

Supplemental Table 3. Functional classification of probe sets showing significant increased transcript levels that were unique to the susceptible line in soybean cyst nematode-infected root tissue as compared to mock control.

Probe ID	p-value	Fold Change	G. max GenBankID	TIGR (PlantTA) Description	Arabidopsis ID	Arabidopsis Description	Functional Category
Gma.12040.4.A1_at	0.0169113	2.23049	CA785568	Nucleolar protein-like [Oryza sativa (japonica cultivar-group)]	AT4G39870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G05590.2); similar to Os06g0221100 [Oryza sativa (japonica cultivar-group)] (GB:NP001057175.1); similar to Os02g0754000 [Oryza sativa (japonica cultivar-group)] (GB:NP001048151.1)	Cell Growth & Division
Gma.12710.1.A1_at	0.0021542	2.12366	CD395311	Replication factor A-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G61000	replication protein, putative	Cell Growth & Division
Gma.13469.1.A1_at	0.00930252	2.09691	CD398557	Chromosome condensation protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G48600	ATSMC3 (Arabidopsis thaliana structural maintenance of chromosome 3); ATP binding	Cell Growth & Division
Gma.14125.1.A1_at	0.00459589	4.36517	CD416082	Homolog of Homo sapiens "Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen). [Takifugu rubripes]	0	0	Cell Growth & Division
Gma.4218.2.S1_at	0.000139137	2.14983	BE805868	Targeting for Xklp2 [Medicago truncatula (Barrel medic)]	AT3G23090	similar to WDL1 (WVD2-LIKE 1) [Arabidopsis thaliana] (TAIR:AT3G04630.3); similar to seed specific protein Bn15D14A [Brassica napus] (GB:AAP37969.1); contains InterPro domain Targeting for Xklp2; (InterPro:IPR009675)	Cell Growth & Division
Gma.5155.1.A1_at	0.000147095	2.07847	BI971134	Methyladenine glycosylase [Medicago truncatula (Barrel medic)]	AT3G12710	methyladenine glycosylase family protein	Cell Growth & Division
Gma.5911.1.S1_at	1.03629E-05	2.01295	AW349281	Mitotic spindle checkpoint protein MAD2 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G25980	mitotic spindle checkpoint protein, putative (MAD2)	Cell Growth & Division
GmaAffx.12370.1.S1_at	0.000247132	2.48065	BE059411	Microtubule-associated protein-like [Oryza sativa (japonica cultivar-group)]	AT5G62250	microtubule associated protein (MAP65/ASE1) family protein	Cell Growth & Division
GmaAffx.23381.1.S1_at	0.00196154	2.20962	BI973984	Replication protein A1 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G08020	replication protein, putative	Cell Growth & Division
GmaAffx.29662.1.S1_at	0.00138673	2.07966	CD415526	DNA-directed RNA polymerase II subunit-like protein [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Cell Growth & Division
GmaAffx.39169.1.S1_at	0.00624022	2.021	AW350332	Cellular retinaldehyde-binding/triple function, C-terminal [Medicago truncatula (Barrel medic)]	AT2G33560	spindle checkpoint protein-related	Cell Growth & Division
GmaAffx.69489.1.S1_at	0.0047083	2.59824	BG238202	Cyclin delta-1 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G70210	CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	Cell Growth & Division
GmaAffx.79262.1.S1_at	0.00423359	2.16573	CA801774	Origin recognition complex 4 subunit [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Cell Growth & Division
GmaAffx.81472.1.S1_at	0.00218429	2.17974	AW570625	PREG regulatory protein-like [Arabidopsis thaliana (Mouse-ear cress)]	AT2G44740	CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Cell Growth & Division

GmaAffx.82879.1.S1_at	0.00676461	2.03124	BM731508	GIN5 complex, Psf1 component [Medicago truncatula (Barrel medic)]	AT1G80190	similar to GIN5 complex, Psf1 component [Medicago truncatula] (GB:ABE94320.1); contains InterPro domain GIN5 complex, Psf1 component; (InterPro:IPR005339)	Cell Growth & Division
Gma.10795.1.S1_at	5.20863E-05	3.10956	AI442845	Glycoside hydrolase, family 16; Xyloglucan endo-transglycosylase, C-terminal [Medicago truncatula (Barrel medic)]	AT2G36870	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Cell Structure
Gma.10997.1.S1_at	3.97293E-05	2.05758	CD396418	F25I16.1 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G18650	glycosyl hydrolase family protein 17	Cell Structure
Gma.11298.2.S1_at	6.39553E-07	2.81386	CD415329	Pectate lyase [Fragaria ananassa (Strawberry)]	0	0	Cell Structure
Gma.1254.1.S1_at	0.00040179	2.11707	CF921991	Homolog of Homo sapiens "Histone 1, H2ai [Takifugu rubripes]	0	histone H4	Cell Structure
Gma.13759.1.A1_at	0.002855	2.14069	CD404860	NA	AT5G34940	glycosyl hydrolase family 79 N-terminal domain-containing protein	Cell Structure
Gma.1458.1.S1_at	2.95776E-05	2.19014	BI970708	Pectinesterase, putative, 5' partial; 91413-90223 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G76160	SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Cell Structure
Gma.14802.1.S1_at	0.00215347	2.54259	AW201116	Emb[CAB70981.1 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G54070	ankyrin repeat family protein	Cell Structure
Gma.16107.1.S1_at	6.87008E-05	2.12611	CD405936	Polygalacturonase-1 non-catalytic subunit beta precursor [Lycopersicon esculentum (Tomato)]	AT1G23760	JP630; polygalacturonase	Cell Structure
Gma.16122.1.S1_at	3.99453E-05	2.13583	CD413696	Endo-1,4-beta-glucanase [Glycine max (Soybean)]	AT4G02290	glycosyl hydrolase family 9 protein	Cell Structure
Gma.18013.1.A1_at	4.56956E-05	2.03044	CD400520	PREDICTED: similar to H3 histone, family 2 isoform 2 [Canis familiaris]	AT5G65360	histone H3	Cell Structure
Gma.2224.1.S1_at	0.000087503	2.03541	CD406086	Tubulin beta-1 chain [Zea mays (Maize)]	AT5G23860	TUB8 (tubulin beta-8)	Cell Structure
Gma.2224.1.S1_s_at	0.000250639	2.0777	CD406086	Tubulin beta-1 chain [Zea mays (Maize)]	AT5G23860	TUB8 (tubulin beta-8)	Cell Structure
Gma.2307.1.S1_at	3.55433E-05	2.10591	CA785639	Putative PS60 [Oryza sativa (japonica cultivar-group)]	AT1G76160	SKS5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Cell Structure
Gma.3064.1.S1_at	0.000998553	2.0179	CD403129	Histone H3 [Triticum aestivum (Wheat)]	AT5G65360	histone H3	Cell Structure
Gma.3594.2.S1_x_at	1.94473E-05	2.13815	CD393884	NA	AT4G37450	AGP18 (Arabinogalactan protein 18)	Cell Structure
Gma.361.1.S1_at	3.50561E-05	2.12466	AW349280	Xyloglucan endo-transglycosylase [Carica papaya (Papaya)]	AT2G36870	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Cell Structure
Gma.4216.1.S1_a_at	0.000159209	2.04154	BI970653	Xyloglucan endotransglucosylase/hydrolase protein A precursor [Phaseolus angularis (Adzuki bean) (Vigna angularis)]	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds	Cell Structure
Gma.4216.2.S1_s_at	5.65473E-07	2.30864	CD405657	Xyloglucan endotransglucosylase/hydrolase protein A precursor [Phaseolus angularis (Adzuki bean) (Vigna angularis)]	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds	Cell Structure

Gma.4220.2.S1_at	0.000195773	2.19759	AW164216	Xyloglucan endotransglucosylase/hydrolase protein 9 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT4G03210	XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds	Cell Structure
Gma.4385.1.S1_at	0.000191899	2.63008	BU762481	Putative fasciclin-like arabinogalactan protein FLA2 [Trifolium pratense (Red clover)]	AT4G12730	FLA2 (FLA2)	Cell Structure
Gma.4385.1.S1_s_at	1.84665E-08	2.16215	BU762481	Putative fasciclin-like arabinogalactan protein FLA2 [Trifolium pratense (Red clover)]	AT4G12730	FLA2 (FLA2)	Cell Structure
Gma.4418.1.S1_at	0.000254546	2.08281	AW310969	Putative beta-1,3-glucanase [Oryza sativa (japonica cultivar-group)]	0	glycosyl hydrolase family protein 17	Cell Structure
Gma.4491.1.S1_at	0.000601478	2.59955	BI967493	NA	AT2G20520	FLA6 (FLA6)	Cell Structure
Gma.5666.2.S1_at	1.90723E-05	2.00872	BE609637	Tubulin beta-1 chain [Zea mays (Maize)]	AT1G75780	TUB1 (tubulin beta-1 chain); structural molecule	Cell Structure
Gma.5744.1.S1_at	0.000132273	2.0912	CA802118	Multicopper oxidase, type 1 [Medicago truncatula (Barrel medic)]	AT4G22010	SKS4 (SKU5 Similar 4); copper ion binding / oxidoreductase	Cell Structure
Gma.5744.2.S1_at	0.00253025	2.41092	BF068954	Multicopper oxidase, type 1 [Medicago truncatula (Barrel medic)]	AT4G22010	SKS4 (SKU5 Similar 4); copper ion binding / oxidoreductase	Cell Structure
Gma.5949.1.A1_at	0.000215126	2.15627	CD412339	Histone H3 [Triticum aestivum (Wheat)]	AT5G65360	histone H3	Cell Structure
Gma.6199.1.S1_at	1.45469E-06	4.13159	BQ612015	AT5g66920/MUD21 18 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G66920	SKS17 (SKU5 Similar 17); copper ion binding / oxidoreductase	Cell Structure
Gma.8546.1.S1_at	0.00116003	2.23542	AW349424	Putative phi-1 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G44130	fasciclin-like arabinogalactan-protein, putative	Cell Structure
Gma.987.1.S1_at	0.00445076	2.88416	AW100853	Alpha-expansin precursor [Gossypium hirsutum (Upland cotton)]	0	0	Cell Structure
GmaAffx.11204.2.S1_at	0.00116073	2.08404	AW706352	NA	AT2G45470	FLA8 (Arabinogalactan protein 8)	Cell Structure
GmaAffx.12832.1.S1_at	0.000651927	2.16193	BG363116	Probable xyloglucan endotransglucosylase/hydrolase protein 33 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT1G10550	XTH33 (xyloglucan:xyloglucosyl transferase 33); hydrolase, acting on glycosyl bonds	Cell Structure
GmaAffx.16018.1.S1_at	2.9704E-06	2.50998	BE821618	Beta-Ig-H3/fasciclin [Medicago truncatula (Barrel medic)]	AT5G03170	FLA11 (fasciclin-like arabinogalactan-protein 11)	Cell Structure
GmaAffx.22677.1.S1_at	0.000143557	2.39514	BG507403	Beta-Ig-H3/fasciclin [Medicago truncatula (Barrel medic)]	AT5G03170	FLA11 (fasciclin-like arabinogalactan-protein 11)	Cell Structure
GmaAffx.248.1.S1_at	0.000133983	2.37155	AW311298	F21M11.2 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G04040	acid phosphatase class B family protein	Cell Structure
GmaAffx.3369.1.S1_at	0.00432528	2.01261	BU548983	Probable xyloglucan endotransglucosylase/hydrolase protein 32 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT2G36870	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Cell Structure
GmaAffx.34085.1.A1_at	1.07639E-06	2.07645	CD418272	Tubulin beta-1 chain [Zea mays (Maize)]	0	0	Cell Structure
GmaAffx.34532.1.S1_at	0.000300672	2.21911	BG362816	Glycoside hydrolase, family 1 [Medicago truncatula (Barrel medic)]	AT1G61810	BGLU45; hydrolase, hydrolyzing O-glycosyl compounds	Cell Structure
GmaAffx.34697.1.S1_at	7.27331E-08	2.60921	AW433263	EXGT1 [Pisum sativum (Garden pea)]	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds	Cell Structure
GmaAffx.41724.1.S1_at	0.000207097	2.06249	BI968713	Microtubule-associated protein EB1-like protein [Medicago truncatula (Barrel medic)]	0	ATEB1A (Arabidopsis thaliana Microtubule End Binding Protein EB1A); microtubule binding	Cell Structure

GmaAffx.41724.2.S1_at	0.00612844	2.0318	BG047062	Microtubule-associated protein EB1-like protein [Medicago truncatula (Barrel medic)]	AT5G62500	ATEB1B (Arabidopsis thaliana Microtubule End Binding Protein EB1A); microtubule binding	Cell Structure
GmaAffx.46389.1.S1_at	0.00125731	2.31477	BM522568	CG4869-PA [Drosophila melanogaster (Fruit fly)]	AT5G44340	TUB4 (tubulin beta-4 chain)	Cell Structure
GmaAffx.50714.1.S1_at	8.09042E-05	2.43888	BE021980	Alpha-L-arabinofuranosidase [Raphanus sativus (Radish)]	AT5G64572; AT5G64570	[AT5G64570, XYL4 (beta-xylosidase 4); hydrolase, hydrolyzing O-glycosyl compounds]	Cell Structure
GmaAffx.51445.1.S1_at	0.000193689	2.03362	BQ612160	Monocopper oxidase-like protein SKS1 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT4G25240	SKS1 (SKU5 SIMILAR 1); copper ion binding	Cell Structure
GmaAffx.54479.2.A1_s_at	0.011099	2.75256	CD405056	Gonadotropin, beta chain; Gibberellin regulated protein [Medicago truncatula (Barrel medic)]	AT5G14920	gibberellin-regulated family protein	Cell Structure
GmaAffx.54716.1.S1_s_at	0.000041334	2.20116	BI699590	Kinesin related protein [Lycopersicon esculentum (Tomato)]	AT4G26660	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G55520.2); similar to kinesin related protein [Lycopersicon esculentum] (GB:AAO15358.1); contains InterPro domain Kinesin-related; (InterPro:IPR010544)	Cell Structure
GmaAffx.62345.1.S1_at	3.02761E-06	2.3404	BQ630544	Endo-1,4-beta-glucanase precursor [Pisum sativum (Garden pea)]	AT1G22880	glycosyl hydrolase family 9 protein	Cell Structure
GmaAffx.65868.1.A1_at	0.000101145	2.21476	CD401651	Calponin-like actin-binding; Kinesin, motor region [Medicago truncatula (Barrel medic)]	0	0	Cell Structure
GmaAffx.671.1.S1_at	7.81714E-05	2.07901	CA785167	Alpha-expansin 4 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT2G39700	ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Cell Structure
GmaAffx.68709.1.A1_at	3.19641E-05	2.33765	BI969418	Endo-1,4-beta-glucanase precursor [Pisum sativum (Garden pea)]	AT1G71380	glycosyl hydrolase family 9 protein	Cell Structure
GmaAffx.69508.1.S1_at	0.0113959	2.19323	BQ299262	Cellulose synthase [Populus tremula x Populus tremuloides]	0	0	Cell Structure
GmaAffx.69994.1.S1_at	0.000336577	2.12783	CD417025	Phi-1 protein [Nicotiana tabacum (Common tobacco)]	AT4G08950	phosphate-responsive protein, putative (EXO)	Cell Structure
GmaAffx.71683.1.S1_at	0.00522031	2.24667	AW734979	Protein At3g52525 [Arabidopsis thaliana (Mouse-ear cress)]	0	ATOFP6/OFPP6 (Arabidopsis thaliana ovate family protein 6)	Cell Structure
GmaAffx.71901.1.S1_s_at	1.31755E-05	2.34451	BE022356	Beta-1,3-glucanase [Camellia sinensis (Tea)]	AT1G66250	glycosyl hydrolase family 17 protein	Cell Structure
GmaAffx.75219.1.S1_at	0.000371607	2.13801	BE020773	Hypothetical protein At2g35860 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G52370	beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein	Cell Structure
GmaAffx.75875.1.S1_at	0.0125658	2.37611	AW598284	Actin bundling protein ABP135 [Lilium longiflorum (Trumpet lily)]	AT3G57410	VLN3 (VILLIN 3); actin binding	Cell Structure
GmaAffx.77113.1.S1_at	0.00797976	4.96571	BG238990	Ankyrin [Medicago truncatula (Barrel medic)]	0	0	Cell Structure
GmaAffx.79075.1.S1_at	0.000210264	2.03581	BE824264	Endo-1,4-beta-glucanase precursor [Glycine max (Soybean)]	AT4G39010	glycosyl hydrolase family 9 protein	Cell Structure
GmaAffx.79361.1.S1_at	0.0009741	2.56043	CA785641	Glycoside hydrolase, family 28 [Medicago truncatula (Barrel medic)]	AT5G17200	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Cell Structure
GmaAffx.85140.1.S1_at	0.000261433	2.01794	BF069014	Phytochelatin synthetase-like protein [Phaseolus vulgaris (Kidney bean) (French bean)]	AT5G60920	COB (COBRA)	Cell Structure

