Table S5. List of transcripts differentially regulated in *M. truncatula* roots in comparison to

AM+K (268)	log2	Annotation	AM+K (85)	log2	Annotation
Medtr2g088610	inf	Late embryog	Medtr1g062590	-1.49338	Pathogenesis
Medtr3g036335	inf	F-box family	Medtr1g037310	-1.40851	Zinc finger, C
Medtr4g036300	inf	0	Medtr1g099310	-1.15929	chitinase A
Medtr4g091150	inf	FAD-binding	Medtr4g088375	-1.14066	homeobox-1
Medtr4g020520	inf	disease resist	Medtr5g041190	-1.09455	0
Medtr4g036290	inf	0	Medtr3g007650	-1.08921	S-locus lectin
Medtr4g064873	inf	C2H2 and C2	Medtr1g040525	-1.06538	Leucine-rich
Medtr4g083110	inf	0	Medtr8g019330	-1.05667	0
Medtr4g097670	inf	xyloglucan en	Medtr6g071895	-1.05405	disease resist
Medtr5g005290	inf	0	Medtr7g101800	-1.0118	Protein kinas
Medtr5g005570	inf	gibberellin 2-	Medtr7g027960	-0.994467	cytochrome
Medtr5g058320	inf	UDP-Glycosyl	Medtr4g114250	-0.983062	receptor-like
Medtr5g062030	inf	0	Medtr3g013970	-0.979009	Ubiquitin car
Medtr6g014040	inf	UDP-glucosyl	Medtr4g070370	-0.902565	NmrA-like ne
Medtr6g071605	inf	annexin 5	Medtr4g128580	-0.888797	xyloglucan en
Medtr7g011630	inf	related to AP	Medtr1g101250	-0.888548	disease resist
Medtr7g076960	inf	0	Medtr1g086390	-0.879515	Pectin lyase-l
Medtr7g080530	inf	2-phosphogly	Medtr3g110330	-0.853762	NADP-malic e
Medtr7g076970	inf	0	Medtr8g022790	-0.848232	GDSL lipase 1
Medtr7g076990	inf	0	Medtr4g019225	-0.838075	laccase 7
Medtr7g087170	inf	F-box family	Medtr5g079890	-0.837402	Calcium-depe
Medtr7g096660	inf	0	Medtr1514s0010	-0.836582	NB-ARC dom
Medtr7g105400	inf	alpha/beta-H	Medtr6g021870	-0.83216	0
Medtr8g012870	inf	Arabidopsis	Medtr2g011270	-0.831936	S-locus lectin
Medtr8g031120	inf	0	Medtr5g055680	-0.820116	senescence-r
Medtr8g031160	inf	0	Medtr4g052620	-0.819511	NAC domain
Medtr8g067960	inf	Concanavalin	Medtr7g013240	-0.817202	UDP-Glycosyl
Medtr8g074750	inf	ammonium t	Medtr4g087100	-0.812621	2-oxoglutarat
Medtr8g019710	inf	RING/U-box	Medtr2g073420	-0.809852	cytochrome
Medtr8g467650	inf	chitinase A	Medtr6g021850	-0.807173	0
Medtr8g071815	inf	RING/U-box	Medtr5g048050	-0.807162	ARM repeat
Medtr0302s0030	inf	kunitz trypsin	Medtr8g031400	-0.798247	GDSL-motif li
Medtr0328s0040	inf	Thioredoxin	Medtr5g021390	-0.795541	ferulic acid 5-
Medtr2g010320	inf	cytochrome	Medtr7g113410	-0.794228	lipoxygenase
Medtr2g093750	inf	Seven transm	Medtr1g080990	-0.792262	0

Medtr3g112470	4.73182	peptide trans	Medtr4g114980	-0.784751	WUS-interact
Medtr7g098150	4.71822	peptide trans	Medtr5g077760	-0.781865	0
Medtr4g080730	4.52235	senescence-a	Medtr6g082130	-0.779729	0
Medtr2g034950	4.22856	COBRA-like p	Medtr3g109820	-0.776679	Leucine-rich
Medtr1g090783	4.01004	AGAMOUS-lil	Medtr2g102640	-0.769432	pleiotropic dr
Medtr4g057865	3.83154	nitrate transp	Medtr4g057960	-0.76302	P-loop contai
Medtr8g078300	3.52813	Protein kinas	Medtr4g053785	-0.757493	Jojoba acyl C
Medtr2g062310	3.52226	Domain of ur	Medtr2g099470	-0.751249	homolog of c
Medtr2g090050	3.29012	Family of unk	Medtr6g021830	-0.737307	0
Medtr4g109380	3.20387	0	Medtr7g028432	-0.734544	Leucine-rich
Medtr4g057890	3.15432	nitrate transp	Medtr6g088450	-0.732968	polyol/mono
Medtr7g106880	2.96923	ABC-2 type tr	Medtr6g071340	-0.730774	ARM repeat s
Medtr1g096030	2.79556	GRAS family t	Medtr8g093010	-0.722223	RING/U-box s
Medtr6g011860	2.72648	NAC (No Apic	Medtr4g060890	-0.698485	0
Medtr2g438310	2.59705	0	Medtr3g094630	-0.697665	Peroxidase su
Medtr1g027570	2.55122	wall-associate	Medtr8g010200	-0.697439	0
Medtr5g017290	2.54927	Remorin fam	Medtr2g031530	-0.695685	Wall-associat
Medtr7g105460	2.50513	NAD(P)-bindi	Medtr4g094772	-0.684681	cytochrome P
Medtr5g004650	2.45669	0	Medtr1g008740	-0.676104	NAC domain
Medtr4g104410	2.43951	Transducin/W	Medtr2g015050	-0.67565	Integrase-typ
Medtr7g091570	2.43648	NB-ARC dom	Medtr5g006160	-0.673908	receptor-like
Medtr2g438320	2.39359	0	Medtr0052s0070	-0.671857	0
Medtr5g012270	2.26557	nitrate transp	Medtr8g040080	-0.67109	VQ motif-cor
Medtr2g438560	2.20139	0	Medtr7g100240	-0.658474	Protein phosp
Medtr1g079440	2.16166	Protein kinas	Medtr4g119790	-0.655131	flowering pro
Medtr8g010530	2.09416	Seven transm	Medtr3g055610	-0.654912	PLC-like phos
Medtr6g045097	2.06121	Kunitz family	Medtr5g036410	-0.653254	matrix metall
Medtr4g111975	2.04298	Duplicated ho	Medtr3g464650	-0.651389	Protein phosp
Medtr4g018760	1.92797	Nucleotide-su	Medtr5g004800	-0.647537	Calcium-depe
Medtr3g081040	1.92384	Myzus persic	Medtr4g126920	-0.647468	Xyloglucan er
Medtr1g054035	1.8732	fatty acid des	Medtr3g088760	-0.642588	wall-associate
Medtr5g010350	1.84539	root hair spe	Medtr4g064887	-0.640506	NAD(P)-bindi
Medtr8g042870	1.80808	zinc induced	Medtr6g009720	-0.635402	P-loop contai
Medtr7g033325	1.80643	beta-1,4-N-ac	Medtr5g076170	-0.634614	Late embryog
Medtr0391s0020	1.73442	Disease resist	Medtr4g087925	-0.632822	glutamate rec
Medtr3g058630	1.72676	zinc transpor	Medtr5g016440	-0.630822	cytochrome P
Medtr8g068300	1.71633	Deoxyxylulos	Medtr2g089120	-0.62978	terpene synth
Medtr3g085630	1.68128	0	Medtr7g058640	-0.626432	synaptobrevi
Medtr5g092150	1.64574	cytochrome P	Medtr3g021430	-0.624004	O-methyltrar
Medtr5g084090	1.5965	0	Medtr6g091680	-0.61409	S-adenosyl-L-
Medtr4g029270	1.59515	0	Medtr5g010640	-0.611803	osmotin 34
Medtr4g052040	1.59158	ovate family	Medtr6g005330	-0.605061	RmlC-like cup
Medtr4g119500	1.58053	nuclear facto	Medtr5g027810	-0.598492	NB-ARC doma

Medtr7g085810	1.57723	related to AP	Medtr6g034930	-0.595482	extensin 3
Medtr7g101190	1.56383	plasma mem	Medtr4g020110	-0.595243	delta 1-pyrro
Medtr3g467130	1.52884	cytochrome	Medtr3g088750	-0.593824	wall associat
Medtr7g082810	1.50472	MATE efflux	Medtr8g080770	-0.589097	histidine kina
Medtr3g008760	1.4917	Plant inverta	Medtr1g105820	-0.588637	cysteine-rich
Medtr8g018570	1.47837	lipoxygenase	Medtr5g095120	-0.587996	receptor like
Medtr3g057970	1.47164	cytochrome	Medtr5g013260	-0.585609	FAD/NAD(P)-
Medtr8g069350	1.46429	0			
Medtr4g087120	1.41967	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe			
Medtr1g103110	1.40657	Acyl-CoA N-acyltransferases (NAT) superfamily protein			
Medtr4g075150	1.40558	serine carboxypeptidase-like 34			
Medtr2g104130	1.37026	Calcium-binding EF-hand family protein			
Medtr2g028980	1.36442	peroxidase 2			
Medtr2g036260	1.34827	0			
Medtr8g066280	1.34185	P-loop containing nucleoside triphosphate hydrolases supe			
Medtr4g066330	1.31562	beta glucosidase 13			
Medtr4g050140	1.30802	alpha/beta-Hydrolases superfamily protein			
Medtr8g074920	1.30018	protein kinase family protein			
Medtr7g079440	1.28297	cytochrome P450, family 97, subfamily A, polypeptide 3			
Medtr6g051680	1.27387	Heavy metal transport/detoxification superfamily protein			
Medtr5g020960	1.26971	Heavy metal transport/detoxification superfamily protein			
Medtr8g024310	1.24763	pyruvate dehydrogenase E1 alpha			
Medtr2g438260	1.23551	0			
Medtr5g072570	1.23001	serine carboxypeptidase-like 42			
Medtr5g023370	1.21223	Arabidopsis protein of unknown function (DUF241)			
Medtr4g068290	1.20568	CSL zinc finger domain-containing protein			
Medtr3g068030	1.20131	rubisco activase			
Medtr7g077313	1.19697	0			
Medtr1g073700	1.19683	Cyclopropane-fatty-acyl-phospholipid synthase			
Medtr7g088790	1.1967	Major facilitator superfamily protein			
Medtr4g096690	1.19465	3-ketoacyl-acyl carrier protein synthase I			
Medtr8g031900	1.15979	NAD(P)-binding Rossmann-fold superfamily protein			
Medtr1g070250	1.15906	C2H2 and C2HC zinc fingers superfamily protein			
Medtr7g088350	1.13713	DHHC-type zinc finger family protein			
Medtr7g024950	1.1303	Cysteine/Histidine-rich C1 domain family protein			
Medtr5g084950	1.12993	Myzus persicae-induced lipase 1			
Medtr2g034260	1.12864	RGA-like 2			
Medtr4g021725	1.11814	metallothionein 2A			
Medtr3g007770	1.11594	cellulose synthase 5			
Medtr1g105965	1.11408	Pyruvate kinase family protein			
Medtr3g087980	1.11241	long chain acyl-CoA synthetase 9			
Medtr3g107393	1.08349	SPX domain gene 2			
Medtr7g053290	1.07523	NAD(P)-binding Rossmann-fold superfamily protein			

Medtr1g044105	1.07108	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe
Medtr8g074530	1.06839	Arabidopsis protein of unknown function (DUF241)
Medtr8g066770	1.06626	basic helix-loop-helix (bHLH) DNA-binding superfamily prot
Medtr8g059425	1.06261	UDP-Glycosyltransferase superfamily protein
Medtr2g064400	1.05216	F-box family protein
Medtr2g040690	1.03659	chitinase A
Medtr1g081290	1.03654	zeta-carotene desaturase
Medtr1g019640	1.02488	Calcium-binding EF-hand family protein
Medtr3g462710	1.0246	peptide transporter 1
Medtr2g025080	1.0164	RING/U-box superfamily protein
Medtr4g121880	1.01324	lipoamide dehydrogenase 1
Medtr5g080660	1.01221	zinc-finger protein 10
Medtr1g099360	1.01047	plastidic pyruvate kinase beta subunit 1
Medtr3g085740	1.00875	NAD(P)-binding Rossmann-fold superfamily protein
Medtr8g027820	1.00697	Protein of unknown function (DUF 3339)
Medtr2g012320	1.00278	Protein of unknown function (DUF761)
Medtr4g131180	0.99283	aldehyde dehydrogenase 11A3
Medtr7g078010	0.992139	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe
Medtr4g133750	0.992026	cytochrome P450, family 71, subfamily B, polypeptide 34
Medtr6g034195	0.989187	plastidic pyruvate kinase beta subunit 1
Medtr3g040370	0.989162	S-adenosyl-L-methionine-dependent methyltransferases su
Medtr7g117730	0.98606	myb domain protein 12
Medtr5g011060	0.980598	phospholipase D beta 1
Medtr2g096230	0.977868	exocyst subunit exo70 family protein H7
Medtr3g088565	0.974742	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe
Medtr3g049330	0.968162	TRICHOME BIREFRINGENCE-LIKE 43
Medtr7g024750	0.961974	Uncharacterised protein family (UPF0497)
Medtr7g105320	0.961372	F-box family protein
Medtr8g085960	0.961178	related to AP2 11
Medtr2g078730	0.949933	D-aminoacid aminotransferase-like PLP-dependent enzyme
Medtr1g044225	0.947581	telomerase activator1
Medtr4g063885	0.94541	0
Medtr4g057595	0.941721	serine carboxypeptidase-like 48
Medtr1g062200	0.940311	0
Medtr7g044980	0.936351	0
Medtr4g094265	0.934746	Thioesterase superfamily protein
Medtr7g044920	0.931519	0
Medtr3g031380	0.929743	catalytics;transferases;[acyl-carrier-protein] S-malonyltrans
Medtr6g082330	0.928783	Copper transport protein family
Medtr5g014370	0.922306	0
Medtr2g010970	0.915447	Protein of unknown function, DUF538
Medtr7g056803	0.912462	0
Medtr1g103020	0.910207	3-ketoacyl-acyl carrier protein synthase I

