Appendix 2b Genes down-regulated following the acclimation treatment. This table contains the full set of genes that were responsive to the acclimation treatment (P <0.05) and that were down-regulated (log2 fold change in expression >-1).

Probe ID	Fold change	AGI Code	TAIR annotation
253040_at	-5.1421	At4g37800	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
260221_at	-5.0661	At1g74670	gibberellin-responsive protein, putative
266123_at	-4.9344	At2g45180	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
247266_at	-4.9237	At5g64570 At5g64572	XYL4_ATBXL4__XYL4 (beta-xylosidase 4); hydrolase, hydrolyzing O-glycosyl compounds
258054_at	-4.7918	At3g16240	DELTA-TIP_AQP1_ATTIP2;1_DELTA-TIP1_TIP2;1__DELTA-TIP (delta tonoplast integral protein); water channel
265066_at	-4.3500	At1g03870	FLA9__FLA9
259788_at	-4.3176	At1g29670	GDSL-motif lipase/hydrolase family protein
248566_s_at	-4.2659	At5g49730 At5g49740	ATFRO6_FRO6__ATFRO6/FRO6 (FERRIC REDUCTION OXIDASE 6); ferric-chelate reductase/ oxidoreductase
266790_at	-4.0745	At2g28950	ATEXPA6_ATEXP6_ATHEXP ALPHA 1.8__ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)
259272_at	-4.0049	At3g01290	band 7 family protein
266899_at	-3.8172	At2g34620	mitochondrial transcription termination factor-related / mTERF-related
248186_at	-3.7084	At5g53880	similar to unknown [Populus trichocarpa] (GB:ABK92577.1)
266215_at	-3.6984	At2g06850	EXGT-A1_EXT__EXGT-A1 (ENDOXYLOGLUCAN TRANSFERASE); hydrolase, acting on glycosyl bonds
256772_at	-3.6881	At3g13750	BGAL1__BGAL1 (BETA GALACTOSIDASE 1); beta-galactosidase
247162_at	-3.6739	At5g65730	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
246487_at	-3.6344	At5g16030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02500.1); similar to hypothetical protein [Cleome spinosa] (GB:ABD96956.1)
252367_at	-3.6103	At3g48360	BT2__BT2 (BTB AND TAZ DOMAIN PROTEIN 2); protein binding / transcription factor/ transcription regulator
265400_at	-3.5247	At2g10940	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
246011_at	-3.4940	At5g08330	TCP family transcription factor, putative
255786_at	-3.3898	At1g19670	ATCLH1_ATHCOR1_CORI1__ATCLH1 (CORONATINE-INDUCED PROTEIN 1)
258993_at	-3.3466	At3g08940	LHCB4.2__LHCB4.2 (LIGHT HARVESTING COMPLEX PSII)
255822_at	-3.3412	At2g40610	ATEXPA8_ATEXP8_ATHEXP ALPHA 1.11_EXP8__ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)
254573_at	-3.2922	At4g19420	pectinacetylesterase family protein
260603_at	-3.2885	At1g55960	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13062.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13062.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41766.1); contains InterPro domain Lipid-binding START (InterPro:IPR002913)
250437_at	-3.2868	At5g10430	AGP4__AGP4 (ARABINOGALACTAN-PROTEIN 4)
259786_at	-3.2844	At1g29660	GDSL-motif lipase/hydrolase family protein
245041_at	-3.2444	At2g26530	AR781__AR781
267083_at	-3.2337	At2g41100	TCH3_ATCAL4__TCH3 (TOUCH 3)
259431_at	-3.2253	At1g01620	PIP1;3_PIP1C_PIP1;3_TMP-B__PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3)
247377_at	-3.1629	At5g63180	pectate lyase family protein
258791_at	-3.1361	At3g04720	PR4_HEL_PR-4__PR4 (PATHOGENESIS-RELATED 4)

258497_at	-3.1267	At3g02380	COL2__COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding
251509_at	-3.1135	At3g59010	pectinesterase family protein
264672_at	-3.1086	At1g09750	chloroplast nucleoid DNA-binding protein-related
258552_at	-3.0465	At3g07010	pectate lyase family protein
252712_at	-3.0102	At3g43800	ATGSTU27__ATGSTU27 (Arabidopsis thaliana Glutathione S-transferase (class tau) 27); glutathione transferase
260237_at	-2.9479	At1g74430	AtMYB95_AtMYBCP66_MYB95__MYB95 (myb domain protein 95); DNA binding / transcription factor
250007_at	-2.9459	At5g18670	BMY3__BMY3 (BETA-AMYLASE 9); beta-amylase
264016_at	-2.8753	At2g21220	auxin-responsive protein, putative
266001_at	-2.8508	At2g24150	HHP3__HHP3 (heptahelical protein 3); receptor
259544_at	-2.8343	At1g20620	CAT3_SEN2__CAT3 (CATALASE 3); catalase
251304_at	-2.8339	At3g61990	O-methyltransferase family 3 protein
250110_at	-2.8239	At5g15350	plastocyanin-like domain-containing protein
267393_at	-2.8175	At2g44500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G07900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15104.1); contains InterPro domain Protein of unknown function DUF246, plant (InterPro:IPR004348)
265342_at	-2.8142	At2g18300	basic helix-loop-helix (bHLH) family protein
267517_at	-2.8067	At2g30520	RPT2__RPT2 (ROOT PHOTOTROPISM 2)
267262_at	-2.7652	At2g22990	SNG1_SCPL8__SNG1 (SINAPOYLGLUCOSE 1); serine carboxypeptidase
263114_at	-2.7646	At1g03130	PSAD-2__PSAD-2 (photosystem I subunit D-2)
259842_at	-2.7602	At1g73600	phosphoethanolamine N-methyltransferase
257203_at	-2.7464	At3g23730	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
246270_at	-2.7394	At4g36500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18210.1); similar to hypothetical protein [Thellungiella halophila] (GB:ABB45855.1)
261598_at	-2.7328	At1g49750	leucine-rich repeat family protein
262832_s_at	-2.7179	At1g14870 At1g14880	Identical to Uncharacterized protein At1g14870 [Arabidopsis Thaliana] (GB:Q9LQU4); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35525.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42338.1); contains InterPro domain Aspartic acid and asparagine hydroxylation site (InterPro:IPR000152); contains InterPro domain Protein of unknown function Cys-rich (InterPro:IPR006461)
251575_at	-2.7115	At3g58120	bZIP transcription factor family protein
258750_at	-2.6909	At3g05910	pectinacetylesterase, putative
246917_at	-2.6896	At5g25280	serine-rich protein-related
264348_at	-2.6813	At1g12110	NRT1.1_ATNRT1_B-1_CHL1_NRT1__NRT1.1 (NITRATE TRANSPORTER 1.1); transporter
254328_at	-2.6755	At4g22570	APT3__APT3 (ADENINE PHOSPHORIBOSYL TRANSFERASE 3); adenine phosphoribosyltransferase
249073_at	-2.6749	At5g44020	acid phosphatase class B family protein
263161_at	-2.6678	At1g54020	myrosinase-associated protein, putative
248964_at	-2.6654	At5g45340	CYP707A3__CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding
265118_at	-2.6612	At1g62660	beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar
249928_at	-2.6575	At5g22250	CCR4-NOT transcription complex protein, putative
253534_at	-2.6560	At4g31500	CYP83B1_ATR4_RED1_RNT1_SUR2__CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxygen binding
245465_at	-2.6355	At4g16590	ATCSLA01_ATCSLA1_CSLA01__ATCSLA01 (Cellulose synthase-like A1); glucosyltransferase/ transferase, transferring glycosyl groups
246603_at	-2.6256	At1g31690	copper ion binding
250178_at	-2.6200	At5g14430	dehydration-responsive protein-related
255842_at	-2.6191	At2g33530	SCPL46__SCPL46 (serine carboxypeptidase-like 46); serine carboxypeptidase
266989_at	-2.5960	At2g39330	jacalin lectin family protein
250000_at	-2.5890	At5g18650	zinc finger (C3HC4-type RING finger) family protein
264507_at	-2.5853	At1g09415	NIMIN-3__NIMIN-3 (NIM1-INTERACTING 3)

258156_at	-2.5831	At3g18050	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G28100.1); similar to unknown [Populus trichocarpa] (GB:ABK95654.1)
249847_at	-2.5783	At5g23210	SCPL34__SCPL34
264279_s_at	-2.5777	At1g78820 At1g78830	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein
253643_at	-2.5733	At4g29780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43835.1); contains domain PTHR22930 (PTHR22930)
255774_at	-2.5678	At1g18620	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74160.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49165.1)
265149_at	-2.5594	At1g51400	photosystem II 5 kD protein
245558_at	-2.5591	At4g15430	similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] (TAIR:AT4G04340.1); similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] (TAIR:AT4G04340.3); similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] (TAIR:AT3G21620.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24038.1); similar to CM0545.360.nc [Lotus japonicus] (GB:BAF98597.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69661.1); contains InterPro domain Protein of unknown function DUF221; (InterPro:IPR003864)
257615_at	-2.5503	At3g26510	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
258976_at	-2.5499	At3g01980	short-chain dehydrogenase/reductase (SDR) family protein
262232_at	-2.5430	At1g68600	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G25480.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G17470.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42118.1); contains InterPro domain Protein of unknown function UPF0005 (InterPro:IPR006214)
250669_at	-2.5347	At5g06870	PGIP2__PGIP2 (POLYGALACTURONASE INHIBITING PROTEIN 2); protein binding
260254_at	-2.5285	At1g74210	glycerophosphoryl diester phosphodiesterase family protein
247440_at	-2.5127	At5g62680	proton-dependent oligopeptide transport (POT) family protein
263207_at	-2.5025	At1g10550	XET_XTH33__XTH33 (xyloglucan:xyloglucosyl transferase 33); hydrolase, acting on glycosyl bonds
249862_at	-2.5020	At5g22920	zinc finger (C3HC4-type RING finger) family protein
245318_at	-2.4947	At4g16980	arabinogalactan-protein family
258003_at	-2.4913	At3g29030	ATEXPA5_ATEXP5_ATHEXP ALPHA 1.4__ATEXPA5 (ARABIDOPSIS THALIANA EXPANSIN A5)
259927_at	-2.4772	At1g75100	JAC1__JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding
257966_at	-2.4715	At3g19800	similar to unnamed protein product [Vitis vinifera] (GB:CAO15360.1)
248419_at	-2.4650	At5g51550	phosphate-responsive 1 family protein
256237_at	-2.4288	At3g12610	DRT100__DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100); protein binding
251413_at	-2.4261	At3g60320	DNA binding
256548_at	-2.4236	At3g14770	nodulin MtN3 family protein
260427_at	-2.3923	At1g72430	auxin-responsive protein-related
264022_at	-2.3702	At2g21185 At2g21187	unknown protein
259104_at	-2.3685	At3g02170	LNG2__LNG2 (LONGIFOLIA2)
247573_at	-2.3546	At5g61160	AACT1__AACT1 (ANTHOCYANIN 5-AROMATIC ACYLTRANSFERASE 1);
256299_at	-2.3483	At1g69530	EXP1_ATEXPA1_ATEXP1_AT-EXP1_ATHEXP ALPHA 1.2_EXP1__ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)
266805_at	-2.3282	At2g30010	similar to PMR5 (POWDERY MILDEW RESISTANT 5) [Arabidopsis thaliana] (TAIR:AT5G58600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21434.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
254105_at	-2.3257	At4g25080	CHLM__CHLM (MAGNESIUM-PROTOPORPHYRIN IX METHYLTRANSFERASE)

