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Supplementary Materials

Distinct Signatures of Host Defense Suppression by Plant-Feeding Mites

Figure S1. Relative transcript abundances of defense-associated tomato (*Solanum lycopersicum*) genes in leaflets after seven days of infestation with herbivorous mites. Tomato leaves were infested with either a single mite species (*Tetranychus urticae* [Tu], *Tetranychus evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]). Non-infested plants served as controls [C]. The figure shows the average (+ SEM) normalized transcript abundances of: (**A**) *Jasmonate-inducible protein 21* (*JIP-21*); (**B**) *Proteinase inhibitor IIc* (*PI-IIc*); (**C**) *Kunitz-type trypsin inhibitor* (*KTI_20*); (**D**) *Kunitz-type trypsin inhibitor* (*KTI_40*); (**E**) *Leucine aminopeptidase A1* (*LapA1*); (**F**) *Cytochrome P450* (*CYP450*); (**G**) *Serine proteinase inhibitor* (*Ser PI*); (**H**) *Isochorismate synthase* (*ICS*); (**I**) *β-1-3-glucanase* (*β-1-3-gluc*), and; (**J**) *Pathogenesis-related protein* (*PR-P*), as determined by qPCR. Transcript abundances were normalized to *Actin* and then scaled to the overall lowest average value per gene panel. Different letters above the bars indicate significant differences at a level of $P \leq 0.05$, after applying a generalized linear model followed by Fisher's Least Significant Difference test.

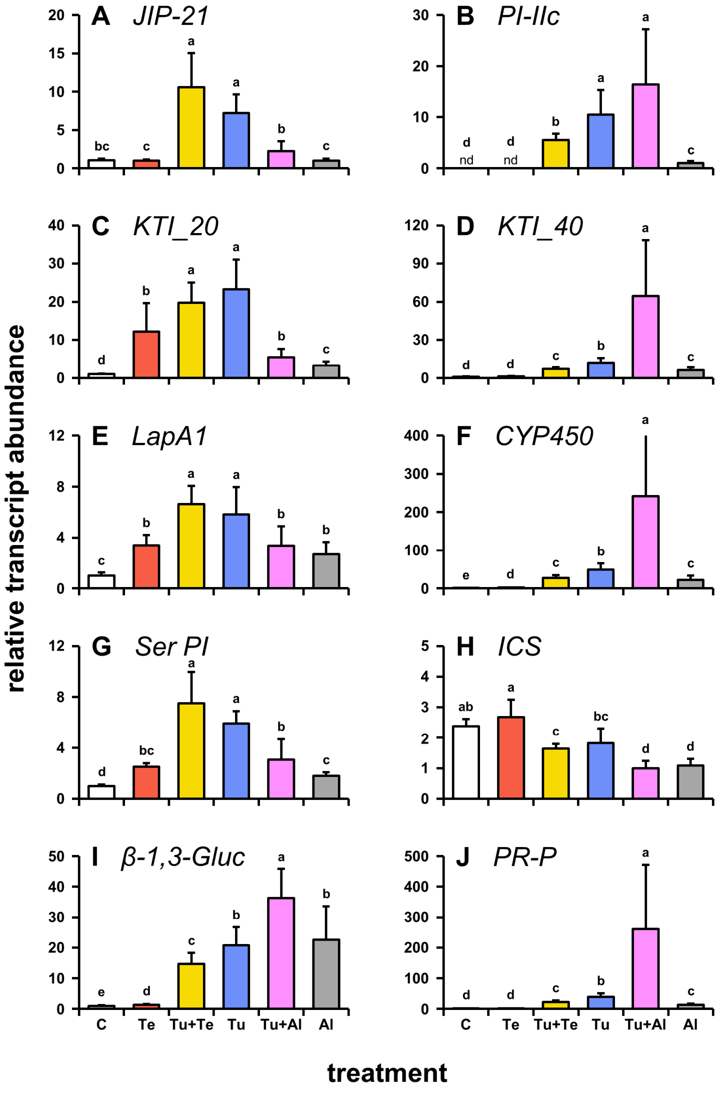


Figure S2. Relative transcript abundances of flavonoid and steroidal (glycol)alkaloid biosynthetic tomato (*Solanum lycopersicum*) genes in leaflets after seven days of infestation with herbivorous mites. Tomato leaves were infested with either a single mite species (*Tetranychus urticae* [Tu], *Tetranychus evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]). Non-infested plants served as controls [C]. The figure shows the average (+ SEM) normalized transcript abundances of: (**A**) *Chalcone synthase 1* (*CHS1*); (**B**) *Chalcone synthase 2* (*CHS2*); (**C**) *Glycoalkaloid metabolism 1* (*GAME1*), and; (**D**) *Glycoalkaloid metabolism 9 / Jasmonate-responsive ethylene response factor 4* (*GAME9/JRE4*), as determined by qPCR. Transcript abundances were normalized to *Actin* and then scaled to the overall lowest average value per gene panel. Different letters above the bars indicate significant differences at a level of $P \leq 0.05$, after applying a generalized linear model followed by Fisher's Least Significant Difference test.