GmaAffx.87042.1.S1_at	0.000282542	2.25383	AW596159	Putative monocopper oxidase precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT5G51480	SKS2 (SKU5 SIMILAR 2); copper ion binding	Cell Structure
GmaAffx.87808.1.S1_at	4.6095E-06	2.39379	BM522465	NA	AT5G60490	FLA12 (fasciclin-like arabinogalactan-protein 12)	Cell Structure
GmaAffx.88219.1.S1_at	0.000447929	2.61308	BE330621	Endo-xyloglucan transferase like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G11545	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Cell Structure
GmaAffx.89045.1.A1_s_at	3.44631E-05	2.20908	CK605938	Endo-xyloglucan transferase like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G11545	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Cell Structure
GmaAffx.90617.1.S1_s_at	0.00177939	2.28856	CF806342	Glycoside hydrolase, family 1 [Medicago truncatula (Barrel medic)]	AT2G44480	glycosyl hydrolase family 1 protein	Cell Structure
GmaAffx.91763.1.S1_s_at	4.01948E-05	3.38683	CF807488	Xyloglucan endotransglucosylase/hydrolase protein A precursor [Phaseolus angularis (Adzuki bean) (Vigna angularis)]	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds	Cell Structure
GmaAffx.91763.1.S1_x_at	3.19428E-07	2.65594	CF807488	Xyloglucan endotransglucosylase/hydrolase protein A precursor [Phaseolus angularis (Adzuki bean) (Vigna angularis)]	AT5G13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds	Cell Structure
GmaAffx.93073.1.S1_s_at	0.000207027	2.54114	CF808798	Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) [Glycine max (Soybean)]	AT3G57270	BG1 (BETA-1,3-GLUCANASE 1); hydrolase, hydrolyzing O-glycosyl compounds	Cell Structure
GmaAffx.93198.1.S1_x_at	0.00449282	2.10203	CF808912	Tubulin beta-1 chain [Zea mays (Maize)]	AT1G75780	TUB1 (tubulin beta-1 chain); structural molecule	Cell Structure
GmaAffx.93619.1.S1_s_at	0.000970792	2.80204	CF809344	Putative phi-1 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G20520	FLA6 (FLA6)	Cell Structure
Gma.10658.1.A1_at	0.000128524	2.78816	CA852384	Ripening related protein [Glycine max (Soybean)]	AT1G70890	major latex protein-related / MLP-related	Disease & Defense
Gma.11336.2.S1_at	1.03319E-05	2.06177	CA852094	NA	AT1G18250	ATLP-1 (Arabidopsis thaumatin-like protein 1)	Disease & Defense
Gma.12018.1.S1_at	0.000117013	2.72187	CD398677	Phytoalexin-deficient 4-2 protein [Solanum tuberosum (Potato)]	AT3G52430	PAD4 (PHYTOALEXIN DEFICIENT 4); triacylglycerol lipase	Disease & Defense
Gma.12286.1.S1_at	0.00244569	2.64097	AW396660	NA	0	0	Disease & Defense
Gma.14288.1.S1_at	0.00187607	2.37165	CA852004	Peroxidase precursor [Quercus suber (Cork oak)]	0	peroxidase, putative	Disease & Defense
Gma.1539.1.S1_at	4.35981E-05	2.36881	CA802612	Haem peroxidase, plant/fungal/bacterial [Medicago truncatula (Barrel medic)]	AT4G37530; AT4G37520	[AT4G37530, peroxidase, putative];[AT4G37520, peroxidase 50 (PER50) (P50) (PRXR2)]	Disease & Defense
Gma.17816.2.S1_s_at	0.00834722	2.06875	BE020641	Cationic peroxidase 1 precursor [Arachis hypogaea (Peanut)]	AT5G05340	peroxidase, putative	Disease & Defense
Gma.363.1.S1_at	0.00298367	2.32988	AW349408	NA	AT1G75800	pathogenesis-related thaumatin family protein	Disease & Defense
Gma.4829.1.S1_at	8.84768E-05	3.14015	AW309606	Class III peroxidase [Gossypium hirsutum (Upland cotton)]	AT5G05340	peroxidase, putative	Disease & Defense
Gma.4919.1.S1_at	0.000113466	2.28861	AW350788	Class III peroxidase [Gossypium hirsutum (Upland cotton)]	AT5G05340	peroxidase, putative	Disease & Defense

Gma.6332.1.S1_at	2.35716E-06	2.26315	BG237174	F5M15.18 [Arabidopsis thaliana (Mouse-ear cross)]	AT5G63380	4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Disease & Defense
Gma.6452.1.A1_at	0.00464534	2.87695	BQ298226	Polyphenol oxidase [Trifolium pratense (Red clover)]	0	0	Disease & Defense
Gma.7180.1.S1_at	0.00402761	4.71503	AI794693	Subtilisin inhibitor CLSI-II [Contains: Subtilisin inhibitor CLSI- III] [Canavalia lineata]	0	0	Disease & Defense
Gma.8365.1.S1_at	0.000509395	2.59409	CD396813	Hypothetical protein At2g37330 [Arabidopsis thaliana (Mouse-ear cross)]	AT2G37330	ALS3 (ALUMINUM SENSITIVE 3)	Disease & Defense
Gma.8524.1.S1_at	1.23134E-06	3.40053	U51194	Peroxidase [Glycine max (Soybean)]	AT5G42180	peroxidase 64 (PER64) (P64) (PRXR4)	Disease & Defense
Gma.8525.1.S1_s_at	1.08457E-06	3.35138	AI966178	NA	AT5G42180	peroxidase 64 (PER64) (P64) (PRXR4)	Disease & Defense
Gma.8957.1.A1_at	0.000664082	3.23347	BU764905	NA	AT1G70890	major latex protein-related / MLP-related	Disease & Defense
Gma.9638.1.A1_at	7.23535E-05	2.1419	CA936403	ADR6 protein [Glycine max (Soybean)]	AT5G25610	RD22 (RESPONSIVE TO DESSICATION 22)	Disease & Defense
GmaAffx.10710.1.S1_s_at	0.00016012	2.4075	AW278629	Pathogenesis-related protein PR-1 precursor [Medicago truncatula (Barrel medic)]	AT4G30320	allergen V5/Tpx-1-related family protein	Disease & Defense
GmaAffx.12305.1.S1_at	0.000521764	2.50572	BE022059	NA	AT5G23400	disease resistance family protein / LRR family protein	Disease & Defense
GmaAffx.1833.1.A1_at	0.000577231	5.04181	BU547841	Hcr2-p3 [Lycopersicon pimpinellifolium (Currant tomato)]	AT5G23400	disease resistance family protein / LRR family protein	Disease & Defense
GmaAffx.2172.1.S1_at	0.00901625	2.13704	CD402944	AT3g63200/F16M2 50 [Arabidopsis thaliana (Mouse-ear cross)]	AT3G63200	PLA IIIB/PLP9 (Patatin-like protein 9); nutrient reservoir	Disease & Defense
GmaAffx.23295.1.S1_at	0.000051639	2.13061	BI968028	T19F11.6 protein [Arabidopsis thaliana (Mouse-ear cross)]	AT3G11660	NHL1 (NDR1/HIN1-like 1)	Disease & Defense
GmaAffx.47160.1.A1_at	0.00552876	5.29989	BU550419	Crocin dialdehyde-like [Oryza sativa (japonica cultivar-group)]	AT3G63520	CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1)	Disease & Defense
GmaAffx.50446.1.S1_at	0.00363158	4.87596	BQ080496	Cationic peroxidase 1 precursor [Arachis hypogaea (Peanut)]	AT5G05340	peroxidase, putative	Disease & Defense
GmaAffx.50446.2.S1_at	0.00450739	2.7686	BG508856	Peroxidase precursor [Picea abies (Norway spruce) (Picea excelsa)]	AT5G05340	peroxidase, putative	Disease & Defense
GmaAffx.5076.1.S1_s_at	0.00232575	2.05889	BM139563	Harpin-induced 1 [Medicago truncatula (Barrel medic)]	0	0	Disease & Defense
GmaAffx.53152.1.S1_at	0.0121161	2.00875	BE823592	RING-H2 subgroup RHE protein [Populus alba x Populus tremula]	AT3G16720	ATL2 (Arabidopsis T?xicos en Levadura 2); protein binding / zinc ion binding	Disease & Defense
GmaAffx.57878.1.S1_at	0.0154542	3.90746	CA799481	Probable polygalacturonase non-catalytic subunit JP650 precursor [Arabidopsis thaliana (Mouse-ear cross)]	AT1G70370	BURP domain-containing protein / polygalacturonase, putative	Disease & Defense
GmaAffx.57878.2.S1_at	0.00286445	2.18002	BE610836	NA	AT1G60390	BURP domain-containing protein / polygalacturonase, putative	Disease & Defense
GmaAffx.73174.1.S1_at	0.00261227	2.70355	BI699854	Protein At4g14723 [Arabidopsis thaliana (Mouse-ear cross)]	0	allergen-related	Disease & Defense
GmaAffx.73978.1.S1_at	8.00217E-05	2.24923	BQ629101	NA	AT3G07040	RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1)	Disease & Defense
GmaAffx.792.3.S1_at	0.00219519	2.68169	AW509489	Putative epoxide hydrolase [Oryza sativa (japonica cultivar-group)]	AT4G02340	epoxide hydrolase, putative	Disease & Defense
GmaAffx.86757.1.S1_at	0.000679911	2.22103	BM567976	NA	AT5G28010	Bet v I allergen family protein	Disease & Defense

GmaAffx.8704.1.A1_at	0.0121119	3.24452	BG156185	NA	AT1G49570	peroxidase, putative	Disease & Defense
GmaAffx.8704.2.S1_at	0.00695909	3.21946	BG042982	NA	AT1G49570	peroxidase, putative	Disease & Defense
GmaAffx.88699.1.S1_s_at	0.000441136	2.29853	CK606025	OSJNBa0006A01.6 protein [Oryza sativa (Rice)]	AT5G28010	Bet v I allergen family protein	Disease & Defense
GmaAffx.90350.1.A1_at	0.000205848	2.15889	CF806075	Class1 chitinase [Pisum sativum (Garden pea)]	AT1G05850	POM1 (POM-POM1); chitinase	Disease & Defense
GmaAffx.91353.1.S1_s_at	0.000216846	2.2138	CF807078	Peroxidase [Glycine max (Soybean)]	AT1G05260	RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Disease & Defense
GmaAffx.91353.1.S1_x_at	9.04652E-05	2.00445	CF807078	Peroxidase [Glycine max (Soybean)]	AT1G05260	RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Disease & Defense
GmaAffx.92917.1.S1_s_at	0.000016668	2.37355	CF808642	Peroxidase precursor [Glycine max (Soybean)]	AT1G05260	RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Disease & Defense
GmaAffx.93041.1.S1_s_at	0.00405513	2.17042	CF808766	Thaumatococcus, pathogenesis-related [Medicago truncatula (Barrel medic)]	AT1G18250	ATLP-1 (Arabidopsis thaumatin-like protein 1)	Disease & Defense
GmaAffx.93487.1.S1_s_at	0.000265235	2.00354	CF809212	Major pollen allergen Bet v 1-M/N [Betula verrucosa (White birch) (Betula pendula)]	AT1G24020	Bet v I allergen family protein	Disease & Defense
Gma.13278.1.A1_at	5.42495E-05	2.11342	CD391349	Emb[CAB72177.1 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G03870	glutaredoxin family protein	Energy
Gma.17884.1.S1_s_at	0.00017731	2.39633	BE023599	Thioredoxin domain 2 [Medicago truncatula (Barrel medic)]	AT1G11530	ATCXXS1 (C-TERMINAL CYSTEINE RESIDUE IS CHANGED TO A SERINE 1); thiol-disulfide exchange intermediate	Energy
Gma.2590.10.S1_at	0.000165129	2.31959	BM086662	Blue (Type 1) copper domain [Medicago truncatula (Barrel medic)]	AT2G25060	plastocyanin-like domain-containing protein	Energy
Gma.3160.1.S1_at	6.93511E-05	3.33634	BG507816	Thioredoxin H [Nicotiana glauca (Winged tobacco) (Persian tobacco)]	AT5G39950	ATTRX2 (Arabidopsis thioredoxin h2, thioredoxin H-type 1); thiol-disulfide exchange intermediate	Energy
Gma.6151.1.S1_at	2.11195E-05	2.86404	BQ611806	Dimethylaniline monooxygenase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G07800	flavin-containing monooxygenase family protein / FMO family protein	Energy
Gma.883.1.S1_at	0.000167623	2.22505	CD395912	Hypothetical protein OSJNBa0078O01.30 [Oryza sativa (japonica cultivar-group)]	AT5G53490	thylakoid lumenal 17.4 kDa protein, chloroplast	Energy
GmaAffx.1943.1.S1_at	1.56385E-06	2.73724	BU765258	AX110P [Daucus carota (Carrot)]	AT4G09670	oxidoreductase family protein	Energy
GmaAffx.53622.1.S1_s_at	0.0097445	3.41534	BE583854	Probable protein disulfide-isomerase A4 precursor [Caenorhabditis elegans]	AT2G47470	ATPDIL2-1/MEE30/UNE5 (PDI-LIKE 2-1, maternal effect embryo arrest 30, unfertilized embryo sac 5); thiol-disulfide exchange intermediate	Energy
GmaAffx.60443.1.S1_at	0.0116375	2.0472	BG238788	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta [Ricinus communis (Castor bean)]	AT1G12000	pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Energy
GmaAffx.77264.1.S1_at	0.0124794	2.27892	CA935091	OSJNBa0073L04.11 protein [Oryza sativa (japonica cultivar-group)]	AT5G03870	glutaredoxin family protein	Energy
GmaAffx.80064.1.S1_at	0.000681034	2.18155	BQ081542	ATP citrate lyase b-subunit [Lupinus albus (White lupin)]	AT1G10670	ACLA-1 (ATP-citrate lyase A-1)	Energy
GmaAffx.92537.1.S1_at	0.00285842	2.15875	CF808262	Thioredoxin domain 2 [Medicago truncatula (Barrel medic)]	AT1G11530	ATCXXS1 (C-TERMINAL CYSTEINE RESIDUE IS CHANGED TO A SERINE 1); thiol-disulfide exchange intermediate	Energy
GmaAffx.92895.1.S1_at	0.0125941	3.10104	CF808620	Putative fructose bisphosphate aldolase [Arabidopsis thaliana (Mouse-ear cress)]	AT2G36460	fructose-bisphosphate aldolase, putative	Energy

GmaAffx.92935.1.S1_s_at	0.0129849	2.14637	CF808660	Light harvesting chlorophyll a /b binding protein of PSII [Euglena gracilis]	0	LHCB2.1 (Photosystem II light harvesting complex gene 2.1); chlorophyll binding	Energy
GmaAffx.9843.1.S1_at	5.89746E-05	2.47888	CD416791	At1g64640 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G64640	plastocyanin-like domain-containing protein	Energy
Gma.11175.1.S1_at	4.51315E-05	2.23516	AW349743	Alcohol dehydrogenase 7 [Vitis vinifera (Grape)]	AT3G18280	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.1494.1.S1_x_at	0.000082433	2.00842	BF598755	NA	AT2G10940	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.15048.2.S1_at	0.00825785	2.19357	BG238374	Putative zinc finger protein [Arabidopsis thaliana (Mouse-ear cress)]	AT3G15680	zinc finger (Ran-binding) family protein	Intracellular Traffic
Gma.2972.1.S1_at	9.45156E-05	2.1598	AW350602	Hypothetical protein [Cicer arietinum (Chickpea) (Garbanzo)]	AT1G72160	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Intracellular Traffic
Gma.3291.1.S1_at	2.44021E-05	2.46814	AF248055	Proline-rich protein [Glycine max (Soybean)]	AT2G45180	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.3440.1.S1_s_at	5.53801E-06	2.17774	BE820653	Annexin, putative [Medicago truncatula (Barrel medic)]	AT5G12380	annexin, putative	Intracellular Traffic
Gma.3440.2.S1_a_at	0.00015716	2.08471	CD418071	Annexin, putative [Medicago truncatula (Barrel medic)]	AT5G12380	annexin, putative	Intracellular Traffic
Gma.3723.1.S1_at	0.000668464	2.04496	BI424448	Nonspecific lipid-transfer protein 2 [Prunus armeniaca (Apricot)]	AT3G18280	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.4050.1.S1_at	1.05879E-05	3.41604	AW317179	Putative 14-kDa proline-rich protein [Cicer arietinum (Chickpea) (Garbanzo)]	AT2G45180	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.5357.1.S1_at	0.000344168	2.25283	AW164593	Annexin, putative [Medicago truncatula (Barrel medic)]	AT5G12380	annexin, putative	Intracellular Traffic
Gma.6146.1.S1_at	0.000132394	4.53386	BI969869	Putative 14-kDa proline-rich protein [Cicer arietinum (Chickpea) (Garbanzo)]	AT2G45180	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
Gma.6427.2.S1_a_at	0.000219656	2.19575	AW349057	Calnexin [Glycine max (Soybean)]	AT5G61790	calnexin 1 (CNX1)	Intracellular Traffic
Gma.6427.2.S1_x_at	0.00229631	2.04856	AW349057	Calnexin [Glycine max (Soybean)]	AT5G61790	calnexin 1 (CNX1)	Intracellular Traffic
Gma.8016.1.S1_at	9.50517E-05	2.66122	BU547223	Generic methyltransferase [Medicago truncatula (Barrel medic)]	AT4G00750	dehydration-responsive family protein	Intracellular Traffic
GmaAffx.20084.1.S1_at	0.00890168	2.22757	CA799812	Vacuolar protein sorting-associated protein 26-like protein [Solanum tuberosum (Potato)]	AT5G53530	vacuolar protein sorting-associated protein 26, putative / VPS26, putative	Intracellular Traffic
GmaAffx.52578.1.S1_at	0.00294291	2.0145	CD406471	Copine I-like protein [Oryza sativa (japonica cultivar-group)]	AT1G79380	copine-related	Intracellular Traffic
GmaAffx.67979.1.S1_at	0.000687035	2.3807	BG238184	transporter [Arabidopsis thaliana]	AT5G10840	endomembrane protein 70, putative	Intracellular Traffic
GmaAffx.68244.1.S1_at	0.000987451	2.10841	BE210278	Patellin-4 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G30690	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Intracellular Traffic
GmaAffx.80464.1.S1_at	0.0153943	2.55364	CA850542	Arachidonic acid-induced DEA1 [Capsicum chinense (Scotch bonnet) (Bonnet pepper)]	AT1G62510	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
GmaAffx.81641.1.S1_s_at	0.000126558	2.42529	BG156396	Extensin-like protein [Glycine max (Soybean)]	AT1G62510	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Intracellular Traffic
GmaAffx.90865.1.S1_s_at	0.00415807	2.12453	CF806590	Calnexin [Glycine max (Soybean)]	AT5G61790	calnexin 1 (CNX1)	Intracellular Traffic
Gma.10072.1.S1_at	0.00394523	3.40765	CD399353	Protein HOTHEAD precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT1G72970	HTH (HOTHEAD); aldehyde-lyase	Metabolism
Gma.10521.1.A1_at	5.09192E-06	2.26093	AW310958	NA	AT1G13710	CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding	Metabolism