255604_at	-2.3232	At4g01080	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01430.1); similar to unknown protein Cr17 [Brassica napus] (GB:AAX51387.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
264701_at	-2.3218	At1g70160	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54870.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27020.1); similar to unknown [Picea sitchensis] (GB:ABK24649.1); similar to hypothetical protein OsI_030218 [Oryza sativa (indica cultivar-group)] (GB:EAZ08986.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40967.1)
262162_at	-2.3197	At1g78020	senescence-associated protein-related
249835_s_at	-2.2774	At5g23490 At5g23510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G08440.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67077.1)
245362_at	-2.2639	At4g17460	HAT1__HAT1 (homeobox-leucine zipper protein 1); DNA binding / transcription factor
253597_at	-2.2629	At4g30690	translation initiation factor 3 (IF-3) family protein
265042_at	-2.2616	At1g04040	acid phosphatase class B family protein
248404_at	-2.2606	At5g51460	ATTPPA__ATTPPA (Arabidopsis thaliana trehalose-6-phosphate phosphatase); trehalose-phosphatase
245117_at	-2.2499	At2g41560	ACA4__ACA4 (AUTO-INHIBITED CA(2+)-ATPASE, ISOFORM 4); calcium-transporting ATPase/ calmodulin binding
254163_s_at	-2.2416	At4g24340 At4g24350	phosphorylase family protein
245885_at	-2.2295	At5g09440	phosphate-responsive protein, putative
267516_at	-2.2253	At2g30520	RPT2__RPT2 (ROOT PHOTOTROPISM 2)
264609_at	-2.2242	At1g04530	binding
250109_at	-2.2229	At5g15230	GASA4__GASA4 (GAST1 PROTEIN HOMOLOG 4)
246919_at	-2.2216	At5g25460	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G11420.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946)
261570_at	-2.2212	At1g01120	KCS1__KCS1 (3-KETOACYL-COA SYNTHASE 1); acyltransferase
249327_at	-2.2192	At5g40890	ATCLC-A_CLCA_CLC-A__ATCLC-A (CHLORIDE CHANNEL A); voltage-gated chloride channel
245196_at	-2.2138	At1g67750	pectate lyase family protein
254915_s_at	-2.2078	At4g11310 At4g11320	RD21__cysteine proteinase, putative
248263_at	-2.1916	At5g53370	ATPMEPCRF__ATPMEPCRF; pectinesterase
262797_at	-2.1901	At1g20840	TMT1__TMT1 (TONOPLAST MONOSACCHARIDE TRANSPORTER1); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen ion symporter
267034_at	-2.1774	At2g38310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G05440.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48777.1); contains InterPro domain Bet v I allergen; (InterPro:IPR000916); contains InterPro domain Streptomyces cyclase/dehydrase (InterPro:IPR005031)
264590_at	-2.1656	At2g17710	similar to unnamed protein product [Vitis vinifera] (GB:CAO42932.1)
253871_at	-2.1652	At4g27440	PORB__PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); oxidoreductase/ protochlorophyllide reductase
262899_at	-2.1432	At1g59870	PDR8_PEN3__PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter
253440_at	-2.1398	At4g32570	TIFY8__TIFY8
260014_at	-2.1362	At1g68010	HPR__HPR (HYDROXYPYRUVATE REDUCTASE); glycerate dehydrogenase/ poly(U) binding
253736_at	-2.1354	At4g28780	GDSL-motif lipase/hydrolase family protein
253286_at	-2.1338	At4g34260	catalytic
264001_at	-2.1250	At2g22420	peroxidase 17 (PER17) (P17)
251864_at	-2.1240	At3g54920	PMR6__PMR6 (POWDERY MILDEW RESISTANT 6); lyase/ pectate lyase
265795_at	-2.1231	At2g35780	SCPL26__SCPL26 (serine carboxypeptidase-like 26); serine carboxypeptidase
254384_at	-2.1222	At4g21870	26.5 kDa class P-related heat shock protein (HSP26.5-P)

261308_at	-2.1153	At1g48480	RKL1__RKL1 (Receptor-like kinase 1); ATP binding / kinase/ protein serine/threonine kinase
263156_at	-2.1145	At1g54030	GDSL-motif lipase, putative
266363_at	-2.1057	At2g41250	haloacid dehalogenase-like hydrolase family protein
254785_at	-2.1053	At4g12730	FLA2__FLA2
257701_at	-2.1037	At3g12710	methyladenine glycosylase family protein
253048_at	-2.1036	At4g37560	formamidase, putative / formamide amidohydrolase, putative
254185_at	-2.0988	At4g23990	ATCSLG3_CSLG3__ATCSLG3 (Cellulose synthase-like G3); transferase/ transferase, transferring glycosyl groups
260227_at	-2.0988	At1g74450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18740.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43630.1); contains InterPro domain Protein of unknown function DUF793 (InterPro:IPR008511)
245866_s_at	-2.0982	At1g57980 At1g57990	purine permease-related
254221_at	-2.0940	At4g23820	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
247694_at	-2.0858	At5g59750	riboflavin biosynthesis protein, putative
245321_at	-2.0856	At4g15545	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16520.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71054.1); contains InterPro domain Paired amphipathic helix; (InterPro:IPR003822)
261769_at	-2.0843	At1g76100	plastocyanin
258468_at	-2.0843	At3g06070	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19190.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71112.1)
252346_at	-2.0836	At3g48650	
266552_at	-2.0764	At2g46330	AGP16__AGP16 (ARABINOGALACTAN PROTEIN 16)
259671_at	-2.0726	At1g52290	protein kinase family protein
254363_at	-2.0719	At4g22010	SKS4__SKS4 (SKU5 Similar 4); copper ion binding / oxidoreductase
259839_at	-2.0640	At1g52190	proton-dependent oligopeptide transport (POT) family protein
260453_s_at	-2.0613	At1g72510 At2g09970	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G09970.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73516.1); contains InterPro domain Protein of unknown function DUF1677, plant (InterPro:IPR012876)
262598_at	-2.0604	At1g15260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G16070.1)
260302_at	-2.0584	At1g80310	sulfate transmembrane transporter
245574_at	-2.0556	At4g14750	IQD19__IQD19 (IQ-DOMAIN 19); calmodulin binding
264037_at	-2.0547	At2g03750	sulfotransferase family protein
261480_at	-2.0503	At1g14280	PKS2__PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)
245906_at	-2.0497	At5g11070	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35090.1)
264987_at	-2.0476	At1g27030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27020.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAN05517.1); similar to Os10g0463800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001064789.1)
250649_at	-2.0445	At5g06690	(THIOREDOXIN-LIKE 5); thiol-disulfide exchange intermediate
247188_at	-2.0323	At5g65430	GRF8_GF14 KAPPA__GRF8 (GENERAL REGULATORY FACTOR 8); protein phosphorylated amino acid binding
250734_at	-2.0117	At5g06270	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15841.1)
260665_at	-2.0113	At1g19360	similar to RRA2 (REDUCED RESIDUAL ARABINOSE 2) [Arabidopsis thaliana] (TAIR:AT1G75110.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61198.1); contains InterPro domain Reticulon; (InterPro:IPR003388)
245253_at	-2.0023	At4g15440	HPL1_CYP74B2__HPL1 (HYDROPEROXIDE LYASE 1); heme binding / iron ion binding / monooxygenase
262884_at	-2.0011	At1g64720	CP5__CP5
259181_at	-2.0001	At3g01690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14390.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14651.1); contains InterPro domain Alpha/beta hydrolase fold-1 (InterPro:IPR000073)
261594_at	-1.9999	At1g33240	AT-GTL2__AT-GTL1 (Arabidopsis thaliana GT2-like 1); transcription factor
251324_at	-1.9967	At3g61430	PIP1A_ATPIP1_PIP1__PIP1A (PLASMA MEMBRANE INTRINSIC PROTEIN 1A)

254612_at	-1.9908	At4g19100	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52780.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN79943.1)
258055_at	-1.9869	At3g16250	ferredoxin-related
266476_at	-1.9838	At2g31090	unknown protein
253548_at	-1.9774	At4g30993	similar to hypothetical protein [Vitis vinifera] (GB:CAN67945.1); contains domain Metallo-dependent phosphatases (SSF56300)
256894_at	-1.9674	At3g21870	CYCP2;1__CYCP2;1 (cyclin p2;1); cyclin-dependent protein kinase
251688_at	-1.9590	At3g56480	myosin heavy chain-related
246154_at	-1.9586	At5g19940	plastid-lipid associated protein PAP-related / fibrillin-related
247214_at	-1.9550	At5g64850	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09960.1); similar to 80C09_15 [Brassica rapa subsp. pekinensis] (GB:AAZ41826.1)
255856_at	-1.9506	At1g66940	protein kinase-related
253609_at	-1.9496	At4g30190	AHA2_PMA2__AHA2 (Arabidopsis H(+)-ATPase 2); ATPase
250842_at	-1.9395	At5g04490	VTE5__VTE5 (VITAMIN E PATHWAY GENE5); phosphatidate cytidylyltransferase/ phytol kinase
251248_at	-1.9376	At3g62150	PGP21__PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances
251705_at	-1.9281	At3g56400	WRKY70__WRKY70 (WRKY DNA-binding protein 70); transcription factor
247388_s_at	-1.9044	At3g48590 At5g63470	HAP5A__HAP5A (Heme activator protein (yeast) homolog 5A); DNA binding / transcription factor
264355_at	-1.8984	At1g03210	phenazine biosynthesis PhzC/PhzF family protein
259840_at	-1.8968	At1g52230	PSAH2_PSAH-2_PSI-H__PSAH-2/PSAH2/PSI-H (PHOTOSYSTEM I SUBUNIT H-2)
252377_at	-1.8843	At3g47960	proton-dependent oligopeptide transport (POT) family protein
265471_at	-1.8824	At2g37130	peroxidase 21 (PER21) (P21) (PRXR5)
252033_at	-1.8801	At3g51950	zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein
265387_at	-1.8748	At2g20670	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G32480.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69754.1); contains InterPro domain Protein of unknown function DUF506, plant (InterPro:IPR006502)
261577_at	-1.8747	At1g01080	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative
253049_at	-1.8743	At4g37300	MEE59__MEE59 (maternal effect embryo arrest 59)
259039_at	-1.8697	At3g09250	DNA binding / nuclease
253085_s_at	-1.8660	At4g36280	ATP-binding region, ATPase-like domain-containing protein
266460_at	-1.8556	At2g47930	AGP26__AGP26/ATAGP26 (ARABINOGALACTAN PROTEINS 26)
261692_at	-1.8493	At1g08450	CRT3__CRT3 (CALRETICULIN 3); calcium ion binding
245349_at	-1.8446	At4g16690	esterase/lipase/thioesterase family protein
257651_at	-1.8445	At3g16850	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
266545_at	-1.8445	At2g35290	similar to unnamed protein product [Vitis vinifera] (GB:CAO63442.1)
247963_at	-1.8357	At5g56590	glycosyl hydrolase family 17 protein
247447_at	-1.8297	At5g62730	proton-dependent oligopeptide transport (POT) family protein
252282_at	-1.8171	At3g49360	glucosamine/galactosamine-6-phosphate isomerase family protein
253806_at	-1.8165	At4g28270	zinc finger (C3HC4-type RING finger) family protein
250511_at	-1.8153	At5g09960	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64850.1); similar to 4D11_4 [Brassica rapa subsp. pekinensis] (GB:AAZ67518.1)
259664_at	-1.8149	At1g55330	AGP21__AGP21 (ARABINOGALACTAN PROTEIN 21)
266893_at	-1.8137	At2g26070	RTE1__RTE1 (REVERSION-TO-ETHYLENE SENSITIVITY1)
252430_at	-1.8117	At3g47470	LHCA4_CAB4__LHCA4 (Photosystem I light harvesting complex gene 4); chlorophyll binding
245123_at	-1.8112	At2g47450	CAO__CAO (CHAOS); chromatin binding
261982_at	-1.8098	At1g33780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64828.1); contains InterPro domain Protein of unknown function DUF179 (InterPro:IPR003774)
260317_at	-1.8075	At1g63800	UBC5__UBC5 (UBIQUITIN-CONJUGATING ENZYME 5); ubiquitin-protein ligase
255411_at	-1.8061	At4g03110	RNA-binding protein, putative
249375_at	-1.8023	At5g40730	AGP24__AGP24 (ARABINOGALACTAN PROTEIN 24)

