New Phytologist

***New Phytologist* Supporting Information**

Article title: **Induced ligno-suberin vascular coating and tyramine-derived hydroxycinnamic acid amides restrict *Ralstonia solanacearum* colonization in resistant tomato**

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The following Supporting Information is available for this article:

Figure S1: Tissue used for analysis and bacterial dynamics.

Figure S2: H7996 plants show mild symptoms upon challenge inoculation of *R. solanacearum.*

Figure S3: *R. solanacearum*-induced xylem vascular ferulic acid deposition occurs in resistant H7996, but not in susceptible Marmande.

Figure S4: Expression of suberin biosynthetic genes in xylem vasculature of taproots upon infection of *R. solanacearum*.

Figure S5: Phylogeny of Feruloyl transferase (FHT) orthologues in different plant species and expression of the putative tomato FHT ortholog in response to *Ralstonia solanacearum* infection.

Figure S6: Phylogeny of tyramine hydroxycinnamoyl transferase (THT) orthologues in different plant species and expression of the tomato THT gene family members in response to *R. solanacearum* infection.

Figure S7: Expression of phenylpropanoid pathway genes in xylem vasculature of taproots upon invasion of *R. solanacearum*.

Figure S8: Immunoblot of *35S::SlFHT-HA* in independent Marmande tomato lines expressing *35S::SlFHT-HA* (Marmande).

Figure S9: Fresh weight of *35S::SlFHT-HA* plants.

Figure S10: Fresh weight of *35S::SlTHT1-3* plants.

Figure S11: Overexpression of *SlTHT1-3* in tomato results in restricted colonization by *R. solanacearum*.

Table S1: List of primers used in this study.

Table S2: Assignments of the correlation signals in the 2D HSQC spectra.

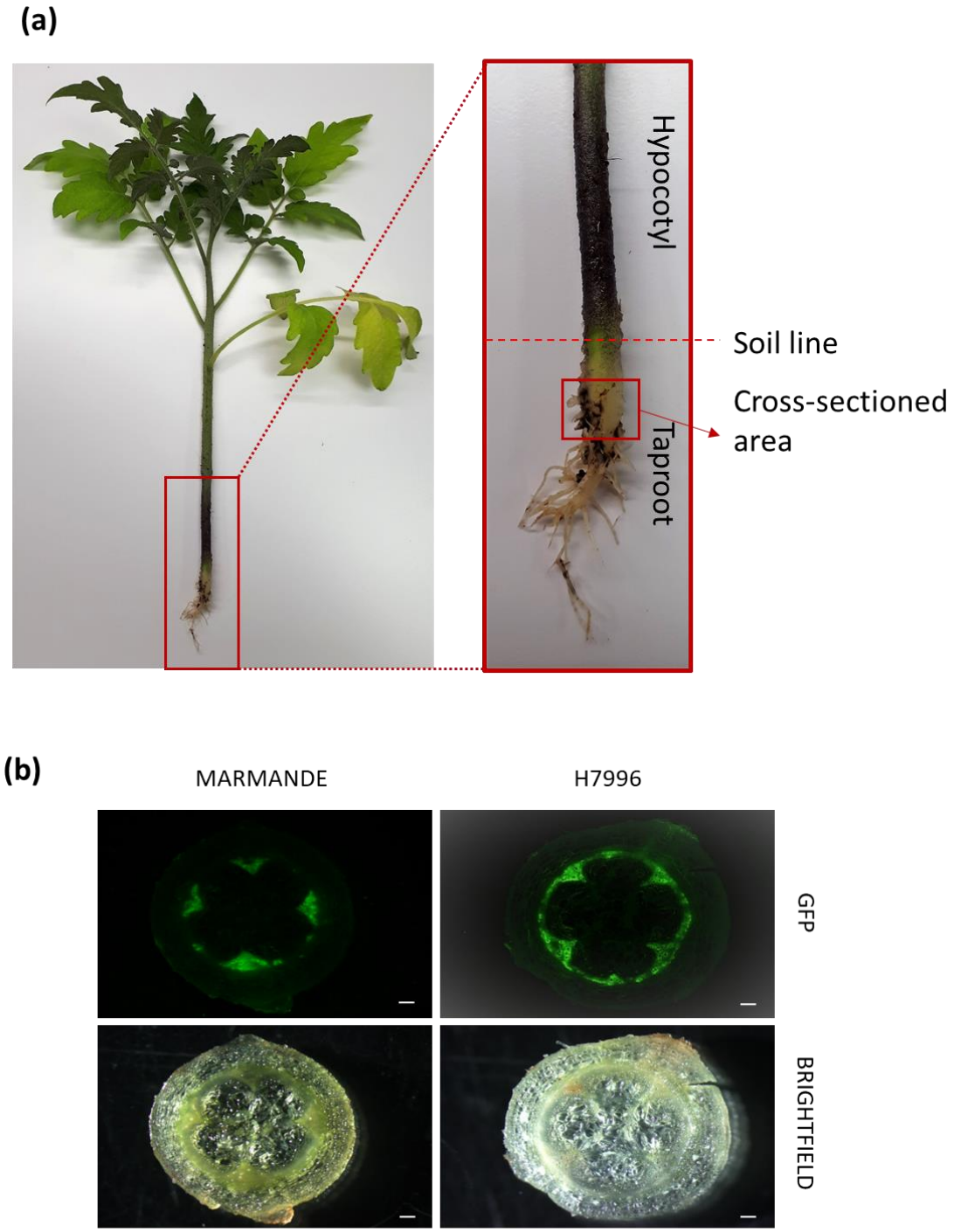

Fig. S1 Tissue used for analysis and bacterial dynamics. (a) A picture of a tomato plant is shown, highlighting in red the selected region for all cross-sections used in this work, both for histological methods and molecular analysis. The transition zone between the taproot and the hypocotyl, down the soil line, was chosen because of their implications on *R. solanacearum*-

tomato interactions, as discussed in the manuscript. **(b)** Plants (4–5 weeks old) of the susceptible variety Marmande and the resistant variety H7996 were inoculated with ~$1x10^7$ CFU/ml of a fluorescent *R. solanacearum* strain by soil drenching. Cross-sections of the taproot-to-hypocotyl area containing 10^5 CFU g^{-1} of *R. solanacearum* were obtained and photographed with a fluorescence stereomicroscope under brightfield and UV light. Images from a representative experiment out of 3 with n=5 plants per cultivar. Scale bar = 500 µm.

