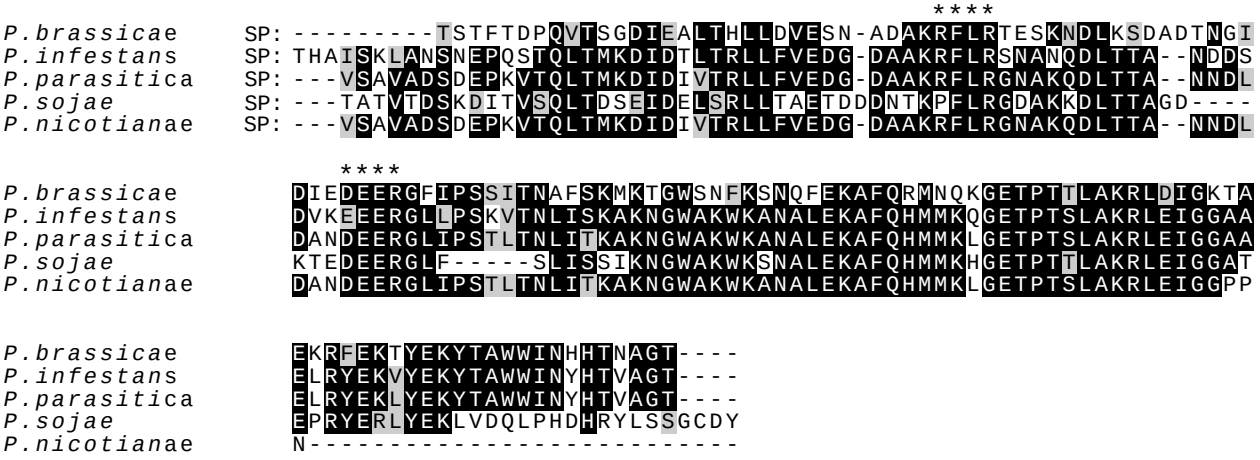
Supplemental File S1. List of peptide sequences derived from proteins associated with *Pb*RxLR24 in Co-IP experiment.

Supplemental Movie S1. Movement of GFP-RxLR24 positive vesicles in leaf cells. Movie (15 fps) shows vesicle movement observed with confocal microscopy in epidermal leaf cells. The movie consists of 100 time points and was recorded with use of EMCCD camera and 60 x magnification. Exposure time was 200 ms.

Supplemental Movie S2. Movement of GFP-RxLR24 positive vesicles in leaf cells. Movie (15 fps) shows vesicle movement observed with confocal microscopy in the root cells. The movie consists 300 time points and was recorded with use of EMCCD camera and 60x magnification. Exposure time was 500 ms.

SUPPORTING FIGURES



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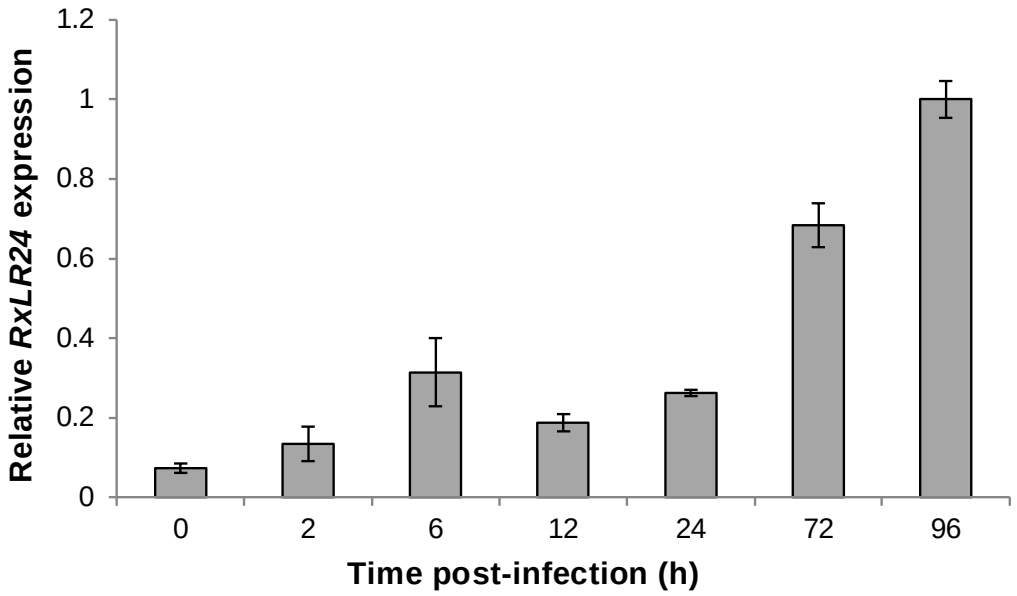

