

Accessory Publication

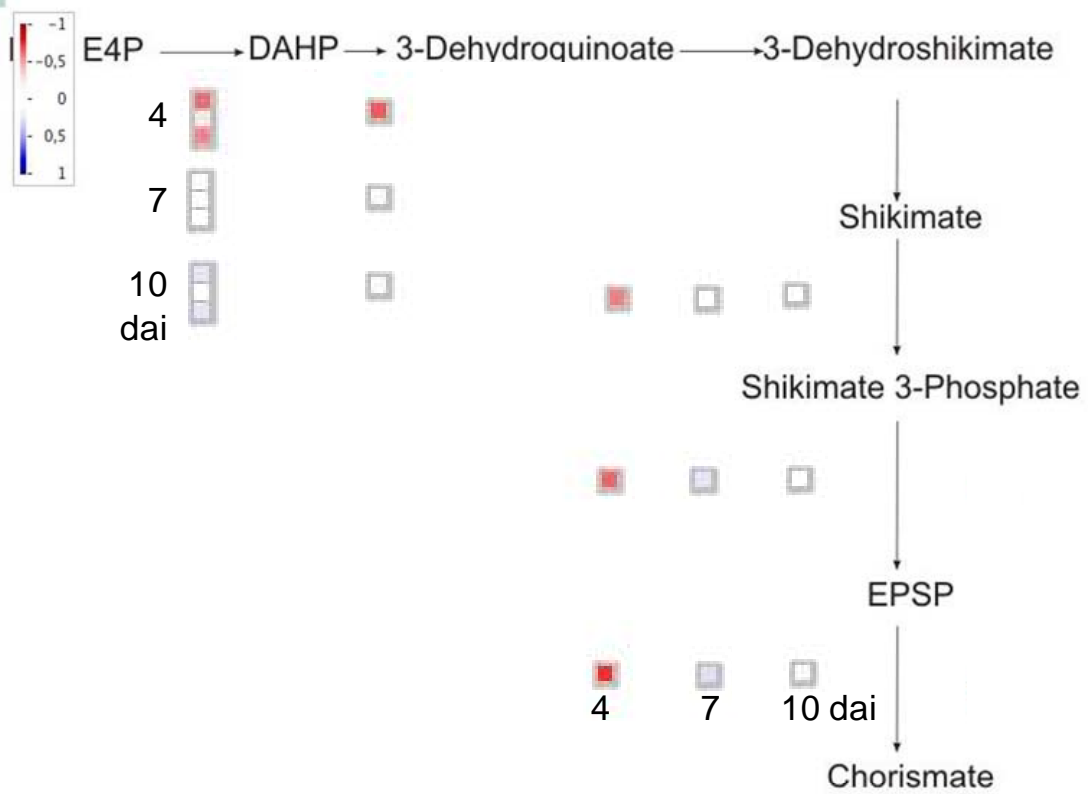


Fig. S1. Shikimate pathway during three different time points of clubroot development analysed using the MAPMAN software comparing up- and down-regulated genes from control and infected *Arabidopsis* roots at 4, 7 and 10 days after inoculation (dai).

Table S1. Primers designed for transcripts whose expression level was verified using quantitative real-time RT-PCR analysis

Gene name	AGI ID	Sequence size	Product size	Primer sequence (5' to 3')
Actin 2	At3g18780	586	492	FP, 5'-TGC TGG ACG TGA CCT TAC TG-3' RP, 5'-GAA CCA CCG ATC CAG ACA CT-3'
WRKY18	At4g31800	544	482	FP, 5'-ACA GCT CCA GCA ACG AAG AT-3' RP, 5'-CGC CAT TTG TTG AAT CAG AA-3'
Lipoxygenase 4	At1g72520	546	451	FP, 5'-ATC TCG TCT CCG TCA TCA CC-3' RP, 5'-GAA CTC GGA GCC ATC AAC TC-3'
TIR-NBS-LRR	At5g46470	529	403	FP, 5'-TCC GTG GAA CTT TCC TCA AC-3' RP, 5'-GCC CAG TTC GGA GAA TGA TA-3'
Phytoalexin-deficient 4	At3g52430	455	381	FP, 5'-CAA CTC TTA GCC GAG CCA CT-3' RP, 5'-ATT CGC CTC CCA CAC ACT AT-3'