255344_s_at	-1.7941	At4g04540 At4g04570	protein kinase family protein
260015_at	-1.7863	At1g67980	CCoAMT__CCoAMT (caffeoyl-CoA 3-O-methyltransferase)
247284_at	-1.7839	At5g64410	ATOPT4__ATOPT4 (oligopeptide transporter 4); oligopeptide transporter
267569_at	-1.7837	At2g30790	PSBP-2__PSBP-2 (photosystem II subunit P-2); calcium ion binding
255895_at	-1.7812	At1g17990 At1g18020	12-oxophytodienoate reductase, putative
252421_at	-1.7767	At3g47540	chitinase, putative
248942_at	-1.7710	At5g45480	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45470.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45530.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39193.1); contains InterPro domain Protein of unknown function DUF594 (InterPro:IPR007658)
247817_at	-1.7668	At5g58375	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14602.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21327.1); contains domain PTHR12133 (PTHR12133)
262134_at	-1.7666	At1g77990	AST56_SULTR2;2__AST56 (sulphate transporter 2;2); sulfate transmembrane transporter
252011_at	-1.7659	At3g52720	carbonic anhydrase family protein
253915_at	-1.7633	At4g27280	calcium-binding EF hand family protein
263761_at	-1.7622	At2g21330	fructose-bisphosphate aldolase, putative
263987_at	-1.7603	At2g42690	lipase, putative
257071_at	-1.7586	At3g28180	ATCSLC04_ATCSLC4_CSLC04_CSLC4__ATCSLC04 (CELLULOSE-SYNTHASE LIKE C 4); transferase, transferring glycosyl groups
267367_at	-1.7579	At2g44210	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67164.1); contains InterPro domain Protein of unknown function DUF239, plant (InterPro:IPR004314)
257299_at	-1.7578	At3g28050	nodulin MtN21 family protein
255065_s_at	-1.7562	At4g08870 At4g08900	arginase, putative
261491_at	-1.7556	At1g14350	AtMYB124_FLP_MYB124__FLP (FOUR LIPS)
264340_at	-1.7486	At1g70280	NHL repeat-containing protein
267635_at	-1.7434	At2g42220	rhodanese-like domain-containing protein
261834_at	-1.7414	At1g10640	polygalacturonase, putative / pectinase, putative
250735_at	-1.7412	At5g06280	similar to hypothetical protein [Vitis vinifera] (GB:CAN67410.1)
264521_at	-1.7409	At1g10020	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61535.1); contains InterPro domain Protein of unknown function DUF1005 (InterPro:IPR010410)
255779_at	-1.7363	At1g18650	glycosyl hydrolase family protein 17
245060_at	-1.7323	At2g39770	CYT1_EMB101_GMP1_SOZ1_VTC1__CYT1 (CYTOKINESIS DEFECTIVE 1); nucleotidyltransferase
263142_at	-1.7300	At1g65230	similar to hypothetical protein [Vitis vinifera] (GB:CAN76393.1)
251722_at	-1.7277	At3g56200	amino acid transporter family protein
261751_at	-1.7264	At1g76080	ATCDSP32_CDSP32__ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD); thiol-disulfide exchange intermediate
250793_at	-1.7251	At5g05600	oxidoreductase, 2OG-Fe(II) oxygenase family protein
250960_at	-1.7220	At5g02940	similar to phosphotransferase-related [Arabidopsis thaliana] (TAIR:AT5G43745.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71282.1); similar to hypothetical protein OsI_009890 [Oryza sativa (indica cultivar-group)] (GB:EAY88657.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAN06856.1); contains InterPro domain Protein of unknown function DUF1012
262388_at	-1.7218	At1g49320	BURP domain-containing protein

266583_at	-1.7201	At2g46220	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79510.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16320.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G79510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39696.1); contains domain NTF2-like (SSF54427)
265005_at	-1.7189	At1g61667	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G54530.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64729.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493)
260297_at	-1.7143	At1g80280	hydrolase, alpha/beta fold family protein
257636_at	-1.7109	At3g26200	CYP71B22__CYP71B22 (cytochrome P450, family 71, subfamily B, polypeptide 22); oxygen binding
266984_at	-1.7075	At2g39570	ACT domain-containing protein
261426_at	-1.7031	At1g18680	HNH endonuclease domain-containing protein
248683_at	-1.6996	At5g48490	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
251886_at	-1.6988	At3g54260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70127.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
262286_at	-1.6987	At1g68585	metal ion binding
258606_at	-1.6985	At3g02840	immediate-early fungal elicitor family protein
266749_at	-1.6979	At2g47060	serine/threonine protein kinase, putative
266474_at	-1.6958	At2g31110	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69853.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
248622_at	-1.6925	At5g49360	BXL1__BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds
266334_at	-1.6914	At2g32380	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05210.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24140.1); contains InterPro domain Transmembrane protein 97, predicted (InterPro:IPR016964)
264839_at	-1.6882	At1g03630	POR C_PORC__POR C (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE); oxidoreductase/ protochlorophyllide reductase
250547_at	-1.6878	At5g08100	L-asparaginase / L-asparagine amidohydrolase
267001_at	-1.6876	At2g34470	UREG_PSKF109__UREG (urease accessory protein G); metal ion binding / nucleotide binding
261825_at	-1.6853	At1g11545	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
259586_at	-1.6848	At1g28100	similar to unnamed protein product [Vitis vinifera] (GB:CAO68677.1)
256751_at	-1.6845	At3g27170	CLC-B__CLC-B (chloride channel protein B); anion channel/ voltage-gated chloride channel
253386_at	-1.6836	At4g33030	SQD1__SQD1 (sulfoquinovosyldiacylglycerol 1); UDPsulfoquinovose synthase
261084_at	-1.6816	At1g07440	tropinone reductase, putative / tropine dehydrogenase, putative
248507_at	-1.6801	At5g50420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G53770.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17270.1); similar to Os07g0572600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001060060.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN80219.1); contains domain PTHR13398 (PTHR13398)
246033_at	-1.6782	At5g08280	HEMC__HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase
251427_at	-1.6779	At3g60130	glycosyl hydrolase family 1 protein / beta-glucosidase, putative (YLS1)
251327_at	-1.6753	At3g61540	peptidase family protein
260651_at	-1.6730	At1g32460	unknown protein
251640_at	-1.6710	At3g57450	similar to unnamed protein product [Vitis vinifera] (GB:CAO40798.1)
259738_at	-1.6691	At1g64355	similar to unnamed protein product [Vitis vinifera] (GB:CAO65822.1)
254815_at	-1.6639	At4g12420	SKU5__SKU5 (skewed 5); copper ion binding
249777_at	-1.6637	At5g24210	lipase class 3 family protein
256627_at	-1.6633	At3g19970	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18245.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66476.1); contains InterPro domain Protein of unknown function DUF829, eukaryotic (InterPro:IPR008547)
262464_at	-1.6632	At1g50280	phototropic-responsive NPH3 family protein

249876_at	-1.6547	At5g23060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59780.1); similar to extracellular Ca2+ sensing receptor [Glycine max] (GB:ABY57763.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)
254701_at	-1.6502	At4g18030	dehydration-responsive family protein
253859_at	-1.6493	At4g27657	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27652.1)
249378_at	-1.6487	At5g40450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28770.1); similar to hypothetical protein Kpol_1058p4 [Vanderwaltozyma polyspora DSM 70294] (GB:XP_001645325.1)
245242_at	-1.6444	At1g44446	CH1_ATCAO_CAO__CH1 (CHLOROPHYLL B BIOSYNTHESIS); chlorophyllide a oxygenase
253666_at	-1.6416	At4g30270	MERI5B_BRU1_MERI-5__MERI5B (MERISTEM-5); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase
260983_at	-1.6401	At1g53560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17080.1); similar to unknown [Populus trichocarpa] (GB:ABK95219.1); contains domain PTHR10052 (PTHR10052); contains domain PTHR10052:SF2 (PTHR10052:SF2)
260083_at	-1.6396	At1g63220	C2 domain-containing protein
261037_at	-1.6383	At1g17420	LOX3__LOX3 (Lipoxygenase 3); iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
249894_at	-1.6341	At5g22580	Identical to Uncharacterized protein At5g22580 [Arabidopsis Thaliana] (GB:Q9FK81); similar to stable protein 1-related [Arabidopsis thaliana] (TAIR:AT3G17210.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68720.1); contains InterPro domain Dimeric alpha-beta barrel (InterPro:IPR011008); contains InterPro domain Stress responsive alpha-beta barrel (InterPro:IPR013097)
257072_at	-1.6338	At3g14220	GDSL-motif lipase/hydrolase family protein
264611_at	-1.6325	At1g04680	pectate lyase family protein
258369_at	-1.6262	At3g14310	ATPME3__ATPME3 (Arabidopsis thaliana pectin methylesterase 3)
252976_s_at	-1.6224	At4g38550	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G20950.1); contains InterPro domain Phospholipase-like, arabidopsis (InterPro:IPR007942)
259491_at	-1.6220	At1g15820	LHCB6_CP24__LHCB6 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding
258038_at	-1.6212	At3g21260	GLTP3__GLTP3 (GLYCOLIPID TRANSFER PROTEIN 3); glycolipid binding / glycolipid transporter
253477_at	-1.6196	At4g32320	APX6__APX6 (ASCORBATE PEROXIDASE 6); L-ascorbate peroxidase
267381_at	-1.6134	At2g26190	calmodulin-binding family protein
251516_s_at	-1.6128	At3g59300 At3g59310 At3g59320	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67773.1); contains domain PTHR10483:SF11 (PTHR10483:SF11); contains domain PTHR10483 (PTHR10483)
252167_at	-1.6121	At3g50560	short-chain dehydrogenase/reductase (SDR) family protein
264164_at	-1.6102	At1g65295	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G01015.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22991.1)
266296_at	-1.6074	At2g29420	ATGSTU7_GST25__ATGSTU7 (GLUTATHIONE S-TRANSFERASE 25); glutathione transferase
249008_at	-1.6055	At5g44680	methyladenine glycosylase family protein
250936_at	-1.6038	At5g03120	similar to hypothetical protein [Vitis vinifera] (GB:CAN68657.1)
259242_at	-1.6018	At3g33520	ATARP6_ARP6_ESD1_SUF3__ATARP6; structural constituent of cytoskeleton
251028_at	-1.6010	At5g02230	haloacid dehalogenase-like hydrolase family protein
257510_at	-1.5986	At1g55360	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56530.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22094.1); similar to unknown [Populus trichocarpa] (GB:ABK93966.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72570.1); contains InterPro domain Protein of unknown function DUF239, plant (InterPro:IPR004314)
246576_at	-1.5977	At1g31650	ATROPGEF14_ROPGEF14__ATROPGEF14/ROPGEF14 (KINASE PARTNER PROTEIN-LIKE); Rho guanyl-nucleotide exchange factor/
254938_at	-1.5973	At4g10770	ATOPT7__ATOPT7 (oligopeptide transporter 7); oligopeptide transporter