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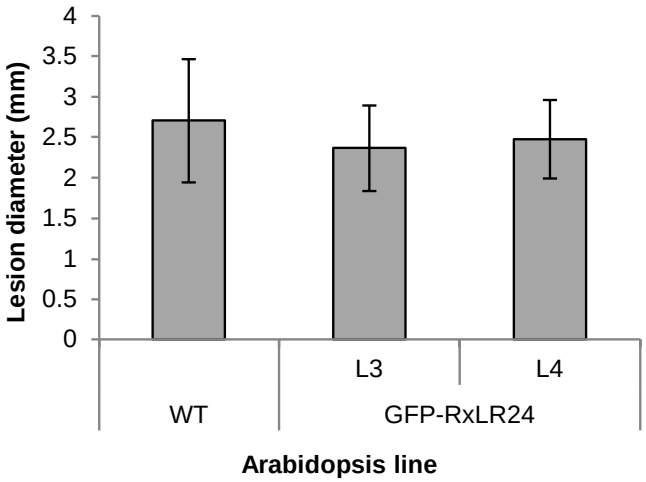

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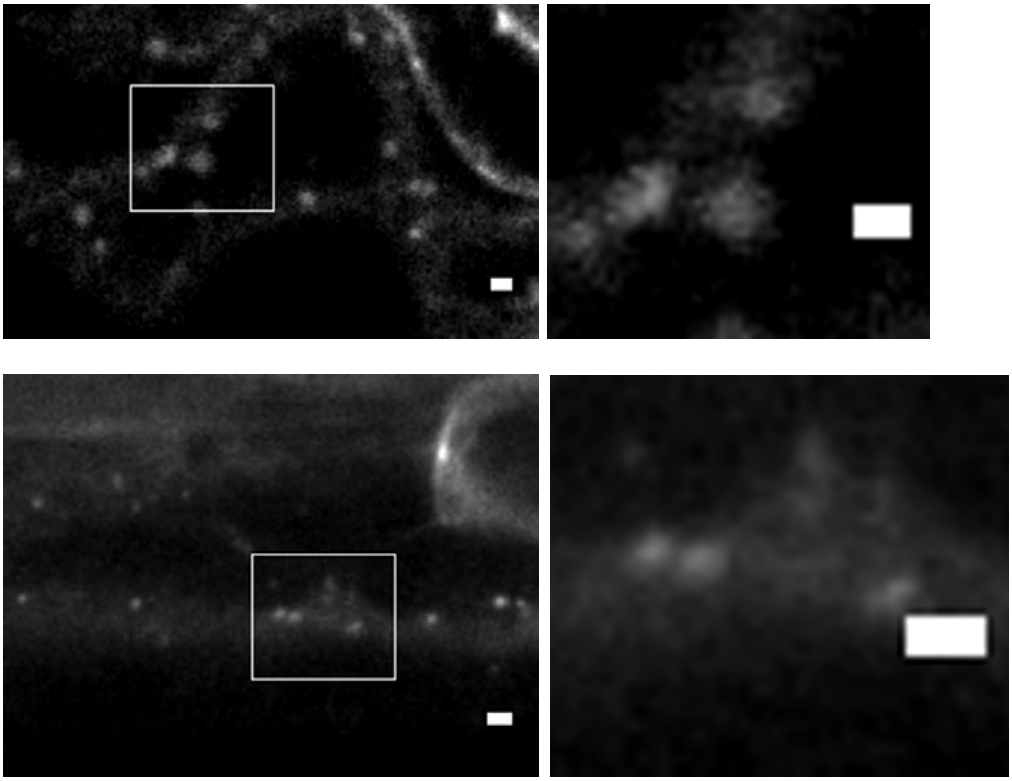

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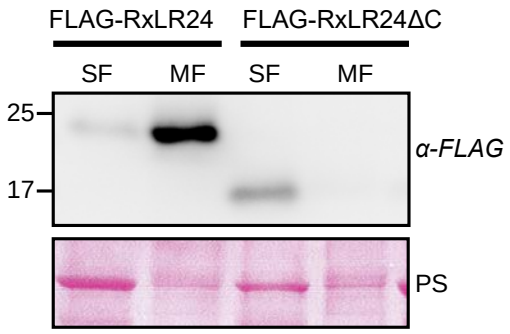

