

Supplementary Tables

Table S1. Overview of the total number of clean reads generated after filtering and the read mapping rates to *S. lycopersicum* and *S. indica* genome. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants

Samples	Total clean reads	Mapped to <i>S. lycopersicum</i> genome ^a	Mapped to <i>S. indica</i> genome ^b	Mapping rate to <i>S. lycopersicum</i> gene models ^c
RC1	38227240	35487214 (92.83%)	244 (0%)	83.94%
RC2	47270758	43673880 (92.39%)	8 (0%)	83.96%
RC3	41130072	37796991 (91.9%)	0 (0%)	82.07%
RC4	46475282	42823753 (92.14%)	0 (0%)	83.16%
RS1	45532784	40862604 (89.74%)	1195995 (2.63%)	80.68%
RS2	48436740	42962249 (88.7%)	1752964 (3.62%)	79.55%
RS3	46513138	41191437 (88.56%)	1575329 (3.39%)	80.13%
RS4	45271188	40389016 (89.22%)	1498744 (3.31%)	80.61%
LC1	46198574	42966834 (93%)	0 (0%)	86.83%
LC2	53771394	49928827 (92.85%)	0 (0%)	86.52%
LC3	41846030	39049561 (93.32%)	2 (0%)	86.1%
LC4	44246664	41039108 (92.75%)	0 (0%)	86.15%
LS1	51285910	47739147 (93.08%)	57168 (0.11%)	86.06%
LS2	49844254	46353638 (93%)	10252 (0.02%)	85.84%
LS3	47361048	44102554 (93.12%)	681 (0%)	86.2%
LS4	48618546	45273435 (93.12%)	2370 (0%)	86.22%

^a Mapping to *S. lycopersicum* genome (release41, Ensembl) was performed using TopHat2 [86] from Novogene Bioinformatics Technology Co. Ltd (Hong Kong). ^b Mapping to *S. indica* genome (JGI genome portal) was performed using Bowtie 2 [87] from Novogene Bioinformatics Technology Co. Ltd (Hong Kong). ^c Mapping to *S. lycopersicum* gene models (ITAG3.2, SolGenomics) was performed with Salmon version 0.12.0 [40]

Table S2. GO terms enriched in statistically up-regulated genes (≥ 2 -fold change) in leaves of tomato plants colonised by *S. indica*. Simulation corrected $P \leq 0.05$.

GO number	Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P-value
	unannotated	30 out of 391 genes, 7.7%	8 out of 34727 genes, 0.0%	<0.001
GO:0042254	ribosome biogenesis	48 out of 391 genes, 12.3%	1141 out of 34727 genes, 3.3%	<0.001
GO:0006364	rRNA processing	41 out of 391 genes, 10.5%	1027 out of 34727 genes, 3.0%	<0.001
GO:0016072	rRNA metabolic process	41 out of 391 genes, 10.5%	1048 out of 34727 genes, 3.0%	<0.001
GO:0009220	pyrimidine ribonucleotide biosynthetic process	21 out of 391 genes, 5.4%	272 out of 34727 genes, 0.8%	<0.001
GO:0009218	pyrimidine ribonucleotide metabolic process	21 out of 391 genes, 5.4%	283 out of 34727 genes, 0.8%	<0.001
GO:0022613	ribonucleoprotein complex biogenesis and assembly	52 out of 391 genes, 13.3%	1646 out of 34727 genes, 4.7%	<0.001
GO:0006221	pyrimidine nucleotide biosynthetic process	21 out of 391 genes, 5.4%	293 out of 34727 genes, 0.8%	<0.001
GO:0030490	maturation of SSU-rRNA	14 out of 391 genes, 3.6%	116 out of 34727 genes, 0.3%	<0.001
GO:0006220	pyrimidine nucleotide metabolic process	21 out of 391 genes, 5.4%	310 out of 34727 genes, 0.9%	<0.001
GO:0034470	ncRNA processing	43 out of 391 genes, 11.0%	1273 out of 34727 genes, 3.7%	<0.001
GO:0000478	endonucleolytic cleavages during rRNA processing	10 out of 391 genes, 2.6%	61 out of 34727 genes, 0.2%	<0.001
GO:0000469	cleavages during rRNA processing	11 out of 391 genes, 2.8%	85 out of 34727 genes, 0.2%	<0.001
GO:0034660	ncRNA metabolic process	43 out of 391 genes, 11.0%	1455 out of 34727 genes, 4.2%	<0.001
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	10 out of 391 genes, 2.6%	81 out of 34727 genes, 0.2%	<0.001
GO:0000480	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8 out of 391 genes, 2.0%	45 out of 34727 genes, 0.1%	<0.001
GO:0000472	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8 out of 391 genes, 2.0%	49 out of 34727 genes, 0.1%	<0.001
GO:0006606	protein import into nucleus	18 out of 391 genes, 4.6%	342 out of 34727 genes, 1.0%	<0.001
GO:0000967	rRNA 5'-end processing	8 out of 391 genes, 2.0%	52 out of 34727 genes, 0.1%	<0.001
GO:0034471	ncRNA 5'-end processing	8 out of 391 genes, 2.0%	52 out of 34727 genes, 0.1%	<0.001
GO:0000966	RNA 5'-end processing	8 out of 391 genes, 2.0%	56 out of 34727 genes, 0.2%	<0.001
GO:0051170	nuclear import	18 out of 391 genes, 4.6%	367 out of 34727 genes, 1.1%	<0.001
GO:0000479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8 out of 391 genes, 2.0%	57 out of 34727 genes, 0.2%	<0.001
GO:0006396	RNA processing	64 out of 391 genes, 16.4%	2972 out of 34727 genes, 8.6%	<0.001
GO:0009260	ribonucleotide biosynthetic process	21 out of 391 genes, 5.4%	511 out of 34727 genes, 1.5%	<0.001

GO:0009451	RNA modification	28 out of 391 genes, 7.2%	861 out of 34727 genes, 2.5%	0.002
GO:0051169	nuclear transport	24 out of 391 genes, 6.1%	688 out of 34727 genes, 2.0%	0.003
GO:0006913	nucleocytoplasmic transport	23 out of 391 genes, 5.9%	672 out of 34727 genes, 1.9%	0.005
GO:0009165	nucleotide biosynthetic process	29 out of 391 genes, 7.4%	1062 out of 34727 genes, 3.1%	0.019
GO:0016554	cytidine to uridine editing	9 out of 391 genes, 2.3%	142 out of 34727 genes, 0.4%	0.049

Table S3. GO terms enriched in statistically down-regulated genes (>2-fold change) in leaves of tomato plants colonised by *S. indica*. Simulation corrected $P \leq 0.05$.

GO number	Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P -value
	unannotated	36 out of 868 genes, 4.1%	3 out of 34727 genes, 0.0%	<0.001
GO:0003700	transcription factor activity	110 out of 868 genes, 12.7%	2215 out of 34727 genes, 6.4%	<0.001
GO:0016758	transferase activity, transferring hexosyl groups	49 out of 868 genes, 5.6%	655 out of 34727 genes, 1.9%	<0.001
GO:0035251	UDP-glucosyltransferase activity	32 out of 868 genes, 3.7%	316 out of 34727 genes, 0.9%	<0.001
GO:0046527	glucosyltransferase activity	32 out of 868 genes, 3.7%	333 out of 34727 genes, 1.0%	<0.001
GO:0047893	flavonol 3-O-glucosyltransferase activity	20 out of 868 genes, 2.3%	136 out of 34727 genes, 0.4%	<0.001
GO:0008194	UDP-glycosyltransferase activity	39 out of 868 genes, 4.5%	490 out of 34727 genes, 1.4%	<0.001
GO:0016757	transferase activity, transferring glycosyl groups	52 out of 868 genes, 6.0%	830 out of 34727 genes, 2.4%	<0.001
GO:0030528	transcription regulator activity	114 out of 868 genes, 13.1%	2579 out of 34727 genes, 7.4%	<0.001
GO:0050403	trans-zeatin O-beta-D-glucosyltransferase activity	16 out of 868 genes, 1.8%	106 out of 34727 genes, 0.3%	<0.001
GO:0050502	cis-zeatin O-beta-D-glucosyltransferase activity	11 out of 868 genes, 1.3%	56 out of 34727 genes, 0.2%	<0.001
GO:0008509	anion transmembrane transporter activity	28 out of 868 genes, 3.2%	378 out of 34727 genes, 1.1%	<0.001
GO:0015293	symporter activity	26 out of 868 genes, 3.0%	341 out of 34727 genes, 1.0%	<0.001
GO:0042937	tripeptide transporter activity	12 out of 868 genes, 1.4%	82 out of 34727 genes, 0.2%	<0.001
GO:0032795	heterotrimeric G-protein binding	5 out of 868 genes, 0.6%	9 out of 34727 genes, 0.0%	<0.001
GO:0042936	dipeptide transporter activity	12 out of 868 genes, 1.4%	84 out of 34727 genes, 0.2%	<0.001
GO:0015103	inorganic anion transmembrane transporter activity	20 out of 868 genes, 2.3%	233 out of 34727 genes, 0.7%	<0.001
GO:0016762	xyloglucan:xyloglucosyl transferase activity	8 out of 868 genes, 0.9%	38 out of 34727 genes, 0.1%	<0.001
GO:0015334	high affinity oligopeptide transporter activity	10 out of 868 genes, 1.2%	65 out of 34727 genes, 0.2%	0.001
GO:0015291	secondary active transmembrane transporter activity	34 out of 868 genes, 3.9%	594 out of 34727 genes, 1.7%	0.002
GO:0015198	oligopeptide transporter activity	12 out of 868 genes, 1.4%	103 out of 34727 genes, 0.3%	0.002
GO:0015197	peptide transporter activity	12 out of 868 genes, 1.4%	106 out of 34727 genes, 0.3%	0.008
GO:0004604	phosphoadenylyl-sulfate reductase (thioredoxin) activity	3 out of 868 genes, 0.3%	3 out of 34727 genes, 0.0%	0.013
GO:0009973	adenylyl-sulfate reductase activity	3 out of 868 genes, 0.3%	3 out of 34727 genes, 0.0%	0.013
GO:0033741	adenylyl-sulfate reductase (glutathione) activity	3 out of 868 genes, 0.3%	3 out of 34727 genes, 0.0%	0.013

