Appendix 2a Genes up-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 up-regulated (log2 fold change in expression >1).

Probe ID	Fold change (log2)	AGI Code	TAIR annotation
264211_at	7.3677	At1g22770	GI_FB__GI (GIGANTEA); binding
245306_at	7.1462	At4g14690	ELIP2__ELIP2 (EARLY LIGHT-INDUCIBLE PROTEIN 2); chlorophyll binding
264511_at	6.7448	At1g09350	ATGOLS3__ATGOLS3 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl
253416_at	6.5656	At4g33070	pyruvate decarboxylase, putative
247095_at	6.3543	At5g66400	RAB18_ATDI8__RAB18 (RESPONSIVE TO ABA 18)
252102_at	6.1259	At3g50970	LTI30_XERO2__LTI30 (LOW TEMPERATURE-INDUCED 30)
264612_at	5.8457	At1g04560	AWPM-19-like membrane family protein
245627_at	5.8352	At1g56600	ATGOLS2__ATGOLS2 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl
247851_at	5.8249	At5g58070	lipocalin, putative
258979_at	5.7350	At3g09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)
248337_at	5.5474	At5g52310	LTI78_RD29A_COR78_LTI140_LTI78_RD29A__COR78 (COLD REGULATED
255521_at	5.5254	At4g02280	SUS3__SUS3; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups
266462_at	5.4409	At2g47770	benzodiazepine receptor-related
262644_at	5.3020	At1g62710	BETA-VPE_BETAVPE__BETA-VPE (vacuolar processing enzyme beta); cysteine-type endopeptidase
258321_at	5.1929	At3g22840	ELIP1_ELIP__ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll
266578_at	5.0904	At2g23910	cinnamoyl-CoA reductase-related
256245_at	4.9662	At3g12580	HSP70__HSP70 (heat shock protein 70); ATP binding
264147_at	4.6517	At1g02205	CER1__CER1 (ECERIFERUM 1)
254952_at	4.6488	At4g10955 At4g10960	lipase class 3 family protein
253627_at	4.6442	At4g30650	hydrophobic protein, putative / low temperature and salt responsive protein,
245749_at	4.5267	At1g51090	heavy-metal-associated domain-containing protein
252956_at	4.5073	At4g38580	ATFP6__ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding
259426_at	4.4764	At1g01470	LEA14_LSR3__LEA14 (LATE EMBRYOGENESIS ABUNDANT 14)
257237_at	4.3944	At3g14890	phosphoesterase
263497_at	4.3651	At2g42540	COR15A_COR15__COR15A (COLD-REGULATED 15A)
258735_at	4.2467	At3g05880	RCI2A__RCI2A (RARE-COLD-INDUCIBLE 2A)
259570_at	4.2324	At1g20440	COR47_RD17__COR47 (cold regulated 47)
264436_at	4.1704	At1g10370	ATGSTU17_ERD9_GST30__ATGSTU17/ERD9/GST30/GST30B (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase
256114_at	4.1413	At1g16850	unknown protein
264146_at	4.1075	At1g02205	CER1__CER1 (ECERIFERUM 1)
263495_at	4.0904	At2g42530	COR15B
266141_at	4.0833	At2g02120	LCR70_PDF2.1__LCR70/PDF2.1 (Low-molecular-weight cysteine-rich 70); protease inhibitor
246922_at	4.0728	At5g25110	SnRK3.25_CIPK25__CIPK25 (CBL-INTERACTING PROTEIN KINASE 25);
245433_at	4.0637	At4g17140	pleckstrin homology (PH) domain-containing protein
263249_at	3.9850	At2g31360	ADS2__ADS2 (16:0DELTA9 ARABIDOPSIS DESATURASE 2); oxidoreductase
262113_at	3.9828	At1g02820	late embryogenesis abundant 3 family protein / LEA3 family protein
254085_at	3.9623	At4g24960	HVA22D__ATHVA22D (Arabidopsis thaliana HVA22 homologue D)
250826_at	3.9321	At5g05220	similar to hypothetical protein [Vitis vinifera] (GB:CAN82940.1)

250648_at	3.9270	At5g06760	late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein
248043_s_at	3.9249	At5g56000 At5g56010	heat shock protein 81-4 (HSP81-4)
250558_at	3.8553	At5g07990	TT7_CYP75B1_D501__TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding
264953_at	3.8029	At1g77120	ADH1_ADH__ADH1 (ALCOHOL DEHYDROGENASE 1)
251668_at	3.7737	At3g57010	strictosidine synthase family protein
265480_at	3.7191	At2g15970	COR413-PM1_FL3-5A3_WCOR413__COR413-PM1 (cold regulated 413 plasma membrane 1)
251084_at	3.6685	At5g01520	zinc finger (C3HC4-type RING finger) family protein
264787_at	3.6435	At2g17840	ERD7__ERD7 (EARLY-RESPONSIVE TO DEHYDRATION 7)
247061_at	3.6252	At5g66780	similar to unknown [Ammopiptanthus mongolicus] (GB:AAW33981.1)
247776_at	3.6227	At5g58700	phosphoinositide-specific phospholipase C family protein
247463_at	3.5860	At5g62210	embryo-specific protein-related
259588_at	3.5846	At1g27930	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67330.1); similar to unknown [Populus trichocarpa] (GB:ABK93495.1); contains InterPro domain Protein of unknown function DUF579, plant (InterPro:IPR006514)
249204_at	3.5481	At5g42570	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G11905.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24012.1); contains InterPro domain B-cell receptor-associated 31-like; (InterPro:IPR008417)
255259_at	3.5216	At4g05020	NDB2__NDB2 (NAD(P)H DEHYDROGENASE B2); disulfide oxidoreductase
259516_at	3.5113	At1g20450	LTI29_ERD10_LTI45__ERD10/LTI45 (EARLY RESPONSIVE TO
263574_at	3.5025	At2g16990	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G16980.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO61976.1); contains InterPro domain Major facilitator superfamily MFS-1 (InterPro:IPR011701); contains InterPro domain MFS general substrate transporter (InterPro:IPR016196)
261651_at	3.4917	At1g27760	interferon-related developmental regulator family protein / IFRD protein family
262881_at	3.4846	At1g64890	integral membrane transporter family protein
267080_at	3.4572	At2g41190	amino acid transporter family protein
245052_at	3.4373	At2g26440	pectinesterase family protein
260556_at	3.4207	At2g43620	chitinase, putative
247937_at	3.4104	At5g57110	ACA8__ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calmodulin
252315_at	3.3801	At3g48690	ATCXE12__ATCXE12 (ARABIDOPSIS THALIANA CARBOXYESTERASE 12); carboxylesterase
262452_at	3.3628	At1g11210	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G11220.1); similar to cotton fiber expressed protein 1 [Gossypium hirsutum] (GB:AAC33276.1); contains InterPro domain Protein of unknown function DUF761, plant
248722_at	3.3137	At5g47810	phosphofructokinase family protein
264529_at	3.2987	At1g30820	CTP synthase, putative / UTP--ammonia ligase, putative
253872_at	3.2878	At4g27410	ANAC072_RD26__RD26 (RESPONSIVE TO DESSICATION 26)
266142_at	3.2823	At2g39030	GCN5-related N-acetyltransferase (GNAT) family protein
247268_at	3.2748	At5g64080	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
263221_at	3.2711	At1g30620	HSR8_MUR4_MURUS4_MUR4_HSR8_UXE1__HSR8/MUR4/UXE1 (MURUS
250971_at	3.2546	At5g02810	PRR7__PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator
264968_at	3.2092	At1g67360	rubber elongation factor (REF) family protein
265561_s_at	3.1876	At2g05440 At2g05510	glycine-rich protein
250083_at	3.1824	At5g17220	ATGSTF12_GST26_TT19__ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase
257876_at	3.1511	At3g17130	invertase/pectin methylesterase inhibitor family protein
265119_at	3.1448	At1g62570	flavin-containing monooxygenase family protein / FMO family protein
252123_at	3.1190	At3g51240	F3H_F3'H_TT6__F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase
256338_at	3.1148	At1g72100	late embryogenesis abundant domain-containing protein / LEA domain-containing protein
263811_at	3.1115	At2g04350	long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)

245200_at	3.0828	At1g67850	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13000.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42517.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)
251432_at	3.0824	At3g59820	calcium-binding mitochondrial protein-related
254304_at	3.0732	At4g22270	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G03820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23242.1)
259105_at	3.0661	At3g05500	rubber elongation factor (REF) family protein
256595_x_at	3.0650	At1g36770 At3g28530	
260264_at	3.0573	At1g68500	similar to hypothetical protein [Vitis vinifera] (GB:CAN66643.1)
247487_at	3.0547	At5g62150	peptidoglycan-binding LysM domain-containing protein
248045_at	3.0529	At5g56030	HSP81-2_ERD8__HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP binding
266327_at	3.0498	At2g46680	ATHB-7_ATHB7__ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7)
249411_at	3.0443	At5g40390	SIP1__SIP1 (SEED IMBIBITION 1-LIKE); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds
245434_at	3.0318	At4g17120	
267461_at	3.0253	At2g33830	dormancy/auxin associated family protein
258719_at	2.9643	At3g09540	pectate lyase family protein
246481_s_at	2.9550	At5g15960 At5g15970	KIN1__KIN1
267168_at	2.9508	At2g37770	aldo/keto reductase family protein
262440_at	2.9377	At1g47710	(ATSERPIN1); cysteine protease inhibitor/ serine-type endopeptidase inhibitor
264400_at	2.9355	At1g61800	GPT2__GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transmembrane transporter
248100_at	2.8839	At5g55180	glycosyl hydrolase family 17 protein
251753_at	2.8795	At3g55760	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G42430.1); similar to hypothetical protein [Trifolium pratense] (GB:BAE71279.1)
259990_s_at	2.8660	At1g68050 At5g23410 At5g42730	FKF1_ADO3__FKF1 (FLAVIN-BINDING KELCH DOMAIN F BOX PROTEIN); ubiquitin-protein ligase
263548_at	2.8616	At2g21660	GRP7_GR-RBP7_ATGRP7_CCR2__ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding
262164_at	2.8562	At1g78070	WD-40 repeat family protein
261613_at	2.8450	At1g49720	ABF1__ABF1 (ABSCISIC ACID RESPONSIVE ELEMENT-BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor
245998_at	2.8410	At5g20830	SUS1__SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase
264458_at	2.8269	At1g10410	similar to CW14 [Arabidopsis thaliana] (TAIR:AT1G59650.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF98316.1); contains InterPro domain Protein of unknown function DUF1336
258830_at	2.8206	At3g07090	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46108.1); contains InterPro domain Protein of unknown function DUF862, eukaryotic (InterPro:IPR008580)
250994_at	2.8172	At5g02490	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)
255331_at	2.8095	At4g04330	similar to unnamed protein product [Vitis vinifera] (GB:CAO69665.1)
257271_at	2.7883	At3g28007	nodulin MtN3 family protein
255364_s_at	2.7831	At4g04020 At4g22240	FIB__FIB (FIBRILLIN); structural molecule
257252_at	2.7817	At3g24170	ATGR1__ATGR1 (GLUTATHIONE-DISULFIDE REDUCTASE)
260876_at	2.7751	At1g21460	nodulin MtN3 family protein
258449_s_at	2.7603	At3g22310 At3g22330	PMH1 (PUTATIVE MITOCHONDRIAL RNA HELICASE 1); ATP-dependent helicase
247399_at	2.7409	At5g62960	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10660.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10660.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10660.4); similar to unnamed protein product [Vitis vinifera] (GB:CAO64308.1)