Table S2. List of genes up-regulated ($\geq 1.5x$) after 4 days of inoculation in comparison with 4 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Signal transduction, transcription				
250277_at	At5g12940	Leucine-rich repeat family protein	3.3	Signal transduction
253284_at	At4g34150	C2 domain-containing protein	1.9	G-protein coupled receptor protein signalling pathway
247137_at	At5g66210	Calcium-dependent protein kinase family protein/CDPK family protein	2.3	Protein amino acid phosphorylation
247962_at	At5g56580	Mitogen-activated protein kinase kinase (MAPKK), putative (MKK6)	2.2	Protein amino acid phosphorylation
250102_at	At5g16590	Leucine-rich repeat transmembrane protein kinase, putative	2.2	Protein amino acid phosphorylation
251636_at	At3g57530	Calcium-dependent protein kinase, putative/CDPK, putative	1.8	Protein amino acid phosphorylation
255716_at	At4g00330	Protein kinase family protein	1.6	Protein amino acid phosphorylation
257784_at	At3g26970	Ubiquitin family protein	2.0	Protein modification
259012_at	At3g07360	Armadillo/beta-catenin repeat family protein/U-box domain-containing protein	1.6	Protein ubiquitination
264862_at	At1g24330	Armadillo/beta-catenin repeat family protein/U-box domain-containing family protein	1.8	Protein ubiquitination
249557_at	At5g38280	Serine/threonine protein kinase (PR5K)	1.5	Response to pathogenic fungi
253485_at	At4g31800	WRKY family transcription factor	3.6	Regulation of transcription, DNA-dependent
Metabolism				

245325_at	At4g14130	Xyloglucan:xyloglucosyl transferase, putative/endo-xyloglucan transferase, putative (XTR7)	3.0	Carbohydrate metabolism
250335_at	At5g11650	Hydrolase, alpha/beta fold family protein	1.7	Aromatic compound metabolism
252060_at	At3g52430	Phytoalexin-deficient 4 protein (PAD4)	1.7	Lipid metabolism
256736_at	At3g29410	Terpene synthase/cyclase family protein	2.6	Metabolism
259518_at	At1g20510	4-coumarate-CoA ligase family protein/4-coumaroyl-CoA synthase family protein	2.5	Phenylpropanoid metabolism
Response to stimulus				
248845_at	At5g46470	Disease resistance protein (TIR-NBS-LRR class), putative	1.6	Defense response to pathogen
255479_at	At4g02380	Late embryogenesis abundant 3 family protein/LEA3 family protein	2.2	Response to reactive oxygen species/response to cold/embryonic development
260941_at	At1g44970	Peroxidase, putative	1.6	Response to oxidative stress
262947_at	At1g75750	Gibberellin-regulated protein 1 (GASA1)/gibberellin-responsive protein 1	1.6	Response to gibberellic acid stimulus/response to abscisic acid stimulus
Transport				
250053_at	At5g17850	Cation exchanger, putative (CAX8)	1.6	Cation transport
257185_at	At3g13100	ABC transporter family protein	1.6	Transport
258377_at	At3g17690	Cyclic nucleotide-binding transporter 2/CNBT2 (CNGC19)	2.5	Ion transport
266526_at	At2g16980	Expressed protein	2.1	Tetracycline transport
Cell wall modification				
250490_at	At5g09760	Pectinesterase family protein	1.7	Cell wall modification