GO:0031683	G-protein beta/gamma-subunit binding	5 out of 868 genes, 0.6%	15 out of 34727 genes, 0.0%	0.015
GO:0016759	cellulose synthase activity	8 out of 868 genes, 0.9%	56 out of 34727 genes, 0.2%	0.046
GO:0016760	cellulose synthase (UDP-forming) activity	8 out of 868 genes, 0.9%	56 out of 34727 genes, 0.2%	0.046
GO:0022892	substrate-specific transporter activity	73 out of 868 genes, 8.4%	1842 out of 34727 genes, 5.3%	0.047

Table S4. GO terms enriched in statistically up-regulated genes (≥ 2 -fold change) in tomato roots colonised by *S. indica*. Simulation corrected $P \leq 0.05$.

GO number	Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P -value
	unannotated	7 out of 128 genes, 5.5%	8 out of 34727 genes, 0.0%	<0.001
GO:0006952	defence response	60 out of 128 genes, 46.9%	6089 out of 34727 genes, 17.5%	<0.001
GO:0006950	response to stress	84 out of 128 genes, 65.6%	12568 out of 34727 genes, 36.2%	<0.001
GO:0042742	defence response to bacterium	33 out of 128 genes, 25.8%	2350 out of 34727 genes, 6.8%	<0.001
GO:0009617	response to bacterium	38 out of 128 genes, 29.7%	3151 out of 34727 genes, 9.1%	<0.001
GO:0009607	response to biotic stimulus	56 out of 128 genes, 43.8%	6463 out of 34727 genes, 18.6%	<0.001
GO:0045087	innate immune response	43 out of 128 genes, 33.6%	4265 out of 34727 genes, 12.3%	<0.001
GO:0050896	response to stimulus	92 out of 128 genes, 71.9%	15482 out of 34727 genes, 44.6%	<0.001
GO:0006955	immune response	43 out of 128 genes, 33.6%	4428 out of 34727 genes, 12.8%	<0.001
GO:0009814	defence response, incompatible interaction	36 out of 128 genes, 28.1%	3304 out of 34727 genes, 9.5%	<0.001
GO:0051707	response to other organism	49 out of 128 genes, 38.3%	5651 out of 34727 genes, 16.3%	<0.001
GO:0002376	immune system process	44 out of 128 genes, 34.4%	4830 out of 34727 genes, 13.9%	<0.001
GO:0045088	regulation of innate immune response	30 out of 128 genes, 23.4%	2611 out of 34727 genes, 7.5%	<0.001
GO:0010200	response to chitin	28 out of 128 genes, 21.9%	2359 out of 34727 genes, 6.8%	<0.001
GO:0050776	regulation of immune response	30 out of 128 genes, 23.4%	2749 out of 34727 genes, 7.9%	<0.001
GO:0010363	regulation of plant-type hypersensitive response	28 out of 128 genes, 21.9%	2447 out of 34727 genes, 7.0%	<0.001
GO:0031347	regulation of defence response	31 out of 128 genes, 24.2%	2971 out of 34727 genes, 8.6%	<0.001
GO:0002682	regulation of immune system process	30 out of 128 genes, 23.4%	2882 out of 34727 genes, 8.3%	<0.001
GO:0009863	salicylic acid mediated signalling pathway	25 out of 128 genes, 19.5%	2215 out of 34727 genes, 6.4%	<0.001
GO:0006612	protein targeting to membrane	27 out of 128 genes, 21.1%	2645 out of 34727 genes, 7.6%	0.001
GO:0051704	multi-organism process	51 out of 128 genes, 39.8%	7325 out of 34727 genes, 21.1%	0.001
GO:0031640	killing of cells of another organism	8 out of 128 genes, 6.2%	210 out of 34727 genes, 0.6%	0.001

GO:0010033	response to organic substance	38 out of 128 genes, 29.7%	4667 out of 34727 genes, 13.4%	0.001
GO:0009743	response to carbohydrate stimulus	34 out of 128 genes, 26.6%	3915 out of 34727 genes, 11.3%	0.001
GO:0007242	intracellular signalling cascade	47 out of 128 genes, 36.7%	6527 out of 34727 genes, 18.8%	0.001
GO:0001906	cell killing	8 out of 128 genes, 6.2%	216 out of 34727 genes, 0.6%	0.002
GO:0009719	response to endogenous stimulus	47 out of 128 genes, 36.7%	6589 out of 34727 genes, 19.0%	0.002
GO:0009751	response to salicylic acid stimulus	27 out of 128 genes, 21.1%	2749 out of 34727 genes, 7.9%	0.002
GO:0046483	heterocycle metabolic process	26 out of 128 genes, 20.3%	2617 out of 34727 genes, 7.5%	0.002
GO:0042445	hormone metabolic process	21 out of 128 genes, 16.4%	1810 out of 34727 genes, 5.2%	0.002
GO:0042435	indole derivative biosynthetic process	13 out of 128 genes, 10.2%	741 out of 34727 genes, 2.1%	0.003
GO:0042430	indole and derivative metabolic process	14 out of 128 genes, 10.9%	863 out of 34727 genes, 2.5%	0.003
GO:0042434	indole derivative metabolic process	14 out of 128 genes, 10.9%	863 out of 34727 genes, 2.5%	0.003
GO:0006725	cellular aromatic compound metabolic process	34 out of 128 genes, 26.6%	4125 out of 34727 genes, 11.9%	0.004
GO:0009611	response to wounding	28 out of 128 genes, 21.9%	3029 out of 34727 genes, 8.7%	0.004
GO:0006995	cellular response to nitrogen starvation	10 out of 128 genes, 7.8%	434 out of 34727 genes, 1.2%	0.004
GO:0009627	systemic acquired resistance	24 out of 128 genes, 18.8%	2374 out of 34727 genes, 6.8%	0.004
GO:0048583	regulation of response to stimulus	32 out of 128 genes, 25.0%	3810 out of 34727 genes, 11.0%	0.004
GO:0042436	indole derivative catabolic process	10 out of 128 genes, 7.8%	448 out of 34727 genes, 1.3%	0.004
GO:0009605	response to external stimulus	44 out of 128 genes, 34.4%	6280 out of 34727 genes, 18.1%	0.007
GO:0043562	cellular response to nitrogen levels	10 out of 128 genes, 7.8%	456 out of 34727 genes, 1.3%	0.008
GO:0031348	negative regulation of defence response	19 out of 128 genes, 14.8%	1647 out of 34727 genes, 4.7%	0.011
GO:0042446	hormone biosynthetic process	18 out of 128 genes, 14.1%	1499 out of 34727 genes, 4.3%	0.011
GO:0009753	response to jasmonic acid stimulus	26 out of 128 genes, 20.3%	2848 out of 34727 genes, 8.2%	0.012
GO:0043067	regulation of programmed cell death	29 out of 128 genes, 22.7%	3393 out of 34727 genes, 9.8%	0.012
GO:0007165	signal transduction	49 out of 128 genes, 38.3%	7570 out of 34727 genes, 21.8%	0.016
GO:0006569	tryptophan catabolic process	9 out of 128 genes, 7.0%	418 out of 34727 genes, 1.2%	0.023
GO:0046218	indolalkylamine catabolic process	9 out of 128 genes, 7.0%	418 out of 34727 genes, 1.2%	0.023
GO:0010817	regulation of hormone levels	24 out of 128 genes, 18.8%	2649 out of 34727 genes, 7.6%	0.032
GO:0009867	jasmonic acid mediated signalling pathway	20 out of 128 genes, 15.6%	1965 out of 34727 genes, 5.7%	0.032
GO:0009074	aromatic amino acid family catabolic process	9 out of 128 genes, 7.0%	449 out of 34727 genes, 1.3%	0.047
GO:0002679	respiratory burst during defence response	11 out of 128 genes, 8.6%	682 out of 34727 genes, 2.0%	0.049

GO:0042221	response to chemical stimulus	62 out of 128 genes, 48.4%	10951 out of 34727 genes, 31.5%	0.05
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Table S5. GO terms enriched in statistically down-regulated genes (≥ 2 -fold change) in tomato roots colonised by *S. indica*. Simulation corrected $P \leq 0.05$.