266690_at	2.7034	At2g19900	ATNADP-ME1__ATNADP-ME1 (NADP-MALIC ENZYME 1); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor
259616_at	2.6859	At1g47960	C/VIF1__C/VIF1 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1); pectinesterase inhibitor
245164_at	2.6829	At2g33210	chaperonin, putative
250207_at	2.6804	At5g13930	CHS_TT4__ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
261661_at	2.6802	At1g18360	hydrolase, alpha/beta fold family protein
251975_at	2.6674	At3g53230	cell division cycle protein 48, putative / CDC48, putative
254188_at	2.6568	At4g23920	UGE2__UGE2 (UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 2); UDP-glucose 4-epimerase/ protein dimerization
253343_at	2.6565	At4g33540	metallo-beta-lactamase family protein
251090_at	2.6475	At5g01340	mitochondrial substrate carrier family protein
253695_at	2.6450	At4g29510	ATPRMT11_PRMT11__ATPRMT11/PRMT11 (ARABIDOPSIS ARGININE METHYLTRANSFERASE 11); protein-arginine N-methyltransferase
261376_at	2.6311	At1g18660	zinc finger (C3HC4-type RING finger) family protein
253989_at	2.6236	At4g26130	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G56980.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72576.1)
249134_at	2.6207	At5g43150	similar to unnamed protein product [Vitis vinifera] (GB:CAO61459.1)
251221_at	2.6128	At3g62550	universal stress protein (USP) family protein
260489_at	2.6053	At1g51610	cation efflux family protein / metal tolerance protein, putative (MTPc4)
253254_at	2.6016	At4g34650	SQS2__SQS2 (SQUALENE SYNTHASE 2); farnesyl-diphosphate farnesyltransferase
261187_at	2.5946	At1g32860	glycosyl hydrolase family 17 protein
252010_at	2.5762	At3g52740	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G44450.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70571.1)
248381_at	2.5757	At5g51830	pfkB-type carbohydrate kinase family protein
246189_at	2.5680	At5g20910	zinc finger (C3HC4-type RING finger) family protein
248410_at	2.5599	At5g51570	band 7 family protein
267035_at	2.5521	At2g38400	AGT3__AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3); alanine-glyoxylate transaminase
250502_at	2.5438	At5g09590	mtHSC70-2_HSC70-5__mtHSC70-2 (HEAT SHOCK PROTEIN 70); ATP binding / unfolded protein binding
253252_at	2.5417	At4g34740	ATASE2_CIA1_ATD2_ATPURF2__ATASE2 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 2);
264054_at	2.5410	At2g22540	SVP_AGL22__SVP (SHORT VEGETATIVE PHASE); transcription factor
253824_at	2.5325	At4g27940	mitochondrial substrate carrier family protein
249677_at	2.5308	At5g35970	DNA-binding protein, putative
249456_at	2.5224	At5g39410	binding / catalytic
265154_at	2.5210	At1g30960	GTP-binding protein (ERG)
264676_at	2.5105	At1g09870	histidine acid phosphatase family protein
248625_at	2.5048	At5g48880	KAT5_PKT1_KAT5_PKT2__KAT5/PKT1/PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 1, PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase
247097_at	2.4920	At5g66460	(1-4)-beta-mannan endohydrolase, putative
250794_at	2.4897	At5g05270	chalcone-flavanone isomerase family protein
259248_at	2.4897	At3g07770	ATP binding
252006_at	2.4823	At3g52820	ATPAP22_PAP22__ATPAP22/PAP22 (purple acid phosphatase 22); acid phosphatase/ protein serine/threonine phosphatase
251109_at	2.4792	At5g01600	ATFER1__ATFER1 (FERRETIN 1); ferric iron binding
259173_at	2.4673	At3g03640	GLUC__GLUC (Beta-glucosidase homolog); hydrolase, hydrolyzing O-glycosyl compounds
266368_at	2.4589	At2g41380	embryo-abundant protein-related
264652_at	2.4566	At1g08920	sugar transporter, putative
245523_at	2.4528	At4g15910	ATDI21_DI21__ATDI21 (Arabidopsis thaliana drought-induced 21)
249769_at	2.4522	At5g24120	SIGE_SIG5__SIGE (RNA polymerase sigma subunit E); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor

247318_at	2.4474	At5g63990	3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative
247378_at	2.4442	At5g63120	ethylene-responsive DEAD box RNA helicase, putative (RH30)
257702_at	2.4432	At3g12670	EMB2742__EMB2742 (EMBRYO DEFECTIVE 2742); CTP synthase
247983_at	2.4152	At5g56630	phosphofructokinase family protein
262626_at	2.3897	At1g06430	FTSH8__FTSH8 (FtsH protease 8); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding
262050_at	2.3721	At1g80130	binding
266503_at	2.3699	At2g47780	rubber elongation factor (REF) protein-related
258402_at	2.3689	At3g15450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27450.1); similar to unknown [Populus trichocarpa] (GB:ABK93866.1); contains domain N-terminal nucleophile aminohydrolases (Ntn hydrolases) (SSF56235); contains domain no description (G3DSA:3.60.20.10)
AFFX-r2-At-G	2.3596	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
257713_at	2.3574	At3g27380	SDH2-1__SDH2-1 (succinate dehydrogenase 2-1)
248744_at	2.3545	At5g48250	zinc finger (B-box type) family protein
248258_at	2.3543	At5g53400	nuclear movement family protein
260444_at	2.3439	At1g68300	universal stress protein (USP) family protein
247525_at	2.3416	At5g61380	TOC1_APRR1_PRR1__TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator
265886_at	2.3414	At2g25620	protein phosphatase 2C, putative / PP2C, putative
267361_at	2.3407	At2g39920	acid phosphatase class B family protein
262691_at	2.3233	At1g62740	stress-inducible protein, putative
248118_at	2.3230	At5g55050	GDSL-motif lipase/hydrolase family protein
251323_at	2.3210	At3g61580	delta-8 sphingolipid desaturase (SLD1)
252134_at	2.3124	At3g50910	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66480.1); similar to hypothetical protein [Thellungiella halophila] (GB:ABB45854.1)
256905_at	2.3116	At3g23990	HSP60__HSP60 (Heat shock protein 60); ATP binding / protein binding / unfolded protein binding
262526_at	2.3106	At1g17050	SPS2__SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyltranstransferase/ trans-octaprenyltranstransferase
264186_at	2.3102	At1g54570	esterase/lipase/thioesterase family protein
255225_at	2.3058	At4g05410	transducin family protein / WD-40 repeat family protein
266170_at	2.3040	At2g39050	hydroxyproline-rich glycoprotein family protein
259789_at	2.2956	At1g29395	COR414-TM1__COR414-TM1 (cold regulated 414 thylakoid membrane 1)
266510_at	2.2950	At2g47990	EDA13_EDA19_SWA1__SWA1 (SLOW WALKER1); nucleotide binding
247060_at	2.2914	At5g66760	SDH1-1__SDH1-1 (Succinate dehydrogenase 1-1)
264261_at	2.2877	At1g09240	nicotianamine synthase, putative
249148_at	2.2870	At5g43260	chaperone protein dnaJ-related
255594_at	2.2833	At4g01660	ABC1At_ATATH10__ABC1At (ARABIDOPSIS THALIANA ABC
246973_at	2.2746	At5g24970	ABC1 family protein
259226_at	2.2643	At3g07700	ABC1 family protein
260903_at	2.2642	At1g02460	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family
264102_at	2.2491	At1g79270	ECT8__ECT8 (evolutionarily conserved C-terminal region 8)
251800_at	2.2481	At3g55510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18220.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68987.1); contains InterPro domain Protein of unknown function UPF0120 (InterPro:IPR005343)
247989_at	2.2450	At5g56350	pyruvate kinase, putative
245352_at	2.2444	At4g15490	UGT84A3__UGT84A3; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups
251503_at	2.2387	At3g59140	ATMRP14__ATMRP14 (Arabidopsis thaliana multidrug resistance-associated protein 14)
255325_at	2.2347	At4g04210	PUX4__PUX4 (PLANT UBX DOMAIN-CONTAINING PROTEIN 4)
262281_at	2.2195	At1g68570	proton-dependent oligopeptide transport (POT) family protein
246744_at	2.2089	At5g27760	hypoxia-responsive family protein
256965_at	2.1978	At3g13450	DIN4__DIN4 (DARK INDUCIBLE 4); 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)
263995_at	2.1932	263995_at	