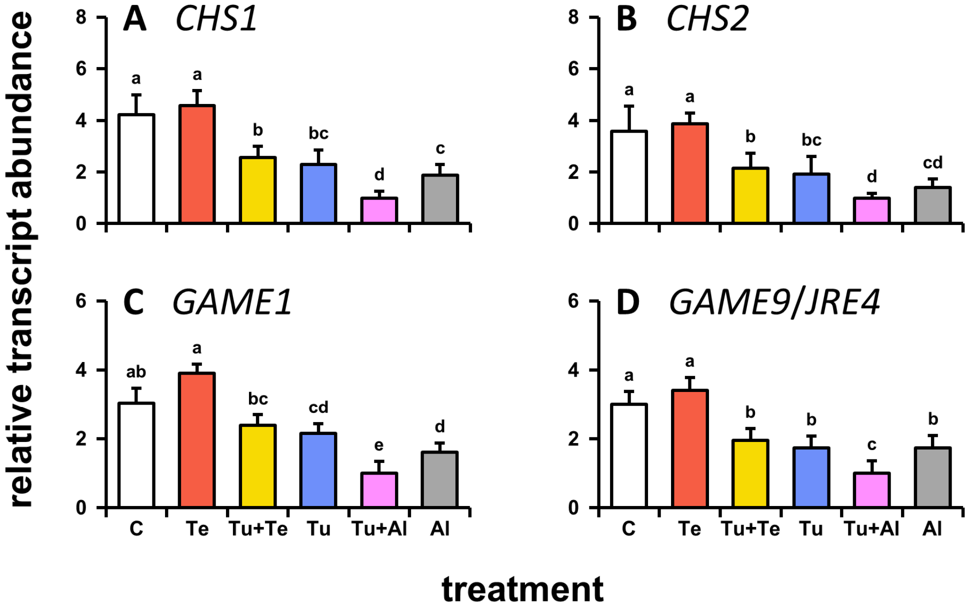
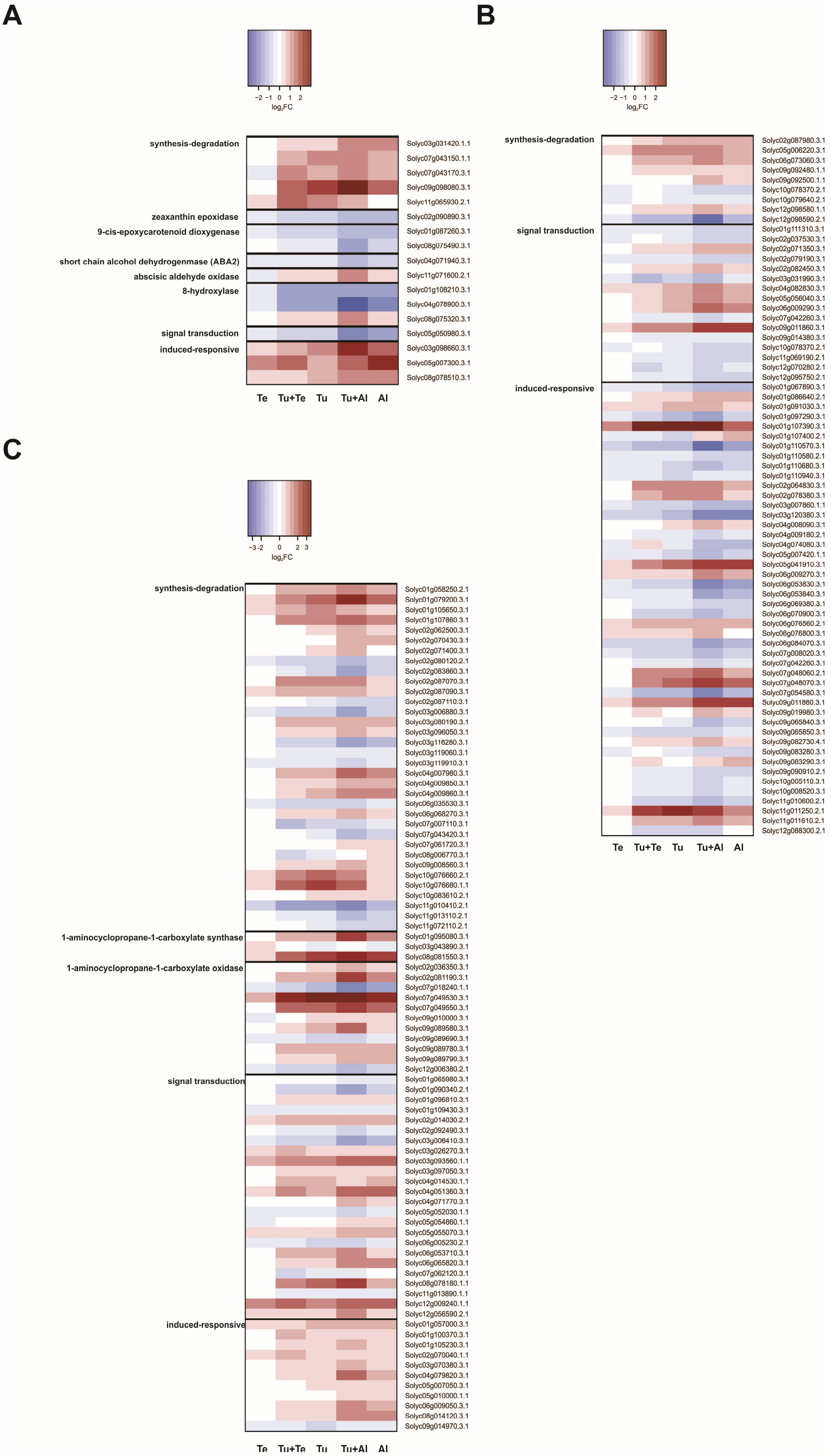


Figure S3. Gene-expression heat map depicting the relative transcript levels of tomato (*Solanum lycopersicum*) genes that encode proteins with a (predicted) function in phytohormone biosynthesis/signaling and that were differentially expressed in leaves after seven days of infestation with herbivorous mites. Tomato leaves were infested with either a single mite species (*Tetranychus urticae* [Tu], *Tetranychus evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]). Non-infested plants served as controls and were used as a common reference in the transcriptional comparisons. The figure shows heat maps for the following phytohormones: (**A**) abscisic acid, (**B**) auxin, (**C**) ethylene, (**D**) brassinosteroids, (**E**) gibberellins, and (**F**) cytokinins. Presented genes were differentially expressed (Benjamini and Hochberg false discovery rate adjusted $P \leq 0.05$; Log_2 fold change (FC) ≥ 0.585) in at least one of the mite-infestation treatments. The different (sub)sections of each pathway are specified on the left.


A
−2 −1 0 1 2
log2FC
synthesis-degradation
zeaxanthin epoxidase
9-cis-epoxycarotenoid dioxygenase
short chain alcohol dehydrogenmase (ABA2)
abscisic aldehyde oxidase
8-hydroxylase
signal transduction
induced-responsive
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Tu+Te
Tu
Tu+Al
Al
B
−2 −1 0 1 2
log2FC
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signal transduction
induced-responsive
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Te
Tu+Te
Tu
Tu+Al
Al
C
−3 -2 0 2 3
log2FC
synthesis-degradation
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1-aminocyclopropane-1-carboxylate oxidase
signal transduction
induced-responsive
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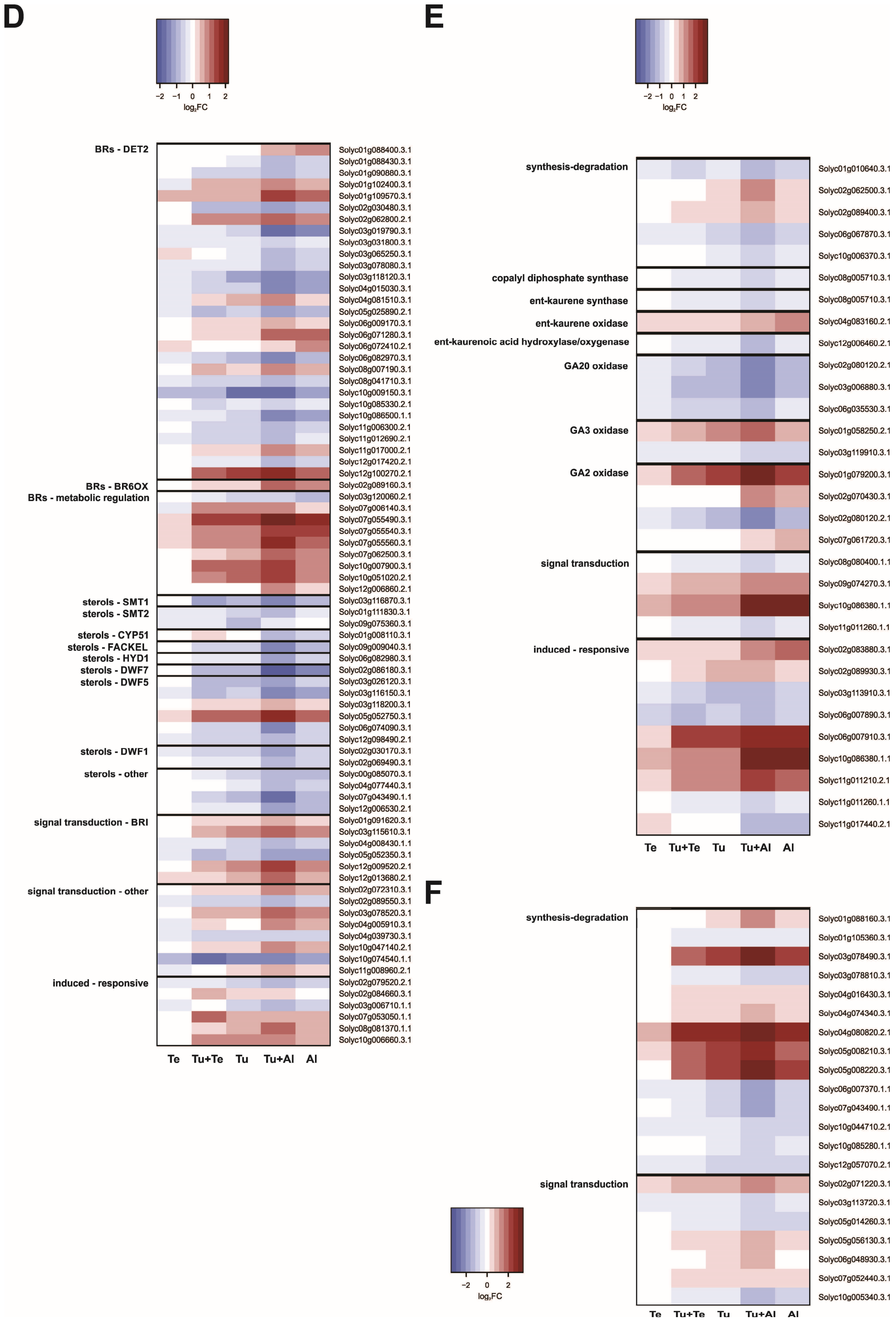
Tu+Te
Tu
Tu+Al
Al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log2FC
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Te Tu+Te Tu Tu+Al Al
F
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−2 0 2
log2FC
Te Tu+Te Tu Tu+Al Al