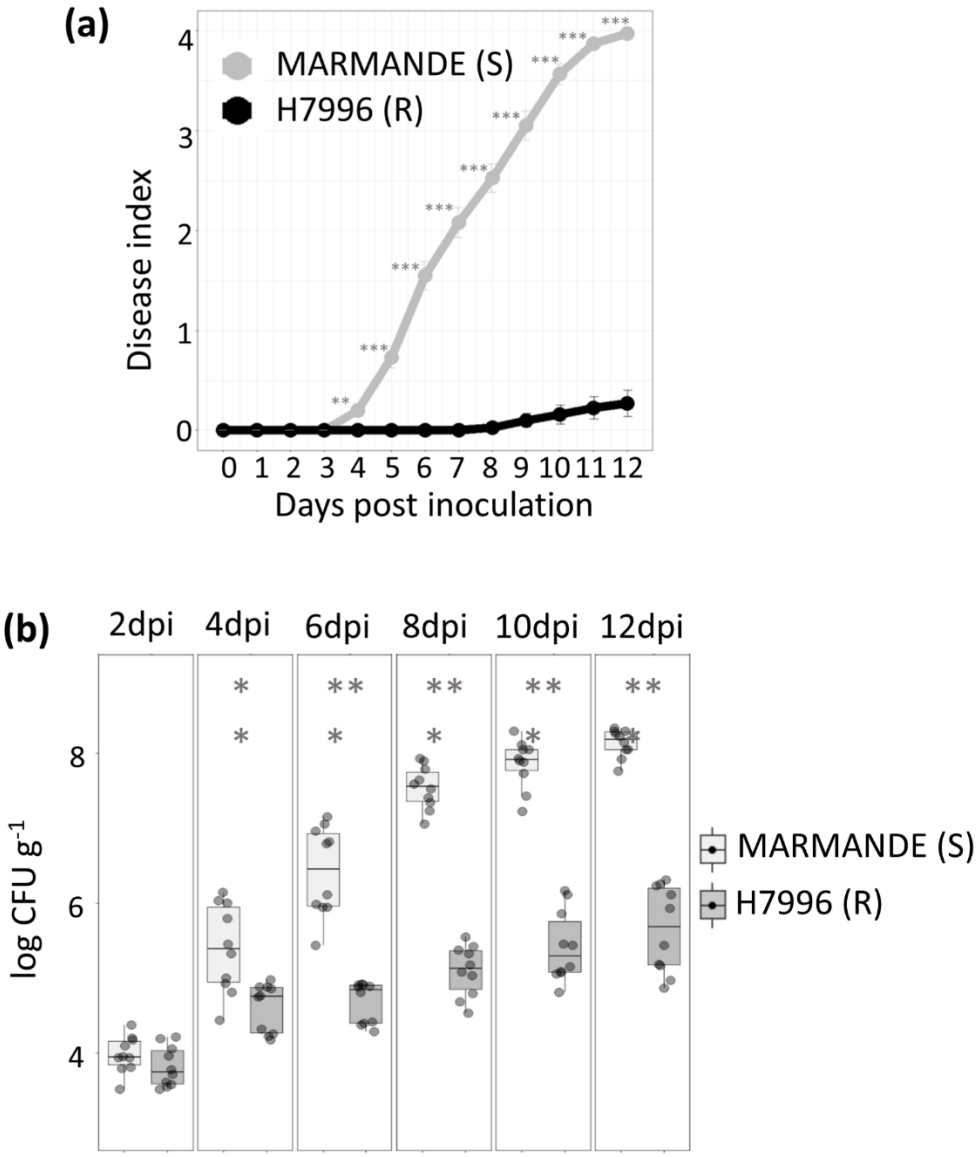

Fig. S2 H7996 plants show mild symptoms upon challenge inoculation of *R. solanacearum*. Susceptible (Marmande) and resistant (H7996), 5-week-old tomato plants were inoculated through roots by soil-soak with ~1x10^{7} CFU/ml of *R. solanacearum* GMI1000 and incubated at 28°C. **(a)** Wilting progress was assayed in both cultivars by rating plants daily on a 0 to 4 disease index scale where 0 = healthy and 4 =100% wilted. Data presented are means ± SE of a representative experiment with n=20 plants for each cultivar, out of a total of 3 experiments. **(b)** The level of in planta colonization by *R. solanacearum* was calculated as colony forming units per gram of fresh taproot tissue (CFU·g $^{-1}$) at the indicated days post-infection (dpi). Data presented are of a

representative experiment with n=10 plants for each time point each cultivar out of a total of 3 experiments. Asterisks indicate statistically significant difference between Marmande and H7996 in a paired Student´s t-test (** p-value of $p < 0.01$ and *** p-value of $p < 0.001$). Supports Figure 1 of the main manuscript.

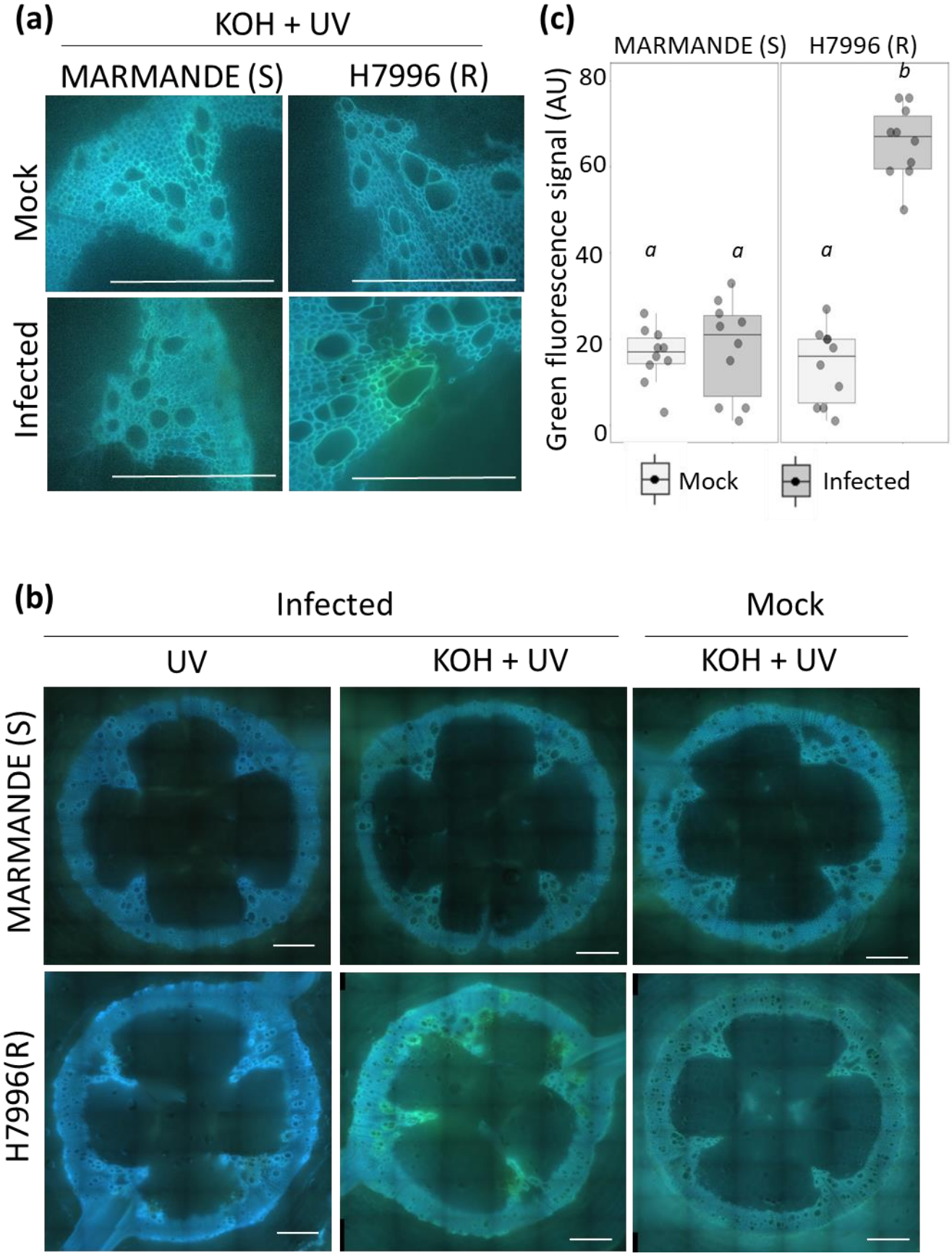
(a)
KOH + UV
MARMANDE (S)
H7996 (R)
Mock
Infected
(c)
MARMANDE (S)
H7996 (R)
Green fluorescence signal (AU)
80
60
40
20
0
a
a
a
b
Mock
Infected
(b)
Infected
Mock
UV
KOH + UV
KOH + UV
MARMANDE (S)
H7996(R)