253304_at	-1.5966	At4g33640	similar to Os03g0690000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050950.1); similar to Protein C6orf115, putative [Medicago truncatula] (GB:ABD28547.2); contains domain PD022054 (PD022054); contains domain
254262_at	-1.5935	At4g23470	hydroxyproline-rich glycoprotein family protein
253486_at	-1.5876	At4g31600	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related
247439_at	-1.5868	At5g62670	AHA11__AHA11 (ARABIDOPSIS H(+)-ATPASE 11); ATPase
255503_at	-1.5866	At4g02420	lectin protein kinase, putative
264920_at	-1.5858	At1g60550	naphthoate synthase, putative / dihydroxynaphthoic acid synthetase, putative / DHNA synthetase, putative
257198_at	-1.5847	At3g23690	basic helix-loop-helix (bHLH) family protein
264513_at	-1.5832	At1g09420	G6PD4__G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 4); glucose-6-phosphate dehydrogenase
259609_at	-1.5831	At1g52410	TSA1__TSA1 (TSK-ASSOCIATING PROTEIN 1)
263606_at	-1.5802	At2g16280	very-long-chain fatty acid condensing enzyme, putative
245611_at	-1.5799	At4g14390	ankyrin repeat family protein
264299_s_at	-1.5797	At1g78850 At1g78860	curculin-like (mannose-binding) lectin family protein
248591_at	-1.5787	At5g49650	xylulose kinase, putative
263647_at	-1.5777	At2g04690	cellular repressor of E1A-stimulated genes (CREG) family
248448_at	-1.5774	At5g51190	AP2 domain-containing transcription factor, putative
250102_at	-1.5774	At5g16590	leucine-rich repeat transmembrane protein kinase, putative
251122_at	-1.5761	At5g01020	protein kinase family protein
253958_at	-1.5697	At4g26400	zinc finger (C3HC4-type RING finger) family protein
255064_at	-1.5695	At4g08950	phosphate-responsive protein, putative (EXO)
245478_at	-1.5655	At4g16130	ARA1_ATISA1_ISA1__ARA1 (ARABINOSE KINASE); ATP binding / galactokinase
263421_at	-1.5648	At2g17230	phosphate-responsive 1 family protein
253160_at	-1.5638	At4g35760	electron carrier/ protein disulfide oxidoreductase
264837_at	-1.5633	At1g03600	photosystem II family protein
258989_at	-1.5629	At3g08920	rhodanese-like domain-containing protein
262582_at	-1.5628	At1g15410	aspartate-glutamate racemase family
249188_at	-1.5620	At5g42830	transferase family protein
263687_at	-1.5559	At1g26940	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein
261143_at	-1.5551	At1g19770	ATPUP14__ATPUP14 (Arabidopsis thaliana purine permease 14); purine transmembrane transporter
260831_at	-1.5536	At1g06830	glutaredoxin family protein
263153_s_at	-1.5509	At1g54000 At1g54010	myrosinase-associated protein, putative
264201_at	-1.5506	At1g22630	heat shock protein binding / unfolded protein binding
259106_at	-1.5484	At3g05490	RALFL22__RALFL22 (RALF-LIKE 22)
260236_at	-1.5469	At1g74470	geranylgeranyl reductase
247627_at	-1.5458	At5g60360	AALP__AALP (ARABIDOPSIS ALEURAIN-LIKE PROTEASE)
249917_at	-1.5451	At5g22460	esterase/lipase/thioesterase family protein
260498_at	-1.5435	At2g41710	ovule development protein, putative
258393_at	-1.5416	At3g15480	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G52910.1); similar to fiber protein Fb34 [Gossypium barbadense] (GB:AAR07596.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR009606)
258495_at	-1.5390	At3g02690	integral membrane family protein
261354_at	-1.5386	At1g79690	ATNUDT3__ATNUDT3 (Arabidopsis thaliana Nudix hydrolase homolog 3); hydrolase
259434_at	-1.5379	At1g01490	heavy-metal-associated domain-containing protein
245736_at	-1.5356	At1g73330	ATDR4__ATDR4 (Arabidopsis thaliana drought-repressed 4)
250257_at	-1.5329	At5g13770	pentatricopeptide (PPR) repeat-containing protein
265737_at	-1.5277	At2g01180	ATPAP1_ATLPP1_LPP1_PAP1__ATPAP1 (PHOSPHATIDIC ACID PHOSPHATASE 1); phosphatidate phosphatase
247604_at	-1.5247	At5g60950	COBL5 (COBRA-LIKE PROTEIN 5 PRECURSOR)
266279_at	-1.5195	At2g29290	tropinone reductase, putative / tropine dehydrogenase, putative

264986_at	-1.5188	At1g27130	ATGSTU13_GST12__ATGSTU13 (GLUTATHIONE S-TRANSFERASE 12); glutathione transferase
246636_at	-1.5133	At5g34850	ATPAP26_PAP26__ATPAP26/PAP26 (purple acid phosphatase 26); acid phosphatase/ protein serine/threonine phosphatase
257171_at	-1.5122	At3g23760	similar to transferase, transferring glycosyl groups [Arabidopsis thaliana] (TAIR:AT4G14100.1); similar to unknown [Populus trichocarpa] (GB:ABK94230.1)
252280_at	-1.5119	At3g49260	IQD21__IQD21 (IQ-DOMAIN 21, IQ-domain 21); calmodulin binding
245337_at	-1.5072	At4g16566	histidine triad family protein / HIT family protein
258956_at	-1.5057	At3g01440	oxygen evolving enhancer 3 (PsbQ) family protein
258866_at	-1.5017	At3g03180	Got1-like family protein
265994_at	-1.5012	At2g24170	endomembrane protein 70, putative
261405_at	-1.5002	At1g18740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G74450.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43630.1); contains InterPro domain Protein of unknown function DUF793 (InterPro:IPR008511)
252158_at	-1.4985	At3g50530	CRK__CRK (CDPK-RELATED KINASE); calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase
255549_at	-1.4984	At4g01950	ATGPAT3_GPAT3__ATGPAT3/GPAT3 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 3); acyltransferase
251820_at	-1.4884	At3g55040	In2-1 protein, putative
263365_at	-1.4874	At2g20550	DNAJ chaperone C-terminal domain-containing protein
246620_at	-1.4873	At5g36220	CYP81D1_CYP91A1__CYP81D1 (CYTOCHROME P450 91A1); oxygen binding
259072_at	-1.4868	At3g11700	FLA18__FLA18 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 18 PRECURSOR)
266588_at	-1.4858	At2g14890	AGP9__AGP9 (ARABINOGALACTAN PROTEIN 9)
250249_at	-1.4858	At5g13760	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04440.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03700.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40758.1); contains InterPro domain Protein of unknown function DUF580 (InterPro:IPR007603)
255694_at	-1.4838	At4g00050	UNE10__UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor
246651_at	-1.4835	At5g35170	adenylate kinase family protein
264624_at	-1.4795	At1g08930	ERD6__ERD6 (EARLY RESPONSE TO DEHYDRATION 6); carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter
259731_at	-1.4766	At1g77460	binding
262830_at	-1.4745	At1g14700	ATPAP3_PAP3__ATPAP3/PAP3 (purple acid phosphatase 3)
265952_at	-1.4736	At2g37480	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G53670.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77855.1)
264960_at	-1.4722	At1g76930	ATEXT4_ATEXT1_ORG5__ATEXT4 (EXTENSIN 4)
263199_at	-1.4680	At1g05590	ATHEX3_HEXO2__ATHEX3/HEXO2 (BETA-HEXOSAMINIDASE 2); beta-N-acetylhexosaminidase/ hexosaminidase/ hydrolase, hydrolyzing O-glycosyl compounds
251661_at	-1.4668	At3g56950	SIP2__SIP2;1 (SMALL AND BASIC INTRINSIC PROTEIN 2); transporter
252972_at	-1.4658	At4g38840	auxin-responsive protein, putative
256547_at	-1.4650	At3g14840	leucine-rich repeat family protein / protein kinase family protein
251454_at	-1.4646	At3g60080	zinc finger (C3HC4-type RING finger) family protein
252679_at	-1.4642	At3g44260	CCR4-NOT transcription complex protein, putative
260968_at	-1.4632	At1g12250	thylakoid lumenal protein-related
245868_at	-1.4609	At1g58030	CAT2__CAT2 (CATIONIC AMINO ACID TRANSPORTER 2); amino acid transmembrane transporter
267391_at	-1.4576	At2g44480	glycosyl hydrolase family 1 protein
264504_at	-1.4516	At1g09430	ACLA-3__ACLA-3 (ATP-citrate lyase A-3)
248276_at	-1.4508	At5g53550	YSL3__YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter
261975_at	-1.4448	At1g64640	plastocyanin-like domain-containing protein
266101_at	-1.4434	At2g37940	similar to phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] (TAIR:AT3G54020.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15746.1); contains domain PTHR21290:SF1 (PTHR21290:SF1); contains domain PTHR21290 (PTHR21290)
261572_at	-1.4424	At1g01170	ozone-responsive stress-related protein, putative

264736_at	-1.4396	At1g62200	proton-dependent oligopeptide transport (POT) family protein
251720_at	-1.4387	At3g56160	bile acid:sodium symporter
253099_s_at	-1.4373	At4g37520 At4g37530	peroxidase 50 (PER50) (P50) (PRXR2)
261031_at	-1.4369	At1g17360	COP1-interacting protein-related
264240_at	-1.4349	At1g54820	protein kinase family protein
245987_at	-1.4341	At5g13180	ANAC083__ANAC083 (Arabidopsis NAC domain containing protein 83); transcription factor
261230_at	-1.4329	At1g20010	TUB5__TUB5 (tubulin beta-5 chain)
261191_at	-1.4299	At1g32900	starch synthase, putative
254239_at	-1.4278	At4g23400	PIP1;5_PIP1D__PIP1;5/PIP1D (plasma membrane intrinsic protein 1;5); water channel
247816_at	-1.4274	At5g58260	Encodes subunit NDH-N of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.
248656_at	-1.4267	At5g48460	fimbrin-like protein, putative
251261_at	-1.4243	At3g62110	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
251218_at	-1.4241	At3g62410	CP12-2_CP12__CP12-2
255486_at	-1.4237	At4g02600	ATMLO1_MLO1__ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); calmodulin binding
253647_at	-1.4208	At4g29950	microtubule-associated protein
246231_at	-1.4162	At4g37080	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G42690.2); similar to hypothetical protein [Populus tremula] (GB:CAM84232.1); contains InterPro domain Protein of unknown function DUF547 (InterPro:IPR006869)
262978_at	-1.4159	At1g75780	TUB1__TUB1 (tubulin beta-1 chain); structural molecule
246906_at	-1.4147	At5g25475	DNA binding
249864_at	-1.4146	At5g22830	ATMGT10_GMN10__GMN10 (Arabidopsis thaliana Mg transporter 10)
261129_at	-1.4144	At1g04820	TUA4__TUA4 (tubulin alpha-4 chain)
256186_at	-1.4136	At1g51680	4CL1_4CL.1_AT4CL1__4CL1 (4-COUMARATE:COA LIGASE 1)
267028_at	-1.4120	At2g38470	WRKY33__WRKY33 (WRKY DNA-binding protein 33); transcription factor
266070_at	-1.4117	At2g18660	EXLB3__EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)
258151_at	-1.4114	At3g18080	glycosyl hydrolase family 1 protein
256796_at	-1.4112	At3g22210	unknown protein
266533_s_at	-1.4098	At2g16850 At4g35100	PIP2;8_PIP3B__PIP2;8/PIP3B (plasma membrane intrinsic protein 2;8); water channel
263151_at	-1.4048	At1g54120	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G14060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO45609.1)
248050_at	-1.3996	At5g56100	glycine-rich protein / oleosin
258797_at	-1.3961	At3g04730	IAA16__IAA16 (indoleacetic acid-induced protein 16); transcription factor
251087_at	-1.3922	At5g01460	LMBR1 integral membrane family protein
250366_at	-1.3907	At5g11420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25460.1); similar to unknown [Ricinus communis] (GB:CAB02653.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946); contains InterPro domain Galactose-binding like (InterPro:IPR008979)
258676_at	-1.3893	At3g08600	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO45372.1); contains InterPro domain Protein of unknown function DUF1191 (InterPro:IPR010605)
254547_at	-1.3874	At4g19860	lecithin:cholesterol acyltransferase family protein / LACT family protein
256754_at	-1.3862	At3g25690	CHUP1__CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)
245115_at	-1.3852	At2g41530	ATSFGH__ATSFGH (ARABIDOPSIS THALIANA S-FORMYLGLUTATHIONE HYDROLASE); S-formylglutathione hydrolase/ hydrolase, acting on ester bonds
261197_at	-1.3832	At1g12900	GAPA-2__GAPA-2
254578_at	-1.3831	At4g19410	pectinacetylesterase, putative
264582_at	-1.3824	At1g05230	homeobox-leucine zipper family protein / lipid-binding START domain-containing protein
255886_at	-1.3818	At1g20340	DRT112__DRT112 (DNA-damage-repair/toleration protein 112); copper ion binding / electron carrier

