

Functional category	CloneID	annotation	1 dpi M	5 dpi M	15 dpi M	Cluster
Metabolism						
	16_G12	inorganic phosphatase	-1,4			1
	22_E07	arginine decarboxylase	-1,6			1
	24_C06	5-methyltetrahydropteroyltriglutamate (methionine synthase)	-1,4			1
	27_D07	enoyl-CoA-hydratase		1,4		4
	38_B04	enolase 2-phosphoglycerate		1,4		4
	NXCI_001_H08	SWP:IFRH_ARATH P52577 ISOFLAVONE REDUCTASE		-1,5		7
	NXCI_018_A08	pectate lyase	1,4			2
	NXCI_032_E01	ASPARTATE CARBAMOYL TRANSFERASE	1,3	1,5		5
	NXCI_040_H05	SWP:METE_MESCR P93263 5-METHYLTETRAHYDROPTEROYLTR		-1,4		7
	NXCI_048_B08	DIHYDROLIPOAMIDE ACETYLTRANSFERASE	1,4			2
	NXCI_055_D02	srg1 protein - aanthocyanidin synthase	1,4			2
	NXCI_066_G08	3-KETOACYL-COA THIOLASE B PEROXISOMAL	-1,4			1
	NXCI_068_C12	polygalacturonase-like protein		1,4		4
	NXCI_082_E07	xyloglucan endo-transglycosylase		2,2		4
	NXCI_094_E12	PECTATE LYASE		1,5		4
	NXCI_098_D10	cytochrome P450	1,4			2
	NXCI_102_C08	PROBABLE MANNITOL DEHYDROGENASE	1,4			2
	NXCI_114_H07	putative uridylate kin	1,6			2
	NXCI_123_C05	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECUR...	1,6			2
	NXCI_127_G06	SWP:SPE1_PEA Q43075 ARGININE DECARBOXYLASE (EC 4.1.1.19)		-1,4		7
	NXNV_002_E08	adenylate kinase		1,4		4
	NXNV_067_G03	nucleotide pyrophosphatase homolog	1,3	1,4		5
	NXNV_074_D01	galactose-1-phosphate uridyltransferase	1,5			2
	NXNV_106_C07	Beta-xylosidase		1,6		4
	NXNV_127_E04	ISOFLAVONE REDUCTASE HOMOLOG	1,3	1,4		5
	NXNV_132_G06	endoglucanase 1 (ec 3.2.1.4) (endo-1,4-beta-glucanase) (cellulase)	1,3	1,4		5
	NXNV_136_H04	EMB:Q43781 Q43781 ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1)		1,7		4
	NXNV_165_G01	methionine synthase		1,4		4
	NXSI_025_H02	alpha-pinene synthase		-1,4		7
	NXSI_040_H09	phosphogluconate dehydrogenase (decarboxylatin... 286 1e-76	-1,4			1
	NXSI_062_B08	no hit		-1,4		7
	NXSI_066_A02	2-oxoglutarate dehydrogenase		1,5		4
	NXSI_083_G03	putative lipase (catalytic hydrolase)		1,7		4
	NXSI_099_F10	adenosylmethionine decarboxylase (EC 4.1.1.50)	-1,7			1
	NXSI_107_B01	Sorbitol dehydrogenase-like protein	-1,4			1
	NXSI_132_B10	LANATOSIDE 15'-O-ACETYLESTERASE PRECURSOR	-1,3	-1,4		7
	NXSI_134_B11	EMB:Q9SFU6 Q9SFU6 PUTATIVE GLUCAN SYNTHASE.		1,4		4

