

1 **Supplementary material 1.** Complete list of differentially expressed genes by TSH1188 cacao meristems challenged with *M. pernicioso* at early
2 stages, 30 dai and 60 dai compared to un-inoculated meristems (Control). The genes were determined as differentially expressed if the fold
3 change was greater than 2 or below -2. The differentially expressed genes were classified in 8 regulatory patterns (clusters I to VIII). Asterisk
4 indicates the genes analyzed by RT-qPCR. ^a (-) indicates the genes for with no *A. thaliana* ortholog were found. ^b indicates the genes which were
5 found in the *A. thaliana* PPPI network. ^c indicates the genes in common with Catongo.
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Accession number	Putative function	Early stage vs Control	30 dai vs Control	60 dai vs Control	30 dai vs Early stage	60 dai vs Early stage	60 dai vs 30 dai	Cluster	<i>Arabidopsis thaliana</i> ortholog ^a
ES439941	18S ribosomal protein	-2.2		-2.1				I	-
ES441521	21 kDa seed protein ^c	2.4			-2.7	-4.2		IV	At1g17860
FC072453	26S ribosomal protein				2.3		-2.1	VIII	RBOHI
ES439999	26S ribosomal protein	2.2			-2.7	-2.1		IV	-
ES439794	40S ribosomal protein ^{b, c}		-2.0	-2.5				I	RPS3C
ES441508	60S ribosomal protein L11 ^{b, c}			2.6		2.8		VI	AT4G18730.1
ES440648	60S ribosomal protein L15 ^b			2.0				VII	RPL15A
ES441839	60S ribosomal protein L31 ^{b, c}			-2.1				II	RPL31A
ES441252	6-phosphogluconolactonase ^b			2.2				VII	EMB2024
ES442366	ADP-ribosylation factor				2.3			VIII	At3g22950
ES441819	Aminoacyl-Trna synthetase ^b	2.9			-2.8	-2.4		IV	ALATS
ES440568	Arabidopsis thaliana clone T17M13			3.0		2.4	2.1	VII	SHL1
ES441616	ATP synthase ^b			2.0				VII	atpF
ES442546	Autophagy protein Apg6 ^b			2.0		3.5	2.5	V	At3g61710
ES441005	Calcineurin B-like protein 10 ^b	2.5			-2.1			IV	CBL4
ES441056	Calmodulin-binding family protein		2.6	2.5				VIII	At5g62390
ES439863	Cathepsin B-like cysteine proteinase ^b				-2.0			III	T7I23.13
ES441714	Chlorophyll A-B binding protein ^b			2.8		2.5		VIII	LHCB4.3
ES441545	Chlorophyll a-binding protein of LHCII type I ^b					2.6		VIII	Lhb1B2
ES442086	Cinnamoyl-CoA reductase ^b			2.1				VII	At5g58490
ES440300	C-myc binding protein / prefoldin ^{b, c}		-2.6	-2.2				I	At5g23290
ES440774	Cytochrome c oxidase subunit 3	-2.0						II	At3g49450
ES441868	Cytochrome oxidase subunit II	5.5			-4.4	-4.2		IV	-
ES441607	DC1 domain-containing protein ^b			2.5		2.5	2.2	VI	At1g60420

ES441755	DEAD-box ATP-dependent RNA helicase 42 ^c	-2.3			3.6	2.2	V	-
ES440693	Dihydroxy-acid dehydratase ^b	2.1					IV	At3g23940
ES440909	DnaJ (I18-12) ^b	2.0					IV	ATJ3
ES439984	Elongation factor 1 beta 2 ^{b, c}	-2.2	-2.2	-2.2			I	At1g30230
ES442358	Epsilon-adaptin ^b			2.0			VIII	F27M3_7
ES440398	Eukaryotic translation initiation factor 5A ^b	-3.2			2.1	2.7	II	At1g69410
ES440399	Expressed protein			2.6		2.4	VIII	T19L5_60
ES441735	Expressed protein					2.1	VIII	At3g01680
ES440746	Expressed protein			2.3		2.8	VI	At5g59410
ES440753	Expressed protein	3.4			-3.0	-2.8	IV	At5g01750
ES442164	Expressed protein			2.2			VII	At2g44360
ES440494	Expressed protein			2.0			VIII	AT3G18240.1
ES442282	Expressed protein	2.7					IV	At5g22580
ES440574	Expressed protein			2.0			VIII	AT4g12700
ES441509	Expressed protein ^c			2.0		2.4	VI	At3g20430
ES442350	F-box family protein			2.0	2.0	3.1	V	At1g10780
ES440219	F-box protein ^c	-2.1					I	AT1G20750.1
ES440575	Formate-tetrahydrofolate ligase ^b			2.1			VIII	THFS
ES442460	GDP-D-mannose-4,6-dehydratase ^b			2.1			VII	GMD1
ES441593	Glutathione S-transferase ^b			2.1			VII	Gst8
ES442509	Glutathione S-transferase ^c					2.6	II	ATGSTF9
ES441788	Glycine/D-amino acid oxidases ^b			2.3			VII	At2g32640
ES441743	Glycoside hydrolase ^b			2.2		2.7	VIII	At2g04280
ES442487	Glycosyl hydrolase family 38 protein ^c			2.0		2.2	VIII	At3g26720
ES440961	Gm347 ^b			2.5			VII	ALA1
ES440707	Heat shock protein 90 ^b	-2.1					II	HSP81-3
ES440392	Heat-shock protein 80 ^b				-2.0		III	HSP81-2
ES442529	Homo sapiens clone CTD-2249K22				2.5	3.2	VIII	-
ES440528	Homo sapiens clone RP11-472A1 ^c					2.3	VI	T22N19_110
ES440133	HSP 17.3 ^c		-2.3				I	At2g29500
ES442283	Hydroxyproline-rich glycoprotein family protein ^{*,b}	4.1			-3.2	-2.4	IV	At3g22440

ES441576	Hypothetical mitochondrial protein				2.6		VIII	AtMg00030
ES441127	Hypothetical protein	2.2		2.0			VIII	MIJ24.9
ES440565	Hypothetical protein		2.4		2.6		VIII	T17B22.7
ES440539	Hypothetical protein		2.0		2.1		VIII	At2g01210
ES441015	Hypothetical protein F13N6.4		2.1				VII	F13N6.4
ES441505	Late embryogenesis abundant protein		2.6		3.1	2.7	VI	dl3995w
ES441600	Leucine-rich repeat family protein				2.4		VIII	At1g49750
ES440650	Leucine-rich repeat transmembrane protein kinase		2.1		2.0		VIII	At5g61480
ES441718	Lipoxygenase ^b		2.8		2.4		VIII	LOX5
ES442238	Methyltransferase PMT28		2.6		2.2		VI	At1g19430
ES442545	Microsomal glutathione S-transferase ^b		2.6				VII	At1g65820
ES442473	Monodehydroascorbate reductase ^b		2.3		2.1		VI	At3g52880
ES441694	NADH dehydrogenase ^b	2.1		-2.3	-2.2		IV	ND2
ES441096	NBS-LRR type resistance protein		2.2				VII	ADR1-L2
ES442582	No-Hit	2.7	5.0		3.8	2.3	VII	-
ES442523	No-Hit		2.0				VII	AT1G10400.
ES441833	No-Hit		2.2			2.2	III	AT1G10450.
ES442530	No-Hit	-3.7		2.3	3.3		II	At1g68740
ES441230	No-Hit		2.2		3.7		V	KNAT3
ES441133	No-Hit		2.6		2.5		VI	At1g34500
ES441750	No-Hit		3.0		3.5		VIII	F28D10_10
ES441426	No-Hit	2.5					IV	-
ES441782	No-Hit	4.7		-3.8	-3.3		IV	-
ES440573	No-Hit		2.4				VII	At2g44580
ES441426	No-Hit	2.5					IV	-
ES442306	No-Hit		2.0				VII	T18C15_1
ES441024	No-Hit		2.4				VII	At5g11250
ES441764	No-Hit	2.4					IV	-
ES441699	No-Hit				2.1		II	AERO1
ES441324	No-Hit				2.5		V	At4g26190
ES440104	No-Hit		2.5				VII	At5g59260