253875_at	2.1891	At4g27520	plastocyanin-like domain-containing protein
258588_s_at	2.1889	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
258696_at	2.1857	At3g09650	HCF152_CRM3__HCF152 (HIGH CHLOROPHYLL FLUORESCENCE 152)
260832_at	2.1853	At1g06780	GAUT6__GAUT6 (Galacturonosyltransferase 6); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups
248207_at	2.1832	At5g53970	aminotransferase, putative
262503_at	2.1802	At1g21670	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21680.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73514.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61906.1); contains InterPro domain WD40-like Beta Propeller (InterPro:IPR011659); contains InterPro domain Six-bladed beta-propeller, TolB-like (InterPro:IPR011042)
256854_at	2.1752	At3g15180	proteasome-related
261664_s_at	2.1543	At1g18320 At3g10110	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
AFFX-r2-At-G	2.1523	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
257122_at	2.1518	At3g20250	APUM5__APUM5 (ARABIDOPSIS PUMILIO 5); RNA binding
246527_at	2.1396	At5g15750	RNA-binding S4 domain-containing protein
252863_at	2.1394	At4g39800	MI-1-P SYNTHASE__MI-1-P SYNTHASE (Myo-inositol-1-phosphate synthase); inositol-3-phosphate synthase
254077_at	2.1365	At4g25640	MATE efflux family protein
260986_at	2.1305	At1g53580	ETHE1_GLX2-3_GLY3__ETHE1/GLX2-3/GLY3 (GLYOXALASE 2-3); hydroxyacylglutathione hydrolase
263517_at	2.1278	At2g21620	RD2__RD2 (RESPONSIVE TO DESSICATION 2)
264042_at	2.1265	At2g03760	ST_RAR047__ST (steroid sulfotransferase); sulfotransferase
254079_at	2.1230	At4g25730	FtsJ-like methyltransferase family protein
251827_at	2.1113	At3g55120	TT5_A11_CFI__A11/CFI/TT5 (TRANSPARENT TESTA 5); chalcone
256221_at	2.1111	At1g56300	DNAJ heat shock N-terminal domain-containing protein
260323_at	2.1073	At1g63780	IMP4__IMP4
246461_at	2.0874	At5g16930	AAA-type ATPase family protein
256235_at	2.0789	At3g12490	cysteine protease inhibitor, putative / cystatin, putative
261655_at	2.0778	At1g01940	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein
245702_at	2.0751	At5g04220	ATSYTC_NTMCTYPE1.3_SYTC__ATSYTC/NTMC2T1.3/NTMC2TYPE1.3/SYT
264019_at	2.0611	At2g21130	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase
261318_at	2.0584	At1g53035	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15358.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69750.1)
255543_at	2.0535	At4g01870	tolB protein-related
257253_at	2.0507	At3g24190	ABC1 family protein
251272_at	2.0454	At3g61890	ATHB-12_ATHB12__ATHB-12 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 12); transcription factor
249233_at	2.0415	At5g42150	electron carrier/ protein disulfide oxidoreductase
262751_at	2.0410	At1g16310	cation efflux family protein
258452_at	2.0404	At3g22370	AOX1A__AOX1A (alternative oxidase 1A); alternative oxidase
261907_at	2.0365	At1g65060	4CL3__4CL3 (4-coumarate:CoA ligase 3); 4-coumarate-CoA ligase
247593_at	2.0323	At5g60790	ATGCN1__ATGCN1 (Arabidopsis thaliana general control non-repressible 1)
250413_at	2.0297	At5g11160	APT5__APT5 (ADENINE PHOSPHORIBOSYLTRANSFERASE 5); adenine phosphoribosyltransferase
262634_at	2.0264	At1g06690	aldo/keto reductase family protein
255462_at	2.0240	At4g02940	oxidoreductase, 2OG-Fe(II) oxygenase family protein
AFFX-Athal-G	2.0233	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
267261_at	2.0129	At2g23120	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23110.1)
260025_at	2.0025	At1g30070	SGS domain-containing protein
245600_at	1.9988	At4g14230	CBS domain-containing protein-related
250279_at	1.9959	At5g13200	GRAM domain-containing protein / ABA-responsive protein-related
254818_at	1.9859	At4g12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
247120_at	1.9857	At5g65990	amino acid transporter family protein
245699_at	1.9776	At5g04250	OTU-like cysteine protease family protein

262054_s_at	1.9720	At1g79920 At1g79930	heat shock protein 70, putative / HSP70, putative
247323_at	1.9720	At5g64170	dentin sialophosphoprotein-related
253013_at	1.9679	At4g37910	MTHSC70-1__MTHSC70-1 (mitochondrial heat shock protein 70-1); ATP binding / unfolded protein binding
250845_at	1.9630	At5g04600	RNA recognition motif (RRM)-containing protein
266119_at	1.9594	At2g02100	LCR69_PDF2.2__LCR69/PDF2.2 (Low-molecular-weight cysteine-rich 69); protease inhibitor
260727_at	1.9556	At1g48100	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family
253237_at	1.9519	At4g34240	ALDH3I1_ALDH3__ALDH3I1 (Aldehyde dehydrogenase 3I1); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)
257654_at	1.9461	At3g13310	DNAJ heat shock N-terminal domain-containing protein
260331_at	1.9406	At1g80270	DNA-binding protein, putative
266093_at	1.9375	At2g37990	ribosome biogenesis regulatory protein (RRS1) family protein
267280_at	1.9357	At2g19450	TAG1_ABX45_AS11_ATDGAT_DGAT1_RDS1__TAG1 (TRIACYLGLYCEROL BIOSYNTHESIS DEFECT 1); diacylglycerol O-acyltransferase
248833_at	1.9329	At5g47120	ATBI1_BI-1__ATBI-1 (ARABIDOPSIS BAX INHIBITOR 1)
264091_at	1.9312	At1g79110	protein binding / zinc ion binding
AFFX-Athal-G	1.9297	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
263845_at	1.9279	At2g37040	PAL1__PAL1 (PHE AMMONIA LYASE 1); phenylalanine ammonia-lyase
247025_at	1.9268	At5g67030	ABA1_ATZEP_IBS3_LOS6_NPQ2_ZEP__ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase
265244_at	1.9233	At2g43020	ATPAO2__ATPAO2 (POLYAMINE OXIDASE 2); amine oxidase
266097_at	1.9208	At2g37970	SOUL-1__SOUL-1; binding
260157_at	1.9196	At1g52930	brix domain-containing protein
267036_at	1.9136	At2g38465	similar to unnamed protein product [Vitis vinifera] (GB:CAO61577.1)
253188_at	1.9134	At4g35300	TMT2__TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter
250358_at	1.9086	At5g11740	AGP15__AGP15 (ARABINOGALACTAN PROTEIN 15)
245686_at	1.9065	At5g22060	ATJ2__ATJ2 (Arabidopsis thaliana DnaJ homologue 2)
253394_at	1.9040	At4g32770	VTE1_ATSDX1__VTE1 (VITAMIN E DEFICIENT 1)
245319_at	1.9027	At4g16146	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69510.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69510.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G69510.3); similar to unnamed protein product [Vitis vinifera] (GB:CAO44882.1); contains InterPro domain Lg106-like (InterPro:IPR012482)
259992_at	1.9018	At1g67970	AT-HSFA8_HSFA8__AT-HSFA8 (Arabidopsis thaliana heat shock transcription factor A8); DNA binding / transcription factor
245365_at	1.8994	At4g17720	RNA recognition motif (RRM)-containing protein
251529_at	1.8952	At3g58570	DEAD box RNA helicase, putative
263415_at	1.8944	At2g17250	EMB2762__EMB2762 (EMBRYO DEFECTIVE 2762)
257144_at	1.8915	At3g27300	G6PD5__G6PD5 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 5)
258193_at	1.8851	At3g29090	pectinesterase family protein
260870_at	1.8829	At1g43890	AtRab18_AtRABC1_ATRAB18__ATRAB18 (Arabidopsis Rab GTPase
253778_at	1.8828	At4g28480	DNAJ heat shock family protein
250155_at	1.8802	At5g15160	bHLH family protein
264452_at	1.8757	At1g10270	GRP23__GRP23 (GLUTAMINE-RICH PROTEIN23); binding
251793_at	1.8735	At3g55580	regulator of chromosome condensation (RCC1) family protein
254080_at	1.8694	At4g25630	FIB2__FIB2 (FIBRILLARIN 2)
266938_at	1.8671	At2g18950	HPT1_ATHPT_HPT_TPT1_VTE2__HPT1 (HOMOGENTISATE PHYTYLTRANSFERASE 1); prenyltransferase
263921_at	1.8628	At2g36460	fructose-bisphosphate aldolase, putative
249984_at	1.8530	At5g18400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G18362.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15382.1); contains InterPro domain Protein of unknown function DUF689 (InterPro:IPR007785)
258751_at	1.8492	At3g05890	RCI2B__RCI2B (RARE-COLD-INDUCIBLE 2B)
259137_at	1.8409	At3g10300	calcium-binding EF hand family protein

250147_at	1.8384	At5g14600	similar to unnamed protein product [Vitis vinifera] (GB:CAO14741.1); contains InterPro domain tRNA methyltransferase complex GCD14 subunit (InterPro:IPR014816)
257822_at	1.8380	At3g25230	ROF1__ROF1 (ROTAMASE FKBP 1)
259077_s_at	1.8372	At3g02230 At5g15650	RGP1_ATRGP__RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1)
246468_at	1.8355	At5g17050	UDP-glucoronosyl/UDP-glucosyl transferase family protein
245427_at	1.8297	At4g17550	transporter-related
267509_at	1.8254	At2g45660	AGL20_SOC1__AGL20 (AGAMOUS-LIKE 20); transcription factor
248505_at	1.8238	At5g50360	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63350.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68256.1)
258679_at	1.8234	At3g08590	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative
245528_at	1.8225	At4g15530	PPDK__PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE)
265828_at	1.8207	At2g14520	CBS domain-containing protein
263074_at	1.8143	At2g17560	HMGB4_NFD04_NFD4__HMGB4 (HIGH MOBILITY GROUP B 4)
246939_at	1.8086	At5g25390	SHN2__SHN2 (SHINE2); DNA binding / transcription factor
246070_at	1.8068	At5g20160	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
246125_at	1.8067	At5g19875	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G31940.1); similar to hypothetical protein MtrDRAFT_AC155880g29v2 [Medicago truncatula] (GB:ABN08129.1)
252670_at	1.8033	At3g44110	ATJ3_ATJ__ATJ3 (Arabidopsis thaliana DnaJ homologue 3)
258218_at	1.8028	At3g18000	PEAMT_XIPOTL1_NMT1__NMT1 (N-METHYLTRANSFERASE 1); phosphoethanolamine N-methyltransferase
250096_at	1.8018	At5g17190	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03160.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42347.1)
246831_at	1.8015	At5g26340	STP13_MSS1__MSS1 (SUGAR TRANSPORT PROTEIN 13); carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen ion symporter
259008_at	1.7988	At3g09390	MT2A_ATMT-1_ATMT-K_MT2__MT2A (METALLOTHIONEIN 2A)
264992_at	1.7970	At1g67300	hexose transporter, putative
252591_at	1.7970	At3g45600	TET3__TET3 (TETRASPANIN3)
262940_at	1.7922	At1g79520	cation efflux family protein
250293_s_at	1.7841	At5g13360 At5g13370	auxin-responsive GH3 family protein
250849_at	1.7817	At5g04410	ANAC078_NAC2__NAC2 (Arabidopsis NAC domain containing protein 78); transcription factor
255953_at	1.7811	At1g22070	TGA3__TGA3 (TGA1a-related gene 3); DNA binding / calmodulin binding / transcription factor
247351_at	1.7739	At5g63790	ANAC102__ANAC102 (Arabidopsis NAC domain containing protein 102); transcription factor
247795_at	1.7709	At5g58620	zinc finger (CCCH-type) family protein
253994_at	1.7687	At4g26080	ABI1__ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein serine/threonine phosphatase
245724_at	1.7649	At1g73390	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G17940.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62047.1); contains domain PCD6 INTERACTING PROTEIN-RELATED (PTHR23030)
258224_at	1.7627	At3g15670	late embryogenesis abundant protein, putative / LEA protein, putative
245512_at	1.7612	At4g15770	60S ribosome subunit biogenesis protein, putative
258965_at	1.7572	At3g10530	transducin family protein / WD-40 repeat family protein
256092_at	1.7547	At1g20696	HMGB3_NFD03_NFD3__HMGB3 (HIGH MOBILITY GROUP B 3)
251227_at	1.7542	At3g62700	ATMRP10__ATMRP10 (Arabidopsis thaliana multidrug resistance-associated protein 10)
261377_at	1.7531	At1g18850	similar to hypothetical protein [Vitis vinifera] (GB:CAN63140.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62515.1)
263352_at	1.7521	At2g22080	unknown protein
259381_s_at	1.7425	At3g16390 At3g16400 At3g16410	jacalin lectin family protein