GO number	Gene Ontology term	Cluster frequency	Genome frequency of use	Corrected P -value
GO:0009416	response to light stimulus	58 out of 172 genes, 33.7%	4203 out of 34727 genes, 12.1%	<0.001
	unannotated	6 out of 172 genes, 3.5%	8 out of 34727 genes, 0.0%	<0.001
GO:0009314	response to radiation	58 out of 172 genes, 33.7%	4446 out of 34727 genes, 12.8%	<0.001
GO:0010218	response to far red light	18 out of 172 genes, 10.5%	431 out of 34727 genes, 1.2%	<0.001
GO:0010114	response to red light	18 out of 172 genes, 10.5%	444 out of 34727 genes, 1.3%	<0.001
GO:0009765	photosynthesis, light harvesting	9 out of 172 genes, 5.2%	59 out of 34727 genes, 0.2%	<0.001
GO:0009639	response to red or far red light	29 out of 172 genes, 16.9%	1456 out of 34727 genes, 4.2%	<0.001
GO:0009637	response to blue light	16 out of 172 genes, 9.3%	397 out of 34727 genes, 1.1%	<0.001
GO:0018298	protein-chromophore linkage	10 out of 172 genes, 5.8%	146 out of 34727 genes, 0.4%	<0.001
GO:0009628	response to abiotic stimulus	78 out of 172 genes, 45.3%	8617 out of 34727 genes, 24.8%	<0.001
GO:0009698	phenylpropanoid metabolic process	28 out of 172 genes, 16.3%	1650 out of 34727 genes, 4.8%	<0.001
GO:0019748	secondary metabolic process	46 out of 172 genes, 26.7%	4093 out of 34727 genes, 11.8%	<0.001
GO:0050896	response to stimulus	111 out of 172 genes, 64.5%	15482 out of 34727 genes, 44.6%	<0.001
GO:0042221	response to chemical stimulus	87 out of 172 genes, 50.6%	10951 out of 34727 genes, 31.5%	<0.001
GO:0009699	phenylpropanoid biosynthetic process	23 out of 172 genes, 13.4%	1311 out of 34727 genes, 3.8%	<0.001
GO:0042440	pigment metabolic process	23 out of 172 genes, 13.4%	1371 out of 34727 genes, 3.9%	<0.001
GO:0006575	amino acid derivative metabolic process	34 out of 172 genes, 19.8%	2805 out of 34727 genes, 8.1%	0.001
GO:0009812	flavonoid metabolic process	19 out of 172 genes, 11.0%	1085 out of 34727 genes, 3.1%	0.002
GO:0043647	inositol phosphate metabolic process	8 out of 172 genes, 4.7%	173 out of 34727 genes, 0.5%	0.003
GO:0043455	regulation of secondary metabolic process	21 out of 172 genes, 12.2%	1319 out of 34727 genes, 3.8%	0.003
GO:0009642	response to light intensity	18 out of 172 genes, 10.5%	999 out of 34727 genes, 2.9%	0.003
GO:0015698	inorganic anion transport	22 out of 172 genes, 12.8%	1448 out of 34727 genes, 4.2%	0.003
GO:0006725	cellular aromatic compound metabolic process	42 out of 172 genes, 24.4%	4125 out of 34727 genes, 11.9%	0.003
GO:0009744	response to sucrose stimulus	18 out of 172 genes, 10.5%	1048 out of 34727 genes, 3.0%	0.003
GO:0034285	response to disaccharide stimulus	18 out of 172 genes, 10.5%	1048 out of 34727 genes, 3.0%	0.003
GO:0006629	lipid metabolic process	50 out of 172 genes, 29.1%	5426 out of 34727 genes, 15.6%	0.003

GO:0010264	myo-inositol hexakisphosphate biosynthetic process	7 out of 172 genes, 4.1%	137 out of 34727 genes, 0.4%	0.003
GO:0033517	myo-inositol hexakisphosphate metabolic process	7 out of 172 genes, 4.1%	137 out of 34727 genes, 0.4%	0.003
GO:0010033	response to organic substance	45 out of 172 genes, 26.2%	4667 out of 34727 genes, 13.4%	0.003
GO:0019684	photosynthesis, light reaction	15 out of 172 genes, 8.7%	765 out of 34727 genes, 2.2%	0.004
GO:0015979	photosynthesis	17 out of 172 genes, 9.9%	970 out of 34727 genes, 2.8%	0.004
GO:0019751	polyol metabolic process	9 out of 172 genes, 5.2%	265 out of 34727 genes, 0.8%	0.004
GO:0032958	inositol phosphate biosynthetic process	7 out of 172 genes, 4.1%	146 out of 34727 genes, 0.4%	0.004
GO:0006020	inositol metabolic process	8 out of 172 genes, 4.7%	205 out of 34727 genes, 0.6%	0.004
GO:0042754	negative regulation of circadian rhythm	3 out of 172 genes, 1.7%	9 out of 34727 genes, 0.0%	0.007
GO:0043496	regulation of protein homodimerization activity	3 out of 172 genes, 1.7%	9 out of 34727 genes, 0.0%	0.007
GO:0009963	positive regulation of flavonoid biosynthetic process	14 out of 172 genes, 8.1%	692 out of 34727 genes, 2.0%	0.007
GO:0006021	inositol biosynthetic process	7 out of 172 genes, 4.1%	149 out of 34727 genes, 0.4%	0.007
GO:0006631	fatty acid metabolic process	27 out of 172 genes, 15.7%	2202 out of 34727 genes, 6.3%	0.009
GO:0009644	response to high light intensity	14 out of 172 genes, 8.1%	713 out of 34727 genes, 2.1%	0.013
GO:0009813	flavonoid biosynthetic process	17 out of 172 genes, 9.9%	1035 out of 34727 genes, 3.0%	0.015
GO:0046173	polyol biosynthetic process	7 out of 172 genes, 4.1%	163 out of 34727 genes, 0.5%	0.015
GO:0010155	regulation of proton transport	8 out of 172 genes, 4.7%	234 out of 34727 genes, 0.7%	0.02
GO:0042398	amino acid derivative biosynthetic process	26 out of 172 genes, 15.1%	2161 out of 34727 genes, 6.2%	0.02
GO:0009725	response to hormone stimulus	51 out of 172 genes, 29.7%	5884 out of 34727 genes, 16.9%	0.024
GO:0048572	short-day photoperiodism	6 out of 172 genes, 3.5%	116 out of 34727 genes, 0.3%	0.026
GO:0006820	anion transport	22 out of 172 genes, 12.8%	1677 out of 34727 genes, 4.8%	0.028
GO:0009719	response to endogenous stimulus	55 out of 172 genes, 32.0%	6589 out of 34727 genes, 19.0%	0.028
GO:0044255	cellular lipid metabolic process	45 out of 172 genes, 26.2%	4970 out of 34727 genes, 14.3%	0.028
GO:0048575	short-day photoperiodism, flowering	5 out of 172 genes, 2.9%	74 out of 34727 genes, 0.2%	0.034
GO:0009648	photoperiodism	9 out of 172 genes, 5.2%	329 out of 34727 genes, 0.9%	0.041
GO:0046148	pigment biosynthetic process	17 out of 172 genes, 9.9%	1123 out of 34727 genes, 3.2%	0.043
GO:0006520	cellular amino acid and derivative metabolic process	39 out of 172 genes, 22.7%	4118 out of 34727 genes, 11.9%	0.043

Table S6. Key genes involved in the biosynthesis of sterols and glycoalkaloids in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [47].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc03g032010.3.1	HMGR1	-1,071862292	2,71E-12	0,103935545	0,464283426
Solyc01g110290.3.1	SQS	-0,345804369	0,007375011	-0,032854916	0,760343841
Solyc12g006530.2.1	TTS1	-1,955851209	0,115840374	-1,276454187	0,011412626
Solyc12g006520.2.1	TTS2	0,015512455	0,993705338	0,090562205	0,743155339
Solyc04g070980.3.1	CAS1	-0,292381932	0,193009074	-0,041647917	0,798240379
Solyc01g087560.3.1	SMT1	0,141969113	0,597019637	0,048563191	0,763076686
Solyc02g069490.3.1	SSR2	-1,431619619	8,38E-16	-0,237390468	0,146353048
Solyc02g086180.3.1	C5-SD	-1,93644664	2,22E-09	-0,142034096	0,630482937
Solyc07g043420.3.1	GAME11	-1,503566951	9,14E-09	-0,151616616	0,52471162
Solyc12g006460.2.1	GAME4	-0,815255056	1,04E-05	-0,196100414	0,235506181
Solyc12g006470.2.1	GAME12	-0,863429161	0,000111696	-0,425103646	0,031294329
Solyc07g043460.3.1	GAME6	-1,359318681	1,27E-08	-0,190700908	0,376037687
Solyc07g062520.3.1	GAME7	-1,662185084	1,26E-14	-0,636557794	0,001151219
Solyc07g043490.1.1	GAME1	-0,884034983	1,32E-05	-0,210908043	0,231842813
Solyc07g043410.1.1	GAME2	0	NA	-1,390168387	0,745721125
Solyc07g043480.1.1	GAME17	-1,03607763	1,69E-07	0,003807049	0,982918559
Solyc07g043500.1.1	GAME18	-1,283048358	6,02E-06	-0,24149352	0,326668836
Solyc01g090340.2.1	GAME9	-1,238433425	1,43E-06	-0,305221634	0,188539735