263865_at	-1.3812	At2g36910	PGP1_ATMDR1__ATPGP1 (ARABIDOPSIS THALIANA P GLYCOPROTEIN1); calmodulin binding
247819_at	-1.3808	At5g58350	WNK4_ZIK2__WNK4 (Arabidopsis WNK kinase 4); kinase
260530_at	-1.3801	At2g47320	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein
252353_at	-1.3792	At3g48200	similar to hypothetical protein OsI_020499 [Oryza sativa (indica cultivar-group)] (GB:EAY99266.1); similar to hypothetical protein OsJ_018975 [Oryza sativa (japonica cultivar-group)] (GB:EAZ35492.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64300.1)
254926_at	-1.3773	At4g11280	ACS6__ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE
263132_at	-1.3763	At1g78560	bile acid:sodium symporter family protein
247443_at	-1.3746	At5g62720	integral membrane HPP family protein
253220_s_at	-1.3744	At4g34920 At4g34930	1-phosphatidylinositol phosphodiesterase-related
258499_at	-1.3742	At3g02540	RAD23-3__RAD23-3 (PUTATIVE DNA REPAIR PROTEIN RAD23-3)
261788_at	-1.3734	At1g15980	similar to unnamed protein product [Vitis vinifera] (GB:CAO49411.1); contains domain G3DSA:3.40.50.2000 (G3DSA:3.40.50.2000); contains domain SSF53756 (SSF53756)
249264_s_at	-1.3705	At5g41740 At5g41750	disease resistance protein (TIR-NBS-LRR class), putative
254723_at	-1.3704	At4g13505 At4g13510	
253849_at	-1.3690	At4g28080	binding
254931_at	-1.3672	At4g11460	protein kinase family protein
263537_at	-1.3667	At2g24790	COL3__COL3 (CONSTANS-LIKE 3); protein binding / transcription factor/ zinc ion binding
265720_at	-1.3661	At2g40110	yippee family protein
247903_at	-1.3601	At5g57340	similar to hypothetical protein MtrDRAFT_AC155282g59v2 [Medicago truncatula] (GB:ABN08100.1)
250409_at	-1.3596	At5g10860	CBS domain-containing protein
254564_at	-1.3580	At4g19170	NCED4__NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)
253815_at	-1.3574	At4g28250	ATEXPB3_ATHEXP BETA 1.6_EXPB3__ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)
262786_at	-1.3566	At1g10740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23330.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42648.1); contains domain SSF53474 (SSF53474); contains domain G3DSA:3.40.50.1820 (G3DSA:3.40.50.1820)
257313_at	-1.3561	At3g26520	TIP2_SITIP_TIP1;2__TIP2 (TONOPLAST INTRINSIC PROTEIN 2); water channel
262725_at	-1.3552	At1g43580	similar to unnamed protein product [Vitis vinifera] (GB:CAO43621.1); contains domain PTHR21290 (PTHR21290)
266275_at	-1.3547	At2g29370	tropinone reductase, putative / tropine dehydrogenase, putative
263804_at	-1.3544	At2g40270	protein kinase family protein
264394_at	-1.3521	At1g11860	aminomethyltransferase, putative
264000_at	-1.3507	At2g22500	mitochondrial substrate carrier family protein
263736_at	-1.3492	At1g60000	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative
266927_at	-1.3472	At2g45960	PIP1B_ATHH2_PIP1;2_TMP-A__PIP1B (plasma membrane intrinsic protein 1;2)
259507_at	-1.3429	At1g43910	AAA-type ATPase family protein
261488_at	-1.3406	At1g14345	oxidoreductase
265680_at	-1.3401	At2g32150	haloacid dehalogenase-like hydrolase family protein
256607_at	-1.3393	At3g32930	similar to unnamed protein product [Vitis vinifera] (GB:CAO22035.1)
259140_at	-1.3386	At3g10230	LYC__LYC (LYCOPENE CYCLASE)
246901_at	-1.3374	At5g25630	pentatricopeptide (PPR) repeat-containing protein
251022_at	-1.3344	At5g02150	binding
247954_at	-1.3339	At5g56870	BGAL4__BGAL4 (beta-galactosidase 4); beta-galactosidase
250217_at	-1.3338	At5g14120	nodulin family protein
254705_at	-1.3315	At4g17870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G46790.1); similar to Streptomyces cyclase/dehydrase family protein [Brassica oleracea] (GB:ABD65175.1); contains InterPro domain Streptomyces cyclase/dehydrase (InterPro:IPR005031)

249922_at	-1.3314	At5g19140	auxin/aluminum-responsive protein, putative
246781_at	-1.3308	At5g27350	SFP1__SFP1; carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter
260637_at	-1.3297	At1g62380	ACO2__ACO2 (ACC OXIDASE 2)
267355_at	-1.3280	At2g39900	LIM domain-containing protein
255457_at	-1.3266	At4g02770	PSAD-1__PSAD-1 (photosystem I subunit D-1)
257784_at	-1.3251	At3g26980	MUB4__MUB4 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 4 PRECURSOR)
250384_at	-1.3248	At5g11500	similar to unknown [Brassica juncea] (GB:ABX10747.1); contains InterPro domain Protein of unknown function DUF814 (InterPro:IPR008532)
250012_x_at	-1.3244	At5g18060	auxin-responsive protein, putative
248037_at	-1.3224	At5g55930	ATOPT1__ATOPT1 (oligopeptide transporter 1); oligopeptide transporter
245513_at	-1.3219	At4g15780	ATVAMP724_VAMP724__ATVAMP724 (Arabidopsis thaliana vesicle-associated membrane protein 724)
250317_at	-1.3211	At5g12250	TUB6__TUB6 (BETA-6 TUBULIN)
250017_at	-1.3210	At5g18140	DNAJ heat shock N-terminal domain-containing protein
257769_at	-1.3203	At3g23050	IAA7_AXR2__IAA7 (AUXIN RESISTANT 2); transcription factor
252542_at	-1.3188	At3g45770	oxidoreductase, zinc-binding dehydrogenase family protein
245592_at	-1.3186	At4g14540	CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family
264963_at	-1.3178	At1g60600	ABC4__ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4)
260560_at	-1.3152	At2g43590	chitinase, putative
255720_at	-1.3150	At1g32060	PRK__PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding
250170_at	-1.3148	At5g14260	SET domain-containing protein
253702_at	-1.3145	At4g29900	ACA10__ACA10 (autoinhibited Ca2+ -ATPase 10); calcium-transporting ATPase/ calmodulin binding
262775_at	-1.3141	At1g13000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G26440.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G26440.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14680.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)
254194_at	-1.3139	At4g23980	ARF9__ARF9 (AUXIN RESPONSE FACTOR 9)
248524_s_at	-1.3130	At5g50570 At5g50670	squamosa promoter-binding protein, putative
253925_at	-1.3104	At4g26690	MRH5_SHV3__MRH5/SHV3 (morphogenesis of root hair 5); glycerophosphodiester phosphodiesterase/ kinase
251408_at	-1.3103	At3g60340	palmitoyl protein thioesterase family protein
265884_at	-1.3103	At2g42320	nucleolar protein gar2-related
261346_at	-1.3081	At1g79720	aspartyl protease family protein
256528_at	-1.3025	At1g66140	ZFP4__ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding
245925_at	-1.3024	At5g28770	ATBZIP63_BZO2H3__BZO2H3 (ARABIDOPSIS THALIANA BASIC LEUCINE ZIPPER 63); DNA binding / transcription factor
266266_at	-1.3024	At2g29560	enolase, putative
253971_at	-1.3016	At4g26530	fructose-bisphosphate aldolase, putative
254669_at	-1.3008	At4g18370	HHOA_DEG5_DEGP5__DEG5/DEGP5/HHOA (DEGP PROTEASE 5); serine-type peptidase/ trypsin
259460_at	-1.3006	At1g44000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11911.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81476.1)
261016_at	-1.2976	At1g26560	glycosyl hydrolase family 1 protein
260073_at	-1.2974	At1g73660	protein kinase family protein
256281_at	-1.2972	At3g12560	TRFL9_ATTBP2__TRFL9 (TRF-LIKE 9); DNA binding
265189_at	-1.2961	At1g23840	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23830.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14801.1)
249918_at	-1.2961	At5g19240	Identical to Uncharacterized GPI-anchored protein At5g19240 precursor [Arabidopsis Thaliana] (GB:Q84VZ5;GB:Q8H7A4); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19230.1); similar to unknown [Populus trichocarpa] (GB:ABK94712.1)

257825_at	-1.2951	At3g26700	protein kinase family protein
266800_at	-1.2935	At2g22880	VQ motif-containing protein
256469_at	-1.2927	At1g32540	LOL1__LOL1 (LSD ONE LIKE 1)
260267_at	-1.2919	At1g68530	CUT1_CER6_G2_POP1__CUT1 (CUTICULAR 1); catalytic
253294_at	-1.2907	At4g33750	unknown protein
254024_at	-1.2867	At4g25780	pathogenesis-related protein, putative
257060_at	-1.2860	At3g18230	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
258368_at	-1.2858	At3g14240	subtilase family protein
260914_at	-1.2841	At1g02640	BXL2__BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyzing O-glycosyl compounds
245999_at	-1.2832	At5g20650	COPT5__COPT5 (copper transporter 5); copper ion transmembrane transporter
249800_at	-1.2820	At5g23660	MTN3__MTN3 (ARABIDOPSIS HOMOLOG OF MEDICAGO TRUNCATULA MTN3)
262813_at	-1.2819	At1g11670	MATE efflux family protein
257749_at	-1.2814	At3g18780	ACT2_DER1_ENL2_LSR2__ACT2 (ACTIN 2); structural constituent of cytoskeleton
254387_at	-1.2801	At4g21850	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein
254386_at	-1.2800	At4g21960	PRXR1__PRXR1 (peroxidase 42); peroxidase
260837_at	-1.2743	At1g43670	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative
254487_at	-1.2735	At4g20780	calcium-binding protein, putative
250742_at	-1.2695	At5g05800	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11290.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69032.1)
253891_at	-1.2691	At4g27720	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64650.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64650.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49310.1); similar to unknown [Populus trichocarpa] (GB:ABK93582.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48607.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62932.1); contains InterPro domain Protein of unknown function DUF791 (InterPro:IPR008509); contains InterPro domain MFS general substrate transporter
260545_at	-1.2681	At2g43350	ATGPX3__ATGPX3 (GLUTATHIONE PEROXIDASE 3); glutathione peroxidase
258927_at	-1.2668	At3g10160	ATDFC__ATDFC (A. THALIANA DHFS-FPGS HOMOLOG C); dihydrofolate synthase
250428_at	-1.2664	At5g10480	PAS2_PEP__PAS2 (PASTICCINO 2)
252080_at	-1.2662	At3g51670	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
254616_at	-1.2662	At4g18710	BIN2_DWF12_UCU1__BIN2 (BRASSINOSTEROID-INSENSITIVE 2); kinase
256246_at	-1.2660	At3g66658	ALDH22a1__ALDH22a1 (ALDEHYDE DEHYDROGENASE 22A1); 3-chloroallyl aldehyde dehydrogenase
267256_s_at	-1.2648	At2g23000 At2g23010	SCPL10__SCPL10 (serine carboxypeptidase-like 10); serine carboxypeptidase
247858_at	-1.2637	At5g58220	TTL__TTL (TRANSTHYRETIN-LIKE PROTEIN); steroid binding
254561_at	-1.2616	At4g19160	binding
248191_at	-1.2610	At5g54130	calcium-binding EF hand family protein
249417_at	-1.2602	At5g39670	calcium-binding EF hand family protein
263972_at	-1.2598	At2g42760	similar to unnamed protein product [Vitis vinifera] (GB:CAO69913.1)
261443_at	-1.2580	At1g28480	GRX480__GRX480; thiol-disulfide exchange intermediate
247137_at	-1.2568	At5g66210	CPK28__CPK28 (calcium-dependent protein kinase 28)
267040_at	-1.2566	At2g34300	dehydration-responsive protein-related
247037_at	-1.2558	At5g67070	RALFL34__RALFL34 (RALF-LIKE 34)
254505_at	-1.2545	At4g19985	GCN5-related N-acetyltransferase (GNAT) family protein
247320_at	-1.2526	At5g64040	PSAN__PSAN (photosystem I reaction center subunit PSI-N); calmodulin binding
250203_at	-1.2518	At5g13980	glycosyl hydrolase family 38 protein
265414_at	-1.2514	At2g16660	nodulin family protein
267400_at	-1.2501	At2g26240	Identical to UPF0136 membrane protein At2g26240 [Arabidopsis Thaliana] (GB:O64847); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43520.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ63811.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)