259001_at	1.7396	At3g01960	unknown protein
249372_at	1.7377	At5g40760	G6PD6__G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); glucose-6-phosphate dehydrogenase
260714_at	1.7360	At1g14980	CPN10__CPN10 (CHAPERONIN 10)
262112_at	1.7356	At1g02870	similar to unnamed protein product [Vitis vinifera] (GB:CAO39998.1); contains domain PD099709 (PD099709)
257149_at	1.7351	At3g27280	ATPHB4__ATPHB4 (PROHIBITIN 4)
248817_at	1.7316	At5g47020	glycine-rich protein
263881_at	1.7271	At2g21820	similar to hypothetical protein MtrDRAFT_AC155884g16v2 [Medicago truncatula] (GB:ABN08202.1)
250527_at	1.7251	At5g08590	ASK2_SNRK2-1_SNRK2.1_SRK2G__ASK2 (ARABIDOPSIS SERINE/THREONINE KINASE 2); kinase
260410_at	1.7208	At1g69870	proton-dependent oligopeptide transport (POT) family protein
252528_at	1.7199	At3g46460	UBC13__UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase
256451_s_at	1.7187	At1g75170	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
257973_at	1.7185	At3g20720	similar to hypothetical protein OsI_016901 [Oryza sativa (indica cultivar-group)] (GB:EAY95668.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ56411.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39040.1); contains domain SUBFAMILY NOT NAMED (PTHR22774:SF4); contains domain UNCHARACTERIZED (PTHR22774)
266118_at	1.7161	At2g02130	LCR68_PDF2.3__LCR68/PDF2.3 (Low-molecular-weight cysteine-rich 68); protease inhibitor
264535_at	1.7159	At1g55690	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
260900_s_at	1.7106	At1g21400 At5g34780	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1
249111_at	1.7023	At5g43770	proline-rich family protein
265730_at	1.6986	At2g32220	60S ribosomal protein L27 (RPL27A)
250516_at	1.6898	At5g09620	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
258166_at	1.6887	At3g21540	transducin family protein / WD-40 repeat family protein
253879_s_at	1.6867	At4g27560 At4g27570	glycosyltransferase family protein
263912_at	1.6858	At2g36390	BE3_SBE2.1__SBE2.1 (STARCH BRANCHING ENZYME 2.1); 1,4-alpha-glucan branching enzyme
251265_at	1.6856	At3g62310	RNA helicase, putative
260943_at	1.6828	At1g45145	ATH5_ATTRX5_LIV1__ATTRX5 (thioredoxin H-type 5); thiol-disulfide exchange intermediate
248352_at	1.6769	At5g52300	RD29B_LTI65__LTI65/RD29B (RESPONSIVE TO DESSICATION 29B)
249528_at	1.6750	At5g38720	similar to hypothetical protein [Vitis vinifera] (GB:CAN75612.1); contains domain PTHR13191 (PTHR13191)
254227_at	1.6747	At4g23630	BTI1__BTI1 (VIRB2-INTERACTING PROTEIN 1)
247723_at	1.6736	At5g59220	protein phosphatase 2C, putative / PP2C, putative
245893_at	1.6732	At5g09270	similar to hypothetical protein OsI_004420 [Oryza sativa (indica cultivar-group)] (GB:EAY76573.1)
261173_at	1.6707	At1g04830	RabGAP/TBC domain-containing protein
263034_at	1.6699	At1g24020	MLP423__MLP423 (MLP-LIKE PROTEIN 423)
248311_at	1.6683	At5g52570	BETA-OHASE 2_B2_CHY2__BETA-OHASE 2 (BETA-CAROTENE HYDROXYLASE 2)
251024_at	1.6658	At5g02180	amino acid transporter family protein
263789_at	1.6637	At2g24560	carboxylesterase
264252_at	1.6630	At1g09180	ATSAR1_ATSARA1A__ATSAR1/ATSARA1A (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 1); GTP binding
245346_at	1.6621	At4g17090	BAM3_BMY8_CT-BMY_BMY8__CT-BMY (BETA-AMYLASE 3, BETA-AMYLASE 8); beta-amylase
264357_at	1.6617	At1g03360	ATRRP4__ATRRP4; exonuclease
247712_at	1.6593	At5g59300	UBC7__UBC7 (UBIQUITIN-CONJUGATING ENZYME 31); ubiquitin-protein
245557_at	1.6544	At4g15410	UBX domain-containing protein
263824_at	1.6519	At2g40360	transducin family protein / WD-40 repeat family protein
248101_at	1.6477	At5g55200	co-chaperone grpE protein, putative

266399_at	1.6468	At2g38670	PECT1__PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); ethanolamine-phosphate cytidylyltransferase
258470_at	1.6417	At3g06035	Identical to Uncharacterized GPI-anchored protein At3g06035 precursor [Arabidopsis Thaliana] (GB:Q84MC0;GB:Q8H7F7;GB:Q8L9J0); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19250.1); similar to unknown [Populus trichocarpa] (GB:ABK94712.1)
262296_at	1.6395	At1g27630	CYCT1;3__CYCT1;3; cyclin-dependent protein kinase
248136_at	1.6384	At5g54910	DEAD/DEAH box helicase, putative
266500_at	1.6353	At2g06925	ATSPLA2-ALPHA_PLA2-ALPHA__ATSPLA2-ALPHA/PLA2-ALPHA (PHOSPHOLIPASE A2-ALPHA); phospholipase A2
253559_at	1.6341	At4g31140	glycosyl hydrolase family 17 protein
245770_at	1.6331	At1g30240	binding
265703_at	1.6292	At2g03430	ankyrin repeat family protein
263134_at	1.6288	At1g78570	RHM1_ROL1__RHM1/ROL1 (RHAMNOSE BIOSYNTHESIS1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic
253700_at	1.6248	At4g29840	MTO2_TS__MTO2 (METHIONINE OVER-ACCUMULATOR); threonine
264818_at	1.6196	At1g03530	ATNAF1_NAF1__ATNAF1/NAF1
266695_at	1.6190	At2g19810	zinc finger (CCCH-type) family protein
247717_at	1.6176	At5g59320	LTP3__LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding
267163_at	1.6173	At2g37520	PHD finger family protein
257484_at	1.6111	At1g01650	peptidase
250316_at	1.6001	At5g12140	ATCYS1__ATCYS1 (A. THALIANA CYSTATIN-1); cysteine protease inhibitor
262851_at	1.5993	At1g20920	DEAD box RNA helicase, putative
259461_at	1.5962	At1g18900	pentatricopeptide (PPR) repeat-containing protein
248126_at	1.5900	At5g54760	eukaryotic translation initiation factor SUI1, putative
247921_at	1.5886	At5g57660	zinc finger (B-box type) family protein
247706_at	1.5871	At5g59480	haloacid dehalogenase-like hydrolase family protein
256676_at	1.5843	At3g52180	ATPTPKIS1_DSP4_SEX4__ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); protein tyrosine/serine/threonine phosphatase
245879_at	1.5811	At5g09420	ATTOC64-V_MTOM64__ATTOC64-V/MTOM64 (ARABIDOPSIS THALIANA TRANSLOCON AT THE OUTER MEMBRANE OF CHLOROPLASTS 64-V);
261220_at	1.5789	At1g19970	ER lumen protein retaining receptor family protein
256765_at	1.5768	At3g22200	POP2_GABA-T__POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase
266358_at	1.5759	At2g32280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21310.1); similar to unknown [Populus trichocarpa] (GB:ABK92874.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR009606)
253039_at	1.5743	At4g37760	SQE3__SQE3 (SQUALENE EPOXIDASE 3); oxidoreductase
257746_at	1.5734	At3g29200	CM1__CM1 (chorismate mutase 1); chorismate mutase
246099_at	1.5733	At5g20230	ATBCB_BCB__ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding
260421_at	1.5728	At1g69640	acid phosphatase, putative
262098_at	1.5711	At1g56170	HAP5B__HAP5B (Heme activator protein (yeast) homolog 5B)
256746_at	1.5702	At3g29320	glucan phosphorylase, putative
259178_at	1.5640	At3g01650	RGLG1__RGLG1 (RING DOMAIN LIGASE1); protein binding / zinc ion binding
253526_at	1.5638	At4g31420	zinc finger (C2H2 type) family protein
265662_at	1.5629	At2g24500	FZF__FZF; transcription factor
262584_at	1.5584	At1g15440	transducin family protein / WD-40 repeat family protein
250350_at	1.5539	At5g12010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G29780.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43835.1); contains domain PTHR22930 (PTHR22930)
260596_at	1.5529	At1g55900	EMB1860_TIM50__TIM50 (EMBRYO DEFECTIVE 1860)
AFFX-Athal-G	1.5479	At3g04120	GAPC__GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase
249237_at	1.5468	At5g42050	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27090.1); similar to unknown [Populus trichocarpa] (GB:ABK95892.1); contains InterPro domain Kelch related (InterPro:IPR013089); contains InterPro domain Development and cell death (InterPro:IPR013989)