Table S7. Key genes involved in the biosynthesis of shikimate, chorismate and phenolic compounds in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [49,50].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Shikimate and chorismate					
Solyc04g074480.3.1	DAHPS1	-0,091029449	0,518884286	-0,055184127	0,909055509
Solyc11g009080.2.1	DAHPS2	-0,448701577	6,02E-06	-0,033685079	0,958259072
Solyc01g067750.3.1	SDH	0,012339708	0,961687305	0,11714096	0,564414714
Solyc02g094420.3.1	SK	-0,129120503	0,288794119	0,030562822	0,966040571
Solyc05g050980.3.1	EPSPS2	-0,44055303	9,06E-05	-0,034775088	0,963068652
Solyc11g017240.2.1	CM	-0,03445038	0,8897592	0,100160649	0,82565885
Solyc11g066890.1.1	PAT	-0,332400037	0,034328115	-0,094208126	0,87374324
Solyc06g074530.1.1	PDH	-0,566282705	0,040209421	0,000422606	1
Solyc02g080620.3.1	PDT	-0,024694318	0,949242727	0,108618928	0,851384887
Phenylpropanoid					
Solyc03g042560.2.1	PAL1	-0,898417661	NA	-0,438509133	NA
Solyc00g282510.2.1	PAL2	-0,89928451	NA	1,247862167	NA
Solyc03g036470.2.1	PAL3	-0,171473141	NA	-0,276371585	NA
Solyc03g071857.1.1	PAL4	0	NA	-0,000240988	NA
Solyc03g078270.1.1	PAL5	NA	NA	NA	NA
Solyc09g007890.1.1	PAL6	-1,174676907	0,479735953	-1,499501221	0,002410206
Solyc09g007900.3.1	PAL7a	-0,572381395	0,015814736	-0,269295136	0,662974208
Solyc09g007910.3.1	PAL7b	-0,914072434	5,03E-05	-0,256718449	0,692940185
Solyc09g007920.3.1	PAL7c	-0,567828609	0,018834789	-0,277928285	0,655692121
Solyc03g071870.1.1	PAL8	NA	NA	NA	NA
Solyc10g086180.2.1	PAL9	-0,736939955	6,76E-09	-0,066904207	0,917584149
Solyc05g056170.3.1	PAL10	-0,412712138	0,019743476	-0,080605723	0,91400179
Solyc01g096670.3.1	C4H1	-0,469518807	0,001664968	0,031852103	0,966552457
Solyc06g082530.2.1	C4H2	-0,777383791	1,72E-06	-0,006173548	1
Solyc03g117870.3.1	4CL1	-0,993874582	2,53E-13	-0,122354545	0,805956778
Solyc12g094520.2.1	4CL2	-0,432336753	1,93E-06	-0,161477051	0,323557117
Solyc03g097030.3.1	4CL3	-0,71530824	6,53E-05	-0,488191598	0,146135686
Solyc06g035960.3.1	4CL-1	-0,780536116	4,33E-06	0,140907509	0,838552808

Table S8. Key genes involved in the biosynthesis of flavonoids, flavonols and anthocyanins in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [49,50].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Flavonoids					
Solyc09g091510.3.1	CHS1	-1,405578312	0,005423215	-1,83876567	0,005020187
Solyc05g053550.3.1	CHS2	-0,644782121	0,240006038	-0,878582371	0,278314997
Solyc05g052240.3.1	CHI2	-1,176352071	0,000760419	-1,337554599	0,002426868
Solyc02g067870.3.1	CHI3	0,555993317	0,869267866	0,033847335	0,999928216
Solyc05g010320.3.1	CHI4	-0,702023761	0,00059892	-0,245995962	0,732607255
Solyc07g062030.3.1	CHI-1	0,206988033	0,132773495	0,004272026	1
Solyc02g083860.3.1	F3H	-0,923618013	0,000303146	-0,25221463	0,766261324
Solyc03g115220.3.1	F3'H	-0,758730163	0,001524057	0,305527499	0,514574674
Solyc12g088460.2.1	F3'H-1	0,338468515	0,208006969	0,051909337	0,96398595
Solyc11g066580.2.1	F3'5'H	-0,578543132	0,133716272	-1,267910327	0,004625226
Flavonols					
Solyc11g013110.2.1	FLS	-0,8996357	1,21E-05	-0,591266349	0,033829586
Solyc10g083440.1.1	F-3GT	-1,403958107	0,001536325	-1,966460645	0,000440105
Solyc12g088170.2.1	AAC	-0,889554061	0,059219576	-1,148257992	0,064127679
Solyc12g098590.2.1	5GT	-0,808655047	0,097344243	-0,712729268	0,443220755
Solyc09g059170.2.1	AN-3GT	-1,202746908	0,016325381	-1,486435009	0,056143105
Solyc07g055930.3.1	UGT	-0,778887335	0,000130513	-0,142167332	0,860014725
Solyc01g107780.3.1	Q-3GT	-0,515763727	0,308559864	0,100130854	0,916793324
Solyc02g081690.1.1	Q-3/4GT	0,287488471	0,404663468	0,442879179	0,108376132
Solyc11g010760.1.1	UDP-GT2	-0,413139373	0,01571682	-0,117639229	0,85390753
Solyc03g078770.3.1	UDP-GT3	-2,89362296	0,04866842	-0,294369572	0,707628688
Solyc05g053890.2.1	UDP-GT1	-0,567965245	0,018152446	-0,033371818	0,986118777
Anthocyanins					
Solyc02g085020.3.1	DFR1	-0,723238213	0,178652891	-1,145239145	0,118180441
Solyc02g089770.3.1	DFR2	-1,456494883	0,322529114	8,37E-05	1
Solyc08g080040.3.1	ANS1	-0,807279345	0,026528347	0,669773387	0,669849519
Solyc10g076660.2.1	ANS2	-3,459172628	0,024767673	0,669773387	0,669849519
Solyc09g059170.2.1	RT	-1,202746908	0,016325381	-1,486435009	0,056143105

Table S9. Key genes involved in the biosynthesis of alignin and hydroxycinnamic acids in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [50,88,89].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Lignin & HCAs					
Solyc03g117600.3.1	HCT	-0,570444609	4,23E-08	-0,223811502	0,138655697
Solyc07g005760.3.1	HQT	-0,084688684	0,707674551	-0,084688684	0,707674551
Solyc11g066670.1.1	UDP-GT1	-1,12031455	5,69E-07	-0,335791729	0,522919538
Solyc02g093250.3.1	CCoAOMT	-0,709810179	0,00967726	0,097779953	0,925918254
Solyc06g068440.3.1	CCR1	-0,815171597	6,71E-05	-0,329673042	0,372474776
Solyc03g116910.3.1	CCR2	-0,909926964	0,014113812	0,15246435	0,934905037
Solyc08g076780.2.1	CCR3	NA	NA	NA	NA
Solyc08g005120.3.1	CCR-l2	1,156093528	0,479227376	-0,098499186	0,973114754
Solyc06g061280.3.1	CCR-l4	0,961251828	0,132557876	-0,485353696	0,601207497
Solyc11g066670.1.1	UDP-GT1	-1,12031455	5,69E-07	-0,335791729	0,522919538
Solyc02g084570.3.1	F5H	-0,484482025	0,033196492	-0,227566525	0,728433888
Solyc01g107590.3.1	CAD	-0,468227374	4,14E-05	-0,290902107	0,062343787
Solyc01g087630.2.1	pCAD	-1,076464456	0,044052911	-0,312590108	0,882116022
Solyc02g069250.3.1	pCAD	-1,318336311	0,003192601	0,993977299	0,019930332
Solyc03g078430.2.1	pCAD	0	NA	-0,785863759	NA
Solyc03g078433.1.1	pCAD	NA	NA	NA	NA
Solyc03g078437.1.1	pCAD	NA	NA	NA	NA
Solyc04g048970.1.1	pCAD	NA	NA	NA	NA
Solyc08g014360.2.1	pCAD	-0,898462445	NA	0	NA
Solyc08g048300.2.1	pCAD	-0,898462445	NA	0	NA
Solyc12g055820.2.1	pCAD	-0,071222154	0,611534601	-0,00820372	0,996038378
Solyc03g080180.3.1	COMT	-0,914019261	2,01E-11	-0,35010867	0,068918999
Solyc10g078240.2.1	SIC3H4	-1,004826422	2,01E-11	-0,201064207	0,635129215
Solyc01g096670.3.1	SIC3H3	-0,469518807	0,001664968	0,031852103	0,966552457
Solyc10g078220.2.1	SIC3H1	3,230724147	0,008537938	3,638829219	0,029683717
Solyc10g078230.2.1	SIC3H2	1,539907	0,084764268	1,308337238	0,345907924
Solyc04g010250.3.1	pCSE	1,223489703	9,48E-15	0,639263733	4,02E-05
Solyc07g052510.4.1	TPX1	1,594725994	0,069343572	0,133663786	0,812490037
Solyc07g017880.3.1	POD	0	1	0,239891571	0,67872875
Solyc02g084790.3.1	POD	-0,163331214	0,983201705	0,467952915	0,372584118
Solyc10g076240.2.1	POD	0	1	0,58482129	0,026963089
Solyc03g006700.3.1	POD	0,329869405	0,31167089	-0,120926361	0,804816973
Solyc02g079500.4.1	POD	0,78714786	0,009665615	0,875455523	2,36E-06
Solyc04g071890.3.1	POD	0,829452925	0,001563457	0,18776353	0,845572452

Table S10. Putative fatty acid desaturases expressed in leaves and roots in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value.