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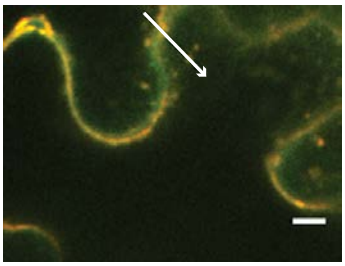
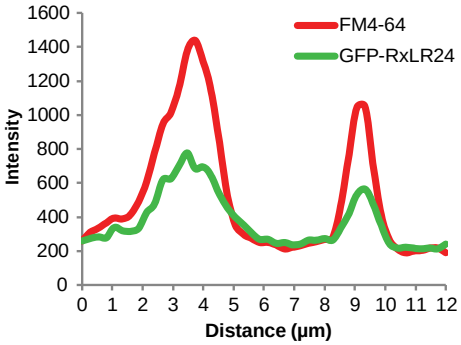
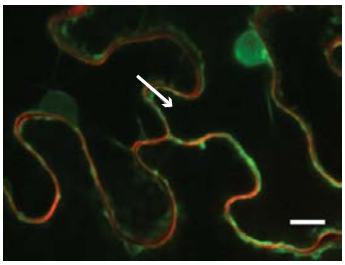
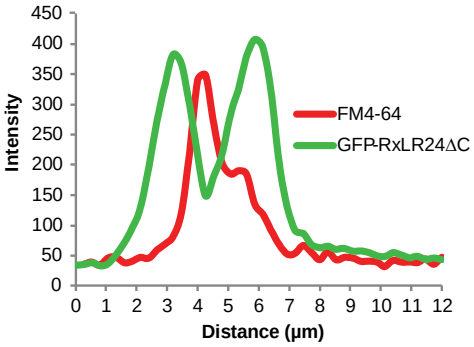


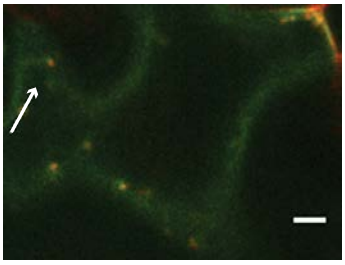
Merged:
FM4-64 + GFP-RxLR24
scale bar 5 µm



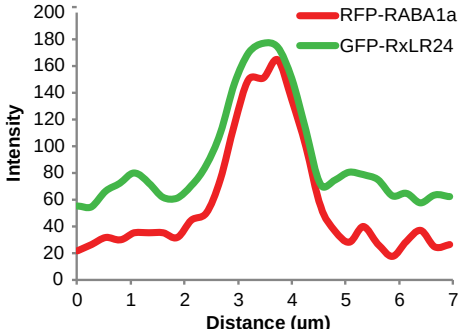


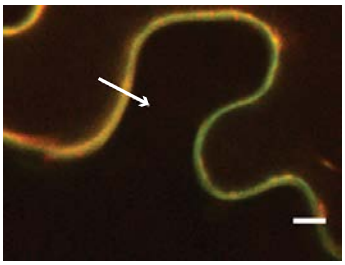
Merged:
FM4-64 + GFP-RxLR24ΔC
scale bar 10 µm





Merged:
RFP-RABA1a + GFP-RxLR24
scale bar 5 µm





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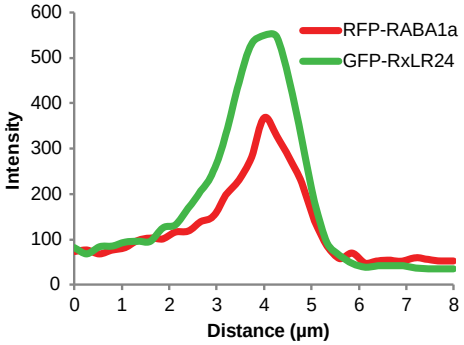
scale bar 5 µm