261566_at	1.5431	At1g33230	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10430.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10430.3); similar to unnamed protein product [Vitis vinifera] (GB:CAO62852.1); contains InterPro domain TMPIT-like; (InterPro:IPR012926)
247810_at	1.5424	At5g58290	RPT3__RPT3 (root phototropism 3); ATPase
259611_at	1.5406	At1g52280	AtRABG3d__AtRABG3d (Arabidopsis Rab GTPase homolog G3d); GTP
253425_at	1.5405	At4g32190	centromeric protein-related
262419_at	1.5390	At1g50380	prolyl oligopeptidase family protein
261768_at	1.5374	At1g15550	GA4_ATGA3OX1__GA4 (GA REQUIRING 4); gibberellin 3-beta-dioxygenase
248328_at	1.5326	At5g52660	myb family transcription factor
245765_at	1.5322	At1g33600	leucine-rich repeat family protein
258575_at	1.5282	At3g04240	SEC__SEC (SECRET AGENT); transferase, transferring glycosyl groups
245264_at	1.5268	At4g17245	zinc finger (C3HC4-type RING finger) family protein
256296_at	1.5255	At1g69480	EXS family protein / ERD1/XPR1/SYG1 family protein
250248_at	1.5217	At5g13740	ZIF1__ZIF1 (ZINC INDUCED FACILITATOR 1); carbohydrate transmembrane transporter/ sugar:hydrogen ion symporter
254059_at	1.5215	At4g25200	ATHSP23.6-MITO__ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)
253358_at	1.5190	At4g32940	GAMMA-VPE_GAMMAVPE__GAMMA-VPE (Vacuolar processing enzyme gamma); cysteine-type endopeptidase
251951_s_at	1.5163	At1g55710 At3g53630	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G53342.1)
248749_at	1.5133	At5g47880	ERF1-1_ERF1__ERF1-1 (EUKARYOTIC RELEASE FACTOR 1-1); translation release factor
261957_at	1.5128	At1g64660	ATMGL__ATMGL; catalytic/ methionine gamma-lyase
258649_at	1.5097	At3g09840	CDC48__CDC48 (CELL DIVISION CYCLE 48); ATPase
251492_at	1.5057	At3g59280	TXR1__TXR1 (THAXTOMIN A RESISTANT 1)
261082_at	1.5046	At1g07360	zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein
265354_at	1.5016	At2g16700	ADF5__ADF5 (ACTIN DEPOLYMERIZING FACTOR 5); actin binding
249180_at	1.5009	At5g43010	RPT4A__RPT4A (regulatory particle triple-A 4A); ATPase
260425_at	1.4977	At1g72440	EDA25__EDA25 (embryo sac development arrest 25); binding
262313_at	1.4947	At1g70900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23110.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23110.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23110.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN77015.1)
262635_at	1.4936	At1g06570	PDS1_HPD__PDS1 (PHYTOENE DESATURATION 1)
265326_at	1.4925	At2g18220	Identical to Nucleolar complex protein 2 homolog [Arabidopsis Thaliana] (GB:Q9ZPV5); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55510.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81729.1); contains InterPro domain Protein of unknown function
245667_at	1.4909	At1g28200	FIP1__FIP1 (FH INTERACTING PROTEIN 1)
261458_at	1.4906	At1g21080	DNAJ heat shock N-terminal domain-containing protein
259188_at	1.4906	At3g01510	5'-AMP-activated protein kinase beta-1 subunit-related
262945_at	1.4892	At1g79510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16320.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64929.1); contains domain NTF2-like (SSF54427)
260049_at	1.4858	At1g29940	NRPA2__NRPA2 (nuclear RNA polymerase A 2); DNA-directed RNA
257672_at	1.4834	At3g20300	extracellular ligand-gated ion channel
258396_at	1.4824	At3g15460	brix domain-containing protein
262496_at	1.4822	At1g21790	similar to unnamed protein product [Vitis vinifera] (GB:CAO61872.1); contains InterPro domain TRAM, LAG1 and CLN8 homology; (InterPro:IPR006634)
246528_at	1.4816	At5g15640	mitochondrial substrate carrier family protein
251826_at	1.4802	At3g55110	ABC transporter family protein
249703_at	1.4704	At5g35560	DENN (AEX-3) domain-containing protein
247280_at	1.4694	At5g64260	phosphate-responsive protein, putative
265499_at	1.4693	At2g15480	UGT73B5__UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B5); UDP-glycosyltransferase/ transferase, transferring glycosyl groups

245956_s_at	1.4648	At5g28540 At5g42020	BIP1; ATP binding
249315_at	1.4640	At5g41190	similar to hypothetical protein [Vitis vinifera] (GB:CAN66411.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62795.1); contains InterPro domain D-site 20S pre-rRNA nuclease (InterPro:IPR017117); contains InterPro domain Nin one binding (NOB1) Zn-ribbon like (InterPro:IPR014881)
251735_at	1.4638	At3g56090	ATFER3__ATFER3 (FERRITIN 3); ferric iron binding
250556_at	1.4637	At5g07920	DGK1__DGK1 (DIACYLGLYCEROL KINASE 1, DIACYLGLYCEROL KINASE1); diacylglycerol kinase
255080_at	1.4623	At4g09030	AGP10__AGP10 (Arabinogalactan protein 10)
260868_at	1.4606	At1g43860	transcription factor
252355_at	1.4580	At3g48250	pentatricopeptide (PPR) repeat-containing protein
251775_s_at	1.4580	At2g39800 At3g55610	P5CS1_ATP5CS__P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1)
266225_at	1.4544	At2g28900	ATOEP16-1_ATOEP16-L_OEP16__OEP16 (OUTER ENVELOPE PROTEIN 16); P-P-bond-hydrolysis-driven protein transmembrane transporter
259965_at	1.4527	At1g53670	MSRB1__MSRB1 (METHIONINE SULFOXIDE REDUCTASE B 1); peptide-methionine-(S)-S-oxide reductase
262706_at	1.4514	At1g16280	DEAD/DEAH box helicase, putative
257211_at	1.4480	At3g15080	exonuclease family protein
250072_at	1.4466	At5g17210	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61065.1); similar to Os06g0114700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001056606.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62222.1); contains InterPro domain Protein of unknown function
254073_at	1.4434	At4g25500	ATRSP35_ATRSP40_AT-SRP40__ATRSP35 (Arabidopsis thaliana arginine/serine-rich splicing factor 35)
256589_at	1.4406	At3g28740	cytochrome P450 family protein
266237_at	1.4390	At2g29540	ATRPC14_ATRPAC14__ATRPC14 (Arabidopsis thaliana RNA polymerase I(A) and III(C) 14 kDa subunit)
248765_at	1.4379	At5g47650	ATNUDT2__ATNUDT2 (Arabidopsis thaliana Nudix hydrolase homolog 2); ADP-ribose diphosphatase/ NAD binding / hydrolase
263010_at	1.4354	At1g23330	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G10740.1); similar to Os05g0408300 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055523.1); 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)
251311_at	1.4323	At3g61140	FUS6_COP11_CSN1_EMB78__FUS6 (FUSCA 6)
262722_at	1.4316	At1g43620	UDP-glucose:sterol glucosyltransferase, putative
248583_at	1.4302	At5g49930	EMB1441__EMB1441 (EMBRYO DEFECTIVE 1441); nucleic acid binding
251091_at	1.4298	At5g01410	ATPDX1.3_RSR4_PDX1__PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); protein heterodimerization/ protein homodimerization
258812_at	1.4294	At3g03950	ECT1__ECT1
257193_at	1.4293	At3g13160	pentatricopeptide (PPR) repeat-containing protein
245445_at	1.4258	At4g16750	DRE-binding transcription factor, putative
254691_at	1.4256	At4g17840	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G35260.1); similar to hypothetical protein 40.t00061 [Brassica oleracea] (GB:ABD65174.1)
257146_at	1.4247	At3g27260	GTE8__GTE8 (GLOBAL TRANSCRIPTION FACTOR GROUP E8); DNA
259037_at	1.4188	At3g09350	armadillo/beta-catenin repeat family protein
256649_at	1.4154	At3g13570	SCL30a__SCL30a (SC35-like splicing factor 30a); RNA binding
251961_at	1.4146	At3g53620	ATPPA4__ATPPA4 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 4); inorganic diphosphatase/ pyrophosphatase
255795_at	1.4130	At2g33380	RD20__RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding
265899_s_at	1.4108	At1g20140 At2g25700	ASK4__ASK4 (ARABIDOPSIS SKP1-LIKE 4); ubiquitin-protein ligase
252475_s_at	1.4099	At3g46640 At5g59570	LUX_PCL1__PCL1 (PHYTOCLOCK 1); DNA binding
253890_s_at	1.4094	At4g27585 At5g54100	band 7 family protein
252884_at	1.4060	At4g39170	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative

255456_at	1.4029	At4g02920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03340.1); similar to hypothetical protein MtrDRAFT_AC161864g5v2 [Medicago truncatula] (GB:ABE86673.1)
262478_at	1.4027	At1g11170	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61240.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61240.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61240.4); similar to unknown [Picea sitchensis] (GB:ABK25584.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)
264024_at	1.4027	At2g21180	similar to Os03g0249700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001049562.1)
248781_at	1.4021	At5g47870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71310.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71310.1); similar to unknown [Populus trichocarpa] (GB:ABK95546.1)
246779_at	1.4009	At5g27520	mitochondrial substrate carrier family protein
246575_at	1.4009	At1g31660	similar to unknown [Populus trichocarpa] (GB:ABK93690.1); contains InterPro domain Bystin (InterPro:IPR007955)
254891_at	1.4002	At4g11740	SAY1__SAY1
248792_at	1.3998	At5g47200	AtRab1A_AtRABD2b__AtRABD2b/AtRab1A (Arabidopsis Rab GTPase homolog D2b); GTP binding
249785_at	1.3993	At5g24300	ATSS1_SSI__ATSS1/SSI (STARCH SYNTHASE I); transferase, transferring glycosyl groups
262959_at	1.3989	At1g54290	eukaryotic translation initiation factor SUI1, putative
253326_at	1.3965	At4g33440	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family
252184_at	1.3939	At3g50660	DWF4_CLM_CYP90B1_SNP2__DWF4 (DWARF 4)
261116_at	1.3901	At1g75370	SEC14 cytosolic factor, putative / phosphatidylinositol transfer-like protein,
251463_at	1.3888	At3g59800	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G43795.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G43795.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO46318.1)
256663_at	1.3887	At3g12050	Aha1 domain-containing protein
256061_at	1.3880	At1g07040	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27030.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41035.1)
245560_at	1.3866	At4g15480	UGT84A1__UGT84A1; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups
261059_at	1.3840	At1g01250	AP2 domain-containing transcription factor, putative
261482_at	1.3840	At1g14530	(TOM THREE HOMOLOG); virion binding
259194_at	1.3825	At3g01540	DRH1__DRH1 (DEAD box RNA helicase 1)
259367_at	1.3810	At1g69070	binding
267066_at	1.3767	At2g41040	methyltransferase-related
265283_at	1.3739	At2g20370	KAM1_MUR3__KAM1/MUR3 (MURUS 3); catalytic/ transferase, transferring glycosyl groups
248582_at	1.3727	At5g49910	cpHSC70-2_HSC70-7__cpHSC70-2 (HEAT SHOCK PROTEIN 70-7); ATP binding / unfolded protein binding
261818_at	1.3726	At1g11390	ABC1 family protein
266746_s_at	1.3674	At2g02930 At4g02520	ATGSTF3_GST16__ATGSTF3 (GLUTATHIONE S-TRANSFERASE 16); glutathione transferase
262600_at	1.3644	At1g15340	MBD10__MBD10 (methyl-CpG-binding domain 10); DNA binding
253755_at	1.3642	At4g29040	RPT2A__RPT2A (REGULATORY PARTICLE AAA-ATPASE 2A); ATPase
250916_at	1.3628	At5g03630	ATMDAR2__ATMDAR2; monodehydroascorbate reductase (NADH)
262953_at	1.3601	At1g75670	DNA-directed RNA polymerase/ RNA binding
267246_at	1.3598	At2g30250	WRKY25__WRKY25 (WRKY DNA-binding protein 25); transcription factor
267364_at	1.3585	At2g40080	ELF4__ELF4 (EARLY FLOWERING 4)
266555_at	1.3542	At2g46270	GBF3__GBF3 (G-BOX BINDING FACTOR 3); transcription factor
249581_at	1.3513	At5g37600	ATGSR1__ATGSR1 (Arabidopsis thaliana glutamine synthase clone R1); glutamate-ammonia ligase
260589_at	1.3511	At1g53400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45740.1); similar to unknown [Brassica rapa] (GB:ABL97984.1); contains domain PTHR13609 (PTHR13609)
254268_at	1.3506	At4g23040	UBX domain-containing protein
251943_at	1.3497	At3g53500	RSZ32__RSZ32; nucleic acid binding