248302_at	-1.2481	At5g53160	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69376.1); contains domain SSF55961 (SSF55961)
264071_at	-1.2470	At2g27920	SCPL51__SCPL51; serine carboxypeptidase
247306_at	-1.2469	At5g63870	PP7__PP7 (protein phosphatase 7); protein serine/threonine phosphatase
252486_at	-1.2461	At3g46510	armadillo/beta-catenin repeat family protein / U-box domain-containing family protein
262082_s_at	-1.2446	At1g56120 At1g56130 At1g56140	leucine-rich repeat family protein / protein kinase family protein
256655_at	-1.2445	At3g18890	binding / catalytic/ coenzyme binding
260399_at	-1.2437	At1g72520	lipoxygenase, putative
262612_at	-1.2431	At1g14150	oxygen evolving enhancer 3 (PsbQ) family protein
249598_at	-1.2422	At5g37970	S-adenosyl-L-methionine:carboxyl methyltransferase family protein
259073_at	-1.2410	At3g02290	zinc finger (C3HC4-type RING finger) family protein
248529_at	-1.2408	At5g50000	protein kinase, putative
260656_at	-1.2403	At1g19380	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65650.1); similar to unknown [Vitis pseudoreticulata] (GB:ABC69762.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61173.1); contains InterPro domain Protein of unknown function DUF1195 (InterPro:IPR010608)
263737_at	-1.2398	At1g60010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10530.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40951.1)
251142_at	-1.2393	At5g01015	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G65295.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN82885.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO45347.1)
251745_at	-1.2358	At3g55980	zinc finger (CCCH-type) family protein
259474_at	-1.2357	At1g19130	similar to unknown [Populus trichocarpa] (GB:ABK94529.1); contains InterPro domain Protein of unknown function DUF985 (InterPro:IPR009327); contains InterPro domain RmlC-like jelly roll fold (InterPro:IPR014710)
252255_at	-1.2348	At3g49220	pectinesterase family protein
263628_at	-1.2347	At2g04780	FLA7__FLA7
256074_at	-1.2303	At1g18260	suppressor of lin-12-like protein-related / sel-1 protein-related
266022_at	-1.2289	At2g05920	subtilase family protein
266615_s_at	-1.2284	At2g29720 At2g35660	CTF2B__CTF2B; monooxygenase
251055_at	-1.2275	At5g01710	similar to methyltransferase [Arabidopsis thaliana] (TAIR:AT4G24805.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48800.1); contains InterPro domain Methyltransferase FkbM (InterPro:IPR006342)
249366_at	-1.2272	At5g40610	glycerol-3-phosphate dehydrogenase (NAD+) / GPDH
246028_at	-1.2270	At5g21170	5'-AMP-activated protein kinase beta-2 subunit, putative
247069_at	-1.2255	At5g66920	SKS17__SKS17 (SKU5 Similar 17); copper ion binding / oxidoreductase
253136_at	-1.2253	At4g35470	leucine-rich repeat family protein
263690_at	-1.2249	At1g26960	ATHB23__ATHB23 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 23); DNA binding / transcription factor
261586_at	-1.2238	At1g01640	speckle-type POZ protein-related
260602_at	-1.2236	At1g55920	AtSerat2;1_SAT1_SAT5__AtSerat2;1 (SERINE ACETYLTRANSFERASE 1)
257611_at	-1.2229	At3g26580	binding
265472_at	-1.2209	At2g15580	zinc finger (C3HC4-type RING finger) family protein
248619_at	-1.2168	At5g49630	AAP6__AAP6 (AMINO ACID PERMEASE 6); amino acid transmembrane transporter
261149_s_at	-1.2149	At1g19550 At1g19570	dehydroascorbate reductase, putative
253606_at	-1.2149	At4g30530	defense-related protein, putative
253578_at	-1.2139	At4g30340	ATDGK7__ATDGK7 (DIACYLGLYCEROL KINASE 7); diacylglycerol kinase
253273_at	-1.2138	At4g34180	cyclase family protein
266922_s_at	-1.2114	At2g45950 At3g61415	ASK20__ASK20 (ARABIDOPSIS SKP1-LIKE 20)

247563_at	-1.2110	At5g61130	glycosyl hydrolase family protein 17
263442_at	-1.2100	At2g28605	Identical to PsbP-related thylakoid lumenal protein 3, chloroplast precursor [Arabidopsis Thaliana] (GB:Q8VY52;GB:P83050;GB:Q8S8B1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71682.1); contains InterPro domain Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich (InterPro:IPR016124); contains InterPro domain Mog1/PsbP, alpha/beta/alpha sandwich (InterPro:IPR016123)
245251_at	-1.2094	At4g17615	CBL1_SCABP5__CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion binding
248509_at	-1.2085	At5g50335	unknown protein
251391_at	-1.2070	At3g60910	catalytic
263499_at	-1.2042	At2g42580	TTL3__TTL3 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 3); protein binding
266285_at	-1.2040	At2g29180	similar to 80C09_19 [Brassica rapa subsp. pekinensis] (GB:AAZ41830.1)
260079_s_at	-1.2024	At1g35460 At5g33210	basic helix-loop-helix (bHLH) family protein
260368_at	-1.2013	At1g69700	ATHVA22C__ATHVA22C (Arabidopsis thaliana HVA22 homologue C)
264940_at	-1.2008	At1g60470	ATGOLS4__ATGOLS4 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 4); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
258617_at	-1.1997	At3g03000	calmodulin, putative
246170_at	-1.1980	At5g32450	RNA recognition motif (RRM)-containing protein
249216_at	-1.1927	At5g42240	SCPL42__SCPL42 (serine carboxypeptidase-like 42); serine carboxypeptidase
266018_at	-1.1919	At2g18710	SCY1__SCY1 (SECY HOMOLOG 1); P-P-bond-hydrolysis-driven protein transmembrane transporter
257745_at	-1.1908	At3g29240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33780.1); similar to hypothetical protein OsI_032014 [Oryza sativa (indica cultivar-group)] (GB:EAY78055.1); similar to Os10g0330400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001064365.1); contains InterPro domain Protein of unknown function DUF179
250738_at	-1.1904	At5g05730	ASA1_AMT1_TRP5_WEI2__ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase
259541_at	-1.1903	At1g20650	protein kinase
261685_at	-1.1878	At1g47290	AT3BETAHSD/D1__AT3BETAHSD/D1 (3BETA-HYDROXYSTEROID-DEHYDROGENASE/DECARBOXYLASE ISOFORM 1); 3-beta-hydroxy-delta5-steroid dehydrogenase
251296_at	-1.1878	At3g62010	metal ion binding / oxidoreductase
245408_at	-1.1878	At4g17180	glycosyl hydrolase family 17 protein
248681_at	-1.1854	At5g48900	pectate lyase family protein
259838_at	-1.1852	At1g52220	similar to PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA) [Arabidopsis thaliana] (TAIR:AT2G46820.2); similar to PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA), DNA binding [Arabidopsis thaliana] (TAIR:AT2G46820.1); similar to unknown [Populus trichocarpa] (GB:ABK95860.1)
264007_at	-1.1829	At2g21140	ATPRP2__ATPRP2 (PROLINE-RICH PROTEIN 2)
267142_at	-1.1821	At2g38290	ATAMT2__ATAMT2 (AMMONIUM TRANSPORTER 2); ammonium transmembrane transporter
261144_s_at	-1.1820	At1g19660 At1g75380	wound-responsive family protein
265573_at	-1.1782	At2g28200	nucleic acid binding / transcription factor/ zinc ion binding
258359_s_at	-1.1777	At3g14415 At3g14420	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative
255118_at	-1.1769	At4g08790	nitrilase, putative
247219_at	-1.1765	At5g64920	CIP8__CIP8 (COP1-INTERACTING PROTEIN 8); protein binding / zinc ion binding
256225_at	-1.1761	At1g56220	dormancy/auxin associated family protein
258394_at	-1.1744	At3g15530	methyltransferase
261979_at	-1.1737	At1g37130	NIA2_B29_CHL3_NIA2-1_NR__NIA2 (NITRATE REDUCTASE 2)
265648_at	-1.1737	At2g27500	glycosyl hydrolase family 17 protein

256396_at	-1.1732	At3g06150	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71094.1); contains InterPro domain Immunoglobulin E-set (InterPro:IPR014756)
265053_at	-1.1722	At1g52000	jacalin lectin family protein
266591_at	-1.1713	At2g46225	ABI1L1__ABIL1 (ABI-1-LIKE 1)
266322_at	-1.1709	At2g46690	auxin-responsive family protein
267154_at	-1.1699	At2g30870	ATGSTF10_ATGSTF4_ERD13__ATGSTF10 (EARLY DEHYDRATION-INDUCED 13); glutathione transferase
266348_at	-1.1698	At2g01450	ATMPK17__ATMPK17 (Arabidopsis thaliana MAP kinase 17); MAP kinase
253855_at	-1.1679	At4g28050	TET7__TET7 (TETRASPANIN7)
251108_at	-1.1675	At5g01620	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G38320.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48780.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
260877_at	-1.1671	At1g21500	similar to hypothetical protein OsI_030994 [Oryza sativa (indica cultivar-group)] (GB:EAZ09762.1); similar to Os09g0517000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063677.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD33829.1)
248886_at	-1.1651	At5g46110	APE2_TPT__APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT)
250318_at	-1.1650	At5g12200	dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)
260730_at	-1.1642	At1g48030	dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1)
251890_at	-1.1635	At3g54220	SCR_SGR1__SCR (SCARECROW); transcription factor
263478_at	-1.1631	At2g31880	leucine-rich repeat transmembrane protein kinase, putative
258489_at	-1.1624	At3g02520	GRF7_GF14 NU__GRF7 (GENERAL REGULATORY FACTOR 7); protein phosphorylated amino acid binding
249810_at	-1.1623	At5g23920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52420.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49441.1)
267130_at	-1.1620	At2g23390	similar to hypothetical protein OsI_015489 [Oryza sativa (indica cultivar-group)] (GB:EAY94256.1); similar to Os04g0442200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001052881.1); contains InterPro domain Acyl-CoA N-acyltransferase (InterPro:IPR016181); contains InterPro domain Protein of unknown function DUF482 (InterPro:IPR007434)
260271_at	-1.1611	At1g63690	protease-associated (PA) domain-containing protein
264781_at	-1.1609	At1g08540	SIGB_SIG1_SIG2_SIGA__SIGB (SIGMA FACTOR B); DNA binding / DNA-directed RNA polymerase/ transcription factor
245499_at	-1.1605	At4g16480	ATINT4__ATINT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen ion symporter
252326_at	-1.1603	At3g48680	GAMMA CAL2__GAMMA CAL2 (GAMMA CARBONIC ANHYDRASE-LIKE 2); acyltransferase/ transferase
254770_at	-1.1600	At4g13340	leucine-rich repeat family protein / extensin family protein
266314_at	-1.1597	At2g27040	AGO4__AGO4 (ARGONAUTE 4); nucleic acid binding
253562_at	-1.1582	At4g31130	similar to hypothetical protein [Vitis vinifera] (GB:CAN64246.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR009606)
256755_at	-1.1581	At3g25600	calmodulin, putative
245046_at	-1.1573	At2g26510	PDE135__PDE135 (PIGMENT DEFECTIVE EMBRYO 135); transmembrane
265826_at	-1.1571	At2g35795	DNAJ heat shock N-terminal domain-containing protein
264313_at	-1.1569	At1g70410	carbonic anhydrase, putative / carbonate dehydratase, putative
264745_at	-1.1550	At1g62180	APR2_APSR_ATAPR2_PRH__APR2 (5'ADENYLYLPHOSPHOSULFATE REDUCTASE 2)
264446_at	-1.1545	At1g27310	NTF2A__NTF2A (NUCLEAR TRANSPORT FACTOR 2A); Ran GTPase binding / protein transporter
259545_at	-1.1526	At1g20560	AMP-dependent synthetase and ligase family protein
266483_at	-1.1525	At2g47910	CRR6__CRR6 (CHLORORESPIRATORY REDUCTION 6)
257413_at	-1.1520	At1g22910	RNA recognition motif (RRM)-containing protein