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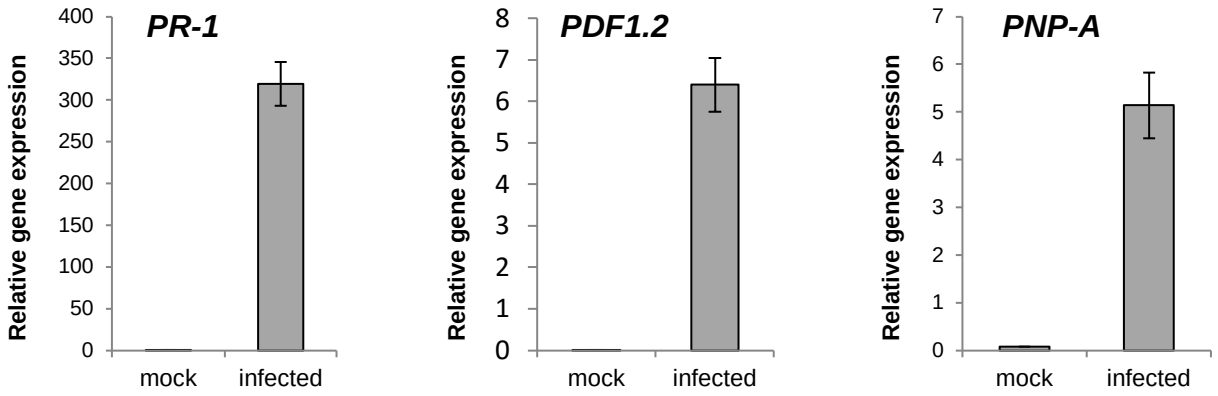

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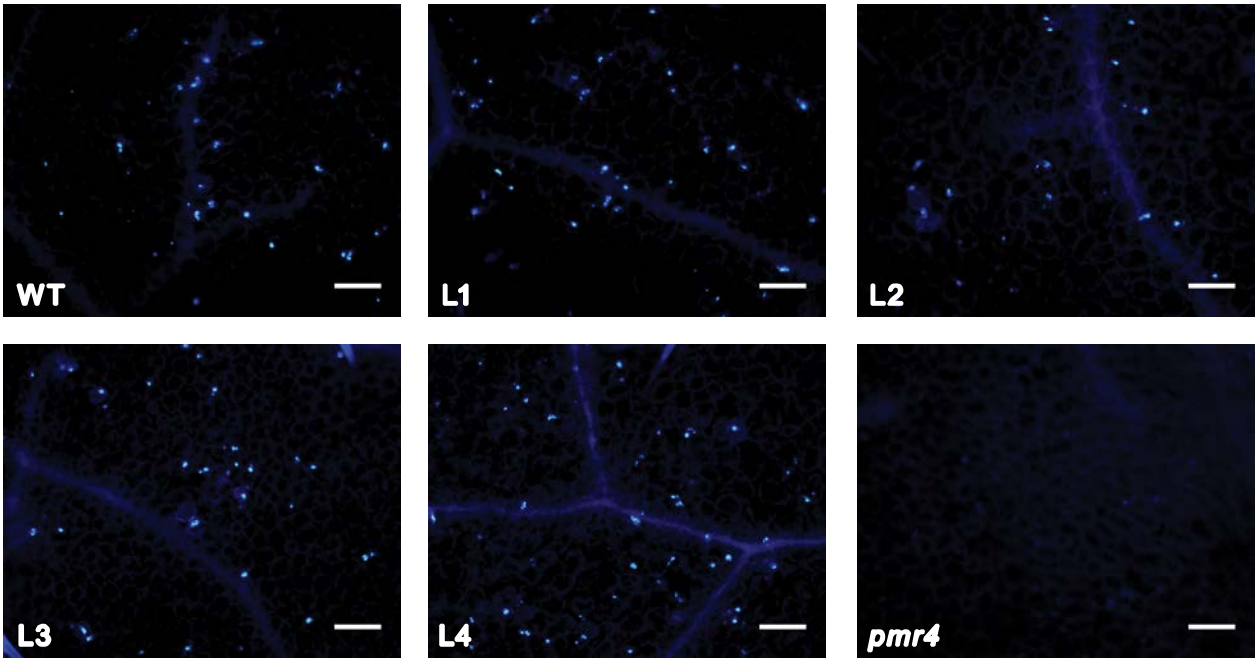

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	P. brassicae	***P. infestans***	***P. parasitica***	***P. sojae***	***P. nicotianae***
P. brassicae		51.0% (64.6%)	54.3% (66.4%)	41.4% (55.2%)	40.0% (50.7%)
P. infestans	51.0% (64.6%)		82.3% (90.8%)	50.0% (62.5%)	64.5% (72.3%)
P. parasitica	54.3% (66.4%)	82.3% (90.8%)		53.7% (65.1%)	81.2% (81.2%)
P. sojae	41.4% (55.2%)	50.0% (62.5%)	53.7% (65.1%)		48.3% (58.0%)
P. nicotianae	40.0% (50.7%)	64.5% (72.3%)	81.2% (81.2%)	48.3% (58.0%)	

