SUPPORTING INFORMATION (SI) APPENDIX

SUPPORTING TABLES:

S1 Table. Comparison of *P. palmivora* transcriptomes

	In planta upregulated transcripts in *LILI/N. benthamiana* [1] and ARI/Marchantia	Transcripts upregulated only in ARI/Marchantia
Overall	784(37%)	1347
Candidate Secreted Proteins	219(53%)	196
Candidate RXLR Effectors	42(45%)	52

S2 Table. Plants Used in This Study

Name/Strain	Species	Reference/Source
TAK1	*Marchantia polymorpha*	Jim Haseloff (University of Cambridge)
nop1	*Marchantia polymorpha*	[2] Ishizaki et al. 2013
MpSYP13A:mCitrine-MpSYP13A	*Marchantia polymorpha*	[3] Kanazawa et al. 2016
MpSYP13B:mCitrine-MpSYP13B	*Marchantia polymorpha*	[3] Kanazawa et al. 2016
35S:mCitrine-MpRab7	*Marchantia polymorpha*	This Study
35S:mCitrine-MpRab11A	*Marchantia polymorpha*	This Study
MpPRX:GUS	*Marchantia polymorpha*	This Study
N/A	*Marchantia paleacea*	Pierre-Marc Delaux (Paul Sabatier University
N/A	*Lunularia cruciata*	Pierre-Marc Delaux (Paul Sabatier University

S3 Table. Pathogen Strains Used in This Study

Organism	Strain (Accession)	Reference
Phytophthora infestans	Pi88069-td	[4] Chaparro-Garcia et al. 2011
Phytophthora palmivora	ARI-tdTomato (P3914)	[5] Le Fevre et al. 2016
Phytophthora palmivora	ADA (P7551)	[5] Le Fevre et al. 2016
Phytophthora palmivora	ALOHA (P6053)	[5] Le Fevre et al. 2016
Phytophthora palmivora	FLIMA (P7545)	[5] Le Fevre et al. 2016
Phytophthora palmivora	FLIP (P7548)	[5] Le Fevre et al. 2016
Phytophthora palmivora	FRED (P7547)	[5] Le Fevre et al. 2016
Phytophthora palmivora	JAKO (P3738)	[5] Le Fevre et al. 2016
Phytophthora palmivora	MAZI (P6375)	[5] Le Fevre et al. 2016
Phytophthora palmivora	TAZI (P6802)	[5] Le Fevre et al. 2016
Phytophthora palmivora	STITCH (P0113)	[5] Le Fevre et al. 2016

S4 Table. Primers Used in This Study

Primer Name	Sequence (5-3)	Reference
qRT-PCR Primers:		
MpACT-qF	AGGCATCTGGTATCCACGAG	[6] Saint-Marcoux et al. 2015
MpACT-qR	ACATGGTCGTTCCTCCAGAC	[6] Saint-Marcoux et al. 2015
MpEF1a-qF	CCGAGATCCTGACCAAGG	[6] Saint-Marcoux et al. 2015
MpEF1a-qR	GAGGTGGGTACTCAGCGAAG	[6] Saint-Marcoux et al. 2015
MpSYP13A-qF	CCAGGTTCAGCAGTAAGCCA	This Study
MpSYP13A-qR	TTTCTCTCTACCGTTCCCG	This Study
MpSYP13B-qF	CGAAATGAGCACGAACGGGA	This Study
MpSYP13B-qR	CCAGCTTCTTCAGCAGCGAC	This Study
MpPRX-qF	ATTTCGATTGCTTCCGAGGC	This Study
MpPRX-qR	AATCCCACATCCCCGAAGTT	This Study
MpDIR-qF	AGACTTCGGTTTCCAGCTGA	This Study
MpDIR-qR	TATGCCTCCTTGCTTCCAC	This Study
Ppal_03573p06550_06960qF	GCAACAATGCGTACATTCTCC	This Study
Ppal_03573p06550_06960qR	ATCGAGTCGTCGGTGTTAGG	This Study
Ppal_08171n02473_03033qF	GTCAAAACATTGTCCGAGTTCA	This Study
Ppal_08171n02473_03033qR	GGCGGATATCTACATCACCTTC	This Study
Ppal_05494p02665_03135qF	ACCAAGGAACAACCGTTTGCC	This Study
Ppal_05494p02665_03135qR	CCTTGCCGCTTATGAGTAGAGT	This Study
Ppal_06531n05739_06188qF	GACTGATCAAGCACACCACACT	This Study
Ppal_06531n05739_06188qR	AGCTGGTCAGGAATCTCTCTGT	This Study
Ppal_03660p04152_04550qF	CAGTTCTTACAAGCGTCATGC	This Study
Ppal_03660p04152_04550qR	TCTGTCGGATCGTTGTTTTG	This Study
Ppal_18465n22905_2647qF	TGCTTTTGTGGAGTGTACTGCT	This Study
Ppal_18465n22905_2647qR	CGTTAAATCCGCTGTTATGTCA	This Study
PpEF1a-qF	CAAGATCCCGTTCGTGCCTA	[5] Le Fevre et al. 2016
PpEF1a-qR	GCGTTCAGGTTGTCAAGAGC	[5] Le Fevre et al. 2016
PpWS21-qF	CTCCAGAACGTGTACATTCG	[1] Evangelisti et al. 2017
PpWS21-qR	TGGCACCCTTCTCCTCGG	[1] Evangelisti et al. 2017
PpCdc14-qF	TCTGCACGAGTTCCAGCATT	[5] Le Fevre et al. 2016
PpCdc14-qR	CACCACTAGCGTCACGTTCT	[5] Le Fevre et al. 2016
PpHmp1-qF	TGCCATTCTTGATCTGCCGT	[5] Le Fevre et al. 2016
PpHmp1-qR	GACGATGCGAAAAGGGCTTC	[5] Le Fevre et al. 2016
REX1-qF	TCTCTTATCCAGACGAGCAACA	[1] Evangelisti et al. 2017
REX1-qR	TGACGTAGCCCTTGTAGATTGA	[1] Evangelisti et al. 2017
REX3-qF	AGTCCAAGAAGGATTTGACGAC	[1] Evangelisti et al. 2017
REX3-qR	TTCTCTAACGCATTAGCCTTCC	[1] Evangelisti et al. 2017
REX4-qF	CAGAACGACAACGAATGGTATC	[1] Evangelisti et al. 2017
REX4-qR	TCGGCAATAAGCCTTTAAATTG	[1] Evangelisti et al. 2017
PiWS21-qF	CTCCAAAACGTGTACATCCGTAAGTGC	This Study
PiWS21-qR	CCTTAGCACCCTTCTCCTCAGCACC	This Study
PiCdc14-qF	TCTGCACGAGTTCCAGCACTATGAAC	This Study
PiCdc14-qR	CCTGCAAAGGCTATGAACTTGGGTG	This Study
PiHmp1-qF	CATGATGGCTGTCATGGTCGGTGAGG	[7] Schoina et al. 2017
PiHmp1-qR	TTAGCTAACATTCAAGCGAGCATGAAG	[7] Schoina et al. 2017
PiAVR3a-qF	CGCCATAAACTTTGCAACCA	[7] Schoina et al. 2017
PiAVR3a-qR	TGCCGGCTGAATCGTGTAT	[7] Schoina et al. 2017
PiAVRblb2-qF	CGTCGCAGCATTCCCAAT	[7] Schoina et al. 2017
PiAVRblb2-qR	GCCACAGTGTCAGGAGATGTCTT	[7] Schoina et al. 2017
Cloning Primers:		
MpRab7-B1F	AAAAAGCAGGCTtcATGTCAGCTCGTAAACGAACTCTG	This Study
MpRab7-B2R	AGAAAGCTGGGTTCAGCATTCACAGACAGATGACT	This Study
MpRab11A-B1F	AAAAAGCAGGCTtcATGGCTTATAGATCCGACGATG	This Study
MpRab11A-B2R	AGAAAGCTGGGTTTACGCTGAGCAACATCCTACT	This Study

SUPPORTING METHODS

Histochemical Staining

GUS staining was performed in mock (water) or infected (*P. palmivora* ARI-td) plants 4 days post inoculation (dpi) essentially as described in [1], except that *M. polymorpha* thalli (TAK1 and *MpPRX:*GUS) were vacuum infiltrated with the GUS staining solution. Thalli were de-stained in a solution containing 70% ethanol and 20-30% glycerol. De-stained thalli were sectioned using a vibratome and imaged using the 3D display option on a Keyence digital microscope. DAB (diaminobenzidine) staining for the detection of H_2O_2 was performed on mock (water) or infected (*P. palmivora* ARI-td) plants 4 days post inoculation (dpi) as described in [8]. Three-week old *M. polymorpha* plants were used for all histochemical staining experiments.

