Table 5. All 179 genes with GO annotations up- and down-regulated by > 1.5 fold

Probe	**Symbol**	**Description**	**Gene Ontology**	Pathway	**Fold**
243158_at	NT5C2	5'-nucleotidase, cytosolic II	cytosol 5'-nucleotidase activity hydrolase activity	Purine metabolism Pyrimidine metabolism Nicotinate and nicotinamide metabolism	4.43
243149_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	RNA cap bindingtranslation initiation factor activity regulation of translational initiation eukaryotic translation initiation factor 4F complex		6.38
239238_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	chromatin chromatin binding transcription coactivator activity protein binding nucleoplasm		3.49

			chromatin assembly/disassembly chromatin remodeling transcription regulation of transcription from Pol II promoter SWI/SNF complex positive regulation of transcription, DNA-dependent		
236128_at					2.39
232138_at	MBNL2	muscleblind-like 2 (Drosophila)	nucleic acid binding		2.71
242695_at					5.66
222266_at	C19orf2	chromosome 19 open reading frame 2	transcription corepressor activity protein binding nucleus DNA-directed RNA polymerase II, core complex cytoplasm regulation of transcription from Pol II promoter protein folding response to virus prefoldin complex		3.94
232528_at	UBE2E3	ubiquitin-	ubiquitin conjugating enzyme activity	Ubiquitin mediated	3.65

		conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	ubiquitin-protein ligase activity ubiquitin cycle ligase activity	proteolysis	
242963_at	MGC26963		Golgi apparatus integral to plasma membrane lipid metabolism sphingolipid metabolism sphingomyelin biosynthesis kinase activity transferase activity integral to Golgi membrane ceramide cholinephosphotransferase activity	Glycosphingolipid metabolism	2.27
229949_at	DKFZP434A0131				0.37
225417_at	EPC1	enhancer of polycomb homolog 1 (Drosophila)	regulation of cell growth nucleus transcription regulation of transcription, DNA-dependent transcriptional activator activity transcriptional repressor activity chromatin modification		4.59

222348_at	MAST4	microtubule associated serine/threonine kinase family member 4	protein kinase activity protein serine/threonine kinase activity calmodulin binding ATP binding protein amino acid phosphorylation transferase activity		2.65
234594_at	ITPK1	inositol 1,3,4-triphosphate 5/6 kinase	catalytic activity mitochondrion signal transduction kinase activity ligase activity		0.32
232356_at	KIAA0143		integral to membrane		4.81
1566903_at	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	receptor activity transmembrane receptor activity transmembrane receptor activity calcium ion binding plasma membrane plasma membrane proteolysis and peptidolysis lipid metabolism lipid metabolism		0.48

			endocytosis endocytosis signal transduction signal transduction lipoprotein binding membrane integral to membrane cytokine and chemokine mediated signaling pathway apolipoprotein E receptor activity apolipoprotein E receptor activity apolipoprotein E receptor activity		
239716_at	TRIM33	tripartite motif-containing 33	ubiquitin ligase complex DNA binding ubiquitin-protein ligase activity nucleus transcription regulation of transcription, DNA-dependent zinc ion binding negative regulation of transcription protein ubiquitination		4.77
242233_at	KIAA1219		GTPase activator activity		2.78

241769_at					2.33
1557360_at	LRPPRC	leucine-rich PPR-motif containing	biological_process unknown single-stranded DNA binding RNA binding binding nucleus nucleus mitochondrion mitochondrion		8.82
230651_at	THOC2	THO complex 2	nuclear mRNA splicing, via spliceosome RNA binding nucleus mRNA-nucleus export transport		2.79
230337_at	SOS1	son of sevenless homolog 1 (Drosophila)	DNA binding Ras guanyl-nucleotide exchange factor activity Rho guanyl-nucleotide exchange factor activity Rho GTPase activator activity RAS protein signal transduction	MAPK signaling pathway Integrin-mediated cell adhesion Jak-STAT signaling pathway NA	3.45
242287_at	RSN	restin (Reed-Steinberg cell-	nucleic acid binding endosome		3.48

		expressed intermediate filament-associated protein)	intermediate filament microtubule binding microtubule cytoskeleton		
226711_at	HTLF	human T-cell leukemia virus enhancer factor	transcription factor activity transcription factor activity nucleus transcription regulation of transcription, DNA-dependent		2.16
238563_at	ABI1	abl-interactor 1	soluble fraction nucleus endoplasmic reticulum cytosol transmembrane receptor protein tyrosine kinase signaling pathway cytoskeletal protein binding negative regulation of cell proliferation		3.34
236778_at	ATRX	alpha thalassemia/mental retardation syndrome X-	DNA binding DNA helicase activity transcription factor activity helicase activity		2.89