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc04g040130.1.1		3,198652	0,004083	2,294026	2,63E-08
Solyc12g044950.2.1		0,897417	0,019481	1,452144	5,23E-05
Solyc12g100240.1.1		0	1	1,377983	0,112193
Solyc12g100250.2.1		0	1	3,304992	1,42E-05
Solyc12g100260.1.1		0	1	3,419097	3,54E-09
Solyc12g100270.2.1		1,581493	0,034177	1,736664	1,20E-06
Solyc12g049030.1.1		3,757193	0,0203	4,57847	5,09E-05
Solyc10g011810.3.1		-0,0151	0,965894	0,438785	0,000647
Solyc01g088400.3.1		-0,16255	0,297263	0,189514	0,628794
Solyc01g006430.3.1		-0,93606	3,26E-17	0,235283	0,24383
Solyc03g063110.3.1		-0,04009	0,872316	0,021389	0,984577
Solyc04g040120.1.1		0	1	0,313254	0,917584
Solyc05g007460.3.1		-0,40774	0,004627	0,057637	0,927733
Solyc08g063090.2.1		-0,20588	0,590021	-0,70359	0,676064
Solyc11g008680.2.1		0,397876	0,183515	-0,1575	0,880243
Solyc07g005510.3.1		-0,63079	3,74E-07	-0,18965	0,568441
Solyc03g116730.3.1		-0,55934	0,001785	-0,22752	0,748806
Solyc04g072180.2.1		-0,23171	0,030744	0,104446	0,706116
Solyc02g086180.3.1		-1,93645	2,22E-09	-0,14203	0,937103
Solyc05g050090.3.1		-0,63783	0,003528	-0,18808	0,879373
Solyc01g091320.3.1		-2,18952	6,15E-19	-0,23474	0,802902
Solyc01g010860.3.1		-0,02066	0,957769	0,060875	0,920814
Solyc06g059710.3.1		-0,26197	0,218846	-1,3699	0,769268
Solyc05g010180.3.1		-0,15995	0,526267	-0,39711	0,218499
Solyc08g079570.3.1		-0,05894	0,69955	0,162848	0,297973
Solyc03g117800.3.1		-0,9662	0,032004	-1,30899	0,000807
Solyc03g058430.2.1		-0,16184	0,348322	0,15178	0,722384
Solyc06g076410.3.1		-0,3262	0,000596	-0,29634	0,004736
Solyc01g088420.3.1		0,141716	0,950398	3,171774	0,166854
Solyc06g051400.3.1		-0,52122	0,000237	-0,34201	0,112681
Solyc06g053480.3.1		-0,04135	0,822722	-0,04946	0,926497
Solyc01g097810.3.1		-0,05769	0,70729	-0,24641	0,087337
Solyc02g063240.3.1		0,199096	0,148221	0,23264	0,227459
Solyc07g006300.3.1		-0,69192	0,003193	0,043613	0,986856
Solyc02g085250.3.1		0,009023	0,990782	-0,00047	1
Solyc10g011820.3.1		-0,94553	6,04E-09	0,109334	0,886557
Solyc06g007130.4.1		0,690138	7,02E-06	0,160779	0,747131
Solyc03g123760.3.1		0,064769	0,793503	-0,10239	0,87071
Solyc10g081650.2.1		-0,04063	0,884182	-0,16263	0,691256
Solyc03g065250.3.1		0,417943	0,034685	-0,66939	0,019346

Table S11. Genes involved in the mevalonate (MVA) and MEP pathway in tomato. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [82].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc07g045350.3.1	AACT.ch7	0,057950542	0,86401304	0,061477604	0,933604967
Solyc05g017760.3.1	AACT.ch5	-0,185388001	0,30353754	-0,009889917	0,997108054
Solyc08g080170.3.1	HMGS.ch8	-0,042359663	0,91085945	-0,050201796	0,961220221
Solyc08g080160.3.1	HMGS.ch8	0,264529744	NA	-1,98178398	NA
Solyc12g056450.2.1	HMGS.ch12	-0,185305786	0,13557104	-0,101299395	0,77041856
Solyc02g082260.3.1	HMGR.ch2	-0,41414197	0,00625572	0,085593114	0,891536188
Solyc02g038740.3.1	HMGR.ch2*	-0,929268138	3,73E-05	0,109239354	0,91996693
Solyc03g032010.3.1	HMGR1.ch3	-1,071862292	2,71E-12	0,103935545	0,886556654
Solyc03g032020.3.1	HMGR.ch3	-1,006995835	4,91E-06	-0,263899143	0,693595505
Solyc01g098840.3.1	MVK.ch1	-0,058623672	0,65514158	0,031626634	0,944435225
Solyc06g066310.3.1	pMVK.ch6	-0,007319725	1	0,035535642	0,959856798
Solyc08g076140.3.1	pMVK.ch8	-0,184895099	0,05873937	0,045112927	0,896239626
Solyc04g009650.3.1	MDC.ch4	-0,418461713	0,09807263	0,132787489	0,859066682
Solyc11g007020.2.1	MDC.ch11	-0,063861507	0,73740772	0,017151174	0,987660236
Solyc04g056390.3.1	IDI.ch4	-0,088246492	0,32845503	0,012939541	0,983146426
Solyc05g055760.3.1	IDI.ch5	-0,131862568	0,5720865	0,08163444	0,90972484
Solyc01g067890.3.1	DXS1.ch1	-0,551888421	0,00566032	-0,151254629	0,846599315
Solyc06g071380.3.1	DXS.ch6	-0,191929361	0,44383373	0,186955286	0,77041856
Solyc11g010850.2.1	DXS2.ch11	-0,919166826	0,0097868	-0,261579324	0,881177812
Solyc03g114340.3.1	DXR.ch3	-0,156834036	0,16013763	-0,136228401	0,560526059
Solyc01g102820.3.1	MCT.ch1a	0,033459324	0,85579128	0,055696128	0,913819537
Solyc01g049890.3.1	MCT.ch1b	0,091507575	0,19974777	-0,008736578	0,987861872
Solyc01g009010.3.1	CMK.ch1	-0,031884314	0,84958923	-0,198349707	0,241942195
Solyc08g081570.3.1	MDS.ch8	0,150892116	0,16638511	0,048971282	0,926754359
Solyc11g069380.2.1	HDS.ch11	-0,129439941	0,30313817	-0,189595803	0,309457903
Solyc01g109300.3.1	HDR.ch1	-0,158669455	0,44433905	-0,074151939	0,925426569

Table S12. Genes encoding for *trans*- and *cis*-prenyltransferases involved in precursor biosynthesis of terpenes in tomato, LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [82].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc08g023470.3.1	GPS.ch8	0,161009402	0,08502987	0,03684977	0,926754359
Solyc12g015860.2.1	FPS.ch12	-0,120645626	0,3868077	0,062953783	0,896942232
Solyc10g005820.2.1	FPS.ch10a	-0,098523742	0,78937338	0,039549313	0,977682299
Solyc10g005840.3.1	FPS.ch10b	0,127272475	0,37757649	-0,111808618	0,754346618
Solyc04g079960.1.1	GGPPS.ch4	0,056239045	0,7208673	0,239430733	0,435398055
Solyc09g008920.3.1	GGPPS.ch9	0,108136192	0,29281316	0,007358012	0,995739606
Solyc02g085700.1.1	GGPPS.ch2	0,056057941	0,68947972	-0,283364382	0,033126615
Solyc08g005680.3.1	CPT1.ch8	-0,168138439	0,83150306	1,703465261	0,645906245
Solyc08g005660.2.1	CPT2.ch8	1,493110427	NA	0	NA
Solyc03g025560.3.1	CPT3.ch3	0,938931372	5,98E-09	0,063686629	0,931339242
Solyc10g085150.2.1	CPT4.ch10	0,085612234	0,7048527	0,089889705	0,880373283
Solyc10g085140.1.1	CPT5.ch10	0,519904248	0,35155701	-0,512426209	0,65582371
Solyc06g059990.3.1	CPT6.ch6	0	1	-0,324919447	0,691476966
Solyc06g076920.3.1	CPT7.ch6	-0,124522285	0,68327154	0,271683457	0,972197923

Table S13. Terpene synthase gene family in tomato. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [54].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc01g105850.3.1	TPS1	-0,54994748	0,7208673	0	NA
Solyc01g105910.2.1	TPS2	NA	NA	NA	NA
Solyc01g105870.3.1	TPS3	0,580415632	NA	0,035808782	NA
Solyc01g105880.4.1	TPS4	0	1	-0,975821005	0,478825032
Solyc01g105890.3.1	TPS5	-1,113476057	2,02E-07	0,62955363	0,946881956
Solyc01g105900.2.1	TPS6	NA	NA	NA	NA
Solyc01g105920.3.1	TPS7	-0,703745041	0,16072763	-0,634129923	0,852887879
Solyc01g105960.2.1	TPS8	-1,64198066	0,46879539	-0,174702613	0,911475706
Solyc06g059885.1.1	TPS9	-0,405747158	0,03477536	-0,059272384	1
Solyc06g059930.3.1	TPS12	-0,418507469	0,28653169	0	1
Solyc09g092470.2.1	TPS14	-0,924272171	0,73448105	-0,172113512	0,844577631
Solyc07g051940.3.1	TPS15	0,215918118	0,86035072	-0,062621214	0,999809093
Solyc07g008690.3.1	TPS16	0,088974328	0,9809211	0	1
Solyc12g006570.2.1	TPS17	0,583108512	0,7444946	-0,508364553	NA
Solyc08g005720.3.1	TPS18	-0,441017097	0,34874294	-0,047332024	0,971318204
Solyc08g005665.1.1	TPS20	0,136657211	0,76722836	3,768573001	0,025929723
Solyc08g005640.3.1	TPS21	-0,213635236	0,66685141	-0,315605501	0,826897157
Solyc07g066670.3.1	TPS24	0,078842979	0,71287643	-0,106766107	0,809565188
Solyc02g079890.2.1	TPS25	-1,336823602	NA	0	NA
Solyc02g079910.2.1	TPS27	-2,682785575	NA	0	NA
Solyc04g054380.1.1	TPS28	NA	NA	NA	NA
Solyc12g019240.2.1	TPS30	NA	NA	NA	NA
Solyc01g101170.3.1	TPS31	-0,035906624	0,99941245	1,214155049	0,091506913
Solyc01g101180.3.1	TPS32	-0,359959576	NA	4,732970263	NA
Solyc01g101190.3.1	TPS33	0,596821351	0,71653315	5,113598894	NA
Solyc01g101210.4.1	TPS35	-1,452780804	NA	-0,611150631	NA
Solyc06g060180.2.1	TPS36	NA	NA	NA	NA
Solyc10g005410.3.1	TPS38	-0,515268314	0,56814557	-0,032229788	1
Solyc02g079840.2.1	TPS39	0,765313276	0,75277623	0,091578319	0,99808769
Solyc06g084240.2.1	TPS40	-1,286341356	0,2674703	-1,052006644	NA
Solyc08g005710.3.1	TPS41	-0,226917392	0,54397277	0,495493666	0,81218199
Solyc10g005420.1.1	TPS42	NA	NA	NA	NA
Solyc03g006550.3.1	TPS46	-0,603841912	0,65298683	0	NA
Solyc03g007730.1.1	TPS47	0,569118998	NA	0,631877319	NA
Solyc04g051620.2.1	TPS48	0	NA	-1,645031122	NA
Solyc07g052120.3.1	TPS51	2,849151536	0,045501	0,797192056	0,532046929