Energy

01_D05	amino acid selective channel protein	1,4	4
03_C08	chlorophyll a/b binding protein CP29 precursor	1,4	4
14_G06	cytochrome C	-1,4	7
19_B07	23-bisphosphoglycerate independent phosphatase	1,6	4
21_E04	glyceraldehyde 3-phosph	1,4	4
22_G10	adenosine kinase-like protein	-1,4	1
26_D05	ATP synthase c-chain	-1,5	7
NXCI_002_H04	H+-transporting ATP synthase (EC 3.6.1.34)	1,5	2
NXCI_008_C01	photosystem ii oxygen-evolving complex protein	1,5	2
NXCI_018_G04	aldehyde dehydrogenase homolog	1,6	2
NXCI_026_A11	PUTATIVE GLUTAREDOXIN	1,4	2
NXCI_031_H08	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHatase	1,6	4
NXCI_075_C07	PROBABLE NADH-GLUTAMATE SYNTHASE	2,1	4
NXCI_094_G11	EMB:Q9ZQY2 Q9ZQY2 PYRUVATE DEHYDROGENASE E1 BETA	1,5	4
NXCI_116_H02	EMB:Q40916 Q40916 NADPH-CYTOCHROME P450 REDUCTASE	-1,5	7
NXSI_007_H12	SUCROSE SYNTHASE	-1,4	1
NXSI_060_A06	EMB:Q9ZS54 Q9ZS54 HIGH PI CUZN-SUPEROXIDE DISMUTASE	1,4	4
NXSI_096_C09	SWP:RUBB_PEA P08927 RUBISCO SUBUNIT BINDING-PROTEIN BETA	1,5	4
NXSI_116_G04	photoassimilate-responsive protein	1,8	4

Cell cycle and DNA processing

NXCI_106_H10	CELL DIVISION CONTROL PROTEIN 12 (SEPTIN)	1,5	2
NXSI_094_B05	EMB:Q43303 Q43303 HISTONE H3 (FRAGMENT	1,6	4
NXSI_096_C12	no hit	1,4	6

Transcription

NXCI_008_H10	putative zinc-finger protein	1,4	2
NXCI_044_A12	PREG-LIKE PROTEIN (FRAGMENT)	1,5	2
NXNV_002_F08	ELONGATION FACTOR-1 ALPHA	1,4	2
NXNV_074_G09	putative bZIP transcription factor	1,5	2
NXSI_021_H06	homeobox protein HAT22	1,4	4
NXSI_063_D09	PIR:T02995 T02995 unspecific monooxygenase (EC 1.14.14.1) -	-1,7	7

Protein synthesis

21_F11	elongation factor 1-AI	-1,4	1
17_H04	acid ribosomal protein	-1,4	7
22_A01	ribo pro L39	1,6	4
28_F06	ribosomal protein S3A	1,7	4
35_B03	40S ribo pro S8	1,6	4
NXCI_029_D03	40S ribosomal protein S15-like	1,3	2
NXCI_044_E02	SWP:R13A_PICMA O65055 60S RIBOSOMAL PROTEIN L13A.	1,4	4
NXCI_050_F08	40S RIBOSOMAL PROTEIN	1,4	2
NXCI_097_F03	POLY(A)-BINDING PROTEIN	1,4	2
NXCI_102_G08	60S acidic ribosomal protein	1,5	2
NXNV_134_B03	PIR:T02039 T02039 acidic ribosomal protein P1a - maize >GEN:2431... -	1,6	4
NXNV_140_F08	SWP:RS18_ARATH P34788 40S RIBOSOMAL PROTEIN S18.	1,5	4
NXSI_052_B04	valine--tRNA ligase-like protein	-1,4	1
NXSI_116_E07	RIBOSOMAL PROTEIN	1,4	4