Phylogenetic Analysis

Amino acid sequences retrieved from phytozome (https://phytozome.jgi.doe.gov/pz/portal.html) and MarpolBase (www.marchantia.info) were aligned using MUSCLE. The evolutionary history was inferred by the Maximum Likelihood method utilizing the Jones, Taylor & Thornton model with discrete Gamma distribution using MEGA 6 [9]. Ten thousand bootstrap replicates were conducted, and percent bootstrap values were placed on corresponding branches. The tree was drawn in MEGA 6. 0

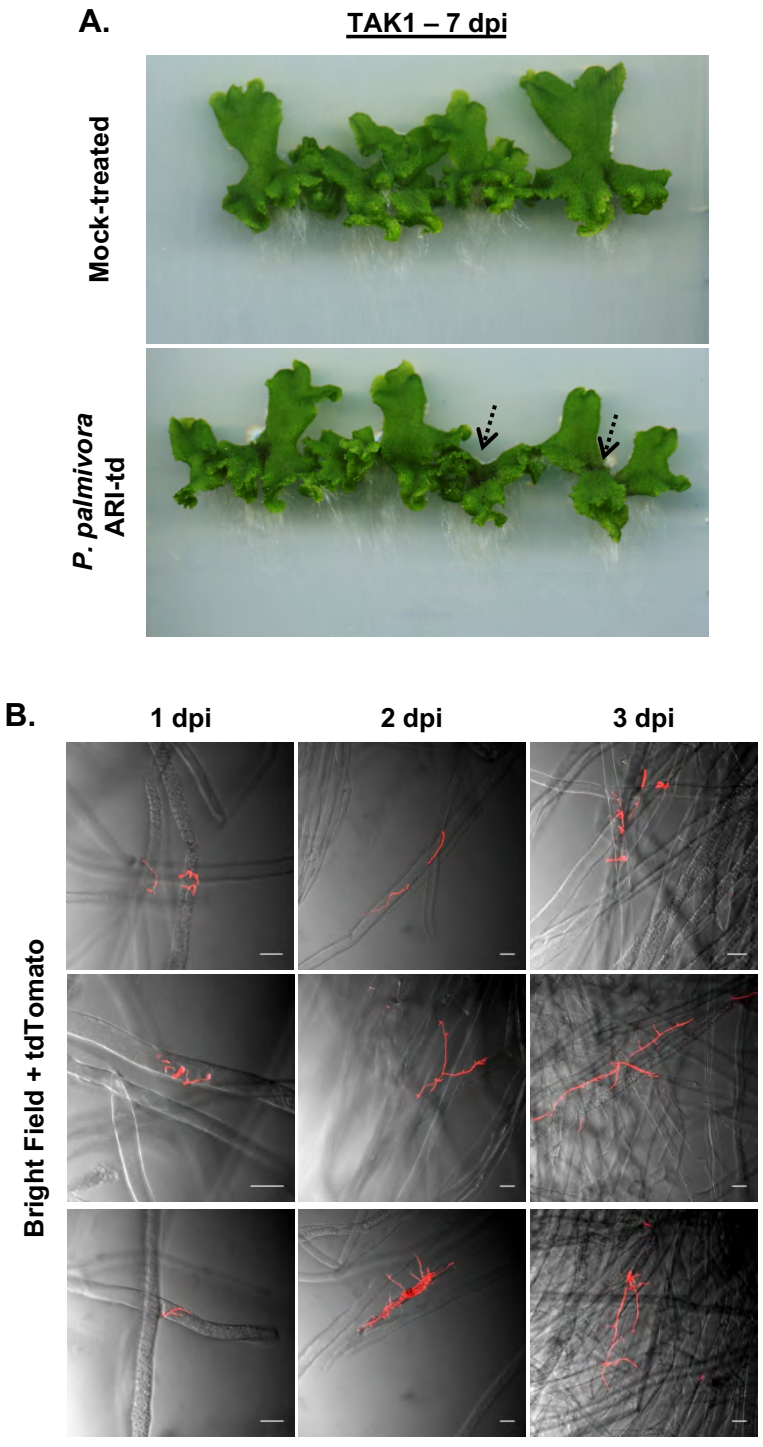
Comparison of *P. palmivora* expression patterns in *M. polymorpha* and *N. benthamiana pathosystems*

To compare *P. palmivora* expression patterns in *M. polymorpha* and *N. benthamiana* [1] pathosystems we applied standardized analysis approach. Reads from *P. palmivora* LILI - *N. benthamiana* experiment were mapped back to the same P. palmivora reference genome [10] using STAR (version 2.5.2b) aligner [11]. Similar to *P. palmivora*-ARI *M. polymorpha* analysis, raw counts were obtained with FeatureCounts [12]. Uniquely mapped and properly paired reads were considered further. Differentially expressed genes were obtained applying EdgeR methodology [13,14] for both *P. palmivora*-LILI *N. benthamiana* and *P. palmivora-ARI M. polymorpha* datasets. In the absence of replicates in *P. palmivora*-LILI *N. benthamiana* dataset 6-18-24 hai and 48-72 hai samples were treated as pseudo-replicates for biotrophic and necrotrophic stages. To get a subset of genes up-regulated *in planta* we compared infected samples against respective *ex-planta*

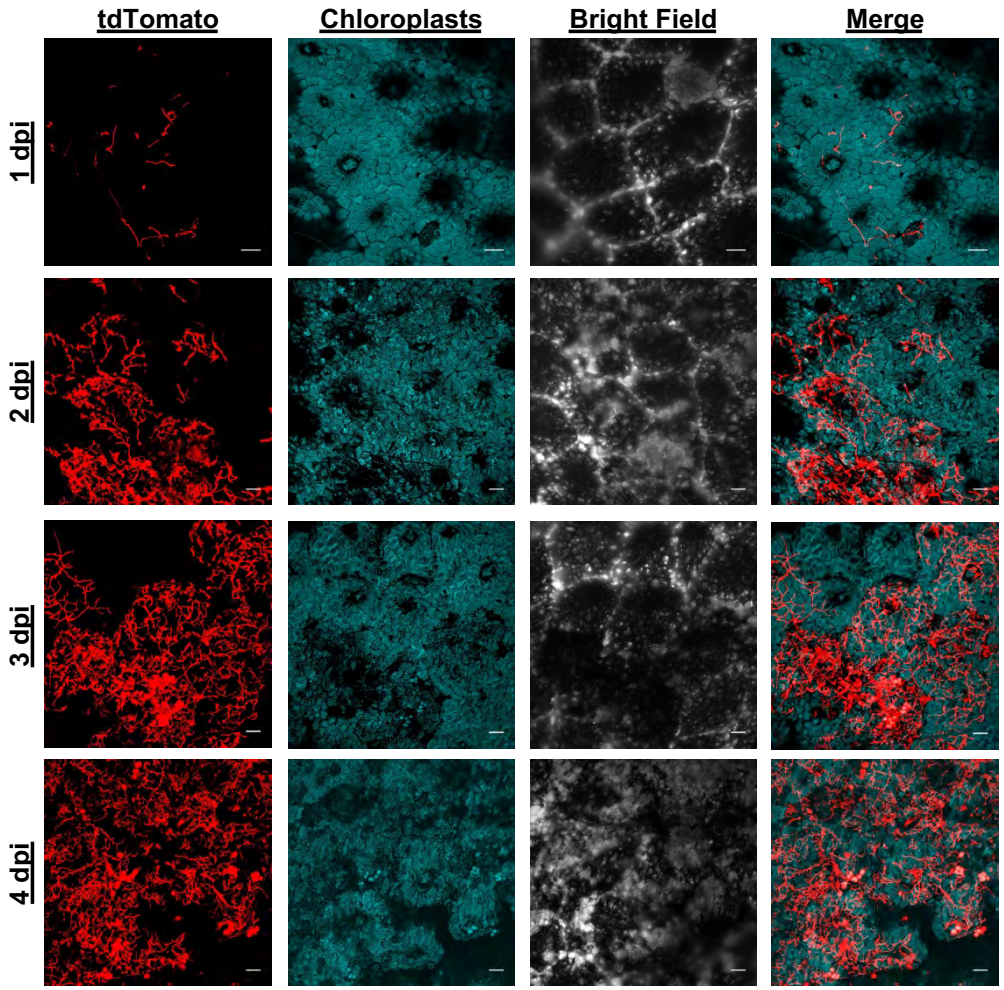
stage: MZ - for *P. palmivora*-LILI *N. benthamiana* and MYC - for *P. palmivora-ARI M. polymorpha*. Lists of *in planta* up-regulated genes (LFC >= 2, adjusted p-value < 10-3) in both pathosystems were compared using UpSetR package [15].