Table S1. Overview of microarray data, showing the transcriptomic changes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with either a single mite species (*Tetranychus urticae* [Tu], *T. evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls. Differentially expressed genes (DEGs) were identified based on a Benjamini and Hochberg false discovery rate adjusted $P \le 0.05$. ▲, up-regulated; ▼, down-regulated

	All DEGs			**DEGs at absolute fold change ≥ 1.5**		
Treatment	▲	▼	**Total**	▲	▼	**Total**
Te	37	1	38	35	1	36
Tu+Te	1,049	983	2,032	795	530	1,325
Tu	1,281	1,179	2,460	925	631	1,556
Tu+Al	2,517	2,635	5,132	1,678	1,672	3,350
Al	1,676	1,524	3,200	1,159	874	2,033

Table S2. Overview of microarray data, showing the results from a gene set enrichment analysis (GSA) of biological process (BP) gene ontology (GO) annotations per mite-infestation treatment. We surveyed transcriptomic changes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with either a single mite species (*Tetranychus urticae* [Tu], *T. evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls. Differentially expressed genes (DEGs) were identified based on a Benjamini and Hochberg (BH) false discovery rate adjusted $P \leq 0.05$ and an absolute fold change ≥ 1.5. The DEGs of each individual mite-infestation treatment were subsequently analyzed for enrichment of BP GO annotations using the PAGE algorithm (BH-adj $P \leq 0.05$). The Te treatment was excluded, because the number of Te-DEGs was insufficient for statistical analysis. (**A**) Results of the GSA for the up-regulated DEGs and (**B**) for the down-regulated DEGs per treatment. Values inside the columns annotated with 'DEGs' denote the number of up-regulated (▲) versus down-regulated (▼) DEGs associated with a particular GO term.

(A) GSA for up-regulated DEGs of each treatment		**Tu+Te**		**Tu**		**Tu+Al**		**Al**	
GO ID	**GO term**	**DEGs ▲ / ▼**	**BH-adj *P***	**DEGs ▲ / ▼**	**BH-adj *P***	**DEGs ▲ / ▼**	**BH-adj *P***	**DEGs ▲ / ▼**	**BH-adj *P***
GO:0006468	protein phosphorylation	64 / 19	0.0204	79 / 22	0.0003	145 / 54	0.0033	104 / 31	0.0046
GO:0042744	hydrogen peroxide catabolic process	14 / 0	0.0200	16 / 2	0.0419	17 / 5	0.0044	13 / 3	0.0107
GO:0048544	recognition of pollen	10 / 0	0.0259	11 / 0	0.0324	15 / 1	0.0033	10 / 0	0.0046
GO:0006032	chitin catabolic process	6 / 0	0.0432	7 / 0	0.0419	8 / 0	0.0066	7 / 0	0.0359
GO:0006629	lipid metabolic process	14 / 3	0.0200	16 / 5	0.0324	22 / 15	0.0451	19 / 8	0.0552
GO:0019752	carboxylic acid metabolic process	5 / 1	0.0120	6 / 3	0.0756	6 / 4	0.0451	6 / 1	0.0264
GO:0006950	response to stress	11 / 0	0.0277	12 / 0	0.0419	18 / 5	0.0264	14 / 3	0.0678
GO:0006952	defense response	7 / 0	0.0259	6 / 1	0.0419	10 / 7	0.2324	6 / 2	0.0581
GO:0009607	response to biotic stimulus	5 / 0	0.0259	-	-	5 / 5	0.2653	5 / 1	0.0376
GO:0055114	oxidation-reduction process	96 / 41	0.0204	107 / 51	0.0324	161 / 155	0.3173	107 / 90	0.9431
GO:0016998	cell wall macromolecule catabolic process	-	-	5 / 0	0.0419	5 / 0	0.0172	5 / 0	0.0552
GO:0006811	ion transport	-	-	5 / 0	0.0419	5 / 1	0.0451	5 / 0	0.0552
GO:0006457	protein folding	5 / 2	0.2463	5 / 0	0.0419	9 / 9	0.5074	7 / 1	0.0678
GO:0006979	response to oxidative stress	18 / 3	0.0532	20 / 6	0.1419	23 / 14	0.0451	16 / 7	0.0678
GO:0006869	lipid transport	6 / 0	0.0713	6 / 0	0.1419	8 / 2	0.0451	6 / 1	0.0678
GO:0009664	plant-type cell wall organization	-	-	-	-	7 / 1	0.0451	-	-

(B) GSA for down-regulated DEGs of each treatment

GO ID	**GO term**								
GO:0015979	photosynthesis	0 / 12	0.0001	0 / 14	0.0001	0 / 38	0.0001	0 / 32	0.0001
GO:0009765	photosynthesis. light harvesting	-	-	0 / 7	0.0021	0 / 17	0.0001	0 / 17	0.0001
GO:0015995	chlorophyll biosynthetic process	-	-	-	-	0 / 6	0.0286	0 / 6	0.0313
GO:0006096	glycolytic process	-	-	-	-	2 / 9	0.1529	0 / 6	0.0313
GO:0008152	metabolic process	44 / 22	0.9997	48 / 32	0.9998	76 / 82	0.7245	47 / 54	0.0313

Table S3. List of the 25 most highly up-regulated genes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with *Tetranychus urticae*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*T. urticae* [Tu], *T. evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]). The asterisk denotes that JA-inducibility of the respective gene was established by [75]. Genes were ranked according to their relative expression level in the Tu sample (shaded grey).