Table S14. Transcription factors considered to be involved in terpene biosynthesis in tomato. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [82].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc05g052050.1.1	SIAP2_9	0,339444074	0,10726132	0,212137882	0,70131784
Solyc11g072600.2.1	SIAP2_6	0,069385254	0,7541838	-0,028227528	0,977664088
Solyc10g050970.1.1	SIAP2_4	-1,702544451	NA	-2,911016156	NA
Solyc06g075510.3.1	SIAP2_10	-0,246252057	0,10915844	-0,189316011	0,515283776
Solyc12g056590.2.1	SIAP2_5	0,311043086	0,58918874	0,329584578	0,323332603
Solyc09g075420.3.1	SIAP2_11	0,794996508	0,00057209	0,203805019	0,806174798
Solyc05g050830.2.1	SIAP2_7	-1,231894948	0,00247871	-2,755635583	0,215330769
Solyc03g026270.3.1	SIAP2_2	-3,028177242	0,1287803	-4,641461137	0,094800438
Solyc01g108240.3.1	SIAP2_1	-1,235683192	0,6562689	-5,205940302	NA
Solyc07g053740.1.1	SIAP2_8	-1,44036617	0,00682981	-0,378952572	0,857937386
Solyc01g095100.3.1	SIWRKY22	-0,765603305	0,00640675	0,06312119	0,97055289
Solyc12g011200.2.1	SIWRKY28	-0,268752572	0,68442332	0,346166031	0,65582371
Solyc03g113120.3.1	SIWRKY73	-0,590197796	0,42635358	0,417725729	0,572987269
Solyc07g055280.3.1	SIWRKY78	0,380688852	0,1476444	0,078348944	0,945974768
Solyc08g005050.3.1	SIMYC1	-0,558751919	0,00177769	-0,477686159	0,03402615
Solyc02g062400.3.1	EOT1	-0,522319521	0,20536434	-0,77095575	0,926770625
Solyc00g117450.2.1	EOT2	-0,850562368	0,38547123	0,551094685	0,911357047
Solyc02g084680.2.1	EOT3	-0,319305473	0,44288983	0,551387136	0,457772107

Table S15. Primer list

No	Name	Sequence 5'-3'	Used for
1	SITPS5Q-F	CTTCGGATGAACTGAAAAGAGG	qRT-PCR
2	SITPS5Q-R	GTGGAGAATTTTGTCTTGAGC	qRT-PCR
3	SITPS12Q-F	CGTTACTGGTTGAGTCTGTCTG	qRT-PCR
4	SITPS12Q-R	CTTGATTATTTGAAATATTCCGGAGG	qRT-PCR
5	SITPS20Q-F	AAGGAAATCTTGGAATGAATAGAA	qRT-PCR
6	SITPS20Q-R	ATAGAAGGAAAGAACAAAAGTCATAA	qRT-PCR
7	SITPS47Q-F	CTTGAAAGACGTCATCTCTATGGTG	qRT-PCR
8	SITPS47Q-R	CTGACACAAAGATAAAACAACATCAAG	qRT-PCR
9	SITPS47_USER-F	GGCTTAAUATGGTCGTTGGATTTGG	USER® cloning for <i>N. benthamiana</i> expression
10	SITPS47_USER-R	GGTTTAAUTCATGCTTTTATAGGATC	USER® cloning for <i>N. benthamiana</i> expression

Table S16. Key genes involved in jasmonic acid (JA) biosynthesis and signalling in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected P-value [90].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc06g051400.3.1	FAD7	-0,52122	0,000237	-0,34201	0,112681
Solyc06g007130.4.1	FAD3	0,690138	7,02E-06	0,160779	0,747131
Solyc02g077110.3.1	LPS1	-0,88486	0,013511	-0,59014	0,533914
Solyc02g077420.3.1	LPS2	0,208364	0,64	-0,83081	0,016525
Solyc02g077430.3.1	LPS3	0,383799	0,153999	-0,54053	0,098868
Solyc08g014000.3.1	LOXa	0,371724	0,665065	-0,24131	0,448477
Solyc01g099190.3.1	LOXb	1,876023	0,388878	-0,98646	NA
Solyc01g006540.3.1	LOXc	-0,01829	0,973535	-1,43732	0,426245
Solyc03g122340.3.1	LOXd	-1,0794	3,56E-08	-0,21732	0,740042
Solyc04g079730.1.1	AOS1	-0,36596	0,669424	-0,23212	0,916888
Solyc11g069800.1.1	AOS2	0,237965	0,148081	0,294209	0,160026
Solyc10g007960.1.1	AOS3	0	1	0,264679	0,920446
Solyc02g085730.3.1	AOC	-0,56523	0,001218	-0,06737	0,943924
Solyc07g007870.3.1	OPR3	-0,213	0,064294	-0,16317	0,39408
Solyc01g103390.3.1	OPR2	-0,1053	0,821924	0,492251	0,122428
Solyc08g078390.3.1	ACX1a	-0,0428	0,673255	-0,10809	0,35879
Solyc10g009600.1.1	SIJAR1	0	NA	-0,8944	NA
Solyc10g011660.3.1	SIJRL1	0,042699	0,87078	-0,05252	0,941463
Solyc05g052620.3.1	COI1	-0,1008	0,457458	0,079088	0,839469
Solyc07g042170.3.1	JAZ1	0,052028	0,832774	-0,37273	0,007447
Solyc12g009220.2.1	JAZ2	0,271821	0,678566	-0,38681	0,821226
Solyc03g122190.3.1	JAZ3	-0,39368	0,0003	-0,09444	0,911305
Solyc12g049400.2.1	JAZ4	0,140274	0,937416	0,54339	0,890906
Solyc03g118500.3.1	JAZ5	-0,01954	0,941306	-0,00302	1
Solyc01g005440.3.1	JAZ6	0,012189	0,984196	0,114442	0,812334
Solyc11g011030.2.1	JAZ7	0,077566	0,908856	-0,75411	0,612208
Solyc06g068930.2.1	JAZ8	0	1	-0,26571	0,574543
Solyc08g036640.3.1	JAZ9	0,541241	NA	-0,90516	NA

Solyc08g036620.3.1	JAZ10	-0,89846	NA	0	NA
Solyc08g036660.3.1	JAZ11	-0,19585	NA	0	NA
Solyc01g009740.2.1	JAZ12	NA	NA	NA	NA
Solyc08g076930.1.1	MYC2	-0,49978	0,00035	-0,17132	0,649645
Solyc08g005050.3.1	MYC10	-0,55875	0,001778	-0,47769	0,034026
Solyc00g071180.3.1	CysPI	2,905347	0,055295	-0,31417	0,892171
Solyc08g074630.2.1	PPO F	-1,04885	0,065938	0,662129	0,945518
Solyc08g074620.3.1	PPO F	0,046456	0,948825	0,651306	0,944637
Solyc08g074680.3.1	PPO B	-0,90066	0,740395	-0,18542	0,709324
Solyc03g098790.3.1	CDI	-0,78679	NA	0	NA
Solyc09g008670.3.1	TD2	0,215593	0,889864	-1,29753	0,226864
Solyc12g010020.2.1	LapA1	-0,07866	0,986593	0	1
Solyc00g187050.3.1	LapA2	0	NA	0,656818	NA
Solyc01g091160.4.1	LeARG1	0,208857	0,524094	-0,08599	0,943413
Solyc01g091170.3.1	LeARG2	0,568832	0,463449	0	1
Solyc09g084470.3.1	PI-I	-0,98887	0,19942	0	1
Solyc03g020080.3.1	PI-II	NA	NA	NA	NA
Solyc09g091540.1.1	SAMT	NA	NA	NA	NA

Table S17. Key genes involved in salicylic acid (SA) biosynthesis and signalling in tomato plants. LS-Leaves from *S. indica*-inoculated plants, LC-Leaves from control plants, RS-Roots from *S. indica*-inoculated plants, RC-Roots from control plants, Padj represents the FDR corrected *P*-value [90].