263715_at	-1.1515	At2g20570	GPRI1_GLK1__GPRI1 (GOLDEN2-LIKE 1); transcription factor
252441_at	-1.1515	At3g46780	PTAC16__PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE18); binding / catalytic
257641_s_at	-1.1502	At3g25760 At3g25770	AOC1_ERD12__AOC1 (ALLENE OXIDE CYCLASE 1)
254492_at	-1.1500	At4g20260	DREPP plasma membrane polypeptide family protein
260499_at	-1.1497	At2g41760	similar to unnamed protein product [Vitis vinifera] (GB:CAO23603.1); contains domain PTHR13035 (PTHR13035)
262951_at	-1.1492	At1g75500	nodulin MtN21 family protein
265716_at	-1.1469	At2g03350	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G08890.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G08890.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO15324.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493)
259445_at	-1.1466	At1g02400	ATGA2OX6_DTA1__ATGA2OX6/DTA1 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase
261534_at	-1.1446	At1g01820	PEX11C__PEX11C
259207_at	-1.1445	At3g09050	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96465.1)
264796_at	-1.1430	At1g08680	AGD14_ZIGA4__ZIGA4 (ARF GAP-LIKE ZINC FINGER-CONTAINING PROTEIN ZIGA4); DNA binding
263662_at	-1.1418	At1g04430	dehydration-responsive protein-related
254970_at	-1.1417	At4g10340	LHCB5__LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding
254120_at	-1.1412	At4g24570	mitochondrial substrate carrier family protein
267357_at	-1.1410	At2g40000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41329.1); contains InterPro domain Hs1pro-1, C-terminal (InterPro:IPR009743); contains InterPro domain Hs1pro-1, N-terminal (InterPro:IPR009869)
261492_at	-1.1399	At1g14290	acid phosphatase, putative
245275_at	-1.1396	At4g15210	BMY1_ATBETA-AMY_AT-BETA-AMY_RAM1__ATBETA-AMY (BETA-AMYLASE); beta-amylase
253414_at	-1.1394	At4g33050	EDA39__EDA39 (embryo sac development arrest 39)
259955_s_at	-1.1386	At1g19350 At1g75080	BES1_BZR2__BES1 (BRI1-EMS-SUPPRESSOR 1)
265637_at	-1.1385	At2g27490	ATCOAE__ATCOAE; ATP binding / dephospho-CoA kinase
266316_at	-1.1367	At2g27080	harpin-induced protein-related / HIN1-related / harpin-responsive protein-related
258623_at	-1.1364	At3g02790	zinc finger (C2H2 type) family protein
248943_s_at	-1.1361	At5g45440 At5g45490	disease resistance protein-related
254331_s_at	-1.1341	At4g22690 At4g22710	CYP706A1__CYP706A1 (cytochrome P450, family 706, subfamily A, polypeptide 1); oxygen binding
264360_at	-1.1339	At1g03310	ATISA2_BE2_DBE1_ISA2__ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYME 1); alpha-amylase/ isoamylase
256633_at	-1.1330	At3g28340	GATL10__GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring hexosyl groups
256872_at	-1.1325	At3g26490	phototropic-responsive NPH3 family protein
260371_at	-1.1322	At1g69690	TCP family transcription factor, putative
254229_at	-1.1317	At4g23610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G54200.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39657.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73280.1)
262577_at	-1.1316	At1g15290	binding
254606_at	-1.1307	At4g19030	NIP1;1_NLM1__NLM1 (NOD26-like intrinsic protein 1;1); water channel
254686_at	-1.1296	At4g13720	inosine triphosphate pyrophosphatase, putative / HAM1 family protein
247696_at	-1.1295	At5g59780	AtMYB59_MYB59__MYB59 (myb domain protein 59); DNA binding / transcription factor
266168_at	-1.1289	At2g38870	protease inhibitor, putative
245304_at	-1.1287	At4g15630	integral membrane family protein
264898_at	-1.1277	At1g23205	invertase/pectin methylesterase inhibitor family protein

261920_at	-1.1266	At1g65930	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative
250272_at	-1.1264	At5g13000	ATGSL12_GSL12__ATGSL12 (GLUCAN SYNTHASE-LIKE 12); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups
259958_at	-1.1263	At1g53730	SRF6__SRF6 (STRUBBELIG-RECEPTOR FAMILY 6)
262902_x_at	-1.1234	At1g59930	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G59920.1); similar to putative MADS-box transcription factor [Arabidopsis lyrata] (GB:AAO42467.1); contains domain PTHR11945 (PTHR11945); contains domain PTHR11945:SF14 (PTHR11945:SF14)
248526_at	-1.1228	At5g50740	similar to ATFP3 (Arabidopsis thaliana farnesylated protein 3), metal ion binding [Arabidopsis thaliana] (TAIR:AT5G63530.1); similar to ATFP3 (Arabidopsis thaliana farnesylated protein 3) [Arabidopsis thaliana] (TAIR:AT5G63530.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO68320.1); contains InterPro domain Heavy metal transport/detoxification protein; (InterPro:IPR006121)
259131_at	-1.1224	At3g02180	SP1L3_SP1L__SP1L3 (SPIRAL 1-LIKE3)
256458_at	-1.1214	At1g75220	integral membrane protein, putative
261881_at	-1.1206	At1g80760	NIP6;1_NLM7_NIP6;1_NIP6__NIP6;1 (NOD26-like intrinsic protein 6;1); water channel
261221_at	-1.1205	At1g19960	similar to transmembrane receptor [Arabidopsis thaliana] (TAIR:AT2G32140.1)
251322_at	-1.1198	At3g61440	ARATH;BSAS3;1_ATCYSC1__ATCYSC1 (BETA-SUBSTITUTED ALA SYNTHASE
259513_at	-1.1196	At1g12430	PAK__PAK (PHOSPHATIDIC ACID KINASE); microtubule motor
253382_at	-1.1187	At4g33040	glutaredoxin family protein
262809_at	-1.1178	At1g11720	ATSS3__ATSS3 (STARCH SYNTHASE 3); starch synthase/ transferase, transferring glycosyl groups
261434_at	-1.1177	At1g07650	leucine-rich repeat transmembrane protein kinase, putative
248557_at	-1.1157	At5g49980	AFB5__AFB5 (AUXIN F-BOX PROTEIN 5); ubiquitin-protein ligase
261420_at	-1.1153	At1g07720	beta-ketoacyl-CoA synthase family protein
246233_at	-1.1142	At4g36550	binding / ubiquitin-protein ligase
255483_at	-1.1125	At4g02500	ATXT2__ATXT2; UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups
249197_at	-1.1116	At5g42380	CML37_CML39__CML37/CML39; calcium ion binding
264342_at	-1.1114	At1g12080	contains domain PTHR22683 (PTHR22683)
258803_at	-1.1099	At3g04670	WRKY39__WRKY39 (WRKY DNA-binding protein 39); transcription factor
247288_at	-1.1082	At5g64330	NPH3_JK218_RPT3__NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3)
265677_at	-1.1073	At2g32080	PUR ALPHA-1__PUR ALPHA-1 (purin-rich alpha 1); nucleic acid binding
248291_at	-1.1066	At5g53020	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G45900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48642.1); contains domain gb def:
248095_at	-1.1016	At5g55230	ATMAP65-1__ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding
246786_at	-1.1008	At5g27410	aminotransferase class IV family protein
248511_at	-1.0997	At5g50375	CPI1__CPI1 (CYCLOPROPYL ISOMERASE)
248401_at	-1.0995	At5g52110	HCF208 (HIGH CHLOROPHYLL FLUORESCENCE 208)
248190_at	-1.0967	At5g54130	calcium-binding EF hand family protein
245176_at	-1.0959	At2g47440	DNAJ heat shock N-terminal domain-containing protein
259152_at	-1.0942	At3g10210	similar to Rho-GTPase-activating protein-related [Arabidopsis thaliana] (TAIR:AT4G35750.1); similar to unknown [Populus trichocarpa] (GB:ABK94010.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251)
259892_at	-1.0937	At1g72610	GLP1__GLP1 (GERMIN-LIKE PROTEIN 1); manganese ion binding / metal ion binding / nutrient reservoir
256226_at	-1.0930	At1g56280	ATDI19__ATDI19 (Arabidopsis thaliana drought-induced 19)
252829_at	-1.0925	At4g40060	ATHB16__ATHB-16/ATHB16 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 16); transcription activator/ transcription factor
255068_at	-1.0918	At4g08920	CRY1_BLU1_HY4_OOP2__CRY1 (CRYPTOCHROME 1)
266037_at	-1.0901	At2g05940	protein kinase, putative
262400_at	-1.0875	At1g49480	RTV1__RTV1 (RELATED TO VERNALIZATION1 1); DNA binding / transcription factor
253302_at	-1.0861	At4g33660	unknown protein

248624_at	-1.0855	At5g48790	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49997.1)
265366_at	-1.0853	At2g13290	glycosyl transferase family 17 protein
263834_at	-1.0842	At2g40316	similar to unnamed protein product [Vitis vinifera] (GB:CAO41434.1); contains domain CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR (PTHR15071); contains domain Q6CBS9_EEEEE_Q6CBS9; (PD106563)
266324_at	-1.0835	At2g46710	rac GTPase activating protein, putative
262557_at	-1.0833	At1g31330	PSAF__PSAF (photosystem I subunit F)
252411_at	-1.0830	At3g47430	PEX11B__PEX11B
263688_at	-1.0826	At1g26920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69760.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48418.1)
254784_at	-1.0822	At4g12720	NUDT7_GFG1__AtNUDT7 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 7); hydrolase
251610_at	-1.0800	At3g57930	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42190.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83221.1); contains InterPro domain HMG-I and HMG-Y, DNA-binding (InterPro:IPR000637)
261597_at	-1.0798	At1g49780	U-box domain-containing protein
251036_at	-1.0787	At5g02160	unknown protein
267188_at	-1.0769	At2g44050	COS1__COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase
264990_at	-1.0756	At1g27210	binding
255860_at	-1.0755	At5g34940	ATGUS3__ATGUS3 (ARABIDOPSIS THALIANA GLUCURONIDASE 3); beta-glucuronidase
246351_at	-1.0755	At1g16570	glycosyl transferase family 1 protein
253493_at	-1.0748	At4g31820	ENP (ENHANCER OF PINOID); signal transducer
248303_at	-1.0747	At5g53170	FTSH11__FTSH11 (FtsH protease 11); ATP-dependent peptidase/ ATPase/ metallopeptidase
262728_at	-1.0737	At1g75820	CLV1_FAS3_FLO5__CLV1 (CLAVATA 1); ATP binding / kinase/ protein serine/threonine kinase
257206_at	-1.0727	At3g16530	legume lectin family protein
246522_at	-1.0726	At5g15830	ATBZIP3__ATBZIP3 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 3); DNA binding / transcription factor
267010_at	-1.0710	At2g39250	SNZ__SNZ (SCHNARCHZAPFEN); DNA binding / transcription factor
263048_s_at	-1.0706	At2g05310 At4g13500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41162.1)
263946_at	-1.0706	At2g36000	mitochondrial transcription termination factor-related / mTERF-related
249144_at	-1.0701	At5g43270	SPL2__SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor
245790_at	-1.0682	At1g32200	ATS1_ACT1__ATS1 (ACYLTRANSFERASE 1)
257008_at	-1.0679	At3g14210	ESM1__ESM1 (EPITHIOSPECIFIER MODIFIER 1); carboxylesterase
252040_at	-1.0669	At3g52060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22070.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66030.1); contains InterPro domain Protein of unknown function DUF266, plant (InterPro:IPR004949)
267460_at	-1.0668	At2g33810 At2g33815	SPL3__SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); transcription factor
261196_at	-1.0664	At1g12860	basic helix-loop-helix (bHLH) family protein / F-box family protein
250524_at	-1.0659	At5g08520	myb family transcription factor
250913_at	-1.0657	At5g03770	3-deoxy-D-manno-octulosonic acid transferase-related
255046_at	-1.0654	At4g09650	ATP synthase delta chain, chloroplast, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative
245913_at	-1.0651	At5g19860	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55265.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23444.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493)
252921_at	-1.0643	At4g39030	EDS5_SID1__EDS5 (ENHANCED DISEASE SUSCEPTIBILITY 5); antiporter/
262399_at	-1.0642	At1g49500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19030.1)
245141_at	-1.0635	At2g45400	BEN1__BEN1; oxidoreductase, acting on CH-OH group of donors