MpPRX **(Mapoly0106s0049) Promoter +** **5' UTR:**

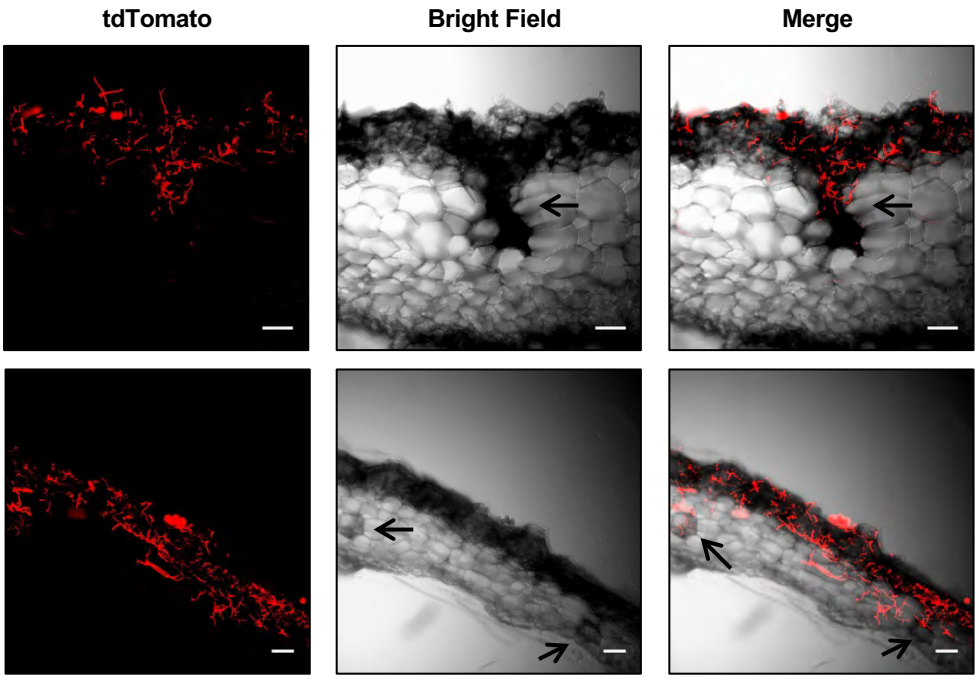
GATCTCAACGTTCTGGCTGAGAGTGTGTTCCACAATTCTGGAAGCGTTTCATGGCTGAGCGAGTTAGAA
GAATCGATTACCTTCTGCTTCTAATCATCACAGAAATTAATGTATCAGAATGCTCAGACATTACTAGATGA
AAAGGGAAATGCAAAGATTGCAAACGTAAGAGTTGCAGTCGGAATTTCTTCCAGGGTTACGAATTGGGA
CTAGCGTCAACGTCATAATAACAGCCCAAGATAGTGGCCTTGTGCATGTCGGCTTTGTGCATAGAATGA
CGTGTATCTAATCACATGCACATCATTCGTCACAAGGTCTTGCATACTTGCATTGGCTTGTAAGCTCGAG
CAATCTAATTGCAGCATTCCTAACCCTCAGAGAATTCCTAACCCTTTCGCATGCAAATTAGTATACAAAAA
GATTGCATCTAGAAGGTGTAATGATGCATGTTCTATACCTAGAGTAGGAGAGATTTATCATGAGAACAAT
AAACTCTGGTGTGAATCTAGAAAGAGGGTTTTCTTTGCGGTATGTAGCCATCGTGTATCCGCAACTAAC
GCGCTATCATCCTTTCGAAATTGGGACTCCTAGCCGCCATCTTAAACACACCAGCCTCCAGAATTGGGG
TCGGAGACTGCAACTTCCCGCCCTACGCATGGTCAGGTCAAACGTAAACCAGGGCTTTCACTGAATTGT
TAGCGTTTCCCAGCCGCCGAAAATGTCTGCGTCGGCCAAATGTAGCTTGAACATAATCGCACATTTTTCT
CACCACGATTTTGCGAAAAGATGGGGCCTATCTTTTCGTATTTCACACCTTTAGCGTCCCATCACCAATT
CGGGTCACTCGTTTGGTTCCAGATGGCGGACTGAGTGGTCGCATTGGAAGACGCTGTGCTCACATGCA
TAGTCTACTCTTCTTCCCGACCTTATCTGAAACTCGTTCCGTTGTGCTCGACTGCAAACGCCTCCAGGG
CTTCACATGATCACGGTGTTTGCATGCCGCGGTCAAATAAGACTCTAGAGGTCACATCTGACCAGTGCA
GCACACACTCTAGTCTGCATGCATGCGCCTGCCGGACGATGTGCGTTCTGATCGCAACTCGGCAGCAC
ACATAGTTATCCCCGTTGGACTGCCCACTTTCCAAGCCTAGGGCAGATGGGGCACAGGCAGTATCCTAT
TGTTTATGTTTGCTTCCGAAGACTCAATACAGTCTTCTAAGGCCATCTACAAGGAAAGGAAATTTTACAA
GGAGACTTAATATACAGGTCCCTTTTGTGTTTCTCACTGTGAATCCGAGAGCAAACACTTTTTTTTGTCTA
TGGTCACCGGAATCGCTTCAACTTGTGCTGCGAAAGCTGCTGTAGTTATGATGACTTAGTCAAAGCTTT
GAGTCGGATGAAAATAGACAGTTTTTGGCGCATGCCATGACCTTGTGGAACCGTTCCACATTGCCACAA
TCTTCAGATCTACGAATCCTCGCTCTTCTGTACCAGGTCCACGTCGTACAGACATTGACGTGTAAAAGAC
TCTCTTTAGCCGGAGTGTATATATCTCCAGGATGAGCACAGCATTCCATCCAAAGCAAAACTATCAGATT
CAATTACTGCCTGCTCACCTGCACTCCCTGAAGTCCAGTACAATCATC**CTTGGAAGGAGAATCAAGTGC**
TTCAAAACTTCAGGCGCATCGAGGATTCATATCAACTTCACAGTTTTAGCGGAGATTCAGAGTCACCT
TTCAGTTTTGTTCGTCGACCTGCACAAGTCGACGCCAAAGGAGCGCATCTATCAGCATTCTCACG



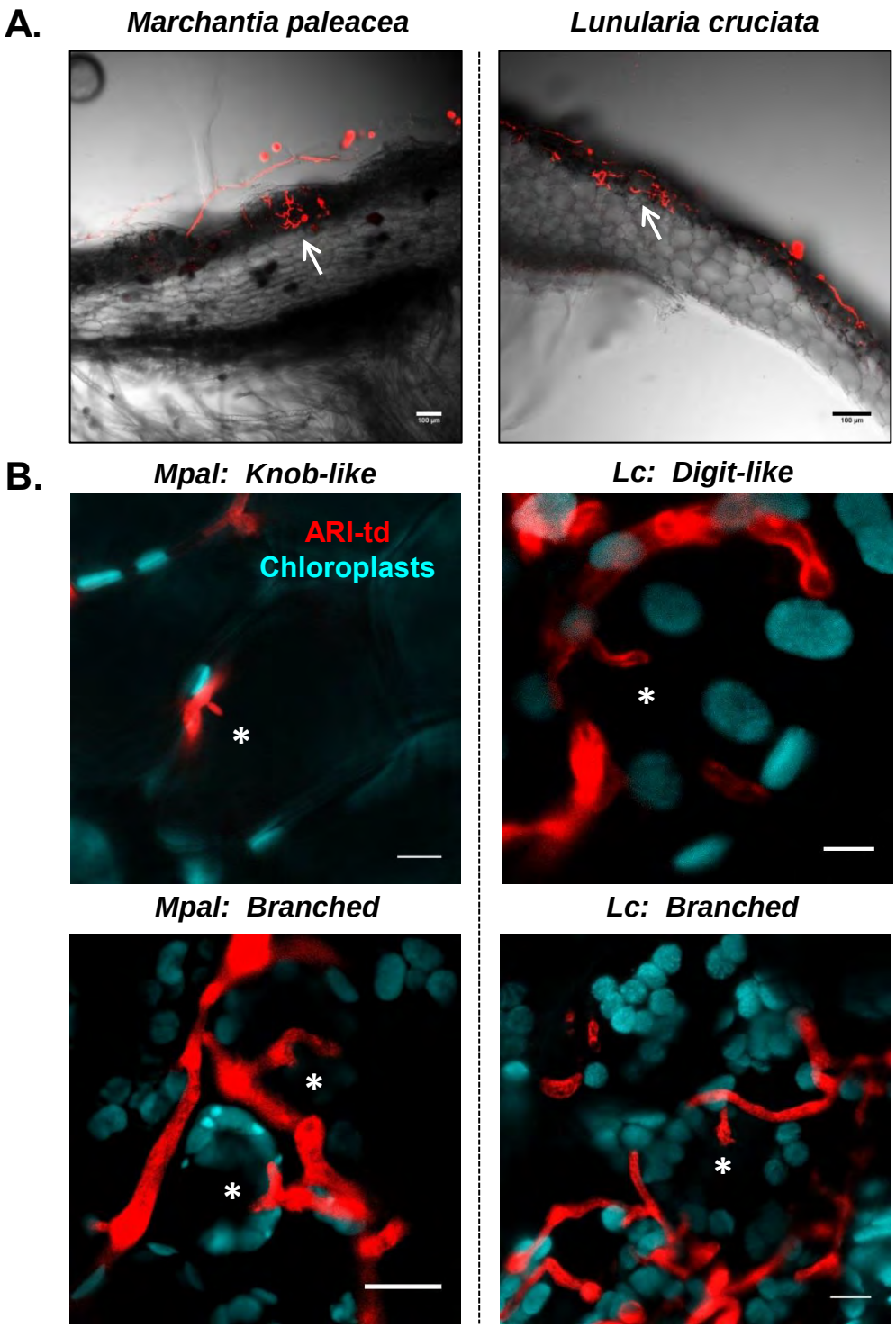
S1 Fig. Rhizoid inoculations do not reliably lead to colonization
(A) Disease symptoms at 7 days post inoculation (dpi) of 3-week-old *M. polymorpha* (TAK1) plants that were inoculated with *P. palmivora* ARI-td zoospores or water directly onto rhizoids. **(B)** Confocal fluorescence microscopy demonstrating *P. palmivora* ARI-td growth on 3-week-old *M. polymorpha* rhizoids from 1-3 dpi. Micrographs represent z-stack projections of merged bright field and tdTomato channels. Scale bars = 50 μm.