Gma.11174.1.S1_at	9.11621E-05	2.38235	CD405503	Apyrase GS50 [Glycine soja (Wild soybean)]	AT5G18280	ATAPY2 (APYRASE 2)	Metabolism
Gma.11848.1.S1_at	0.000763138	2.0814	CD408549	Monogalactosyldiacylglycerol synthase [Medicago truncatula (Barrel medic)]	AT5G20410	MGD2 (monogalactosyldiacylglycerol synthase 2); 1,2-diacylglycerol 3-beta-galactosyltransferase/ transferase, transferring glycosyl groups	Metabolism
Gma.13058.1.A1_at	0.0135706	2.62869	CD394760	E-class P450, group I [Medicago truncatula (Barrel medic)]	AT1G11600	CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding	Metabolism
Gma.13058.1.A1_s_at	0.00512727	4.57097	CD394760	E-class P450, group I [Medicago truncatula (Barrel medic)]	AT1G11600	CYP77B1 (cytochrome P450, family 77, subfamily B, polypeptide 1); oxygen binding	Metabolism
Gma.138.1.S1_at	0.00312514	2.10476	AF022463	Cytochrome P450 78A3 [Glycine max (Soybean)]	AT3G61880	CYP78A9 (CYTOCHROME P450 78A9); oxygen binding	Metabolism
Gma.14900.1.S1_at	0.0125048	2.144	AI496668	Hypothetical protein F5K20 250 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G53950	glyoxal oxidase-related	Metabolism
Gma.15233.1.S1_at	0.00120274	2.8686	CD398582	Putative metallophosphatase [Lupinus luteus (European yellow lupin)]	AT5G50400	ATPAP27/PAP27 (purple acid phosphatase 27); acid phosphatase/ protein serine/threonine phosphatase	Metabolism
Gma.1545.2.S1_at	0.00216415	2.34552	BG239480	Probable mannitol dehydrogenase [Medicago sativa (Alfalfa)]	AT2G21890; AT2G21730	[AT2G21890, mannitol dehydrogenase, putative];[AT2G21730, mannitol dehydrogenase, putative]	Metabolism
Gma.15653.1.S1_at	1.11453E-05	4.75372	BI969594	CPRD49 protein [Vigna unguiculata (Cowpea)]	AT3G11210	GDSL-motif lipase/hydrolase family protein	Metabolism
Gma.16833.1.S1_s_at	0.00571931	4.01798	L34841	Fructose-1,6-bisphosphatase, chloroplast precursor [Glycine max (Soybean)]	AT3G54050	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FB Pase, putative	Metabolism
Gma.17250.1.A1_at	8.31655E-06	2.1506	BI969790	UDP-glucuronosyl/UDP-glucosyltransferase [Medicago truncatula (Barrel medic)]	0	DOGT1 (DON-GLUCOSYLTRANSFERASE); UDP-glucosyltransferase/ transferase, transferring glycosyl groups	Metabolism
Gma.17835.1.S1_at	4.69003E-05	2.21014	BE822840	Galactose-binding like; Alpha-L-arabinofuranosidase, C-terminal [Medicago truncatula (Barrel medic)]	AT3G10740	ASD1 (ALPHA-L-ARABINOFURANOSIDASE); hydrolase, acting on glycosyl bonds	Metabolism
Gma.1988.1.S1_at	4.05846E-06	2.05585	BE659231	Probable 3-beta-hydroxysteroid-delta(8),delta(7)-isomerase [Arabidopsis thaliana (Mouse-ear cress)]	AT1G20050	HYD1 (Hydra 1)	Metabolism
Gma.2019.1.S1_at	1.27187E-05	3.00838	U26457	Lipoxygenase [Glycine max (Soybean)]	AT1G55020	LOX1 (Lipoxygenase 1); lipoxygenase	Metabolism
Gma.2450.1.A1_at	0.00163407	2.21488	BI970853	Anthocyanidin 3-O-glucosyltransferase [Petunia hybrida (Petunia)]	0	glycosyltransferase family protein	Metabolism
Gma.3161.1.S1_at	0.0130601	2.10813	AF353620	Glutamine synthetase [Glycine max (Soybean)]	AT5G35630	GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	Metabolism
Gma.3988.1.S1_at	0.00272086	2.16595	BE658819	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G80160	lactoylglutathione lyase family protein / glyoxalase I family protein	Metabolism
Gma.4429.1.S1_at	0.000456307	2.30983	BI967598	Ascorbate oxidase [Glycine max (Soybean)]	AT5G21105	L-ascorbate oxidase/ copper ion binding	Metabolism
Gma.4958.1.A1_at	5.31447E-05	3.0051	BI969925	F12P19.5 protein [Arabidopsis thaliana (Mouse-ear cress)]	0	AMP-binding protein, putative	Metabolism
Gma.5160.1.S1_at	0.000206327	2.02447	AJ563382	Ornithine decarboxylase [Glycine max (Soybean)]	0	diaminopimelate decarboxylase, putative / DAP carboxylase, putative	Metabolism

Gma.5205.1.A1_at	0.000249296	2.15131	BI970186	AT5g55180/MCO15 13, putative [Medicago truncatula (Barrel medic)]	AT5G67460	glycosyl hydrolase family protein 17	Metabolism
Gma.529.1.S1_x_at	4.56377E-06	2.02918	AI939079	Acid phosphatase precursor [Phaseolus vulgaris (Kidney bean) (French bean)]	AT5G34850	ATPAP26/PAP26 (purple acid phosphatase 26); acid phosphatase/protein serine/threonine phosphatase	Metabolism
Gma.5886.1.A1_at	0.000536655	2.29537	CD395987	Fructokinase-like protein [Cicer arietinum (Chickpea) (Garbanzo)]	AT1G06030; AT1G50390	[AT1G06030, pfkB-type carbohydrate kinase family protein];[AT1G50390, fructokinase-related]	Metabolism
Gma.5992.4.S1_a_at	9.06487E-05	2.39559	BM567831	Aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana (Mouse-ear cress)]	AT3G24503	ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Metabolism
Gma.5992.4.S1_at	0.00220407	3.03528	BM567831	Aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana (Mouse-ear cress)]	AT3G24503	ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Metabolism
Gma.5992.4.S1_x_at	0.000140348	2.22436	BM567831	Aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana (Mouse-ear cress)]	AT3G24503	ALDH2C4 (REDUCED EPIDERMAL FLUORESCENCE1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Metabolism
Gma.6037.1.S1_at	3.40537E-05	2.26918	CD390794	NA	AT2G19070	transferase family protein	Metabolism
Gma.6211.1.S1_at	0.00805578	2.13159	BU089706	Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G41080	glycerophosphoryl diester phosphodiesterase family protein	Metabolism
Gma.6469.1.A1_at	0.000164835	2.61314	BI969830	Immunoglobulin/major histocompatibility complex; 2OG-Fe(II) oxygenase [Medicago truncatula (Barrel medic)]	0	0	Metabolism
Gma.6532.1.S1_at	0.000109952	4.33558	BQ627617	Class III chitinase [Medicago truncatula (Barrel medic)]	AT5G24090	acidic endochitinase (CHIB1)	Metabolism
Gma.7085.1.S1_at	7.01895E-05	2.02664	BE820335	SAM (And some other nucleotide) binding motif [Medicago truncatula (Barrel medic)]	AT1G73600	phosphoethanolamine N-methyltransferase 3, putative (NMT3)	Metabolism
Gma.7418.1.S1_at	0.00602641	3.29549	BU547276	F21F23.15 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G13710	CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding	Metabolism
Gma.7515.1.S1_at	0.00636991	2.09895	BU548256	Expressed protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G06925	ATSPLA2-ALPHA/PLA2-ALPHA (PHOSPHOLIPASE A2-ALPHA); phospholipase A2	Metabolism
Gma.7600.1.S1_at	5.22721E-05	3.03251	BU548955	NA	AT5G51520	invertase/pectin methylesterase inhibitor family protein	Metabolism
Gma.7832.1.S1_s_at	0.0114095	2.37217	CD392810	3-ketoacyl-CoA synthase [Gossypium hirsutum (Upland cotton)]	AT1G68530	CUT1 (CUTICULAR 1); acyltransferase	Metabolism
Gma.8215.2.S1_at	0.000107541	2.10166	BQ296859	Cytochrome P450 family protein, expressed [Oryza sativa (japonica cultivar group)]	AT1G13710	CYP78A5 (cytochrome P450, family 78, subfamily A, polypeptide 5); oxygen binding	Metabolism
Gma.8279.1.A1_at	0.00259387	2.04051	BU549975	NA	AT5G51520	invertase/pectin methylesterase inhibitor family protein	Metabolism
Gma.8489.1.S1_at	0.000517244	2.05662	AB030493	Thiamin biosynthetic enzyme [Glycine max (Soybean)]	AT5G54770	TH1 (THIAZOLE REQUIRING)	Metabolism
Gma.8520.1.S1_at	0.00147126	2.20829	CA802722	Acid phosphatase [Glycine max (Soybean)]	AT5G51260	acid phosphatase, putative	Metabolism

Gma.8867.2.S1_at	0.000511752	4.47747	AW200744	UDP-glucuronosyl/UDP-glucosyltransferase [Medicago truncatula (Barrel medic)]	AT1G22400	UGT85A1 (UDP-glucosyl transferase 85A1); UDP-glycosyltransferase/transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Metabolism
Gma.8966.1.S1_at	4.95548E-05	2.77323	BU765374	Lipase, class 3 [Medicago truncatula (Barrel medic)]	0	lipase class 3 family protein	Metabolism
Gma.9130.1.A1_at	6.53062E-07	6.69047	BI969027	Apyrase GS52 [Glycine soja (Wild soybean)]	AT5G18280	ATAPY2 (APYRASE 2)	Metabolism
Gma.9176.1.S1_at	0.0115441	3.61237	CA802590	UDP-glucuronosyl/UDP-glucosyltransferase [Medicago truncatula]	AT4G01070	UDP-glucuronosyl/UDP-glucosyl transferase family protein	Metabolism
Gma.9185.1.S1_at	0.001033	7.36549	AW459610	Putative GDSL-motif lipase/acylhydrolase [Arabidopsis thaliana (Mouse-ear cress)]	AT3G04290	ATLTL1/LTL1 (LI-TOLERANT LIPASE 1); carboxylic ester hydrolase	Metabolism
Gma.9322.1.A1_at	0.000451046	2.02914	BI969538	Hypothetical protein F15G16.70 [Arabidopsis thaliana (Mouse-ear cress)]	0	lipase class 3 family protein	Metabolism
Gma.9957.1.S1_at	5.21279E-05	2.07223	BE820632	Glucosyltransferase-7 [Phaseolus angularis (Adzuki bean) (Vigna angularis)]	AT1G05680	UDP-glucuronosyl/UDP-glucosyl transferase family protein	Metabolism
GmaAffx.11201.1.A1_at	0.00214946	2.14562	CD409722	Lipolytic enzyme, G-D-S-L [Medicago truncatula (Barrel medic)]	AT1G54790	GDSL-motif lipase/hydrolase family protein	Metabolism
GmaAffx.11815.1.S1_at	0.000518941	3.03525	AW311637	Methyltransferase [Prunus armeniaca (Apricot)]	0	0	Metabolism
GmaAffx.1301.90.S1_s_at	1.59037E-05	4.2662	BU764871	CPRD49 protein [Vigna unguiculata (Cowpea)]	AT3G11210	GDSL-motif lipase/hydrolase family protein	Metabolism
GmaAffx.15940.1.S1_at	0.000452343	2.02141	AI522941	Acid beta-fructofuranosidase precursor (EC 3.2.1.26) (Acid sucrose hydrolase) (Acid invertase) (AI) (Vacuolar invertase) [Contains: Acid beta-fructofuranosidase 30 kDa subunit; Acid beta-fructofuranosidase 38 kDa subunit] [Phaseolus aureus (Mung bean) (Vi	AT1G12240	ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTASE); beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Metabolism
GmaAffx.16966.1.S1_at	0.00621704	2.77424	BG882760	Putative metallophosphatase [Lupinus luteus (European yellow lupin)]	AT5G50400	ATPAP27/PAP27 (purple acid phosphatase 27); acid phosphatase/ protein serine/threonine phosphatase	Metabolism
GmaAffx.18905.1.S1_at	0.000292466	3.19093	BM523606	CXE carboxylesterase [Malus pumila]	AT5G06570	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16080.1); similar to CXE carboxylesterase [Actinidia deliciosa] (GB:ABB89016.1); contains InterPro domain Esterase/lipase/thioesterase; (InterPro:IPR000379)	Metabolism
GmaAffx.19096.1.S1_at	0.000127034	2.02583	BM522826	Cytochrome P450 71D8 [Glycine max (Soybean)]	0	CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23); oxygen binding	Metabolism
GmaAffx.19831.1.S1_at	0.000196569	2.02337	BU549972	Cytochrome P450 monooxygenase CYP716A12 [Medicago truncatula (Barrel medic)]	AT5G36130; AT5G36110	[AT5G36130, cytochrome P450 family];[AT5G36110, CYP716A1 (cytochrome P450, family 716, subfamily A, polypeptide 1); oxygen binding]	Metabolism

GmaAffx.21595.1.S1_at	0.00964574	2.60094	BE059253	Aldehyde dehydrogenase [Medicago truncatula (Barrel medic)]	AT4G34131; AT4G34135	[AT4G34131, UGT73B3 (UDP-glucosyl transferase 73B3); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring hexosyl groups];[AT4G34135, UGT73B2; UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase]	Metabolism
GmaAffx.21753.1.S1_at	0.0126527	2.02138	CA784528	Isopentenyl transferase [Glycine max (Soybean)]	AT5G19040	ATIPT5 (Arabidopsis thaliana isopentenyltransferase 5); transferase, transferring alkyl or aryl (other than methyl) groups	Metabolism
GmaAffx.23311.1.A1_at	0.00760111	2.4733	BI969379	L-galactose-1-phosphate phosphatase [Actinidia deliciosa (Kiwi)]	AT3G02870	VTC4; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Metabolism
GmaAffx.2475.1.S1_at	0.0094571	2.40776	AW100779	NA	AT1G77240	AMP-binding protein, putative	Metabolism
GmaAffx.26533.1.A1_s_at	0.0166872	3.3147	BE659836	Hypothetical protein AT4g28940 [Arabidopsis thaliana (Mouse-ear cress)]	AT4G28940	catalytic	Metabolism
GmaAffx.27192.1.S1_at	3.74894E-05	2.02721	BE823286	TK1-like deoxyribonucleoside kinase [Lycopersicon esculentum (Tomato)]	AT3G07800	thymidine kinase, putative	Metabolism
GmaAffx.28120.1.S1_at	7.08356E-05	2.32216	BM143646	Flavonoid 3-O-galactosyl transferase [Vigna mungo (Rice bean) (Black gram)]	AT5G17050	UDP-glucuronosyl/UDP-glucosyl transferase family protein	Metabolism
GmaAffx.28539.1.S1_at	0.00214091	2.12078	BQ080184	Similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana (Mouse-ear cress)]	AT2G39220	PLA IIB/PLP6 (Patatin-like protein 6); nutrient reservoir	Metabolism
GmaAffx.32023.1.S1_at	0.0139643	2.72734	BG046495	MtN21 protein [Medicago truncatula (Barrel medic)]	AT5G07050	nodulin MtN21 family protein	Metabolism
GmaAffx.33147.1.S1_at	0.00455389	3.44072	BQ452965	Cytochrome P-450 [Phalaenopsis sp. SM9108]	AT1G74110	CYP78A10 (cytochrome P450, family 78, subfamily A, polypeptide 10); oxygen binding	Metabolism
GmaAffx.33480.1.A1_at	0.0144548	2.03103	BU551196	Putative phosphoribosylanthranilate transferase [Arabidopsis thaliana (Mouse-ear cress)]	AT3G03680	C2 domain-containing protein	Metabolism
GmaAffx.33611.1.S1_at	8.42059E-05	2.63663	BU765780	E-class P450, group I [Medicago truncatula (Barrel medic)]	AT2G42247; AT2G42250	[AT2G42250, CYP712A1 (cytochrome P450, family 712, subfamily A, polypeptide 1); oxygen binding]	Metabolism
GmaAffx.34785.21.S1_at	4.19589E-06	5.16698	CA799146	F4H5.9 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G06830	glutaredoxin family protein	Metabolism
GmaAffx.3526.1.S1_at	0.000984765	4.82693	BE658646	Apyrase GS50 [Glycine soja (Wild soybean)]	0	0	Metabolism
GmaAffx.3702.1.S1_at	0.0136128	2.45352	BE821030	Hypothetical protein F28O9.250 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Metabolism
GmaAffx.37316.1.S1_at	0.000436851	2.30726	AW733720	NA	AT5G20740	invertase/pectin methylesterase inhibitor family protein	Metabolism
GmaAffx.37484.1.S1_at	2.69545E-05	2.12908	BG651852	Hypothetical protein F15G16.140 [Arabidopsis thaliana (Mouse-ear cress)]	0	auxin-responsive protein -related	Metabolism
GmaAffx.37484.2.S1_at	0.00860109	2.73352	BQ629925	Hypothetical protein OJ1214 E03.7 [Oryza sativa (japonica cultivar-group)]	0	auxin-responsive protein -related	Metabolism