Fig. S3 *R. solanacearum*-induced xylem vascular ferulic acid deposition occurs in resistant H7996, but not in susceptible Marmande. Cell wall-bound ferulic acid can be detected by emission of a blue fluorescence with UV excitation at neutral pH, which characteristically changes to stronger green emission under conditions of high pH such as in the presence of alkali. Five-week-old Marmande and H7996 plants were inoculated with ~$1x10^7$ CFU/ml of *R. solanacearum* GMI1000 and incubated at 28°C. Taproot cross-sections were obtained at 9 dpi **(a)** or in plants containing a bacterial load of approximately 10^5 CFU g^{-1} of *R. solanacearum* **(b, c)**. **(a)** Autofluorescence emitted from taproot cross-section from mock-treated and infected Marmande and H7996 plants was visualized at 9 dpi under UV before and after treatment with KOH alkali (high pH above 10). In infected H7996 a green/turquoise color appears in vessel walls and surrounding xylem parenchyma cells, indicative of ferulic acid deposition in the cell walls. Scale bars = 500 µm. **(b)** The same as in (a) but cross-sections were obtained from plants containing a bacterial load of approximately 10^5 CFU g^{-1} of *R. solanacearum.* Scale bars = 500 µm. **(c)** Green fluorescence from ferulate deposits in the xylem and surrounding parenchyma cells was measured using ImageJ. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Plots show data from a single representative experiment (n =6) out of a total of 3. Different letters indicate statistically significant differences (α=0.05, Fisher's least significant difference test). Supports Figure 4 of the main manuscript.

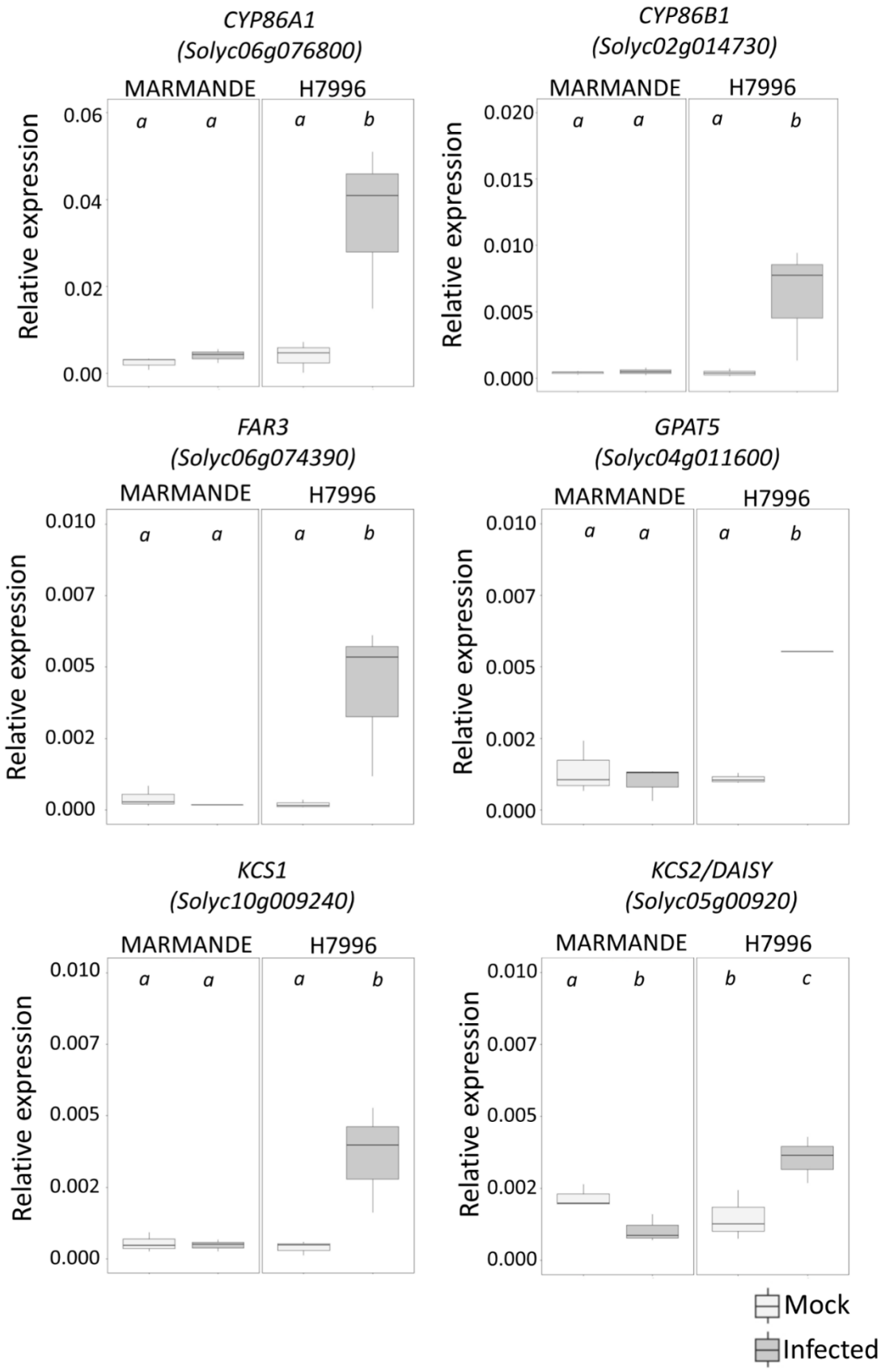
CYP86A1
(Solyc06g076800)
MARMANDE
H7996
Relative expression
0.06
0.04
0.02
0.00
a
a
a
b
CYP86B1
(Solyc02g014730)
MARMANDE
H7996
Relative expression
0.020
0.015
0.010
0.005
0.000
a
a
a
b
FAR3
(Solyc06g074390)
MARMANDE
H7996
Relative expression
0.010
0.007
0.005
0.002
0.000
a
a
a
b
GPAT5
(Solyc04g011600)
MARMANDE
H7996
Relative expression
0.010
0.007
0.005
0.002
0.000
a
a
a
b
KCS1
(Solyc10g009240)
MARMANDE
H7996
Relative expression
0.010
0.007
0.005
0.002
0.000
a
a
a
b
KCS2/DAISY
(Solyc05g00920)
MARMANDE
H7996
Relative expression
0.010
0.007
0.005
0.002
0.000
a
b
b
c
Mock
Infected

Fig. S4 Expression of suberin biosynthetic genes in xylem vasculature of taproots upon infection of *R. solanacearum*. Expression levels of tomato putative orthologs of the suberin fatty acid pathway were analyzed by qPCR in H7996 and Marmande plants infected with *R. solanacearum* or mock-treated. Xylem vascular tissue comprising of metaxylems and surrounding parenchyma cells was collected from infected plants with a *R. solanacearum* inoculum of 10^5 CFU g^{-1} in the taproot or mock-inoculated plants of a similar age. Relative expression values were calculated using the Elongation Factor 1 alpha (eEF1 α) gene as reference. Three biological replicates (n=3) were used, and taproots of 6 plants were used in each replicate. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters indicate statistically significant differences (α=0.05, Fisher's least significant difference test). Supports Figure 5 of the main manuscript.


