

Appendix Table 4	probe sets and gene annotations induced in WT 5dpi and under NIN positive control
<i>Medicago truncatula</i> probesets	<i>M. truncatula</i> gene model name
Mtr.7337.1.S1_at	unknown protein
Mtr.37542.1.S1_at	Encodes a cold-inducible cationic peroxidase that is involved in the stress response. In response to low temperature, RCI3 transcripts accumulate in the aerial part and in roots of etiolated seedlings but only in roots of light-grown seedlings. protein_coding RARE COLD INDUCIBLE GENE 3 (RCI3) RARE COLD INDUCIBLE GENE 3 (RCI3)
Mtr.43433.1.S1_at	phloem protein 2-A10 (PP2-A10)
Mtr.10634.1.S1_at	Encodes a H ⁺ /hexose cotransporter. protein_coding SUGAR TRANSPORTER 1 (STP1) SUGAR TRANSPORTER 1 (ATSTP1)
Mtr.21871.1.S1_at	methylesterase PCR A (PMEPCRA)
Mtr.40562.1.S1_at	F-box/RNI-like superfamily protein
Mtr.13370.1.S1_at	Involved in later steps of the gibberellic acid biosynthetic pathway. Activated by AGAMOUS in a cal-1, ap1-1 background. Deletion of 208 bp from -1016 to -809
Mtr.10819.1.S1_at	Encodes a member of the X8-GPI family of proteins. It localizes to the plasmodesmata and is predicted to bind callose. protein_coding PLASMODESMATA CALLOSE-BINDING PROTEIN 3 (PDCB3) PLASMODESMATA CALLOSE-BINDING PROTEIN 3 (PDCB3)
Mtr.24480.1.S1_at	Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant defensin (PDF) family with the following members: At1g75830/PDF1.1, At5g44420/PDF1.2a, At2g26020/PDF1.2b, At5g44430/PDF1.2c, At2g26010/PDF1.3, At1g19610/PDF1.4, At1g55010/PDF1.5, At2g02120/PDF2.1, At2g02100/PDF2.2, At2g02130/PDF2.3, At1g61070/PDF2.4, At5g63660/PDF2.5, At2g02140/PDF2.6, At5g38330/PDF3.1 and At4g30070/PDF3.2. protein_coding (PDF1.4) LOW-MOLECULAR-WEIGHT CYSTEINE-RICH 78 (LCR78)
Mtr.3807.1.S1_at	encodes a wall-associated kinase protein_coding WALL ASSOCIATED KINASE 5 (WAK5) WALL ASSOCIATED KINASE 5 (WAK5)
Mtr.37585.1.S1_a_at	Encodes extensin 3. protein_coding EXTENSIN 3 (EXT3) EXTENSIN 3 (EXT3)

Mtr.42709.1.S1_at	UDP-glucosyl transferase 85A2 (UGT85A2)
Mtr.45092.1.S1_at	cellulase 5 (CEL5)
Mtr.50491.1.S1_at	Transmembrane amino acid transporter family protein
Mtr.40179.1.S1_at	unknown protein
Mtr.44485.1.S1_at	Encodes MCM2 (MINICHROMOSOME MAINTENANCE 2), a protein essential to embryo development. Overexpression results in altered root meristem function. protein_coding MINICHROMOSOME MAINTENANCE 2 (MCM2) (ATMCM2)
Mtr.44381.1.S1_at	beta-galactosidase 5 (BGAL5)
Mtr.28564.1.S1_at	Transmembrane amino acid transporter family protein
Mtr.11579.1.S1_at	R-protein L3 B (RPL3B)
Mtr.27763.1.S1_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Mtr.43131.1.S1_at	glycosyl hydrolase 9C2 (GH9C2)
Mtr.33549.1.S1_at	member of BETA-EXPANSINS. Naming convention from the Expansin Working Group (Kende et al, 2004. Plant Mol Bio) protein_coding EXPANSIN B2 (EXPB2) (ATHEXP BETA 1.4)
Mtr.1975.1.S1_at	Protein with RING/U-box and TRAF-like domains
Mtr.26489.1.S1_at	Pectate lyase family protein
Mtr.8357.1.S1_s_at	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
Mtr.38321.1.S1_at	Homeodomain-like superfamily protein
Mtr.18064.1.S1_at	GDSL-like Lipase/Acylhydrolase superfamily protein
Mtr.40237.1.S1_at	Encodes PPsPase1, a pyrophosphate-specific phosphatase catalyzing the specific cleavage of pyrophosphate (Km 38.8 uM) with an alkaline catalytic pH optimum. protein_coding PHOSPHATE STARVATION-INDUCED GENE 2 (PS2) PYROPHOSPHATE-SPECIFIC PHOSPHATASE1 (AtPPsPase1)
Mtr.10607.1.S1_at	SKU5 similar 5 (sks5)
Mtr.29216.1.S1_at	DNAJ heat shock N-terminal domain-containing protein
Mtr.33147.1.S1_at	unknown protein
Mtr.33659.1.S1_at	Uncharacterized conserved protein (DUF2358)
Mtr.27817.1.S1_at	Sterile alpha motif (SAM) domain-containing protein
Mtr.8632.1.S1_s_at	Plant invertase/pectin methylesterase inhibitor superfamily protein