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Annotation for proteins identified as potential RxLR24 targets		TAIR accession number	Subcellular location	Number of total unique peptides matched to each plant protein identified for each RxLR effector			
				RxLR24	RxLR23	RxLR27	RxLR29
RAB GTPases subfamilly RABA1	RABA1a*	AT1G06400	endosome membrane, plasma membrane	9	0	0	0
	RABA1b	AT1G16920		9	0	0	0
	RABA1c	AT5G45750		8	0	0	0
	RABA1d	AT4G18800		8	0	0	0
	RABA1f	AT5G60860		9	0	0	0
RAB GTPases subfamilly RABA2	RABA2a*	AT1G09630		9	0	0	0
	RABA2c	AT3G46830		10	0	0	0
	RABA2d	AT5G59150		12	0	0	0
RAB GTPases subfamilly RABA4	RABA4a*	AT5G65270		12	0	0	0
	RABA4b	AT4G39990		5	0	0	0
	RABA4c	AT5G47960		5	0	0	0
RAB GTPases subfamilly RABG3	RABG3f*	AT3G18820		3	0	0	0
Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase		AT3G56940	chloroplast	8	2	0	0
AT2G30950 protein		AT2G30950	chloroplast	6	0	0	3

Supplemental Table S3. List of primers used for PCR amplification of cDNAs and plasmids used for the generation of fusion proteins. † Obtained from gene synthesis service (GenScript).

Gene	Primer forward	Primer reverse	Destination plasmid	Tagged fusion protein
***Pb*RxLR24** (without SP)	CACCACCTCGACGTTCACC GACCCC	TTACGTTCCAGCATTCGTGT GG	pB2GW7 (Karimi *et al*., 2002)	3xFLAG-RxLR24
			pFAST-R06 (Shimada *et al*., 2010)	GFP-RxLR24
***Pb*RxLR24ΔC** (truncated)	CACCACCTCGACGTTCACC GACCCC	TTAAAATTGGTTCGATTTGAA GTTGG	pB2GW7 (Karimi *et al*., 2002)	3xFLAG-RxLR24ΔC
			pFAST-R06 (Shimada *et al*., 2010)	GFP-RxLR24
***Pi*RxLR24**† (without SP)			pB2GW7 (Karimi *et al*., 2002)	3xFLAG-PiRxLR24
RABA1a (*A. thaliana*)	CACCGCTGGTTACAGAGCC GATGAAG	CTAGTTAGAGCAGCAACCCA TTC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA1a
			pB7WGF2 (Karimi *et al*., 2002)	RFP-RABA1a
RABA2a (*A. thaliana*)	CACCGCGAGAAGACCGGA CGAAGAATAC	TCAAGACGATGAGCAACAAG GCTTC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA2a
RABA4a† (*A. thaliana*)			pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA4a
RABG3f (*A. thaliana*)	CACCCCGTCCCGTAGACGT ACCCTCC	TTAGCATTCACACCCTGTAGA CCTC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABG3f
RABA1a (*S. tuberosum*)	GCAGGTTATAGAGGTGATG ATGAG	CTAGCTCGAACAGCACCCAA AC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA1a$_{potato}$
RABA2a (*S. tuberosum*)	GCGAGAAGAGCGGAAGAG GAG	CTATGCAGAGCAACATGCCT TC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA2a$_{potato}$
RABA4a (*S. tuberosum*)	GCAAGTGGGGGTGGGTAT G	TTAAGAACTACAGCATGCCTT C	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA4a$_{potato}$
ph-dependent **secGFP**			pRB35S (Bartetzko *et al*., 2009)	secGFP
PR-1 (*A. thaliana*)	TCAGTCGACATGAATTTTAC TGGCTATTCTCG	AGTGCGGCCGCGAGTATGG CTTCTCGTTCACA	pB2GW7 (Karimi *et al*., 2002)	PR-1-phGFP
PDF1.2 (*A. thaliana*)	TCAGTCGACATGGCTAAGT TTGCTTCCATCATC	AGTGCGGCCGCGAACATGG GACGTAACAGATAC	pB2GW7 (Karimi *et al*., 2002)	PDF1.2-phGFP
PNP-A (*A. thaliana*)	TCAGTCGACATGATAAAAAT GGCAGTAAAATTTG	AGTGCGGCCGCGATATCGGT GTGTATACGACAC	pB2GW7 (Karimi *et al*., 2002)	PNP-A-phGFP

Supplemental Table S4. List of primers used for qPCR analysis.

