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Overlapping sets of transcripts from host and non-host interactions of tomato are expressed early during non-host resistance

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Supplementary Table 1. Primary metabolism (carbohydrate and photosynthesis)-related transcripts that are differentially regulated during compatible and non-host interactions compared to mock-inoculated tomato leaves. hpi-hours post inoculation.

Agilent probe ID	Annonation	*M. grisea*		*A. alternata*	
Carbohydrate metabolism					
	Starch metabolism				
		6hpi	24hpi	6hpi	24hpi
A_96_P150041	Starch-granule-bound R1 protein	1.32	3.36	1.25	2.05
A_96_P136127	α-amylase	2.72	5.05	2.91	6.03
A_96_P070684	α-1,4 glucan phosphorylase L-2	5.62	1.24	5.04	2.30
A_96_P033066	α-glucosidase	8.44	9.55	9.66	10.13
A_96_P183669	Starch phosphorylase L	-4.48	-4.23	-4.47	-3.87
A_96_P005256	Isoamylase isoform 2	-2.66	-2.64	-3.15	-3.27
A_96_P004556	Granule-bound starch synthase 1	-2.66	-2.64	-3.08	-3.97
A_96_P116282	Granule-bound starch synthase 2	-5.64	-8.17	-5.47	-9.18
A_96_P036116	Alpha-glucan water dikinase chloroplastic	-4.73	-5.15	-4.90	-4.90
A_96_P259597	Starch branching enzyme II	-4.83	-4.83	-5.32	-4.84
A_96_P035956	Soluble starch synthase	-3.11	-3.08	-2.94	-4.27
	Sucrose metabolism				
A_96_P065636	β-fructofuranosidase	4.27	3.49	4.28	3.97
A_96_P011256	Sucrose synthase 4	3.19	3.13	3.76	4.17
A_96_P000596	sucrose synthase	1.76	2.02	2.26	2.80
A_96_P031836	Sucrose-phosphate-synthase	2.06	3.35	3.00	4.43
A_96_P008131	Apoplastic invertase	1.95	3.23	2.19	2.44
A_96_P253712	Acid invertase	1.55	1.39	1.81	1.70
A_96_P028286	Sucrose synthase	-1.62	-2.04	-1.86	-3.00
	Glycolysis pathway				
A_96_P037226	Hexokinase	4.21	4.17	4.10	4.22
A_96_P168554	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha	5.06	6.76	5.33	6.76
A_96_P113557	Fructose-bisphosphate aldolase	2.35	2.86		
A_96_P099959	Plastid enolase	1.81	1.65	2.05	1.49
A_96_P010086	Glyceraldehyde-3-phosphate dehydrogenase	-2.92	-5.06	-2.87	-5.41
A_96_P010891	Fructose-bisphosphate aldolase	-3.44	-2.82	-3.22	-5.04
A_96_P019851	Pyruvate kinase, cytosolic isozyme	-3.48	-3.50	-3.94	-3.34
A_96_P150586	Phosphoglycerate kinase	-2.44	-4.16	-2.29	-3.87
A_96_P247337	Enolase	-2.17	-3.67	-2.48	-4.12
	Calvin cycle				
A_96_P027406	Transaldolase 2	8.78	5.42	7.12	6.38
A_96_P019756	RUBISCO- large subunit	4.47	1.75	4.18	2.56
A_96_P086549	Ribulose-1,5-bisphosphate carboxylase, small subunit	-3.78	-4.46	-3.72	-6.58
A_96_P149036	Chloroplast Rubisco activase	-3.44	-3.57	-3.14	-4.46
A_96_P184724	Fructose-1,6-bisphosphatase class 1 2	-2.55	-5.04	-2.55	-4.47
A_96_P220109	Ribulose-phosphate 3-epimerase	-2.31	-4.17	-2.31	-4.47
A_96_P262727	Ribulose bisphosphate carboxylase small chain 3B	-2.85	-4.31	-1.93	-4.45
A_96_P231324	Carbonic anhydrase	-2.35	-5.98	-2.27	-5.33
A_96_P075589	Ribulosebisphosphate carboxylase/oxygenase activase	-2.49	-3.36	-2.72	-3.31
Photosynthesis					