Mtr.10725.1.S1_at	Encodes plantacyanin one of blue copper proteins. Involved in anther development and pollination. Expressed in the transmitting tract of the pistil. protein_coding PLANTACYANIN (ARPN) PLANTACYANIN (ARPN)
Mtr.21136.1.S1_at	Glycine-rich protein family
Mtr.12606.1.S1_at	Subtilase family protein
Mtr.35539.1.S1_at	Member of the minichromosome maintenance complex, involved in DNA replication initiation. Abundant in proliferating and endocycling tissues. Localized in the nucleus during G1, S and G2 phases of the cell cycle, and are released into the cytoplasmic compartment during mitosis. Binds chromatin. protein_coding MINICHROMOSOME MAINTENANCE 5 (MCM5) MINICHROMOSOME MAINTENANCE 5 (MCM5)
Mtr.41121.1.S1_at	putative proline-rich protein (At2g14890) mRNA, complete protein_coding ARABINO GALACTAN PROTEIN 9 (AGP9) ARABINO GALACTAN PROTEIN 9 (AGP9)
Mtr.37688.1.S1_at	Plant basic secretory protein (BSP) family protein
Mtr.39772.1.S1_at	Predicted to encode a PR (pathogenesis-related) protein. Belongs to the lipid transfer protein (PR-14) family with the following members: At2g38540/LTP1, At2g38530/LTP2, At5g59320/LTP3, At5g59310/LTP4, At3g51600/LTP5, At3g08770/LTP6, At2g15050/LTP7, At2g18370/LTP8, At2g15325/LTP9, At5g01870/LTP10, At4g33355/LTP11, At3g51590/LTP12, At5g44265/LTP13, At5g62065/LTP14, At4g08530/LTP15. protein_coding
Mtr.6197.1.S1_s_at	Leucine-rich repeat (LRR) family protein
Mtr.4585.1.S1_s_at	MINICHROMOSOME MAINTENANCE 4 (MCM4)
Mtr.6707.1.S1_s_at	Uncharacterised conserved protein (UCP030210)
Mtr.15220.1.S1_at	Sec14p-like phosphatidylinositol transfer family protein
Mtr.7525.1.S1_at	Encodes a nuclear protein that acts as a floral repressor and that functions within the thermosensory pathway. SVP represses FT expression via direct binding to the vCARG III motif in the FT promoter. protein_coding SHORT VEGETATIVE PHASE (SVP) AGAMOUS-LIKE 22 (AGL22)