Medtr2g069020	0.909122	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe
Medtr4g122110	0.901663	Disease resistance-responsive (dirigent-like protein) family
Medtr4g059680	0.900015	beta-galactosidase 8
Medtr3g020780	0.892262	cytochrome P450, family 93, subfamily D, polypeptide 1
Medtr5g093570	0.887499	PYRIMIDINE B
Medtr0110s0050	0.869118	5\'-3\' exonuclease family protein
Medtr3g087050	0.858054	alpha/beta-Hydrolases superfamily protein
Medtr7g069970	0.854871	0
Medtr3g018790	0.852794	annexin 8
Medtr2g087460	0.852581	Protein of unknown function (DUF3049)
Medtr3g082120	0.84543	Leucine-rich repeat (LRR) family protein
Medtr8g101330	0.844234	acetyl Co-enzyme a carboxylase biotin carboxylase subunit
Medtr7g081805	0.843735	ethylene-responsive element binding factor 13
Medtr8g063200	0.843276	0
Medtr5g035430	0.840408	0
Medtr7g111850	0.839995	galactinol synthase 2
Medtr0161s0050	0.839688	acyl activating enzyme 5
Medtr2g040500	0.833648	homology to ABI1
Medtr5g032060	0.826304	Kinase interacting (KIP1-like) family protein
Medtr7g060460	0.82575	laccase 17
Medtr1g009860	0.823686	Protein kinase superfamily protein
Medtr7g013100	0.814281	biotin carboxyl carrier protein 2
Medtr1g011640	0.813614	pleiotropic drug resistance 12
Medtr8g080230	0.811654	PLAT/LH2 domain-containing lipoxygenase family protein
Medtr4g083620	0.804203	0
Medtr4g073920	0.802039	PLC-like phosphodiesterases superfamily protein
Medtr7g045370	0.80193	carotenoid cleavage dioxygenase 7
Medtr6g009540	0.801162	AAA-ATPase 1
Medtr3g110195	0.798974	carotenoid cleavage dioxygenase 1
Medtr6g049260	0.790884	Heavy metal transport/detoxification superfamily protein
Medtr1g106420	0.788765	LOB domain-containing protein 38
Medtr4g035650	0.787404	0
Medtr7g090230	0.784306	Glutaredoxin family protein
Medtr5g094730	0.784149	Copper transport protein family
Medtr8g432480	0.783724	BON association protein 2
Medtr7g015710	0.782924	PLC-like phosphodiesterases superfamily protein
Medtr2g084120	0.777569	Protein kinase superfamily protein
Medtr4g056520	0.772424	serine carboxypeptidase-like 51
Medtr7g103610	0.770119	Thioredoxin superfamily protein
Medtr8g098375	0.766121	plasma membrane intrinsic protein 1;4
Medtr2g034280	0.764467	RGA-like 2
Medtr2g036440	0.760896	lectin protein kinase family protein
Medtr4g023480	0.758956	Metal-dependent phosphohydrolase

Medtr4g107370	0.754082	AAA-ATPase 1
Medtr2g105100	0.74819	3-ketoacyl-acyl carrier protein synthase III
Medtr7g090560	0.747471	0
Medtr8g095040	0.746883	ammonium transporter 2
Medtr4g117660	0.744665	Copper amine oxidase family protein
Medtr1g090370	0.744501	TGACG motif-binding factor 4
Medtr3g055130	0.744418	PYR1-like 11
Medtr3g479490	0.732334	UDP-glucosyl transferase 85A3
Medtr2g017810	0.722226	Haloacid dehalogenase-like hydrolase (HAD) superfamily pr
Medtr7g109580	0.720358	RGA-like 2
Medtr4g094220	0.718263	UDP-glucosyl transferase 85A3
Medtr2g090710	0.70517	HAESA-like 1
Medtr3g067510	0.702868	0
Medtr8g089830	0.700574	0
Medtr5g026580	0.689993	KAR-UP F-box 1
Medtr8g040070	0.68564	Ribosome recycling factor
Medtr4g105690	0.684936	Inositol 1,3,4-trisphosphate 5/6-kinase family protein
Medtr7g092600	0.683572	cytochrome P450, family 712, subfamily A, polypeptide 1
Medtr4g109020	0.679894	0
Medtr1g112940	0.679069	Protein phosphatase 2A regulatory B subunit family proteir
Medtr2g023890	0.678694	mitogen-activated protein kinase kinase kinase 18
Medtr1g068690	0.677484	glucan synthase-like 12
Medtr8g009270	0.675399	0
Medtr3g073180	0.673955	nitrate reductase 1
Medtr1g090090	0.671461	glutathione S-transferase TAU 15
Medtr1g090920	0.670316	glycosyltransferase family protein 47
Medtr8g081530	0.669828	0
Medtr3g055120	0.667042	0
Medtr1g112750	0.664512	FAD/NAD(P)-binding oxidoreductase family protein
Medtr1g066530	0.663156	0
Medtr1g028560	0.662909	cytokinin response factor 4
Medtr3g108520	0.662077	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase supe
Medtr6g023600	0.659789	NAD(P)-binding Rossmann-fold superfamily protein
Medtr8g090210	0.658046	Mitochondrial substrate carrier family protein
Medtr4g081180	0.657803	Nucleic acid-binding, OB-fold-like protein
Medtr1g076310	0.645974	small subunit ribosomal protein 16
Medtr1g077930	0.644201	alpha/beta-Hydrolases superfamily protein
Medtr5g007210	0.639215	0
Medtr5g017550	0.638553	Calcium-binding EF-hand family protein
Medtr8g061950	0.63845	Glutathione S-transferase family protein
Medtr6g059650	0.637108	Kunitz family trypsin and protease inhibitor protein
Medtr2g102570	0.632199	gibberellin 3-oxidase 1
Medtr5g098020	0.630337	0

Medtr2g072190	0.628685	glyoxalase II 3
Medtr8g007125	0.626126	phospholipase A 2A
Medtr1g054880	0.625278	Plant invertase/pectin methylesterase inhibitor superfamily
Medtr0050s0240	0.617802	Embryo-specific protein 3, (ATS3)
Medtr8g056020	0.616817	ankyrin repeat family protein
Medtr1g105480	0.614453	thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (TH
Medtr2g009220	0.611857	dicarboxylate transport 2.1
Medtr8g008660	0.611831	methyl esterase 10
Medtr8g018510	0.608084	lipoxygenase 1
Medtr4g108330	0.607098	end binding protein 1B
Medtr7g074220	0.602059	0
Medtr4g092515	0.593525	CAP (Cysteine-rich secretory proteins, Antigen 5, and Patho
Medtr2g031930	0.592201	ent-kaurenoic acid hydroxylase 2
Medtr2g064405	0.591499	Cation efflux family protein
Medtr1g076800	0.591297	Protein of unknown function (DUF1442)
Medtr1g111140	0.591266	2-oxoacid dehydrogenases acyltransferase family protein
Medtr2g085370	0.589035	Stigma-specific Stig1 family protein
Medtr8g045300	0.587235	MLP-like protein 28

the NM-K condition. "Log2 f.c." columns indicate the 1.5 cutoff log2 fold-change of transcripts in

AM+K & AM-K (227)	log2 f.c. AM+K	log2 f.c. AM-K	Annotation
Medtr1g009240	inf	inf	Leucine-rich
Medtr2g038675	inf	inf	Leucine-rich
Medtr2g102010	inf	inf	Mitochondria
Medtr1g105130	inf	inf	uclacyanin 1
Medtr3g047190	inf	inf	0
Medtr3g049390	inf	inf	proline-rich family protein
Medtr3g063240	inf	inf	nodulin MtN21 /EamA-like transporter family protein
Medtr3g107650	inf	inf	RING/U-box superfamily protein with ARM repeat doma
Medtr4g049550	inf	inf	Disease resistance-responsive (dirigent-like protein) fam
Medtr4g091010	inf	inf	0
Medtr4g091000	inf	inf	0
Medtr4g091020	inf	inf	0
Medtr4g104020	inf	inf	RGA-like 1
Medtr4g116620	inf	inf	0
Medtr5g081780	inf	inf	Polyketide cyclase/dehydrase and lipid transport superf
Medtr5g005950	inf	inf	Late embryogenesis abundant (LEA) hydroxyproline-rich
Medtr5g068140	inf	inf	phosphate transporter 1;3
Medtr6g073040	inf	inf	Uncharacterised protein family (UPF0497)
Medtr1g014150	inf	inf	Protein of unknown function (DUF567)
Medtr7g057900	inf	inf	0
Medtr7g076770	inf	inf	0
Medtr7g093330	inf	inf	Cysteine/Histidine-rich C1 domain family protein
Medtr7g077010	inf	inf	0
Medtr7g086230	inf	inf	uclacyanin 1
Medtr7g086280	inf	inf	Cupredoxin superfamily protein
Medtr7g089730	inf	inf	F-box family protein
Medtr7g102870	inf	inf	Protein of unknown function (DUF1624)
Medtr8g012865	inf	inf	Arabidopsis defensin-like protein
Medtr8g040940	inf	inf	0
Medtr8g068040	inf	inf	Concanavalin A-like lectin protein kinase family protein
Medtr8g074580	inf	inf	GDSL-like Lipase/Acylhydrolase superfamily protein
Medtr8g035880	inf	inf	Oxidoreductase, zinc-binding dehydrogenase family pro
Medtr0027s0260	inf	inf	chitinase A
Medtr0084s0030	inf	inf	Kunitz family trypsin and protease inhibitor protein
Medtr0147s0050	inf	inf	0

AM+K & AM-K (3)	log2 f.c. AM+K	log2 f.c. AM-K
Medtr3g479470	-1.44193	-2.8418
Medtr2g007880	-1.06145	-0.992466
Medtr0219s0070	-0.677477	-1.39489

Medtr2g460730	inf	inf	ARIA-interacting double AP2 domain protein
Medtr2g075830	inf	inf	senescence-associated gene 12
Medtr2g086640	inf	inf	germin-like protein 5
Medtr8g068030	10.1108	8.58078	Concanavalin A-like lectin protein kinase family protein
Medtr8g031150	10.0788	7.2638	0
Medtr5g075520	10.003	7.87582	0
Medtr4g077180	9.95087	7.94979	Bifunctional inhibitor/lipid-transfer protein/seed storag
Medtr7g068600	9.90378	7.67816	myb-like HTH transcriptional regulator family protein
Medtr5g031090	9.89226	7.98638	Concanavalin A-like lectin protein kinase family protein
Medtr4g052770	9.84962	8.13728	germin-like protein 5
Medtr3g079570	9.79405	8.15294	serine carboxypeptidase-like 40
Medtr1g028600	9.74879	7.79855	phosphate transporter 1;1
Medtr3g107810	9.74627	7.83577	0
Medtr5g031160	9.71758	8.0359	Concanavalin A-like lectin protein kinase family protein
Medtr5g035640	9.64668	7.66238	0
Medtr5g076900	9.61267	7.80558	glutathione S-transferase TAU 19
Medtr8g012835	9.14895	7.33216	Arabidopsis defensin-like protein
Medtr3g081140	9.04025	7.20519	0
Medtr8g059790	8.96675	7.08113	Kunitz family trypsin and protease inhibitor protein
Medtr3g009880	8.90808	7.30858	FAD-binding Berberine family protein
Medtr3g088965	8.70249	6.81701	0
Medtr7g066070	8.4305	6.29007	Ctr copper transporter family
Medtr2g091215	7.96527	5.89057	Protein of unknown function, DUF538
Medtr8g071050	7.8541	6.40503	0
Medtr8g068530	7.7909	5.95475	U-box domain-containing protein kinase family protein
Medtr2g017750	7.77394	6.03243	nitrate transporter 1:2
Medtr7g086160	7.50311	5.81325	uclacyanin 1
Medtr2g030855	7.48879	6.13163	RmlC-like cupins superfamily protein
Medtr1g109110	7.45121	5.50383	fatty acyl-ACP thioesterases B
Medtr8g055940	7.29507	5.25095	chitinase A
Medtr7g102460	7.17417	5.44485	UDP-glucosyl transferase 73C1
Medtr8g091690	7.13991	5.30092	Cytochrome P450 superfamily protein
Medtr1g040500	6.7579	4.7861	glycerol-3-phosphate acyltransferase 6
Medtr3g078623	6.58582	5.05771	formin 8
Medtr3g079630	6.57553	4.97153	serine carboxypeptidase-like 40
Medtr1g079120	6.44041	4.91118	Subtilisin-like serine endopeptidase family protein
Medtr3g104900	5.98034	4.58532	ACT-like protein tyrosine kinase family protein
Medtr7g070810	5.92936	4.73813	UDP-glucosyl transferase 73B3
Medtr7g070800	5.92564	4.2032	UDP-glucosyl transferase 73B3
Medtr3g086430	5.91001	4.3382	ABC transporter family protein
Medtr2g016730	5.8366	4.11461	related to AP2 11
Medtr2g081600	5.7747	4.31748	nuclear factor Y, subunit C1
Medtr8g103227	5.62093	3.93355	Transducin/WD40 repeat-like superfamily protein