ES442511	No-Hit*	3.6			-2.7	-2.5	IV	AT3G20620.1
ES440549	No-Hit ^b	-2.4			3.0	3.0	VIII	At1g79990
ES441706	No-Hit ^b			2.4			VII	BIG
ES441560	No-Hit ^b			2.2		3.2	V	At2g21150
ES440864	No-Hit ^{b, c}					2.0	VIII	WRKY23
ES441777	No-Hit ^{b, c}	2.0					IV	ROT3
ES440515	No-Hit ^c	2.2					IV	F15N18_60
ES441134	ORF25 ^b		2.1				VIII	AtMg00640
ES440594	ORF77					2.7	V	At2g38970
ES440558	Oryza sativa genomic DNA ^b	2.7					IV	ND2
ES442476	OSJNBa0006A01.2 ^{b, c}			2.8		2.2	VII	At1g60850
ES441708	Oxysterol-binding family protein ^b			2.1			VII	At5g59420
ES440257	Pb-reticulocyte binding protein			2.9		2.6	VI	At5g12290
ES441760	PDI-like protein ^{b, c}	-2.1		-2.8			I	At1g60420
ES442202	Pentatricopeptide repeat-containing protein			2.1			III	xpo1
ES442515	Peptide transporter PTR5			2.1		2.8	V	-
ES441587	Peptidyl-prolyl cis-trans isomerase ^{*,b}	2.8			-2.9	-3.7	IV	PAS1
ES439831	Polyphenol oxidase	2.7		2.3			VIII	At4g29230
ES441688	Polyubiquitin ^{b, c}		-2.5				III	At4g05050
ES441776	Predicted protein			2.6		2.6	VI	At5g42710
ES442456	Predicted protein					2.0	III	At4g36960
ES442607	Predicted protein ^c					2.3	III	At1g68570
ES440854	Probable WRKY transcription factor 23 ^b			3.2			VII	PRS5
ES441626	Programmed cell death 4			2.1			VII	At2g25860
ES440131	Proline-rich phosphoprotein ^b			3.0		2.4	VII	At3g63095
ES440244	Proline-rich spliceosome-associated (PSP) family protein ^{b, c}	-2.5		-2.7			II	At4g21660
ES442327	Protease inhibitor 2 ^c	-3.3	-2.4	-2.4			I	-
ES441846	Proteasome 26S					2.9	V	-
ES441746	Protein disulfide isomerase precursor ^b					2.3	V	At1g21750
ES440491	Protein transport protein Sec61 subunit beta			2.1			VII	At2g02080
ES441784	Purine permease			3.0		3.0	VIII	PUP5

ES442652	Putative 20S proteasome beta subunit ^b	2.5			-2.6		IV	PBE1
ES441539	Putative heat shock protein ^b			2.2			VII	At1g36390
ES440500	Rattus norvegicus clone CH230-206L9 ^b	3.3			-3.2	-2.7	IV	nimin-3
ES440181	Resistance protein RGC2 [*]	2.9					IV	S1P
ES440181	Ribosomal protein L2 ^{b, c}			-2.1			I	ATCG01310.1
ES440844	Ribosomal protein S10 ^b	2.1					IV	At3g13120
ES440451	RNA-binding protein ^b			2.0		2.1	VI	At5g46250
ES441112	S18.A ribosomal protein			-2.8		-2.2	II	T1G34030.1
ES441767	SAC1-like protein ^{b, c}					2.3	V	SAC6
ES442470	Secologanin synthase ^c	-2.1				2.4	II	AT4g27710
ES440577	Similar to histone H3 ^b			2.6		3.0	VI	HTR12
ES440601	SoDip22 drought inducible					2.2	VI	At1g22335
ES441678	Tonoplast intrinsic protein ^b	2.2					IV	TIP1-1
ES440677	Translation initiation factor B04 ^{b, c}	2.6	4.6	3.7			VIII	At4g27130
ES439793	Translation initiation factor IF-3-like ^b	-2.1		-2.5			II	T10C21.40
ES441506	Translational activator family protein ^{b, c}	-3.3	-3.8	-3.5			I	F13O11.10
ES442391	tRNA-Leu (UAA)			2.3		2.1	III	-
ES439865	Trnt-trnL intergenic spacer					-2.4	IV	-
ES440233	Ubiquinol-cytochrome C reductase			2.4		2.5	VIII	-
ES440607	Ubiquitin conjugating protein ^{b, c}		-2.0				I	UBC2
ES440384	Ubiquitin family protein ^{b, c}	-2.3			2.2		II	RUB1
ES439868	Ubiquitin-conjugating enzyme			2.0			III	-
ES442447	Ubiquitin-conjugating enzyme ^b			2.3			VII	Ahus5
ES442466	Uncharacterized protein ^c					2.3	VIII	-
ES441723	Uncharacterized RNA-binding protein C660.15 ^c				2.1		VIII	At4g36960
ES439842	Unknown protein	3.4			-2.4	-2.4	IV	SOBER1
ES441721	Unknown ^b	2.0					IV	At2g22570
ES440559	Unnamed protein					2.6	V	AT3G23980.1
ES440563	Unnamed protein	2.6		3.9		2.1	VII	At3g29780
ES441875	Unnamed protein ^b			2.1			VIII	APRR5
ES440507	Vacuolar ATP synthase subunit D ^b			2.0			III	VATD

ES441836	Zea mays mitochondrion genome	2.3	2.3	VIII	-	
ES442510	Zeta-carotene desaturase ^c		2.1	VIII	-	
ES440652	Zinc finger (C3HC4-type RING finger) ^b	2.4		VII	HUB1	
ES442603	Zinc finger (DNL type) family protein	2.2	2.0	VIII	AT5G27280.1	
ES442290	Zinc finger homeobox family protein	3.4	2.4	2.4	VII	AtHB33
ES439941	Zinc finger protein ^b	3.2	2.4	2.3	VII	ARI8