A_96_P136617	Respiratory burst oxidase protein F	3.68	2.13	3.71	2.76
A_96_P204174	Chlorophyll a,b binding protein type I	-8.14	-8.55	-8.42	-8.29
A_96_P010486	Chlorophyll a/b binding protein Lhcb1-4	-4.19	-3.16	-4.31	-4.74
A_96_P088944	Chlorophyll a/b binding protein	-5.20	-8.15	-5.14	-8.58
A_96_P029831	PsaA 1	-2.13	-2.58	-2.50	-2.46
A_96_P012266	Phytochrome B	-2.43	-2.98	-2.59	-2.48
A_96_P136997	Chlorophyll a/b binding protein precursor CAB6A	-3.26	-5.20	-3.33	-5.59
A_96_P149976	Chlorophyll a/b-binding protein precursor	-4.25	-4.26	-4.57	-5.73
A_96_P030561	Cytochrome b6 1	-2.80	-2.63	-3.13	-2.78
A_96_P155001	Apocytochrome f 1	-2.67	-3.73	-3.12	-2.06
A_96_P187539	33kDa precursor protein of oxygen-evolving complex	-2.43	-3.15	-1.79	-2.55
A_96_P150616	Photosystem II oxygen-evolving complex protein 3	-1.43	-2.02	-1.55	-3.71
A_96_P135040	Pre-plastocyanin (AA -64 to 106)	-2.57	-3.61	-2.42	-4.42
A_96_P221374	PsaD	-1.23	-1.80	-1.35	-2.93
A_96_P034001	violaxanthin de-epoxidase	-2.54	-6.04	-2.53	-7.61
A_96_P100959	PSII polypeptide	-2.50	-1.65	-2.35	-3.33
A_96_P044911	NADH-quinone oxidoreductase subunit A 1	-1.13	-4.39	-1.36	-4.63
A_96_P049066	PsaB 1	-1.81	-1.55	-2.11	-1.52
A_96_P060171	Oxygen-evolving enhancer protein 2	-1.25	-1.89	-1.56	-1.87
A_96_P052471	NADPH oxidase RBOHD	-2.75	-4.51	-3.11	-5.77
A_96_P133947	Ferredoxin-I	-2.39	-1.95	-2.40	-2.63
A_96_P133912	Ferredoxin-NADP reductase	-2.22	-3.95	-2.08	-5.19
A_96_P173919	Subunit A of ferredoxin-thioredoxin-reductase	-1.09	-1.96	-1.15	-2.71
A_96_P020791	Cytochrome b6-f complex iron-sulfur subunit	-1.29	-1.11	-1.36	-1.28
A_96_P092199	Ferrochelatase	-1.62	-3.59	-1.48	-4.05

Fold changes in up- (with no prefix) and down-regulated (with negative mark prefix) between mock- and pathogen (*M. grisea* and *A. alternata* f. sp. *lycopersici)* inoculated tomato leaves are given.

Supplementary Table 2. Transport-related transcripts that are differentially regulated during compatible and non-host interactions compared to mock-inoculated tomato leaves. hpi-hours post inoculation.