GmaAffx.377.1.S1_at	1.53853E-06	2.48852	BE822954	Mevalonate kinase/phosphomevalonate kinase [Medicago truncatula (Barrel medic)]	AT5G27450	MK/MVK; mevalonate kinase	Metabolism
GmaAffx.40069.1.A1_at	0.0125783	2.71752	BE658613	AMP-dependent synthetase and ligase [Medicago truncatula (Barrel medic)]	AT3G23790	AMP-binding protein, putative	Metabolism
GmaAffx.40972.1.S1_at	0.0012042	2.01995	BQ453416	Short-chain dehydrogenase/reductase SDR [Medicago truncatula (Barrel medic)]	AT3G26760	short-chain dehydrogenase/reductase (SDR) family protein	Metabolism
GmaAffx.41338.1.A1_at	0.0048453	2.81562	BU550133	Cytochrome P450 monooxygenase CYP716A12 [Medicago truncatula (Barrel medic)]	AT5G36130; AT5G36110	[AT5G36130, cytochrome P450 family];[AT5G36110, CYP716A1 (cytochrome P450, family 716, subfamily A, polypeptide 1); oxygen binding]	Metabolism
GmaAffx.43208.1.A1_at	0.000668289	2.54817	CD412962	NA	AT3G29670	transferase family protein	Metabolism
GmaAffx.45841.1.S1_at	9.08243E-09	2.08353	BI702220	Isoflavone reductase homolog [Lupinus albus (White lupin)]	AT1G32100	pinoresinol-lariciresinol reductase, putative	Metabolism
GmaAffx.4604.1.S1_at	4.60831E-05	2.39233	BI426477	Glucosyltransferase [Ipomoea purpurea (Common morning glory) (Pharbitis purpurea)]	AT5G54010	glycosyltransferase family protein	Metabolism
GmaAffx.46344.2.S1_s_at	0.0023128	2.58344	BQ629356	Phosphoserine phosphatase, chloroplast precursor [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Metabolism
GmaAffx.47583.1.S1_at	0.00424254	2.49802	CA853439	E-class P450, group I [Medicago truncatula (Barrel medic)]	AT4G36220	FAH1 (FERULATE-5-HYDROXYLASE 1); ferulate 5-hydroxylase	Metabolism
GmaAffx.50360.1.S1_at	0.000135029	2.01439	BM309759	CXE carboxylesterase [Actinidia arguta]	AT5G62180	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45600.1); similar to CXE carboxylesterase [Actinidia arguta] (GB:ABB89014.1); contains InterPro domain Esterase/lipase/thioesterase; (InterPro:IPR000379)	Metabolism
GmaAffx.50571.1.S1_s_at	6.53649E-05	2.18452	BI943299	Cytochrome P450 monooxygenase CYP78F1 [Medicago truncatula (Barrel medic)]	AT3G61880	CYP78A9 (CYTOCHROME P450 78A9); oxygen binding	Metabolism
GmaAffx.51505.1.S1_at	0.0117407	2.22647	BE611553	Putative acetone-cyanohydrin lyase [Arabidopsis thaliana (Mouse-ear cress)]	0	ACL (ACETONE-CYANOHYDRIN LYASE); hydrolase	Metabolism
GmaAffx.57896.2.S1_at	0.000493848	2.6375	AW830233	E-class P450, group I [Medicago truncatula (Barrel medic)]	AT3G26230	CYP71B24 (cytochrome P450, family 71, subfamily B, polypeptide 24); oxygen binding	Metabolism
GmaAffx.61867.1.S1_at	0.00181317	2.76492	AW101682	Phenol hydroxylase reductase; Ferric reductase-like transmembrane component [Medicago truncatula (Barrel medic)]	0	FRO2 (FERRIC REDUCTION OXIDASE 2); ferric-chelate reductase	Metabolism
GmaAffx.62309.1.S1_at	0.000659327	2.4525	AW704333	Inositol polyphosphate related phosphatase [Medicago truncatula (Barrel medic)]	AT2G01900	endonuclease/exonuclease/phosphatase family protein	Metabolism
GmaAffx.66451.1.S1_at	2.72993E-05	2.33818	AW309198	Galactose-binding like; Alpha-L-arabinofuranosidase, C-terminal [Medicago truncatula (Barrel medic)]	AT5G26120	glycosyl hydrolase family protein 51	Metabolism
GmaAffx.66649.1.S1_at	0.00164613	2.48088	CA819378	SAM (And some other nucleotide) binding motif [Medicago truncatula (Barrel medic)]	AT1G48600	phosphoethanolamine N-methyltransferase 2, putative (NMT2)	Metabolism
GmaAffx.68419.1.S1_at	0.000176649	2.44177	BI425574	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT3G28050	nodulin MtN21 family protein	Metabolism

GmaAffx.69328.1.S1_at	0.0167255	5.40235	BM891265	PREDICTED: similar to CG6084-PA, isoform A [Tribolium castaneum]	0	mannose 6-phosphate reductase (NADPH-dependent), putative	Metabolism
GmaAffx.72212.1.A1_at	0.000123247	2.06852	BE824300	Glucosyltransferase [Ipomoea purpurea (Common morning glory) (Pharbitis purpurea)]	AT1G64920	glycosyltransferase family protein	Metabolism
GmaAffx.72986.1.S1_at	0.00198784	2.16334	BI317536	Inositol polyphosphate related phosphatase [Medicago truncatula (Barrel	AT2G01900	endonuclease/exonuclease/ phosphatase family protein	Metabolism
GmaAffx.73241.1.S1_at	0.000381389	2.15476	BM188470	Similarity to endo-beta-N-acetylglucosaminidase [Arabidopsis thaliana (Mouse-ear cress)]	AT5G05460	hydrolase, acting on glycosyl bonds	Metabolism
GmaAffx.73653.1.S1_at	0.00196822	2.16258	BE211623	Cytochrome P450 [Petunia hybrida (Petunia)]	AT3G61040	CYP76C7 (cytochrome P450, family 76, subfamily C, polypeptide 7); oxygen binding	Metabolism
GmaAffx.74009.1.S1_at	0.0129326	2.25089	BM093331	UDP-glucosyltransferase HRA25 [Phaseolus vulgaris (Kidney bean) (French bean)]	AT3G02100	UDP-glucuronosyl/UDP-glucosyl transferase family protein	Metabolism
GmaAffx.77438.1.A1_at	0.00861376	6.19412	AW831599	Phosphonopyruvate decarboxylase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	0	2,3-biphosphoglycerate-independent phosphoglycerate mutase-related / phosphoglyceromutase-related	Metabolism
GmaAffx.79229.1.S1_at	0.00113127	2.00074	CA800208	Hypothetical protein T17J13.120 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G62160	transferase family protein	Metabolism
GmaAffx.79891.1.S1_at	0.000469989	4.73411	AI988440	Putative cytochrome P450 monooxygenase [Cicer arietinum (Chickpea) (Garbanzo)]	AT2G02580	CYP71B9 (cytochrome P450, family 71, subfamily B, polypeptide 9); oxygen binding	Metabolism
GmaAffx.80249.1.S1_at	0.0040857	2.32335	AW397976	Probable rhamnose biosynthetic enzyme 2 [Arabidopsis thaliana (Mouse-ear	AT3G14790	RHM3 (RHAMNOSE BIOSYNTHESIS 3); catalytic	Metabolism
GmaAffx.80904.1.A1_s_at	0.00328813	4.41031	BE583523	NA	AT5G62530	ALDH12A1 (Aldehyde dehydrogenase 12A1); 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase	Metabolism
GmaAffx.81018.1.A1_at	3.94856E-05	2.47546	BE657998	Alpha-1,4-glucan-protein synthase [UDP-forming] [Pisum sativum (Garden pea)]	0	0	Metabolism
GmaAffx.81287.1.S1_at	0.0013117	3.18949	BG789983	O-methyltransferase [Prunus dulcis (Almond) (Prunus amygdalus)]	0	O-methyltransferase family 2 protein	Metabolism
GmaAffx.81584.1.S1_at	6.64826E-08	2.42331	BI426969	NA	AT4G37150	esterase, putative	Metabolism
GmaAffx.82528.1.S1_at	0.000159215	2.46999	CA800460	Putative adenosylhomocysteinase [Medicago sativa (Alfalfa)]	AT5G16250	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02640.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78001.1)	Metabolism
GmaAffx.82528.2.S1_at	0.000884804	2.24632	BI702248	Putative adenosylhomocysteinase [Medicago sativa (Alfalfa)]	AT5G16250	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02640.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78001.1)	Metabolism
GmaAffx.82528.2.S1_s_at	7.34402E-05	2.30075	BI702248	Putative adenosylhomocysteinase [Medicago sativa (Alfalfa)]	AT5G16250	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02640.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE78001.1)	Metabolism

GmaAffx.82887.1.S1_at	8.74651E-05	2.18585	BI973946	Probable rhamnose biosynthetic enzyme 1 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G78570	RHM1/ROL1 (RHAMNOSE BIOSYNTHESIS1); UDP-glucose 4,6-dehydratase/ catalytic	Metabolism
GmaAffx.8328.1.S1_at	0.00020746	2.63754	AW831983	Generic methyltransferase [Medicago truncatula (Barrel medic)]	AT2G45750	dehydration-responsive family protein	Metabolism
GmaAffx.84418.1.S1_at	0.000142842	3.36777	BQ576552	Nodulin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT4G08290	nodulin MtN21 family protein	Metabolism
GmaAffx.84946.1.S1_s_at	0.00350102	2.10993	BM523917	Glyoxal oxidase [Vitis pseudoreticulata]	AT3G53950	glyoxal oxidase-related	Metabolism
GmaAffx.85662.2.S1_at	0.00256943	2.21608	AI496432	Hypothetical protein F15G16.140 [Arabidopsis thaliana (Mouse-ear cress)]	0	auxin-responsive protein -related	Metabolism
GmaAffx.86766.1.S1_at	3.36643E-05	2.33196	CA820659	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT1G68170	nodulin MtN21 family protein	Metabolism
GmaAffx.87031.1.S1_at	0.000550399	2.05463	AW507869	L-ascorbate oxidase precursor [Medicago truncatula (Barrel medic)]	AT5G21105	L-ascorbate oxidase/ copper ion binding	Metabolism
GmaAffx.87441.1.S1_at	5.43325E-05	2.17616	BQ273031	UDP-glucose glucosyltransferase [Medicago truncatula (Barrel medic)]	0	UGT73B3 (UDP-glucosyl transferase 73B3); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring hexosyl groups	Metabolism
GmaAffx.87888.1.S1_s_at	5.08991E-05	2.13703	BU578170	NA	AT3G17130	invertase/pectin methylesterase inhibitor family protein	Metabolism
GmaAffx.9102.1.S1_at	0.0034028	2.17852	BI971064	Lipoxygenase [Medicago truncatula (Barrel medic)]	AT1G55020	LOX1 (Lipoxygenase 1); lipoxygenase	Metabolism
GmaAffx.91115.1.S1_at	0.00219045	2.34063	CF806840	Glyoxal oxidase [Vitis pseudoreticulata]	AT3G53950	glyoxal oxidase-related	Metabolism
GmaAffx.91817.1.S1_at	0.0120981	4.38231	CF807542	Galactose mutarotase-like [Medicago truncatula (Barrel medic)]	AT5G15140	aldose 1-epimerase family protein	Metabolism
GmaAffx.93221.1.S1_s_at	1.18629E-05	2.18473	CF808946	O-methyltransferase, family 2 [Medicago truncatula (Barrel medic)]	0	O-methyltransferase family 2 protein	Metabolism
GmaAffx.9437.1.S1_at	0.000217959	2.29671	BI942964	S-adenosylmethionine synthetase 3 [Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle)]	AT1G02500	SAM1 (S-adenosylmethionine synthetase 1); methionine adenosyltransferase	Metabolism
Gma.10234.1.S1_at	0.000127544	2.88406	BE023458	NA	0	0	No Homology to Known Proteins
Gma.12949.1.A1_at	0.00373568	2.12527	CD411827	NA	0	0	No Homology to Known Proteins
Gma.13218.1.A1_s_at	0.0010172	2.04394	CD391892	NA	0	0	No Homology to Known Proteins
Gma.13485.1.A1_at	0.00280427	3.67309	CD398890	NA	0	0	No Homology to Known Proteins
Gma.14318.1.S1_at	0.000287515	2.4869	CA852942	NA	0	0	No Homology to Known Proteins
Gma.15881.1.A1_at	0.00491024	2.03837	CD400159	NA	0	0	No Homology to Known Proteins
Gma.15993.1.A1_at	0.00105921	2.42213	BG237670	NA	0	0	No Homology to Known Proteins
Gma.16139.1.S1_at	0.00194872	2.42011	CD402105	NA	0	0	No Homology to Known Proteins
Gma.17231.1.A1_at	0.000197224	4.22293	AW309582	NA	0	0	No Homology to Known Proteins
Gma.17957.1.S1_at	0.0145657	2.05372	AW760876	NA	0	0	No Homology to Known Proteins

Gma.357.1.A1_at	0.0013379	2.01047	AW348892	NA	0	0	No Homology to Known Proteins
Gma.368.1.S1_at	0.00339802	2.48504	AW349594	NA	0	0	No Homology to Known Proteins
Gma.3965.1.S1_at	1.27158E-05	3.36051	BE821339	NA	0	0	No Homology to Known Proteins
Gma.5399.1.A1_at	0.00830436	2.00448	CD402231	NA	0	0	No Homology to Known Proteins
Gma.6139.1.S1_at	0.000139443	2.16321	CD390793	NA	0	0	No Homology to Known Proteins
Gma.6416.1.S1_at	9.64576E-05	2.37892	BM139646	NA	0	0	No Homology to Known Proteins
Gma.677.1.S1_at	0.0064878	2.37862	BU082252	NA	0	0	No Homology to Known Proteins
Gma.786.1.A1_at	0.00110028	5.41491	BE820386	NA	0	0	No Homology to Known Proteins
Gma.8048.1.S1_at	0.000133916	2.25929	BG511047	NA	0	0	No Homology to Known Proteins
Gma.8594.1.S1_at	0.00546731	3.36555	BU760779	NA	0	0	No Homology to Known Proteins
Gma.9036.1.S1_at	2.31799E-06	2.32052	AW309501	NA	0	0	No Homology to Known Proteins
Gma.9966.1.S1_at	0.00771673	2.02902	CD396068	NA	0	0	No Homology to Known Proteins
GmaAffx.10340.1.S1_s_at	0.00984319	2.59025	CA938421	NA	0	0	No Homology to Known Proteins
GmaAffx.11214.1.A1_at	0.00235835	2.21949	CD413632	NA	0	0	No Homology to Known Proteins
GmaAffx.11297.1.S1_at	2.5971E-06	2.04867	BI967760	NA	0	0	No Homology to Known Proteins
GmaAffx.12519.1.S1_at	7.02111E-06	2.24942	BU080591	NA	0	0	No Homology to Known Proteins
GmaAffx.12723.1.A1_at	0.000470598	6.35926	BE658883	NA	0	0	No Homology to Known Proteins
GmaAffx.15362.1.S1_at	0.000950689	2.10717	BU926414	NA	0	0	No Homology to Known Proteins
GmaAffx.16092.1.A1_at	0.000120542	2.13969	BE658167	NA	0	0	No Homology to Known Proteins
GmaAffx.16437.1.A1_at	0.00106796	2.35877	AW349866	NA	0	0	No Homology to Known Proteins
GmaAffx.1859.1.A1_at	0.016302	2.19089	BU549902	NA	0	0	No Homology to Known Proteins
GmaAffx.18649.1.S1_at	0.0153896	2.08668	AW351025	NA	0	0	No Homology to Known Proteins
GmaAffx.24530.1.S1_at	0.0167466	2.28276	BU762196	NA	0	0	No Homology to Known Proteins
GmaAffx.27508.1.S1_at	0.00110315	4.9673	BI315773	NA	0	0	No Homology to Known Proteins
GmaAffx.27581.1.S1_at	2.19054E-05	2.25049	CD414601	NA	0	0	No Homology to Known Proteins
GmaAffx.28689.1.S1_at	0.00531001	2.08962	BQ610782	NA	0	0	No Homology to Known Proteins