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1 **Supplementary material 2.** Complete list of differentially expressed genes by Catongo cacao meristems challenged with *M. pernicios* at early
2 stages, 30 dai and 60 dai compared to un-inoculated meristems (Control). The genes were determined as differentially expressed if the fold
3 change was greater than 2 or below -2. The differentially expressed genes were classified in 9 regulatory patterns (clusters I to IX). Asterisk
4 indicates the genes analyzed by RT-qPCR. ^a (-) indicates the genes for with no *A. thaliana* ortholog were found. ^b indicates the genes which were
5 found in the *A. thaliana* PPI network. ^c indicates the genes in common with TSH1188.
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Accession number	Putative function	Early stage vs Control	30 dai vs Control	60 dai vs Control	30 dai vs Early stage	60 dai vs Early stage	60 dai vs 30 dai	Cluster	<i>Arabidopsis thaliana</i> ortholog ^a
ES441727	14-3-3 protein ^b			2.0				VIII	F3F9.16
ES440115	18S ribosomal protein			2.3				IX	FIT
ES440256	20S proteasome alpha subunit C ^b			2.4				II	PAC1
ES441521	21 kDa seed protein ^c		-2.1		-2.3			III	At1g17860
ES440959	23S ribosomal protein	-3.3	-3.6	-2.1				III	At1g08125
ES440146	26S proteasome non-ATPase regulatory subunit 3 ^b			2.6				VIII	RPN3a
ES439794	40S ribosomal protein ^{b, c}	2.5		3.0				VIII	RPS3C
ES441508	60S ribosomal protein L11 ^{b, c}	-2.2						IV	RPL11B
ES440960	60S ribosomal protein L13 ^b	-2.8	-3.0					III	RPL13B
ES441839	60S ribosomal protein L31 ^{b, c}	2.8	2.4					VIII	RPL31C
ES440609	60S ribosomal protein L36 ^b		-2.5					III	RPL36A
ES442372	Acidic nuclear phosphoprotein			4.7		3.2	3.8	II	AT5G61190.1
ES440119	ADR122Cp			2.0				V	-
ES440125	Al-induced protein			2.0				II	At5g19140
ES440610	Alpha-tubulin ^b			2.0			2.1	I	TUBA6
ES442520	Ammonium transporter AMT2 ^b			2.4		3.2	3.1	I	AMT2
ES440516	At1g24050			3.0		2.2	2.6	II	AT1G24050.1
ES441937	At1g61040/T7P117			4.5		4.0	4.7	II	At1g61040
FC072112	At5g19590 ^b			2.2				V	At5g19590
ES440526	AT5g25280			2.2				IX	At5g25280
ES441504	Auxin-binding protein ABP20 precursor	2.3		2.0				VIII	GER3
ES440410	BEL1-related homeotic protein 29 ^b			2.2				II	BLH1
ES441962	Beta vulgaris mitochondrial DNA						2.5	I	-
ES442500	Beta-expansin			2.0				V	EXPB3

ES440200	Calcium binding protein ^b			2.1			IX	Cml5	
ES440098	Carboxyl-terminal peptidase			3.9		2.9	3.1	II	At3g13510
ES442468	CBL-interacting protein kinase 16 ^b	2.4						VII	CIPK16
ES440222	Cellulose synthase			2.7				VIII	CESA4
ES440806	ChaC protein			2.0				II	T12C22.6
ES439829	Chloroplast ATP synthase CF0 subunit III						2.2	I	LAG2
ES441826	Cinnamyl-alcohol dehydrogenase ^b			2.0				II	AT5G19440.1
ES441709	Clone LjT16B11			2.1				I	F26C17.6
ES440300	C-myc binding protein / prefoldin ^{b, c}		2.8	3.2				IX	At5g23290
ES441849	Copper chaperone	3.0		2.4				VII	At5g50730
ES441850	Cyclophilin ^b	2.1	3.7	2.4				VIII	CYP63
ES441450	Cysteine proteinase ^b			2.1				V	RD21A
ES439853	Cytosolic class II small heat shock protein HCT2	-2.6						IV	HSP17.6A
ES440981	D-aminoacyl-tRNA deacylase ^b	-2.2						IV	ROT3
ES441755	DEAD-box ATP-dependent RNA helicase 42 ^c	-3.8	-2.0	-2.8				IV	-
ES441722	Deaminase		2.2					IX	At1g68720
ES441947	Disease resistance protein RGA2	2.1						VII	RPPL1
ES441333	DNA repair protein RAD23	2.1						VII	RAD23
ES440020	DnaJ ^b			2.9				IV	ATJ3
ES440969	DnaJ protein ^b	-2.2	-2.4					III	At2g17880
ES441222	Drm3						2.5	VI	At1g56220
ES441403	E3 SUMO-protein ligase SIZ1			2.2				VIII	SIZ1
ES439984	Elongation factor 1 beta 2 ^{b, c}			2.3				VIII	At2g18110
ES440064	Elongation factor 1-gamma ^b			2.6			2.2	V	AT1G09640.1
ES441019	Elongation factor Tu family protein ^b	-2.1						IV	Sco1
ES441175	Endochitinase 1 ^b	2.1				-2.2		VII	CHI-B
ES440123	Eukaryotic translation initiation factor 2 / eIF-2 ^b			2.4				V	At1g76810
ES442536	Expressed protein	2.0						VII	At4g01150
ES441735	Expressed protein		2.5					IX	At3g20430
ES441122	Expressed protein			2.0				II	At1g15940
ES440976	Expressed protein	-2.1	-2.0					III	AT5G51840.1

ES440523	Expressed protein			2.3				II	At1g34350
ES440915	Expressed protein						2.0	I	At1g68490
ES441205	Expressed protein			2.0				II	At1g65720
ES441565	Expressed protein			2.6			2.0	V	MDF20.8
ES441825	Expressed protein			4.2		3.9	4.9	II	At3g54260
ES442519	Expressed protein		-2.5		-2.1		4.1	VI	At3g24490
ES441848	Expressed protein ^b	2.3		2.2				VII	At3g32930
ES441447	Expressed protein ^b				-2.2			VII	At5g42150
ES441509	Expressed protein ^c		3.1					IX	T19L5_60
ES441080	F16A14.15						2.4	VI	F7A19.3
ES440294	F-box protein	3.5	3.2	4.6				VIII	At1g10890
ES440219	F-box protein ^c	3.1	3.0	4.5				VIII	AT1G20750.1
ES442076	Fiber protein (Fb11) ^b	2.6			-2.3			VII	At2g46540
ES442624	Fiber protein Fb31				-2.2			VII	SAG29
ES441669	Flavonoid 3'-hydroxylase ^b			2.2				V	CYP75B1
ES441759	Gigantea protein ^b	2.2	2.3	2.2				VIII	GI
ES442509	Glutathione S-transferase ^{b, c}					2.6	2.0	I	At3g03190
ES442187	Glycine-rich protein	2.2			-2.0			VII	F19K16.3
ES442692	Glycoside hydrolase family 28 protein						2.1	VI	F9D16.290
ES442487	Glycosyl hydrolase family 38 protein ^c	-2.9		-2.4				IV	At3g26720
ES441636	GTP-binding protein ^b			2.0				VIII	SAR1A
ES442508	HB2 homeodomain protein			3.5		4.0	4.7	II	WOX13
ES441273	Heat shock protein ^b	2.8			-3.1			VII	Hsc70-7
ES441498	Heat stress transcription factor B-2a			2.1				V	dl4605c
ES441705	Histone H4 ^b		2.6					IX	At1g07660
ES441356	Homeotic protein knotted-1 ^b			2.0				I	BP
ES440796	Homo sapiens Cdna DKFZp686C17112			2.0				II	-
ES439811	Homo sapiens clone DKFZp686B0962			2.0				II	-
ES440528	Homo sapiens clone RP11-472A1 ^{b, c}			2.3				IX	At5g12040
ES440133	HSP 17.3 ^{b, c}	3.5	2.5	3.3				VIII	HSP17.4
ES441174	Hypothetical protein				-2.0			VII	RER1A