Medtr2g070120	5.49876	3.69924	glutathione S-transferase TAU 20
Medtr6g013440	5.42399	3.77708	UDP-glucosyl transferase 85A3
Medtr4g011120	5.4026	3.96259	RNI-like superfamily protein
Medtr2g104800	5.32724	3.68237	0
Medtr6g043700	5.32645	3.23366	0
Medtr3g107830	5.17015	3.64293	unknown seed protein like 1
Medtr3g118160	5.15989	3.4468	ATPase family associated with various cellular activities
Medtr4g108170	5.14167	3.38825	ABC2 homolog 6
Medtr6g056070	5.12898	3.57363	S-adenosyl-L-methionine-dependent methyltransferases
Medtr2g072260	5.10953	3.32694	cytochrome P450, family 72, subfamily A, polypeptide 1
Medtr3g058000	5.09948	3.11129	cytochrome P450, family 71, subfamily B, polypeptide 3
Medtr3g022830	5.0438	2.88628	scarecrow-like 3
Medtr7g028810	5.00895	3.31609	0
Medtr1g075550	4.93284	3.50868	PLAC8 family protein
Medtr7g076920	4.81469	3.12559	0
Medtr7g077050	4.80983	3.28987	0
Medtr8g091720	4.79743	3.65435	nuclear factor Y, subunit B3
Medtr8g107450	4.6958	3.00271	ABC-2 type transporter family protein
Medtr5g018610	4.67935	2.95027	0
Medtr1g101370	4.66365	3.16515	S-adenosyl-L-methionine-dependent methyltransferases
Medtr3g057980	4.63469	3.05595	cytochrome P450, family 71, subfamily B, polypeptide 3
Medtr2g031270	4.5162	3.44398	RmlC-like cupins superfamily protein
Medtr4g114320	4.42994	2.43803	Mitochondrial substrate carrier family protein
Medtr7g070870	4.42682	2.84207	UDP-glucosyl transferase 73B3
Medtr6g013450	4.29566	2.92507	UDP-Glycosyltransferase superfamily protein
Medtr7g098040	4.22994	2.8307	peptide transporter 3
Medtr3g467150	4.18382	2.76572	extra-large GTP-binding protein 2
Medtr5g030910	3.9312	2.7626	ABC-2 type transporter family protein
Medtr8g103233	3.89145	2.41281	Major facilitator superfamily protein
Medtr8g069775	3.86943	2.1843	nitrate transporter2.5
Medtr1g017910	3.86903	2.05475	exocyst subunit exo70 family protein G1
Medtr2g044100	3.85737	1.95534	GDSL-motif lipase 5
Medtr4g094515	3.8533	2.37902	FAD-binding Berberine family protein
Medtr4g104750	3.80527	2.58225	0
Medtr6g012980	3.76006	2.03377	SNF1 kinase homolog 10
Medtr3g014500	3.72493	2.32737	NB-ARC domain-containing disease resistance protein
Medtr1g098300	3.69379	2.23812	Protein kinase superfamily protein
Medtr1g050525	3.68414	2.56805	pleiotropic drug resistance 6
Medtr4g126930	3.64438	2.26777	Leucine-rich repeat transmembrane protein kinase
Medtr6g079630	3.64362	1.81749	0
Medtr4g102400	3.63102	2.62942	Subtilase family protein
Medtr5g086080	3.62213	2.40431	chitin elicitor receptor kinase 1
Medtr8g036050	3.49403	2.02957	dihydrodipicolinate synthase

Medtr1g069725	3.44487	2.16993	GRAS family transcription factor
Medtr3g011630	3.37247	1.52436	Protein kinase superfamily protein
Medtr2g023150	3.34479	1.93666	Leucine-rich repeat protein kinase family protein
Medtr6g462640	3.33597	1.8266	cytochrome P450, family 71, subfamily B, polypeptide 3
Medtr7g094760	3.31565	2.1286	Receptor-like protein kinase-related family protein
Medtr2g062430	3.30998	1.62343	Plant protein of unknown function (DUF946)
Medtr7g092620	3.23024	2.12915	cytochrome P450, family 93, subfamily D, polypeptide 1
Medtr4g064025	3.22236	1.50756	3-oxo-5-alpha-steroid 4-dehydrogenase family protein
Medtr3g093270	3.14777	1.73521	Major facilitator superfamily protein
Medtr3g021440	3.11653	1.68429	O-methyltransferase 1
Medtr7g111740	3.10093	1.75731	Glycosyl hydrolase superfamily protein
Medtr8g033380	3.0976	1.64382	gibberellin 20 oxidase 2
Medtr3g020880	3.05807	1.61313	0
Medtr2g012790	2.97972	1.55223	Galactose oxidase/kelch repeat superfamily protein
Medtr8g065720	2.96682	2.20881	Thioredoxin superfamily protein
Medtr8g107250	2.94882	1.85375	beta-6 tubulin
Medtr2g062560	2.94868	1.77021	beta-hexosaminidase 2
Medtr6g012970	2.87496	1.81994	related to AP2 11
Medtr3g111900	2.80885	1.58568	AMP-dependent synthetase and ligase family protein
Medtr1g116000	2.80639	1.5937	0
Medtr1g009270	2.80408	1.46564	Leucine-rich repeat protein kinase family protein
Medtr5g010590	2.79987	1.50661	Remorin family protein
Medtr7g105570	2.76498	1.47482	NAD(P)-binding Rossmann-fold superfamily protein
Medtr4g053630	2.7207	1.87912	Subtilisin-like serine endopeptidase family protein
Medtr7g082660	2.71463	1.09716	Plant protein of unknown function (DUF827)
Medtr4g117750	2.70785	1.71201	F-box family protein
Medtr1g080820	2.70413	2.19724	pathogenesis-related 4
Medtr3g058250	2.61534	1.0571	cytochrome P450, family 71, subfamily B, polypeptide 3
Medtr5g083030	2.58327	1.72934	plant U-box 13
Medtr4g130270	2.57523	1.51934	ARIA-interacting double AP2 domain protein
Medtr8g093070	2.43348	2.05007	GRAS family transcription factor
Medtr8g064840	2.41823	1.23208	DC1 domain-containing protein
Medtr7g080950	2.40263	0.916511	UDP-Glycosyltransferase superfamily protein
Medtr0021s0370	2.39766	1.11343	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase s
Medtr8g089190	2.39631	1.25035	cytochrome P450, family 716, subfamily A, polypeptide
Medtr8g068265	2.35878	1.49506	Deoxyxylulose-5-phosphate synthase
Medtr7g117280	2.3437	1.04561	alpha/beta-Hydrolases superfamily protein
Medtr7g112963	2.33832	0.945749	alpha/beta-Hydrolases superfamily protein
Medtr2g437880	2.32914	1.9589	cytochrome P450, family 81, subfamily D, polypeptide 8
Medtr8g068050	2.27992	1.05991	Concanavalin A-like lectin protein kinase family protein
Medtr2g089100	2.27845	0.967669	GRAS family transcription factor
Medtr1g050550	2.2765	0.773947	Major facilitator superfamily protein
Medtr6g027840	2.27226	1.2458	protein kinases;ubiquitin-protein ligases

Medtr3g099740	2.25771	0.901964	purine permease 3
Medtr3g434790	2.2478	1.69447	P-loop containing nucleoside triphosphate hydrolases su
Medtr7g102490	2.19228	1.62283	UDP-glucosyl transferase 73C1
Medtr4g116610	2.18414	0.890161	0
Medtr8g038220	2.10932	0.849897	annexin 8
Medtr1g110290	2.08818	1.03819	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransf
Medtr1g086550	2.07411	1.07163	gibberellin 2-oxidase 6
Medtr4g090600	2.03391	0.950521	sugar transporter 1
Medtr5g026730	1.98693	1.36729	RING/U-box superfamily protein
Medtr3g082200	1.98329	1.07165	Subtilisin-like serine endopeptidase family protein
Medtr4g129010	1.98026	1.23786	Protein kinase superfamily protein
Medtr6g082180	1.96124	1.37846	Heavy metal transport/detoxification superfamily protei
Medtr0045s0060	1.93677	1.61664	cytochrome P450, family 88, subfamily A, polypeptide 3
Medtr1g115195	1.91744	0.836408	glutathione S-transferase tau 7
Medtr1g021638	1.91589	1.2106	cysteine-rich RLK (RECEPTOR-like protein kinase) 26
Medtr7g080180	1.85823	0.795251	serine carboxypeptidase-like 20
Medtr6g015950	1.83682	0.808768	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase su
Medtr5g064990	1.83232	0.711909	RING/U-box superfamily protein
Medtr7g112440	1.82653	1.39622	Protein kinase family protein
Medtr0083s0100	1.81379	1.01663	0
Medtr7g090520	1.81028	0.659839	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase su
Medtr4g127140	1.80762	1.04116	AGAMOUS-like 62
Medtr7g093030	1.79458	1.43658	myb-like HTH transcriptional regulator family protein
Medtr3g020970	1.78424	0.719874	Serine protease inhibitor, potato inhibitor I-type family p
Medtr3g072710	1.76838	1.17385	GRAS family transcription factor
Medtr1g102070	1.76044	0.82218	gibberellin 20 oxidase 2
Medtr6g029180	1.75275	0.99537	related to AP2 11
Medtr5g044220	1.75027	0.746246	Glucose-6-phosphate/phosphate translocator-related
Medtr2g461970	1.74486	0.999925	reversibly glycosylated polypeptide 1
Medtr8g038210	1.70413	0.638672	annexin 8
Medtr0188s0020	1.64446	1.34987	purple acid phosphatase 10
Medtr4g080700	1.64128	1.37084	senescence-associated gene 12
Medtr4g478140	1.59487	0.635016	MLP-like protein 423
Medtr8g045555	1.58689	1.97988	MLP-like protein 43
Medtr1g061540	1.56445	1.28653	Protein of unknown function (DUF668)
Medtr2g099110	1.48094	0.824637	GRAS family transcription factor
Medtr3g109610	1.48068	0.724219	carotenoid cleavage dioxygenase 8
Medtr5g023170	1.4709	1.6852	Rhodanese/Cell cycle control phosphatase superfamily p
Medtr7g062580	1.46805	0.657223	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase su
Medtr2g090240	1.4457	0.801234	alpha/beta-Hydrolases superfamily protein
Medtr8g046240	1.37264	0.947224	cytochrome P450, family 76, subfamily C, polypeptide 6
Medtr6g012960	1.36992	0.992801	0
Medtr6g086560	1.33959	0.625249	alpha/beta-Hydrolases superfamily protein

Medtr1g070135	1.33239	0.643657	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase su
Medtr7g063800	1.29921	1.03156	carotenoid cleavage dioxygenase 8
Medtr4g102280	1.29027	0.787888	cytochrome P450, family 706, subfamily A, polypeptide
Medtr4g133890	1.28948	0.742994	microtubule-associated proteins 70-5
Medtr3g106430	1.09134	0.800882	SPFH/Band 7/PHB domain-containing membrane-associ
Medtr4g097220	0.983834	0.870434	0
Medtr2g105360	0.94618	0.64932	GA requiring 3
Medtr5g030310	0.939335	0.816111	0
Medtr7g075040	0.874958	0.888155	EF hand calcium-binding protein family
Medtr5g026640	0.865377	0.700426	solute:sodium symporters;urea transmembrane transpo
Medtr3g067437	0.853719	1.27221	0
Medtr4g057450	0.840207	0.721659	xyloglucan endotransglucosylase/hydrolase 32
Medtr7g082180	0.837387	0.688643	0
Medtr2g026420	0.81162	0.997231	0
Medtr2g010530	0.801438	1.01273	cytochrome P450, family 71, subfamily B, polypeptide 3
Medtr5g090830	0.799878	0.659976	HXXXD-type acyl-transferase family protein
Medtr1g111510	0.743993	0.739662	Major facilitator superfamily protein
Medtr2g045490	0.722615	0.7775	pyruvate dehydrogenase kinase
Medtr8g041650	0.711831	0.647726	cysteine-rich RLK (RECEPTOR-like protein kinase) 10
Medtr6g092660	0.691818	0.961607	cytidine deaminase 1

rfamily protein

HI4)

genesis-related 1 protein) superfamily protein response to the control condition NM+K. Inf indicates that no transcript was found expressed in the NI