				Te		**Tu+Te**		**Tu**		**Tu+Al**		**Al**	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc03g098760	Kunitz-type trypsin inhibitor	YES	2.85	< 0.0001	4.64	< 0.0001	4.70	< 0.0001	3.48	< 0.0001	2.16	< 0.0001
2	Solyc10g005320	Tryptophan synthase	YES	1.81	0.0004	4.14	< 0.0001	4.36	< 0.0001	4.31	< 0.0001	2.41	< 0.0001
3	Solyc10g083690	Cytochrome P450		0.54	0.9994	3.49	< 0.0001	4.29	< 0.0001	5.30	< 0.0001	3.29	< 0.0001
4	Solyc01g080570	Inosine/uridine-preferring nucleoside hydrolase		0.72	0.9994	3.61	< 0.0001	4.22	< 0.0001	4.65	< 0.0001	3.29	< 0.0001
5	Solyc04g064880	Pathogenesis-related protein		0.17	0.9994	3.28	< 0.0001	3.92	< 0.0001	4.90	< 0.0001	2.58	< 0.0001
6	Solyc05g014590	bHLH DNA-binding protein		2.19	< 0.0001	3.77	< 0.0001	3.89	< 0.0001	4.49	< 0.0001	3.78	< 0.0001
7	Solyc01g106620	Pathogenesis-related protein 1		0.51	0.9994	3.38	< 0.0001	3.83	< 0.0001	4.09	< 0.0001	2.72	< 0.0001
8	Solyc01g105450	ABC transporter	YES	1.55	0.0014	3.32	< 0.0001	3.79	< 0.0001	3.38	< 0.0001	2.36	< 0.0001
9	Solyc01g106630	CBL-interacting protein kinase 23		0.49	0.9994	3.35	< 0.0001	3.79	< 0.0001	4.14	< 0.0001	2.46	< 0.0001
10	Solyc03g098720	Kunitz-type trypsin inhibitor	YES	2.04	0.0104	3.70	< 0.0001	3.69	< 0.0001	1.59	0.0025	1.13	0.0527
11	Solyc09g091550	Salicylic acid methyltransferase	YES*	1.59	< 0.0001	3.58	< 0.0001	3.64	< 0.0001	3.78	< 0.0001	2.87	< 0.0001
12	Solyc08g074682	Polyphenol oxidase precursor		1.35	0.0104	3.52	< 0.0001	3.60	< 0.0001	3.61	< 0.0001	0.85	0.0240
13	Solyc01g060020	β-1,3-glucanase		0.43	0.9994	2.90	< 0.0001	3.53	< 0.0001	4.13	< 0.0001	3.26	< 0.0001
14	Solyc08g067630	Histone deacetylase-like protein		1.58	0.1823	3.31	< 0.0001	3.52	< 0.0001	4.37	< 0.0001	3.39	< 0.0001
15	Solyc01g059990	Serine/threonine protein phosphatase		0.34	0.9994	3.03	< 0.0001	3.51	< 0.0001	3.94	< 0.0001	3.15	< 0.0001
16	Solyc01g059980	β-1,3-glucanase		0.36	0.9994	3.03	< 0.0001	3.45	< 0.0001	3.96	< 0.0001	3.15	< 0.0001
17	Solyc05g050350	Cyclic nucleotide-gated channel		0.97	0.0558	2.89	< 0.0001	3.42	< 0.0001	3.98	< 0.0001	3.23	< 0.0001
18	Solyc12g049030	Fatty acid desaturase		0.33	0.9994	2.75	0.0006	3.36	< 0.0001	3.11	< 0.0001	2.98	0.0001
19	Solyc05g007950	Ribonuclease LE		2.50	< 0.0001	3.41	< 0.0001	3.33	< 0.0001	4.10	< 0.0001	4.16	< 0.0001
20	Solyc01g059965	β-1,3-glucanase		0.34	0.9994	2.82	< 0.0001	3.33	< 0.0001	3.81	< 0.0001	2.96	< 0.0001
21	Solyc04g074770	Unknown protein	YES	1.64	< 0.0001	3.25	< 0.0001	3.26	< 0.0001	2.54	< 0.0001	1.22	0.0001
22	Solyc03g044830	Transducin/WD40 repeat-like protein		0.28	0.9994	2.64	< 0.0001	3.23	< 0.0001	3.79	< 0.0001	2.57	< 0.0001
23	Solyc03g020060	Proteinase inhibitor IId		0.91	0.6783	3.02	< 0.0001	3.17	< 0.0001	1.75	< 0.0001	0.62	0.2031
24	Solyc10g078230	Cytochrome P450		-0.01	0.9994	2.66	< 0.0001	3.17	< 0.0001	4.32	< 0.0001	3.16	< 0.0001
25	Solyc02g067750	Carbonic anhydrase	YES	1.03	0.7322	2.76	< 0.0001	3.13	< 0.0001	3.02	< 0.0001	1.65	0.0010

Table S4. List of the 25 most highly up-regulated genes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with *Tetranychus evansi*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*T. urticae* [Tu], *T. evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]). The asterisk denotes that JA-inducibility of the respective gene was established by [75]. Genes were ranked according to their relative expression level in the Te sample (shaded grey).

				Te		**Tu+Te**		**Tu**		**Tu+Al**		**Al**	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc03g098760	Kunitz-type trypsin inhibitor	YES	2.85	< 0.0001	4.64	< 0.0001	4.70	< 0.0001	3.48	< 0.0001	2.16	< 0.0001
2	Solyc05g007950	Ribonuclease LE		2.50	< 0.0001	3.41	< 0.0001	3.33	< 0.0001	4.10	< 0.0001	4.16	< 0.0001
3	Solyc05g014590	bHLH DNA-binding protein		2.19	< 0.0001	3.77	< 0.0001	3.89	< 0.0001	4.49	< 0.0001	3.78	< 0.0001
4	Solyc03g098720	Kunitz-type trypsin inhibitor	YES	2.04	0.0104	3.70	< 0.0001	3.69	< 0.0001	1.59	0.0025	1.13	0.0527
5	Solyc10g005320	Tryptophan synthase	YES	1.81	0.0004	4.14	< 0.0001	4.36	< 0.0001	4.31	< 0.0001	2.41	< 0.0001
6	Solyc04g074770	Unknown protein	YES	1.64	< 0.0001	3.25	< 0.0001	3.26	< 0.0001	2.54	< 0.0001	1.22	0.0001
7	Solyc09g091550	Salicylic acid methyltransferase	YES*	1.59	< 0.0001	3.58	< 0.0001	3.64	< 0.0001	3.78	< 0.0001	2.87	< 0.0001
8	Solyc12g010020	Leucine aminopeptidase A1	YES	1.58	0.0316	2.63	< 0.0001	2.17	< 0.0001	1.35	0.0024	0.70	0.1912
9	Solyc01g105450	ABC transporter	YES	1.55	0.0014	3.32	< 0.0001	3.79	< 0.0001	3.38	< 0.0001	2.36	< 0.0001
10	Solyc10g075110	Non-specific lipid-transfer protein		1.49	0.0003	1.64	< 0.0001	0.71	0.0354	3.21	< 0.0001	3.76	< 0.0001
11	Solyc02g093580	Pectate lyase		1.45	< 0.0001	2.74	< 0.0001	2.71	< 0.0001	3.35	< 0.0001	2.99	< 0.0001
12	Solyc04g079730	Allene oxide synthase	YES	1.40	< 0.0001	1.72	< 0.0001	1.67	< 0.0001	1.85	< 0.0001	1.72	< 0.0001
13	Solyc08g036640	Jasmonate ZIM-domain protein 9	YES	1.36	0.0004	2.15	< 0.0001	2.30	< 0.0001	2.57	< 0.0001	2.50	< 0.0001
14	Solyc01g094250	Short-chain dehydrogenase/reductase		1.35	0.0329	2.14	< 0.0001	2.12	< 0.0001	2.37	< 0.0001	1.68	< 0.0001
15	Solyc08g074682	Polyphenol oxidase precursor		1.35	0.0104	3.52	< 0.0001	3.60	< 0.0001	3.61	< 0.0001	0.85	0.0240
16	Solyc10g078360	Short-chain dehydrogenase/reductase	YES	1.34	< 0.0001	2.40	< 0.0001	2.34	< 0.0001	1.60	< 0.0001	1.03	< 0.0001
17	Solyc01g021600	Dirigent protein		1.27	0.0027	2.86	< 0.0001	2.91	< 0.0001	4.73	< 0.0001	4.63	< 0.0001
18	Solyc02g077420	Phospholipase A1	YES	1.22	0.0207	2.44	< 0.0001	2.46	< 0.0001	2.37	< 0.0001	2.23	< 0.0001
19	Solyc08g036660	Jasmonate ZIM-domain protein 11		1.19	0.0191	2.35	< 0.0001	2.70	< 0.0001	3.41	< 0.0001	2.66	< 0.0001
20	Solyc02g093250	Caffeoyl-CoA O-methyltransferase		1.16	0.0160	1.63	< 0.0001	1.89	< 0.0001	2.65	< 0.0001	2.75	< 0.0001
21	Solyc01g109710	Universal stress protein	YES	1.03	0.0017	1.90	< 0.0001	1.86	< 0.0001	2.49	< 0.0001	1.81	< 0.0001
22	Solyc06g075690	Auxin-regulated protein		1.02	0.0027	2.17	< 0.0001	2.24	< 0.0001	3.39	< 0.0001	3.06	< 0.0001
23	Solyc03g013160	Amino acid transporter, putative	YES	1.01	0.0034	2.03	< 0.0001	2.07	< 0.0001	2.01	< 0.0001	1.59	< 0.0001
24	Solyc05g051480	DNA-directed RNA polymerase subunit		1.00	0.0473	2.73	< 0.0001	2.66	< 0.0001	3.23	< 0.0001	2.89	< 0.0001
25	Solyc08g068680	Aromatic amino acid decarboxylase 1A		1.00	0.0034	2.84	< 0.0001	3.03	< 0.0001	3.70	< 0.0001	3.01	< 0.0001