ES442678	Hypothetical protein	2.0					VII	PAP27	
ES442099	Hypothetical protein		3.1	2.1			IX	T4P13.15	
ES442465	Hypothetical protein		-2.0				III	At4g27740	
ES440032	Hypothetical protein			2.2			V	ARI8	
ES442052	Hypothetical protein			2.1			I	T22A6.30	
ES442387	Hypothetical protein	2.2		2.0			VIII	At3g05660	
ES442591	Hypothetical protein	2.4					VII	-	
ES440804	Hypothetical protein			2.1			I	At1g63380	
ES440813	Hypothetical protein			2.0			I	F9L1.12	
ES439796	Hypothetical protein			2.2			II	At3g17330	
ES441355	Hypothetical protein			2.4			IX	dl3665c	
ES441206	Hypothetical protein ^b					2.2	VI	CYP38	
ES440529	Hypothetical protein ^b			2.0			V	At2g23090	
ES440823	Hypothetical protein ^b			2.3			IX	RNR1	
ES441783	IgE-binding protein ^b	2.0					VIII	SODA	
ES441474	Integral membrane transporter protein				-2.5		VII	-	
ES441464	Kinesin	2.4			-2.6		VII	AT1G22060.1	
ES441435	Kinesin heavy chain				-2.3		VII	AT3G12020.1	
ES442223	Laccase			2.9		2.3	2.5	II	LAC17
ES440113	Lotus corniculatus clone:LjT17H01			2.0				IX	F2G14_10
ES441081	Medicago truncatula clone mth2-12f13 ^b						2.0	VI	ARF7
ES441511	Metallothionein		2.0					IX	MT2A
ES442183	MGC69563 ^b			2.6			2.0	V	T9C5.30
ES442064	MRG family protein ^{*,b}			5.1		4.5	4.7	II	C7A10.80
ES441854	Mus musculus clone RP23-402A4			2.2				II	-
ES442063	Mus musculus clone RP24-300F2 ^b	3.4			-3.3	-2.0		VII	ATAF1
ES441147	Myb-related protein 1			2.0				II	MYB106
ES439800	Neurofilament triplet M protein ^b			2.4				VIII	ERD10
ES442523	No-Hit	2.8	2.8	3.6				VIII	AT1G10400.1
ES441090	No-Hit	2.3						VII	-
ES442689	No-Hit	2.3						VII	At5g57580

ES441864	No-Hit				2.0			IX	-	
ES441844	No-Hit				2.0			V	-	
ES442120	No-Hit		2.4					IX	-	
ES441707	No-Hit		2.2					IX	AT4g33600	
ES441615	No-Hit		-2.3		-2.0			III	F8F6_270	
ES442445	No-Hit		-2.1		-2.4		2.9	VI	-	
ES440010	No-Hit				2.0			V	GC1	
ES440705	No-Hit				2.2			V	T2J15.14	
ES440807	No-Hit				2.2			II	F28O9.120	
ES440175	No-Hit				2.0			II	CRK8	
ES441058	No-Hit				2.2			II	-	
ES441699	No-Hit	2.4				-2.5		VII	-	
ES440112	No-Hit	-2.2	-3.0				2.0	III	-	
ES441932	No-Hit				2.0			V	At2g14710	
ES442186	No-Hit				2.1			V	At3g14250	
ES440914	No-Hit				2.0			II	dl3250c	
ES441068	No-Hit						2.0	2.9	I	-
ES441798	No-Hit							2.0	I	ACA13
ES441071	No-Hit				2.2			2.1	II	At3g03870
ES442527	No-Hit				3.2		2.7	3.1	II	F6I7.50
ES441212	No-Hit	2.6	3.0		2.7				VIII	-
ES442211	No-Hit				2.2			2.3	I	At5g19420
ES442507	No-Hit							2.1	VI	At1g56420
ES441217	No-Hit				3.3			2.9	V	At2g13295
ES442502	No-Hit							2.0	I	At1g28260
ES441725	No-Hit				2.6				IX	F18B3.120
ES441925	No-Hit ^b							2.6	VI	At2g21150
ES442643	No-Hit ^b				2.5			2.1	V	xpo1
ES441497	No-Hit ^b	2.4				-2.8			VII	PUX4
ES439825	No-Hit ^b		-2.4						III	At5g37830
ES440864	No-Hit ^{b, c}		2.5						IX	MAA21_90

ES441777	No-Hit ^{b, c}	-2.0			2.1	IV	GEK1	
ES440515	No-Hit ^{b, c}	2.7			-2.6	VII	TCP10	
ES440902	Non-cell-autonomous heat shock cognate protein 70 ^b	4.7	4.1	5.1		VIII	hsp70	
ES440558	Orf25 (L16-10)					2.1	I	AtMg00640
ES440903	Organic cation transporter protein		-2.6				III	At4g26190
ES442638	OSJNBa0006A01.2 ^{b, c}				2.3		IV	At1g60850
ES441045	OSJNBa0029K06			2.1		2.1	VI	At1g75190
ES441149	OSJNBa0086P08.14 ^b	2.6			-2.2		VII	At2g33845
ES441752	OTU-like cysteine protease ^b	2.3			-2.4		VII	F17J6.19
ES440614	Oxidoreductase	2.7			-2.6		VII	COG1052
ES439829	P0435B05.20 ^b			2.2			II	AT5G46020.1
ES439858	Panax ginseng chloroplast genome			2.3			VII	-
ES440257	Pathogenesis related protein PR10 [*]			2.5			II	MLP423
ES441596	PDI-like protein ^{b, c}	5.1	4.8	6.2			VIII	At1g60420
ES440722	Peptidyl-prolyl cis-trans isomerase CYP19-4			2.0			VII	LCR
ES441424	Phosphatase type 2C	2.5			-2.6		VII	AtPPC3
ES439810	Phosphoglucosyltransferase ^b		2.9		2.3		IX	At1g70730
ES441527	Polyubiquitin ^b	2.4	2.9	4.2			VIII	T8F5.13
ES439831	Polyubiquitin ^c		2.2	3.3			VIII	-
ES441237	Predicted protein	2.1					VII	AT1G08510.1
ES441959	Predicted protein			2.1		2.8	VI	F9D24.150
ES442607	Predicted protein ^c		2.3				IX	AT3G20620.1
ES440920	Probable acetyl-CoA acetyltransferase			2.2			VII	F9P7.1
FC072054	Profilin 1	3.4	3.6	2.5			VIII	PRF3
ES440794	Proline-rich protein precursor	3.1			-3.2		VII	At2g34700
ES440131	Proline-rich protein PRP1			2.2			II	At5g04290
ES439819	Proline-rich spliceosome-associated (PSP) family protein ^{b, c}	2.9		3.9		2.2	VIII	At4g21660
ES440244	Protease inhibitor / seed storage / lipid transfer protein (LTP)		2.6	4.2	3.0		IX	AT2G37870.1
ES440207	Protease inhibitor 2 ^c	3.1	3.0	4.3			VIII	At2g38870
ES440095	Proteasome inhibitor ^b		2.5	2.8			IX	At3g53970
ES440218	Protein kinase			2.1			I	T5I8.9