246126_at	1.3480	At5g20070	ATNUDT19__ATNUDT19 (Arabidopsis thaliana Nudix hydrolase homolog 19); hydrolase
257970_at	1.3452	At3g27570	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G40510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14698.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold (InterPro:IPR012335); contains InterPro domain Sucraseferredoxin-like (InterPro:IPR009737)
262128_at	1.3416	At1g52690	late embryogenesis abundant protein, putative / LEA protein, putative
253282_at	1.3401	At4g34120	LEJ1__LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)
246452_at	1.3400	At5g16840	RNA recognition motif (RRM)-containing protein
251667_at	1.3397	At3g57150	NAP57_ATCBF5_ATNAP57_CBF5__NAP57 (ARABIDOPSIS THALIANA HOMOLOGUE OF NAP57)
258249_s_at	1.3388	At3g15820 At3g15830	phosphatidic acid phosphatase-related / PAP2-related
246042_at	1.3381	At5g19440	cinnamyl-alcohol dehydrogenase, putative (CAD)
267062_at	1.3372	At2g32600	hydroxyproline-rich glycoprotein family protein
257719_at	1.3340	At3g18440	ATALMT9 (ALUMINUM-ACTIVATED MALATE TRANSPORTER 9); anion
264221_s_at	1.3334	At1g60170 At3g60610	EMB1220__EMB1220 (EMBRYO DEFECTIVE 1220)
258519_at	1.3328	At3g06760	Identical to Protein DEHYDRATION-INDUCED 19 homolog 4 (DI19-4) [Arabidopsis Thaliana] (GB:Q8VXU6;GB:Q9M7Y2); similar to HRB1 (HYPERSENSITIVE TO RED AND BLUE) [Arabidopsis thaliana] (TAIR:AT5G49230.1); similar to fiber protein Fb2 [Gossypium barbadense] (GB:AAN77145.1); contains InterPro domain Drought induced 19
251860_at	1.3326	At3g54660	GR_EMB2360__GR (GLUTATHIONE REDUCTASE); glutathione-disulfide
257658_at	1.3320	At3g13230	RNA binding
250995_at	1.3259	At5g02500	HSC70-1_HSC70_HSP70-1__HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding
260653_at	1.3228	At1g32440	PKP3__PKP3 (PLASTIDIAL PYRUVATE KINASE 3); pyruvate kinase
248049_at	1.3220	At5g56090	COX15__COX15 (CYTOCHROME C OXIDASE 15)
250028_at	1.3216	At5g18130	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G03870.2); similar to unknown [Medicago truncatula] (GB:ABK28852.1)
245751_s_at	1.3213	At1g25682 At1g25988	cell cycle control protein-related
250736_s_at	1.3200	At1g01350 At5g06420	nucleic acid binding
265991_at	1.3187	At2g24120	PDE319_SCA3__PDE319/SCA3 (SCABRA 3); DNA binding / DNA-directed RNA polymerase
263509_s_at	1.3154	At2g07687 AtMg00730	cytochrome c oxidase subunit 3
252127_at	1.3148	At3g50960	PLP3A (PHOSDUCIN-LIKE PROTEIN 3 HOMOLOG)
257019_at	1.3144	At3g19640	magnesium transporter CorA-like family protein (MRS2-3)
263185_at	1.3078	At1g05520	transport protein, putative
264671_at	1.3046	At1g09920	TRAF-type zinc finger-related
267300_at	1.2999	At2g30140	UDP-glucoronosyl/UDP-glucosyl transferase family protein
251020_at	1.2996	At5g02270	ATNAP9__ATNAP9 (Non-intrinsic ABC protein 9)
261062_at	1.2984	At1g07530	scarecrow-like transcription factor 14 (SCL14)
245904_at	1.2911	At5g11110	ATSPS2F_SPS1__ATSPS2F/SPS1 (SUCROSE PHOSPHATE SYNTHASE 1); sucrose-phosphate synthase
265947_at	1.2899	At2g19540	transducin family protein / WD-40 repeat family protein
254920_at	1.2895	At4g11220	BTI2__BTI2 (VIRB2-INTERACTING PROTEIN 2)
262114_at	1.2890	At1g02860	NLA__NLA (NITROGEN LIMITATION ADAPTATION); protein binding / zinc ion binding
258188_at	1.2889	At3g17800	mRNA level of the MEB5.2 gene (At3g17800) remains unchanged after cutting the inflorescence stem
254559_at	1.2878	At4g19200	proline-rich family protein
246073_at	1.2878	At5g20180	ribosomal protein L36 family protein
256797_at	1.2867	At3g18600	DEAD/DEAH box helicase, putative
258678_at	1.2855	At3g08690	UBC11__UBC11 (ubiquitin-conjugating enzyme 11); ubiquitin-protein ligase

247899_at	1.2854	At5g57345	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96592.1)
263325_at	1.2854	At2g04240	XERICO__XERICO; protein binding / zinc ion binding
260525_at	1.2802	At2g47250	RNA helicase, putative
257694_at	1.2801	At3g12860	nucleolar protein Nop56, putative
264123_at	1.2760	At1g02270	endonuclease/exonuclease/phosphatase family protein / calcium-binding EF hand family protein
248466_at	1.2741	At5g50720	ATHVA22E__ATHVA22E (Arabidopsis thaliana HVA22 homologue E)
254278_at	1.2725	At4g22740	glycine-rich protein
251234_s_at	1.2696	At2g47650 At3g62830	UXS4__UXS4 (UDP-XYLOSE SYNTHASE 4); catalytic
253581_at	1.2692	At4g30660	hydrophobic protein, putative / low temperature and salt responsive protein,
246466_at	1.2690	At5g17010	sugar transporter family protein
262766_at	1.2690	At1g13160	SDA1 family protein
252468_at	1.2687	At3g46970	ATPHS2_PHS2__ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups
256598_at	1.2685	At3g30180	BR6OX2_CYP85A2__BR6OX2/CYP85A2 (BRASSINOSTEROID-6-OXIDASE 2); monooxygenase/ oxygen binding
259232_at	1.2671	At3g11420	fringe-related protein
259103_at	1.2654	At3g11690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67416.1)
260336_at	1.2654	At1g73990	SPPA__SPPA (signal peptide peptidase); protease IV/ serine-type
251760_at	1.2636	At3g55605	mitochondrial glycoprotein family protein / MAM33 family protein
257708_at	1.2618	At3g13330	binding
245533_at	1.2608	At4g15130	cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative
251029_at	1.2598	At5g02050	mitochondrial glycoprotein family protein / MAM33 family protein
247999_at	1.2594	At5g56150	UBC30__UBC30 (UBIQUITIN-CONJUGATING ENZYME 30); ubiquitin-protein
248739_at	1.2587	At5g48030	GFA2__GFA2 (GAMETOPHYTIC FACTOR 2); heat shock protein binding / unfolded protein binding
266116_at	1.2564	At2g02180	TOM3__TOM3 (tobamovirus multiplication protein 3)
251936_at	1.2555	At3g53700	MEE40__MEE40 (maternal effect embryo arrest 40)
256110_at	1.2550	At1g16900	sugar binding / transferase, transferring glycosyl groups
263809_at	1.2489	At2g04570	GDSL-motif lipase/hydrolase family protein
251065_at	1.2488	At5g01870	lipid transfer protein, putative
258167_at	1.2438	At3g21560	UGT84A2__UGT84A2; UDP-glycosyltransferase/ sinapate 1-
248607_at	1.2417	At5g49480	ATCP1_ACP1__ATCP1 (CA2+-BINDING PROTEIN 1); calcium ion binding
254804_at	1.2407	At4g13010	oxidoreductase, zinc-binding dehydrogenase family protein
258800_at	1.2397	At3g04550	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1)
248762_at	1.2393	At5g47455	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17310.1); similar to transcription factor [Arabidopsis thaliana] (TAIR:AT4G17310.2); similar to hypothetical protein 25.t00029 [Brassica oleracea] (GB:ABD64980.1)
265228_s_at	1.2387	At2g07698 AtMg01190	ATP synthase alpha chain, mitochondrial, putative
260357_at	1.2372	At1g69260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13740.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41856.1); contains InterPro domain Protein of unknown function DUF1675 (InterPro:IPR012463)
252204_at	1.2362	At3g50340	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G67020.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD09363.1)
264668_at	1.2326	At1g09780	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative
250222_at	1.2320	At5g14050	transducin family protein / WD-40 repeat family protein
264471_at	1.2311	At1g67120	midasin-related
263502_s_at	1.2285	At2g07675 AtMg00980	ribosomal protein S12 mitochondrial family protein
262119_s_at	1.2234	At1g02920 At1g02930	ATGSTF7_ATGSTF8_GST11_GSTF7__ATGSTF7 (GLUTATHIONE S-TRANSFERASE 11); glutathione transferase
250533_at	1.2224	At5g08640	FLS__FLS (FLAVONOL SYNTHASE)
258794_at	1.2174	At3g04710	ankyrin repeat family protein