(a)
Eucgr.H03354
Gorai.011G088000
Gorai.012G084200
Lus10012552.g
Brara.G01504
Brara.D01116
Thhalv10027756m.g
Bostr.7200s0122
Cagra.1914s0020
Carubv10004701m.g
AT5G41040
AL7G48510
Araha.31350s0002
Ciclev10015302m.g
orange1.1g013997m.g
Potri.001G326300
MDP0000258308
Kaladp0006s0052
Kalax.0949s0007
Kalax.0347s0007
Kaladp0056s0026
Kalax.0226s0029
Lus10032554.g
Lus10043189.g
PGSC0003DMG400031731
Solyc03g097500.2
Cucsa.157160
Ciclev10031592m.g
orange1.1g014029m.g
Gorai.003G119000
evm.TU.supercontig_989.1
Potri.015G100800
Manes.06G122500
Manes.14G048500
Medtr3g098980
Tp57577_TGAC_v2_gene35261
Phvul.009G162300
Glyma.04G198000
Glyma.06G167600
gene06484-v1.0-hybrid
Prupe.5G147300
MDP0000312405
MDP0000370643
Eucgr.B00086
Aqcoe3G161400
GRMZM2G034360
Migut.I00559
Zosma27g00520
evm_27.TU.AmTr_v1.0_scaffold00016.187
0.2
(b)
SlFHT
(Solyc03g097500)
MARMANDE
H7996
Relative expression
Mock
Infected

Fig. S5 Phylogeny of Feruloyl transferase (*FHT*) orthologues in different plant species and expression of the putative tomato *FHT* ortholog in response to *Ralstonia solanacearum* infection. (a) Protein homologs of potato *FHT* gene (*PGSC0003DMG400031731*) were obtained from www.phytozome.jgi.doe.gov and matches with more than 80 % similarity were used for phylogenetic analysis using www.phylogeny.fr. **(b)** Gene expression of the putative tomato *FHT* ortholog (*Solyc03g097500*) was analyzed by qPCR. Relative expression levels were calculated using the Elongation Factor 1 alpha (*eEF1 α, Solyc06g005060*) as the reference gene. H7996 and Marmande plants, containing a *R. solanacearum* inoculum of 10^5 CFU g^{-1} in the taproot were selected. Xylem vascular tissue, comprising of metaxylems and surrounding parenchyma cells was collected from taproots for RNA extraction and cDNA synthesis. Similarly, xylem tissue was collected from Marmande mock plants and H7996 mock plants. Three biological replicates (n=3) were used, and taproots of 6 plants were used in each replicate. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters indicate statistically significant differences (α=0.05, Fisher's least significant difference test). Supports Figure 5 of the main manuscript.

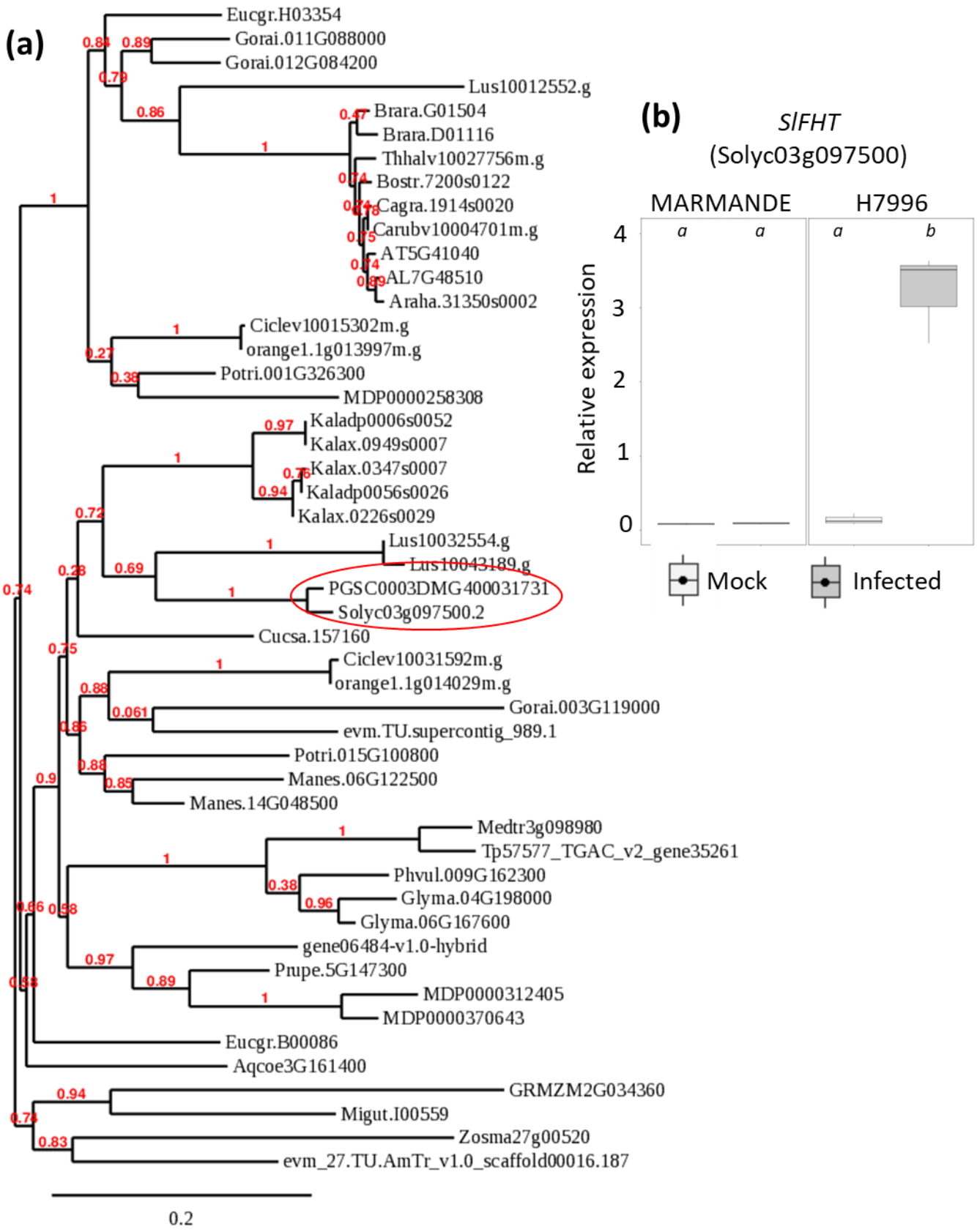
(a)
Eucgr.H03354
Gorai.011G088000
Gorai.012G084200
Lus10012552.g
Brara.G01504
Brara.D01116
Thhalv10027756m.g
Bostr.7200s0122
Cagra.1914s0020
Carubv10004701m.g
AT5G41040
AL7G48510
Araha.31350s0002
Ciclev10015302m.g
orange1.1g013997m.g
Potri.001G326300
MDP0000258308
Kaladp0006s0052
Kalax.0949s0007
Kalax.0347s0007
Kaladp0056s0026
Kalax.0226s0029
Lus10032554.g
Lus10043189.g
PGSC0003DMG400031731
Solyc03g097500.2
Cucsa.157160
Ciclev10031592m.g
orange1.1g014029m.g
Gorai.003G119000
evm.TU.supercontig_989.1
Potri.015G100800
Manes.06G122500
Manes.14G048500
Medtr3g098980
Tp57577_TGAC_v2_gene35261
Phvul.009G162300
Glyma.04G198000
Glyma.06G167600
gene06484-v1.0-hybrid
Prupe.5G147300
MDP0000312405
MDP0000370643
Eucgr.B00086
Aqcoe3G161400
GRMZM2G034360
Migut.I00559
Zosma27g00520
evm_27.TU.AmTr_v1.0_scaffold00016.187
0.2
(b)
SlFHT
(Solyc03g097500)
MARMANDE
H7996
Relative expression
Mock
Infected

Fig. S6 Phylogeny of tyramine hydroxycinnamoyl transferase (*THT*) orthologues in different plant species and expression of the tomato *THT* gene family members in response to *R. solanacearum* infection. (a) Protein homologs of tomato *THT1-3* gene (*Solyc08g068730*) were obtained from www.phytozome.jgi.doe.gov and matches with more than 60 % similarity were used for phylogenetic analysis using the webpage www.phylogeny.fr. **(b)** Gene expression of the tomato *THT* gene family members was analyzed by qPCR. Relative expression levels were calculated using the Elongation Factor 1 alpha (*eEF1 α, Solyc06g005060*) as the reference gene. H7996 and Marmande plants, containing a *R. solanacearum* inoculum of 10^5 CFU g^{-1} in the taproot were selected. Xylem vascular tissue, comprising of metaxylems and surrounding parenchyma cells was collected from taproots for RNA extraction and cDNA synthesis. Similarly, xylem tissue was collected from Marmande mock plants and H7996 mock plants. Three biological replicates (n=3) were used, and taproots of 6 plants were used in each replicate. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters indicate statistically significant differences (α=0.05, Fisher's least significant difference test). Supports Figure 5 of the main manuscript.