Table S5. List of the 25 most highly up-regulated genes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with *Aculops lycopersici*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*Tetranychus urticae* [Tu], *T. evansi* [Te], or *A. lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]; note that none of the genes in this top list were JA-inducible according to these criteria). Genes were ranked according to their relative expression level in the Al sample (shaded grey).

				Te		Tu+Te		Tu		Tu+Al		Al	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc01g021600	Dirigent protein		1.27	0.0027	2.86	< 0.0001	2.91	< 0.0001	4.73	< 0.0001	4.63	< 0.0001
2	Solyc05g007950	Ribonuclease LE		2.50	< 0.0001	3.41	< 0.0001	3.33	< 0.0001	4.10	< 0.0001	4.16	< 0.0001
3	Solyc02g062890	Polyol monosaccharide transporter 5		0.02	0.9994	2.44	< 0.0001	2.77	< 0.0001	4.06	< 0.0001	3.85	< 0.0001
4	Solyc05g014590	bHLH DNA-binding protein		2.19	< 0.0001	3.77	< 0.0001	3.89	< 0.0001	4.49	< 0.0001	3.78	< 0.0001
5	Solyc10g075110	Non-specific lipid-transfer protein		1.49	0.0003	1.64	< 0.0001	0.71	0.0354	3.21	< 0.0001	3.76	< 0.0001
6	Solyc01g105070	Peroxidase precursor		0.78	0.0539	2.12	< 0.0001	2.37	< 0.0001	3.84	< 0.0001	3.75	< 0.0001
7	Solyc02g071130	WRKY transcription factor 71		0.76	0.5048	2.39	< 0.0001	2.50	< 0.0001	3.91	< 0.0001	3.43	< 0.0001
8	Solyc08g067630	Histone deacetylase-like protein		1.58	0.1823	3.31	< 0.0001	3.52	< 0.0001	4.37	< 0.0001	3.39	< 0.0001
9	Solyc05g005865	Major latex-like protein		0.73	0.6783	1.00	0.0078	0.34	0.4910	2.51	< 0.0001	3.36	< 0.0001
10	Solyc04g071070	Extensin		0.96	0.5886	2.28	< 0.0001	1.83	< 0.0001	3.56	< 0.0001	3.34	< 0.0001
11	Solyc10g083290	Extracellular invertase LIN6		0.36	0.9994	1.93	< 0.0001	2.55	< 0.0001	3.62	< 0.0001	3.29	< 0.0001
12	Solyc10g083690	Cytochrome P450		0.54	0.9994	3.49	< 0.0001	4.29	< 0.0001	5.30	< 0.0001	3.29	< 0.0001
13	Solyc01g080570	Inosine-uridine preferring nucleoside hydrolase		0.72	0.9994	3.61	< 0.0001	4.22	< 0.0001	4.65	< 0.0001	3.29	< 0.0001
14	Solyc01g060020	β-1,3-glucanase		0.43	0.9994	2.90	< 0.0001	3.53	< 0.0001	4.13	< 0.0001	3.26	< 0.0001
15	Solyc05g050350	Cyclic nucleotide-gated channel		0.97	0.0558	2.89	< 0.0001	3.42	< 0.0001	3.98	< 0.0001	3.23	< 0.0001
16	Solyc01g073820	Unknown protein		0.52	0.9743	1.98	< 0.0001	2.46	< 0.0001	3.23	< 0.0001	3.22	< 0.0001
17	Solyc10g078230	Cytochrome P450		-0.01	0.9994	2.66	< 0.0001	3.17	< 0.0001	4.32	< 0.0001	3.16	< 0.0001
18	Solyc01g059980	β-1,3-glucanase		0.36	0.9994	3.03	< 0.0001	3.45	< 0.0001	3.96	< 0.0001	3.15	< 0.0001
19	Solyc01g059990	Serine/threonine protein phosphatase		0.34	0.9994	3.03	< 0.0001	3.51	< 0.0001	3.94	< 0.0001	3.15	< 0.0001
20	Solyc04g072000	Chitinase		0.65	0.5372	2.89	< 0.0001	3.00	< 0.0001	3.89	< 0.0001	3.13	< 0.0001
21	Solyc02g036480	Unknown protein		0.77	0.3696	2.59	< 0.0001	2.83	< 0.0001	3.56	< 0.0001	3.09	< 0.0001
22	Solyc01g006950	Syntaxin		0.85	0.3007	2.71	< 0.0001	2.84	< 0.0001	3.74	< 0.0001	3.07	< 0.0001
23	Solyc06g075690	Auxin-regulated protein		1.02	0.0027	2.17	< 0.0001	2.24	< 0.0001	3.39	< 0.0001	3.06	< 0.0001
24	Solyc09g009985	Unknown protein		0.57	0.7793	1.87	< 0.0001	2.19	< 0.0001	3.37	< 0.0001	3.04	< 0.0001
25	Solyc04g011750	Unknown protein		0.18	0.9994	1.52	0.0002	1.80	< 0.0001	3.32	< 0.0001	3.02	< 0.0001

Table S6. List of the 25 most strongly down-regulated genes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with *Aculops lycopersici*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*Tetranychus urticae* [Tu], *T. evansi* [Te], or *A. lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]); note that none of the genes in this top list were JA-inducible according to these criteria. Genes were ranked according to their relative expression level in the Al sample (shaded grey).