GmaAffx.30176.1.A1_at	0.00563407	2.33176	CD417988	NA	0	0	No Homology to Known Proteins
GmaAffx.310.1.S1_at	0.00522693	2.05526	AW458428	NA	0	0	No Homology to Known Proteins
GmaAffx.31311.1.S1_at	0.000770496	2.36164	BI970399	NA	0	0	No Homology to Known Proteins
GmaAffx.36823.1.S1_at	0.000740925	2.31888	BI967614	NA	0	0	No Homology to Known Proteins
GmaAffx.37221.1.S1_at	0.00127179	2.10356	BM523361	NA	0	0	No Homology to Known Proteins
GmaAffx.41990.1.S1_at	6.09011E-05	2.17972	CA936708	NA	0	0	No Homology to Known Proteins
GmaAffx.42417.1.S1_at	0.00345275	2.99937	BE611786	NA	0	0	No Homology to Known Proteins
GmaAffx.43784.1.A1_s_at	5.23362E-05	2.00181	AW350840	NA	0	0	No Homology to Known Proteins
GmaAffx.4508.1.S1_at	0.0130478	2.09929	BI316036	NA	0	0	No Homology to Known Proteins
GmaAffx.45755.1.S1_at	0.00980368	2.17519	BI470908	NA	0	0	No Homology to Known Proteins
GmaAffx.45991.1.A1_at	8.27217E-05	2.3342	BI969588	NA	0	0	No Homology to Known Proteins
GmaAffx.45999.1.A1_at	0.00110648	2.24693	BI969944	NA	0	0	No Homology to Known Proteins
GmaAffx.47744.1.A1_at	2.24009E-05	2.11407	CD401867	NA	0	0	No Homology to Known Proteins
GmaAffx.48416.1.S1_at	0.00954002	2.73209	AW318337	NA	0	0	No Homology to Known Proteins
GmaAffx.50999.1.S1_at	0.00190615	2.93303	AW509187	NA	0	0	No Homology to Known Proteins
GmaAffx.51463.1.S1_at	0.0014568	3.04263	BE659841	NA	0	0	No Homology to Known Proteins
GmaAffx.5272.1.S1_at	0.000869998	2.48204	BM522624	NA	0	0	No Homology to Known Proteins
GmaAffx.53121.1.A1_at	1.78099E-05	2.07845	BE820032	NA	0	0	No Homology to Known Proteins
GmaAffx.54537.1.S1_at	0.000986107	2.18685	BG551770	NA	0	0	No Homology to Known Proteins
GmaAffx.55928.1.S1_at	0.0166232	2.06929	BQ612397	NA	0	0	No Homology to Known Proteins
GmaAffx.56672.1.S1_at	0.000704607	9.30944	CB063595	NA	0	0	No Homology to Known Proteins
GmaAffx.58518.1.A1_at	0.00564482	4.6987	BE820428	NA	0	0	No Homology to Known Proteins
GmaAffx.59486.1.S1_at	0.000406688	4.18728	BI471586	NA	0	0	No Homology to Known Proteins
GmaAffx.59971.1.S1_at	0.0124067	4.25506	BM177559	NA	0	0	No Homology to Known Proteins
GmaAffx.6000.1.A1_at	0.00150827	3.45645	BU549774	NA	0	0	No Homology to Known Proteins
GmaAffx.60846.1.A1_at	0.0148787	2.97343	BU550268	NA	0	0	No Homology to Known Proteins

GmaAffx.60949.1.S1_at	0.0010799	2.75577	BU763299	NA	0	0	No Homology to Known Proteins
GmaAffx.61526.1.A1_s_at	0.00998914	2.39038	CD417915	NA	0	0	No Homology to Known Proteins
GmaAffx.62017.1.S1_at	0.0155725	3.59733	AW278559	NA	0	0	No Homology to Known Proteins
GmaAffx.6302.1.S1_at	0.000357569	2.77094	CA801413	NA	0	0	No Homology to Known Proteins
GmaAffx.64250.1.A1_at	0.00638959	3.31674	BI967675	NA	0	0	No Homology to Known Proteins
GmaAffx.65566.1.A1_at	0.00897138	5.29732	CA785452	NA	0	0	No Homology to Known Proteins
GmaAffx.66587.1.S1_at	0.000920814	2.00937	AW432768	NA	0	0	No Homology to Known Proteins
GmaAffx.66986.1.S1_at	0.000671663	2.19805	BI970793	NA	0	0	No Homology to Known Proteins
GmaAffx.69470.1.S1_at	0.00511029	2.03976	BE803881	NA	0	0	No Homology to Known Proteins
GmaAffx.70540.1.A1_at	0.00727855	5.0674	CD409006	NA	0	0	No Homology to Known Proteins
GmaAffx.71084.1.S1_at	0.000135428	2.07567	AW311116	NA	0	0	No Homology to Known Proteins
GmaAffx.73005.1.S1_at	0.00900279	2.05139	BI321220	NA	0	0	No Homology to Known Proteins
GmaAffx.75079.1.A1_at	0.00252922	2.32316	CD404293	NA	0	0	No Homology to Known Proteins
GmaAffx.75247.1.S1_at	0.00635648	6.44793	AI748250	NA	0	0	No Homology to Known Proteins
GmaAffx.768.1.A1_at	0.00147998	8.59958	BE821548	NA	0	0	No Homology to Known Proteins
GmaAffx.76964.1.S1_at	0.00587084	3.77259	BU577127	NA	0	0	No Homology to Known Proteins
GmaAffx.78787.1.S1_at	0.0168538	3.81853	CA938386	NA	0	0	No Homology to Known Proteins
GmaAffx.79321.1.S1_at	0.00583871	2.48375	CA850892	NA	0	0	No Homology to Known Proteins
GmaAffx.79963.1.S1_at	0.00320399	2.21214	BG362727	NA	0	0	No Homology to Known Proteins
GmaAffx.80099.1.S1_at	0.000211308	3.33284	BQ298229	NA	0	0	No Homology to Known Proteins
GmaAffx.81947.1.S1_at	0.00032969	2.03898	BE609705	NA	0	0	No Homology to Known Proteins
GmaAffx.8248.1.S1_at	0.000625367	2.35108	BI426579	NA	0	0	No Homology to Known Proteins
GmaAffx.82574.1.S1_at	0.0104627	2.82687	BE806391	NA	0	0	No Homology to Known Proteins
GmaAffx.84445.1.S1_at	0.00018297	2.58507	AI974106	NA	0	0	No Homology to Known Proteins
GmaAffx.85440.1.A1_at	0.0116542	3.46879	BM731559	NA	0	0	No Homology to Known Proteins
GmaAffx.85650.1.S1_at	0.00132984	2.02929	BQ473221	NA	0	0	No Homology to Known Proteins

GmaAffx.85713.1.S1_at	0.00740383	2.77904	AW396379	NA	0	0	No Homology to Known Proteins
GmaAffx.86032.1.S1_at	0.00704285	2.17216	BF597286	NA	0	0	No Homology to Known Proteins
GmaAffx.86352.1.S1_at	0.0057152	2.19792	BG238111	NA	0	0	No Homology to Known Proteins
GmaAffx.87005.1.A1_at	0.014086	2.2356	BI971502	NA	0	0	No Homology to Known Proteins
GmaAffx.87886.1.S1_at	0.0128853	2.04975	BU082696	NA	0	0	No Homology to Known Proteins
GmaAffx.88555.1.A1_at	0.00705419	2.05705	CD390916	NA	0	0	No Homology to Known Proteins
GmaAffx.90548.1.S1_s_at	2.40638E-06	10.2272	CF806273	NA	0	0	No Homology to Known Proteins
GmaAffx.90548.1.S1_x_at	0.000473379	2.35554	CF806273	NA	0	0	No Homology to Known Proteins
GmaAffx.9778.1.S1_at	0.000678389	2.20488	BM308105	NA	0	0	No Homology to Known Proteins
Gma.5236.1.S1_at	0.000398881	2.42359	BI969602	RNA binding protein-like [Arabidopsis thaliana (Mouse-ear cress)]	AT3G54770	RNA recognition motif (RRM)-containing protein	Post-Transcription
GmaAffx.79131.1.A1_at	0.0138604	4.27703	BE660395	NA	AT3G23900	RNA recognition motif (RRM)-containing protein	Post-Transcription
GmaAffx.9348.1.S1_at	0.000333914	2.19983	AW350108	NA	AT1G78260	RNA recognition motif (RRM)-containing protein	Post-Transcription
Gma.16526.1.S1_at	0.000131887	2.6704	CD407998	Bifunctional nuclease [Zinnia elegans (Zinnia)]	AT3G12203	SCPL17 (serine carboxypeptidase-like 17); serine carboxypeptidase	Protein Destination & Storage
Gma.16870.1.A1_at	0.00458966	4.12079	CD404774	Peptidase M14, carboxypeptidase A [Medicago truncatula (Barrel medic)]	AT1G12330	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12900.1); similar to Peptidase M14, carboxypeptidase A [Medicago truncatula] (GB:ABE94280.1); contains domain TNF receptor-like (SSF57586)	Protein Destination & Storage
Gma.2488.1.S1_at	9.50855E-05	2.50106	CD406079	Serine carboxypeptidase 2 precursor (EC 3.4.16.6) (Serine carboxypeptidase II) (Carboxypeptidase D) (Bri1 suppressor 1) [Contains: Serine carboxypeptidase 2 chain A (Serine carboxypeptidase II chain A); Serine carboxypeptidase 2 chain B (Serine carboxypep	AT4G30610	BRS1 (BRI1 SUPPRESSOR 1)	Protein Destination & Storage
Gma.3460.1.S1_at	0.0161624	6.63307	BQ629044	Subtilisin-like protease C1 [Glycine max (Soybean)]	AT5G59190	subtilase family protein	Protein Destination & Storage
Gma.4914.2.S1_at	0.00355553	2.40298	BI973233	Root cap protein 2-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G54370	late embryogenesis abundant protein-related / LEA protein-related	Protein Destination & Storage
Gma.5139.1.S1_at	0.000783436	2.08465	AF243376	Glutathione S-transferase GST 21 [Glycine max (Soybean)]	AT3G62760	ATGSTF13 (Arabidopsis thaliana Glutathione S-transferase (class phi) 13); glutathione transferase	Protein Destination & Storage
Gma.5994.1.S1_at	1.03325E-05	2.11194	CD408043	Proteinase inhibitor I25, cystatin [Medicago truncatula (Barrel medic)]	AT5G47550	cysteine protease inhibitor, putative / cystatin, putative	Protein Destination & Storage
Gma.6374.2.S1_at	0.00292293	2.28711	CA799123	Peptidase A1, pepsin [Medicago truncatula (Barrel medic)]	AT5G07030	pepsin A	Protein Destination & Storage
Gma.6633.2.S1_at	6.96022E-05	2.00504	BE020127	Ubiquitin conjugating protein-like [Arabidopsis thaliana (Mouse-ear cress)]	AT1G50490	UBC20 (ubiquitin-conjugating enzyme 20); ubiquitin-protein ligase	Protein Destination & Storage

GmaAffx.179.1.S1_at	0.000699045	2.06946	AW164770	Hypothetical protein F5A18.27 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Protein Destination & Storage
GmaAffx.17961.2.S1_at	0.000653676	2.13985	BG511562	Heat shock protein Hsp70; Actin/actin-like [Medicago truncatula (Barrel medic)]	AT1G16030	HSP70B (heat shock protein 70B); ATP binding	Protein Destination & Storage
GmaAffx.21968.1.A1_at	1.92955E-05	5.91406	BE660774	Orn/DAP/Arg decarboxylase 2; Protease-associated PA; Proteinase inhibitor I9, subtilisin propeptide [Medicago truncatula (Barrel medic)]	AT5G67360	ARA12; subtilase	Protein Destination & Storage
GmaAffx.28861.1.S1_at	0.000118839	2.21926	BU080561	Orn/DAP/Arg decarboxylase 2; Protease-associated PA; Proteinase inhibitor I9, subtilisin propeptide [Medicago truncatula (Barrel medic)]	AT5G51750	subtilase family protein	Protein Destination & Storage
GmaAffx.31196.1.S1_s_at	0.00420302	2.3675	BE821537	Subtilisin-like protease C1 [Glycine max (Soybean)]	AT4G15040	subtilase family protein	Protein Destination & Storage
GmaAffx.35346.1.S1_at	0.0011887	2.47671	AW432825	NA	AT5G59190	subtilase family protein	Protein Destination & Storage
GmaAffx.39703.1.S1_at	0.000694126	2.52857	BE023656	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G23000; AT2G23010	[AT2G23000, SCPL10 (serine carboxypeptidase-like 10); serine carboxypeptidase];[AT2G23010, SCPL9; serine carboxypeptidase]	Protein Destination & Storage
GmaAffx.39703.2.S1_s_at	9.58739E-06	2.47004	AW307363	Serine carboxypeptidase, putative; 88458-86107 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G73300; AT5G36180	[AT1G73300, SCPL2 (serine carboxypeptidase-like 2); serine carboxypeptidase];[AT5G36180, SCPL1 (serine carboxypeptidase-like 1); serine carboxypeptidase]	Protein Destination & Storage
GmaAffx.5537.1.S1_at	0.00230214	2.4529	BQ081493	H ⁺ -transporting two-sector ATPase, delta (OSCP) subunit; Peptidase, metallopeptidases [Medicago truncatula (Barrel medic)]	AT1G59970	matrixin family protein	Protein Destination & Storage
GmaAffx.61125.1.S1_at	0.000741727	2.56712	CA799403	MtN5 protein precursor [Medicago truncatula (Barrel medic)]	0	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Protein Destination & Storage
GmaAffx.6733.1.S1_at	0.000181925	2.01779	AI736161	Peptidase M14, carboxypeptidase A [Medicago truncatula (Barrel medic)]	AT1G70230	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01430.1); similar to Protein of unknown function DUF231, plant [Medicago truncatula] (GB:ABE83215.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)	Protein Destination & Storage
GmaAffx.68175.1.S1_at	0.00251251	4.12142	BG650945	Subtilisin-like protease C1 [Glycine max (Soybean)]	AT5G59190	subtilase family protein	Protein Destination & Storage
GmaAffx.69661.1.S1_at	0.00581155	2.01876	BQ741578	F611.14 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G16860	merozoite surface protein-related	Protein Destination & Storage
GmaAffx.71056.1.S1_at	0.00170768	2.11577	BE329937	Signal recognition particle 9 kDa protein [Arabidopsis thaliana (Mouse-ear cress)]	AT3G49100	signal recognition particle 9 kDa protein, putative / SRP9, putative	Protein Destination & Storage
GmaAffx.82151.1.S1_at	0.00125325	4.91236	BI471566	Sali3-2 [Glycine max (Soybean)]	AT5G25610	RD22 (RESPONSIVE TO DESSICATION 22)	Protein Destination & Storage
GmaAffx.85056.1.S1_at	0.000404087	2.69211	AI900723	Hypothetical protein F2J7.6 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G25510	aspartyl protease family protein	Protein Destination & Storage
GmaAffx.85056.2.S1_at	0.000338398	2.89919	BU964909	Hypothetical protein F2J7.6 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G25510	aspartyl protease family protein	Protein Destination & Storage
GmaAffx.88625.1.A1_at	0.00211561	2.87771	CD405589	NA	0	0	Protein Destination & Storage