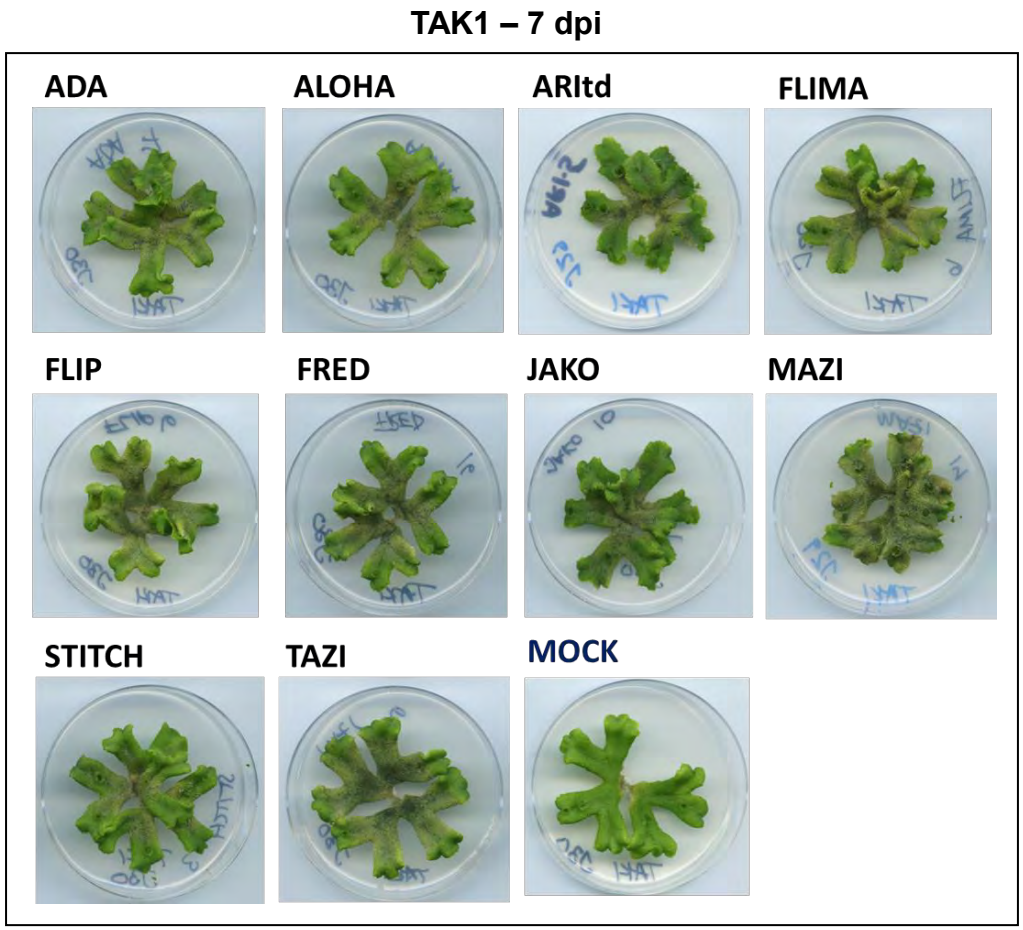
S2 Fig. *P. palmivora* colonizes TAK1 thalli. Confocal fluorescence microscopy demonstrating *P. palmivora* ARI-td growth on 3-week-old *M. polymorpha* thalli from 1-4 days post inoculation (dpi). Micrographs represent z-stack projections. The merged micrographs display red pathogen fluorescence (tdTomato) overlaid on top of chlorophyll autofluorescence (turquoise). Scale bars = 100 µm.



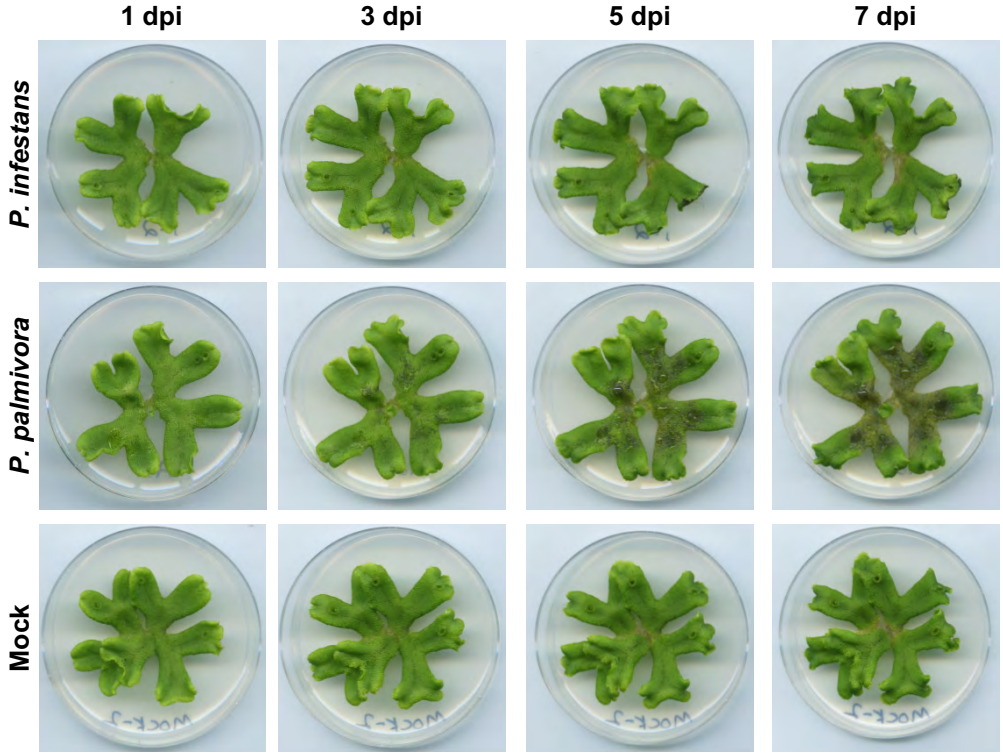
S3 Fig. *P. palmivora* hyphae access the storage region during necrotrophy. Confocal fluorescence microscopy demonstrating the co-occurrence of *P. palmivora* ARI-td hyphae and necrotrophic disease symptoms in the storage region of *M. polymorpha* thalli at 7 days post inoculation (dpi). Red pathogen fluorescence is merged with bright field images. Micrographs represent z-stacked images. Scale bars = 100 μm.



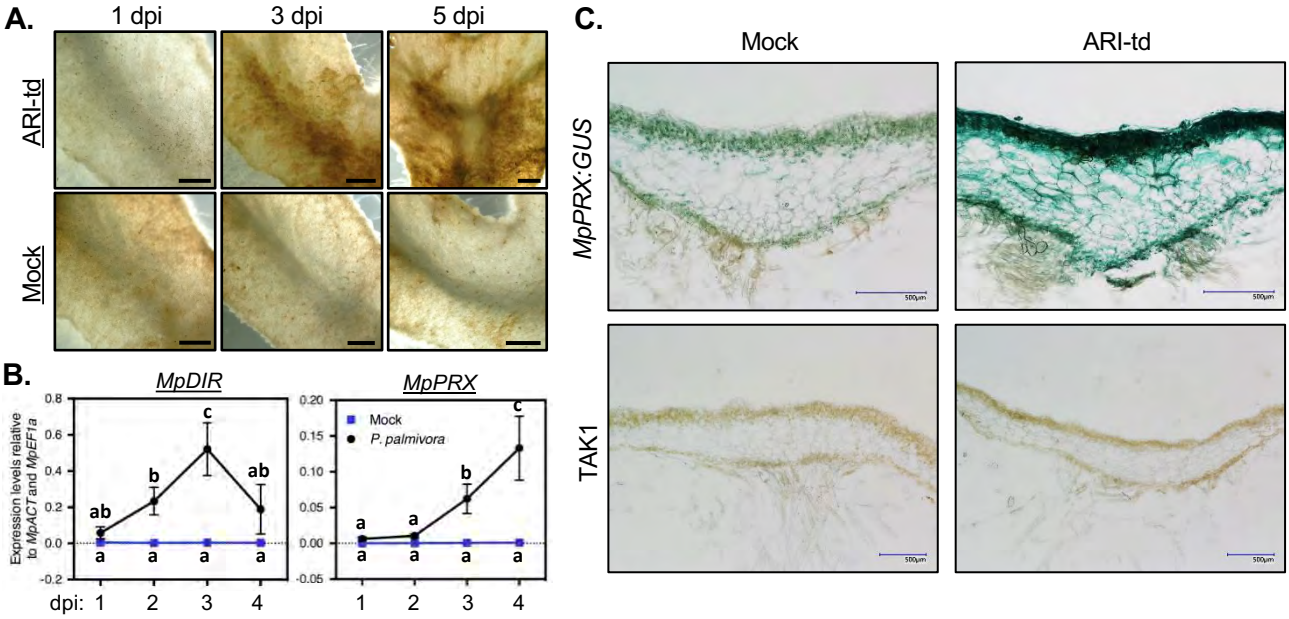
S4 Fig. Intracellular colonization of the photosynthetic layer in *Marchantia paleacea* and *Lunularia cruciata*.
(A) Confocal fluorescence microscopy of sectioned thalli of *M. paleacea* and *L. cruciata* colonized by *P. palmivora* ARI-td at 7 days post inoculation (dpi). Z-stacked images represent red pathogen fluorescence (tdTomato) merged with the bright field channel. Colonized air chambers are denoted by arrows. Scale bars = 100 μm
(B) Confocal fluorescence microscopy demonstrating haustoria morphology in *P. palmivora* ARI-td-colonized *M. paleacea* (*Mpal*) and *L. cruciata* (*Lc*) thalli at 3 dpi. Z-stacked images display red pathogen fluorescence (ARI-td) merged with plastid autofluorescence. Scale bars = 10 μm.