				Te		Tu+Te		Tu		Tu+Al		Al	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc11g056680	LRR receptor-like kinase		-0.63	0.9994	-1.00	0.0387	-1.57	0.0004	-3.03	< 0.0001	-2.39	< 0.0001
2	Solyc07g063905	RING/U-box protein		-0.23	0.9994	-0.27	0.7215	-0.55	0.3009	-2.32	< 0.0001	-2.08	< 0.0001
3	Solyc08g005680	Cis-prenyltransferase 1 / Neryl diphosphate synthase 1		-0.26	0.9994	-0.07	0.9190	-0.61	0.0948	-2.35	< 0.0001	-1.97	< 0.0001
4	Solyc03g120380	IAA19		-0.92	0.1316	-0.85	0.0148	-1.35	< 0.0001	-2.15	< 0.0001	-1.94	< 0.0001
5	Solyc10g008720	GDSL esterase/lipase		-0.31	0.9994	-0.78	0.1329	-0.93	0.0508	-2.72	< 0.0001	-1.93	< 0.0001
6	Solyc06g069730	Chlorophyll A-B binding protein		-0.60	0.9994	-1.18	0.0391	-1.27	0.0177	-2.18	< 0.0001	-1.93	0.0002
7	Solyc08g067030	Unknown protein		-0.50	0.9994	-0.45	0.6107	-1.11	0.0622	-2.32	< 0.0001	-1.86	0.0008
8	Solyc07g018240	Long-chain fatty acid elongase		-0.42	0.9994	-0.90	0.0055	-1.16	0.0002	-2.39	< 0.0001	-1.77	< 0.0001
9	Solyc06g071320	Unknown protein		-0.48	0.9994	-1.43	0.0004	-1.60	< 0.0001	-2.49	< 0.0001	-1.75	< 0.0001
10	Solyc08g014430	Formin 3 (actin-binding)		-0.21	0.9994	-0.84	0.0313	-0.78	0.0390	-1.99	< 0.0001	-1.75	< 0.0001
11	Solyc03g116730	Stearoyl-CoA 9-desaturase		-0.30	0.9994	-0.93	0.0146	-0.83	0.0234	-1.89	< 0.0001	-1.70	< 0.0001
12	Solyc12g055970	Endoglucanase		-0.13	0.9994	-0.60	0.1126	-0.61	0.0828	-1.58	< 0.0001	-1.64	< 0.0001
13	Solyc12g011010	Meiosis 5		-0.42	0.9994	-0.96	0.0918	-1.83	0.0003	-2.72	< 0.0001	-1.64	0.0009
14	Solyc09g082660	Caffeoyl-CoA O-methyltransferase		-0.15	0.9994	-1.43	0.0001	-1.27	0.0003	-2.84	< 0.0001	-1.63	< 0.0001
15	Solyc10g083670	Glycosyltransferase		-0.23	0.9994	-0.26	0.7009	-0.75	0.0796	-1.84	< 0.0001	-1.62	< 0.0001
16	Solyc06g009190	Pectinesterase		-0.35	0.9994	-1.01	0.0279	-1.24	0.0036	-2.74	< 0.0001	-1.62	0.0001
17	Solyc03g098480	Unknown protein		0.04	0.9994	-1.00	0.0023	-0.79	0.0138	-2.31	< 0.0001	-1.61	< 0.0001
18	Solyc05g053550	Chalcone synthase 2		-0.12	0.9994	-0.62	0.1086	-0.99	0.0036	-2.36	< 0.0001	-1.59	< 0.0001
19	Solyc02g080200	Pectinesterase		-0.68	0.9994	-1.04	0.0300	-1.07	0.0184	-2.03	< 0.0001	-1.59	0.0003
20	Solyc10g083300	Extracellular invertase LIN8		-0.46	0.9994	-1.17	0.0014	-1.00	0.0049	-2.12	< 0.0001	-1.56	< 0.0001
21	Solyc08g076820	bHLH transcription factor 146		-0.49	0.9994	-1.23	0.0003	-1.46	< 0.0001	-2.03	< 0.0001	-1.56	< 0.0001
22	Solyc01g006330	Plastid-lipid-associated protein		-0.49	0.9994	-1.23	0.0002	-1.25	0.0001	-2.01	< 0.0001	-1.56	< 0.0001
23	Solyc12g044280	Photosystem I reaction center subunit		-0.21	0.9994	-0.86	0.0465	-0.96	0.0169	-1.79	< 0.0001	-1.54	0.0001
24	Solyc01g110570	Small auxin up-regulated RNA 4		-0.72	0.9994	-1.22	0.0240	-1.33	0.0091	-2.35	< 0.0001	-1.54	0.0017
25	Solyc05g009270	Long-chain fatty acid elongase		-0.37	0.9994	-0.54	0.0493	-0.69	0.0063	-1.68	< 0.0001	-1.53	< 0.0001

Table S7. List of the 25 tomato (*Solanum lycopersicum*) genes that are most highly up-regulated in leaves after seven days of infestation with *Aculops lycopersici* while not differentially regulated after infestation with *Tetranychus urticae*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*T. urticae* [Tu], *T. evansi* [Te], or *A. lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Differentially expressed genes were identified based on a BH-adj $P \leq 0.05$. Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]). Genes were ranked according to their relative expression level in the Al sample (shaded grey).

				Te		Tu+Te		Tu		Tu+Al		Al	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc05g005865	Major latex-like protein		0.73	0.6783	1.00	0.0078	0.34	0.4910	2.51	< 0.0001	3.36	< 0.0001
2	Solyc02g071620	GDSL-motif lipase/hydrolase		0.37	0.9994	0.27	0.6431	0.52	0.2246	2.14	< 0.0001	2.43	< 0.0001
3	Solyc09g018020	Expansin		0.04	0.9994	0.14	0.8012	-0.05	0.9338	2.13	< 0.0001	2.42	< 0.0001
4	Solyc09g063060	GDSL esterase/lipase		0.09	0.9994	0.26	0.5577	0.19	0.7104	1.77	< 0.0001	2.25	< 0.0001
5	Solyc06g061280	Cinnamoyl-CoA reductase		0.20	0.9994	0.71	0.0529	0.56	0.1252	2.24	< 0.0001	2.22	< 0.0001
6	Solyc01g011430	O-acyltransferase		0.22	0.9994	0.29	0.5379	0.23	0.6339	1.39	< 0.0001	1.95	< 0.0001
7	Solyc01g105710	Peptidyl-prolyl isomerase		0.43	0.6890	0.21	0.4765	-0.28	0.2811	1.34	< 0.0001	1.90	< 0.0001
8	Solyc01g079940	Xylanase inhibitor		0.22	0.9994	0.36	0.2379	0.44	0.0961	1.78	< 0.0001	1.90	< 0.0001
9	Solyc07g052135	Sesquiterpene synthase		-0.17	0.9994	1.24	0.1438	1.46	0.0576	2.42	0.0003	1.88	0.0085
10	Solyc11g067190	Fatty acyl-CoA reductase		0.01	0.9994	0.54	0.4487	0.79	0.1684	2.72	< 0.0001	1.86	0.0002
11	Solyc12g011030	Xyloglucan endotransglucosylase-hydrolase		0.02	0.9994	0.73	0.0868	0.73	0.0667	1.71	< 0.0001	1.82	< 0.0001
12	Solyc05g009430	Endonuclease		0.19	0.9994	0.50	0.1407	0.57	0.0643	1.81	< 0.0001	1.81	< 0.0001
13	Solyc03g082690	U-box domain-containing protein		0.31	0.9994	0.68	0.3305	1.04	0.0672	1.54	0.0017	1.66	0.0015
14	Solyc01g098590	Phosphoglycerate mutase		0.50	0.9994	0.82	0.4476	0.99	0.3009	1.30	0.0801	1.61	0.0401
15	Solyc02g070890	LRR receptor like kinase FLS2		0.06	0.9994	0.46	0.3107	0.62	0.1103	1.46	< 0.0001	1.60	< 0.0001
16	Solyc09g097770	Glycine-rich cell wall protein		0.67	0.9994	1.32	0.1063	1.28	0.1020	1.79	0.0069	1.53	0.0347
17	Solyc05g055400	Cytochrome P450		0.04	0.9994	0.43	0.4237	0.12	0.8797	0.95	0.0074	1.49	0.0001
18	Solyc06g065820	Ethylene Response Factor H.1		-0.17	0.9994	0.56	0.0485	0.35	0.2647	1.44	< 0.0001	1.47	< 0.0001
19	Solyc07g049440	GDSL esterase/lipase		0.30	0.9994	0.14	0.8380	-0.36	0.4600	0.54	0.1168	1.45	< 0.0001
20	Solyc06g007460	Epidermal patterning factor		0.12	0.9994	0.90	0.0038	0.57	0.0738	1.61	< 0.0001	1.44	< 0.0001
21	Solyc06g074790	Histone H2B	YES	0.18	0.9994	0.71	0.3261	0.74	0.2685	1.15	0.0273	1.41	0.0102
22	Solyc03g093120	Xyloglucan endotransglucosylase-hydrolase		0.26	0.9994	0.84	0.0356	0.76	0.0512	1.39	0.0001	1.39	0.0001
23	Solyc05g055080	Unknown protein		0.27	0.9994	0.60	0.1773	0.63	0.1241	1.36	0.0001	1.33	0.0003
24	Solyc04g050440	Ammonium transporter		0.23	0.9994	0.39	0.2389	0.42	0.1671	1.29	< 0.0001	1.33	< 0.0001
25	Solyc01g010390	β-glucosidase		0.22	0.9994	0.70	0.1031	0.54	0.2225	1.18	0.0007	1.31	0.0004