Agilent probe ID	Annotations	*M. grisea*		*A. alternata*	
		6hpi	24hpi	6hpi	24hpi
A_96_P031266	Voltage-dependent anion-selective channel	8.56	9.27	8.98	9.43
A_96_P115122	Probable polyol transporter 6	6.71	7.37	7.10	9.50
A_96_P104604	Transporter-related	5.88	3.76	6.43	5.30
A_96_P000286	Inorganic phosphate transporter	5.21	4.38	5.62	5.30
A_96_P129327	Alternative oxidase 1b	4.48	2.96	6.00	3.90
A_96_P000681	st3 protein	4.11	3.55	3.98	3.64
A_96_P014501	Plastid quinol oxidase	3.46	1.80	3.37	1.33
A_96_P114627	Amino acid permease	3.94	3.07	4.24	4.27
A_96_P05525	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 4	3.13	4.98	3.29	4.45
A_96_P037226	HXK3	4.21	4.17	4.10	4.22
A_96_P105434	Plastidic ATP/ADP-transporter	2.94	1.87	3.00	1.70
A_96_P177884	Ferritin	2.63	3.19	2.67	2.56
A_96_P012886	Hexose transporter 1	2.45	2.70	2.70	4.12
A_96_P013666	Amino acid transporter	2.44	1.97	2.82	2.95
A_96_P012881	Hexose transporter 3	2.08	1.46	1.92	1.81
A_96_P100969	ADP,ATP carrier protein-like	2.22	2.51	2.00	2.13
A_96_P089619	Sucrose transport protein	1.25	1.76	1.43	1.34
A_96_P105434	Plastidic ATP/ADP-transporter	1.87	2.94	3.00	1.70
A_96_P078044	Sucrose transport protein-SUT1	1.85	1.09	1.42	1.75
A_96_P220224	Envelope membrane protein 1	1.74	1.89	1.60	1.90
A_96_P037246	Plasmalemma Na+/H+ antiporter-like	1.49	1.29	1.23	1.24
A_96_P209334	LeOPT1 protein	1.29	1.24	1.25	1.56
A_96_P111092	ABCG subfamily transporter	-8.86	-6.83	-8.74	-7.06
A_96_P097079	Glucose-6-phosphate/phosphate translocator	-7.66	-10.77	-10.06	-11.57
A_96_P255817	Neryl diphosphate synthase 1	-5.81	-4.77	-3.81	-5.14
A_96_P026886	Triose phosphate/phosphate translocator	-6.78	-5.85	-6.68	-7.23
A_96_P254777	ABC transporter-like	-6.06	-4.41	-6.43	-4.69
A_96_P101554	ATP synthase subunit a	-6.05	-6.13	-5.40	-6.90
A_96_P085139	Non-specific lipid-transfer protein	-3.88	-2.91	-1.83	-2.88

A_96_P020251	H(+)-transporting ATPase	-3.08	-5.07	-3.36	-4.26
A_96_P231219	Non-specific lipid-transfer protein	-3.34	-3.47	-3.25	-4.59
A_96_P012061	Ammonium transporter	-3.10	-6.56	-3.87	-6.76
A_96_P233459	X intrinsic protein	-3.14	-3.79	-2.96	-2.58
A_96_P088629	Non-specific lipid transfer protein	-3.87	-5.23	-4.30	-8.78
A_96_P149221	Potassium channel	-2.05	-1.87	-1.69	-2.06
A_96_P000121	Ca2+-ATPase	-2.26	-2.83	-2.26	-2.58
A_96_P016631	Membrane channel protein	-2.07	-1.26	-3.83	-3.76
A_96_P094704	ABCG subfamily transporter protein (PDR4)	-2.43	-2.89	-2.28	-4.50
A_96_P073814	ABCG subfamily transporter protein	-1.77	-1.90	-1.55	-2.65
A_96_P182969	P-glycoprotein	-1.25	-2.62	-1.71	-2.27
A_96_P001316	Putative inward rectifying potassium channel	-1.03	-2.70	-1.10	-3.59
A_96_P104919	Hexose transporter (Fragment)	-1.90	-4.04	-1.93	-4.12
A_96_P205469	Oxoglutarate/malate translocator	-1.15	-1.10	-1.49	-1.47
A_96_P241279	ATPase-like	-1.18	-1.16	-1.12	-1.67
A_96_P231969	Remorin (pp34)	-1.10	-2.84	-1.28	-3.28

Fold changes in up- (with no prefix) and down-regulated (with negative mark prefix) between mock- and pathogen (*M. grisea* and *A. alternata* f. sp. *lycopersici)* inoculated tomato leaves are given.

Supplementary Table 3. Fatty acid and amino acid metabolism-related transcripts that are differentially regulated during compatible and non-host interactions compared to mock-inoculated tomato leaves. hpi-hours post inoculation.