Annotation	AM-K (246)	log2 f.c. AM-K	Annotation	AM-K (265)	log2 f.c. AM-K	Annotation
UDP-Glycosyl	Medtr5g011340	8.4835	Subtilase fam	Medtr8g091320	-4.55672	myo-inositol-
HXXXD-type a	Medtr1g090737	6.855	OPC-8:0 CoA	Medtr6g465030	-2.54719	0
alpha carbon	Medtr1g090707	6.31504	SKU5 similar	Medtr7g062250	-2.5197	laccase 17
	Medtr2g063560	2.86477	HSP20-like ch	Medtr6g039440	-2.35304	terpene synth
	Medtr1g087200	2.64534	Adenine nucl	Medtr1g046070	-2.34444	0
	Medtr4g011230	2.4046	Late embryog	Medtr2g095800	-2.27528	xyloglucan en
	Medtr3g466980	2.27527	AGAMOUS-lil	Medtr3g034640	-2.22218	0
in	Medtr8g042900	2.14694	root hair spe	Medtr1g075230	-2.21875	0
ily protein	Medtr4g029190	2.10615	Peroxidase su	Medtr3g063140	-2.11081	terpene synth
	Medtr3g088845	2.02649	Thiamin diph	Medtr7g013710	-2.01884	0
	Medtr7g108250	1.97414	Thioredoxin s	Medtr8g045735	-1.97078	Polyketide cy
	Medtr6g088320	1.87461	xyloglucan en	Medtr1g054935	-1.96152	ABC-2 type tr
	Medtr5g025800	1.75596	0	Medtr1g074070	-1.92178	nodulin MtN
	Medtr7g092090	1.73762	0	Medtr1g035360	-1.91774	Cyclophilin-lil
amily protein	Medtr1g083440	1.72544	Dormancy/au	Medtr5g094550	-1.90643	cytochrome P
glycoprotein	Medtr4g102450	1.69244	expansin A7	Medtr7g085150	-1.89869	apyrase 2
	Medtr1g023700	1.68266	cytochrome P	Medtr7g057330	-1.88482	F-box family
	Medtr3g085020	1.65014	Protein of un	Medtr3g466200	-1.86661	Peroxidase su
	Medtr7g101270	1.64898	0	Medtr1g062500	-1.79829	Phenazine bio
	Medtr6g084640	1.6426	cold-regulate	Medtr3g465090	-1.7701	terpene synth
	Medtr1g098760	1.6257	0	Medtr5g094540	-1.6958	cytochrome P
	Medtr4g099010	1.61548	Plant inverta	Medtr7g081410	-1.68538	Leucine-rich r
	Medtr7g109920	1.60318	galactinol syr	Medtr7g090590	-1.64305	Gibberellin-re
	Medtr3g102970	1.56649	0	Medtr8g020560	-1.61822	growth-regul
	Medtr1g110870	1.55694	B-box type zi	Medtr4g078535	-1.5837	Leucine-rich r
	Medtr4g055170	1.55133	HXXXD-type a	Medtr4g085790	-1.46949	0
	Medtr4g063940	1.54197	protein kinas	Medtr6g021950	-1.45855	Pectin lyase-l
	Medtr2g437770	1.53209	Peroxidase su	Medtr4g059840	-1.44364	FASCICLIN-lik
	Medtr5g009370	1.5162	highly ABA-in	Medtr5g094560	-1.42983	cytochrome P
	Medtr2g070200	1.4356	glutathione S	Medtr2g069300	-1.42874	2-oxoglutarat
	Medtr4g092640	1.43541	FAD/NAD(P)-	Medtr3g112120	-1.38594	cytochrome P
tein	Medtr8g022990	1.41773	0	Medtr4g069810	-1.38534	0
	Medtr1g066380	1.39955	Peroxidase su	Medtr2g062280	-1.36673	0
	Medtr1g104555	1.38581	receptor-like	Medtr8g018170	-1.35676	disease resist
	Medtr7g068650	1.36576	2-oxoglutarat	Medtr1g018200	-1.33782	beta-galactos

	Medtr1g013100	1.36453	Plant protein	Medtr6g047900	-1.33325	0
	Medtr7g427690	1.33698	homeodoma	Medtr3g034030	-1.32685	Disease resist
	Medtr8g102430	1.31383	MATE efflux f	Medtr1g112210	-1.32185	TRICHOME B
	Medtr8g015250	1.28897	basic leucine	Medtr7g091830	-1.30318	0
	Medtr1173s0010	1.2542	Heavy metal	Medtr1g069935	-1.29601	phosphate tr
	Medtr1g026070	1.24492	RING/U-box s	Medtr7g070390	-1.28494	Disease resist
e 2S albumin s	Medtr8g028600	1.23866	ACC synthase	Medtr8g020990	-1.26824	lipoxygenase
	Medtr4g029200	1.23275	Peroxidase su	Medtr2g040740	-1.26074	chitinase A
	Medtr6g042660	1.21151	Pectin lyase-l	Medtr2g090265	-1.25113	expansin B3
	Medtr4g133800	1.1934	Peroxidase su	Medtr5g094570	-1.23915	cytochrome P
	Medtr5g090740	1.18953	0	Medtr6g078070	-1.22699	Kunitz family
	Medtr2g079990	1.18743	NAC (No Apic	Medtr7g021130	-1.2269	serine carbox
	Medtr4g084480	1.16374	Glycosyl hydr	Medtr8g446430	-1.21323	potassium ch
	Medtr2g017570	1.16366	NOD26-like in	Medtr3g109030	-1.2089	cyclic nucleot
	Medtr7g085220	1.15453	NAC domain	Medtr8g016370	-1.20026	Late embryog
	Medtr7g028780	1.1517	0	Medtr5g074680	-1.19977	O-methyltran
	Medtr8g066860	1.12649	0	Medtr4g066380	-1.19872	basic helix-lo
	Medtr4g063945	1.10994	Protein kinas	Medtr2g102450	-1.19045	AP2/B3-like t
	Medtr4g066240	1.10922	beta glucosid	Medtr5g091050	-1.18969	hydroxy meth
	Medtr5g090250	1.10372	Serine protea	Medtr4g087890	-1.18454	formin homo
	Medtr3g106420	1.09648	SPFH/Band 7	Medtr6g088810	-1.18304	Pectin lyase-l
	Medtr4g132010	1.07489	0	Medtr8g085390	-1.17792	Carbohydrate
	Medtr4g017050	1.07476	RmlC-like cup	Medtr6g012730	-1.16197	Pyridoxal pho
	Medtr2g030100	1.07042	Plant self-inc	Medtr6g017150	-1.15611	0
	Medtr8g059170	1.06036	NAC (No Apic	Medtr2g032710	-1.15379	Pectin lyase-l
	Medtr3g101960	1.05792	HXXXD-type a	Medtr4g109140	-1.14977	Protein of un
	Medtr7g112560	1.05244	phloem prote	Medtr1g057560	-1.14561	exocyst subu
	Medtr3g096400	1.04259	xylem NAC do	Medtr4g079760	-1.12247	basic helix-lo
	Medtr2g080010	1.03573	NAC domain	Medtr8g086600	-1.11838	cellulose synt
	Medtr4g039540	1.032	0	Medtr3g099580	-1.11399	Cupredoxin s
	Medtr1g077890	1.01764	methionine g	Medtr4g094212	-1.11252	tobamovirus
	Medtr2g068880	1.01085	NAC domain	Medtr2g462000	-1.10633	COBRA-like e
	Medtr8g026960	1.01068	homeobox 7	Medtr2g102730	-1.10082	Phototropic-r
	Medtr8g019370	1.00329	0	Medtr4g065370	-1.10082	Integrase-typ
	Medtr8g023790	1.00052	photosystem	Medtr7g092580	-1.09743	0
	Medtr5g083500	1.0002	0	Medtr2g043900	-1.09145	Riboflavin syn
	Medtr3g106480	0.99898	SPFH/Band 7	Medtr0011s0020	-1.0787	cellulose synt
	Medtr3g071470	0.998387	Pollen Ole e 1	Medtr4g027800	-1.07801	lipid transfer
	Medtr2g034350	0.997015	0	Medtr2g018990	-1.06881	Protein kinas
	Medtr3g092400	0.996036	0	Medtr7g417750	-1.05184	allene oxide c
	Medtr5g016410	0.995309	cytochrome P	Medtr6g044780	-1.03997	Kunitz family
	Medtr3g114530	0.99111	DC1 domain-	Medtr3g091620	-1.03985	RING/U-box s
	Medtr4g094550	0.990909	0	Medtr4g023550	-1.03036	0

	Medtr8g432390	0.986459	BON associat	Medtr1g071450	-1.02267	Plant protein
	Medtr5g091060	0.985974	phytoene de	Medtr1g044130	-1.01123	Ribosomal pr
	Medtr1g081840	0.982386	gibberellin 2	Medtr2g093980	-0.992054	FASCICLIN-lik
	Medtr5g020060	0.981838	0	Medtr2g072270	-0.977147	cytochrome
	Medtr4g076255	0.979052	Glycosyl hydr	Medtr3g115120	-0.976342	Protein of un
	Medtr4g128410	0.978643	xyloglucan e	Medtr3g087740	-0.972965	slufate transp
(AAA)	Medtr4g094302	0.976509	xylem NAC d	Medtr1g075180	-0.963947	0
	Medtr4g134290	0.962912	phosphofruct	Medtr1g101120	-0.961244	PAR1 protein
s superfamily	Medtr3g091350	0.960239	2-oxoglutara	Medtr3g106290	-0.949811	Integrase-typ
5	Medtr3g078160	0.959655	plant U-box 1	Medtr6g047880	-0.945563	0
5	Medtr3g460790	0.959422	nudix hydrol	Medtr8g065010	-0.944741	Pectin lyase-l
	Medtr1g069805	0.95086	NAC domain	Medtr4g132840	-0.943695	EPS15 homol
	Medtr4g094340	0.950644	nodulin MtN	Medtr8g102800	-0.936551	Integrase-typ
	Medtr1g035690	0.944121	glutaredoxin-	Medtr1g026740	-0.936368	Major facilita
	Medtr8g096320	0.940383	Nodulin MtN	Medtr5g078215	-0.934422	0
	Medtr2g104910	0.935843	golgi snare 1	Medtr4g128770	-0.931341	CAP (Cystein
	Medtr7g112860	0.933067	Dormancy/a	Medtr1g084050	-0.925818	nicotianamin
	Medtr6g464320	0.932511	carboxyester	Medtr5g085850	-0.917473	Major facilita
	Medtr3g057800	0.92513	cytochrome	Medtr4g011970	-0.916275	sulfate transp
s superfamily	Medtr5g005850	0.923686	alpha/beta-H	Medtr8g479390	-0.915384	SKU5 similar
4	Medtr1g100777	0.921951	heat shock tr	Medtr4g053380	-0.913703	FASCICLIN-lik
	Medtr8g445170	0.921322	BURP domai	Medtr3g118010	-0.909451	plasma mem
	Medtr0189s0010	0.921183	mitogen-acti	Medtr3g071890	-0.903513	laccase 12
	Medtr7g102770	0.912956	Pollen Ole e	Medtr3g014290	-0.894466	Eukaryotic as
	Medtr7g100100	0.891603	C2H2 and C2	Medtr5g084260	-0.892212	0
	Medtr1g019110	0.890398	DREB and EA	Medtr5g021840	-0.890387	0
	Medtr3g051530	0.886476	0	Medtr3g028740	-0.887365	myb domain
	Medtr1g043350	0.88618	ethylene resp	Medtr3g070850	-0.885343	Double Clp-N
	Medtr7g099800	0.885528	cation/H+ ex	Medtr3g116440	-0.880237	0
	Medtr2g088930	0.884781	Receptor-like	Medtr4g007740	-0.878427	Eukaryotic as
	Medtr3g435530	0.873233	0	Medtr8g087450	-0.868708	FASCICLIN-lik
	Medtr5g011990	0.87011	0	Medtr4g065017	-0.867025	myb domain
	Medtr3g103580	0.853852	branched-ch	Medtr4g132270	-0.8659	glyoxalase I h
	Medtr5g066020	0.850482	Predicted AT	Medtr8g090265	-0.86166	0
	Medtr0015s0030	0.846003	Concanavalin	Medtr4g031820	-0.857034	cytochrome
	Medtr8g432400	0.844134	BON associat	Medtr8g069925	-0.853955	0
	Medtr2g035430	0.837742	cationic amin	Medtr5g004980	-0.849187	0
	Medtr2g094790	0.833894	Putative lysin	Medtr5g021180	-0.848342	thioredoxin
	Medtr4g066580	0.83046	beta glucosid	Medtr2g017980	-0.84728	AAA-type AT
	Medtr4g087920	0.829365	basic helix-lo	Medtr8g013680	-0.844861	delta tonopla
	Medtr7g017880	0.826473	basic leucine	Medtr3g075320	-0.831328	Pectate lyase
	Medtr7g108650	0.822572	TSPO(outer	Medtr5g009660	-0.831198	Leucine-rich
	Medtr3g108860	0.820863	Galactose ox	Medtr2g026760	-0.828899	Bifunctional