ES441577	Protein kinase			2.4			II	AT4g03230
ES441950	Protein kinase			2.3			VIII	F20H23.1
ES441334	Protein kinase family	2.0			-2.4		VII	AT3G13690
ES441465	Putative trehalose-6-phosphate synthase ^b	2.0					VII	TPS7
ES441771	Putative zinc finger POZ domain protein ^b	2.3			-2.3		VII	At3g03740
ES441358	RabGAP/TBC domain-containing protein		2.4		2.6		IX	T15C9_20
ES440181	Receptor-like kinase RHG1			2.7		2.6	II	T18N14.120
ES439992	Ribosomal protein L2 ^{b, c}	3.1	3.4	4.2			VIII	ATCG01310.1
ES441112	Ribosomal protein S8	3.0			-2.4		VII	HSC70-1
ES441624	SAC1-like protein ^{b, c}				2.2		IV	SAC6
ES441930	Sadtomato protein			4.6		3.9	II	XTH9
ES440570	SAH7			2.2			VII	SAH7
ES441664	SecA-type chloroplast protein transport factor ^b			2.4			II	secA
ES442470	Secologanin synthase ^c					2.6	I	AT4g27710
ES439901	Skp1				-2.0		VII	-
ES442375	Skp1 ^b	-2.3	-2.3	-2.7			IV	SKP1B
ES440808	Splicing factor			2.5			VIII	At2g35170
ES440225	Sulfite oxidase ^b			2.0			II	SOX
ES441720	T19E23.14 ^b			2.5			II	At1g31350
ES441216	TCP family transcription factor			2.4			V	TCP20
ES442017	Thaumatococcus			2.5		2.4	V	At4g11650
ES439918	Threonine synthase ^b	2.8	4.3	2.6			VIII	At4g29840
ES441678	Translation initiation factor 3 ^{b, c}	-2.3	-2.5				III	TIF3B1
ES439922	Translation initiation factor B04		-3.4		-2.4	2.2	III	At1g54290
ES439793	Translation initiation factor B04	3.1	3.1	4.0			VIII	COG0023
ES441079	Translational activator family protein ^{b, c}			2.3			VIII	F13O11.10
ES442391	TrnC			2.1		2.2	VI	T22E16.2
ES441717	TrnT-trnL intergenic spacer		-2.7		-2.2		III	-
ES439841	Ubiquitin conjugating enzyme	2.4		2.4			VII	UEV1D
ES440233	Ubiquitin conjugating protein ^{b, c}		-2.3				III	UBC1
ES440607	Ubiquitin conjugating protein ^{b, c}	2.5	2.8	3.3			VIII	UBC2

ES442021	Ubiquitin family protein ^b					2.1	III	RUB1	
ES440615	Uncharacterized protein			2.1			II	-	
ES441208	Uncharacterized protein			3.7		3.7	4.2	II	-
ES440723	Uncharacterized protein			2.0				II	-
ES442466	Uncharacterized protein ^c					-2.0		VI	-
ES441723	Uncharacterized RNA-binding protein C660.15 ^c	2.3	3.7	2.5				VIII	At4g36960
ES440905	Unknown			2.1			2.2	I	At5g67070
ES441828	Unknown protein						2.1	I	At5g43150
ES440821	Unknown protein			2.0			2.1	VI	At2g26110
ES441644	Unknown ^b			2.5				VIII	F22L4.5
ES442661	Unnamed protein	2.5				-2.4		VII	RCI2B
ES441239	Unnamed protein						2.0	I	At3g17450
ES440817	Vf14-3-3c protein ^b			2.1				VIII	GRF8
ES442510	Zeta-carotene desaturase ^c			2.2				II	At5g48050
ES440083	Zinc finger (C2H2 type) family protein			2.4				V	At3g02790
ES441727	Zinc finger (CCCH-type) family protein			2.4				II	At3g55980
ES441551	Zinc finger CCCH domain-containing protein 20		2.2					IX	At5g41750

1 **Supplementary material 3.** Specific gene ontology (GO) classes derived from PPPI observed in the *A. thaliana* network in relation to the
2 TSH1188-*M. pernicioso* interaction.
3

Description	GO number	p-value	Corrected p-value ^a	k ^b	f ^c	Proteins
Developmental process	32502	1.61×10 ⁻²¹	1.72×10 ⁻¹⁹	82	1052	LOX1; ZWICHEL; ELF3; AT2G02560; GSH1; IAA14; RPS2; AT2G04842; FLC; RPS3; PAS1; COP1; BAK1; SHD; AT5G22290; CUL4; CDF1; FKBP42; ATG5; COL3; CRM2; LPR1; DDB1A; SAG101; APRR5; BRI1; EMB2024; CRY1; F16M19.8; AXR6; TIR1; SERK2; AT1G64440; AHK2; ADO1; NDR1; ADO3; AXR1; MUR1; EMB1467; KAPP; AT5G61960; AT5G10480; AT5G41480; RIN4; AT4G04350; PAD4; EID1; F14O23.21; AT3G01420; SPLAYED; SKP1B; CAM1; SPA1; MYB23; CPR5; CLV1; AT3G08850; GPA1; SHM1; PEX10; TSF; HUB1; TIP1; AT3G02570; PIF1; AFB1; AT1G02140; AT2G18510; NPR1; PHYB; ATE1; OPR1; BI-1; DET1; F26B6.8; SVP; CO; TOR; PAD2; ROT3; GI
Circadian rhythm	7623	1.93×10 ⁻²¹	1.72×10 ⁻¹⁹	16	23	ELF3; ADO1; WNK1; SRR1; ADO2; PHYB; CCA1; FLC; APRR9; ARR4; APRR7; APRR5; APRR3; CRY1; GI; APRR1
Response to stress	6950	6.99×10 ⁻²¹	5.71×10 ⁻¹⁹	65	705	CAX1; EDS1; ELF3; LOX2; NIT3; NIT4; GSH1; CYP74A; TSB1; HSP70; FLC; ATG5; AVP1; CRY1; ATMYB2; AT4G02580; NDPK2; SRK2E; AT1G17870; AT3G27820; AXR1; AXR2; HDT3; EMB1467; ATPK1; COI1; AT3G52880; AT1G12780; AOC2; AOC1; AOC4; HOS1; AOC3; HSC70-7; MPK6; MPK4; AT3G01420; MPK3; AT3G26090; HSP81-1; HSP81-2; AT4G10960; CIPK24; ABI1; SKP1B; AT3G01520; HSC70-1; AT4G21150; T2A6.110; CBL4; HSFA1A; AT3G03190; NPR1; MYB75; PHYB; CIPK1; MEKK1; OPR1; OPR3; MKK1; MKK2; GST8; PAD2; CYT1; GI
Innate immune response	45087	1.16×10 ⁻¹⁹	8.16×10 ⁻¹⁸	26	103	PAD4; MPK6; EDS1; MPK4; LOX2; GSH1; CYP74A; RPS2; RPS3; CPR5; SHM1; NDR1;