256249_at	1.2154	At3g11270	MEE34__MEE34 (maternal effect embryo arrest 34)
259655_at	1.2132	At1g55210	disease resistance response
260176_at	1.2127	At1g71950	identical protein binding / subtilase
250457_at	1.2124	At5g09880	RNA recognition motif (RRM)-containing protein
254998_at	1.2086	At4g09760	choline kinase, putative
245986_at	1.2073	At5g13160	PBS1__PBS1 (AVRPPHB SUSCEPTIBLE 1); kinase
253949_at	1.2071	At4g26780	AR192__AR192; adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization
264118_at	1.2051	At1g79150	binding
247488_at	1.2043	At5g61820	similar to MtN19-like protein [Pisum sativum] (GB:AAU14999.2); contains InterPro domain Stress up-regulated Nod 19 (InterPro:IPR011692)
265614_at	1.2038	At2g25355	exonuclease-related
251879_at	1.2028	At3g54200	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05975.1); similar to Harpin-induced 1 [Medicago truncatula] (GB:ABE93043.1); contains InterPro domain Harpin-induced 1 (InterPro:IPR010847)
257914_at	1.2016	At3g25545	similar to unknown [Populus trichocarpa] (GB:ABK95265.1)
259672_at	1.2014	At1g68990	DNA-directed RNA polymerase, mitochondrial (RPOMT)
267366_at	1.2004	At2g44310	calcium-binding EF hand family protein
249122_at	1.2003	At5g43850	ATARD4__ATARD4; acireductone dioxygenase [iron(II)-requiring]/ metal ion
263556_at	1.1997	At2g16365	F-box family protein
266471_at	1.1982	At2g31060	elongation factor family protein
254106_at	1.1961	At4g24990	ATGP4__ATGP4 (Arabidopsis thaliana geranylgeranylated protein)
251187_at	1.1959	At3g62770	AtATG18a__AtATG18a (Arabidopsis thaliana homolog of yeast autophagy 18 (ATG18) a)
247014_at	1.1934	At5g67630	DNA helicase, putative
255303_at	1.1932	At4g04860	DER2.2__DER2.2 (DERLIN-2.2)
248200_at	1.1900	At5g54160	ATOMT1_OMT1__ATOMT1 (O-METHYLTRANSFERASE 1)
267639_at	1.1899	At2g42200	squamosa promoter-binding protein-like 9 (SPL9)
254440_at	1.1882	At4g21020	late embryogenesis abundant domain-containing protein / LEA domain-containing protein
252968_at	1.1853	At4g38890	dihydrouridine synthase family protein
256983_at	1.1837	At3g13470	chaperonin, putative
261866_at	1.1824	At1g50420	SCL3__SCL3 (SCARECROW-LIKE 3); transcription factor
254850_at	1.1822	At4g12000	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22850.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63604.1); contains InterPro domain SNARE associated Golgi protein (InterPro:IPR015414)
251177_at	1.1796	At3g63400	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein
247498_at	1.1794	At5g61810	mitochondrial substrate carrier family protein
262590_at	1.1792	At1g15100	RHA2A__RHA2A (RING-H2 finger A2A); protein binding / zinc ion binding
247175_at	1.1788	At5g65280	GCL1__GCL1 (GCR2-LIKE 1); catalytic
251768_at	1.1788	At3g55940	phosphoinositide-specific phospholipase C, putative
253245_at	1.1780	At4g34590	ATBZIP11_GBF6_ATB2_ATBZIP11_BZIP11__GBF6 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 11); DNA binding / protein heterodimerization/ transcription factor
259198_at	1.1768	At3g03610	phagocytosis and cell motility protein ELMO1-related
253171_at	1.1758	At4g35040	bZIP transcription factor family protein
267470_at	1.1752	At2g30490	ATC4H_C4H_CYP73A5__ATC4H/C4H/CYP73A5 (CINNAMATE 4-HYDROXYLASE, CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-
259977_at	1.1750	At1g76590	zinc-binding family protein
264239_at	1.1733	At1g54770	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G30495.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G30495.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO70928.1); contains InterPro domain Fcf2 pre-rRNA processing (InterPro:IPR014810)
245639_at	1.1725	At1g25260	acidic ribosomal protein P0-related
262716_at	1.1724	At1g16470	PAB1__PAB1 (PROTEASOME SUBUNIT PAB1); peptidase
246486_at	1.1718	At5g15910	dehydrogenase-related

255501_at	1.1717	At4g02400	similar to U3 ribonucleoprotein (Utp) family protein [Arabidopsis thaliana] (TAIR:AT5G08600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40032.1); contains InterPro domain Small-subunit processome, Utp14; (InterPro:IPR006709)
257333_at	1.1707	AtMg01360	COX1__cytochrome c oxidase subunit 1
256657_at	1.1705	At3g18860	transducin family protein / WD-40 repeat family protein
260005_at	1.1682	At1g67920	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G24600.1)
261635_at	1.1667	At1g50020	similar to unnamed protein product [Vitis vinifera] (GB:CAO49863.1)
262956_at	1.1662	At1g54270	EIF4A-2__EIF4A-2 (eukaryotic translation initiation factor 4A-2); ATP-dependent helicase
254684_at	1.1646	At4g13850	GRP2_GR-RBP2_ATGRP2__ATGRP2 (GLYCINE-RICH RNA-BINDING
255070_at	1.1634	At4g09020	ATISA3_ISA3__ATISA3/ISA3 (ISOAMYLASE 3); alpha-amylase
266556_at	1.1628	At2g46230	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26530.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39702.1); contains InterPro domain Nucleotide binding protein, PINc (InterPro:IPR006596); contains InterPro domain Protein of unknown function DUF652 (InterPro:IPR006984)
252888_at	1.1617	At4g39210	APL3__APL3 (large subunit of AGP 3)
246995_at	1.1596	At5g67470	formin homology 2 domain-containing protein / FH2 domain-containing protein
258545_at	1.1596	At3g07050	GTP-binding family protein
257058_at	1.1591	At3g15352	ATCOX17_COX17__ATCOX17 (Arabidopsis thaliana cytochrome c oxidase
249866_at	1.1589	At5g23010	IMS3_MAM1_IMS3__MAM1 (2-isopropylmalate synthase 3); 2-isopropylmalate synthase
259146_at	1.1572	At3g10370	glycerol-3-phosphate dehydrogenase, putative
265478_at	1.1565	At2g15890	MEE14__MEE14 (maternal effect embryo arrest 14)
246403_at	1.1559	At1g57590	carboxylesterase
248313_at	1.1556	At5g52590	
261064_at	1.1528	At1g07510	FTSH10__FTSH10 (FtsH protease 10); ATPase
256385_at	1.1528	At1g66580	60S ribosomal protein L10 (RPL10C)
252872_at	1.1518	At4g40010	SNRK2-7_SNRK2.7_SRK2F__SNRK2-7/SNRK2.7/SRK2F (SNF1-RELATED PROTEIN KINASE 2.7); kinase
255946_at	1.1497	At1g22020	SHM6__SHM6 (serine hydroxymethyltransferase 6); glycine hydroxymethyltransferase
260814_at	1.1496	At1g43710	EMB1075__EMB1075 (EMBRYO DEFECTIVE 1075); carboxy-lyase
252828_at	1.1494	At4g39960	DNAJ heat shock family protein
249582_at	1.1461	At5g37780	CAM1_ACAM-1_TCH1__CAM1 (CALMODULIN 1); calcium ion binding
262686_at	1.1444	At1g75990	26S proteasome regulatory subunit S3, putative (RPN3)
246147_s_at	1.1443	At5g19990 At5g20000	RPT6A_ATSUG1__RPT6A; ATPase
250370_at	1.1426	At5g11430	transcription elongation factor-related
267048_at	1.1424	At2g34200	zinc finger (C3HC4-type RING finger) family protein
248021_at	1.1418	At5g56500	ATP binding / protein binding / unfolded protein binding
252293_at	1.1393	At3g48990	AMP-dependent synthetase and ligase family protein
249344_at	1.1379	At5g40770	ATPHB3__ATPHB3 (PROHIBITIN 3)
250418_at	1.1371	At5g11240	transducin family protein / WD-40 repeat family protein
261183_at	1.1355	At1g34550	EMB2756__EMB2756 (EMBRYO DEFECTIVE 2756)
252022_at	1.1346	At3g52930	fructose-bisphosphate aldolase, putative
261911_at	1.1341	At1g80750	60S ribosomal protein L7 (RPL7A)
251372_at	1.1309	At3g60520	zinc ion binding
261622_at	1.1296	At1g01970	pentatricopeptide (PPR) repeat-containing protein
252479_at	1.1273	At3g46560	EMB2474_TIM9__TIM9 (EMBRYO DEFECTIVE 2474); P-P-bond-hydrolysis-driven protein transmembrane transporter
259712_at	1.1264	At1g77440	PBC2__PBC2 (20S proteasome beta subunit C 2); peptidase
253215_at	1.1257	At4g34950	nodulin family protein
259800_at	1.1240	At1g72175	zinc finger (C3HC4-type RING finger) family protein
250866_at	1.1224	At5g03905	hesB-like domain-containing protein
254211_at	1.1218	At4g23570	SGT1A__SGT1A (Suppressor of G2 (Two) 1A)
248132_at	1.1212	At5g54840	GTP-binding family protein
262941_at	1.1202	At1g79490	EMB2217__EMB2217 (EMBRYO DEFECTIVE 2217)
252864_at	1.1201	At4g39740	electron transport SCO1/SenC family protein

253779_at	1.1199	At4g28490	HAESA_HAE_RLK5__HAESA (RECEPTOR-LIKE PROTEIN KINASE 5); ATP binding / kinase/ protein serine/threonine kinase
249888_s_at	1.1199	At5g22480 At5g37340	zinc finger (ZPR1-type) family protein
255067_at	1.1195	At4g08960	phosphotyrosyl phosphatase activator (PTPA) family protein
248300_at	1.1194	At5g53000	TAP46__TAP46 (2A PHOSPHATASE ASSOCIATED PROTEIN OF 46 KD)
257707_at	1.1194	At3g12650	similar to unnamed protein product [Vitis vinifera] (GB:CAO15069.1)
250938_at	1.1175	At5g03180	zinc finger (C3HC4-type RING finger) family protein
246017_at	1.1169	At5g10730	binding / catalytic/ coenzyme binding
253521_at	1.1168	At4g31300	PBA1__PBA1 (20S proteasome beta subunit A 1); peptidase
267500_s_at	1.1148	At2g44890 At2g45510	CYP704A1__CYP704A1 (cytochrome P450, family 704, subfamily A, polypeptide 1); oxygen binding
246623_at	1.1118	At1g48920	ATNUC-L1_PARL1__ATNUC-L1/PARL1 (PARALLEL 1); nucleic acid binding
256022_at	1.1109	At1g58360	AAP1_NAT2__AAP1 (AMINO ACID PERMEASE 1); amino acid transmembrane transporter
251562_at	1.1109	At3g57890	tubulin-specific chaperone C-related
247555_at	1.1095	At5g61020	ECT3__ECT3 (evolutionary conserved C-terminal 3)
266514_at	1.1090	At2g47890	zinc finger (B-box type) family protein
248243_at	1.1080	At5g53590	auxin-responsive family protein
257954_at	1.1079	At3g21755 At3g21760	
263922_s_at	1.1071	At2g36580 At3g52990	pyruvate kinase, putative
254451_at	1.1071	At4g21090	adrenodoxin-like ferredoxin 1
253722_at	1.1059	At4g29190	zinc finger (CCCH-type) family protein
264650_at	1.1039	At1g08970	HAP5C__HAP5C (HEME ACTIVATED PROTEIN 5C); DNA binding / transcription factor
253784_at	1.1031	At4g28610	PHR1__PHR1 (PHOSPHATE STARVATION RESPONSE 1); transcription
260955_at	1.1005	At1g06000	UDP-glucoronosyl/UDP-glucosyl transferase family protein
262607_at	1.1005	At1g13990	similar to unnamed protein product [Vitis vinifera] (GB:CAO68469.1)
254321_at	1.1001	At4g22590	trehalose-6-phosphate phosphatase, putative
258776_at	1.0995	At3g11830	chaperonin, putative
251078_at	1.0985	At5g01990	auxin efflux carrier family protein
261176_at	1.0975	At1g04780	ankyrin repeat family protein
250703_at	1.0965	At5g06360	ribosomal protein S8e family protein
253865_at	1.0962	At4g27470	zinc finger (C3HC4-type RING finger) family protein
248082_at	1.0958	At5g55400	fimbrin-like protein, putative
249712_at	1.0957	At5g35620	LSP1_EIF(ISO)4E_LSP__LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES); RNA binding / translation initiation factor
252527_at	1.0956	At3g46440	UXS5__UXS5 (UDP-Xyl synthase 5); catalytic
255452_at	1.0919	At4g02880	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03290.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22500.1)
249244_at	1.0915	At5g42270	VAR1_FTSH5__VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase
264803_at	1.0907	At1g08580	similar to Pm52 [Prunus mume] (GB:BAE48663.1)
259587_at	1.0845	At1g28120	Identical to Ubiquitin thioesterase otubain-like [Arabidopsis Thaliana] (GB:Q8LG98;GB:Q9C7E1); similar to otubain-like cysteine protease [Populus trichocarpa] (GB:ABU93349.1); contains InterPro domain Ovarian tumour, otubain (InterPro:IPR003323); contains InterPro domain Ubiquitin thioesterase Otubain (InterPro:IPR016615)
248271_at	1.0839	At5g53420	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27900.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27900.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV59385.1)
256310_at	1.0834	At1g30360	ERD4__ERD4 (EARLY-RESPONSIVE TO DEHYDRATION 4)
263157_at	1.0828	At1g54100	ALDH7B4__ALDH7B4 (ALDEHYDE DEHYDROGENASE 7B4); 3-chloroallyl aldehyde dehydrogenase
259688_at	1.0809	At1g63120	ATRBL2__ATRBL2 (ARABIDOPSIS THALIANA RHOMBOID-LIKE 2); serine-type endopeptidase
246131_at	1.0769	At5g20990	CHL6_CNX_SIR4_B73__B73 (CHLORATE RESISTANT 6); molybdenum ion