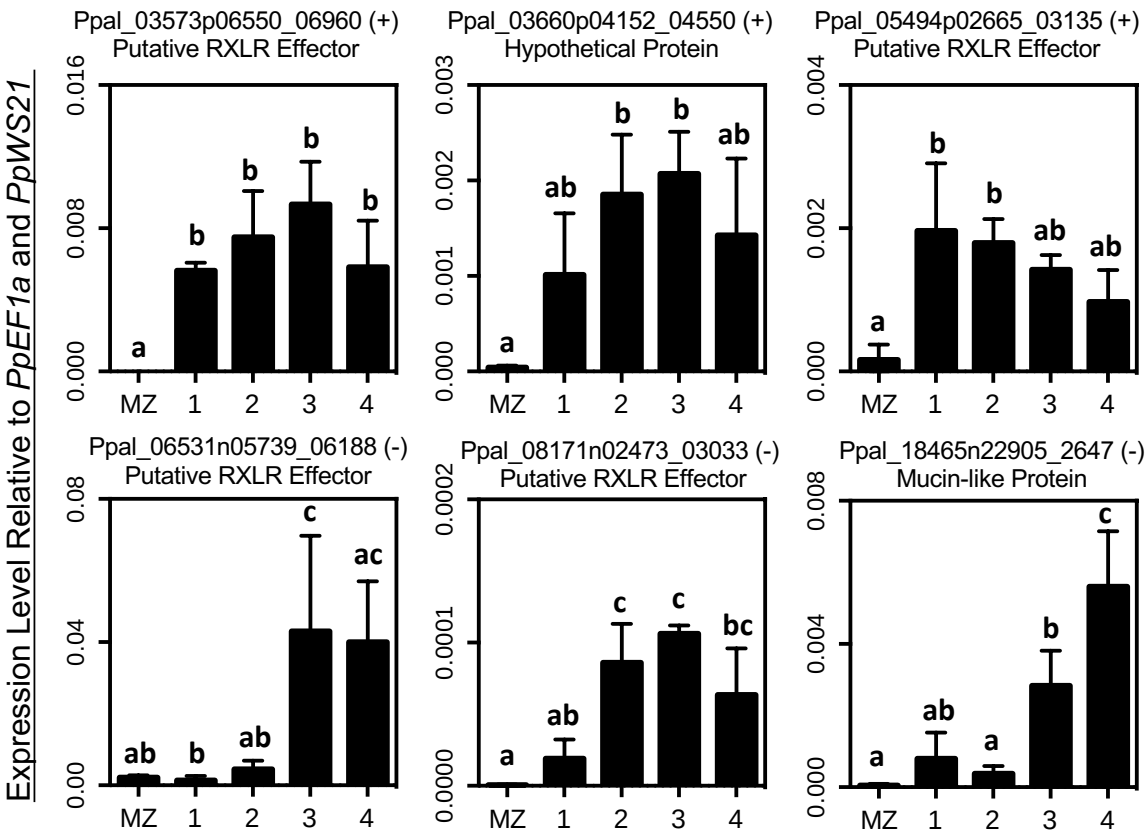
S5 Fig. *P. palmivora* strains vary in aggressiveness in TAK1. Disease symptoms of *M. polymorpha* TAK1 plants inoculated with water (mock) or zoospores of *P. palmivora* strains 7 days post inoculation (dpi). Images displayed are representative of consistent symptoms observed from 8-16 infected plants per strain.



S6 Fig. *P. infestans* does not cause disease symptoms on TAK1
Disease progression of *M. polymorpha* TAK1 plants inoculated with water, *P. palmivora* (ARI-td) zoospores or *P. infestans* (*Pi88069*-td) zoospores. Images display consistent disease symptoms (n=8) at 1, 3, 5, and 7 days post inoculation (dpi).

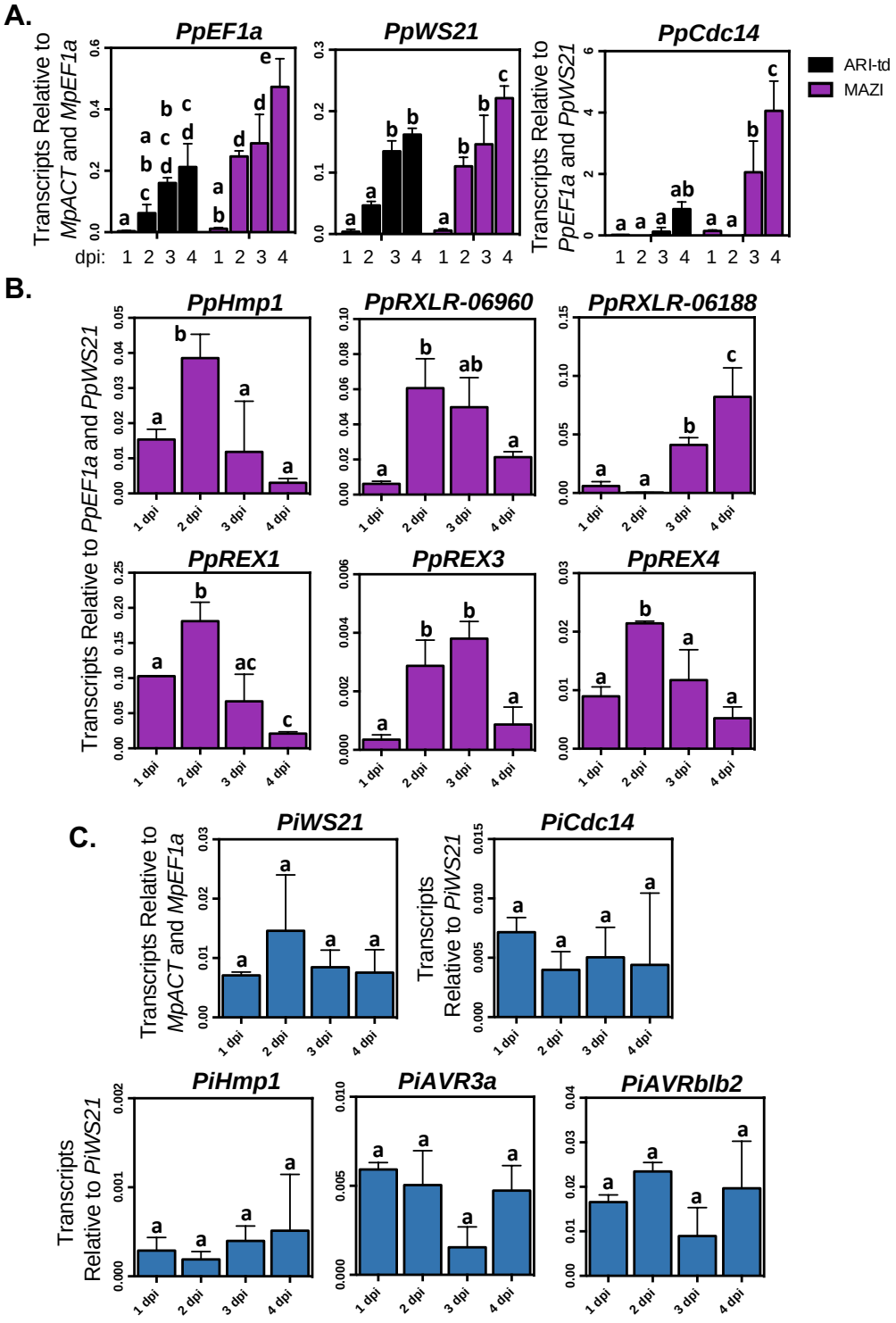


S7 Fig. Host responses to colonization are activated in *Marchantia* air chambers.
(A) Histochemical staining of mock-treated or *P. palmivora* ARI-td infected *M. polymorpha* TAK1 using DAB (diaminobenzidine) to detect hydrogen peroxide (H_2O_2) accumulation at 1, 3, and 5 days post inoculation (dpi). Scale bars = 1000 µm.
(B) qRT-PCR analysis of *MpDIR* and *MpPRX* transcripts in mock-treated (blue) and infected (*P. palmivora* ARI-td, black) *M. polymorpha* TAK1 from 1-4 dpi. Expression was quantified relative to endogenous *MpACT* and *MpEF1a* controls. Different letters indicate statistically significant differences in transcript abundance (ANOVA, Tukey's HSD, $p < 0.05$).
(C) GUS staining of mock-treated and infected (*P. palmivora* ARI-td) *MpPRX:GUS* and wild-type TAK1 thalli at 4 dpi. Thalli were sectioned using a vibratome and images were collected using the 3D display option on a Keyence digital microscope. Scale bars = 500 µm.