252557_at	At3g45960	Expansin family protein (EXPL3)	4.2	Unidimensional cell growth/cell wall loosening
252563_at	At3g45970	Expansin family protein (EXPL1)	5.0	Unidimensional cell growth/cell wall loosening
262105_at	At1g02810	Pectinesterase family protein	2.8	Cell wall modification
Biosynthesis				
260399_at	At1g72520	Lipoxygenase, putative	3.8	Defense response/jasmonic acid biosynthesis
Cell adhesion				
259072_at	At3g11700	Beta-Ig-H3 domain-containing protein/fasciclin domain-containing protein	1.8	Cell adhesion
Unknown function				
245115_at	At2g41530	Esterase, putative	1.5	---
245906_at	At5g11070	Expressed protein	4.2	---
246063_at	At5g19340	Expressed protein	1.6	---
247071_at	At5g66640	LIM domain-containing protein-related	2.7	---
247208_at	At5g64870	Expressed protein	5.5	---
247426_at	At5g62570	Calmodulin-binding protein	2.2	---
247477_at	At5g62340	Invertase/pectin methylesterase inhibitor family protein	3.2	---
248526_at	At5g50730	Expressed protein	1.6	---
251105_at	At5g01730	Expressed protein	1.6	---
251281_at	At3g61640	Arabinogalactan-protein (AGP20)	2.9	---
251886_at	At3g54260	Expressed protein	1.7	---
251982_at	At3g53190	Pectate lyase family protein	1.5	---

252906_at	At4g39640	Gamma-glutamyltranspeptidase family protein	1.8	---
255945_at	At5g28610	Expressed protein	4.3	---
256747_at	At3g29180	Expressed protein	1.6	---
257029_at	At3g19240	Expressed protein	2.5	---
259291_at	At3g11550	Integral membrane family protein	1.6	---
260401_at	At1g69840	Band 7 family protein	1.8	---
261454_at	At1g21090	Hydroxyproline-rich glycoprotein family protein	1.7	---
262452_at	At1g11210	Expressed protein	1.5	---
263800_at	At2g24600	Ankyrin repeat family protein	3.6	---
264512_at	At1g09575	Expressed protein	1.9	---
264661_at	At1g09950	Transcription factor-related	2.5	---
265204_at	At2g36650	Expressed protein	2.6	---
265737_at	At2g01180	Phosphatidic acid phosphatase family protein/PAP2 family protein	2.2	---
266215_at	At2g06850	Xyloglucan:xyloglucosyl transferase/xyloglucan endotransglycosylase/endo-xyloglucan transferase (EXT) (EXGT-A1)	2.3	---
266545_at	At2g35290	Expressed protein	3.7	---

Table S3. List of genes down-regulated ($\leq 1.5x$) after 4 days of inoculation in comparison with 4 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Transport				
247284_at	At5g64410	Oligopeptide transporter OPT family protein	-1.9	Oligopeptide transport
247679_at	At5g59540	Oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1.7	ATP synthesis coupled proton transport
247851_at	At5g58070	Lipocalin, putative	-2.0	Transport
250045_at	At5g17700	MATE efflux family protein	-2.2	Multidrug transport
250252_at	At5g13750	Transporter-related	-1.6	Tetracycline transport
251752_at	At3g55740	Proline transporter 2 (ProT2)	-1.5	Amino acid transport/L-proline transport
251882_at	At3g54140	Proton-dependent oligopeptide transport (POT) family protein	-1.8	Oligopeptide transport
254608_at	At4g18910	Aquaglyceroporin/NOD26-like major intrinsic protein 2 (NLM2)	-2.0	Transport
254710_at	At4g18050	ABC transporter family protein	-2.0	Transport
258179_at	At3g21690	MATE efflux family protein	-2.5	Multidrug transport
259846_at	At1g72140	Proton-dependent oligopeptide transport (POT) family protein	-2.0	Oligopeptide transport
261021_at	At1g26380	FAD-binding domain-containing protein	-1.8	Electron transport
261023_at	At1g12200	Flavin-containing monooxygenase family protein/FMO family protein	-1.7	Electron transport
262912_at	At1g59740	Proton-dependent oligopeptide transport (POT) family protein	-1.7	Oligopeptide transport