		linked (RAD54 homolog, S. cerevisiae)	ATP binding nucleus nuclear heterochromatin DNA repair DNA methylation DNA recombination regulation of transcription, DNA-dependent chromosome organization and biogenesis (sensu Eukarya) perception of sound hydrolase activity		
232696_at	C16orf46	chromosome 16 open reading frame 46			0.30
239780_at					2.33
231087_at	hSyn		binding		2.81
236703_at					3.69
1556126_s_at	GPATC2	G patch domain containing 2	nucleic acid binding intracellular		3.93
243827_at	TEX27	testis expressed sequence 27	DNA binding zinc ion binding		2.75
209735_at	ABCG2	ATP-binding cassette, sub-	nucleotide binding ATP binding		6.71

		family G (WHITE), member 2	transport xenobiotic-transporting ATPase activity membrane integral to membrane ATPase activity response to drug		
204700_x_at	MGC29875				2.30
242920_at	KIAA0999		protein serine/threonine kinase activity ATP binding protein amino acid phosphorylation transferase activity		4.65
243037_at	FUBP1	far upstream element (FUSE) binding protein 1	single-stranded DNA binding transcription factor activity nucleus cytoplasm transcription regulation of transcription, DNA-dependent transcription from Pol II promoter phosphate transport		1.78
237216_at	GARNL1	GTPase activating	GTPase activator activity nucleus		3.12

		Rap/RanGAP domain-like 1			
240765_at	HCMOG T-1				1.85
244165_at	C10orf18	chromosome 10 open reading frame 18			2.37
244546_at	CYCS	cytochrome c, somatic	protein binding mitochondrial electron transport chain mitochondrial intermembrane space mitochondrial intermembrane space cytosol cytosol electron transport DNA fragmentation DNA fragmentation transport apoptosis caspase activation via cytochrome c caspase activation via cytochrome c heme binding electron transporter, transferring electrons from CoQH2-	Apoptosis	0.23

			cytochrome c reductase complex and cytochrome c oxidase complex activity electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity cellular respiration cellular respiration		
243450_at	AKAP13	A kinase (PRKA) anchor protein 13	cAMP-dependent protein kinase activity signal transducer activity receptor activity Rho guanyl-nucleotide exchange factor activity membrane fraction intracellular signaling cascade kinase activity		3.64
234969_s_at					3.57
244633_at	PIAS2	protein inhibitor of activated STAT, 2	DNA binding nucleus transcription regulation of transcription, DNA-dependent ubiquitin cycle development	Jak-STAT signaling pathway	2.84

			zinc ion binding		
239227_at	EXT1	exostoses (multiple) 1	skeletal development endoplasmic reticulum membrane Golgi apparatus glycosaminoglycan biosynthesis cell cycle signal transduction membrane integral to membrane transferase activity, transferring glycosyl groups negative regulation of cell cycle N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	Chondroitin / Heparan sulfate biosynthesis	4.07
216321_s_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	transcription factor activity glucocorticoid receptor activity steroid binding nucleus cytoplasm mitochondrial matrix regulation of transcription, DNA-dependent transcription from Pol II promoter inflammatory response	Neuroactive ligand-receptor interaction	5.48

			signal transduction		
236809_at	MGC40405				3.55
242761_s_at	ZNF420	zinc finger protein 420	nucleic acid binding DNA binding nucleus regulation of transcription, DNA-dependent zinc ion binding		2.56
232431_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	transcription factor activity glucocorticoid receptor activity steroid binding nucleus cytoplasm mitochondrial matrix regulation of transcription, DNA-dependent transcription from Pol II promoter inflammatory response signal transduction	Neuroactive ligand-receptor interaction	8.48
237006_at	MLLT2	myeloid/lymphoid or mixed-lineage leukemia (trithorax	transcription factor activity nucleus		4.66

		homolog, Drosophila), translocated to, 2			
227541_at	WDR20	WD repeat domain 20			2.63
202724_s_at	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	transcription factor activity nucleus transcription regulation of transcription from Pol II promoter anti-apoptosis		2.56
215786_at	HBXAP	hepatitis B virus x associated protein	DNA binding nucleus nucleosome assembly transcription transcriptional activator activity transcriptional repressor activity chromatin modification histone binding negative regulation of transcription, DNA-dependent positive regulation of viral transcription		2.61
243003_at	MLLT10	myeloid/lymphoid or mixed-	DNA binding transcription factor activity		2.24