Table S8. List of the 25 tomato (*Solanum lycopersicum*) genes that are most strongly down-regulated in leaves after seven days of infestation with *Aculops lycopersici* while not differentially regulated after infestation with *Tetranychus urticae*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*T. urticae* [Tu], *T. evansi* [Te], or *A. lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Differentially expressed genes were identified based on a BH-adj *P* ≤ 0.05. Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]). Genes were ranked according to their relative expression level in the Al sample (shaded grey).

				Te		**Tu+Te**		**Tu**		**Tu+Al**		**Al**	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc07g063905	RING/U-box protein		-0.23	0.9994	-0.27	0.7215	-0.55	0.3009	-2.32	< 0.0001	-2.08	< 0.0001
2	Solyc08g005680	Cis-prenyltransferase 1 / Neryl diphosphate synthase 1		-0.26	0.9994	-0.07	0.9190	-0.61	0.0948	-2.35	< 0.0001	-1.97	< 0.0001
3	Solyc10g008720	GDSL esterase/lipase		-0.31	0.9994	-0.78	0.1329	-0.93	0.0508	-2.72	< 0.0001	-1.93	< 0.0001
4	Solyc08g067030	Unknown protein		-0.50	0.9994	-0.45	0.6107	-1.11	0.0622	-2.32	< 0.0001	-1.86	0.0008
5	Solyc12g055970	Endoglucanase		-0.13	0.9994	-0.60	0.1126	-0.61	0.0828	-1.58	< 0.0001	-1.64	< 0.0001
6	Solyc10g083670	Glycosyltransferase		-0.23	0.9994	-0.26	0.7009	-0.75	0.0796	-1.84	< 0.0001	-1.62	< 0.0001
7	Solyc06g066530	Unknown protein		0.01	0.9994	-0.30	0.5819	-0.50	0.2325	-2.14	< 0.0001	-1.50	< 0.0001
8	Solyc04g007825	MLP-like protein		-0.28	0.9994	-0.17	0.7947	-0.38	0.3891	-1.69	< 0.0001	-1.47	< 0.0001
9	Solyc06g084050	Photosystem II reaction center subunit		-0.24	0.9994	-0.57	0.4402	-0.93	0.1103	-1.95	0.0001	-1.41	0.0073
10	Solyc04g050820	Inositol-3-phosphate synthase		-0.28	0.9994	-0.45	0.5232	-0.65	0.2673	-1.87	< 0.0001	-1.35	0.0044
11	Solyc01g108630	Nitrite reductase		-0.34	0.9994	-0.32	0.5939	-0.26	0.6997	-1.34	0.0003	-1.34	0.0006
12	Solyc04g071340	Fructose-1,6-bisphosphatase		-0.27	0.9994	-0.80	0.0811	-0.67	0.1434	-1.57	< 0.0001	-1.31	0.0011
13	Solyc02g091920	Xyloglucan endotransglucosylase-hydrolase		-0.24	0.9994	-0.62	0.3978	-0.02	0.9863	-1.20	0.0176	-1.30	0.0156
14	Solyc06g064550	Aspartokinase-homoserine dehydrogenase		-0.20	0.9994	-0.81	0.0368	-0.64	0.0950	-1.49	< 0.0001	-1.30	0.0002
15	Solyc10g078530	Patatin (lipid acyl hydrolase)		-0.22	0.9994	0.28	0.4569	-0.20	0.6326	-1.45	< 0.0001	-1.29	< 0.0001
16	Solyc01g087040	Thylakoid luminal protein		-0.28	0.9994	-1.00	0.0237	-0.84	0.0509	-1.68	< 0.0001	-1.27	0.0015
17	Solyc06g072710	RNA polymerase sigma factor		-0.16	0.9994	-0.69	0.1283	-0.74	0.0780	-1.47	0.0001	-1.26	0.0010
18	Solyc06g060830	Homeobox-leucine zipper protein		-0.28	0.9994	-0.47	0.3721	-0.31	0.6067	-1.01	0.0060	-1.26	0.0012
19	Solyc12g099650	Photosystem II subunit		-0.01	0.9994	-0.20	0.8556	-0.49	0.5258	-1.81	0.0003	-1.26	0.0175
20	Solyc06g053840	IAA4		-0.34	0.9994	-0.41	0.4022	-0.55	0.1793	-1.51	< 0.0001	-1.26	0.0004
21	Solyc06g062370	Acid phosphatase	YES	-0.10	0.9994	1.35	0.0180	0.62	0.3598	-0.97	0.0536	-1.24	0.0189
22	Solyc03g006410	Unknown protein		-0.53	0.9994	-0.83	0.2320	-0.81	0.2161	-1.73	0.0008	-1.24	0.0271
23	Solyc10g054870	Triosephosphate isomerase		-0.64	0.9994	-0.48	0.4413	-0.89	0.0587	-1.58	0.0001	-1.24	0.0046
24	Solyc12g011280	Chlorophyll A-B binding protein		-0.27	0.9994	-0.87	0.0519	-0.82	0.0549	-1.76	< 0.0001	-1.23	0.0020
25	Solyc10g054380	Fructose-bisphosphate aldolase		-0.42	0.9994	-0.70	0.1008	-0.49	0.2920	-1.53	< 0.0001	-1.22	0.0010

Table S9. List of the 25 most strongly down-regulated genes in tomato (*Solanum lycopersicum*) leaves after seven days of infestation with *Tetranychus urticae*. Shown are Log$_2$ fold change (Log$_2$FC) values, representing relative expression levels of tomato genes upon infestation with either a single mite species (*T. urticae* [Tu], *T. evansi* [Te], or *Aculops lycopersici* [Al]) or two species simultaneously (*T. urticae* plus *T. evansi* [Tu+Te], or *T. urticae* plus *A. lycopersici* [Tu+Al]) as compared to non-infested controls, along with their corresponding Benjamini and Hochberg false discovery rate adjusted *P* values (BH-adj *P*). Information in the column with header 'JA' indicates whether expression of the respective gene was found to be significantly induced in the tomato JA-biosynthesis mutant *def-1*, 24 hours after exogenous application of JA (for details see [39]; note that none of the genes in this top list were JA-inducible according to these criteria. Genes were ranked according to their relative expression level in the Tu sample (shaded grey).