263228_at	At1g30700	FAD-binding domain-containing protein	-1.5	Electron transport
264527_at	At1g30760	FAD-binding domain-containing protein	-2.4	Electron transport
265482_at	At2g15780	Glycine-rich protein	-7.1	Electron transport
266000_at	At2g24180	Cytochrome P450 family protein	-2.0	Electron transport
267024_s_at	At2g34390	Major intrinsic family protein	-2.3	Transport
267414_at	At2g34790	FAD-binding domain-containing protein	-1.7	Electron transport
Biosynthesis				
247138_at	At5g66120	3-dehydroquinate synthase, putative	-1.6	Aromatic amino acid family biosynthesis
249773_at	At5g24140	Squalene monooxygenase 2/squalene epoxidase 2 (SQP2)	-2.8	Sterol biosynthesis
250533_at	At5g08640	Flavonol synthase 1 (FLS1)	-2.7	Flavonoid biosynthesis
253162_at	At4g35630	Phosphoserine aminotransferase, chloroplast (PSAT)	-1.7	L-serine biosynthesis / metabolism
253277_at	At4g34230	Cinnamyl-alcohol dehydrogenase, putative	-2.3	Lignin biosynthesis
254575_at	At4g19460	Glycosyl transferase family 1 protein	-3.3	Biosynthesis
258122_at	At3g14570	Glycosyl transferase family 48 protein	-1.6	Beta-1,3 glucan biosynthesis
259149_at	At3g10340	Phenylalanine ammonia-lyase, putative	-1.7	L-phenylalanine catabolism / biosynthesis
259439_at	At1g01480	1-aminocyclopropane-1-carboxylate synthase 2/ACC synthase 2 (ACS2) (ACC1)	-1.7	Ethylene biosynthesis
260335_at	At1g74000	Strictosidine synthase family protein	-2.5	Biosynthesis
260386_at	At1g74010	Strictosidine synthase family protein	-1.9	Biosynthesis
262526_at	At1g17050	Geranyl diphosphate synthase, putative	-1.9	Isoprenoid biosynthesis
263429_at	At2g22250	Aminotransferase class I and II family protein	-1.5	Biosynthesis

256186_at	At1g51680	4-coumarate--CoA ligase 1/4-coumaroyl-CoA synthase 1 (4CL1)	-1.9	Response to pathogenic fungi/phenylpropanoid metabolism
Response to stimulus				
246228_at	At4g36430	Peroxidase, putative	-1.6	Response to pest, pathogen or parasite
246463_at	At5g16970	NADP-dependent oxidoreductase, putative (P1)	-4.2	Response to oxidative stress
247091_at	At5g66390	Peroxidase 72 (PER72) (P72) (PRXR8)	-1.6	Response to oxidative stress
248551_at	At5g50200	Expressed protein	-1.6	Response to wounding
251895_at	At3g54420	Class IV chitinase (CHIV)	-2.3	Hypersensitive response
257922_at	At3g23150	Ethylene receptor, putative (ETR2)	-1.9	Negative regulation of ethylene mediated signalling pathway
258979_at	At3g09440	Heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	-2.6	Protein folding/response to heat
259443_at	At1g02360	Chitinase, putative	-2.0	Response to pest, pathogen or parasite/cell wall catabolism
260248_at	At1g74310	Heat shock protein 101 (HSP101)	-2.3	Response to heat
262099_s_at	At1g59500	Auxin-responsive GH3 family protein	-1.8	Response to auxin stimulus/auxin homeostasis
266743_at	At2g02990	Ribonuclease 1 (RNS1)	-3.2	Aging/cellular response to phosphate starvation
248582_at	At5g49910	Heat shock protein 70/HSP70 (HSC70-7)	-1.9	Protein folding
262518_at	At1g17170	Glutathione S-transferase, putative	-1.8	Toxin catabolism
Metabolism				
248381_at	At5g51830	PfkB-type carbohydrate kinase family protein	-1.8	D-ribose metabolism