Gene	Organism	Forward sequence	Reverse sequence
RxLR24	*P. brassicae*	AGAAGGGAGAGACGCCAAC	ATTCGTGTGGTGGTTGATCC
Actin		GCAGATGTGGATCTCGAAGG	CAGCAGCGATGTATCTCCAG
Beta-tubulin		CCAAGGGACTGAAGATGAGC	AGCCTTACGACGGAACATTG
PR1	Arabidopsis	ACTACAACTACGCTGCGAACAC	GTTACACCTCACTTTGGCACATC
PDF1.2		ATCACCCTTATCTTCGCTGCTC	ACTTGGCTTCTCGCACAACTTC
PNP-A		CCGTAGACGTGAAGGTAGTTGA	CGAATGTTACCGGCATCAGTAT
ExpG		GAGCTGAAGTGGCTTCCATGAC	GGTCCGACATACCCATGATCC

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	RABA2d	AT5G59150		12	0	0	0
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	RABA4c	AT5G47960		5	0	0	0
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Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase		AT3G56940	chloroplast	8	2	0	0
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RABA2a (*A. thaliana*)	CACCGCGAGAAGACCGGA CGAAGAATAC	TCAAGACGATGAGCAACAAG GCTTC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA2a
RABA4a† (*A. thaliana*)			pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA4a
RABG3f (*A. thaliana*)	CACCCCGTCCCGTAGACGT ACCCTCC	TTAGCATTCACACCCTGTAGA CCTC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABG3f
RABA1a (*S. tuberosum*)	GCAGGTTATAGAGGTGATG ATGAG	CTAGCTCGAACAGCACCCAA AC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA1a$_{potato}$
RABA2a (*S. tuberosum*)	GCGAGAAGAGCGGAAGAG GAG	CTATGCAGAGCAACATGCCT TC	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA2a$_{potato}$
RABA4a (*S. tuberosum*)	GCAAGTGGGGGTGGGTAT G	TTAAGAACTACAGCATGCCTT C	pEarleyGate203 (Earley *et al*., 2006)	Myc-RABA4a$_{potato}$
ph-dependent **secGFP**			pRB35S (Bartetzko *et al*., 2009)	secGFP
PR-1 (*A. thaliana*)	TCAGTCGACATGAATTTTAC TGGCTATTCTCG	AGTGCGGCCGCGAGTATGG CTTCTCGTTCACA	pB2GW7 (Karimi *et al*., 2002)	PR-1-phGFP
PDF1.2 (*A. thaliana*)	TCAGTCGACATGGCTAAGT TTGCTTCCATCATC	AGTGCGGCCGCGAACATGG GACGTAACAGATAC	pB2GW7 (Karimi *et al*., 2002)	PDF1.2-phGFP
PNP-A (*A. thaliana*)	TCAGTCGACATGATAAAAAT GGCAGTAAAATTTG	AGTGCGGCCGCGATATCGGT GTGTATACGACAC	pB2GW7 (Karimi *et al*., 2002)	PNP-A-phGFP

Supplemental Table S4. List of primers used for qPCR analysis.

Gene	Organism	Forward sequence	Reverse sequence
RxLR24	*P. brassicae*	AGAAGGGAGAGACGCCAAC	ATTCGTGTGGTGGTTGATCC
Actin		GCAGATGTGGATCTCGAAGG	CAGCAGCGATGTATCTCCAG
Beta-tubulin		CCAAGGGACTGAAGATGAGC	AGCCTTACGACGGAACATTG
PR1	Arabidopsis	ACTACAACTACGCTGCGAACAC	GTTACACCTCACTTTGGCACATC
PDF1.2		ATCACCCTTATCTTCGCTGCTC	ACTTGGCTTCTCGCACAACTTC
PNP-A		CCGTAGACGTGAAGGTAGTTGA	CGAATGTTACCGGCATCAGTAT
ExpG		GAGCTGAAGTGGCTTCCATGAC	GGTCCGACATACCCATGATCC