	Medtr4g012850	0.82059	Mitochondria	Medtr0246s0020	-0.818683	basic helix-lo
	Medtr1g018320	0.814333	alpha/beta-H	Medtr1g100787	-0.813069	Leucine-rich r
	Medtr8g069450	0.812864	Tetratricopep	Medtr1g070220	-0.794031	lateral organ
5	Medtr3g028210	0.809017	HXXXD-type a	Medtr2g093990	-0.793381	FASCICLIN-lik
	Medtr4g485550	0.808822	Leucine-rich r	Medtr3g095480	-0.793112	0
	Medtr4g115330	0.805225	Raffinose syn	Medtr5g019220	-0.789816	galacturonosy
	Medtr1g027580	0.799808	wall-associat	Medtr2g055470	-0.788493	cytochrome P
	Medtr1g103290	0.798259	homocystein	Medtr5g040420	-0.78823	NAC (No Apic
	Medtr4g011020	0.797588	Lactoylglutat	Medtr7g074935	-0.786303	AT-hook moti
	Medtr7g115120	0.794307	bZIP transcrip	Medtr3g083620	-0.785749	O-methyltran
	Medtr2g070870	0.788645	Arabidopsis t	Medtr4g063130	-0.782898	Domain of un
	Medtr4g089020	0.788211	cytochrome P	Medtr5g031880	-0.782153	AINTEGUMEN
	Medtr1g006695	0.78326	Regulator of	Medtr1g030630	-0.775181	Heavy metal t
	Medtr6g088525	0.782881	0	Medtr8g102400	-0.775027	IQ-domain 26
	Medtr8g009110	0.780313	2-oxoglutarat	Medtr2g081590	-0.774732	BURP domain
	Medtr4g067040	0.780009	beta glucosid	Medtr4g105430	-0.773737	UBX domain-
	Medtr1g098460	0.769413	Integrase-typ	Medtr6g027920	-0.768812	Cobalamin-in
	Medtr2g024010	0.768866	Stigma-specif	Medtr3g076930	-0.766784	P-loop contai
	Medtr1g086510	0.766856	myb domain	Medtr5g022870	-0.766369	Peroxidase su
	Medtr2g080280	0.765907	0	Medtr1g088885	-0.764506	Phototropic-r
	Medtr1g013090	0.76448	pre-mRNA sp	Medtr2g022370	-0.762521	Eukaryotic as
	Medtr3g070880	0.764246	zinc finger (C	Medtr6g066190	-0.76051	Kunitz family
	Medtr5g041940	0.759543	NAC-like, acti	Medtr4g050590	-0.75968	Protein of un
	Medtr3g092150	0.758473	homeobox 7	Medtr5g022530	-0.748322	Protein of un
	Medtr8g099065	0.756211	P-loop contai	Medtr3g086090	-0.746634	TPX2 (targetin
	Medtr2g034720	0.753687	beta-xylosida	Medtr5g041700	-0.743239	expansin A15
	Medtr6g027660	0.752499	cationic amin	Medtr2g017950	-0.73421	FASCICLIN-lik
5	Medtr4g011060	0.75021	0	Medtr0006s0240	-0.730991	NB-ARC doma
	Medtr5g082150	0.749788	ortholog of su	Medtr2g096900	-0.730156	outer plastid
	Medtr7g106820	0.749426	0	Medtr7g011060	-0.728681	expansin A15
	Medtr1g083580	0.749033	phloem prote	Medtr8g098360	-0.727753	beta-6 tubulin
	Medtr2g435690	0.747553	0	Medtr2g090660	-0.725261	0
	Medtr3g104780	0.740258	17.6 kDa clas	Medtr2g081050	-0.72481	HSP20-like ch
uperfamily pro	Medtr4g082360	0.738343	0	Medtr3g112370	-0.724315	beta-galactos
1	Medtr3g111800	0.737434	Protein of un	Medtr8g023310	-0.723085	pectin methy
	Medtr4g129270	0.733183	trehalose pho	Medtr1g013040	-0.722501	Protein kinas
	Medtr2g075550	0.731549	0	Medtr2g014400	-0.721881	0
	Medtr5g066330	0.730249	0	Medtr4g081950	-0.721406	expansin A1
	Medtr4g105250	0.729656	Raffinose syn	Medtr4g116870	-0.719192	Minichromos
	Medtr7g069740	0.729102	RGA-like 1	Medtr8g024060	-0.718189	Protein kinas
	Medtr4g088760	0.728159	Protein of un	Medtr8g100135	-0.716392	cytochrome P
	Medtr4g081500	0.726895	0	Medtr8g098835	-0.713338	Protein of un
	Medtr1g032010	0.726333	tolB protein-r	Medtr7g062310	-0.710235	laccase 17

	Medtr0001s0660	0.721128	Zinc-binding	Medtr2g086580	-0.709801	Rho GTPase a
uperfamily pro	Medtr4g129020	0.719983	glutamine du	Medtr7g056103	-0.709478	cytochrome P
	Medtr6g015815	0.7156	HXXXD-type a	Medtr8g070700	-0.709252	Domain of un
	Medtr5g013440	0.699165	expansin-like	Medtr5g091690	-0.70812	phy rapidly re
	Medtr1g092420	0.694711	0	Medtr7g103440	-0.706207	Leucine-rich r
erase family p	Medtr0015s0090	0.69148	Concanavalin	Medtr8g018040	-0.706163	disease resist
	Medtr7g117415	0.690652	Protein with	Medtr4g011720	-0.70252	2-oxoglutarat
	Medtr5g082130	0.690262	Tetratricopep	Medtr7g096090	-0.702487	indole-3-acet
	Medtr5g079950	0.687385	expansin A4	Medtr5g054730	-0.702081	Transmembra
	Medtr1g105885	0.687261	cysteine-rich	Medtr4g036990	-0.695675	0
	Medtr1g007905	0.682399	0	Medtr1g098680	-0.695283	0
in	Medtr2g435310	0.682354	MLP-like prot	Medtr5g078210	-0.69495	SGNH hydrola
	Medtr1g097910	0.680104	Chalcone and	Medtr2g016460	-0.694608	Xanthine/ura
	Medtr2g086920	0.679323	F-box family	Medtr3g102180	-0.693372	Leucine-rich r
	Medtr1g102370	0.678372	basic helix-lo	Medtr8g075100	-0.692152	Peroxidase su
	Medtr7g024765	0.677612	Acyl-CoA N-a	Medtr5g017260	-0.691392	alpha/beta-H
uperfamily pro	Medtr7g024280	0.675501	delta(3), delt	Medtr4g128750	-0.691052	CAP (Cysteine
	Medtr6g028100	0.672787	Glycosyl hydr	Medtr3g106510	-0.690556	0
	Medtr8g015220	0.672469	myo-inositol	Medtr8g044230	-0.690184	Leucine-rich r
	Medtr1g015410	0.669822	cytokinin oxi	Medtr1g105495	-0.689151	xyloglucan en
uperfamily pro	Medtr1g028300	0.668307	highly ABA-in	Medtr2g007960	-0.688989	nodulin MtN2
	Medtr4g108830	0.668084	RING/U-box s	Medtr2g034810	-0.688566	0
	Medtr8g039090	0.66616	NADPH:quino	Medtr2g063110	-0.687395	Eukaryotic as
protein	Medtr5g071560	0.662624	mitogen-activ	Medtr4g063090	-0.683901	gamma tonop
	Medtr4g478130	0.661528	0	Medtr4g100590	-0.682043	2-oxoglutarat
	Medtr8g079360	0.661068	Disease resis	Medtr5g015840	-0.680612	0
	Medtr4g100975	0.659203	0	Medtr7g105850	-0.680191	Eukaryotic as
	Medtr8g105190	0.657882	0	Medtr5g063620	-0.678126	histone H4
	Medtr2g096120	0.652989	0	Medtr8g018690	-0.676766	PLAT/LH2 do
	Medtr3g102980	0.651629	salt tolerance	Medtr5g074500	-0.676028	Nuclear trans
	Medtr3g030850	0.651351	Photosystem	Medtr4g088055	-0.674799	RAC-like 2
	Medtr2g061780	0.650561	0	Medtr4g011880	-0.67428	indole-3-acet
	Medtr1g106730	0.650127	salt tolerance	Medtr5g015260	-0.672706	Galactosyl tra
	Medtr4g104540	0.648913	cytochrome P	Medtr5g064345	-0.672646	Phosphate-re
	Medtr6g027480	0.646069	0	Medtr6g088670	-0.672134	ABC transpor
	Medtr4g081870	0.645083	NAC-like, acti	Medtr2g062730	-0.671113	NAC (No Apic
	Medtr3g104030	0.644227	Protein of Un	Medtr8g072010	-0.670666	Pectinacetyle
protein	Medtr3g084990	0.640596	0	Medtr3g085270	-0.670463	Protein of un
uperfamily pro	Medtr3g075390	0.63938	Cysteine prot	Medtr2g094060	-0.670173	beta-galactos
	Medtr3g078240	0.639098	NHL domain-	Medtr2g097030	-0.669238	expansin A4
	Medtr7g095170	0.638035	Protein of un	Medtr4g485630	-0.662561	UDP-glucosyl
	Medtr5g024020	0.636183	lipoxygenase	Medtr1g084120	-0.662225	Galactose oxi
	Medtr8g104290	0.635854	0	Medtr7g059080	-0.660551	0

uperfamily pr	Medtr1g075340	0.634131	Serine protea	Medtr8g104820	-0.660548	glycosyl hydr
	Medtr4g107720	0.632365	SPFH/Band 7,	Medtr3g081030	-0.659343	RING/U-box s
4	Medtr3g464580	0.630302	glutamine-de	Medtr7g024480	-0.654957	0
	Medtr4g080020	0.629324	RNI-like supe	Medtr4g073770	-0.652035	like AUXIN RE
ated protein f	Medtr1g077660	0.628815	Aluminium ac	Medtr5g081560	-0.649626	RING/FYVE/P
	Medtr1g105555	0.628513	0	Medtr0305s0020	-0.647959	Calcium-depe
	Medtr6g033280	0.628393	phosphate tr	Medtr3g087700	-0.647218	Protein of un
	Medtr1g104610	0.628386	Haloacid deh	Medtr4g075690	-0.644894	SKU5 similar
	Medtr4g122800	0.6255	cell wall / vac	Medtr1g085500	-0.642443	germin-like p
rters	Medtr4g007710	0.624548	0	Medtr4g063630	-0.639976	Pathogenesis
	Medtr2g019370	0.623936	gibberellin 2-	Medtr3g109450	-0.63871	Protein of un
	Medtr4g006970	0.623268	CBL-interacti	Medtr3g108290	-0.638677	Protein of un
	Medtr2g031590	0.623067	FAD-binding	Medtr3g115050	-0.637193	SKU5 similar
	Medtr5g029910	0.622657	Tetratricopep	Medtr7g096880	-0.636795	phosphate tr
5	Medtr1g015650	0.619257	0	Medtr6g022020	-0.635844	Ubiquitin-like
	Medtr4g128840	0.619148	xylose isome	Medtr5g019120	-0.632865	PQ-loop repe
	Medtr5g091930	0.616455	citrate syntha	Medtr8g099375	-0.631881	0
	Medtr1g074170	0.615213	electron tran	Medtr1g071480	-0.631126	NIMA-related
	Medtr6g016650	0.614782	Methylenete	Medtr5g018110	-0.630182	Reticulan like
	Medtr7g108260	0.611886	Thioredoxin s	Medtr7g061020	-0.63009	ATP binding r
	Medtr4g085890	0.611316	3-methylcrot	Medtr4g074190	-0.627416	Phototropic-r
	Medtr4g051515	0.608403	plant U-box 2	Medtr4g088735	-0.626721	Pollen Ole e 1
	Medtr4g094332	0.606515	Vacuolar iron	Medtr7g051910	-0.625045	Auxin-respon
	Medtr3g102100	0.60607	related to AP	Medtr8g063940	-0.623938	spermidine sy
	Medtr3g070230	0.605817	ortholog of su	Medtr1g099150	-0.620834	0
	Medtr8g066820	0.603724	PLATZ transc	Medtr1g019800	-0.620544	0
	Medtr5g017850	0.603173	Peroxidase su	Medtr1g090987	-0.617974	cytochrome P
	Medtr4g118800	0.600901	Uncharacteri	Medtr4g104320	-0.617972	Pectin lyase-l
	Medtr6g086805	0.600735	heat shock tr	Medtr4g094925	-0.61443	S-adenosyl-L-
	Medtr4g089100	0.59736	Protein of un	Medtr4g081220	-0.613566	Pentatricopep
	Medtr1g034030	0.597088	Protein kinas	Medtr1g047370	-0.612142	Pectin lyase-l
	Medtr2g039320	0.592756	0	Medtr2g065360	-0.611164	cytochrome P
	Medtr6g088500	0.591629	NAD(P)-bindi	Medtr4g048060	-0.610493	0
	Medtr8g041620	0.590847	2-oxoglutarat	Medtr2g084020	-0.609931	Peroxidase su
	Medtr0113s0040	0.589313	phloem prote	Medtr1g087240	-0.609161	beta-xylosida
	Medtr5g053920	0.587963	AP2/B3 trans	Medtr3g060880	-0.608796	Leucine-rich r
	Medtr3g092720	0.587754	30S ribosoma	Medtr4g023730	-0.607921	NAD(P)-bindi
	Medtr7g095960	0.587405	Protein of un	Medtr6g059760	-0.607686	Kunitz family
	Medtr7g093040	0.585554	0	Medtr8g076160	-0.606338	Lactoylglutatl
				Medtr2g089490	-0.605332	Cyclin D6;1
				Medtr4g014070	-0.605274	inflorescence
				Medtr4g107110	-0.604833	ARM repeat s
				Medtr4g057470	-0.604402	Protein of un