250753_at	At5g05860	UDP-glucuronosyl/UDP-glucosyl transferase family protein	-2.2	Metabolism
259173_at	At3g03640	Glycosyl hydrolase family 1 protein	-1.6	Carbohydrate metabolism
260126_at	At1g36370	Glycine hydroxymethyltransferase, putative/serine hydroxymethyltransferase, putative	-1.8	Glycine metabolism/L-serine metabolism
262118_at	At1g02850	Glycosyl hydrolase family 1 protein	-1.9	Carbohydrate metabolism
267300_at	At2g30140	UDP-glucuronosyl/UDP-glucosyl transferase family protein	-2.2	Metabolism
Signal transduction, transcription				
259421_at	At1g13910	Leucine-rich repeat family protein	-2.3	Signal transduction
263128_at	At1g78600	Zinc finger (B-box type) family protein	-1.9	Regulation of transcription
263210_at	At1g10585	Expressed protein	-4.6	Regulation of transcription
Growth/Development				
256299_at	At1g69530	Expansin, putative (EXP1)	-2.5	Unidimensional cell growth/cell wall loosening
Cell adhesion				
249037_at	At5g44130	Fasciclin-like arabinogalactan-protein, putative	-1.7	Cell adhesion
Photosynthesis				
245306_at	At4g14690	Chlorophyll A-B binding family protein/early light-induced protein, putative	-2.6	Photosynthesis light harvesting
Unknown function				
247729_at	At5g59530	2-oxoglutarate-dependent dioxygenase, putative	-1.8	---
248154_at	At5g54400	Expressed protein	-3.8	---

248424_at	At5g51680	Hydroxyproline-rich glycoprotein family protein	-2.3	---
250307_at	At5g12170	Expressed protein	-1.6	---
250662_at	At5g07010	Sulfotransferase family protein	-1.7	---
251379_at	At3g60680	Expressed protein	-1.6	---
252202_at	At3g50300	Transferase family protein	-1.6	---
254343_at	At4g21990	5'-adenylylsulfate reductase (APR3)/PAPS reductase homolog (PRH26)	-2.2	---
254453_at	At4g21120	Amino acid permease family protein	-2.3	---
254691_at	At4g17840	Expressed protein	-1.8	---
256964_at	At3g13520	Arabinogalactan-protein (AGP12)	-1.6	---
257173_at	At3g23810	Adenosylhomocysteinase, putative/S-adenosyl-L-homocysteine hydrolase, putative/AdoHcyase, putative	-2.4	---
257253_at	At3g24190	ABC1 family protein	-1.6	---
258487_at	At3g02550	LOB domain protein 41/lateral organ boundaries domain protein 41 (LBD41)	-1.7	---
258830_at	At3g07090	Expressed protein	-1.6	---
259033_at	At3g09410	Pectinacetyltransferase family protein	-1.8	---
259134_at	At3g05390	Expressed protein	-1.6	---
259892_at	At1g72610	Germin-like protein (GER1)	-1.8	---
260058_at	At1g78100	F-box family protein	-2.0	---
260232_at	At1g74640	Expressed protein	-1.6	---
261177_at	At1g04770	Male sterility MS5 family protein	-3.3	---
261607_at	At1g49660	Expressed protein	-2.0	---