261177_at	-1.0632	At1g04770	male sterility MS5 family protein
266204_at	-1.0631	At2g02410	similar to unnamed protein product [Vitis vinifera] (GB:CAO46936.1); contains InterPro domain Protein of unknown function DUF901 (InterPro:IPR010298)
264177_at	-1.0626	At1g02150	pentatricopeptide (PPR) repeat-containing protein
246759_at	-1.0606	At5g27950	kinesin motor protein-related
256979_at	-1.0602	At3g21055	PSBTN__PSBTN (photosystem II subunit T)
262539_at	-1.0601	At1g17200	integral membrane family protein
263836_at	-1.0589	At2g40330	Bet v I allergen family protein
266188_at	-1.0581	At2g39000	GCN5-related N-acetyltransferase (GNAT) family protein
261560_at	-1.0579	At1g01710	acyl-CoA thioesterase family protein
248941_s_at	-1.0574	At5g45460 At5g45470	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45470.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39193.1)
247396_at	-1.0563	At5g62930	GDSL-motif lipase/hydrolase family protein
261078_at	-1.0563	At1g07320	RPL4__RPL4 (ribosomal protein L4); poly(U) binding / structural constituent of
266856_at	-1.0539	At2g26910	ATPDR4_PDR4__ATPDR4/PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances
254270_at	-1.0535	At4g23100	GSH1_RML1_CAD2_GSH1_PAD2__RML1 (ROOT MERISTEMLESS 1)
251714_at	-1.0529	At3g56370	leucine-rich repeat transmembrane protein kinase, putative
258616_at	-1.0521	At3g02880	leucine-rich repeat transmembrane protein kinase, putative
267076_at	-1.0510	At2g41090	calmodulin-like calcium-binding protein, 22 kDa (CaBP-22)
249932_at	-1.0506	At5g22390	similar to unnamed protein product [Vitis vinifera] (GB:CAO48728.1)
251554_at	-1.0504	At3g58670	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42670.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48045.1); contains InterPro domain Protein of unknown function DUF1637 (InterPro:IPR012864)
257311_at	-1.0503	At3g26570	PHT2;1_ORF02__PHT2;1 (phosphate transporter 2;1)
256570_at	-1.0473	At3g19540	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G49840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70870.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68554.1); contains InterPro domain Protein of unknown function DUF620 (InterPro:IPR006873)
255177_at	-1.0473	At4g08040	ACS11__ACS11 (1-Amino-cyclopropane-1-carboxylate synthase 11); 1-aminocyclopropane-1-carboxylate synthase
254300_at	-1.0453	At4g22780	ACR7__ACR7 (ACT Domain Repeat 7)
258413_at	-1.0430	At3g17300	similar to unnamed protein product [Vitis vinifera] (GB:CAO70895.1)
261926_at	-1.0426	At1g22530	PATL2__PATL2; transporter
266535_s_at	-1.0424	At2g16930 At5g15220	ribosomal protein L27 family protein
254385_s_at	-1.0424	At4g21830 At4g21840	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein
264978_at	-1.0420	At1g27120	galactosyltransferase family protein
253372_at	-1.0420	At4g33220	pectinesterase family protein
261958_at	-1.0394	At1g64500	glutaredoxin family protein
257814_at	-1.0393	At3g25110	ATFATA__ATFATA (ARABIDOPSIS FATA ACYL-ACP THIOESTERASE); acyl carrier/ acyl-ACP thioesterase
250892_at	-1.0365	At5g03760	ATCSLA09_ATCSLA9_CSLA09_CSLA9_RAT4__ATCSLA09 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 4); transferase, transferring glycosyl groups
262155_at	-1.0361	At1g52420	glycosyl transferase family 1 protein
248197_at	-1.0341	At5g54190	PORA__PORA (Protochlorophyllide reductase A); oxidoreductase/ protochlorophyllide reductase
265175_at	-1.0329	At1g23480	ATCSLA03_ATCSLA3_CSLA03__ATCSLA03 (Cellulose synthase-like A3); transferase, transferring glycosyl groups
247286_at	-1.0328	At5g64280	DIT2.2__DIT2.2 (DICARBOXYLATE TRANSPORTER 2.2); oxoglutarate:malate
258932_at	-1.0303	At3g10150	ATPAP16_PAP16__ATPAP16/PAP16 (purple acid phosphatase 16); acid phosphatase/ protein serine/threonine phosphatase
248970_at	-1.0293	At5g45380	sodium:solute symporter family protein

256145_at	-1.0291	At1g48750 At1g48760	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
261131_at	-1.0291	At1g19835	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48232.1); similar to hypothetical protein OsI_010472 [Oryza sativa (indica cultivar-group)] (GB:EAY89239.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60525.1); contains InterPro domain Protein of unknown function DUF869, plant (InterPro:IPR008587)
267612_at	-1.0291	At2g26690	nitrate transporter (NTP2)
266268_at	-1.0289	At2g29510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G59020.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21541.1); contains InterPro domain Tubby, C-terminal (InterPro:IPR000007)
246631_at	-1.0279	At1g50740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G20510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO38976.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)
253921_at	-1.0274	At4g26900	AT-HF_HISHF_HISN4__AT-HF (ARABIDOPSIS THALIANA HISF PROTEIN)
256578_at	-1.0272	At3g28200	peroxidase, putative
246275_at	-1.0262	At4g36540	BEE2__BEE2 (BR ENHANCED EXPRESSION 2); DNA binding / transcription factor
252062_at	-1.0260	At3g52640	nicastrin-related
247865_at	-1.0247	At5g57815	cytochrome c oxidase subunit 6b, putative
267239_at	-1.0238	At2g02510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G14450.1); similar to unknown [Populus trichocarpa] (GB:ABK94107.1)
247725_at	-1.0227	At5g59410	similar to Rab5-interacting family protein [Arabidopsis thaliana] (TAIR:AT2G29020.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21636.1); contains InterPro domain Rab5-interacting (InterPro:IPR010742)
252373_at	-1.0222	At3g48090	EDS1__EDS1 (ENHANCED DISEASE SUSCEPTIBILITY 1); signal transducer/ triacylglycerol lipase
257789_at	-1.0222	At3g27020	YSL6__YSL6 (YELLOW STRIPE LIKE 6); oligopeptide transporter
245152_at	-1.0222	At2g47490	mitochondrial substrate carrier family protein
258109_at	-1.0203	At3g23640	HGL1__HGL1 (HETEROGLYCAN GLUCOSIDASE 1)
245876_at	-1.0196	At1g26230	chaperonin, putative
259383_at	-1.0195	At3g16470	JR1__JR1 (Jacalin lectin family protein)
245877_at	-1.0194	At1g26218 At1g26220	
250368_at	-1.0182	At5g11280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G80200.1); similar to unknown [Populus trichocarpa] (GB:ABK96125.1)
256332_at	-1.0180	At1g76890	GT2__GT2; transcription factor
261165_at	-1.0178	At1g34430	EMB3003__EMB3003 (EMBRYO DEFECTIVE 3003); dihydrolipoyllysine-residue acetyltransferase
250498_at	-1.0172	At5g09660	PMDH2__PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2)
261876_at	-1.0165	At1g50590	pirin, putative
252917_at	-1.0163	At4g38960	zinc finger (B-box type) family protein
249398_at	-1.0162	At5g40250	zinc finger (C3HC4-type RING finger) family protein
263031_at	-1.0161	At1g24070	ATCSLA10_CSLA10__ATCSLA10 (Cellulose synthase-like A10); transferase, transferring glycosyl groups
257674_at	-1.0159	At3g20390	endoribonuclease L-PSP family protein
258039_at	-1.0158	At3g21200	similar to hypothetical protein [Vitis vinifera] (GB:CAN79599.1); contains InterPro domain FMN-binding split barrel, related (InterPro:IPR009002)
257623_at	-1.0148	At3g26210	CYP71B23__CYP71B23 (cytochrome P450, family 71, subfamily B, polypeptide 23); oxygen binding
254688_at	-1.0143	At4g13830	J20__J20 (DNAJ-LIKE 20); heat shock protein binding
267377_at	-1.0140	At2g26250	FDH__FDH (FIDDLEHEAD); acyltransferase
256922_at	-1.0138	At3g19010	oxidoreductase, 2OG-Fe(II) oxygenase family protein
259523_at	-1.0138	At1g12500	phosphate translocator-related
260215_at	-1.0130	At1g74530	similar to unnamed protein product [Vitis vinifera] (GB:CAO62539.1)
266979_at	-1.0111	At2g39470	PPL2__PPL2 (PSBP-LIKE PROTEIN 2); calcium ion binding

261563_at	-1.0103	At1g01630	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative
245266_at	-1.0100	At4g17070	peptidyl-prolyl cis-trans isomerase
253208_at	-1.0098	At4g34830	binding
261469_at	-1.0092	At1g28340	leucine-rich repeat family protein
260360_at	-1.0080	At1g69370	CM3_CM-3__CM3 (CHORISMATE MUTASE 3); chorismate mutase
261832_at	-1.0068	At1g10650	protein binding / zinc ion binding
251764_at	-1.0063	At3g55830	EPC1__EPC1 (ECTOPICALLY PARTING CELLS); transferase, transferring glycosyl groups
246143_at	-1.0062	At5g19980	integral membrane family protein
262878_at	-1.0060	At1g64770	carbohydrate binding / catalytic
261421_at	-1.0057	At1g18840	IQD30__IQD30; calmodulin binding
248793_at	-1.0057	At5g47240	ATNUDT8__ATNUDT8 (Arabidopsis thaliana Nudix hydrolase homolog 8); hydrolase
265912_at	-1.0055	At2g25570	binding
261650_at	-1.0042	At1g27770	ACA1_PEA1__ACA1 (autoinhibited Ca2+ -ATPase 1); calmodulin binding
252824_at	-1.0039	At4g40030	histone H3.2
252213_at	-1.0038	At3g50210	2-oxoacid-dependent oxidase, putative
246200_at	-1.0034	At4g37240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO45438.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN61825.1)
246300_at	-1.0033	At3g51830	ATG5__ATG5 (G5p-related protein); phosphoinositide 5-phosphatase
253887_at	-1.0032	At4g27730	ATOPT6__ATOPT6 (oligopeptide transporter 6); oligopeptide transporter
254549_at	-1.0032	At4g19880	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45020.1); similar to Intracellular chloride channel [Medicago truncatula] (GB:ABC75353.2); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Glutathione S-transferase, C-terminal-like (InterPro:IPR010987); contains InterPro domain Glutathione S-transferase, predicted (InterPro:IPR016639)
262919_at	-1.0021	At1g79380	copine-related
262341_at	-1.0021	At1g64230	UBC28__UBC28; ubiquitin-protein ligase