				Te		Tu+Te		Tu		Tu+Al		Al	
#	**Locus identifier**	**Annotation (ITAG 3.2)**	**JA**	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***	**Log$_2$FC**	**BH-adj *P***
1	Solyc11g010410	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase		-0.74	0.9994	-1.81	0.0001	-1.84	0.0001	-2.17	< 0.0001	-1.51	0.0006
2	Solyc12g011010	Meiosis 5		-0.42	0.9994	-0.96	0.0918	-1.83	0.0003	-2.72	< 0.0001	-1.64	0.0009
3	Solyc06g068130	Tetratricopeptide repeat protein		0.39	0.9994	-1.68	0.0153	-1.75	0.0077	-1.93	0.0012	-0.48	0.5980
4	Solyc12g009650	Lipid-transfer protein, putative		-0.61	0.9994	-1.52	0.0078	-1.75	0.0013	-2.28	< 0.0001	-1.44	0.0066
5	Solyc09g008320	Xyloglucan endotrans-glucosylase/hydrolase		-0.38	0.9994	-1.26	0.0035	-1.75	< 0.0001	-2.42	< 0.0001	-1.34	0.0009
6	Solyc10g009150	Organ-specific protein S2		-0.90	0.9994	-0.90	0.3200	-1.72	0.0159	-1.57	0.0151	-1.06	0.1590
7	Solyc00g272810	N-acetyltransferase		-0.85	0.9994	-0.94	0.1176	-1.68	0.0014	-1.38	0.0042	-0.42	0.5598
8	Solyc06g071320	Unknown protein		-0.48	0.9994	-1.43	0.0004	-1.60	< 0.0001	-2.49	< 0.0001	-1.75	< 0.0001
9	Solyc11g056680	LRR receptor-like kinase		-0.63	0.9994	-1.00	0.0387	-1.57	0.0004	-3.03	< 0.0001	-2.39	< 0.0001
10	Solyc07g041720	Oxalate oxidase-like germin protein		-0.50	0.9994	-1.61	0.0015	-1.53	0.0018	-2.16	< 0.0001	-0.96	0.0534
11	Solyc01g089850	Cyclin-dependent protein kinase		-0.73	0.3304	-1.50	< 0.0001	-1.52	< 0.0001	-2.03	< 0.0001	-0.98	0.0007
12	Solyc10g074540	Unknown protein		-0.86	0.8643	-1.60	0.0008	-1.51	0.0010	-1.42	0.0008	-1.23	0.0061
13	Solyc08g063090	Delta-6-desaturase		-0.41	0.9994	-1.59	0.0001	-1.49	0.0002	-2.16	< 0.0001	-0.97	0.0144
14	Solyc03g112540	Short-chain dehydrogenase/reductase		-0.46	0.9994	-1.44	0.0005	-1.48	0.0002	-1.86	< 0.0001	-1.10	0.0046
15	Solyc02g076690	Cysteine protease		-0.77	0.9994	-1.56	0.0028	-1.47	0.0034	-2.15	< 0.0001	-1.04	0.0391
16	Solyc01g005300	F box protein		-0.88	0.9994	-1.32	0.0582	-1.47	0.0249	-1.39	0.0185	-0.61	0.4502
17	Solyc08g076820	bHLH transcription factor 146		-0.49	0.9994	-1.23	0.0003	-1.46	< 0.0001	-2.03	< 0.0001	-1.56	< 0.0001
18	Solyc07g052980	Xyloglucan endotrans-glycosylase/hydrolase		-0.57	0.9994	-1.23	0.0003	-1.44	< 0.0001	-2.11	< 0.0001	-1.07	0.0009
19	Solyc03g058160	Zinc finger transcription factor		-0.51	0.9994	-1.20	0.0007	-1.37	0.0001	-1.73	< 0.0001	-0.59	0.0972
20	Solyc03g120380	IAA19		-0.92	0.1316	-0.85	0.0148	-1.35	< 0.0001	-2.15	< 0.0001	-1.94	< 0.0001
21	Solyc01g110570	Small auxin up-regulated RNA 4		-0.72	0.9994	-1.22	0.0240	-1.33	0.0091	-2.35	< 0.0001	-1.54	0.0017
22	Solyc05g026490	Phosphomannomutase/phosphor-glucomutase		-0.44	0.9994	-1.33	0.0002	-1.32	0.0001	-1.63	< 0.0001	-1.04	0.0017
23	Solyc01g099630	Xyloglucan endotrans-glycosylase/hydrolase		-0.57	0.9994	-1.04	0.0024	-1.32	0.0001	-0.95	0.0016	-0.33	0.4166
24	Solyc02g085020	Dihydroflavonol 4-reductase		-0.17	0.9994	-1.21	0.0034	-1.30	0.0010	-1.98	< 0.0001	-1.26	0.0011
25	Solyc07g053540	Fasciclin-like arabinogalactan protein		-0.71	0.9994	-1.30	0.0037	-1.30	0.0026	-1.47	0.0002	-0.97	0.0229

Table S10. qPCR primer specifications

Target Gene	**Name**	**Gene Identifier**	**Forward Primer (5' → 3')**	**Reverse Primer (5' → 3')**	**References**
JIP-21	*Jasmonate-inducible protein 21*	Solyc03g098790	ACTCGTCCTGTGCTTTGTCC	CCCAAGAGGATTTTCGTTGA	Lisón et al. [61]
PI-IIc	*Proteinase inhibitor IIc*	Solyc03g020050	CAGGATGTACGACGTGTTGC	GAGTTTGCAACCCTCTCCTG	Gadea et al. [147]
KTI_20	*Kunitz-type trypsin inhibitor*	Solyc03g098720	CTTGGGAATCCGACTGTTTG	GCCTGCTTTACCGTTTGTTG	This study
KTI_40	*Kunitz-type trypsin inhibitor*	Solyc03g098740	CGTCCGGGGTACACCTACTA	TTTCGGGCTTGAAAAACATC	This study
LapA1	*Leucine aminopeptidase A1*	Solyc12g010020	TGATACTCTTGGTCTTACTAGGC	GACCAACTAGAGTAATCCTTCCA	Chao et al. [148]
CYP450	*Cytochrome P450*	Solyc10g083690	ATATGGATGAAAGCATGGGAGT	TGGGAAAACAATGTTATGTATCG	This study
Ser PI	*Serine proteinase inhibitor*	Solyc09g084480	GGGTGGCTTAATATAATGGAT	GGAATTAATTAATGAGAGAACATA	This study
ICS	*Isochorismate synthase*	Solyc06g071030	AACTTGAGGCACCTCTTTTGA	CCCAAAATTGCATATGACAGG	This study
β-1-3-Gluc	*β-1-3-glucanase*	Solyc01g060020	TGCAACACCAAATAAATTCGTA	TTTGCAGTTACCAGATCAGAGTG	This study
PR-P	*Pathogenesis-related protein*	Solyc04g064880	GCGTCAACATGTCCTTTTATGA	AAATTTGCGTAAACAGAATTACAA	This study
CHS1	*Chalcone synthase 1*	Solyc09g091510	TCCTTCACAGTGTTGCTGCT	TAGCAAACACATTAATAACCAAGAAA	O'Neill et al. [88]
CHS2	*Chalcone synthase 2*	Solyc05g053550	GGCTCCCACTCGAGACATAA	CCACAAATCTAATTTCCAAATTCTT	O'Neill et al. [88]
GAME1	*Glycoalkaloid metabolism 1*	Solyc07g043490	GCATTTTGGTCCGCTCTCTC	GCGCATTCAACCAATCTACAAC	Itkin et al. [107]
GAME9/JRE4	*Glycoalkaloid metabolism 9 / Jasmonate-responsive ethylene response factor 4*	Solyc01g090340	TGTTTCCTCCGGTGTTACGG	CGATTTTTTCGAAACTCTTTCC	Cárdenas et al. [113] Thagun et al. [114]
Actin	*Actin*	Solyc03g078400	TCAGCACATTCCAGCAGATGT	AACAGACAGGACACTCGCACT	Schimmel et al. [41]