Mtr.13656.1.S1_at	Galactosyl transferase GMA12/MNN10 family protein
Mtr.19174.1.S1_at	Member of a large family of putative ligands homologous to the Clavata3 gene. Consists of a single exon. protein_coding CLAVATA3/ESR-RELATED 5 (CLE5) (AtCLE5)
Mtr.41528.1.S1_at	LIGHT SENSITIVE HYPOCOTYLS 3 (LSH3)
Mtr.32565.1.S1_at	ent-kaurenoic acid hydroxylase (KAO2) protein_coding ENT-KAURENOIC ACID HYDROXYLASE 2 (KAO2) ARABIDOPSIS ENT-KAURENOIC ACID HYDROXYLASE 2 (ATKAO2)
Mtr.8806.1.S1_at	Encodes a protein with C22-sterol desaturase activity. The enzyme was shown to catalyze in the presence of NADPH the conversion of &beta
Mtr.10356.1.S1_at	Peroxidase superfamily protein
Mtr.18523.1.S1_at	O-acyltransferase (WSD1-like) family protein
Mtr.41561.1.S1_at	putative expansin. Naming convention from the Expansin Working Group (Kende et al, 2004. Plant Mol Bio). Involved in the formation of nematode-induced syncytia in roots of Arabidopsis thaliana. protein_coding EXPANSIN A4 (EXPA4) EXPANSIN A4 (EXPA4)
Mtr.1114.1.S1_at	SGNH hydrolase-type esterase superfamily protein
Mtr.17492.1.S1_at	Encodes a novel plant-specific protein of unknown function. The UVI4 gene is expressed mainly in actively dividing cells. The hypocotyl cells in mutant seedlings undergo one extra round of endoreduplication. The uvi4 mutation also promoted the progression of endo-reduplication during leaf development. protein_coding UV-B-INSENSITIVE 4 (UVI4) UV-B-INSENSITIVE 4 (UVI4)
Mtr.25019.1.S1_at	involved in the regulation of brassinosteroid metabolic pathway protein_coding (BEN1) (BEN1)
Mtr.41489.1.S1_at	ARM repeat superfamily protein
Mtr.12634.1.S1_at	AT hook motif DNA-binding family protein
Mtr.10543.1.S1_at	Adenine nucleotide alpha hydrolases-like superfamily protein
Mtr.20961.1.S1_at	zinc knuckle (CCHC-type) family protein
Mtr.10426.1.S1_at	Ribosomal protein S3Ae

Mtr.43750.1.S1_at	Encodes a subunit of CCAAT-binding complex, binds to CCAAT box motif present in some plant promoter sequences. One of three members of this class (HAP2A, HAP2B, HAP2C), it is expressed in vegetative and reproductive tissues. protein_coding "NUCLEAR FACTOR Y, SUBUNIT A2" (NF-YA2) "NUCLEAR FACTOR Y, SUBUNIT A2" (NF-YA2)
Mtr.50074.1.S1_at	RmlC-like cupins superfamily protein
Mtr.1774.1.S1_at	Similar to fatty acid reductases. protein_coding MALE STERILITY 2 (MS2) FATTY ACID REDUCTASE 2 (FAR2)
Mtr.31750.1.S1_at	Encodes sulfate transporter Sultr3
Mtr.4980.1.S1_at	Encodes a protein with ABA 8'-hydroxylase activity, involved in ABA catabolism. Member of the CYP707A gene family. protein_coding "CYTOCHROME P450, FAMILY 707, SUBFAMILY A, POLYPEPTIDE 4" (CYP707A4) "CYTOCHROME P450, FAMILY 707, SUBFAMILY A, POLYPEPTIDE 4" (CYP707A4)
Mtr.35738.1.S1_at	Leucine-rich repeat (LRR) family protein
Mtr.10626.1.S1_at	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
Mtr.40069.1.S1_at	Encodes a Protease inhibitor/seed storage/LTP family protein protein_coding
Mtr.13368.1.S1_at	putative cytochrome P450 protein_coding "CYTOCHROME P450, FAMILY 71, SUBFAMILY B, POLYPEPTIDE 35" (CYP71B35) "CYTOCHROME P450, FAMILY 71, SUBFAMILY B, POLYPEPTIDE 35" (CYP71B35)
Mtr.8510.1.S1_at	GDSL-like Lipase/Acylhydrolase superfamily protein
Mtr.19487.1.S1_at	kinesin-like protein 1 (KP1)
Mtr.43850.1.S1_at	Encodes a protein that is the product of a fusion gene with a C-terminal GSI like sequence and an N-terminal part sharing homology with nodulins. It self-assembles into oligomers and its expression is increased in response to flagellin treatment. The protein co-localizes with microtubules and binds gamma-tubulin. RNAi lines are affected in root morphogenesis. protein_coding NODULIN/GLUTAMINE SYNTHASE-LIKE PROTEIN (NodGS) NODULIN/GLUTAMINE SYNTHASE-LIKE PROTEIN (NodGS)