GmaAffx.91908.1.S1_at	0.004226	2.1586	CF807624	Hypothetical protein [Trifolium pratense (Red clover)]	AT1G09750	chloroplast nucleoid DNA-binding protein-related	Protein Destination & Storage
Gma.17934.1.S1_at	0.000866582	2.69531	BG237988	Translation initiation factor-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G54940	eukaryotic translation initiation factor SU11, putative	Protein Synthesis
Gma.8953.1.S1_at	0.000247208	2.47603	BU764603	NA	0	0	Protein Synthesis
GmaAffx.16959.1.S1_at	0.000921763	2.0857	CD486940	Ribosomal protein L6, signature 2 [Medicago truncatula (Barrel medic)]	AT5G53880	unknown protein	Protein Synthesis
GmaAffx.28702.1.S1_at	0.00520442	4.44574	BQ611373	RS17 NEUCR 40S ribosomal protein S17 [Emericella nidulans (Aspergillus nidulans)]	AT2G04390; AT5G04800; AT2G05220	[AT2G04390, 40S ribosomal protein S17 (RPS17A)];[AT5G04800, 40S ribosomal protein S17 (RPS17D)];[AT2G05220, 40S ribosomal protein S17 (RPS17B)]	Protein Synthesis
Gma.10150.1.A1_at	0.000122734	2.04816	AW277321	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MHC9 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G21420	oxidoreductase, 2OG-Fe(II) oxygenase family protein	Secondary Metabolism
Gma.11298.3.S1_a_at	3.01151E-06	2.5471	BE059139	Pectate lyase [Fragaria ananassa (Strawberry)]	AT1G04680	pectate lyase family protein	Secondary Metabolism
Gma.1326.3.S1_at	0.000244884	2.49259	AI442263	Pectate lyase [Gossypium hirsutum (Upland cotton)]	AT4G24780	pectate lyase family protein	Secondary Metabolism
Gma.14846.1.A1_at	0.0121714	6.73894	AW310268	Gibberellin 20-oxidase [Phaseolus vulgaris (Kidney bean) (French bean)]	0	0	Secondary Metabolism
Gma.2826.1.S1_at	3.49057E-05	2.30248	CD397710	Chalcone isomerase 1B1 [Glycine max (Soybean)]	AT3G55120	TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Secondary Metabolism
Gma.2826.1.S1_s_at	0.000118766	2.1247	CD397710	Chalcone isomerase 1B1 [Glycine max (Soybean)]	AT3G55120	TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Secondary Metabolism
Gma.2826.1.S1_x_at	4.91566E-05	2.07693	CD397710	Chalcone isomerase 1B1 [Glycine max (Soybean)]	AT3G55120	TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Secondary Metabolism
Gma.3668.3.S1_a_at	8.46034E-05	2.42804	AW704362	1-aminocyclopropane-1-carboxylic acid oxidase [Cicer arietinum (Chickpea) (Garbanzo)]	AT1G77330	1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	Secondary Metabolism
Gma.3668.3.S1_at	0.000196378	2.4025	AW704362	1-aminocyclopropane-1-carboxylic acid oxidase [Cicer arietinum (Chickpea) (Garbanzo)]	AT1G77330	1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	Secondary Metabolism
Gma.4438.2.S1_at	0.00518023	2.05404	BQ630502	2OG-Fe(II) oxygenase [Medicago truncatula (Barrel medic)]	AT5G24530	oxidoreductase, 2OG-Fe(II) oxygenase family protein	Secondary Metabolism
Gma.5026.1.A1_at	0.000909206	2.05195	BI970500	Chlorophyllase 1 [Brassica oleracea (Wild cabbage)]	AT1G19670	ATCLH1 (CORONATINE-INDUCED PROTEIN 1)	Secondary Metabolism
GmaAffx.13717.1.S1_at	0.00083662	2.59805	BI316021	Pectate lyase [Prunus mume (Japanese flowering apricot)]	AT4G24780	pectate lyase family protein	Secondary Metabolism
GmaAffx.24016.1.S1_at	0.0118319	2.66799	BQ253682	2OG-Fe(II) oxygenase [Medicago truncatula (Barrel medic)]	AT4G21200	ATGA2OX8 (GIBBERELLIN 2-OXIDASE 8); gibberellin 2-beta-dioxygenase	Secondary Metabolism
GmaAffx.2941.2.S1_at	0.00545684	2.81791	BM885445	Putative chalcone isomerase 3 [Glycine max (Soybean)]	AT1G53520	chalcone-flavanone isomerase-related	Secondary Metabolism
GmaAffx.6567.1.S1_at	0.00895537	2.17877	CD403256	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT4G27560; AT4G27570	[AT4G27560, glycosyltransferase family protein];[AT4G27570, glycosyltransferase family protein]	Secondary Metabolism
GmaAffx.77765.1.S1_at	4.97307E-05	2.91973	BI945137	NA	AT3G27400	pectate lyase family protein	Secondary Metabolism
GmaAffx.79052.1.S1_at	0.000804657	2.17064	BG726168	Brassinosteroid biosynthetic protein LKB [Pisum sativum (Garden pea)]	AT3G19820	DWF1 (DIMINUTO 1); catalytic	Secondary Metabolism
GmaAffx.86023.1.S1_at	0.000592774	2.23219	BU761776	Cytochrome P450 monooxygenase CYP701A16 [Glycine max (Soybean)]	AT5G25900	GA3 (GA REQUIRING 3); oxygen binding	Secondary Metabolism

GmaAffx.86830.1.S1_at	0.000735565	2.12983	AW734373	AT5g39050/MXF12 60 [Medicago truncatula (Barrel medic)]	AT3G29590	AT5MAT; O-malonyltransferase/transferase	Secondary Metabolism
GmaAffx.92003.1.S1_at	0.000296649	2.15973	CF807728	Chalcone isomerase 1B1 [Glycine max (Soybean)]	AT3G55120	TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Secondary Metabolism
GmaAffx.92003.1.S1_x_at	0.000121417	2.31169	CF807728	Chalcone isomerase 1B1 [Glycine max (Soybean)]	AT3G55120	TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Secondary Metabolism
GmaAffx.9455.1.S1_at	0.00232266	7.32026	BI945275	NA	AT3G01270	pectate lyase family protein	Secondary Metabolism
Gma.11076.1.S1_at	9.57253E-06	2.13766	BE658385	Rapid Alkalinization Factor [Medicago truncatula (Barrel medic)]	AT4G14010	RALFL32 (RALF-LIKE 32)	Signal Transduction
Gma.11349.1.S1_at	3.72972E-05	3.14681	AI442660	Protein kinase [Medicago truncatula (Barrel medic)]	AT2G36570	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
Gma.11810.1.S1_at	0.0119365	3.97345	AW706115	Serine/threonine-specific kinase like protein [Arabidopsis thaliana (Mouse-ear	AT5G55830	lectin protein kinase, putative	Signal Transduction
Gma.12435.1.S1_at	0.00538075	2.27114	BE657686	Calcium-binding EF-hand [Medicago truncatula (Barrel medic)]	AT5G54490	PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding	Signal Transduction
Gma.12435.1.S1_x_at	0.0147231	2.06463	BE657686	Calcium-binding EF-hand [Medicago truncatula (Barrel medic)]	AT5G54490	PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding	Signal Transduction
Gma.16705.1.S1_at	0.00548205	2.41237	BM177533	Receptor protein kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT4G18250	receptor serine/threonine kinase, putative	Signal Transduction
Gma.18035.1.S1_at	0.00291612	3.23714	BQ452873	Protein phosphatase 2C [Mesembryanthemum crystallinum (Common ice plant)]	AT4G31750	protein phosphatase 2C, putative / PP2C, putative	Signal Transduction
Gma.3986.1.S1_at	6.34712E-05	2.12148	BQ453397	F10O3.17 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G03010	phototropic-responsive NPH3 family protein	Signal Transduction
Gma.4832.1.A1_at	0.00404289	2.01709	AW310458	OSJNBb0015D13.18 protein [Oryza sativa (Rice)]	AT4G27290	S-locus protein kinase, putative	Signal Transduction
Gma.4868.1.A1_at	0.000912328	2.60305	BI969469	NA	AT4G00970	protein kinase family protein	Signal Transduction
Gma.5627.1.S1_at	0.00414238	2.15976	BE917603	Receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris (Kidney bean) (French bean)]	AT4G00970	protein kinase family protein	Signal Transduction
Gma.7726.1.A1_at	0.000800957	2.71447	BM886413	Calcium-binding EF-hand [Medicago truncatula (Barrel medic)]	AT4G27280	calcium-binding EF hand family protein	Signal Transduction
Gma.9436.1.S1_at	0.00251902	2.07435	CA802734	NA	AT2G45890	ATROPGEF4/ROPGEF4 (KINASE PARTNER PROTEIN-LIKE); Rho guanyl-nucleotide exchange factor	Signal Transduction
GmaAffx.10790.1.S1_at	0.000146021	2.00587	BU965333	Protein kinase [Medicago truncatula (Barrel medic)]	AT2G36570	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAffx.11598.1.S1_at	1.04285E-05	2.06658	BE659531	40S ribosomal protein S5 [Cicer arietinum (Chickpea) (Garbanzo)]	AT3G26700	protein kinase family protein	Signal Transduction
GmaAffx.15140.1.A1_at	0.0026194	2.02072	BU545778	Protein kinase; Heat shock protein Hsp20; Concanavalin A-like lectin/glucanase [Medicago truncatula	AT5G10530	lectin protein kinase, putative	Signal Transduction
GmaAffx.17677.1.S1_at	0.00391296	2.0242	BF425713	Putative calmodulin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G15680; AT2G15690	[AT2G15680, calmodulin-related protein, putative];[AT2G15690, pentatricopeptide (PPR) repeat-containing protein]	Signal Transduction
GmaAffx.19467.1.S1_at	0.000470887	3.02634	BQ453237	Hypothetical protein At5g18910/F17K4 160 [Arabidopsis thaliana (Mouse-ear	AT5G18910	protein kinase family protein	Signal Transduction
GmaAffx.21782.1.S1_at	0.0146575	4.5773	BE555420	Putative kinase interacting protein [Solanum demissum (Wild potato)]	0	0	Signal Transduction

GmaAfx.25687.1.S1_at	0.00253343	2.4365	BU551389	Integrase, catalytic region [Medicago truncatula (Barrel medic)]	0	protein kinase family protein	Signal Transduction
GmaAfx.257.1.S1_at	0.00217338	2.25463	AW348658	Lectin-like protein kinase [Populus nigra (Lombardy poplar)]	AT5G06740	lectin protein kinase family protein	Signal Transduction
GmaAfx.26457.1.S1_at	0.00393179	2.14181	BE608818	Putative leucine-rich repeat/receptor protein kinase [Oryza sativa (japonica cultivar-group)]	AT3G57830	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.27056.1.S1_at	0.000023216	2.08363	BG154596	NA	AT5G66330	leucine-rich repeat family protein	Signal Transduction
GmaAfx.30164.1.A1_at	0.000294623	2.9449	AW348715	Putative receptor kinase [Malus domestica (Apple) (Malus sylvestris)]	AT2G36570	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.32123.1.S1_at	0.0142908	2.95041	BI497881	Lectin-like protein [Medicago truncatula (Barrel medic)]	AT5G10530	lectin protein kinase, putative	Signal Transduction
GmaAfx.38701.1.S1_at	0.000492158	2.05128	AW706276	C2 [Medicago truncatula (Barrel medic)]	0	0	Signal Transduction
GmaAfx.41382.1.S1_at	0.00170274	2.02093	BI892866	Hypothetical protein OJ1607A12.17 [Oryza sativa (japonica cultivar-group)]	AT4G14750	IQD19 (IQ-DOMAIN 19); calmodulin binding	Signal Transduction
GmaAfx.45212.1.S1_at	0.00867029	2.47789	BG154732	Protein kinase [Medicago truncatula (Barrel medic)]	AT4G23300	protein kinase family protein	Signal Transduction
GmaAfx.46684.1.S1_at	0.00256092	2.03272	BQ081034	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT3G03770	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.47851.1.S1_at	0.0149042	2.10042	AI437780	Receptor protein kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G61480	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.51790.1.S1_at	0.0114946	4.00891	BU761362	Receptor protein kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G67200	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.52613.2.S1_at	0.00772588	2.1045	BU765614	Putative serine/threonine protein kinase [Oryza sativa (japonica cultivar-group)]	AT4G38470	protein kinase family protein	Signal Transduction
GmaAfx.55178.1.S1_at	0.00873587	2.01325	BI974216	WD40-like [Medicago truncatula (Barrel medic)]	AT5G15550	transducin family protein / WD-40 repeat family protein	Signal Transduction
GmaAfx.62304.1.S1_at	4.63039E-05	2.40488	BM178289	NA	AT4G38830	protein kinase family protein	Signal Transduction
GmaAfx.66617.1.S1_at	0.00259996	2.24681	BU760718	Leucine-rich receptor-like protein kinase [Malus domestica (Apple) (Malus sylvestris)]	AT1G28440	HSL1 (HAESA-LIKE 1); ATP binding / kinase/ protein serine/threonine kinase	Signal Transduction
GmaAfx.68209.1.A1_at	0.0015247	2.16913	BE660689	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G37660	receptor-like protein kinase-related	Signal Transduction
GmaAfx.70542.1.A1_at	0.000166298	2.008	CD409235	30S ribosomal protein S9, chloroplast precursor [Spinacia oleracea (Spinach)]	AT3G28040	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.71066.1.S1_at	0.0146505	4.45409	AW307302	Serine/threonine kinase [Persea americana (Avocado)]	AT5G58380	CIPK10 (CBL-INTERACTING PROTEIN KINASE 10); kinase	Signal Transduction
GmaAfx.78253.1.S1_at	0.00046158	3.05465	BM954563	NA	AT4G38830	protein kinase family protein	Signal Transduction
GmaAfx.82216.1.S1_at	9.17258E-06	2.4785	BI967512	Rac small GTPase [Zinnia elegans (Zinnia)]	AT1G75840	AT1G75840.1/ATGP3/ATROP4 (RHO-LIKE GTP BINDING PROTEIN 4); GTP binding / GTPase	Signal Transduction
GmaAfx.82254.1.S1_at	0.00432817	2.25016	BI786489	Leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT4G22730	leucine-rich repeat transmembrane protein kinase, putative	Signal Transduction
GmaAfx.84209.1.S1_at	0.000828725	2.04429	BQ610588	Probable histidine kinase [imported]-Arabidopsis thaliana [Medicago truncatula (Barrel medic)]	AT2G17820	ATHK1 (HISTIDINE KINASE 1)	Signal Transduction
GmaAfx.87745.1.S1_at	0.00523098	2.0096	BQ627642	NA	AT3G25905	CLE27 (CLAVATA3/ESR-RELATED 27); receptor binding	Signal Transduction

GmaAffx.88195.1.S1_at	0.000509323	4.77881	AI440894	Protein kinase; EPSP synthase [Medicago truncatula (Barrel medic)]	AT4G21390	B120; protein kinase/ sugar binding	Signal Transduction
GmaAffx.88241.1.S1_at	0.00419798	2.19113	BU927089	Putative kinase-like protein TMKL1 precursor [Arabidopsis thaliana (Mouse-ear cress)]	AT3G24660	TMKL1 (TRANSMEMBRANE KINASE-LIKE 1); ATP binding / kinase/ protein serine/threonine kinase	Signal Transduction
GmaAffx.8939.1.S1_at	0.00981589	2.11386	BU549481	Protein kinase; N-6 Adenine-specific DNA methylase [Medicago truncatula (Barrel medic)]	0	ARK2 (Arabidopsis Receptor Kinase 2); kinase	Signal Transduction
GmaAffx.93253.1.S1_at	0.00103167	2.25597	CF808047	NA	AT2G44310	calcium-binding EF hand family protein	Signal Transduction
Gma.15943.1.S1_at	0.000217077	2.20589	BM732034	Putative ethylene response factor 5 [Vitis aestivalis (Grape)]	AT4G17490	ATERF6 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 6); DNA binding / transcription factor	Transcription
Gma.15943.2.S1_at	0.00263529	2.16151	BE057404	Putative ethylene response factor 5 [Vitis aestivalis (Grape)]	AT5G47230	ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription factor/ transcriptional activator	Transcription
Gma.163.1.A1_at	0.0120514	5.41469	AB029269	Homeodomain-related [Medicago truncatula (Barrel medic)]	AT3G06490	MYB108 (BOTRYTIS-SUSCEPTIBLE1, myb domain protein 108); DNA binding / transcription factor	Transcription
Gma.17944.1.S1_at	0.000806951	2.23502	AW570024	Auxin-induced protein 22C [Phaseolus aureus (Mung bean) (Vigna radiata)]	AT3G15540	IAA19 (indoleacetic acid-induced protein 19); transcription factor	Transcription
Gma.18091.1.S1_at	0.00262449	2.1199	BE347570	NA	AT4G00950	MEE47 (maternal effect embryo arrest 47); transcription factor	Transcription
Gma.1920.1.A1_at	0.00337364	5.55743	BE059071	NA	AT2G45190	AFO (ABNORMAL FLORAL ORGANS); transcription factor	Transcription
Gma.2115.1.S1_at	0.00130284	2.02411	J03920	Auxin-induced protein AUX22 [Glycine max (Soybean)]	AT3G15540	IAA19 (indoleacetic acid-induced protein 19); transcription factor	Transcription
Gma.3975.1.S1_s_at	0.00140622	2.29833	BQ453039	Heat shock transcription factor 31 [Glycine max (Soybean)]	AT1G46264	AT-HSFB4 (Arabidopsis thaliana heat shock transcription factor B4); DNA binding / transcription factor	Transcription
Gma.561.1.S1_at	8.23569E-05	2.34791	BQ741052	Helix-loop-helix DNA-binding [Medicago truncatula (Barrel medic)]	0	basic helix-loop-helix (bHLH) family protein (bHLH096)	Transcription
Gma.6324.1.S1_at	0.000220164	2.35678	BQ612900	NA	0	0	Transcription
Gma.8067.1.A1_at	0.00001049	2.49583	BU548251	OSJNBb0096E05.11 protein [Oryza sativa (japonica cultivar-group)]	AT1G66040; AT1G66050; AT5G39550	[AT1G66040, zinc finger (C3HC4-type RING finger) family protein];[AT1G66050, zinc finger (C3HC4-type RING finger) family protein];[AT5G39550, zinc finger (C3HC4-type RING finger) family protein]	Transcription
Gma.8495.1.S1_at	0.0140158	2.96197	AJ311808	WIP1 protein [Glycine max (Soybean)]	0	TT1 (TRANSPARENT TESTA 1); transcription factor	Transcription
Gma.9913.2.S1_a_at	0.00113162	2.28741	CD390580	NA	AT3G56400	WRKY70 (WRKY DNA-binding protein 70); transcription factor	Transcription
GmaAffx.10908.2.S1_at	0.00691999	2.65354	CA802289	Gb AAF15936.1 [Arabidopsis thaliana (Mouse-ear cress)]	0	MIF2 (MINI ZINC FINGER 2); DNA binding	Transcription
GmaAffx.15955.1.S1_at	0.00942921	2.24346	AI495284	Hypothetical protein At2g30420 [Arabidopsis thaliana (Mouse-ear cress)]	AT2G46410	CPC (CAPRICE); DNA binding / transcription factor	Transcription
GmaAffx.18746.1.S1_at	0.00326625	2.0254	BU081844	NA	AT3G44460	DPBF2 (BASIC LEUCINE ZIPPER TRANSCRIPTION FACTOR 67); DNA binding / transcription factor	Transcription