						NPR1; MKS1; OPR1; OPR3; MKK4; MKK5; COI1; AOC2; PAD2; AOC1; PAD1; AOC4; RIN4; AOC3
Carboxylic acid metabolic process	19752	3.82×10^{-19}	1.97×10^{-17}	50	462	AT1G29870; NIT2; LOX2; AT5G57850; CYP74A; TSB1; TSB2; AT1G63660; AT2G13560; AT2G04842; AT1G09620; AT2G31810; AT4G00600; AT5G56720; AT1G01600; DXR; AAO2; AT4G23850; T16L1.160; ATSR; AAO3; AT4G13780; AT2G04400; AT1G72810; AT4G24830; HPL1; AT5G10480; AT5G16290; AT3G58610; AOC2; AOC1; AOC4; AOC3; AT4G04350; AT3G01420; AT4G00620; AT5G66120; AT5G43330; SHM1; PEX10; AT3G23940; AT4G02610; LPD1; AT3G02760; PHYB; CSR1; OPR1; OPR3; AT1G04410; CYT1
Defense response, incompatible interaction	9814	3.85×10^{-17}	1.64×10^{-15}	21	75	PAD4; EDS1; MPK4; LOX2; NPR1; NDR1; GSH1; CYP74A; OPR1; OPR3; CPR5; MKK4; COI1; MKK5; PAD2; AOC2; PAD1; AOC1; RIN4; AOC4; AOC3
Response to other organism	51707	3.46×10^{-16}	1.42×10^{-14}	34	253	MPK6; PAD4; EDS1; MPK4; NIT2; LOX2; FLS2; GSH1; CYP74A; HSP70; RPS2; HSC70-1; RPS4; CPR5; TIR1; SRK2E; AFB1; NDR1; NPR1; OPR1; OPR3; MKK1; MKK4; MKK5; COI1; PAD2; AOC2; CYT1; PAD1; WRKY33; AOC1; RIN4; AOC4; AOC3
Anatomical structure development	48856	2.02×10^{-15}	6.83×10^{-14}	58	742	ZWICHEL; ELF3; LOX1; AT2G02560; GSH1; IAA14; AT2G04842; FLC; PAS1; BAK1; CUL4; CDF1; SHD; FKBP42; CRM2; LPR1; BRI1; EMB2024; AXR6; TIR1; AHK2; AT1G64440; ADO1; ADO3; AXR1; MUR1; EMB1467; KAPP; AT5G61960; AT5G41480; AT4G04350; PAD4; EID1; F14O23.21; SPLAYED; CAM1; SKP1B; SPA1; MYB23; CPR5; CLV1; AT3G08850; PEX10; TSF; HUB1; TIP1; AT3G02570; AT2G18510; AT1G02140; ATE1; OPR1; SVP; F26B6.8; CO; TOR; PAD2; ROT3; GI
Response to endogenous stimulus	9719	1.57×10^{-11}	3.57×10^{-10}	46	625	MPK6; PAD4; EDS1; MPK4; MPK3; ELF3;

						LOX2; AT3G26090; MPK1; AT2G02560; IAA3; GSH2; IAA1; IAA14; ABI1; IAA8; PAS1; BAK1; ARR5; LPR1; ARR4; GPA1; BRI1; PRN1; AT3G09940; AXR6; ATMYB2; AXR3; TIR1; NDPK2; SRK2E; AFB1; DHAR1; NPR1; MYB75; AT4G21670; AXR1; HDT3; AXR2; CIPK1; OPR1; F26B6.8; COI1; RUB1; CYT1; AT1G76030
Jasmonic acid and ethylene-dependent systemic resistance	9861	4.89×10^{-11}	1.07×10^{-09}	10	23	OPR1; MPK4; OPR3; LOX2; COI1; CYP74A; AOC2; AOC1; AOC4; AOC3
Phototransduction	7602	4.87×10^{-10}	8.06×10^{-09}	7	10	EID1; NDPK2; ELF3; PKS1; HFR1; SRR1; SPA1 AT4G09650; AT5G08680; AT4G26710; AT4G02580; AT5G08530; AT4G38510; ATPC2; ATPC1; AT5G08690; AT5G47030; AT5G06160; AT4G32260
Oxidative phosphorylation	6119	1.65×10^{-09}	2.31×10^{-08}	12	50	
Oxylipin biosynthetic process	31408	2.05×10^{-09}	2.79×10^{-08}	8	17	OPR1; OPR3; LOX2; CYP74A; AOC2; AOC1; AOC4; AOC3
Photomorphogenesis	9640	2.28×10^{-09}	3.07×10^{-08}	9	24	EID1; CUL4; COL3; LPR1; DDB1A; DET1; APRR5; CRY1; SPA1
Response to hormone stimulus	9725	5.51×10^{-09}	6.67×10^{-08}	33	433	MPK6; ELF3; AT3G26090; MPK1; AT2G02560; IAA3; IAA1; IAA14; ABI1; IAA8; PAS1; ARR5; BAK1; LPR1; ARR4; GPA1; BRI1; PRN1; AXR6; ATMYB2; AXR3; TIR1; NDPK2; SRK2E; AFB1; MYB75; AXR1; AT4G21670; HDT3; AXR2; CIPK1; F26B6.8; RUB1
Monocarboxylic acid metabolic process	32787	1.33×10^{-08}	1.43×10^{-07}	21	198	AT3G01420; LOX2; AT4G00620; LPD1; AT5G57850; CYP74A; PHYB; OPR1; HPL1; OPR3; AT4G00600; DXR; AT1G01600; AT4G23850; AAO2; AOC2; AAO3; PEX10; AOC1; AOC4; AOC3
Purine ribonucleotide biosynthetic process	9150	2.66×10^{-08}	2.69×10^{-07}	11	51	AT4G09650; AT5G08680; AT4G26710; AT4G38510; ATPC2; ATPC1; AT5G08690; AT5G47030; AT1G63660; AT5G06160; AT4G32260
Response to reactive oxygen species	302	1.27×10^{-07}	1.10×10^{-06}	9	36	MPK6; EDS1; NDPK2; MKK1; AT1G17870;