geneID	Annotation	log2FoldChange (LSvsLC)	Padj (LSvsLC)	log2FoldChange (RSvsRC)	Padj (RSvsRC)
Solyc03g042560.2.1	PAL1	-0,89842	NA	-0,43851	NA
Solyc00g282510.2.1	PAL2	-0,89928	NA	1,247862	NA
Solyc03g036470.2.1	PAL3	-0,17147	NA	-0,27637	NA
Solyc03g071857.1.1	PAL4	0	NA	-0,00024	NA
Solyc03g078270.1.1	PAL5	NA	NA	NA	NA
Solyc09g007890.1.1	PAL6	-1,17468	0,479736	-1,4995	0,00241
Solyc09g007900.3.1	PAL7a	-0,57238	0,015815	-0,2693	0,662974
Solyc09g007910.3.1	PAL7b	-0,91407	5,03E-05	-0,25672	0,69294
Solyc09g007920.3.1	PAL7c	-0,56783	0,018835	-0,27793	0,655692
Solyc03g071870.1.1	PAL8	NA	NA	NA	NA
Solyc10g086180.2.1	PAL9	-0,73694	6,76E-09	-0,0669	0,917584
Solyc05g056170.3.1	PAL10	-0,41271	0,019743	-0,08061	0,914002
Solyc06g071030.3.1	ICS	-0,64177	1,03E-06	-0,21447	0,775642
Solyc07g040690.3.1	NPR1	-0,51342	2,99E-05	-0,06393	0,909451
Solyc04g011670.3.1	TGA1a	0,123371	0,588393	0,005003	1
Solyc10g080770.2.1	TGA2.1.	-0,68935	8,16E-08	0,130224	0,766083
Solyc11g064950.2.1	TGA2.2.	-0,15307	0,444841	0,055487	0,937103
Solyc01g095630.3.1	WRKY70	-0,37616	0,317893	-0,29719	0,775505
Solyc01g008620.3.1	β -1,3-glucanase	3,278558	3,16E-11	3,464475	1,83E-09
Solyc08g080620.1.1	PR-5	-1,85628	NA	-0,49681	NA
Solyc01g097240.3.1	PR-2	0,815339	0,132863	4,411324	1,71E-18
Solyc09g007010.1.1	PR-1	0	NA	1,954777	NA
Solyc08g079870.3.1	Subtilisin	0,676755	0,584392	4,560762	0,000319
Solyc08g079840.2.1	Subtilisin	0,46431	0,000379	0,33405	0,763955
Solyc02g082920.3.1	Chi2	0,239727	0,655921	1,961853	2,21E-08
Solyc05g050130.3.1	acidic chitinase	0,261984	0,561059	0,648983	0,1249
Solyc09g090990.2.1	PRP-like	0,576715	0,856787	1,319672	3,11E-05
Solyc08g080650.3.1	Osmotin-like	0,867424	0,003283	0,392173	0,54484
Solyc04g049090.3.1	MLO-like	0,490008	0,000686	0,413785	0,028852
Solyc01g006350.3.1	glucan synthase	-0,08513	0,303008	0,065758	0,752887
Solyc02g069310.3.1	Nim	-1,14235	6,48E-16	0,003057	1
Solyc10g011910.3.1	WRKY22	-0,25548	0,715676	-0,26804	0,852181
Solyc01g095100.3.1	WRKY22.1	-0,7656	0,006407	0,063121	0,970553

Supplementary Figures

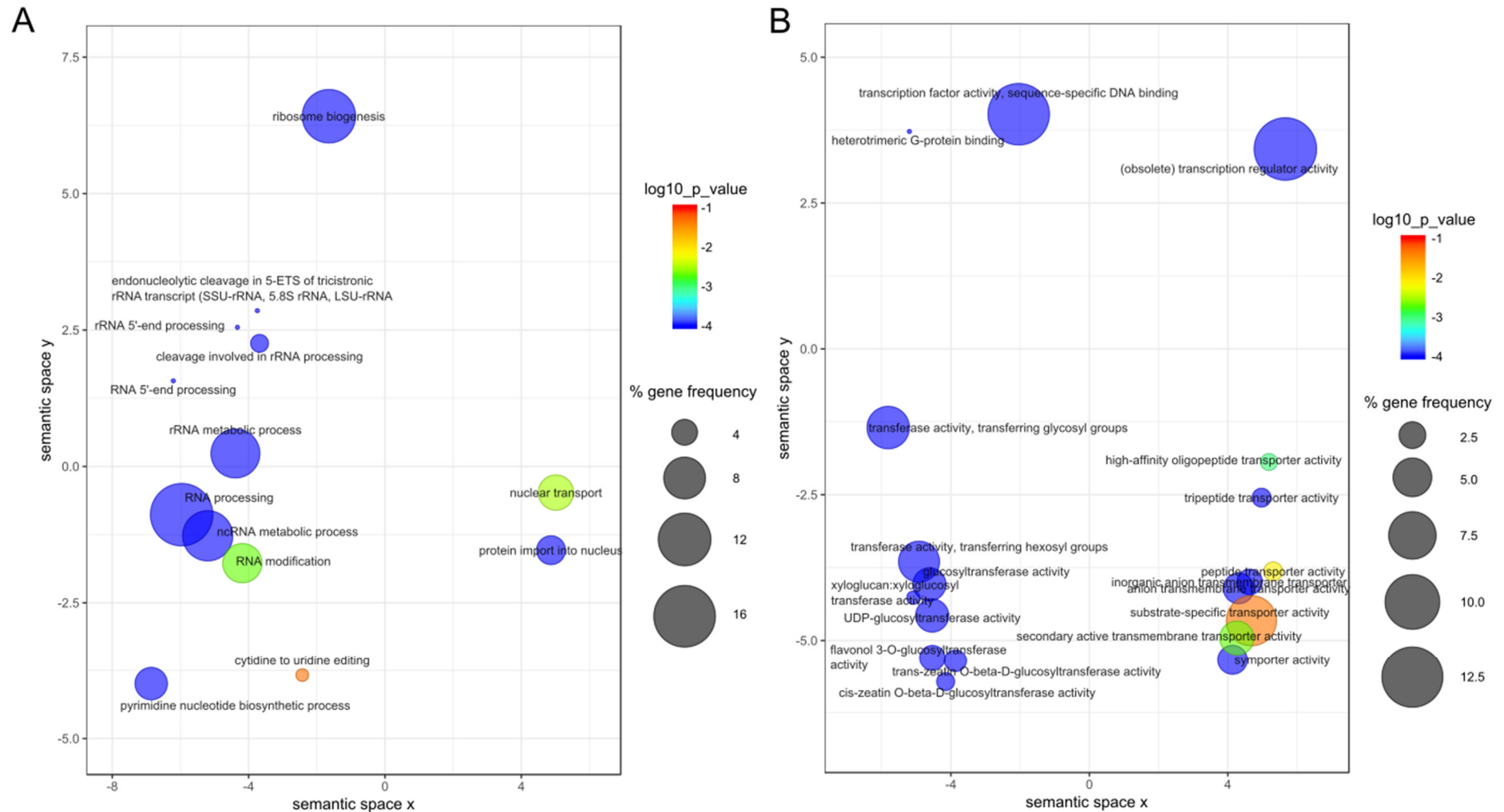


Figure S1. REVIGO scatter plot showing the selected GO terms enriched (FDR corrected $P \leq 0.05$) in the significantly **A**) up-regulated and **B**) down-regulated genes in leaves of *S. indica*-colonised plants. Cluster representatives are presented here (i.e. terms remaining after the redundancy reduction) in a two dimensional space derived by applying multidimensional scaling to a matrix of the GO terms' semantic similarities. Colour range is showing the Log_{10} of the simulation corrected P -value of enrichment and the size of the bubbles reflects the percentage of gene frequency (The percentage of genes involved in the GO category in the total number of significantly up-regulated genes).