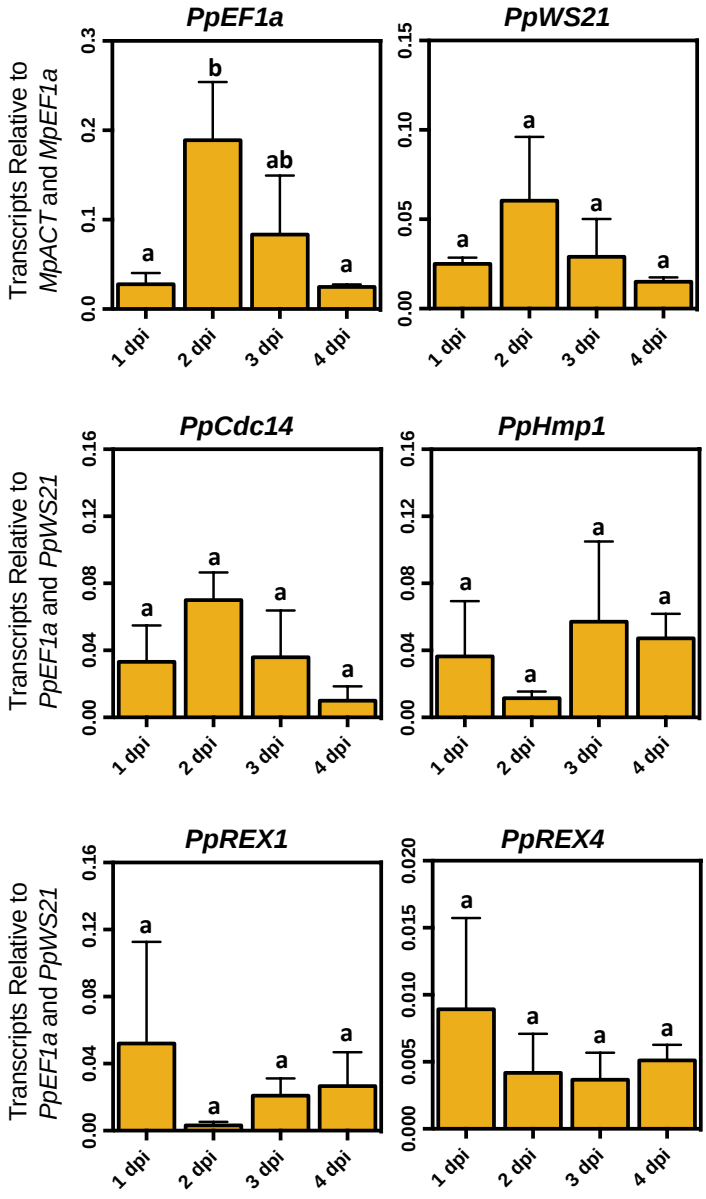
S8 Fig. Validation of colonization-induced *P. palmivora* genes

qRT-PCR analysis of *P. palmivora* (ARI-td) genes identified by RNA-seq analyses. Expression levels were quantified in an axenically propagated MZ (mycelia + zoospores) sample and during the colonization of *M. polymorpha* thalli from 1-4 days post inoculation (dpi). Expression levels were quantified relative to internal controls *PpEF1a* and *PpWS21.* Different letters indicate statistically significant differences in expression levels (ANOVA, Tukey' HSD, $p < 0.05$). Performed twice with similar results.

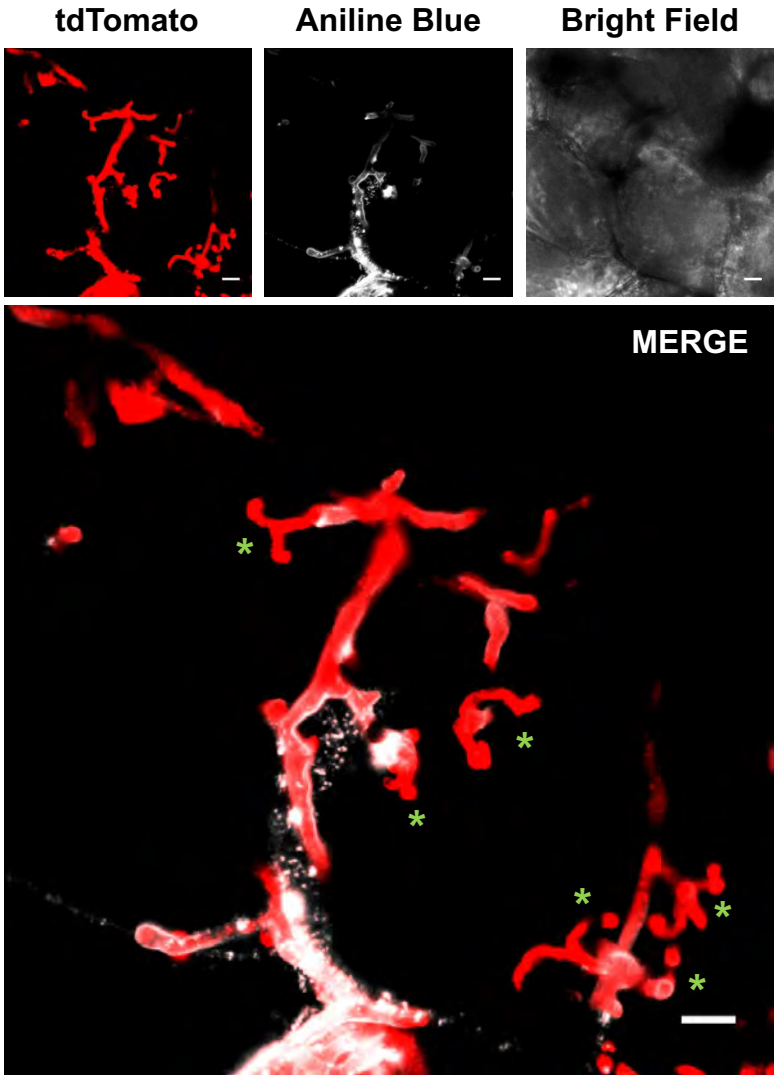


S9 Fig. Expression analysis of *Phytophthora* lifestyle markers during compatible and incompatible interactions with *Marchantia* thalli.

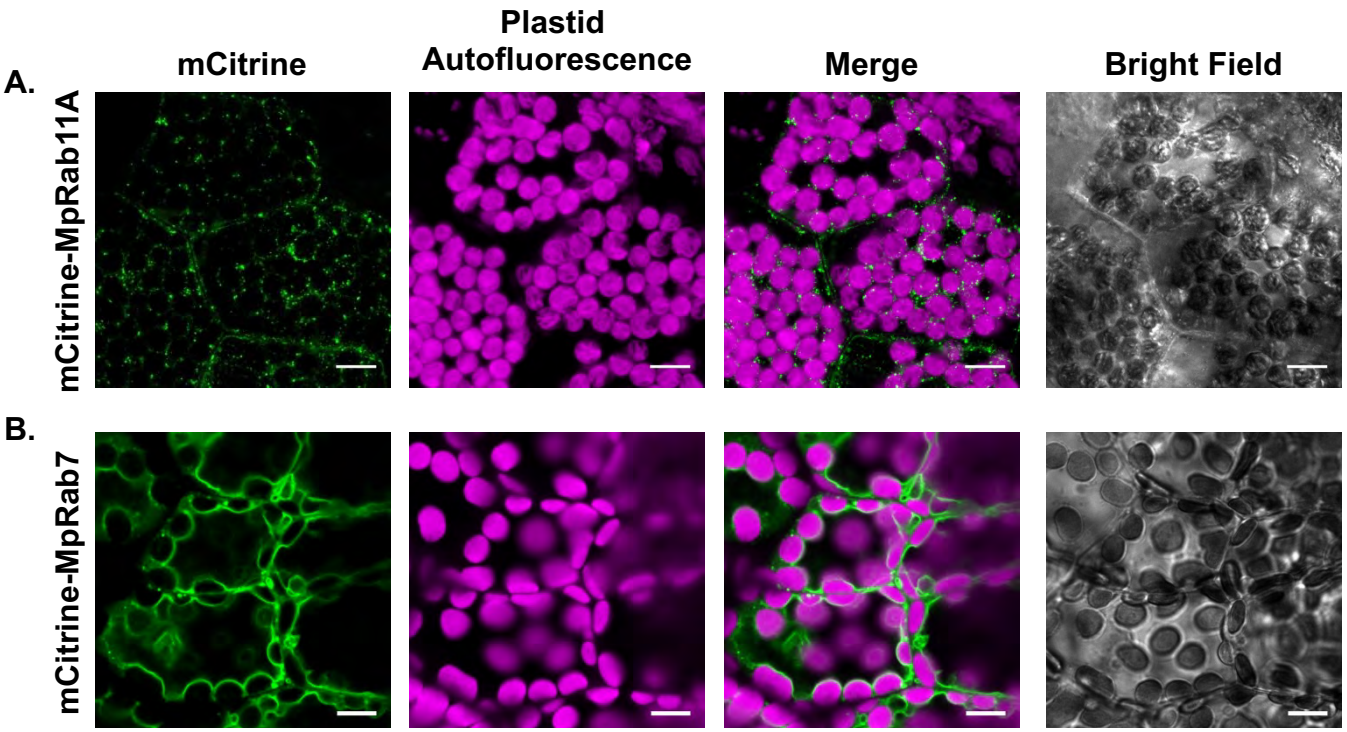
(A) Comparative qRT-PCR analysis of pathogen biomass (*PpEF1a* and *PpWS21*) and sporulation (*PpCdc14*) during interactions between 3-week-old *M. polymorpha* thalli and *P. palmivora* ARI-td (black) or MAZI (magenta) from 1-4 days post inoculation (dpi). **(B)** Expression analysis of haustoria-associated *PpHmp1* and RXLR effectors (*PpREX1,3,4*) in the *P. palmivora* isolate MAZI during compatible interactions with *M. polymorpha* thalli. Additional RXLR effectors *PpRXLR-06960* and *PpRXLR-06188* represent the *P. palmivora* loci Ppal_03573p06550_06960 (+) and Ppal_06531n05739_06188 (-), respectively. **(C)** Expression analysis of *P. infestans* biomass (*PiWS21*), sporulation (*PiCdc14*) , haustoria-associated (*PiHmp1*), and RXLR effector genes (*PiAVR3a* and *PiAVRblb2*) during incompatible interactions with *M. polymorpha* thalli. Different letters indicate statistically significant differences in transcript levels (ANOVA, Tukey's HSD, $p < 0.05$). Performed twice with similar results.