Agilent probe ID	Annotations	*M. grisea*		*A. alternata*	
Fatty acid metabolism					
		6hpi	24hpi	6hpi	24hpi
A_96_P020924	alpha-DOX1	7.51	8.25	8.63	9.08
A_96_P229839	Linoleate 9S-lipoxygenase 2	4.02	4.60	4.87	4.19
A_96_P047816	Linoleate 13S-lipoxygenase 2-1	4.36	1.06	4.16	1.93
A_96_P048591	Putative sterol desaturase	2.45	2.43	2.41	2.22
A_96_P045126	Phosphatidate cytidylyltransferase	1.76	2.49	1.64	2.51
A_96_P116072	Peroxisomal acetoacetyl-coenzyme A thiolase	1.26	2.28	1.38	3.28
A_96_P111547	Oxysterol-binding protein	1.81	1.33	1.97	1.98
A_96_P028291	Linoleate 13S-lipoxygenase 3-1	-2.75	-3.43	-2.81	-2.55
A_96_P019761	Fatty acid hydroperoxide lyase	-2.70	-2.73	-2.63	-2.17
A_96_P171254	Gamma-tocopherol methyltransferase	-5.09	-6.45	-6.28	-7.89
A_96_P026701	Probable linoleate 9S-lipoxygenase 5	-1.82	-2.87	-1.92	-3.02
A_96_P121767	Phosphoinositide-specific phospholipase C	-3.40	-3.35	-3.97	-4.80
A_96_P252582	Omega-3 fatty acid desaturase	-4.40	-6.62	-4.84	-3.72
A_96_P101004	3-ketoacyl-CoA synthase	-9.09	-8.15	-8.22	-9.48
Amino acid metabolism					
A_96_P092815	Aromatic amino acid decarboxylase 1B	5.02	3.72	5.93	4.09
A_96_P225834	Aromatic amino acid decarboxylase 1A	5.77	4.89	6.50	5.43
A_96_P048981	Aromatic amino acid decarboxylase 2	4.97	5.03	5.85	5.82
A_96_P074419	Asparagine synthetase	3.49	7.42	4.21	9.45
A_96_P011256	γ-aminobutyrate transaminase subunit precursor isozyme 1	3.19	3.13	3.76	4.17
A_96_P011291	Arginase 2	2.32	3.00	2.65	5.63
A_96_P065591	Glutamate--tRNA ligase-like protein	2.79	3.95	2.79	3.77
A_96_P250667	Glutamine synthetase	-3.41	-6.37	-3.24	-6.23
A_96_P219879	Aminomethyltransferase	-2.52	-5.08	-2.63	-4.41
A_96_P086199	Glutamate decarboxylase isoform3	-2.91	-5.73	-6.24	-9.59
A_96_P268433	Arginine decarboxylase	-2.17	-2.39	-1.64	-2.10
A_96_P220394	Glycine dehydrogenase	-2.64	-4.17	-3.02	-4.43
A_96_P064401	Polyprotein, putative	-1.78	-3.66	-1.91	-3.87

Fold changes in up- (with no prefix) and down-regulated (with negative mark prefix) between mock- and pathogen (*M. grisea* and *A. alternata* f. sp. *lycopersici)* inoculated tomato leaves are given.

Supplementary Table 4. Transcription factors that are differentially-regulated during compatible and non-host interactions compared to mock-inoculated tomato leaves. hips-hours post inoculation.