Mtr.20645.1.S1_at	CytADR/SDR1 is an aldehyde reductase that catalyzes the reduction of the aldehyde carbonyl groups on alpha,beta-unsaturated aldehydes with more than 5 carbons in vitro. It can also act on menthone and neomenthol in vitro, but these do not represent likely endogenous activities of this enzyme in planta. GFP-tagged CytADR appears to localize to the cytosol where it likely plays a role in detoxifying reactive carbonyls. sdr1 mutants have altered responses to pathogens. protein_coding SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1 (SDR1) SHORT-CHAIN DEHYDROGENASE/REDUCTASE 1 (SDR1)
Mtr.37992.1.S1_at	Member of the minichromosome maintenance complex, involved in DNA replication initiation. Abundant in proliferating and endocycling tissues. Localized in the nucleus during G1, S and G2 phases of the cell cycle, and are released into the cytoplasmic compartment during mitosis. Binds chromatin. protein_coding PROLIFERA (PRL) PROLIFERA (PRL)
Mtr.229.1.S1_at	unknown protein
Mtr.25006.1.S1_at	Catalyzes the conversion of geranylgeranyl pyrophosphate (GGPP) to copalyl pyrophosphate (CPP) of gibberellin biosynthesis protein_coding GA REQUIRING 1 (GA1) GA REQUIRING 1 (GA1)
Mtr.43798.1.S1_at	Inositol 1,3,4-trisphosphate 5/6-kinase family protein
Mtr.12384.1.S1_at	glycosyl hydrolase 9C3 (GH9C3)
Mtr.38726.1.S1_at	Transducin/WD40 repeat-like superfamily protein
Mtr.37525.1.S1_at	Encodes an aquaporin homolog. Functions in arsenite transport and tolerance. When expressed in yeast cells can conduct hydrogen peroxide into those cells. protein_coding NOD26-LIKE INTRINSIC PROTEIN 1
Mtr.6153.1.S1_at	chromomethylase 2 (CMT2)
Mtr.2246.1.S1_at	an aquaporin whose expression level is reduced by ABA, NaCl, dark, and dessication. is expressed at relatively low levels under normal conditions. Also functions in arsenite transport and tolerance. protein_coding NOD26-LIKE MAJOR INTRINSIC PROTEIN 1 (NLM1) NOD26-LIKE MAJOR INTRINSIC PROTEIN 1 (ATNLM1)
Mtr.40699.1.S1_at	Pectinacetylerase family protein

Mtr.39553.1.S1_at	ChiC encodes a Class V chitinase that is a part of glycoside hydrolase family 18 based on CAZy groupings. It appears to primarily act as an exochitinase in vitro where it predominantly cleaves a chitobiose (GlcNAc) ₂ residue from the non-reducing end of a chitin oligosaccharide. However, it shows some minor endochitinase activity in vitro, as well. A putative 24 amino-acid signal peptide may direct this protein to the secretory system and it has been detected in cell wall apoplastic fluid. RT-PCR experiments demonstrate that ChiC transcript levels are increased in response to abscisic acid, jasmonic acid, and NaCl stress. Microarray results also suggest that transcript levels rise in response to osmotic stress, two fungal pathogens, a bacterial pathogen, and the elicitor flagellin. protein_coding
Mtr.45462.1.S1_at	Putative sugar transporter. Expressed in nematode-induced root syncytia. protein_coding SUGAR TRANSPORTER PROTEIN 12 (STP12) SUGAR TRANSPORTER PROTEIN 12 (STP12)
Mtr.39654.1.S1_at	Encodes a receptor-like protein kinase. Naming convention from Chen et al 2003 (PMID 14756307) protein_coding CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 10 (CRK10) (RLK4)
Mtr.20845.1.S1_at	Nodulin MtN3 family protein
Mtr.25315.1.S1_at	Encodes GPI-anchored SKU5-like protein. protein_coding SKU5 SIMILAR 1 (SKS1) SKU5 SIMILAR 1 (SKS1)
Mtr.43405.1.S1_at	SAUR-like auxin-responsive protein family
Mtr.27961.1.S1_s_at	Predicted to encode a PR (pathogenesis-related) protein. Belongs to the lipid transfer protein (PR-14) family with the following members: At2g38540/LTP1, At2g38530/LTP2, At5g59320/LTP3, At5g59310/LTP4, At3g51600/LTP5, At3g08770/LTP6, At2g15050/LTP7, At2g18370/LTP8, At2g15325/LTP9, At5g01870/LTP10, At4g33355/LTP11, At3g51590/LTP12, At5g44265/LTP13, At5g62065/LTP14, At4g08530/LTP15. protein_coding