S10 Fig. Expression analysis of *P. palmivora* lifestyle markers during incompatible interactions with *Marchantia* rhizoids.
qRT-PCR expression analysis of pathogen biomass (*PpEF1a* and *PpWS21*), sporulation (*PpCdc14*), haustoria development (*PpHmp1*), and RXLR effectors (*PpREX1* and *PpREX4*) during interactions between 3-week-old *M. polymorpha* rhizoids and *P. palmivora* ARI-td from 1-4 days post inoculation (dpi). Different letters indicate statistically significant differences in transcript levels (ANOVA, Tukey's HSD, $p < 0.05$). The data are representative of two experimental replicates.



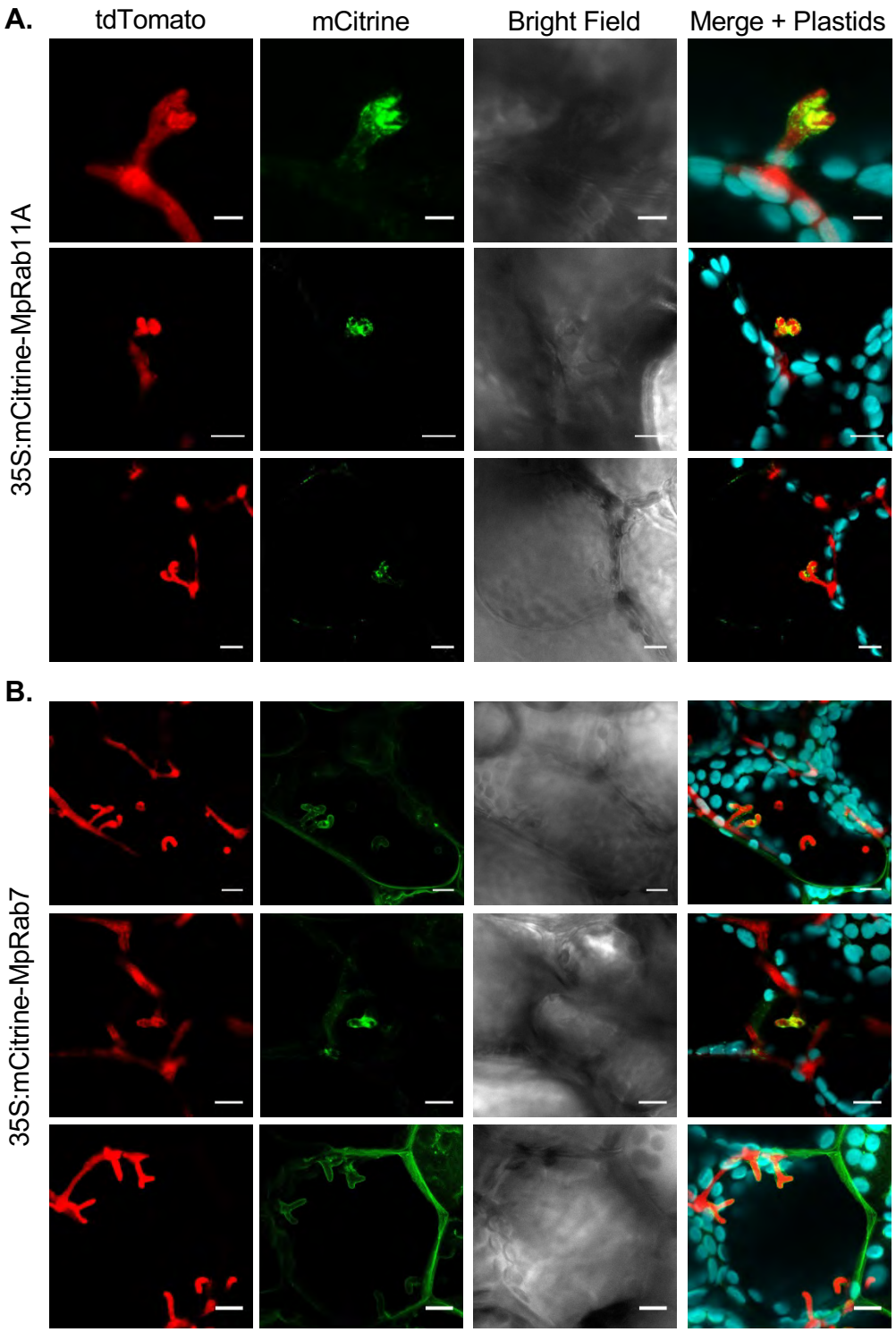
S11 Fig. Callose does not envelope *P. palmivora* infection structures
Confocal fluorescence microscopy of aniline blue stained *M. polymorpha* TAK1 thalli infected with *P. palmivora* ARI-td at 3 days post inoculation (dpi). Images represent z-stack projections displaying red fluorescence from the pathogen (tdTomato), callose deposition through aniline blue staining (white), bright field, or tdTomato merged with aniline blue. Asterisks (*) denote intracellular infection structures that are not enveloped by callose.



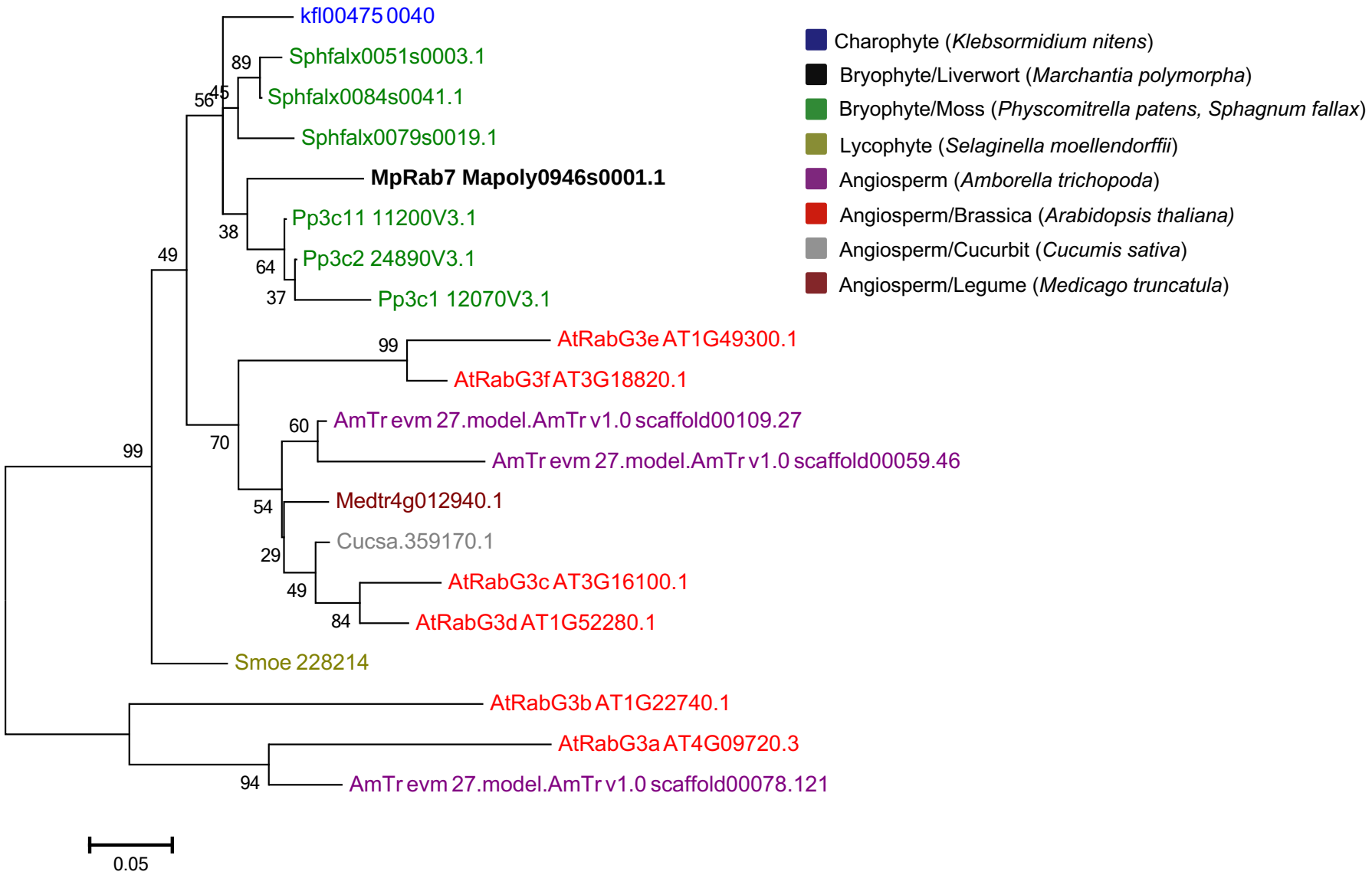
S12 Fig. Subcellular localization of MpRab11A and MpRab7

(A) Confocal fluorescence microscopy showing subcellular localization patterns of MpRab11A in 35S:mCitrine-MpRab11A/TAK1 gemmae. Micrographs display mCitrine fluorescence, plastid autofluorescence (magenta), both channels merged, or bright field images. Scale bars = 10 μm.