Medtr7g028740	-0.602335	Squamosa pr
Medtr8g035780	-0.599937	cytochrome F
Medtr7g026340	-0.595415	O-Glycosyl hy
Medtr4g066460	-0.594416	basic helix-loo
Medtr2g070730	-0.593471	interactor of
Medtr3g014280	-0.592413	sequence-spe
Medtr8g022870	-0.591742	Subtilase fam
Medtr2g105390	-0.589674	tubby like pro
Medtr4g101310	-0.589449	Bifunctional i
Medtr3g074930	-0.588543	purple acid p
Medtr7g081750	-0.587984	Subtilase fam
Medtr5g017160	-0.587567	ralf-like 34
Medtr1g028610	-0.585923	arabinogalact
Medtr8g036080	-0.585658	SEC7-like gua
Medtr8g089745	-0.585355	Melibiase fan

M+K dataset. Transcripts were annotated with the Mt4.0v1 version of M. truncatula genomic data

AM-K & NM-K (115)	log2 f.c. AM-K	log2 f.c. NM-K	Annotation	AM-K & NM-K (88)	log2 f.c. AM-K	log2 f.c. NM-K
Medtr5g064060	4.36151	3.57357	HSP20-like ch	Medtr4g033200	-2.71108	-1.09344
Medtr6g078250	3.74545	3.59813	Kunitz family	Medtr4g087810	-2.44991	-1.23116
Medtr6g078280	3.66779	2.90316	Kunitz family	Medtr2g055940	-2.28557	-1.21548
Medtr5g081530	3.48819	3.59721	HSP20-like ch	Medtr4g095010	-1.8417	-1.53393
Medtr4g086750	3.19828	1.73828	Cupredoxin s	Medtr7g405710	-1.73632	-1.89221
Medtr4g086740	3.05608	1.76327	Cupredoxin s	Medtr2g087470	-1.5354	-1.45906
Medtr8g466220	2.87403	2.63485	Leucine-rich r	Medtr4g033085	-1.48612	-1.06185
Medtr4g017200	2.8295	1.71014	Thiamine pyr	Medtr7g070910	-1.39537	-1.16091
Medtr8g088830	2.67966	1.27902	plantacyanin	Medtr6g087780	-1.36167	-0.762031
Medtr1g015165	2.65897	2.62677	17.6 kDa clas	Medtr8g088330	-1.35421	-0.927998
Medtr8g093560	2.52908	2.27813	chloroplastic	Medtr4g078885	-1.3024	-1.32751
Medtr4g106860	2.4905	1.51169	Gibberellin-re	Medtr7g070740	-1.2782	-0.861948
Medtr8g075780	2.39854	1.43051	Chaperone D	Medtr4g033170	-1.27338	-0.821685
Medtr4g090525	2.39266	1.04389	HAL2-like	Medtr6g022040	-1.26935	-0.897474
Medtr3g087280	2.28542	2.69031	0	Medtr5g025730	-1.23867	-1.45854
Medtr3g086200	2.0726	2.88649	0	Medtr2g088190	-1.2189	-0.719258
Medtr2g007970	1.98553	3.48148	nodulin MtN	Medtr7g085120	-1.19859	-0.797378
Medtr1g066640	1.97853	1.07482	Peroxidase su	Medtr4g117670	-1.14499	-0.907592
Medtr8g461390	1.96195	1.50753	SOUL heme-b	Medtr2g040830	-1.12602	-0.717756
Medtr2g045280	1.91601	1.17989	Cytidine/deo	Medtr5g034810	-1.11978	-0.926011
Medtr3g030540	1.87571	1.07383	Pectin lyase-l	Medtr7g070930	-1.11096	-0.73156
Medtr6g059410	1.83902	1.10406	kunitz trypsin	Medtr0118s0070	-1.10997	-0.60346
Medtr4g081380	1.83562	0.867099	C-terminal cy	Medtr4g062500	-1.06323	-1.96034
Medtr1g103150	1.79516	1.14321	Acyl-CoA N-a	Medtr2g044810	-1.03467	-0.595938
Medtr3g098580	1.77398	2.29116	Integrase-typ	Medtr2g087390	-1.03454	-1.22953
Medtr1g088110	1.70375	0.720833	Pollen Ole e 1	Medtr2g008225	-1.02977	-0.767911
Medtr4g130540	1.68067	1.7221	heat shock pr	Medtr3g070290	-1.02092	-0.658775
Medtr2g022490	1.66791	1.33757	Eukaryotic as	Medtr7g062550	-1.00565	-1.8818
Medtr7g086320	1.66483	2.94028	0	Medtr0088s0100	-1.00556	-1.00083
Medtr3g107500	1.65542	1.04342	plant natriure	Medtr5g069180	-1.00242	-0.660775
Medtr6g061850	1.58356	1.63229	HSP20-like ch	Medtr5g081030	-0.977034	-1.22837
Medtr3g024520	1.57991	1.09907	Cytochrome I	Medtr4g094828	-0.971991	-0.690146
Medtr8g096900	1.57238	0.952874	osmotin 34	Medtr4g032750	-0.971897	-0.749561
Medtr7g102380	1.55525	1.61299	Pathogenesis	Medtr7g065740	-0.968115	-1.68541
Medtr1g029500	1.50343	1.19818	F-box/RNI-lik	Medtr7g104460	-0.968057	-1.4291

Medtr3g100470	1.50088	1.87083	Predicted AT-	Medtr4g022290	-0.939143	-0.912601
Medtr8g102350	1.49359	0.90281	oxidative stre	Medtr1g035770	-0.93033	-0.802931
Medtr8g089110	1.4214	1.07979	plantacyanin	Medtr5g040250	-0.913293	-0.888488
Medtr4g080360	1.3808	1.45599	Cysteine prot	Medtr1g061340	-0.909182	-0.749421
Medtr4g091590	1.34999	2.28681	HSP20-like ch	Medtr7g114990	-0.898454	-0.83325
Medtr7g045860	1.34547	0.803489	Protein kinas	Medtr8g039540	-0.89657	-0.830587
Medtr3g449930	1.33511	1.55881	photosystem	Medtr2g023680	-0.889291	-0.742794
Medtr4g035880	1.29469	1.38938	Plant inverta	Medtr7g059285	-0.876601	-0.889949
Medtr7g102520	1.28894	1.50418	UDP-Glycosyl	Medtr8g069770	-0.875018	-0.985465
Medtr6g452730	1.27894	1.40566	PAR1 protein	Medtr1g087710	-0.846797	-0.708341
Medtr2g027550	1.27366	1.45411	0	Medtr1g019715	-0.824975	-0.666767
Medtr3g064350	1.22317	1.21115	oxidative stre	Medtr4g077160	-0.823287	-1.05208
Medtr1g017700	1.22242	0.75599	phytosulfokir	Medtr5g083960	-0.815699	-0.623977
Medtr7g103390	1.21511	2.03136	0	Medtr4g051880	-0.815555	-0.739296
Medtr7g107710	1.19654	0.78409	Flavin-contai	Medtr1g104840	-0.80896	-0.790534
Medtr7g079900	1.17834	1.32078	photosystem	Medtr5g016320	-0.808888	-1.53606
Medtr7g096830	1.17159	1.27157	ethylene-resp	Medtr4g088870	-0.791803	-0.906272
Medtr4g066210	1.15638	0.808154	beta glucosid	Medtr2g436710	-0.762097	-0.672426
Medtr7g117900	1.15609	0.89955	ATPase, F1 cc	Medtr2g080230	-0.760011	-0.894008
Medtr8g107010	1.15421	1.22743	FKBP-like pep	Medtr7g026990	-0.759658	-1.12505
Medtr2g034360	1.13459	0.908426	0	Medtr8g006270	-0.751752	-1.33167
Medtr4g088450	1.11537	0.979063	HSP20-like ch	Medtr3g083230	-0.746573	-0.811191
Medtr3g077870	1.1117	1.76349	similar to RCI	Medtr5g071200	-0.732469	-0.814098
Medtr8g085650	1.10531	0.599627	Galactose oxi	Medtr7g083110	-0.725256	-0.779711
Medtr3g103960	1.10467	1.8242	CCCH-type zi	Medtr5g040940	-0.724138	-1.08022
Medtr8g096880	1.09725	0.698475	UDP-D-gluco	Medtr1g107460	-0.718119	-0.805371
Medtr8g074040	1.06396	0.797997	AMP-depend	Medtr2g055430	-0.71438	-0.827122
Medtr6g090460	1.04089	0.748138	oxidative stre	Medtr3g086310	-0.711563	-0.721705
Medtr8g094980	1.02019	0.919041	SAUR-like aux	Medtr4g071090	-0.709992	-0.855956
Medtr8g022300	1.0196	0.725453	Dormancy/au	Medtr5g061880	-0.702641	-0.880902
Medtr1g030600	0.999947	1.5365	nodulin MtN2	Medtr8g019730	-0.6947	-0.762537
Medtr6g037610	0.981083	1.09063	Integrase-typ	Medtr3g464720	-0.694078	-0.65011
Medtr3g106920	0.975493	1.01374	0	Medtr4g094285	-0.693213	-0.616699
Medtr5g022210	0.951758	0.703816	Chaperone D	Medtr8g028460	-0.688815	-0.741272
Medtr7g084000	0.94296	0.801788	CCR-like	Medtr5g089170	-0.684954	-0.728499
Medtr3g076960	0.934376	1.23072	0	Medtr6g048910	-0.6797	-0.764931
Medtr2g093760	0.931085	1.35888	0	Medtr4g011630	-0.675508	-0.77298
Medtr4g022920	0.911117	1.34364	tobamovirus	Medtr4g005190	-0.670585	-0.655115
Medtr4g098930	0.906091	0.730434	expansin-like	Medtr8g018590	-0.670158	-0.669985
Medtr8g010320	0.896596	0.929908	low-molecula	Medtr7g080460	-0.666378	-0.821698
Medtr1g083950	0.892393	1.7899	Adenine nucl	Medtr7g053500	-0.665794	-0.619197
Medtr1g052470	0.842603	0.63999	basic helix-lo	Medtr5g037930	-0.66511	-0.718586
Medtr7g066690	0.816643	0.667521	plant uncoup	Medtr7g111500	-0.662513	-1.10145

Medtr8g096860	0.813606	0.805148	0
Medtr5g083690	0.805975	1.13876	dehydration-
Medtr2g016650	0.805715	1.48078	0
Medtr6g008560	0.800548	0.762568	terpene synt
Medtr3g053890	0.799141	0.764036	alanine:glyox
Medtr3g062600	0.786251	0.793753	Ribosomal pr
Medtr7g016060	0.785418	2.03235	B12D protein
Medtr4g121930	0.770603	0.698551	0
Medtr3g466180	0.762746	0.656326	Peroxidase s
Medtr2g008710	0.762348	0.661104	Peroxidase s
Medtr8g091590	0.75691	1.49546	0
Medtr5g062190	0.753231	1.01878	0
Medtr3g072170	0.749199	1.9811	Hypoxia-responsive family protein
Medtr1g090683	0.748804	0.638406	Protein of unknown function (DUF594)
Medtr8g075510	0.742632	0.713265	Pathogenesis-related thaumatin superfamily protein
Medtr2g013140	0.739469	0.611734	Aluminium induced protein with YGL and LRDR motifs
Medtr0018s0170	0.73004	1.21967	Galactose oxidase/kelch repeat superfamily protein
Medtr5g022390	0.716216	1.61974	sulfurtransferase 18
Medtr3g087278	0.711619	0.636765	0
Medtr7g072575	0.707287	0.841455	SOS3-interacting protein 1
Medtr1g030480	0.705755	0.770282	Pheophorbide a oxygenase family protein with Rieske [2
Medtr8g009090	0.703379	0.620523	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase s
Medtr4g057310	0.697796	0.987831	CHY-type/CTCHY-type/RING-type Zinc finger protein
Medtr7g065150	0.68681	0.614849	0
Medtr7g086340	0.674311	0.612821	0
Medtr5g089820	0.670673	0.591565	0
Medtr8g094290	0.656945	1.01456	amino acid permease 2
Medtr2g014240	0.653548	0.64463	dormancy-associated protein-like 1
Medtr6g059530	0.652451	0.845735	kunitz trypsin inhibitor 1
Medtr2g021150	0.640301	0.606486	F-box and associated interaction domains-containing pr
Medtr7g077180	0.620701	0.66755	0
Medtr2g021690	0.601953	0.58987	Family of unknown function (DUF716)
Medtr8g083450	0.59825	0.736639	0
Medtr1g088640	0.594906	1.25979	Adenine nucleotide alpha hydrolases-like superfamily pr
Medtr2g010590	0.592388	0.720985	basic pathogenesis-related protein 1
Medtr1g038680	0.588104	0.59106	Peroxidase superfamily protein
Medtr3g013500	0.58564	0.709349	sulfotransferase 2A