Mtr.17067.1.S1_at	Encodes a basic domain leucine zipper (bZip) transcription factor bZIP11. Translation is repressed by sucrose. Directly regulates gene expression of ASN1 and ProDH2, which are enzyme-coding genes involved in amino acid metabolism. protein_coding G-BOX BINDING FACTOR 6 (GBF6) (ATBZIP11)
Mtr.31299.1.S1_at	RAD-like 1 (RL1)
Mtr.30698.1.S1_at	encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4. protein_coding
Mtr.25211.1.S1_at	Peroxidase superfamily protein
Mtr.4787.1.S1_at	nodulin MtN21 /EamA-like transporter family protein
Mtr.37909.1.S1_at	Encodes a homolog of Replication Protein A. rpa70b mutants are hypersensitive to UV-B radiation and MMS treatments suggesting a role for this protein in DNA damage repair. protein_coding RPA70-KDA SUBUNIT B (RPA70B) RPA70-KDA SUBUNIT B (RPA70B)
Mtr.37152.1.S1_at	Concanavalin A-like lectin protein kinase family protein
Mtr.41073.1.S1_at	BEST Arabidopsis thaliana protein match is: flowering promoting factor 1 (TAIR:AT5G24860.1)
Mtr.43132.1.S1_at	Eukaryotic aspartyl protease family protein
Mtr.20364.1.S1_at	annexin 8 (ANNAT8)
Mtr.14503.1.S1_at	zinc ion binding
Mtr.45966.1.S1_at	Encodes phytoene synthase. protein_coding PHYTOENE SYNTHASE (PSY) PHYTOENE SYNTHASE (PSY)
Mtr.37708.1.S1_at	Encodes sulfate transporter Sultr3
Mtr.43995.1.S1_at	Protein of unknown function (DUF1635)
Mtr.38633.1.S1_at	Encodes a member of the CYP701A cytochrome p450 family that is involved in later steps of the gibberellin biosynthetic pathway. protein_coding GA REQUIRING 3 (GA3) CYTOCHROME P450 701 A3 (CYP701A3)

Mtr.12673.1.S1_at	Encodes a protein with aspartic protease activity (also known as aspartate-type endopeptidase activity). Overexpression of the gene was shown to lead to salicylic acid (SA)-mediated disease resistance upon exposure to the pathogen <i>Pseudomonas syringae</i> . Moreover, overexpression of this gene led to the upregulation of two pathogenesis-related genes PR1 and PR2. This upregulation was no longer observed in transgenic lines expressing the bacterial NahG gene encoding a hydroxylase suppressing SA accumulation. protein_coding CONSTITUTIVE DISEASE RESISTANCE 1 (CDR1) CONSTITUTIVE DISEASE RESISTANCE 1 (CDR1)
Mtr.10704.1.S1_at	Uncharacterised protein family (UPF0497)
Mtr.41598.1.S1_at	MINICHROMOSOME MAINTENANCE 6 (MCM6)
Mtr.20496.1.S1_at	MINICHROMOSOME MAINTENANCE 3 (MCM3)
Mtr.28858.1.S1_at	MATE efflux family protein
Mtr.23516.1.S1_at	FUNCTIONS IN: molecular_function unknown
Mtr.41691.1.S1_at	encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily. protein_coding CYTOKININ RESPONSE FACTOR 3 (CRF3) CYTOKININ RESPONSE FACTOR 3 (CRF3)
Mtr.25945.1.S1_at	myb-like transcription factor family protein
Mtr.13449.1.S1_at	FUNCTIONS IN: molecular_function unknown
Mtr.49594.1.S1_at	Embryo-specific protein 3, (ATS3)
Mtr.39333.1.S1_at	Protein of unknown function (DUF1442)
Mtr.37927.1.S1_at	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
Mtr.9232.1.S1_at	unknown protein
Mtr.44769.1.S1_at	encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4. protein_coding
Mtr.13206.1.S1_at	Histone superfamily protein
Mtr.25510.1.S1_at	Glycosyl hydrolase superfamily protein
Mtr.12557.1.S1_at	SKU5 similar 17 (sks17)