GmaAffx.2553.1.S1_at	0.00507303	2.08688	AW164352	Putative PETHy;ZPT4-1 [<i>Oryza sativa</i> (japonica cultivar-group)]	0	zinc finger (C2H2 type) family protein	Transcription
GmaAffx.28599.1.S1_at	0.00330319	2.51814	BE330504	GRAS transcription factor [<i>Medicago truncatula</i> (Barrel medic)]	AT4G37650	SHR (SHORT ROOT); transcription factor	Transcription
GmaAffx.32120.1.S1_at	3.07787E-05	3.5046	BE059196	MYB transcription factor MYB142 [<i>Glycine max</i> (Soybean)]	AT2G21650	MEE3 (maternal effect embryo arrest 3); DNA binding / transcription factor	Transcription
GmaAffx.35033.1.S1_at	1.85912E-05	2.20155	BI969048	Response regulator receiver [<i>Medicago truncatula</i> (Barrel medic)]	AT3G57040	ARR9 (RESPONSE REACTOR 4); transcription regulator	Transcription
GmaAffx.38738.1.S1_at	0.00383102	2.26518	BI967222	KNOX1; KNOX2 [<i>Medicago truncatula</i> (Barrel medic)]	AT4G08150	KNAT1 (BREVIPEDICELLUS 1); transcription factor	Transcription
GmaAffx.40657.2.A1_at	0.000478035	2.13883	CA937243	Nuclear transcription factor Y subunit A-2 [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	0	0	Transcription
GmaAffx.42856.1.S1_at	0.00489186	2.20421	BM567981	Hypothetical protein [<i>Oryza sativa</i> (japonica cultivar-group)]	AT1G51070	basic helix-loop-helix (bHLH) family protein	Transcription
GmaAffx.43188.1.A1_at	0.00118769	2.50937	CD408888	NA	0	0	Transcription
GmaAffx.47784.1.A1_at	0.00871219	3.44013	CD408214	Transcription factor E2F/dimerisation partner [<i>Medicago truncatula</i> (Barrel medic)]	0	DEL1 (DP-E2F-like 1); transcription factor	Transcription
GmaAffx.50536.1.A1_x_at	0.0122537	3.56831	BI892928	DNA-binding WRKY [<i>Medicago truncatula</i> (Barrel medic)]	0	0	Transcription
GmaAffx.50660.1.A1_at	5.74666E-05	2.09624	BI971027	NA	AT5G19790	RAP2.11 (related to AP2 11); DNA binding / transcription factor	Transcription
GmaAffx.5069.1.S1_at	0.00347416	2.10346	BM884991	BZIP transcription factor BZI-2 [<i>Nicotiana tabacum</i> (Common tobacco)]	AT4G34590	GBF6 (G-box binding factor 6); DNA binding / transcription factor	Transcription
GmaAffx.52983.1.A1_at	0.00198139	2.92284	BE820933	NA	AT3G01140	MYB106 (myb domain protein 106); DNA binding / transcription factor	Transcription
GmaAffx.53324.1.A1_at	0.00829058	2.26768	AW309251	Putative bHLH transcription factor [<i>Arabidopsis thaliana</i> (Mouse-ear cress)]	AT2G22750	basic helix-loop-helix (bHLH) family protein	Transcription
GmaAffx.5686.2.S1_at	0.00784549	3.52283	BM526174	NA	AT1G63900	zinc finger (C3HC4-type RING finger) family protein	Transcription
GmaAffx.5879.1.S1_at	0.00512101	2.19835	BI968201	Transcription factor-like protein- <i>Arabidopsis thaliana</i> [<i>Medicago truncatula</i> (Barrel medic)]	0	0	Transcription
GmaAffx.69720.1.S1_at	0.00180858	2.43284	BU080896	Putative pollen specific LIM domain-containing protein [<i>Lycopersicon esculentum</i> (Tomato)]	AT1G10200	transcription factor LIM, putative	Transcription
GmaAffx.70292.1.S1_at	0.000416037	2.06816	AW101778	NA	AT1G67030	ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding	Transcription
GmaAffx.72367.1.S1_at	0.00309959	2.27749	BU082623	AG-motif binding protein-1 [<i>Nicotiana tabacum</i> (Common tobacco)]	AT3G54810	BME3/BME3-ZF (BLUE MICROPLYLAR END3); transcription factor	Transcription
GmaAffx.73751.1.S1_at	6.71205E-05	3.82856	BM522529	NA	AT1G22380	transcription factor/ transferase, transferring glycosyl groups	Transcription
GmaAffx.75209.1.S1_at	0.00130999	2.24963	AI441434	NA	AT2G44840	ATERF13/EREBP (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Transcription
GmaAffx.77156.1.S1_at	0.000242476	8.59688	BI425820	Helix-loop-helix DNA-binding [<i>Medicago truncatula</i> (Barrel medic)]	AT2G40200	basic helix-loop-helix (bHLH) family protein	Transcription

GmaAffx.80889.1.S1_at	0.000329117	2.35784	BU084219	NAC domain protein NAC1 [Phaseolus vulgaris (Kidney bean) (French bean)]	AT1G56010	NAC1 (Arabidopsis NAC domain containing protein 21, Arabidopsis NAC domain containing protein 22); transcription factor	Transcription
GmaAffx.84825.1.S1_at	0.00349108	2.06057	BI968165	TCP family transcription factor containing protein, expressed [Oryza sativa (japonica cultivar-group)]	0	TCP family transcription factor, putative	Transcription
GmaAffx.86848.1.S1_at	0.00538459	2.34548	BE211253	Leucine zipper, homeobox-associated; Homeodomain-related [Medicago truncatula (Barrel medic)]	AT3G01220	ATHB20 (ARABIDOPSIS THALIANA HOMEODOMAIN PROTEIN 20); DNA binding / transcription factor	Transcription
GmaAffx.8854.1.S1_at	0.00585296	2.45601	AI496452	Hypothetical protein F9D24.30 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G58120	bZIP transcription factor family protein	Transcription
GmaAffx.88598.1.S1_s_at	0.0121767	3.39817	CD400102	NA	0	0	Transcription
GmaAffx.91895.1.S1_at	0.00645243	4.31131	CF807620	DNA-binding WRKY [Medicago truncatula (Barrel medic)]	0	0	Transcription
GmaAffx.93343.1.S1_s_at	0.00581041	2.30124	CF809068	DNA-binding WRKY [Medicago truncatula (Barrel medic)]	AT3G56400	WRKY70 (WRKY DNA-binding protein 70); transcription factor	Transcription
GmaAffx.976.1.S1_at	0.00358191	2.38431	BG238528	BTB/POZ; NPH3 [Medicago truncatula (Barrel medic)]	AT5G64330	NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); signal transducer	Transcription
Gma.10253.1.S1_at	0.00259475	2.10408	AW310916	Amino acid transporter [Vicia faba (Broad bean)]	AT1G77380	AAP3 (amino acid permease 3); amino acid permease	Transporter
Gma.11661.1.A1_at	7.35967E-05	2.3016	CD416993	Metal transport protein [Medicago truncatula (Barrel medic)]	AT1G05300	ZIP5 (ZINC TRANSPORTER 5 PRECURSOR); cation transporter	Transporter
Gma.11661.1.A1_x_at	0.000217527	2.44822	CD416993	Metal transport protein [Medicago truncatula (Barrel medic)]	AT1G05300	ZIP5 (ZINC TRANSPORTER 5 PRECURSOR); cation transporter	Transporter
Gma.12731.1.S1_at	0.000255434	2.13709	BF009846	NA	AT5G18290	SIP1;2 (SMALL AND BASIC INTRINSIC PROTEIN1B)	Transporter
Gma.13252.1.S1_at	0.00306351	2.82078	AW423744	Nod26-like major intrinsic protein [Cicer arietinum (Chickpea) (Garbanzo)]	AT5G37810; AT5G37820	[AT5G37810, NIP4;1/NLM4 (NOD26-LIKE INTRINSIC PROTEIN 4;1); water channel];[AT5G37820, NIP4;2/NLM5 (NOD26-LIKE INTRINSIC PROTEIN 4;2); water channel]	Transporter
Gma.2972.2.S1_at	0.000952537	2.52383	BM522991	NA	AT1G72150	PATL1 (PATELLIN 1); transporter	Transporter
Gma.4779.1.A1_at	0.000207846	2.04623	AW396769	Nodulin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT3G25190	nodulin, putative	Transporter
Gma.5330.2.S1_at	0.0123377	2.0435	BM092298	F19K23.20 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G62280	C4-dicarboxylate transporter/malic acid transport family protein	Transporter
Gma.5998.1.A1_at	0.000930332	2.36272	BI968591	Plasma membrane intrinsic protein 2;5 [Mimosa pudica (Sensitive plant)]	0	PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Transporter
Gma.6352.1.S1_at	0.00631524	2.02664	BQ613046	Nitrate transporter [Populus tremula x Populus tremuloides]	AT1G12940	ATNRT2.5 (NITRATE TRANSPORTER2.5); nitrate transporter	Transporter
GmaAffx.1203.1.A1_at	0.00361197	2.12261	BU548965	NA	AT3G02850	SKOR (stelar K+ outward rectifier); cyclic nucleotide binding / outward rectifier potassium channel	Transporter
GmaAffx.20414.1.S1_at	0.00344558	2.85149	CD410957	Major intrinsic protein [Medicago truncatula (Barrel medic)]	0	0	Transporter
GmaAffx.26311.1.S1_at	0.000707262	2.1497	BE348003	Nodulin-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G39210	nodulin family protein	Transporter
GmaAffx.31403.1.S1_at	0.00002635	2.98251	BF424943	Metal transport protein [Medicago truncatula (Barrel medic)]	AT3G12750	ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transporter	Transporter

GmaAffx.35303.1.S1_at	0.00392741	2.27541	BE440840	Hypothetical protein AT4g05130 [Arabidopsis thaliana (Mouse-ear cress)]	0	equilibrative nucleoside transporter, putative (ENT4)	Transporter
GmaAffx.35364.4.S1_at	0.00290651	2.04824	AW706990	Importin alpha-1 subunit [Arabidopsis thaliana (Mouse-ear cress)]	AT3G06720	AT-IMP (Arabidopsis thaliana importin alpha); protein transporter	Transporter
GmaAffx.36156.1.S1_at	0.000374386	2.06676	BG405325	Probable sulfate transporter 3.4 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G15990	SULTR3;4 (SULTR3;4); sulfate transporter	Transporter
GmaAffx.38430.1.S1_at	0.00716402	2.37859	CA936241	NA	AT4G30360	ATCNGC17 (cyclic nucleotide gated channel 17); calmodulin binding / cyclic nucleotide binding / ion channel	Transporter
GmaAffx.39397.1.S1_at	0.000412966	2.11995	BE657958	TGF-beta receptor, type I/II extracellular region [Medicago truncatula (Barrel	AT1G27040	nitrate transporter, putative	Transporter
GmaAffx.48172.1.S1_at	0.000286434	2.47118	BF009291	Putative phosphate transporter 1 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G23430	PHO1 (PHOSPHATE 1)	Transporter
GmaAffx.51409.1.S1_at	0.00133101	2.05632	BM309035	F3O9.19 protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G16390	organic cation transporter-related	Transporter
GmaAffx.52051.1.S1_at	0.000441912	2.69672	CA802879	Sugar transporter superfamily [Medicago truncatula (Barrel medic)]	0	0	Transporter
GmaAffx.5538.1.A1_at	5.07748E-05	2.85651	BQ081719	Amino acid transporter [Pisum sativum (Garden pea)]	0	0	Transporter
GmaAffx.61311.1.S1_at	0.00370223	2.23777	CA936951	OSJNBb0103I08.20 protein [Oryza sativa (japonica cultivar-group)]	AT3G10600	CAT7 (CATIONIC AMINO ACID TRANSPORTER 7); cationic amino acid transporter	Transporter
GmaAffx.65095.1.S1_at	0.000744654	2.96438	BM108105	Putative organic cation transport protein [Phaseolus vulgaris (Kidney bean) (French bean)]	AT1G73220	sugar transporter family protein	Transporter
GmaAffx.66101.2.S1_at	0.00536583	2.25798	AW620528	Zinc/iron permease [Medicago truncatula (Barrel medic)]	AT1G10970	ZIP4 (ZINC TRANSPORTER 4 PRECURSOR); cation transporter	Transporter
GmaAffx.70959.1.S1_at	0.000252745	2.18414	BE611219	Phosphate translocator-like [Oryza sativa (japonica cultivar-group)]	AT1G06890	transporter-related	Transporter
GmaAffx.76516.1.S1_at	0.00215799	3.25476	BE661181	Putative organic cation transport protein [Phaseolus vulgaris (Kidney bean) (French bean)]	AT1G73220	sugar transporter family protein	Transporter
GmaAffx.80532.2.S1_at	0.000702366	2.04573	AW757083	Transporter-related-like [Oryza sativa (japonica cultivar-group)]	AT5G42420	transporter-related	Transporter
GmaAffx.81056.1.S1_at	0.00307772	3.95321	AW597777	Putative organic cation transport protein [Phaseolus vulgaris (Kidney bean) (French bean)]	AT1G73220	sugar transporter family protein	Transporter
GmaAffx.81873.1.S1_at	1.64401E-05	2.17007	BM522600	TGF-beta receptor, type I/II extracellular region [Medicago truncatula (Barrel	AT3G53960	proton-dependent oligopeptide transport (POT) family protein	Transporter
GmaAffx.82105.1.S1_at	0.0151501	2.09678	AI938690	Sucrose transporter [Glycine max (Soybean)]	AT5G06170	ATSUC9 (SUCROSE-PROTON SYMPORTER 9); carbohydrate transporter/ sucrose:hydrogen symporter/ sugar porter	Transporter
GmaAffx.82168.1.S1_at	0.00680717	2.40647	BI498123	Ammonium transporter [Oryza sativa (japonica cultivar-group)]	AT2G38290	ATAMT2 (AMMONIUM TRANSPORTER 2); ammonium transporter	Transporter
GmaAffx.84719.1.S1_at	0.00038243	2.12813	BE058555	Phosphate/phosphoenolpyruvate translocator-like protein [Arabidopsis thaliana (Mouse-ear cress)]	AT5G04160	phosphate translocator-related	Transporter

GmaAffx.89363.1.S1_s_at	0.00117405	2.03525	CK606317	Aquaglyceroporin (Tonoplast intrinsic protein (Tipa)) [Nicotiana tabacum (Common tobacco)]	AT2G25810	TIP4;1 (tonoplast intrinsic protein 4;1); water channel	Transporter
GmaAffx.42439.1.S1_at	0.00282589	2.56682	BU084039	Transposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]	0	0	Transposon
Gma.12342.1.S1_s_at	0.0142664	3.49334	CD405864	Unidentified precursor [Medicago sativa (Alfalfa)]	AT5G11420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25460.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Galactose-binding like; (InterPro:IPR008979); contains InterPro domain Protein of unknown function DUF642	Unclassified
Gma.13034.1.S1_at	0.000499648	3.78521	CD395146	Putative auxin-regulated protein [Arabidopsis thaliana (Mouse-ear cress)]	AT1G75580	auxin-responsive protein, putative	Unclassified
Gma.13042.1.S1_at	8.50055E-05	2.1986	CD390874	NA	AT5G03210	unknown protein	Unclassified
Gma.13240.1.A1_at	0.000268384	2.00101	CD407026	Hypothetical protein T5J8.12 [Arabidopsis thaliana (Mouse-ear cress)]	AT4G02800	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01970.1); similar to Os04g0228100 [Oryza sativa (japonica cultivar-group)] (GB:NP001052288.1); similar to H0209A05.2 [Oryza sativa (indica cultivar-group)] (GB:CAH66085.1)	Unclassified
Gma.13501.1.A1_at	1.61015E-06	2.13499	CD399296	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
Gma.1402.1.S1_at	0.00287231	3.0679	BU548218	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G23690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G37240.1); similar to TMV response-related gene product [Nicotiana tabacum] (GB:BAB41200.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAC83793.1)	Unclassified
Gma.14054.1.S1_at	0.00301276	2.53162	CD414577	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT2G30900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G78710.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unknown [Pisum sativum] (GB:ABA29158.1); similar to Os01g0652100 [Oryza sativa (japonica cultivar-group)]	Unclassified
Gma.14176.1.A1_at	8.43034E-05	2.22962	CD417226	Hypothetical protein T5J8.12 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
Gma.144.1.S1_at	0.00365002	2.57218	AF065435	Nodulin [Glycine max (Soybean)]	0	0	Unclassified
Gma.15511.1.S1_s_at	0.00133563	2.9795	CD415063	NA	0	0	Unclassified
Gma.15577.1.S1_at	8.48008E-05	2.39855	CD399075	NA	AT1G31335	similar to Os03g0780200 [Oryza sativa (japonica cultivar-group)] (GB:NP001051448.1)	Unclassified