						AT3G27820; AT3G52880; HSP70; GI
Death	16265	1.88×10^{-07}	1.51×10^{-06}	11	61	CDF1; AT3G01420; BI-1; GPA1; SHM1; NDR1; NPR1; CRY1; RPS2; RIN4; RPS3
Response to hydrogen peroxide	42542	1.05×10^{-06}	7.46×10^{-06}	7	24	NDPK2; MKK1; AT1G17870; AT3G27820; AT3G52880; HSP70; GI
Cell differentiation	30154	6.05×10^{-06}	3.88×10^{-05}	17	198	AT3G01420; ZWICHEL; AT1G64440; NPR1; NDR1; RPS2; RPS3; PAS1; MYB23; CDF1; CPR5; BI-1; GPA1; SHM1; AT5G10480; CRY1; RIN4
Hypersensitive response	9626	3.76×10^{-05}	1.98×10^{-04}	5	17	SHM1; NDR1; RPS2; RIN4; RPS3
Phytoalexin biosynthetic process	52315	2.58×10^{-04}	1.09×10^{-03}	3	6	GSH1; PAD2; PAD1

^a Values calculated from p-value after FDR application.
^b Total number of proteins found in the network that belong to a specific GO.
^c Total number of proteins belonging to a specific GO.

1 **Supplementary material 4.** Specific gene ontology (GO) classes derived from PPPI observed in the *A. thaliana* network in relation to the
2 Catongo-*M. pernicioso* interaction.
3

Description	GO number	p-value	Corrected p-value ^a	<i>k</i> ^b	<i>f</i> ^c	Proteins
Response to abiotic stimulus	9628	3.67×10 ⁻²⁵	7.29×10 ⁻²³	55	569	NIA2; HSP70; GSH1; KNAT4; ADA2B; RGA; FLC; AKT1; IAA19; BRI1; CBF1; AT1G16030; CSN5B; CSN5A; NDPK2; SRK2E; ADS3; HAG1; ACS6; AXR2; GAI; AUX1; UBC2; SUS1; HSC70-7; EID1; MPK6; MPK4; MPK3; HSP81-1; HSP81-2; CIPK24; SKP1B; ABI1; CAM1; ACP1; HSC70-1; ORE9; F7G19.5; AT5G28540; ERD15; CHS; PHOT1; HSFA1A; F3H; PSBO1; MEKK1; TT5; CSN8; GORK; ACT7; MKK2; AT4G01900; PAD2; GI
Innate immune response	45087	1.79×10 ⁻²⁰	2.37×10 ⁻¹⁸	24	103	PAD4; MPK6; EDS1; PBS1; MPK4; PBS2; LOX2; WRKY70; NDR1; GSH1; RPS2; RPS5; RPS3; CHI-B; OPR3; MKK4; MKK5; COI1; AOC2; PAD2; AOC1; PAD1; AOC4; RIN4
Protein folding	6457	3.53×10 ⁻²⁰	4.01×10 ⁻¹⁸	30	189	F14G9.9; AT2G17880; AT4G39960; AT5G23290; ATJ3; AT5G20890; F24J7.140; HSP70; AT3G22480; AT5G37750; AT2G22360; AT5G37440; AT2G07340; AT1G77930; F7G19.5; AT3G08970; AT5G28540; F28P5.5; AT3G08910; AT1G16030; AT1G36390; AT5G16070; AT3G10220; AT3G11830; T1P2.3; AT4G39920; AT1G61770; AT2G43560; AT5G49510; AT5G05750
Immune response	6955	4.70×10 ⁻²⁰	4.68×10 ⁻¹⁸	24	107	PAD4; MPK6; EDS1; PBS1; MPK4; PBS2; LOX2; WRKY70; NDR1; GSH1; RPS2; RPS5; RPS3; CHI-B; OPR3; MKK4; MKK5; COI1; AOC2; PAD2; AOC1; PAD1; AOC4; RIN4
Defense response, incompatible interaction	9814	6.91×10 ⁻²⁰	5.50×10 ⁻¹⁸	21	75	PAD4; EDS1; PBS1; PBS2; MPK4; LOX2; WRKY70; NDR1; GSH1; RPS5; CHI-B; OPR3; MKK4; COI1; MKK5; AOC2; PAD2; AOC1; PAD1; AOC4; RIN4
Response to other organism	51707	2.29×10 ⁻¹⁹	1.66×10 ⁻¹⁷	33	253	AT4G11260; PAD4; MPK6; EDS1; PBS1; PBS2;

						MPK4; LOX2; FLS2; WRKY70; GSH1; HSP70; RPS2; HSC70-1; CHI-B; ERD15; TIR1; SRK2E; AFB1; NDR1; RPS5; OPR3; MKK1; MKK4; COI1; MKK5; AOC2; PAD2; AOC1; WRKY33; PAD1; AOC4; RIN4
Response to hormone stimulus	9725	1.36×10^{-18}	8.99×10^{-17}	41	433	ARR10; MPK6; AT4G11260; MPK1; AT2G02560; IAA3; IAA1; IAA14; ABI1; IAA12; ADA2B; IAA8; RGA; IAA13; IAA6; BAK1; CHI-B; AT3G15730; IAA19; IAA18; BRI1; BZR1; AXR6; TIR1; AXR3; CSN5B; NDPK2; CSN5A; SRK2E; AFB1; RBOHF; MP; CPK6; AXR2; ACS6; AUX1; GAI; GORK; ACT7; F26B6.8; RUB1
Response to biotic stimulus	9607	1.54×10^{-17}	8.78×10^{-16}	33	290	AT4G11260; PAD4; MPK6; EDS1; PBS1; PBS2; MPK4; LOX2; FLS2; WRKY70; GSH1; HSP70; RPS2; HSC70-1; CHI-B; ERD15; TIR1; SRK2E; AFB1; NDR1; RPS5; OPR3; MKK1; MKK4; COI1; MKK5; AOC2; PAD2; AOC1; WRKY33; PAD1; AOC4; RIN4
Response to stress	6950	3.73×10^{-17}	1.98×10^{-15}	50	705	EDS1; LOX2; HSP70; GSH1; ADA2B; RGA; FLC; AKT1; CBF1; ATAF1; AT1G16030; AT4G02580; NDPK2; SRK2E; AXR2; GAI; COI1; SUS1; AOC2; TSO2; AOC1; AOC4; HSC70-7; MPK6; MPK4; MPK3; HSP81-1; HSP81-2; CIPK24; ABI1; SKP1B; ACP1; HSC70-1; CHI-B; ORE9; F7G19.5; ERD15; AT5G28540; CHS; HSFA1A; AT3G03190; MEKK1; GORK; OPR3; ACT7; MKK1; MKK2; PAD2; GI; CEF
Response to auxin stimulus	9733	1.82×10^{-15}	8.50×10^{-14}	26	200	AT4G11260; AT2G02560; MPK1; IAA3; IAA14; IAA1; ADA2B; IAA12; IAA13; IAA8; IAA6; IAA19; IAA18; AXR6; CSN5B; AXR3; TIR1; CSN5A; NDPK2; AFB1; MP; ACS6; AXR2; AUX1; ACT7; RUB1
Developmental process	32502	2.12×10^{-15}	8.89×10^{-14}	59	1052	ZWICHEL; AT2G02560; GSH1; IAA14; RPS2; IAA12; RGA; FLD; FLC; RPS3; AKT1; BAK1; SHD; FKBP42; AT3G02660; BRI1; LFY; AXR6; CSN5B; TIR1; CSN5A; ASP3; HAG1; NDR1; MP; ADO3; ACS6; GAI; AUX1; AG; KAPP;