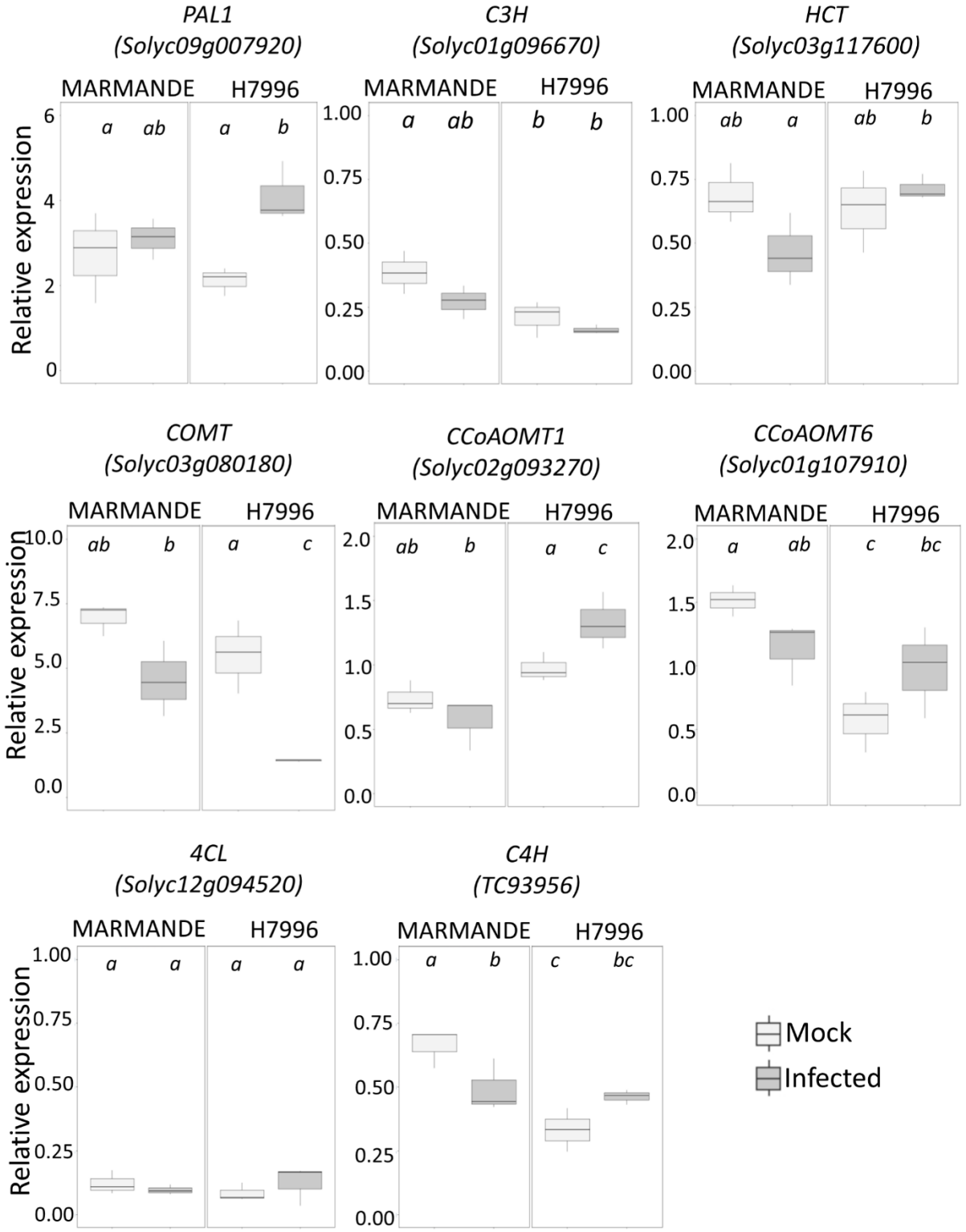
PAL1
(Solyc09g007920)
C3H
(Solyc01g096670)
HCT
(Solyc03g117600)
COMT
(Solyc03g080180)
CCoAOMT1
(Solyc02g093270)
CCoAOMT6
(Solyc01g107910)
4CL
(Solyc12g094520)
C4H
(TC93956)
MARMANDE
H7996
Relative expression
Mock
Infected

Fig. S7 Expression of phenylpropanoid pathway genes in xylem vasculature of taproots upon invasion of *R. solanacearum*. Expression levels of tomato putative orthologs of the phenylpropanoid pathway were analyzed by qPCR in H7996 and Marmande plants infected with *R. solanacearum* or mock-treated. Xylem vascular tissue comprising of metaxylems and surrounding parenchyma cells was collected from infected plants with a *R. solanacearum* inoculum of 10^5 CFU g^{-1} in the taproot or mock-inoculated plants of a similar age. Relative expression values were calculated using the Elongation Factor 1 alpha (*eEF1 α*) gene as reference. Three biological replicates (n=3) were used, and taproots of 6 plants were used in each replicate. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters indicate statistically significant differences (α=0.05, Fisher's least significant difference test). Supports Figure 5 of the main manuscript.

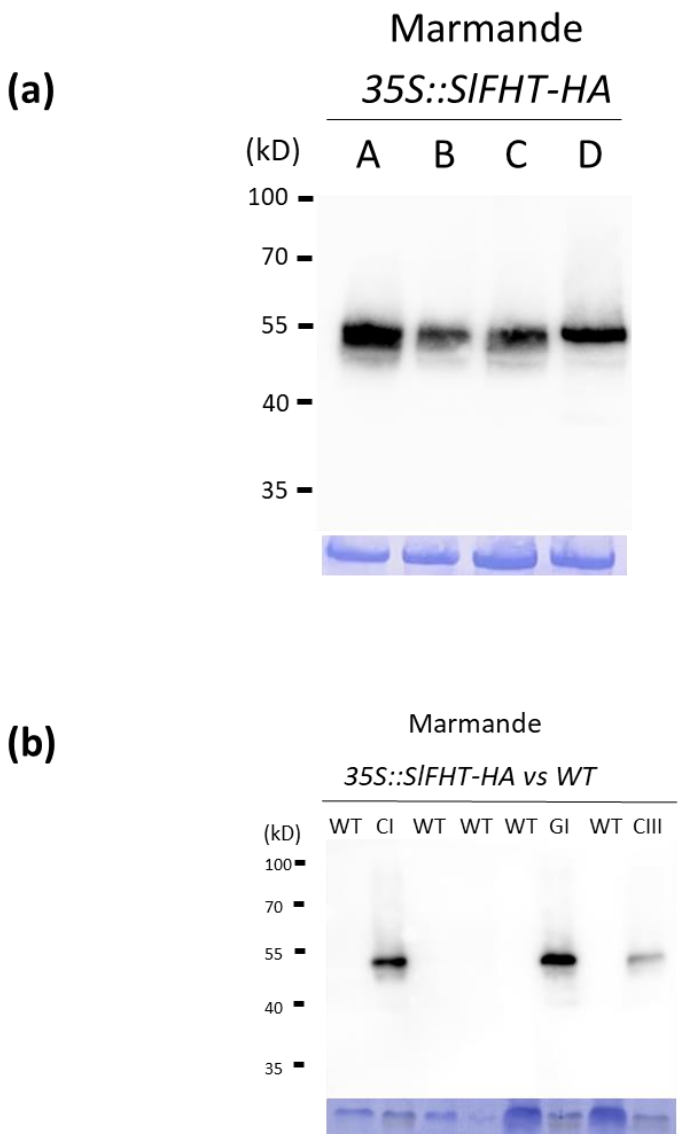

Fig. S8 Immunoblots of SlFHT-HA in independent Marmande tomato lines expressing *35S::SlFHT-HA*. Immunoblots using anti-HA antibody showing SlFHT-HA protein (predicted protein size: 49kDa) levels of independent transgenic lines stably overexpressing *SlFHT-HA* on a susceptible Marmande background (*35S::SlFHT-HA*). **(a)** Independent lines A, B, C and D. **(b)** Independent lines C (siblings CI and CIII) and G. Several wild-type Marmande are included as a control (WT lanes), to ensure specificity of the observed band. Coomasie blue staining showing similar protein load in all the lanes are included.