Gma.17329.1.S1_at	0.00612722	2.21098	AW568528	NA	AT1G11915	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17350.1); similar to Os05g0409100 [Oryza sativa (japonica cultivar-group)] (GB:NP001055526.1); similar to Os06g0364500 [Oryza sativa (japonica cultivar-group)] (GB:NP001057608.1)	Unclassified
Gma.1735.1.A1_at	0.00230676	2.4092	BE658596	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
Gma.17490.1.S1_at	0.00104572	3.6105	BG047161	Expressed protein, putative [Medicago truncatula (Barrel medic)]	0	0	Unclassified
Gma.17587.1.S1_at	2.04707E-05	3.06039	BG791179	Hypothetical protein F24B22.22 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G54260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unknown [Pisum sativum] (GB:ABA29157.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)	Unclassified
Gma.17587.2.S1_at	0.000352681	3.80892	BI316791	Hypothetical protein F24B22.22 [Arabidopsis thaliana (Mouse-ear cress)]	AT3G54260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unknown [Pisum sativum] (GB:ABA29157.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)	Unclassified
Gma.17784.1.S1_at	0.00332216	2.69541	BE822305	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT5G01360	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55990.1); similar to Protein of unknown function DUF231, plant [Medicago truncatula] (GB:ABE79610.1); contains InterPro domain Protein of unknown function DUF231, plant; (InterPro:IPR004253)	Unclassified
Gma.17885.1.S1_at	0.00351918	4.5857	CD410373	NA	0	0	Unclassified
Gma.17917.1.S1_at	0.000136304	2.60265	CF921609	Suspensor-specific protein [Phaseolus coccineus (Scarlet runner bean)]	AT1G49310	unknown protein	Unclassified
Gma.17951.1.S1_at	0.00218074	2.13294	BE821378	NA	AT2G01870	unknown protein	Unclassified
Gma.17992.1.S1_at	0.0156238	2.07213	BG157311	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
Gma.2062.2.S1_a_at	0.000317438	3.16054	BF424226	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
Gma.3175.1.S1_at	0.00363611	2.17824	AI736154	NA	AT3G13950	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13266.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABE80572.1)	Unclassified
Gma.3766.1.S1_at	0.00414787	3.13268	BE023976	NA	0	0	Unclassified
Gma.3806.1.S1_at	0.000534773	2.05565	BQ452617	At2g46890/F19D11.17 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
Gma.4036.1.S1_at	0.000144259	2.23267	BQ453552	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified

Gma.407.1.A1_at	0.0010207	2.34128	AW348889	NA	AT1G76240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17080.1); similar to Os06g0725700 [Oryza sativa (japonica cultivar-group)] (GB:NP001058624.1); similar to Os06g0725500 [Oryza sativa (japonica cultivar-group)] (GB:NP001058623.1)	Unclassified
Gma.4736.1.A1_at	0.00195824	2.40149	BI968966	NA	AT2G28580	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44930.1); similar to Plant protein of unknown function [Medicago truncatula] (GB:ABE78995.1); contains InterPro domain Protein of unknown function DUF247, plant; (InterPro:IPR004158)	Unclassified
Gma.5367.1.S1_at	0.0159509	4.72674	BM092848	Hypothetical protein At2g40435 [Arabidopsis thaliana (Mouse-ear cress)]	AT2G40435	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G56220.1); similar to Os03g0338400 [Oryza sativa (japonica cultivar-group)] (GB:NP001050055.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAC10078.1)	Unclassified
Gma.5812.1.S1_at	1.41837E-06	2.331	AI855901	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
Gma.6219.1.S1_at	0.000218772	2.58734	BQ612268	NA	AT1G23840	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23830.1)	Unclassified
Gma.6529.2.S1_s_at	0.000225389	2.15963	BM309390	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT1G55360	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56530.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13510.1); similar to Os07g0205500 [Oryza sativa (japonica cultivar-group)] (GB:NP001059148.1); similar to Os07g0573400 Oryza sativa	Unclassified
Gma.7107.1.S1_at	0.00195472	2.05946	AI855972	NA	AT5G40210	nodulin MtN21 family protein	Unclassified
Gma.7837.1.A1_at	0.00128937	2.19476	BU550576	Hypothetical protein At3g44150 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
Gma.8021.2.S1_at	1.83839E-05	2.05243	CA782136	NA	AT3G54500	similar to dentin sialophosphoprotein-related [Arabidopsis thaliana] (TAIR:AT5G64170.2); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD28297.1)	Unclassified
Gma.817.1.A1_s_at	0.000162936	4.5241	BQ741341	Zinc finger, RanBP2-type [Medicago truncatula (Barrel medic)]	0	binding	Unclassified

Gma.9696.1.S1_at	0.00987717	2.29359	AW317636	Protein At5g22580 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G22580	Identical to Protein At5g22580 [Arabidopsis Thaliana] (GB:Q9FK81); similar to stable protein 1-related [Arabidopsis thaliana] (TAIR:AT3G17210.1); similar to hypothetical protein [Cucumis melo] (GB:BAD93607.1); contains InterPro domain Stress responsive al	Unclassified
Gma.9852.1.S1_at	0.000702627	2.35723	AW432620	NA	AT3G29370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39240.1); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)	Unclassified
GmaAffx.10491.1.S1_at	0.00220125	2.02497	AW598141	Similarity to unknown protein [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
GmaAffx.11889.1.S1_at	0.00213523	2.02973	BE657528	NA	AT4G10920; AT4G10910	[AT4G10920, KELP];[AT4G10910, unknown protein]	Unclassified
GmaAffx.14034.1.S1_at	0.00665715	4.83199	BI944018	Hypothetical protein At2g16050 [Arabidopsis thaliana (Mouse-ear cress)]	0	DC1 domain-containing protein	Unclassified
GmaAffx.15275.1.A1_at	0.000802672	7.72897	BU761115	NA	0	0	Unclassified
GmaAffx.1814.1.S1_at	1.92181E-05	2.40546	BM271403	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT5G03190	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G53400.1); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD32814.1); contains domain no description (G3D.3.40.50.150); contains domain S-adenosyl-L-methionine-dependent	Unclassified
GmaAffx.19785.1.A1_at	0.00320597	3.27577	BU547380	NA	0	0	Unclassified
GmaAffx.19896.1.S1_at	0.00063434	2.43046	BE660048	Nodulin-like protein [Plantago major (Common plantain)]	AT3G56620	integral membrane family protein / nodulin MtN21-related	Unclassified
GmaAffx.21178.1.S1_at	0.010082	2.16061	AW508670	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT3G03130	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G17160.1); similar to hypothetical protein MtrDRAFT AC144806g2v1 [Medicago truncatula] (GB:ABE91887.1)	Unclassified
GmaAffx.22178.1.S1_at	0.00208848	2.28312	CD416292	T3P18.8 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G62520	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G12450.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD25627.1); contains domain ADP-ribosylation (SSF56399)	Unclassified
GmaAffx.23063.1.S1_at	0.01636	2.63738	BI470614	Hypothetical protein [Oryza sativa (japonica cultivar-group)]	AT1G03055	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64680.1); similar to hypothetical protein LOC Os11g37650 [Oryza sativa (japonica cultivar-group)] (GB:ABA94460.1)	Unclassified

GmaAffx.2310.1.A1_at	4.16119E-05	2.27098	AI736226	NA	AT5G26910	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58650.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05750.1); similar to srpA [Streptococcus cristatus] (GB:AAF34780.1); similar to Os03g0831700 [Oryza sativa (japonica cultivar)]	Unclassified
GmaAffx.25415.1.S1_at	0.00125533	2.1606	BE659702	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
GmaAffx.26690.1.S1_at	0.000117339	3.94099	BE821303	At2g26695 [Arabidopsis thaliana (Mouse-ear cress)]	0	binding	Unclassified
GmaAffx.27632.1.A1_at	0.000036062	2.24236	BI969421	T30F21.12 protein [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
GmaAffx.29769.3.S1_at	0.00668378	2.22426	BM188726	Zinc finger (C3HC4-type RING finger)-like protein [Oryza sativa (japonica cultivar-group)]	AT5G62460	zinc finger (C3HC4-type RING finger) family protein	Unclassified
GmaAffx.38544.1.A1_at	1.64761E-06	2.17305	CD402591	Hypothetical protein F12B17 70 [Arabidopsis thaliana (Mouse-ear cress)]	AT4G31330	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G10580.1); similar to Os09g0494600 [Oryza sativa (japonica cultivar-group)] (GB:NP001063551.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAC55679.1)	Unclassified
GmaAffx.42607.1.A1_at	0.00722675	2.17577	BU551023	NA	AT5G24290	integral membrane family protein	Unclassified
GmaAffx.45034.1.S1_at	0.000756295	2.16352	CD410308	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT3G18050	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G28100.1); similar to hypothetical protein MtrDRAFT AC139526g8v1 [Medicago truncatula] (GB:ABE80139.1)	Unclassified
GmaAffx.51291.1.S1_at	0.00269346	2.09916	BQ080608	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
GmaAffx.53185.1.S1_at	0.000312053	2.1494	BE609308	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
GmaAffx.55536.1.S1_at	0.00136003	2.1481	BM525054	NA	0	0	Unclassified
GmaAffx.56381.1.S1_at	0.00629976	2.20735	BU927066	NA	AT3G04970	zinc finger (DHHC type) family protein	Unclassified
GmaAffx.56804.1.A1_at	0.0107501	4.77222	CD415337	NA	AT5G52030	TraB protein-related	Unclassified
GmaAffx.57322.1.S1_at	0.000446382	2.68736	AW203377	Arabidopsis conserved protein [Medicago truncatula (Barrel medic)]	AT2G17070	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17080.1); similar to hypothetical protein [Glycine max] (GB:AAK01735.1); contains InterPro domain Protein of unknown function DUF241, plant; (InterPro:IPR004320)	Unclassified
GmaAffx.57415.1.S1_at	0.00165068	2.40283	AW311518	NA	0	0	Unclassified
GmaAffx.58952.1.S1_at	0.000213372	3.56699	BG156156	Specific tissue protein 2 [Cicer arietinum (Chickpea) (Garbanzo)]	0	0	Unclassified
GmaAffx.61868.1.S1_at	0.0101727	3.12172	AW101706	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified

GmaAffx.62247.1.S1_at	0.00010447	2.52488	BM519738	Gb AAB82627.1 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G62280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45360.1); similar to Os02g0455400 [Oryza sativa (japonica cultivar-group)] (GB:NP 001046773.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD19988.1)	Unclassified
GmaAffx.62958.1.S1_at	8.65894E-05	2.59774	AW569146	Sali3-2 [Glycine max (Soybean)]	0	0	Unclassified
GmaAffx.65048.1.S1_s_at	0.00437248	2.23326	BQ628412	NA	0	0	Unclassified
GmaAffx.65462.1.S1_at	0.00157749	2.90984	BU765323	Pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa (japonica cultivar-group)]	AT3G02650	pentatricopeptide (PPR) repeat-containing protein	Unclassified
GmaAffx.65596.1.S1_at	1.01746E-05	3.26336	AW459469	NA	AT3G06840	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G49170.1)	Unclassified
GmaAffx.66676.1.S1_at	0.000432861	2.02111	BQ610288	NA	AT1G75500	nodulin MtN21 family protein	Unclassified
GmaAffx.68853.1.S1_at	0.000720388	2.91373	CA803108	Hypothetical protein At1g15260 [Arabidopsis thaliana (Mouse-ear cress)]	AT1G15260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G16070.1)	Unclassified
GmaAffx.69270.1.S1_at	0.000647925	4.94687	BM732932	Protein At1g51340 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
GmaAffx.69982.1.S1_at	0.00547498	2.01501	BG238181	NA	AT3G48490	unknown protein	Unclassified
GmaAffx.70536.1.A1_at	0.00359309	2.91591	CD412979	NA	AT1G31335	similar to Os03g0780200 [Oryza sativa (japonica cultivar-group)] (GB:NP 001051448.1)	Unclassified
GmaAffx.72117.1.S1_at	0.00255683	2.11483	CA800442	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT2G38320	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01620.2); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF95402.1); similar to Os03g0817500 [Oryza sativa (japonica cultivar-group)] (GB:NP 001051701.1)	Unclassified
GmaAffx.73732.1.S1_at	0.0132212	3.77585	BM954799	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT3G56620	integral membrane family protein / nodulin MtN21-related	Unclassified
GmaAffx.76135.1.S1_at	0.00123951	2.07494	BE329894	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT4G39840	similar to hypothetical protein MtrDRAFT AC125389g23v2 [Medicago truncatula] (GB:ABE94089.1)	Unclassified
GmaAffx.76251.1.S1_at	0.00540915	2.44184	AW704352	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cress)]	AT4G15830	binding	Unclassified
GmaAffx.78119.1.S1_at	0.00243471	2.22616	BE803157	Hypothetical protein At5g49170 [Arabidopsis thaliana (Mouse-ear cress)]	AT5G49170	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G06840.1)	Unclassified
GmaAffx.78194.1.S1_at	0.000349234	2.64764	BE440278	Hypothetical protein At3g44150 [Arabidopsis thaliana (Mouse-ear cress)]	0	0	Unclassified
GmaAffx.80180.1.A1_at	0.00325774	2.59188	AW349390	Protein kinase; EPSP synthase [Medicago truncatula (Barrel medic)]	0	0	Unclassified

GmaAfx.80731.1.S1_at	0.00457366	2.3314	BE475096	Gb AAD22996.1 [Arabidopsis thaliana (Mouse-ear cross)]	AT2G30900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G78710.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unknown [Pisum sativum] (GB:ABA29158.1); similar to Os01g0652100 [Oryza sativa (japonica cultivar-group)]	Unclassified
GmaAfx.80810.1.S1_at	0.00477898	2.31882	BE346738	T21P5.16 protein [Arabidopsis thaliana (Mouse-ear cross)]	AT3G03420	Ku70-binding family protein	Unclassified
GmaAfx.80917.1.A1_at	0.0113643	2.65723	BE583981	NA	AT5G32440	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80040.1); similar to Os06g0642900 [Oryza sativa (japonica cultivar-group)] (GB:NP 001058174.1); similar to Ubiquitin system component Cue; UBA-like [Medicago truncatula] (GB:ABE77893.1)	Unclassified
GmaAfx.80959.1.S1_at	2.30222E-05	2.03043	AW349777	Gb AAF34826.1 [Arabidopsis thaliana (Mouse-ear cross)]	AT3G12870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56120.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAK09219.1); similar to Os03g0778400 [Oryza sativa (japonica cultivar-group)] (GB:NP 001051445.1)	Unclassified
GmaAfx.81156.1.S1_at	0.000164	2.10227	CA819098	Zinc finger, BED-type predicted [Medicago truncatula (Barrel medic)]	no_match	no match	Unclassified
GmaAfx.82408.1.A1_at	0.000881533	2.17588	BI971488	F12A21.9 [Arabidopsis thaliana (Mouse-ear cross)]	AT5G38690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67780.1); similar to PREDICTED: hypothetical protein [Strongylocentrotus purpuratus] (GB:XP 001188312.1); similar to PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus]	Unclassified
GmaAfx.82795.1.S1_at	0.0151364	3.11145	CD487797	Hypothetical protein [Arabidopsis thaliana (Mouse-ear cross)]	AT5G18460	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23340.2); similar to Protein of unknown function DUF239, plant [Medicago truncatula] (GB:ABE82132.1); contains InterPro domain Protein of unknown function DUF239, plant; (InterPro:IPR004314)	Unclassified
GmaAfx.82900.1.S1_at	0.00306892	2.37492	BM884903	NA	0	0	Unclassified
GmaAfx.83805.1.S1_at	0.00118599	2.40369	CA800952	NA	AT3G42725	unknown protein	Unclassified
GmaAfx.84421.1.A1_at	0.00428394	2.62284	AI965725	NA	AT3G09280	unknown protein	Unclassified
GmaAfx.85434.1.S1_at	0.000622191	3.01446	BG882734	Hypothetical protein [Medicago truncatula (Barrel medic)]	AT4G21780	similar to hypothetical protein MtrDRAFT AC152499g5v1 [Medicago truncatula] (GB:ABE77785.1)	Unclassified
GmaAfx.93519.1.S1_at	0.00353498	2.33998	CF809244	Hypothetical protein At4g15970 [Arabidopsis thaliana (Mouse-ear cross)]	0	0	Unclassified

GmaAffx.9529.1.S1_at	0.00438662	2.34428	BI971547	Hypothetical protein [Medicago truncatula (Barrel medic)]	0	0	Unclassified
GmaAffx.9539.1.S1_at	2.77678E-07	2.19616	BI972166	Putative fasciclin-like arabinogalactan protein FLA2 [Trifolium pratense (Red clover)]	0	0	Unclassified
GmaAffx.981.1.S1_at	0.0130711	6.1259	BG239687	NA	0	0	Unclassified
GmaAffx.9844.1.S1_at	0.00006235	2.13669	BM522926	Hypothetical protein upa9 [Capsicum annuum (Bell pepper)]	0	AGP41	Unclassified