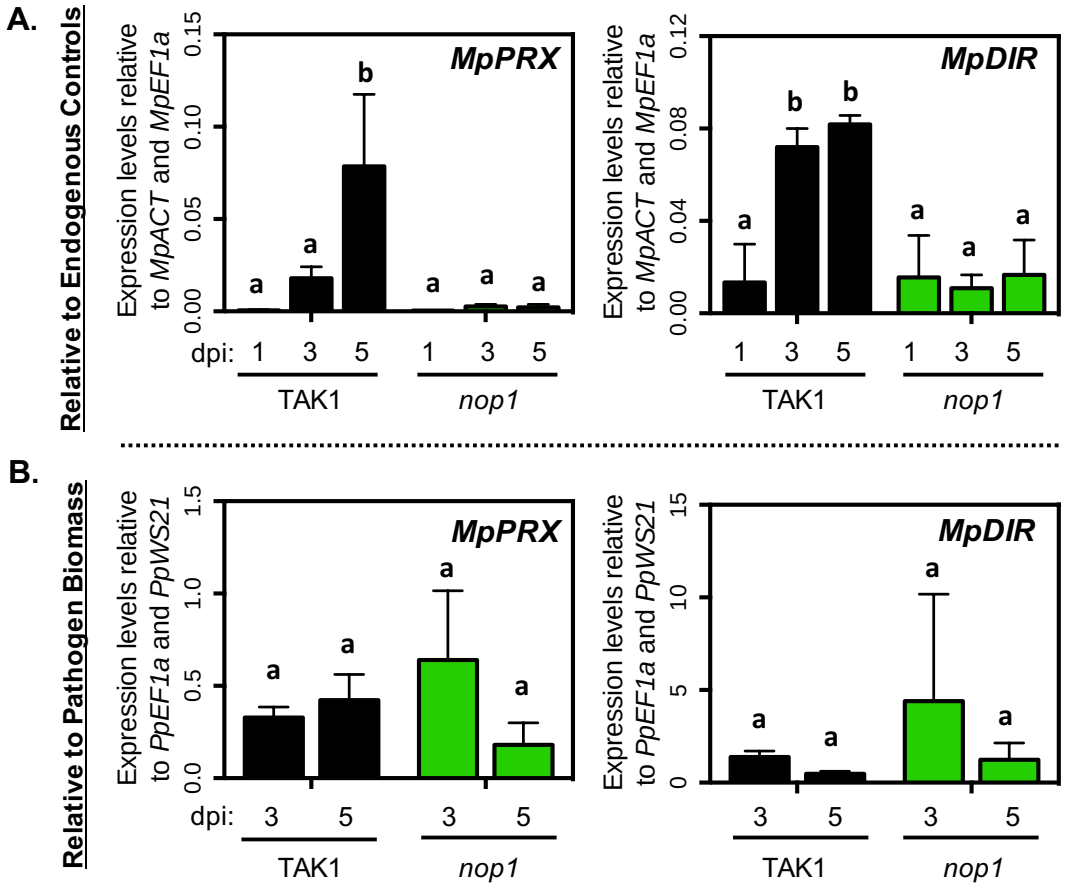
(B) Confocal fluorescence microscopy showing subcellular localization patterns of MpRab7 in 35S:mCitrine-MpRab7/TAK1 gemmae. Micrographs display mCitrine fluorescence, plastid autofluorescence (magenta), both channels merged, or bright field images. Scale bars = 10 μm.



S13 Fig. MpRab11A and MpRab7 accumulate at *P. palmivora* intracellular infection structures in living *Marchantia* cells. Confocal fluorescence microscopy showing subcellular localization patterns of MpRab11A **(A)** and MpRab7 **(B)** in 35S:mCitrine-MpRab11A/TAK1 or 35S:mCitrine-MpRab7/TAK1 thalli infected with *P. palmivora* ARI-td at 2-3 days post inoculation (dpi). Z-stacked micrographs display tdTomato pathogen fluorescence, mCitrine fluorescence, bright field images, and a merged image displaying mCitrine, tdTomato and plastid autofluorescence (cyan), both channels merged, or bright field images. Scale bars = 10 µm.



S14 Fig. Rab7 phylogeny. Maximum likelihood phylogram of Rab7 proteins from the green-plant lineage. Amino acid sequences were aligned using MUSCLE. The evolutionary history was inferred by the Maximum Likelihood method utilizing the Jones, Taylor & Thornton model with discrete Gamma distribution using MEGA 6. Ten thousand bootstrap replicates were conducted and percent bootstrap values were placed on corresponding branches.



S15 Fig. Colonization-induced *MpPRX* and *MpDIR* expression is not compromised in *nop1* mutants.

(A) qRT-PCR analysis of *MpDIR* and *MpPRX* transcripts in wild-type TAK1 and *nop1* mutants at 1, 3, and 5 days post inoculation (dpi) with *P. palmivora* ARI-td in 3 week-old plants. Expression was quantified relative to endogenous *MpACT* and *MpEF1a* controls. Different letters indicate statistically significant differences in transcript abundance (ANOVA, Tukey's HSD, $p < 0.05$).

(B) qRT-PCR analysis of *MpDIR* and *MpPRX* transcripts in wild-type TAK1 and *nop1* mutants at 3 and 5 days post inoculation (dpi) with *P. palmivora* ARI-td in 3 week-old plants. Expression was quantified relative to pathogen biomass (*PpEF1a* and *PpWS21*). Different letters indicate statistically significant differences in transcript abundance (ANOVA, Tukey's HSD, $p < 0.05$).

SUPPORTING REFERENCES:

[1] Evangelisti E, Gogleva A, Hainaux T, Doumane M, Tulin F, Quan C, Yunusov T, Floch K, Schornack S. Time-resolved dual root-microbe transcriptomics reveals early induced Nicotiana benthamiana genes and conserved infection-promoting Phytophthora palmivora effectors. BMC Biology 2017; 15(1): 39. doi: 10.1186/s12915-017-0379-1

[2] Ishizaki K, Mizutani M, Shimamura M, Nishihama R, Kohchi T. Essential role of the E3 ubiquitin ligase nopperabo1 in schizogenous intercellular space formation in the liverwort Marchantia polymorpha. Plant Cell 2013; 25(10): 4075-84

[3] Kanazawa T, Era A, Minamino N, Shikano Y, Fujimoto M, Uemura T, Nishihama R, Yamato KT, Ishizaki K, Nishiyama T, Kohchi T, Nakano A, Ueda T. SNARE molecules in Marchantia polymorpha: unique and conserved features of the membrane fusion machinery. Plant and Cell Physiology 2016; 57(2): 307-24.

[4] Chaparro-Garcia A, Wilkinson RC, Gimenez-Ibanez S, Findlay K, Coffey MD, Zipfel C, Rathjen JP, Kamoun S, Schornack S. The receptor-like kinase SERK3/BAK1 is required for basal resistance against the late blight pathogen phytophthora infestans in Nicotiana benthamiana. PLoS One 2011; 6(1): e16608. doi: 10.1371/journal.pone.0016608

[5] Le Fevre R, O'Boyle B, Moscou MJ, Schornack S. Colonization of barley by the broad-host hemibiotrophic pathogen Phytophthora palmivora uncovers a leaf development-dependent involvement of Mlo. Molecular Plant Microbe Interactions 2016; 29(5): 385-95.

[6] Saint-Marcoux D, Proust H, Dolan L, Langdale JA. Identification of reference genes for real-time quantitative PCR experiments in the liverwort Marchantia polymorpha. PLoS One 2015; 10(3): e0118678. doi: 10.1371/journal.pone.0118678.

[7] Schoina C, Bouwmeester K, Govers F: Infection of a tomato cell culture by Phytophthora infestans; a versatile tool to study Phytophthora-host interactions. Plant Methods 2017; 13:88.

[8] Castro A, Vidal S, Ponce de Leon I. Moss pathogenesis-related-10 protein enhances resistance to Pythium irregular in Physcomitrella patens and Arabidopsis thaliana. Frontiers in Plant Science 2016; 7:580. doi: 10.3389/fpls.2016.00580

[9] Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: Molecular evolutionary genetics analysis version 6.0. Molecular Biology and Evolution 2013; 30(12): 2725-29

[10] Ali SS, Shao J, Lary DJ, Kronmiller BA, Shen D, Strem MD, Amoako-Attah I, Akrofi AY, Begoude BAD, ten Hoopen GM, Coulibaly K, Kebe BI, Melnick RL, Guiltinan MJ, Tyler BM, Meinhardt LW, Bailey BA. Phytophthora megakarya and Phytophthora palmivora, closely related causal agents of cacao black pod rot, underwent increases in genome sizes and gene numbers by different mechanisms. Genome Biology and Evolution 2017; 9(3): 536-57

[11] Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, Batut P, Chaisson M, Gingeras TR. STAR: ultrafast universal RNA-seq aligner. Bioinformatics 2013; 29(1): 15-21

[12] Liao Y, Smyth GK, Shi W. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics 2014; 30(7): 923-30

[13] Robinson MD, McCarthy DJ and Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics 2010; 26(1): 139-140

[14] McCarthy JD, Chen Y, Smyth GK. Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. Nucleic Acids Research 2012; 40(10): 4288-4297

[15] Lex A, Gehlenborg N, Strobelt H, Vuillemot R, Pfister H. UpSet: Visualization of Intersecting Sets, IEEE Transactions on Visualization and Computer Graphics (InfoVis '14), vol. 20, no. 12, pp. 1983–1992, 2014. doi:10.1109/TVCG.2014.2346248