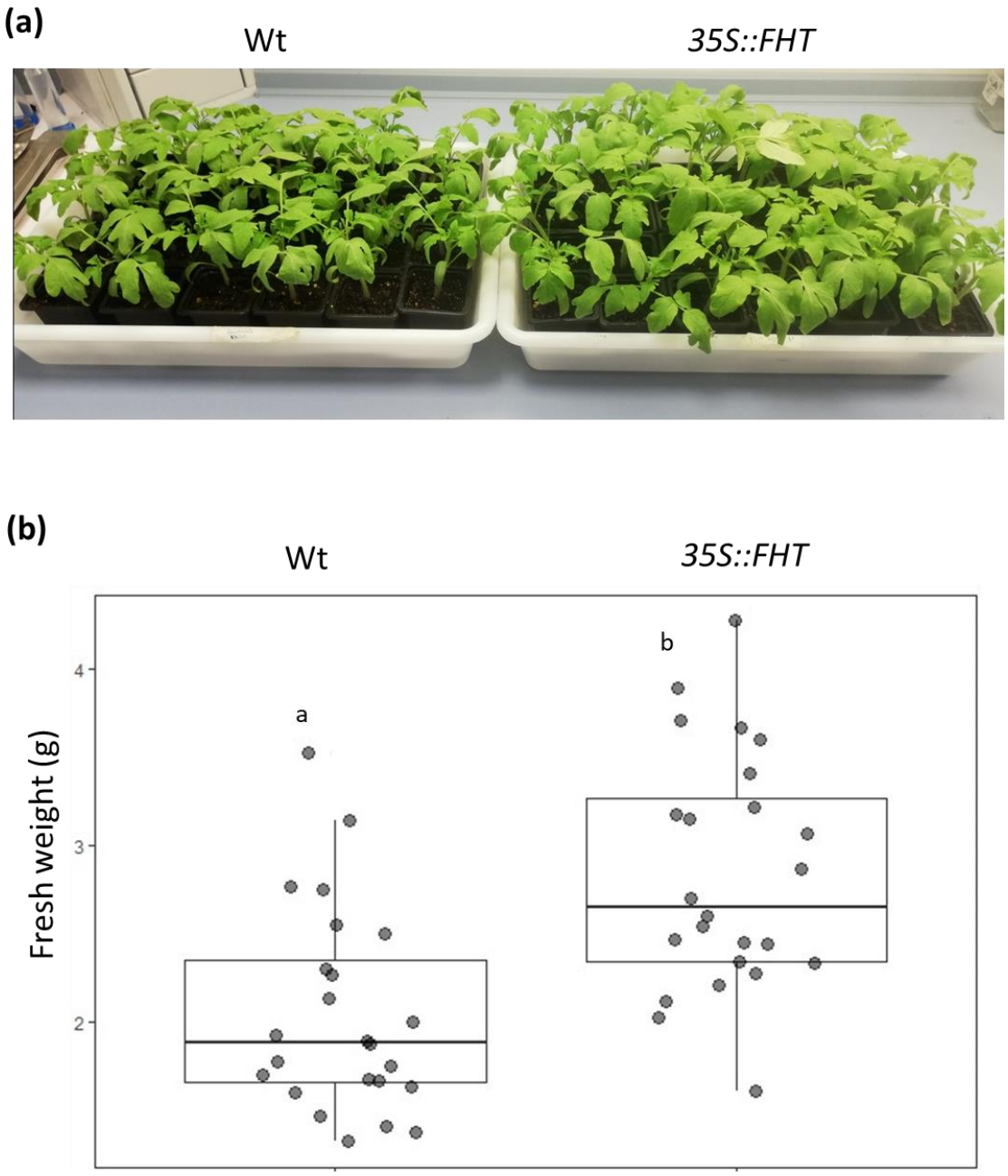

Fig. S9 Fresh weight of *35S::SlFHT-HA* plants. (a) Photographs of Wt Marmande and transgenic *35S::FHT-HA* plants were taken 3 weeks after germination. **(b)** Fresh weight was measured at this point. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters represent statistically significant differences (α=0.05, Fisher's least significant difference test).