Protein fate

02_C01	protease regulatory subunit 7	-1,4	1
02_C09	antifreeze-like protein (af70) - Norway Spruce	1,6	4
03_C11	ubiquitin precursor	1,6	4
03_G03	10 kda chaperonin	1,6	4
14_G12	polyubiquitin	-1,4	7
30_B06	ligumine like protease precursor	-1,4	7
NXCI_032_H03	cullin-like protein	1,4	2
NXCI_053_D08	EMB:O49977 O49977 UBIQUITIN (FRAGMENT). >GEN:2760349	1,3 -1,4	2
NXCI_068_D10	COP9 signalosome complex subunit 4	1,4	4
NXCI_085_H12_F	tau class glutathione S-transferase [Pinus tabuliformis]	1,6	4
NXNV_123_D06	EMB:Q41067 Q41067 POLYUBIQUITIN. >GEN:1332579	1,5	4
NXNV_128_D10	Ubiquitin ligase	2,1	4
NXSI_066_H06	SWP:R11A_LOTJA Q40191 RAS-RELATED PROTEIN RAB11A.	1,4	4
NXSI_101_H03_F	glycosyl hydrolase family 1 protein [Arabidopsis thaliana]	1,4	4
NXSI_104_H10	SWP:RERA_ARATH O48670 RER1A PROTEIN (ATRER1A). >PIR:T08570	1,4	4
NXSI_128_E05	copper chaperone homolog	1,7	4
NXSI_128_E08	DNAJ PROTEIN HOMOLOG	1,4	4
NXSI_135_B02	Glycosylation enzyme-like protein	1,9	4

Transport

03_E05	protein translocase	-1,4		1
19_E08	non specific lipid tra	-1,5		1
28_G07	Ran binding protein		1,6	4
33_E11	phosphate transporter [Sesbania rostrata]	-1,4		1
40_A03	Porine MIP1	-1,4		1
NXCI_034_F04	no hit		-1,4	7
NXCI_048_E08	PROBABLE AQUAPORIN	1,4		2
NXCI_070_E11	vacuolar proton pyrophosphatase	-1,4		1
NXCI_102_F06	putative signal sequence receptor	1,6		2
NXCI_124_E12	transporter	1,4		2
NXNV_085_G09	vesicle-associated membrane protein		1,5	4
NXNV_129_F09	VACUOLAR V-H+ATPASE SUBUNIT E	1,4		2
NXSI_116_G10	proton pump putative	1,5		2

Cellular communication and Signal transduction mechanisms

39_C02	putitive casein kinase II catalitic subunit		-1,4	7
02_D01	ser/thre prot kinase	-1,4		1
NXCI_005_G03	PURPLE ACID PHOSPHATASE	1,5	1,6	5
NXCI_067_D08	Ras	1,6		2
NXCI_075_B02	GTP-binding protein		1,7	4
NXNV_010_D03	calreticulin	1,5		2
NXNV_012_H01	TIR/P-loop/LRR [Pinus taeda]	1,3		2
NXNV_077_C07	14-3-3 PROTEIN	1,4		2
NXNV_132_H07	hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]		1,5	4
NXNV_136_E11	putative TIR/NBS/LRR disease resistance protein [Pinus taeda]		1,5	4
NXNV_148_H07	CC-NBS-LRR resistance-like protein [Pinus lambertiana]	-1,5		1
NXNV_162_E05	TIR/P-loop/LRR [Pinus taeda]		1,6	4
NXNV_166_H02	EMB:Q17063 Q17063 HEMOLYSIN. >GEN:7144507 U12823 hemolysin	-1,4		1
NXPV_037_F09	NBS/LRR [Pinus taeda]		-1,4	7
NXSI_008_B02	thaumatin-like protein PR5 family [Pinus monticola]		1,5	4
NXSI_021_A09	CLAVATA1 receptor kinase(CLV1)-like protein	1,2	1,4	5
NXSI_026_H06	similar to stress responsive lectin-like cDNAs from rice	-1,4		1
NXSI_036_H01	protein binding / signal transducer	1,4	1,4	5
NXSI_039_G02	putative TIR/NBS/LRR disease resistance protein [Pinus taeda]		1,5	4
NXSI_042_E12	NBS-LRR disease resistance protein homologue [Hordeum vulgare]	1,4		2
NXSI_048_D03	EMB:P92963 P92963 RAB2-LIKE PROTEIN (GTP-BINDING RAB2A		1,6	4
NXSI_052_C04	putative TIR/NBS/LRR disease resistance protein [Pinus taeda]		1,4	4
NXSI_052_D08	putative TIR/NBS/LRR disease resistance protein [Pinus taeda]		1,4	4
NXSI_054_F05	glycine-rich protein homolog [Pinus taeda]	1,3		3
NXSI_056_B12	no hit		1,4	4