Agilent probe ID	Annotations	*M. grisea*		*A. alternata*	
		6hpi	24hpi	6hpi	24hpi
A_96_P032431	RNA1 polyprotein	7.14	7.90	7.72	9.24
A_96_P213164	NAC domain protein NAC2	5.53	6.79	5.69	8.37
A_96_P031561	LeCBF1 protein	4.95	3.60	4.48	3.05
A_96_P131262	Putative NAC domain protein	4.91	4.58	5.73	5.01
A_96_P151666	C2H2-type zinc finger protein	4.75	4.03	5.19	5.46
A_96_P042826	Cup-shaped cotyledon3	4.24	6.47	5.44	3.78
A_96_P121127	Probable WRKY transcription factor 71	4.44	4.86	5.50	6.37
A_96_P073524	Ripening regulated protein DDTFR10/A	4.09	2.48	3.60	3.83
A_96_P055916	Putative regulator of chromosome condensation	5.73	5.97	5.60	6.56
A_96_P012306	ERF transcription factor	4.66	5.52	5.36	7.34
A_96_P121127	Probable WRKY transcription factor 71	4.44	4.86	5.50	6.37
A_96_P134222	Putative arginine/serine-rich protein-like	2.22	3.51	2.24	2.91
A_96_P012681	Ethylene-responsive factor 1	3.62	5.04	4.10	4.29
A_96_P073889	Pti4	3.85	3.87	4.20	4.82
A_96_P028806	DREB3	2.30	2.20	2.26	2.16
A_96_P127002	Histone H2B	2.61	4.00	3.19	4.75
A_96_P078759	WRKY protein	2.54	2.55	2.83	2.47
A_96_P037931	Heat stress transcription factor A-5	2.34	3.79	2.42	5.07
A_96_P117257	Mitochondrial SBP40	3.78	3.44	4.61	3.66
A_96_P124087	Myb-related protein MYBAS1	3.10	2.73	2.06	2.36
A_96_P078954	APETALA2-like protein	1.88	1.30	2.19	2.23
A_96_P012666	myb-related transcription factor	1.88	2.19	1.99	1.38
A_96_P112732	GAGA-binding transcriptional activator	1.74	2.86	1.44	2.29
A_96_P072144	Nam-like protein 1	1.78	2.46	2.26	2.77
A_96_P020926	Anaerobic basic leucine zipper protein	1.66	5.70	2.77	6.42
A_96_P001303	Class II knotted-like homeodomain protein	1.67	1.90	1.43	1.64
A_96_P011876	EIL3 protein	1.44	2.31	1.72	2.28
A_96_P023541	Nam-like protein 4	1.55	2.28	1.65	3.07
A_96_P123222	PGPD14	1.58	3.13	1.59	3.62
A_96_P001641	Transcription factor JERF1	2.61	2.68	2.40	2.06
A_96_P097544	WRKY transcription factor 2	2.66	2.32	3.19	4.02
A_96_P001641	Transcription factor JERF1	2.61	2.68	2.40	2.06
A_96_P000191	Ribonuclease	2.86	3.19	3.14	4.53
A_96_P041326	Adenosine kinase isoform 1T-like protein	2.31	2.05	2.30	3.08
A_96_P084244	MADS transcriptional factor	2.10	2.18	2.78	2.58
A_96_P000181	MADS-box protein 5	-6.13	-5.35	-5.45	-6.18
A_96_P000181	Agamous-like MADS-box protein	-6.13	-5.35	-5.45	-6.18
A_96_P057596	Dof zinc finger protein	-5.85	-2.42	-6.55	-1.98
A_96_P124492	DREB	-4.04	-2.97	-4.15	-3.93
A_96_P010706	40S ribosomal protein S27	-3.79	-4.67	-3.73	-4.60
A_96_P012781	IAA11 protein	-2.10	-3.07	-3.00	-4.99
A_96_P013726	IAA7 protein	-3.20	-1.92	-3.30	-2.94
A_96_P072744	Self-pruning G-box protein	-3.00	-2.16	-2.95	-3.43
A_96_P187004	CRT binding factor 2A	-2.66	-3.14	-2.74	-3.89
A_96_P079884	vsf-1 protein	-2.09	-1.57	-2.14	-1.98
A_96_P005166	NO APICAL MERISTEM	-2.28	-2.13	-2.69	-2.29
A_96_P142062	Transcription factor	-2.54	-3.01	-2.95	-3.88
A_96_P014181	Bell-like homeodomain protein 4	-2.28	-5.14	-3.39	-5.82
A_96_P103334	VP1-ABI3-like protein	-2.00	-2.17	-2.26	-2.25
A_96_P000186	TDR3 protein	-2.75	-1.61	-2.23	-1.40
A_96_P232034	Translation initiation factor eIF(Iso)4E	-1.90	-2.55	-2.22	-2.85
A_96_P012801	IAA2 protein	-1.29	-1.68	-3.28	-2.58
A_96_P054666	RNA polymerase IV largest subunit	-1.88	-2.64	-2.39	-2.69
A_96_P036056	Ribonuclease E	-1.41	-2.45	-1.56	-2.50
A_96_P012386	Deoxyuridine triphosphatase	-1.35	-3.15	-1.61	-3.56
A_96_P248382	Transcription factor MYB48	-1.44	-1.28	-2.42	-2.58
A_96_P016486	Deficiens analogue	-1.40	-1.16	-2.64	-2.30

Fold changes in up- (with no prefix) and down-regulated (with negative mark prefix) between mock- and pathogen (*M. grisea* and *A. alternata* f. sp. *lycopersici)* inoculated tomato leaves are given.