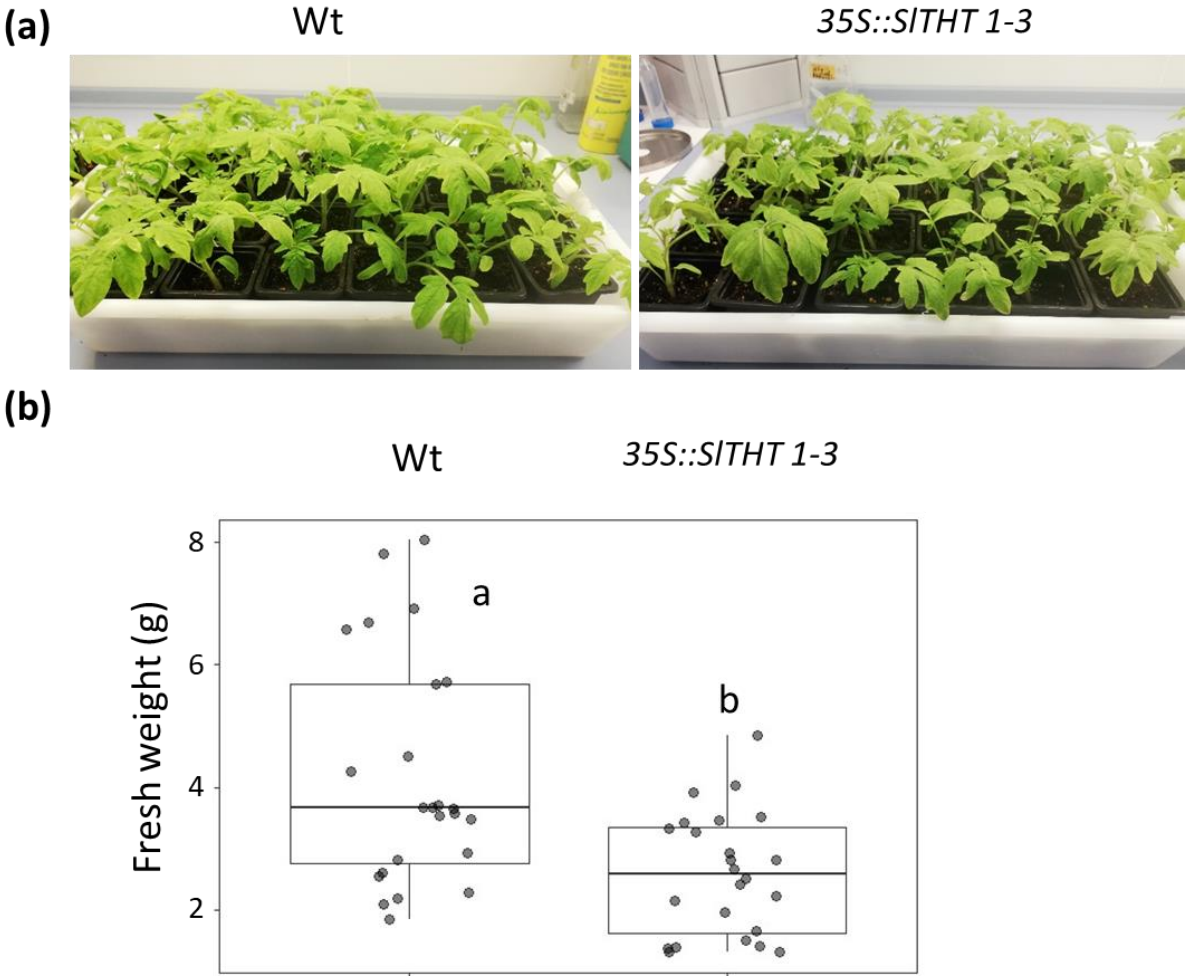

Fig. S10 Fresh weight of *35S::SlTHT1-3* plants. (a) Photographs of Wt Marmande and transgenic *35S::THT-1-3* plants were taken 3 weeks after germination. **(b)** Fresh weight was measured at this point. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Different letters represent statistically significant differences (α=0.05, Fisher's least significant difference test).

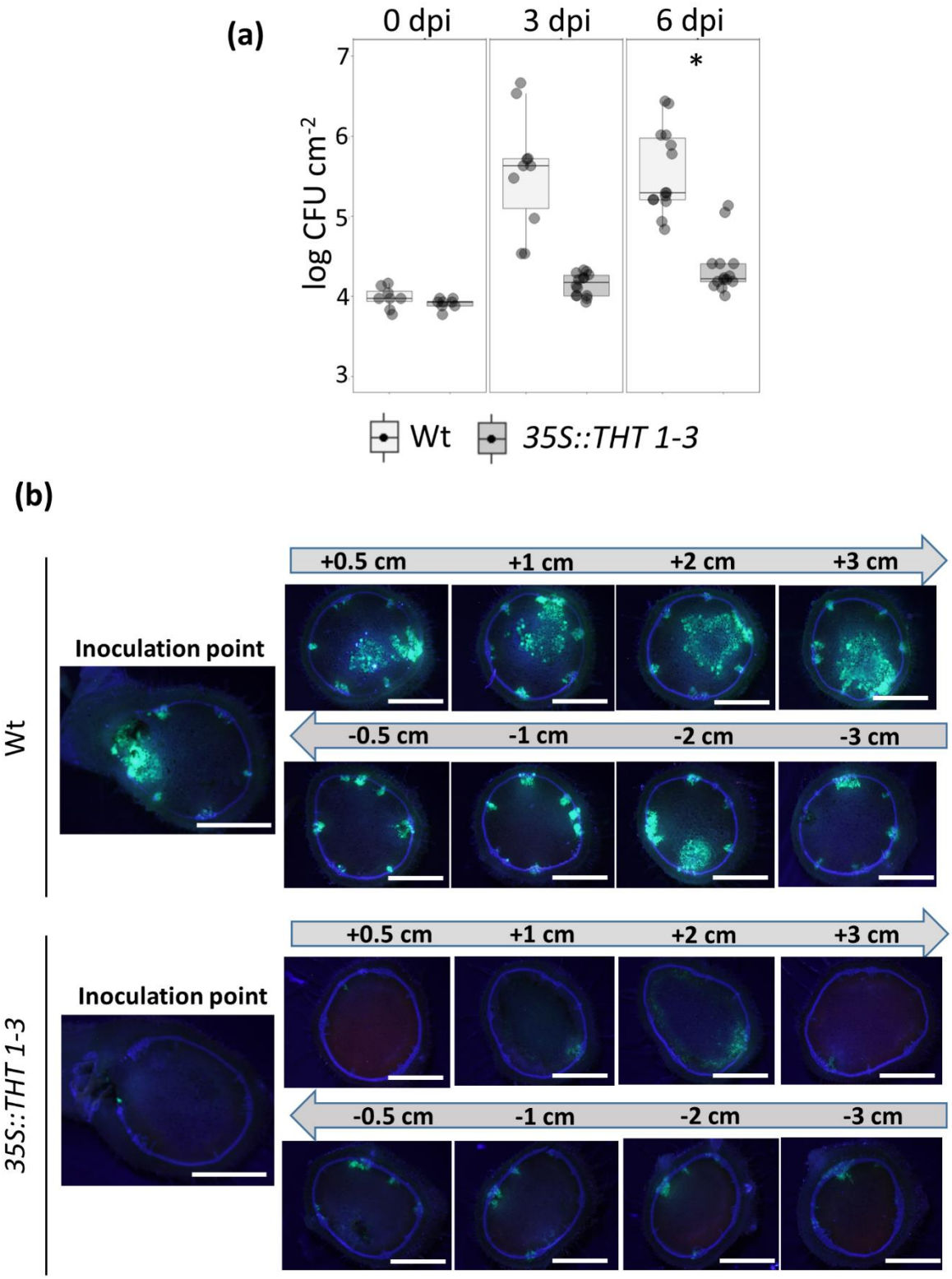
(a)
0 dpi
3 dpi
6 dpi
log CFU cm-2
7
6
5
4
3
*
Wt
35S::THT 1-3
(b)
Wt
Inoculation point
+0.5 cm
+1 cm
+2 cm
+3 cm
-0.5 cm
-1 cm
-2 cm
-3 cm
35S::THT 1-3
Inoculation point
+0.5 cm
+1 cm
+2 cm
+3 cm
-0.5 cm
-1 cm
-2 cm
-3 cm

Fig. S11 Overexpression of *SlTHT1-3* in tomato results in restricted colonization by *R. solanacearum*. (a) Growth of *R. solanacearum* GMI1000 in planta was monitored in leaves of *35S::THT1-3* transgenic plant compared with Wt Moneymaker tomato lines over time. The bacterium was vacuum infiltrated into the leaves at a concentration of ~$1x10^5$ CFU/ml and growth was recorded at 0, 3 and 6 dpi. Data are represented with box and whiskers plots: whiskers indicate variability outside the upper and lower quartiles and boxes indicate second quartile, median and third quartile. Plots show data of 6 to 8 independent plants (n=6-8) from a representative experiment out of 3. Asterisk indicates statistically significant difference between Wt and overexpression line in a paired Student´s t-test (* corresponds to p-value of $p < 0.05$). **(b)** Representative images of tomato stem cross-sections showing colonization by the *R. solanacearum* GMI1000 GFP reporter strain at 6 dpi. *R. solanacearum* was directly injected into the xylem vasculature of the first internode through the petiole at a concentration of 10^5 CFU ml^{-1}. Colonization progress was analyzed at the point of inoculation, at higher (+0.5, +1, +2 and +3 cm) and lower -0.5, -1, -2 and -3 cm) sections. Images from a representative experiment out of 3 with *n*=5 plants each. Scale bar = 2 mm. Supports Figure 7 of the main manuscript.