	NXSI_113_D07	no hit	1,4	4	
	NXSI_141_G01	Receptor protein kinase-like protein	1,5	4	
Cell rescue and defense					
	15_F09	multiple stress-responsive zinc-finger protein	1,6	4	
	38_A10	metallothionine-like prot EMB 30	1,6	4	
	NXCI_002_G06	Blast for putative function	1,5	2	
	NXCI_005_C10	LACCASE (EC 1.10.3.2)	1,4	2	
	NXCI_022_G01	HEAT SHOCK 70 KDA PROTEIN, MITOCHONDRIAL	1,6	2	
	NXCI_045_H07	MLO PROTEIN HOMOLOG 1	1,4	2	
	NXCI_055_D03	metallothionein-like protein	1,4	2	
	NXCI_076_F07	no hit	2,4	4	
	NXCI_094_C09	LACCASE (EC 1.10.3.2)	1,4	2	
	NXCI_095_C01	no hit	1,7	4	
	NXCI_124_A12	disease resistance protein (TIR-NBS-LRR class), putative [Arabidopsis	-1,4	1	
	NXNV_056_F03	PUTATIVE DISEASE RESISTANCE PROTEIN	1,5	2	
	NXNV_069_A02	Avr9 elicitor response protein-like	1,6	4	
	NXNV_096_C08	PR10 protein [Pinus monticola]	-1,6	8	
	NXNV_160_F09	disease resistance protein	1,4	4	
	NXNV_162_C02	peroxidase (EC 1.11.1.7) [secretory, cationic]	-1,4	1	
	NXSI_002_D03	drought-induced protein	1,7	4	
	NXSI_080_D06	PIR:T31428 T31428 fiber annexin - upland cotton >EMB:O82090 O820...	1,7	4	
	NXSI_095_H03	no hit	1,5	4	
	NXSI_134_G06	PIR:T46629 T46629 lp6 protein - loblolly pine >EMB:Q41083 Q41083...	1,4	4	
Regulation of interaction with environment					
	23_G07	putative auxin-induced	-1,4	1	
	37_E10	gibberellin regulated protein	-1,4	-1,4	7
	37_H11	putative auxin indepen	-1,6	1	
	NXCI_018_F09	putative auxin-induced	-1,4	1	
	NXPV_038_C08	MtN21 nodulin protein-like	-1,3	-1,7	7
	NXPV_043_G04	MtN21 nodulin protein-like	-1,6	1	
	NXSI_091_E03	nifU-like protein	1,4	4	
	ST_07_C06	putative auxin-induced	1,5	4	
Development					
	NXNV_025_F03	PIR:F71433 F71433 probable growth regulator - Arabidopsis thalia... 188	1,4	4	
	NXCI_020_A02	embryonic abundant protein	1,4	2	
	NXNV_096_G04	argonaute	-1,4	1	
	NXNV_129_B12	leaf development protein Argonaute	1,4	2	
	NXSI_039_E06	putative floral homeot	1,4	4	
	NXSI_041_A07	senescence-associated protein homolog	1,4	4	
	NXSI_110_A07	Argonaute (AGO1)-like protein	-1,4		