						SUS1; TSO2; RIN4; EID1; PAD4; CLPP4; SKP1B; CAM1; PHE1; TCP10; ORE9; BP; AFB1; AT2G18510; RBOHF; CHIV; RPS5; BLH9; ACT7; BI-1; GLN2; CSN1; F26B6.8; TOR; PAD2; ROT3; DRL1; GI
Protein deneddylation	338	7.45×10^{-14}	2.96×10^{-12}	8	9	CSN8; CSN7; CSN5B; CSN5A; CSN1; CSN4; CSN3; CSN2
Anatomical structure development	48856	6.81×10^{-12}	1.87×10^{-10}	43	742	PAD4; EID1; CLPP4; ZWICHEL; AT2G02560; GSH1; IAA14; SKP1B; CAM1; FLD; FLC; AKT1; PHE1; BAK1; TCP10; SHD; FKBP42; ORE9; AT3G02660; BRI1; AXR6; LFY; TIR1; CSN5A; ASP3; AT2G18510; HAG1; ADO3; MP; CHIV; AUX1; BLH9; ACT7; KAPP; AG; CSN1; F26B6.8; TOR; SUS1; PAD2; DRL1; ROT3; GI
Jasmonic acid and ethylene- dependent systemic resistance	9861	3.27×10^{-09}	6.68×10^{-08}	8	23	CHI-B; MPK4; OPR3; LOX2; COI1; AOC2; AOC1; AOC4
Hormone-mediated signaling	9755	3.89×10^{-09}	7.74×10^{-08}	13	87	BZR1; AT4G11260; AXR3; NDPK2; SRK2E; MPK1; RBOHF; ABI1; CPK6; GAI; BAK1; CHI-B; AT3G15730
Carboxylic acid metabolic process	19752	1.48×10^{-08}	2.61×10^{-07}	28	462	AT2G37500; AT1G24360; LOX2; ACP5; HSK; ACP1; AT3G15730; AT3G02660; AT1G01600; TRP1; T16L1.160; AT3G23940; LPD1; ADS3; CSR1; ACS6; AT4G24830; OPR3; ISPD; GLN2; ENR1; LCR; AT1G04410; AT5G53460; AT4G31180; AOC2; AOC1; AOC4
Response to jasmonic acid stimulus	9753	1.01×10^{-07}	1.54×10^{-06}	10	61	CSN8; MPK6; AXR6; GORK; MPK4; VSP1; LOX2; COI1; WRKY70; CHS
Response to fungus	9621	7.20×10^{-07}	7.81×10^{-06}	9	58	AT4G11260; CHI-B; MPK4; PBS2; NDR1; WRKY70; GSH1; PAD2; WRKY33
Death	16265	1.12×10^{-06}	1.16×10^{-05}	9	61	BI-1; NDR1; RBOHF; RPS2; TSO2; RPS5; ACS6; RIN4; RPS3
Oxylipin biosynthetic process	31408	8.46×10^{-06}	6.73×10^{-05}	5	17	OPR3; LOX2; AOC2; AOC1; AOC4
Hypersensitive response	9626	8.46×10^{-06}	6.73×10^{-05}	5	17	NDR1; RPS2; RPS5; RIN4; RPS3

Cell differentiation	30154	1.15×10^{-05}	8.84×10^{-05}	14	198	ZWICHEL; RBOHF; NDR1; RPS2; ACS6; RPS5; RPS3; AKT1; AUX1; AG; BI-1; BP; TSO2; RIN4
Systemic acquired resistance, salicylic acid mediated signaling pathway	9862	2.80×10^{-05}	1.99×10^{-04}	4	11	PAD4; EDS1; MPK4; WRKY70
Response to reactive oxygen species	302	3.52×10^{-05}	2.48×10^{-04}	6	36	MPK6; EDS1; NDPK2; MKK1; HSP70; GI
Auxin mediated signaling pathway	9734	8.15×10^{-05}	5.32×10^{-04}	4	14	AT4G11260; AXR3; NDPK2; MPK1
Anthocyanin metabolic process	46283	8.15×10^{-05}	5.32×10^{-04}	4	14	DFR; LDOX; AT4G01900; CHS
Phytoalexin biosynthetic process	52315	1.03×10^{-04}	6.43×10^{-04}	3	6	GSH1; PAD2; PAD1

^a Values calculated from p-value after FDR application.
^b Total number of proteins found in the network that belong to a specific GO.
^c Total number of proteins belonging to a specific GO.

Supplementary material 5. Self-consistent set (SCS) used in this study.

Accession number	Putative function
ES441715	Regulator of nonsense transcripts
ES441761	No-Hit
ES439863	Cathepsin B-like cysteine proteinase
ES440505	Elongation factor (ef-1alpha gene)
ES440504	Protease inhibitor/seed storage/lipid transfer protein (LTP)
ES440635	Ribosomal protein S12
ES439878	Ribosomal protein S14
ES440373	Ribosomal protein S19
ES440469	RING zinc finger protein
ES440513	Serine carboxypeptidase S10
ES440636	Serine carboxypeptidase S10
ES440566	Stress-induced cysteine proteinase
ES439977	Transducin family protein / WD-40 repeat protein
ES440426	trnT-trnL
ES442484	NADPH-cytochrome P450 oxydoreductase isoform 3
ES440830	Serine/threonine-protein kinase

Supplementary material 6. Primers used in the RT-qPCR analysis.

Name	Sequence	Size of the amplified product (bp)	Tm (°C)
Beta-tubulin-F	5'-CTGGTCTCAGCAGCCAAAATG-3'	193	85
Beta-tubulin-R	5'- TGCAACCATGAGTGGTGTCA-3'		
RGC2-F	5'- TGTCGTGGCCTTCCAATTAAA-3'	150	76
RGC2-R	5'-GGGAACAGACTTTTCAAACCTCCAA-3'		
HRGP-F	5'- CGGAAACCAAGGCCTCACT-3'	150	82
HRGP-R	5'- ACCTCGCCATCAGGATTGTC-3'		
Petidyl-prolyl-cis-trans isomerase-F	5'-GGGAGAATGCAGAAAGTCC-3'	169	84.5
Petidyl-prolyl-cis-trans isomerase-R	5'-CTGGTTCTGCAGACTTGTCG-3'		
NoHit-F	5'-TCCTGGTCACTGATAAACTTTTGC-3'	150	79
NoHit-R	5'-TGTCGCTTTCATTGCTGAATG-3'		
PR10-F	5'- GGTGTCACCACATATACGCAAGA-3'	150	80
PR10-R	5'- AACACCGCCATCTCCATGAA-3'		
MRG-F	5'- CTCCGAAACGAAACTGATGA-3'	150	79
MRG-R	5'- AAATAATGCCAGCCGTTGCT-3'		