Medtr2g069090	-0.659523	-0.646106
Medtr3g099620	-0.64291	-0.679599
Medtr2g098180	-0.640278	-0.647521
Medtr4g077590	-0.632039	-0.910972
Medtr7g098610	-0.624839	-0.878339
Medtr3g090760	-0.623715	-0.796455
Medtr5g057990	-0.61989	-0.74361
Medtr0059s0170	-0.618779	-1.16453
Medtr1g105595	-0.608041	-0.803718
Medtr7g076150	-0.59522	-0.639115

-type 1
Pase family protein
st integral protein
family protein
repeat protein kinase family protein
nhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein

op-helix (bHLH) DNA-binding superfamily protein
repeat transmembrane protein kinase
boundaries-domain 16
e arabinogalactan-protein 11

yltransferase-like 2
P450, family 72, subfamily A, polypeptide 15
al Meristem) domain transcriptional regulator superfamily protein
if nuclear-localized protein 1
sferase family protein
nknown function (DUF966)
NTA-like 6
transport/detoxification superfamily protein
5
n-containing protein
containing protein
dependent synthase family protein
ning nucleoside triphosphate hydrolases superfamily protein
uperfamily protein
responsive NPH3 family protein
partyl protease family protein
trypsin and protease inhibitor protein
known function (DUF3049)
known function (DUF630) ;Protein of unknown function (DUF632)
ng protein for Xklp2) protein family

e arabinogalactan-protein 11
ain-containing disease resistance protein
envelope protein 16-1

n

haperones superfamily protein
sidase 5
lesterase 3
e superfamily protein

ome maintenance (MCM2/3/5) family protein
e superfamily protein
P450, family 716, subfamily A, polypeptide 1
known function (DUF604)

activating protein with PAK-box/P21-Rho-binding domain
P450, family 93, subfamily D, polypeptide 1
nknown function (DUF23)
egulated 1
repeat protein kinase family protein
tance protein (TIR-NBS-LRR class), putative
te (2OG) and Fe(II)-dependent oxygenase superfamily protein
ic acid inducible 14
ane amino acid transporter family protein

ase-type esterase superfamily protein
cil permease family protein
repeat protein kinase family protein
uperfamily protein
ydrolases superfamily protein
e-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein

repeat protein kinase family protein
ndotransglucosylase/hydrolase 8
21 /EamA-like transporter family protein

partyl protease family protein
plast intrinsic protein
te (2OG) and Fe(II)-dependent oxygenase superfamily protein

partyl protease family protein

main-containing lipoxygenase family protein
sport factor 2 (NTF2) family protein

ic acid inducible 19
ansferase GMA12/MNN10 family protein
esponsive 1 family protein
ter family protein
al Meristem) domain transcriptional regulator superfamily protein
esterase family protein
known function (DUF579)
sidase 8

transferase 73B3
dase/kelch repeat superfamily protein

olase 9B1
superfamily protein

ESISTANT 2
HD zinc finger superfamily protein
endent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein
known function (DUF581)
5
rotein 10
-related thaumatin superfamily protein
known function (DUF630 and DUF632)
known function (DUF581)
5
ansporter 1;7
e superfamily protein
at family protein / transmembrane family protein

d kinase 4
e protein B13
microtubule motor family protein
responsive NPH3 family protein
1 allergen and extensin family protein
sive family protein
ynthase 1

P450, family 76, subfamily C, polypeptide 2
ike superfamily protein
-methionine-dependent methyltransferases superfamily protein
ptide repeat (PPR) superfamily protein
ike superfamily protein
P450, family 71, subfamily B, polypeptide 34

uperfamily protein
se 2
receptor-like protein kinase family protein
ng Rossmann-fold superfamily protein
trypsin and protease inhibitor protein
hione lyase / glyoxalase I family protein

e meristem receptor-like kinase 2
superfamily protein
known function (DUF1635)

omoter-binding protein-like (SBP domain) transcription factor family protein
P450, family 704, subfamily A, polypeptide 2
ydrolases family 17 protein
op-helix (bHLH) DNA-binding superfamily protein
constitutive active rops 1
ecific DNA binding transcription factors
nily protein
otein 8
nhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
hosphatase 27
nily protein

tan protein 16
nine nucleotide exchange family protein
nily protein

base (http://jcvi.org/medicago/index.php). Up-regulated transcripts are highlighted in red and down-r

Annotation	NM-K (199)	log2 f.c. NM-K	Annotation	NM-K (188)	log2 f.c. NM-K	Annotation
O-methyltran	Medtr6g078140	inf	Kunitz family	Medtr2g030825	-3.02012	late embryog
alpha/beta-H	Medtr1g062350	3.2228	Pathogenesis	Medtr2g030845	-1.91225	late embryog
O-methyltran	Medtr1g086490	2.78538	Peroxidase su	Medtr2g021580	-1.68919	late embryog
0	Medtr1g062370	2.60101	Pathogenesis	Medtr2g069660	-1.67035	Pathogenesis
senescence-a	Medtr1g060990	2.14439	Duplicated ho	Medtr3g028340	-1.55862	0
Protein of un	Medtr7g024890	2.08806	Calcium-bind	Medtr2g009480	-1.46533	hydroxyprolin
O-methyltran	Medtr7g022490	2.06621	BCL-2-associa	Medtr4g077880	-1.40847	AAA-type AT
UDP-glucosyl	Medtr6g036450	1.97632	nodulin MtN	Medtr7g087047	-1.29522	zinc finger (R
0	Medtr8g098620	1.8864	0	Medtr3g463490	-1.26979	cell division c
0	Medtr7g096750	1.88264	Integrase-typ	Medtr1g084170	-1.2679	0
Disease resist	Medtr1g056370	1.85257	Disease resist	Medtr5g061860	-1.26422	slufate transp
UDP-glucosyl	Medtr7g063270	1.8338	NAD(P)-bindi	Medtr4g044463	-1.25089	Stigma-specif
O-methyltran	Medtr8g468290	1.76563	0	Medtr4g102650	-1.21105	0
Ubiquitin-like	Medtr3g016290	1.75398	0	Medtr4g049640	-1.15353	SLAC1 homol
Copper amin	Medtr1g069825	1.70504	Protein of un	Medtr3g108760	-1.13044	FASCICLIN-lik
Zinc-binding	Medtr4g068453	1.69705	0	Medtr2g086270	-1.13027	centroradialis
apyrase 2	Medtr5g018540	1.67365	0	Medtr4g087240	-1.10768	Zinc-finger do
Copper amin	Medtr7g096700	1.65681	Integrase-typ	Medtr3g117880	-1.06547	minichromos
chitinase A	Medtr2g011690	1.61499	Wound-respo	Medtr7g075790	-1.06339	Calcium-depe
TRICHOME BI	Medtr2g089835	1.60782	Wound-respo	Medtr2g043560	-1.05013	Plant invertas
UDP-glucosyl	Medtr7g024880	1.60461	Calcium-bind	Medtr3g467460	-1.04659	0
expansin B2	Medtr8g101650	1.59435	myb-like tran	Medtr8g479380	-1.04454	SKU5 similar
cytochrome P	Medtr3g058440	1.5826	F-box family	Medtr4g039740	-1.03896	Protein of un
Plant invertas	Medtr4g120950	1.56465	0	Medtr3g056635	-1.01056	NB-ARC doma
Protein of un	Medtr8g036075	1.51605	EF hand calci	Medtr1g028360	-1.00471	spermidine sy
UDP-Glycosyl	Medtr7g024873	1.50455	Calcium-bind	Medtr4g114120	-1.00446	P-loop contai
anthranilate	Medtr1g067660	1.48159	C2H2 and C2	Medtr4g039720	-0.995177	Protein of un
2-oxoglutarat	Medtr4g030210	1.47855	organic catio	Medtr5g026360	-0.993279	UDP-Glycosyl
Arginase/dea	Medtr4g079830	1.47264	Plant Tudor-l	Medtr4g018800	-0.982724	cytochrome P
Heavy metal	Medtr7g067010	1.45615	peptide trans	Medtr6g015905	-0.976746	reversibly gly
haemoglobin	Medtr3g086230	1.43991	photosystem	Medtr5g037250	-0.943383	BIG PETAL P
HXXXD-type a	Medtr7g096930	1.37966	myb domain	Medtr8g042510	-0.935132	RING/FYVE/P
0	Medtr1g088845	1.33841	glutathione S	Medtr3g031040	-0.931001	topoisomeras
glutathione S	Medtr7g083770	1.32968	LYR family of	Medtr1g100180	-0.922385	detoxifying ef
centroradialis	Medtr4g033150	1.32033	O-methyltran	Medtr4g019040	-0.91515	0

HXXXD-type a	Medtr8g096530	1.31495	HXXXD-type a	Medtr4g059670	-0.911104	late embryog
drought-repr	Medtr1g070495	1.29974	photosystem	Medtr3g053240	-0.907269	Stigma-specif
origin recogn	Medtr8g074810	1.27321	2-oxoglutarat	Medtr1g026020	-0.905989	expansin 11
Nucleotide-di	Medtr7g077210	1.25552	0	Medtr1g082390	-0.894292	GDSL-like Lipa
NAD(P)-linked	Medtr8g019440	1.23336	0	Medtr7g109480	-0.885024	Minichromos
Eukaryotic as	Medtr8g093440	1.22901	Protein of un	Medtr1g070120	-0.88131	2-oxoglutarat
cytochrome F	Medtr3g080860	1.21136	0	Medtr7g076080	-0.881021	Homeobox-le
Leucine-rich r	Medtr2g089815	1.20814	Wound-respo	Medtr7g069930	-0.870885	0
nucleolar RNA	Medtr1g006990	1.20378	Subtilisin-like	Medtr8g445730	-0.86588	0
0	Medtr5g022380	1.1957	Major facilita	Medtr3g046880	-0.863149	alpha/beta-H
EF hand calciu	Medtr7g032240	1.1849	CCT motif fam	Medtr2g010450	-0.85786	basic helix-lo
myosin-relate	Medtr1g022440	1.18485	dihydroflavon	Medtr4g059630	-0.855669	late embryog
LOB domain-c	Medtr4g113820	1.18381	early nodulin	Medtr4g108150	-0.851147	Bifunctional i
Late embryog	Medtr5g043930	1.17605	C2H2-like zin	Medtr3g113210	-0.849977	glyoxal oxidas
0	Medtr5g092790	1.15108	RING/U-box s	Medtr1g019280	-0.829157	Remorin fami
Auxin-respon	Medtr2g044140	1.1374	flavin-depend	Medtr5g062320	-0.828105	Glycosyl hydr
RING membra	Medtr3g027940	1.13385	Leucine-rich r	Medtr1g081970	-0.820657	DNAJ heat sh
multidrug res	Medtr1g080210	1.1224	Protein of un	Medtr3g062840	-0.818237	Protein of un
Late embryog	Medtr5g010000	1.12027	glycosyl hydr	Medtr4g122270	-0.817807	minichromos
Peroxidase su	Medtr2g035440	1.11761	Haloacid deh	Medtr7g093220	-0.816752	0
UDP-Glycosyl	Medtr3g089977	1.11583	alcohol dehy	Medtr2g008226	-0.814905	UDP-Glycosyl
Thymidine kin	Medtr8g092930	1.11527	RING/U-box s	Medtr4g132320	-0.81234	SKU5 similar
Mannose-bin	Medtr7g087080	1.11292	0	Medtr8g037170	-0.810187	MATE efflux f
Endosomal ta	Medtr8g045570	1.08567	Polyketide cy	Medtr7g013610	-0.807897	Histone supe
ribonuclease	Medtr3g095540	1.08212	photosystem	Medtr7g035445	-0.807809	zinc finger (C
Leucine-rich r	Medtr7g086380	1.08016	Protein of un	Medtr3g113140	-0.806418	Leucine-rich r
cytochrome F	Medtr6g092620	1.06868	ACC oxidase 1	Medtr0554s0020	-0.806191	cytochrome F
Pectate lyase	Medtr5g010580	1.04745	0	Medtr1g106775	-0.802997	Peroxisomal r
Minichromos	Medtr8g010440	1.0467	NB-ARC doma	Medtr4g132160	-0.800555	0
sulfate transp	Medtr7g061550	1.04253	myb-like HTH	Medtr7g094940	-0.794572	PATATIN-like
Disease resist	Medtr3g048590	1.04128	receptor like	Medtr8g020960	-0.794491	Cytochrome I
Clathrin, heav	Medtr2g104380	1.03984	serine-rich pr	Medtr8g091700	-0.793469	0
beta-D-xylosi	Medtr4g120940	1.03519	0	Medtr4g036050	-0.791581	AGAMOUS-lik
S-adenosyl-L-	Medtr1g093980	1.02584	0	Medtr8g075950	-0.790322	Chalcone-flav
heat shock tr	Medtr8g052100	1.02171	0	Medtr5g017710	-0.788513	0
0	Medtr4g023070	1.02082	F-box family	Medtr1g016070	-0.784028	Fatty acid/spl
pleiotropic dr	Medtr6g076090	1.01477	Disease resist	Medtr8g036660	-0.781699	MATE efflux f
Terpenoid cy	Medtr3g110205	1.01469	Integrase-typ	Medtr3g438070	-0.775457	BANQUO 3
lipoxygenase	Medtr5g074580	1.0084	O-methyltran	Medtr5g009620	-0.775167	cytokinin resp
Integrase-typ	Medtr4g070640	1.0073	0	Medtr1g044120	-0.773212	Helicase prot
O-Glycosyl hy	Medtr5g014040	1.00181	CheY-like two	Medtr4g050060	-0.771951	0
thioredoxin 2	Medtr1g010270	0.997045	molybdate tra	Medtr7g094250	-0.770727	oxidoreducta
0	Medtr6g071990	0.990201	Pyridoxal pho	Medtr5g024340	-0.768248	Protein phosp