Table S1 List of primers used for cloning and qPCR analysis

Gene	Gene ID	Primers	Sequence	Usage	Origin
FHT	Solyc03g097500	part7FHTF1	GGCCCGGGATGGAGAATGGTAAACACAGTGTTGC	Cloning	This paper
		part7FHTHAR1	GGGGATCCTTAAGCGTAGTCTGGGACGTCGTATGGGTAGATCTCCATAAGTTCCTC		
FHT	Solyc03g097500	qSlFHT F1	GGTGGCTCAGGTGACAAAGT	qPCR	This paper
		qSlFHT R1	CCTCTCGCAATTTCACCCCA		
THT 1-3	Solyc08g068730	qTHT1-3F1	CCCCTTTTGACGAACCTAAA	qPCR	(Campos *et al.*, 2014)
		qTHT1-3R1	TTTGGATCGGAATTCCTCAA		
EF	Solyc06g005060	qeEF1αF1	CCACCTCGAGATCCTAATGG	qPCR	(Campos *et al.*, 2014)
		qeEF1αR1	ACCCTCACGTATGCTTCCAG		
PAL1	Solyc09g007920	qSlPAL1 F1	TACGTGTTTGCCTATGCTGATG	qPCR	(Rahim *et al.*, 2019)
		qSlPAL1 R1	CGGCCTTTAATTCGTCCTC		
COMT	Solyc03g080180	qSlCOMT F1	GGTGGTGGAACAGGGGCTACT	qPCR	(Rahim *et al.*, 2019)
		qSlCOMT R1	TAAACAATGCTCATCGCTCCAATC		
CCoAOMT1	Solyc02g093270	qSlCCOAOMT1 F1	GAGAGCCTGAAGCCATGAAAGAGC	qPCR	(Rahim *et al.*, 2019)
		qSlCCOAOMT1 R1	GAGCCATGGCAGTAGCAAGCAGAG		
CCoAOMT6	Solyc01g107910	qSlCCOAOMT6 F1	ATTTTCGAGAGGGCCCTGCTTTAC	qPCR	(Rahim *et al.*, 2019)
		qSlCCOAOMT6 R1	ATCCGATCACACCACCAACTTTCA		
HCT	Solyc03g117600	qSlHCT F1	CCCTCCTCCGTGCTCGTGA	qPCR	(Rahim *et al.*, 2019)
		qSlHCT R1	CCCGGGTTAGTTTGAAGATTGACA		
C3H	Solyc01g096670	qSlC3H F1	CTGCAATGCGTGGCCAAGGAAGC	qPCR	(Rahim *et al.*, 2019)
		qSlC3H R1	TCGCGAGCAACAGCCCAGACATT		
4CL	Solyc12g094520	qSL4CL F1	CGA GCA TGG AAG GGA AAA TTG	qPCR	(Rigano *et al.*, 2016)
		qSL4CL R1	TCA GAG TCT AGA GTG GAA GCA G		
C4H	TC93956	qSlC4H F1	CTAGCTAACAACCCCGCCCA	qPCR	(Zhang *et al.*, 2019)
		qSlC4H R1	AACTCCTCCTGCCAACACCG		
THT 7-8	Solyc08g068780	qSLTHT 7-8 F1	GGAAACTGATAAGGAGAAGGTGG	qPCR	This paper
		qSLTHT 7-8 R1	GTTTGCACGGCGTATGGAG		
THT like 4	Solyc08g068710	qSLTHT4 F1	AGTTTAGGTATGGCAAATTGCATGG	qPCR	This paper
		qSLTHT4 R1	AAGAAAACACACAGTAGCTAACAGC		
THT like 5	Solyc08g068690	qSLTHT6 F1	TCAGTCGATGGAATAGTAGCAGTT	qPCR	This paper
		qSLTHT6 R1	TCCTCAATTTCCCCCTTGTTATG		
CYP86A1	Solyc06g076800	qSlCYP86A1 F1	GGTCTACTGGTGTATCCGCA	qPCR	This paper
		qSlCYP86A1 R1	CCTTTAGGATAGTTATCGAACCTGG		
KCS1	Solyc10g009240	qSlKCS1 F1	GTCGTAGGGGTGTCACTAGC	qPCR	This paper
		qSlKCS1 R1	GTCATGAAAAACCTGAATTGCTCAG		
GPAT5	Solyc04g011600	qSlGPAT5 F2	CCCTAGGCCAATGTATGAGGTAAC	qPCR	This paper
		qSlGPAT5 R2	GTTGCTGCCAAAATCCTCTGG		
DAISY/KCS2	Solyc05g009280	qDAISY F1	TCCGAGTTCATCCCAAGTCG	qPCR	This paper
		qDAISY R1	AACAGTATGGCTGCACCTCC		
FAR3	Solyc06g074390	qSlFAR3 F1	TGGTGCTACTGGATTTCTTGC	qPCR	This paper
		qSlFAR3 R1	TGCCACAGCCTCATTGTTGA		
THT 7-1	Solyc08g068700	qSlTHT7-1 F1	GCTTGAACGCTTGGTTAGTGG	qPCR	This paper
		qSlTHT7-1 R1	AGTCCTCCTTAGAGGGCTTGC		
CY986B1	Solyc02g014730	qSlCYP86B1 F1	TCCGTTGATTTTCAAGCCAGC	qPCR	This paper
		qSlCYP86B1 R1	TCGTCTTCAACAACCTCTTTGTG		

Table S2 Assignments of the correlation signals in the 2D HSQC spectra.

Label	δ_C/δ_H (ppm)	Assignment
Ty_7	34.2/2.62	C_7/H_7 in amides of tyramine (**Ty**)
Ty_8	40.5/3.29	C_8/H_8 in amides of tyramine (**Ty**)
B_β	53.3/3.43	C_β/H_β in phenylcoumarans (**B**)
C_β	53.5/3.05	C_β/H_β in β–β´resinols (**C**)
MeO	55.3/3.72	C/H in aromatic methoxy group
A_γ	59.7/3.23, 3.58	C_γ/H_γ in β–*O*–4´ alkyl-aryl ethers (**A**)
I_γ	61.5/4.06	C_γ/H_γ in cinnamyl alcohol end-groups (**I**)
B_γ	62.6/3.70	C_γ/H_γ in phenylcoumarans (**B**)
C_γ	71.1/3.80, 4.17	C_γ/H_γ in β–β´resinols (**B**)
A_α	71.3/4.79	C_α/H_α in β–*O*–4′ alkyl-aryl ethers (**A**)
$A_{\beta G}$	83.9/4.27	C_β/H_β in β–*O*–4′ alkyl-aryl ethers (**A**) linked to a G unit
C_α	84.9/4.67	C_α/H_α in β–β´resinols (**C**)
$A_{\beta S}$	83.6/4.28	C_β/H_β in β–*O*–4′ alkyl-aryl ethers (**A**) linked to a S unit
B_α	86.9/5.45	C_α/H_α in phenylcoumarans (**B**)
$S_{2,6}$	104.0/6.68	C_2/H_2 and C_6/H_6 in syringyl units (**S**)
$S'_{2,6}$	106.3/7.29	C_2/H_2 and C_6/H_6 in Cα-oxidized syringyl units (**S′**)
G_2	111.1/6.97	C_2/H_2 in guaiacyl units (**G**)
$Ty_{3,5}$	114.8/6.64	C_3/H_3 and C_5/H_5 in amides of tyramine (**Ty**)
$G_{5/6}$	114.9/6.79	C_5/H_5 and C_6/H_6 in guaiacyl units (**G**)
G_6	119.0/6.76	C_6/H_6 in guaiacyl units (**G**)
I_β	128.2/6.21	C_β/H_β in cinnamyl alcohol end-groups (**I**)
I_α	128.6/6.43	C_α/H_α in cinnamyl alcohol end-groups (**I**)
$Ty_{2,6}$	129.3/6.92	C_2/H_2 and C_6/H_6 in amides of tyramine (**Ty**)
U_F	129.4/5.31	-CH=CH- in unsaturated fatty acid structures (**U_F**)
FAm_7	138.6/7.31	C_7/H_7 in feruloyl amides (**FAm**)

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