261792_at	At1g15950	Cinnamoyl-CoA reductase, putative	-1.6	---
262885_at	At1g64740	Tubulin alpha-1 chain (TUA1)	-2.1	---
264186_at	At1g54570	Esterase/lipase/thioesterase family protein	-2.1	---
264436_at	At1g10370	Glutathione S-transferase, putative (ERD9)	-3.8	---
264745_at	At1g62180	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR)/adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase	-2.7	---
265871_at	At2g01680	Ankyrin repeat family protein	-1.6	---
266835_at	At2g29990	Pyridine nucleotide-disulphide oxidoreductase family protein	-1.5	---
267142_at	At2g38290	Ammonium transporter 2 (AMT2)	-1.6	---

Table S4. List of genes up-regulated ($\geq 1.5x$) after 7 days of inoculation in comparison with 7 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Metabolism				
246701_at	At5g28020	Cysteine synthase, putative/O-acetylserine (thiol)-lyase, putative/O-acetylserine sulfhydrylase, putative	1.8	Metabolism/cysteine biosynthesis from serine/cysteine biosynthesis
247983_at	At5g56630	Phosphofructokinase family protein	1.6	Glycolysis
249057_at	At5g44480	NAD-dependent epimerase/dehydratase family protein	1.7	Nucleotide-sugar metabolism/galactose metabolism
249103_at	At5g43600	N-carbamyl-L-amino acid hydrolase, putative	1.5	Proteolysis
262939_s_at	At1g79530	Glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative	1.5	Glycolysis/glucose metabolism
Transport				
251254_at	At3g62270	Anion exchange family protein	1.6	Anion transport
252589_s_at	At3g45650	Proton-dependent oligopeptide transport (POT) family protein	2.2	Oligopeptide transport
254215_at	At4g23700	Cation/hydrogen exchanger, putative (CHX17)	1.6	Cation transport
254971_at	At4g10380	Major intrinsic family protein/MIP family protein	1.5	Transport
Response to stimulus				
258957_at	At3g01420	Pathogen-responsive alpha-dioxygenase, putative	1.6	Fatty acid alpha-oxidation/cell death/response to pathogen

264647_at	At1g09090	Respiratory burst oxidase protein B (RbohB)/NADPH oxidase	2.0	Defense response
Cell wall modification				
258369_at	At3g14310	Pectinesterase family protein	1.6	Cell wall modification
260181_at	At1g70710	Endo-1,4-beta-glucanase (EGASE)/cellulase	1.6	Cell wall modification during multidimensional cell growth
Signal transduction/transcription				
265629_at	At2g27230	transcription factor-related	1.6	regulation of transcription
247819_at	At5g58350	protein kinase family protein	1.9	protein amino acid phosphorylation
Unknown function				
245181_at	At5g12420	expressed protein	2.1	---
252276_at	At3g49490	expressed protein	1.5	---
252379_at	At3g47730	ABC transporter family protein	1.8	---
253533_at	At4g31590	glycosyl transferase family 2 protein	1.6	---
255221_at	At4g05150	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	1.8	---
259862_at	At1g72650	myb family transcription factor	1.6	---
260297_at	At1g80280	hydrolase, alpha/beta fold family protein	1.7	---

Table S5. List of genes down-regulated ($\leq 1.5x$) after 7 days of inoculation in comparison with 7 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Response to stimulus				
259516_at	At1g20450	Dehydrin (ERD10)	-1.6	Response to stress/response to water
266360_at	At2g32250	Far-red impaired responsive protein, putative	-1.7	Response to red or far red light
Signal transduction/transcription				
263222_at	At1g30640	Protein kinase, putative	-1.7	Protein amino acid phosphorylation
Cell death				
248393_at	At5g52060	BAG domain-containing protein	-1.6	Protein modification/apoptosis/regulation of apoptosis
Unknown function				
248466_at	At5g50720	ABA-responsive protein (HVA22e)	-2.0	---