2-oxoglutarat	Medtr1g112740	0.990197	FAD/NAD(P)-	Medtr1g077790	-0.765898	early nodulin
basic helix-lo	Medtr8g009560	0.989463	Fatty acid hy	Medtr7g099820	-0.76209	cation/H+ exc
Integrase-typ	Medtr4g120970	0.979423	0	Medtr5g062430	-0.758044	Glycosyl hydr
0	Medtr5g055800	0.976077	senescence-r	Medtr5g069800	-0.756467	Glycosyl hydr
Leucine-rich r	Medtr3g111970	0.959207	0	Medtr2g030835	-0.754311	late embryog
cytokinin resp	Medtr4g116277	0.937986	serine-rich pr	Medtr7g056817	-0.754246	0
alpha-xylosid	Medtr8g021010	0.930415	0	Medtr5g023660	-0.748316	chromometh
cytochrome P	Medtr2g089930	0.925316	Wound-respo	Medtr3g462730	-0.74668	Histone supe
cysteine-rich	Medtr8g022440	0.924562	SAUR-like aux	Medtr5g068780	-0.744581	Ribosomal pr
S-adenosyl-L-	Medtr3g088970	0.923935	arginosuccina	Medtr1g082920	-0.737194	P-loop contai
	Medtr1g022395	0.921048	0	Medtr8g090000	-0.736981	minichromos
	Medtr8g022040	0.915407	Tetratricopep	Medtr2g436680	-0.735499	multidrug res
	Medtr1g034120	0.914764	2-oxoglutarat	Medtr7g084750	-0.731848	xyloglucan er
	Medtr5g022350	0.905158	Pathogenesis	Medtr5g094310	-0.725471	Kinesin moto
	Medtr1g017080	0.902094	KNOTTED-like	Medtr7g067950	-0.725386	0
	Medtr1g025490	0.901564	0	Medtr8g042910	-0.724164	Plant invertas
	Medtr3g089940	0.90046	alcohol dehy	Medtr0184s0030	-0.723696	UDP-Glycosyl
	Medtr1g029150	0.897026	Plant stearoy	Medtr7g059070	-0.72294	Histone supe
	Medtr4g125080	0.881043	inter-alpha-tr	Medtr3g464330	-0.722652	fatty acid des
	Medtr1g054150	0.877494	0	Medtr8g099305	-0.720291	HMG (high m
Fe-2S] domai	Medtr8g028780	0.863287	ferric reducti	Medtr5g022010	-0.720047	Chalcone-flav
uperfamily pro	Medtr7g092400	0.858419	A20/AN1-like	Medtr0807s0020	-0.718752	0
	Medtr6g033580	0.84304	sucrose-prot	Medtr2g035230	-0.71729	Histone supe
	Medtr0009s0120	0.842604	phosphoinosi	Medtr8g103700	-0.716814	Leucine-rich r
	Medtr5g012390	0.834419	Lactate/mala	Medtr3g063110	-0.713883	DUTP-PYROP
	Medtr4g072980	0.828169	SAUR-like aux	Medtr3g462130	-0.709805	proliferating
	Medtr1g014320	0.828013	aldehyde deh	Medtr1g017490	-0.707553	growth-regul
	Medtr6g014270	0.825082	UDP-glucosyl	Medtr8g080570	-0.707382	Rubber elong
	Medtr4g094608	0.824433	0	Medtr8g471150	-0.69754	basic helix-lo
otein	Medtr4g094428	0.821698	Protein of un	Medtr5g066320	-0.694651	P-loop contai
	Medtr8g069330	0.821636	Phototropic-r	Medtr1g075680	-0.692995	P-loop contai
	Medtr6g477860	0.816745	Homeodoma	Medtr3g054010	-0.685809	Protein of un
	Medtr1g007920	0.809511	IQ-domain 21	Medtr6g032885	-0.683993	ARM repeat s
otein	Medtr6g065460	0.805181	Kunitz family	Medtr5g065900	-0.682232	0
	Medtr5g015470	0.800177	0	Medtr4g064967	-0.677478	histone H2A
	Medtr4g124650	0.794908	ATP binding r	Medtr4g127670	-0.676641	Peroxidase su
	Medtr7g090020	0.78	Ankyrin repea	Medtr3g109320	-0.67518	calmodulin lil
	Medtr8g096840	0.77886	Protein of un	Medtr1g020080	-0.673371	RNA-binding
	Medtr5g097280	0.773864	photosystem	Medtr2g029180	-0.672544	Nucleotide/su
	Medtr1g087920	0.773084	ethylene-resp	Medtr1g017540	-0.671819	P-loop contai
	Medtr5g047060	0.769271	Malectin/rec	Medtr4g128690	-0.669183	UDP-glucosyl
	Medtr4g008050	0.766506	B-box 32	Medtr6g015875	-0.668699	COBRA-like e
	Medtr4g045990	0.766207	Wound-respo	Medtr2g039410	-0.667991	cytokinin oxic

Medtr2g089965	0.762356	Wound-respo	Medtr3g092890	-0.665597	2-oxoglutarat
Medtr7g108200	0.755123	Glutaredoxin	Medtr2g098910	-0.660553	crinkly4
Medtr2g037970	0.755039	0	Medtr4g065850	-0.659236	Leucine-rich
Medtr1g076500	0.750572	Protein of un	Medtr7g015970	-0.659129	reversibly gly
Medtr0025s0110	0.750407	cytochrome	Medtr7g081420	-0.658442	Subtilisin-like
Medtr1g031640	0.748604	Polyketide cy	Medtr2g088320	-0.65729	0
Medtr4g017040	0.744784	RmlC-like cup	Medtr3g065300	-0.655981	ARM repeat s
Medtr5g072500	0.740141	Protein kinas	Medtr5g070680	-0.655484	alternative ox
Medtr1g103420	0.737075	Bifunctional i	Medtr4g122240	-0.654243	GRAS family t
Medtr6g078100	0.728966	Kunitz family	Medtr4g035855	-0.652273	Plant invertas
Medtr8g020650	0.727484	germin-like p	Medtr4g415390	-0.652136	Transmembra
Medtr2g084280	0.727205	FER-like regu	Medtr3g058220	-0.650619	cytochrome
Medtr4g009950	0.726965	VQ motif-con	Medtr8g020610	-0.646901	germin-like p
Medtr7g111260	0.723514	Major facilita	Medtr1g026410	-0.645613	SKU5 similar
Medtr1g013700	0.722798	CBL-interacti	Medtr7g093910	-0.644673	gamma histo
Medtr0027s0230	0.722133	HSP20-like ch	Medtr3g087640	-0.643676	HXXXD-type a
Medtr4g052460	0.721685	F-box family	Medtr3g115990	-0.640388	0
Medtr5g018550	0.717984	0	Medtr4g116070	-0.638724	glucuronidase
Medtr8g028265	0.717129	BCL-2-associa	Medtr3g461540	-0.637501	0
Medtr1g061640	0.712806	sequence-spe	Medtr5g064360	-0.637269	Phosphate-re
Medtr5g015680	0.711283	BTB and TAZ	Medtr6g013420	-0.637008	early nodulin
Medtr4g133040	0.709917	importin alph	Medtr3g084630	-0.636586	xyloglucan en
Medtr1g111240	0.707618	cinnamate-4-	Medtr3g078490	-0.635433	aldehyde deh
Medtr3g092790	0.701985	Late embryog	Medtr4g035980	-0.634356	Plant invertas
Medtr1g075170	0.700789	0	Medtr4g102790	-0.634019	GRAS family t
Medtr2g090060	0.69943	transferases;	Medtr7g024390	-0.632916	heat shock pr
Medtr5g024730	0.699241	RING/U-box s	Medtr1g112230	-0.630498	GHMP kinase
Medtr4g063720	0.698715	heat shock pr	Medtr1g018205	-0.630142	voltage deper
Medtr2g079670	0.698059	Aluminium in	Medtr4g112035	-0.629345	Plant protein
Medtr4g025690	0.694371	Plant invertas	Medtr7g105030	-0.626468	P-loop contai
Medtr7g023590	0.692786	polygalacturo	Medtr5g039180	-0.626465	basic helix-loo
Medtr6g018270	0.688143	LOB domain-	Medtr5g029770	-0.625463	Histone supe
Medtr8g005295	0.684445	Plant protein	Medtr3g112530	-0.62495	SLAC1 homol
Medtr3g008820	0.684144	Plant invertas	Medtr3g058210	-0.624218	cytochrome
Medtr2g089990	0.683767	Wound-respo	Medtr4g065007	-0.623842	dicarboxylate
Medtr4g068560	0.680756	0	Medtr2g089340	-0.622388	dehydratase
Medtr3g104810	0.678368	Mitochondria	Medtr6g087980	-0.621774	RHO-related
Medtr5g016450	0.671663	maternal effe	Medtr2g436750	-0.620957	ARM repeat s
Medtr5g079780	0.670997	0	Medtr7g013850	-0.620604	HXXXD-type a
Medtr4g029550	0.664904	0	Medtr3g110405	-0.620133	ataurora1
Medtr7g055630	0.663104	0	Medtr2g103440	-0.617963	0
Medtr5g081230	0.658689	type one seri	Medtr4g096700	-0.617833	Minichromos
Medtr2g437370	0.655434	CW-type Zinc	Medtr7g089080	-0.617376	Cyclin family

Medtr4g090545	0.649823	0	Medtr1g076700	-0.616427	Microtubule
Medtr3g109920	0.649822	0	Medtr4g071520	-0.616016	squalene syn
Medtr2g086200	0.648403	0	Medtr8g028145	-0.615699	Dihydrodipic
Medtr3g060740	0.647971	0	Medtr7g082230	-0.613477	0
Medtr2g481150	0.645743	Wound-resp	Medtr6g027540	-0.613192	C2 calcium/li
Medtr1g063420	0.643737	0	Medtr7g062150	-0.613041	Haloacid deh
Medtr3g463720	0.642534	RING/U-box	Medtr2g437380	-0.610726	2-oxoglutara
Medtr2g094720	0.639366	Mediator con	Medtr6g037220	-0.610039	0
Medtr4g086620	0.632561	Protein of un	Medtr1g088190	-0.60876	glycosyl hyd
Medtr1g017830	0.631691	Uncharacteri	Medtr7g007090	-0.607662	chrometh
Medtr0055s0050	0.628355	0	Medtr5g009020	-0.604819	ubiquitin-con
Medtr8g074335	0.627604	basic chitinas	Medtr8g075260	-0.603978	Tetratricope
Medtr2g018630	0.626348	serine carbox	Medtr3g110030	-0.602937	GroES-like fa
Medtr2g026040	0.623742	Cystatin/mon	Medtr4g056390	-0.601593	ser/arg-rich
Medtr6g032830	0.623036	GATA transcr	Medtr5g033490	-0.600984	protein kinas
Medtr1g016360	0.622023	Protein of un	Medtr3g055940	-0.598559	Kinesin moto
Medtr7g086770	0.615709	0	Medtr1g091010	-0.598016	cytochrome
Medtr1g072860	0.61284	inhibitor/inte	Medtr5g078200	-0.59782	O-Glycosyl hy
Medtr7g021220	0.612626	Sterile alpha	Medtr2g098250	-0.595926	Leucine-rich
Medtr3g045460	0.611516	0	Medtr5g015600	-0.595437	ARM repeat
Medtr4g126120	0.611195	alpha/beta-H	Medtr1g080440	-0.594617	Leucine-rich
Medtr5g046750	0.610735	0	Medtr3g110028	-0.591075	Homeodoma
Medtr1g072360	0.609979	F-box family	Medtr2g059200	-0.589765	transducin fa
Medtr2g022460	0.607599	Eukaryotic as	Medtr2g060070	-0.58763	Transducin/
Medtr4g123593	0.60732	Transmembrane proteins 14C			
Medtr4g109450	0.606699	heat shock protein 101			
Medtr3g091510	0.603708	Protein with RING/U-box and TRAF-like domains			
Medtr2g014300	0.598466	ERF domain protein 12			
Medtr2g084985	0.596688	Stress responsive A/B Barrel Domain			
Medtr3g072110	0.595617	Transmembrane amino acid transporter family protein			
Medtr2g095060	0.594515	0			
Medtr4g073040	0.594252	farnesylated protein 6			
Medtr1g075153	0.593817	0			
Medtr7g018090	0.593601	glutamine dumper 4			
Medtr3g084520	0.585443	indole-3-acetate beta-D-glucosyltransferase			

egulated ones are highlighted in green.