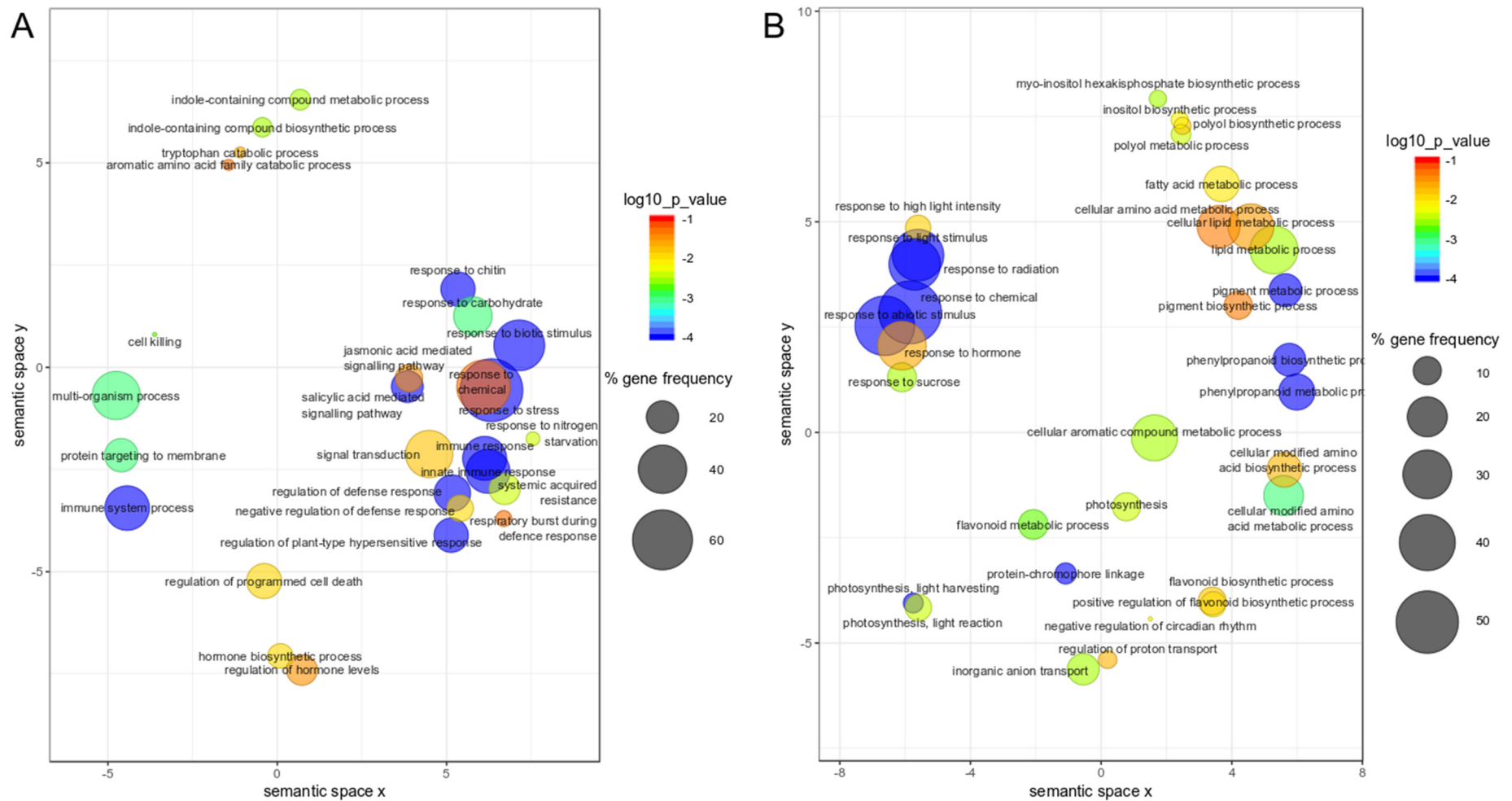
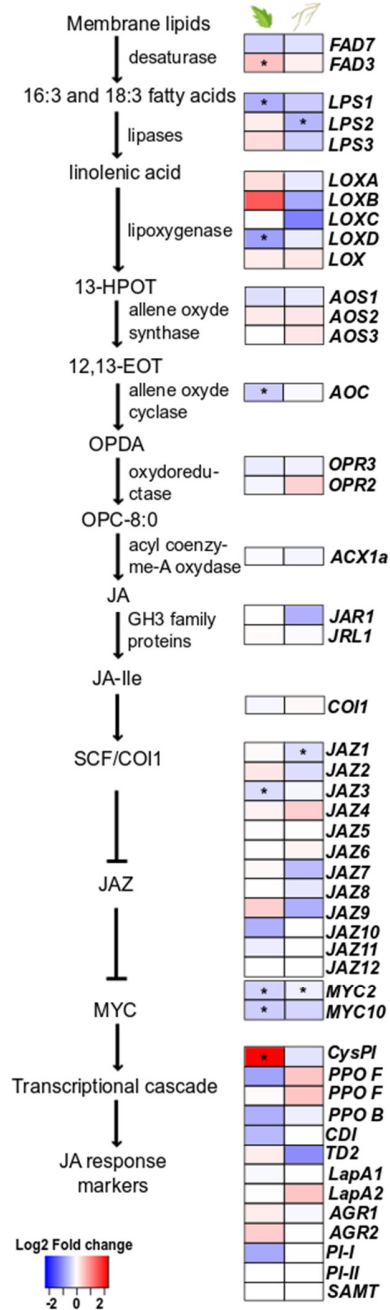


Figure S2. REVIGO scatter plot showing selected GO terms enriched (simulation corrected $P \leq 0.05$) in the significantly A) up-regulated and B) down-regulated genes in roots colonised by *S. indica*. Cluster representatives are presented here (i.e. terms remaining after the redundancy reduction) in a two-dimensional space derived by applying multidimensional scaling to a matrix of the GO terms' semantic similarities. Colour range is showing the Log10 of the simulation corrected P-value of enrichment and the size of the bubbles reflects the percentage of gene frequency (the percentage of genes involved in the GO category to the total number of significantly two-fold up-regulated genes).

Jasmonic acid cascade



Salicylic acid cascade

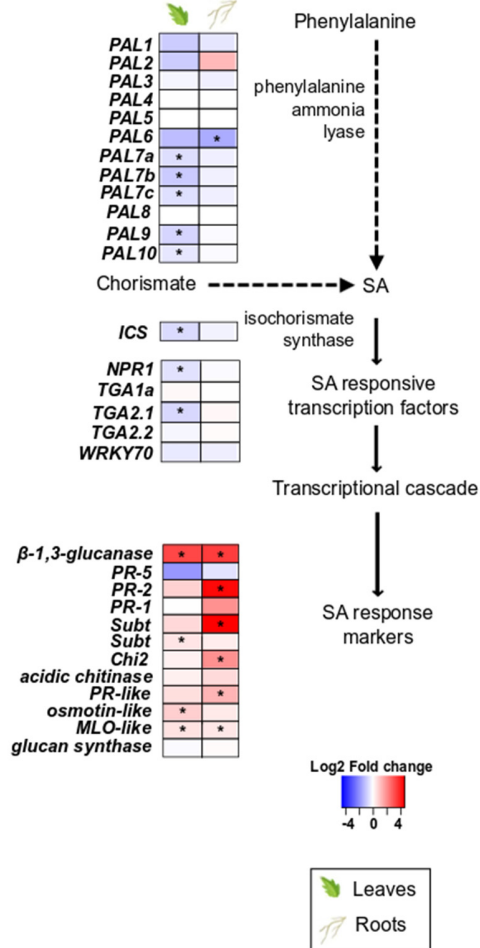


Figure S3. Effect of *S. indica*-colonisation on the expression of genes involved in the JA and SA biosynthesis and signalling pathways. Changes in gene expression between tissues from inoculated plants and tissues from endophyte-free plants are represented as the Log₂ of the fold change in the form of a heatmap. Data derived from RNA sequencing on leaves and roots from *S. indica*- and endophyte-free plants. Asterisks (*) indicate FDR corrected $P \leq 0.05$ (transformed from [90]).

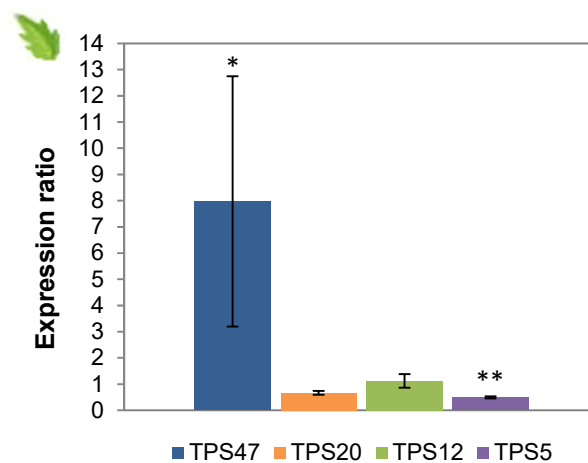


Figure S4. Expression ratio of tomato *TPS*s in leaves of colonised compared to leaves of endophyte-free plants. Data obtained using RT-qPCR on leaf RNA. Normalisation of expression data was done using expression level of *SITUB* (GenBank: DQ205342.1) expression levels. Calculation of gene expression ratio and statistical analyses were performed using the software tool REST© [91]. Error bars represent the standard deviation of the mean (* $P \leq 0.05$, ** $P \leq 0.005$).

Supplementary Methods

Validation of tomato *TPS* expression by RT-qPCR

The RNA samples sent for sequencing were used to synthesize cDNA and validate the expression of tomato *TPS*s. The Revert First Strand cDNA Synthesis kit (Thermo Fisher Scientific, USA) and an oligo-dT primer (Thermo Fisher Scientific, USA) were used to synthesize cDNA according to the manufacturer's instructions. For the RT-PCR, 300 ng of cDNA were used in a 10 μ l reaction using the Phusion High-Fidelity DNA Polymerase (Thermo Fischer Scientific, USA) and 0.5 μ M of *TPS*-specific primers (Supplementary Table S17). A cycling programme of 98°C for 30 sec, followed by 40 cycles of 98°C for 30 sec, 60°C for 20 sec, 72°C for 30 sec, with a final extension step at 72°C for 5 min was used. The amplicons were purified and send for sequencing to verify primer specificity. For the RT-qPCR, the cDNA was diluted 10 times (~300 ng μ l⁻¹) and 2 μ l were used as a template in a 10 μ l reaction, using 5 μ l of the Brilliant III Ultra-Fast SYBR® Green (Agilent Technologies, USA) and *TPS*-specific primers (Supplementary Table S17) in a concentration of 0.3-0.5 μ M. Each RT-qPCR reaction was performed with three technical replications for the four biological replications. The RT-qPCR amplification was performed using the AriaMx Real-Time PCR System-G8830A (Agilent Technologies, USA) with a programme of 95°C for 5 min, followed by 40 cycles of 95°C for 30 sec, 60°C for 1 min, and 72°C for 1 min. A final dissociation step was performed to assess the quality of amplified products and the specificity of the primers. Expression of *TPS*s was normalised using *S. lycopersicum* β -tubulin (TUB, GenBank: DQ205342.1) expression levels. Calculation of gene expression ratio between inoculated and non-inoculated plants and statistical analyses were performed using the software tool REST© [91] (Supplementary Figure S4).