Table S6. List of genes up-regulated ($\geq 1.5x$) after 10 days of inoculation in comparison with 10 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Signal transduction/transcription				
251950_at	At3g53600	Zinc finger (C ₂ H ₂ type) family protein	1.8	Regulation of transcription
254207_at	At4g24060	Dof-type zinc finger domain-containing protein	1.7	Regulation of transcription
248570_at	At5g49780	Leucine-rich repeat transmembrane protein kinase, putative	1.7	Protein amino acid phosphorylation
251479_at	At3g59700	Lectin protein kinase, putative	1.5	Protein amino acid phosphorylation
254660_at	At4g18250	Receptor serine/threonine kinase, putative	1.8	Protein amino acid phosphorylation
263378_at	At2g40180	Protein phosphatase 2C, putative / PP2C, putative	2.3	Protein amino acid dephosphorylation
262131_at	At1g02900	Rapid alkalization factor (RALF) family protein	1.6	Cell-cell signalling
Response to stimulus				
248980_at	At5g45090	Lectin-related	1.5	Defense response
251205_at	At3g63080	Glutathione peroxidase, putative	1.5	Response to oxidative stress
254085_at	At4g24960	ABA-responsive protein (HVA22d)	1.9	Response to abscisic acid stimulus/hyperosmotic salinity response/response to water deprivation
256781_at	At3g13650	Disease resistance response protein-related	1.8	Defense response/lignan biosynthesis/response to pathogenic fungi
Metabolism				
250723_at	At5g06300	Lysine decarboxylase family protein	1.8	Metabolism

251970_at	At3g53150	UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.9	Metabolism
Biosynthesis				
245533_at	At4g15130	Cholinephosphate cytidyltransferase, putative	1.8	Biosynthesis
265194_at	At1g05010	1-aminocyclopropane-1-carboxylate oxidase/ACC oxidase/ethylene-forming enzyme (ACO) (EAT1)	1.7	Ethylene biosynthesis
Unknown function				
245637_at	At1g25230	Purple acid phosphatase family protein	1.7	---
246197_at	At4g37010	Caltractin, putative/centrin, putative	1.8	---
246270_at	At4g36500	Expressed protein	1.5	---
246340_s_at	At3g44860	S-adenosyl-L-methionine:carboxyl methyltransferase family protein	1.6	---
247464_at	At5g62070	Calmodulin-binding family protein	1.9	---
249009_at	At5g44610	DREPP plasma membrane polypeptide-related	1.6	---
249747_at	At5g24600	Expressed protein	1.7	---
253796_at	At4g28460	Hypothetical protein	1.7	---
257480_at	At1g15640	Hypothetical protein	2.0	---
258275_at	At3g15760	Expressed protein	1.7	---
260179_at	At1g70690	Kinase-related	2.0	---
261506_at	At1g71697	Choline kinase, putative	1.6	---
261756_at	At1g08320	Armadillo/beta-catenin repeat family protein	1.5	---
262801_at	At1g21010	Expressed protein	2.5	---

263836_at	At2g40330	Bet v I allergen family protein	1.7	---
266808_at	At2g29995	Expressed protein	1.5	---

Table S7. List of genes down-regulated ($\leq 1.5x$) after 10 days of inoculation in comparison with 10 day control *Arabidopsis* roots at 95% confidence level

Probe set ID	AGI ID	Brief description	Fold change	Gene ontology – Biological function
Photosynthesis				
262632_at	At1g06680	Photosystem II oxygen-evolving complex 23 (OEC23)	-1.5	Photosynthetic water oxidation
267002_s_at	At2g34430	Chlorophyll A-B binding protein/LHCII type I	-2.4	Photosynthesis/photosynthesis light harvesting in photosystem II
Metabolism				
248622_at	At5g49360	Glycosyl hydrolase family 3 protein	-1.6	Carbohydrate metabolism
Response to stimulus				
255078_at	At4g09010	L-ascorbate peroxidase, chloroplast, putative	-1.7	Response to oxidative stress
Signal transduction/transcription				
263962_at	At2g36350	Protein kinase, putative	-1.5	Protein amino acid phosphorylation
Unknown function				
263709_at	At1g09310	Expressed protein	-1.6	---