Transposable elements, viral and plasmid proteins				
25_C11	RNA-directed DNA polymerase (Reverse transcriptase);	-1,4		1
Control of cellular organization				
02_B01	envelope glycoprotein		1,5	4
02_F09	histone-like protein	-1,7		1
06_E01	histone H3	1,4		2
07_F10	actin depolymerizing protein	-1,6		1
NXCI_001_A06	beta tubulin [Arabidopsis thaliana]	1,4		2
NXCI_058_C02	HISTONE H4	1,5		2
NXSI_048_H03	HISTONE-LIKE PROTEIN	-1,6		1
Cell, Tissue and Organ differentiation and localization				
36_B02	plastid protein	-1,4		1
NXSI_046_B05	putative endoplasmatic reticulum retrieval protein Rer1B		1,4	4
Protein with binding function or co-factor requirement				
17_A11	DNA binding / RNA binding	-1,4		1
21_E01	fad binding / aldehyde-lyase/ oxidoreductase/ oxidoreductase,		1,6	4
37_G12	putative T complex protein 1, theta subunit		1,5	4
NXCI_101_D04	polyphosphoinositide binding protein Ssh2	1,4		2
NXNV_005_B04	chloroplast nucleoid DNA binding	1,4		2
Unclassified proteins and Unknown function				
03_F07	no hit	1,5		2
04_B03	no hits found	-1,4		1
04_F02	pyruvate carboxylase (EC6.4.1.1)	-1,4		1
07_A07	hyp pro	-1,4		1
07_E10	unknown	1,4		2
12_A02	FS 1 pro		1,6	4
15_H06	hyp pro		1,5	4
18_H01	no hit		1,6	4
25_C10	hypothetical	1,6		2
27_A08	no hit	-1,5	-1,4	7
28_F04	no hit	-1,4		1
30_H03	hyp pro		-1,4	7
32_F07	hypothetical protein		1,7	4
34_E10	hyp rpo	-1,5	-1,7	7
NXCI_009_C07	no hit	1,5		2
NXCI_027_D03	no hit	1,3	1,4	5
NXCI_027_E04	no hit		-1,5	7
NXCI_056_E02	no hit	1,3	1,8	5
NXCI_071_C03	EMB:Q9LTC1 Q9LTC1 SIMILARITY TO ANKYRIN LIKE PROTEIN.		1,7	4
NXCI_076_C07	EMB:Q9LVU5 Q9LVU5 SIMILARITY TO RIBOSOMAL PROTEIN L9.		1,4	4
NXCI_099_A12	no hit		1,5	4

NXCI_121_D01	PIR:T06667 T06667 argininosuccinate synthase (EC	-1,4		7
NXCI_137_B03	no hit	1,4		2
NXNV_003_C10	hypothetical protein		1,4	4
NXNV_044_E12	fiber protein		1,8	4
NXNV_047_B11	hypothetical protein	1,4	1,4	5
NXNV_074_F12	unknown	1,5		2
NXNV_074_G06	no hit	1,5		2
NXNV_083_G05	EMB:Q9NY06 Q9NY06 INTEGRAL MEMBRANE TRANSPORTER	-1,4		1
NXNV_120_E04	EMB:O14597 O14597 NON- FUNCTIONAL FOLATE BINDING		-1,8	7
NXNV_125_D01	no hit		1,4	4
NXNV_125_G04	no hit		1,4	6
NXNV_128_E01	SWP:IF52_NICPL P24922 INITIATION FACTOR 5A-2 (EIF-5A)		1,7	4
NXNV_129_A06	no hit	1,4		2
NXNV_134_A05	PUTATIVE TYPE 1 MEMBRANE PROTEIN		2	4
NXNV_134_H10	no hit	-1,6	1,4	6
NXNV_139_A05	no hit		1,6	4
NXNV_143_B10	no hit		1,7	4
NXSI_001_G04	no hit	-1,5		1
NXSI_005_F10	no hit	-1,4		1
NXSI_021_D01	no hit		1,6	4
NXSI_040_C01	no hit		1,5	4
NXSI_053_D09	no hit		1,4	4
NXSI_079_E12	EMB:Q9LLZ4 Q9LLZ4 PUTATIVE ARABINOGLACTAN PROTEIN.		1,4	6
NXSI_105_A03	no hit		1,7	4
NXSI_107_C02	PIR:T12958 T12958 copper transport protein homolog T6H20.70 - Ar... 67		1,7	4
NXSI_117_C01	no hit		1,7	4
NXSI_134_C12	no hit		1,7	4