255980_at	1.0760	At1g33970	avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative
246467_at	1.0752	At5g17040	UDP-glucoronosyl/UDP-glucosyl transferase family protein
266532_at	1.0748	At2g16890	UDP-glucoronosyl/UDP-glucosyl transferase family protein
250367_s_at	1.0745	At5g11170 At5g11200	DEAD/DEAH box helicase, putative (RH15)
249067_at	1.0742	At5g43960	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein
258892_at	1.0730	At3g05670	PHD finger family protein
245002_at	1.0729	AtCg00270	PSBD__PSII D2 protein
266181_at	1.0718	At2g02390	ATGSTZ1_GST18__ATGSTZ1 (GLUTATHIONE S-TRANSFERASE 18); glutathione transferase
251541_at	1.0706	At3g58750	CSY2__CSY2 (CITRATE SYNTHASE 2); citrate (SI)-synthase
251732_at	1.0688	At3g56110	prenylated rab acceptor (PRA1) family protein
253276_at	1.0684	At4g34050	caffeoyl-CoA 3-O-methyltransferase, putative
261506_at	1.0676	At1g71697	ATCK1_CK__ATCK1 (CHOLINE KINASE)
247445_at	1.0645	At5g62640	ELF5__ELF5 (EARLY FLOWERING 5)
263901_at	1.0595	At2g36320	zinc finger (AN1-like) family protein
249701_at	1.0593	At5g35460	similar to unknown [Populus trichocarpa] (GB:ABK95300.1); contains domain Acetyl-CoA synthetase-like (SSF56801)
261644_s_at	1.0586	At1g19750 At1g27840	transducin family protein / WD-40 repeat family protein
264921_at	1.0570	At1g60650	glycine-rich RNA-binding protein, putative
250934_at	1.0555	At5g03030	DNAJ heat shock N-terminal domain-containing protein
265850_at	1.0549	At2g35720	DNAJ heat shock N-terminal domain-containing protein
246595_at	1.0549	At5g14780	FDH__FDH (FORMATE DEHYDROGENASE); NAD binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
260937_at	1.0538	At1g45160	similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:AT3G17850.1); similar to hypothetical protein OsJ_011826 [Oryza sativa (japonica cultivar-group)] (GB:EAZ28343.1); similar to putative protein kinase [Oryza sativa] (GB:AAK18843.1); similar to hypothetical protein OsI_012847 [Oryza sativa (indica cultivar-group)] (GB:EAY91614.1); contains InterPro domain Dimeric alpha-beta barrel (InterPro:IPR011008); contains InterPro domain Serine/threonine protein kinase; (InterPro:IPR002290); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase; (InterPro:IPR001245)
254740_s_at	1.0530	At4g13890 At4g13930	EDA36_EDA37_SHM5__SHM5 (SERINE HYDROXYMETHYLTRANSFERASE 5); glycine hydroxymethyltransferase
251657_at	1.0530	At3g57000	nucleolar essential protein-related
262781_s_at	1.0529	At1g13060 At3g26340	PBE1__PBE1 (20S proteasome beta subunit E1); peptidase
259948_at	1.0529	At1g71350	eukaryotic translation initiation factor SUI1 family protein
260081_at	1.0527	At1g78170	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G22250.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61724.1)
260842_at	1.0489	At1g29150	ATS9_RPN6__ATS9 (19S PROTEOSOME SUBUNIT 9)
255968_at	1.0483	At1g22270	Identical to TRM112-like protein At1g22270 [Arabidopsis Thaliana] (GB:Q8LFJ5;GB:Q9LME3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G78190.1); similar to unknown [Picea sitchensis] (GB:ABK23797.1); contains InterPro domain Protein of unknown function DUF343
253603_at	1.0480	At4g30935	WRKY32__WRKY32 (WRKY DNA-binding protein 32); transcription factor
248471_at	1.0480	At5g50840	similar to myosin heavy chain-related [Arabidopsis thaliana] (TAIR:AT5G59210.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68982.1); contains domain PTHR16127 (PTHR16127); contains domain PTHR16127:SF5 (PTHR16127:SF5)
262094_at	1.0469	At1g56110	NOP56__NOP56 (ARABIDOPSIS HOMOLOG OF NUCLEOLAR PROTEIN
262504_at	1.0466	At1g21750	ATPDIL1-1__ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase

246976_s_at	1.0458	At5g24810	ABC1 family protein
263513_at	1.0456	At2g12400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G25270.1); similar to hypothetical protein OsJ_008445 [Oryza sativa (japonica cultivar-group)] (GB:EAZ24962.1)
262219_at	1.0456	At1g74750	pentatricopeptide (PPR) repeat-containing protein
258158_at	1.0442	At3g17790	ATPAP17_PAP17_ATACP5__ATACP5 (acid phosphatase 5); acid phosphatase/ protein serine/threonine phosphatase
251659_at	1.0422	At3g57090	BIGYIN__BIGYIN; binding
247164_at	1.0411	At5g65720	ATNIFS1_NIFS1__ATNFS1/ATNIFS1/NFS1/NIFS1 (ARABIOPSIS THALIANA NITROGEN FIXATION S HOMOLOG 1)
256068_at	1.0395	At1g13690	ATE1__ATE1 (ATPase E1); nucleic acid binding
245496_at	1.0388	At4g16440	iron hydrogenase family protein
267064_at	1.0379	At2g41110	CAM2_ACAM-2_ATCAL5__CAM2 (CALMODULIN-2); calcium ion binding
260979_at	1.0362	At1g53510	ATMPK18__ATMPK18 (ARABIDOPSIS THALIANA MAP KINASE 18); MAP
265987_at	1.0339	At2g24240	potassium channel tetramerisation domain-containing protein
266257_at	1.0292	At2g27820	ADT3_PD1__PD1 (PREPHENATE DEHYDRATASE 1); arogenate dehydratase/ prephenate dehydratase
249199_at	1.0283	At5g42520	ATBPC6_BBR/BPC6_BPC6__ATBPC6/BBR/BPC6/BPC6 (BASIC PENTACYSTEINE 6)
265061_at	1.0270	At1g61640	ABC1 family protein
245605_at	1.0269	At4g14300	heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative
266672_at	1.0266	At2g29650	inorganic phosphate transporter, putative
255559_at	1.0263	At4g02010	protein kinase family protein
252880_at	1.0262	At4g39730	lipid-associated family protein
255586_at	1.0223	At4g01560	MEE49__MEE49 (maternal effect embryo arrest 49)
250752_at	1.0214	At5g05690	CPD_CBB3_CYP90_DWF3__CPD (CABBAGE 3)
254020_at	1.0207	At4g25700	BETA-OHASE 1_B1_CHY1__BETA-OHASE 1 (BETA-HYDROXYLASE 1)
246122_at	1.0204	At5g20380	transporter-related
252419_at	1.0202	At3g47510	unknown protein
258849_at	1.0193	At3g03250	UGP__UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase
257634_s_at	1.0189	At3g26170 At3g26180	CYP71B19__CYP71B19 (cytochrome P450, family 71, subfamily B, polypeptide 19); oxygen binding
263928_at	1.0187	At2g36330	Identical to UPF0497 membrane protein At2g36330 [Arabidopsis Thaliana] (GB:Q84WP5;GB:Q9SJM5); similar to integral membrane protein, putative [Arabidopsis thaliana] (TAIR:AT5G62820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64343.1); contains InterPro domain Protein of unknown function DUF588 (InterPro:IPR006702)
266553_at	1.0181	At2g46170	reticulon family protein (RTNLB5)
250546_at	1.0180	At5g08180	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
246158_at	1.0170	At5g19855	similar to unnamed protein product [Vitis vinifera] (GB:CAO21907.1)
258316_at	1.0169	At3g22660	rRNA processing protein-related
252121_at	1.0169	At3g51160	MUR1_GMD2_MUR_1__MUR1 (MURUS 1)
264131_at	1.0164	At1g79150	binding
259757_at	1.0163	At1g77510	ATPDIL1-2__ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase
266189_at	1.0161	At2g39020	GCN5-related N-acetyltransferase (GNAT) family protein
249074_at	1.0158	At5g44080	bZIP transcription factor family protein
250729_at	1.0128	At5g06460	ATUBA2__ATUBA2 (Arabidopsis thaliana ubiquitin activating enzyme 2); ubiquitin activating enzyme
247608_at	1.0104	At5g60990	DEAD/DEAH box helicase, putative (RH10)
253162_at	1.0077	At4g35630	PSAT__PSAT (phosphoserine aminotransferase); phosphoserine
257908_at	1.0069	At3g25410	bile acid:sodium symporter family protein
260338_at	1.0058	At1g69250	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein
256182_at	1.0045	At1g51740	ATUFE1_SYP81__SYP81 (SYNTAXIN 81); protein binding
247013_at	1.0041	At5g67480	BT4__BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding

247046_at	1.0025	At5g66540	similar to hypothetical protein OsI_036143 [Oryza sativa (indica cultivar-group)] (GB:EAY82184.1); similar to hypothetical protein OsJ_031573 [Oryza sativa (japonica cultivar-group)] (GB:EAZ17364.1); similar to Os12g0133900 [Oryza sativa (japonica cultivar-group)] (GB:NP_001066092.1); contains InterPro domain U3 small nucleolar ribonucleoprotein complex, subunit Mpp10p; (InterPro:IPR012173); contains InterPro domain Mpp10 protein
267183_at	1.0016	At2g44020	mitochondrial transcription termination factor-related / mTERF-related
258399_at	1.0010	At3g15540	IAA19_MSG2__IAA19 (indoleacetic acid-induced protein 19); transcription
263756_at	1.0007	At2g21270	ubiquitin fusion degradation UFD1 family protein