		lineage leukemia (trithorax homolog, Drosophila), translocated to, 10	nucleus regulation of transcription, DNA-dependent		
1562497_at					3.00
1557432_at	RASAL2	RAS protein activator like 2	GTPase activator activity Ras GTPase activator activity signal transduction		2.58
242673_at	UBE3C	ubiquitin protein ligase E3C	protein polyubiquitination ubiquitin-protein ligase activity protein binding intracellular ubiquitin cycle		4.44
227312_at	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	actin binding calcium ion binding calmodulin binding membrane fraction cytoskeleton dystrophin-associated glycoprotein complex		1.91

			membrane		
235374_at	MDH1	malate dehydrogenase 1, NAD (soluble)	L-lactate dehydrogenase activity malic enzyme activity cytosol glycolysis tricarboxylic acid cycle malate metabolism oxidoreductase activity L-malate dehydrogenase activity	Citrate cycle (TCA cycle) Pyruvate metabolism Glyoxylate and dicarboxylate metabolism Carbon fixation Reductive carboxylate cycle (CO2 fixation)	1.87
224336_s_at	DUSP16	dual specificity phosphatase 16	inactivation of MAPK nucleus cytoplasm protein amino acid dephosphorylation hydrolase activity MAP kinase phosphatase activity MAPK nucleus export leptomycin B-sensitive MAPK phosphatase nucleus export	MAPK signaling pathway	2.82
226208_at	MGC40405				3.77
213459_at	RPL37A	ribosomal protein L37a	structural constituent of ribosome ribosome protein biosynthesis	Ribosome	3.25

225957_at	LOC153222		DNA binding nucleus regulation of transcription, DNA-dependent		2.53
239721_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	ubiquitin conjugating enzyme activity ubiquitin-protein ligase activity ubiquitin cycle ligase activity		1.72
241786_at	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	calcium-dependent protein serine/threonine phosphatase activity calcium ion binding calmodulin inhibitor activity calcineurin complex	MAPK signaling pathway Apoptosis Wnt signaling pathway	5.09
218819_at	DDX26	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	helicase activity transmembrane receptor activity		2.85
242068_at	BIRC6	baculoviral IAP repeat-containing	ubiquitin conjugating enzyme activity cysteine protease inhibitor activity		3.11

		6 (apollon)	intracellular ubiquitin cycle apoptosis anti-apoptosis ligase activity		
235556_at					2.80
242919_at	LOC114977		nucleic acid binding nucleus zinc ion binding		2.12
233085_s_at	FLJ22833		nucleic acid binding DNA binding		5.14
232080_at	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	ubiquitin-protein ligase activity intracellular ubiquitin cycle		2.22
227443_at	C9orf150	chromosome 9 open reading frame 150			3.10
227551_at	C9orf77	chromosome 9 open reading frame 77	catalytic activity		3.47

243908_at	ZNF638	zinc finger protein 638	nucleotide binding nucleic acid binding double-stranded DNA binding RNA binding nucleus nucleoplasm cytoplasm zinc ion binding RNA splicing		1.86
241905_at	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	inositol/phosphatidylinositol kinase activity phosphoinositide 3-kinase complex phosphatidylinositol biosynthesis intracellular signaling cascade phosphatidylinositol 3-kinase activity	Phosphatidylinositol signaling system Apoptosis Toll-like receptor signaling pathway Jak-STAT signaling pathway NA	3.57
228038_at	SOX2	SRY (sex determining region Y)-box 2	transcription factor activity nucleus establishment and/or maintenance of chromatin architecture transcription regulation of transcription, DNA-dependent		2.68

232392_at	SFRS3	splicing factor, arginine/serine-rich 3	nuclear mRNA splicing, via spliceosome nucleic acid binding RNA binding nucleus		2.87
231644_at					2.71
1553349_at	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	nucleic acid binding translation initiation factor activity nucleus zinc ion binding		2.22
219662_at	MGC5509				1.61
232472_at					2.67
241775_at	SCFD1	sec1 family domain containing 1	catalytic activity endoplasmic reticulum Golgi apparatus vesicle docking during exocytosis protein transport vesicle-mediated transport		4.78
1556568_a_at	NLK	nemo like kinase	magnesium ion binding protein serine/threonine kinase activity MAP kinase activity ATP binding	MAPK signaling pathway Wnt signaling pathway Cadherin-mediated cell adhesion	2.05

			nucleus regulation of transcription, DNA-dependent protein amino acid phosphorylation protein kinase cascade transferase activity negative regulation of Wnt receptor signaling pathway		
239695_at	KIAA1579		nucleotide binding nucleic acid binding		2.04
1556989_at	ADAMTS9	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9	metalloendopeptidase activity extracellular matrix glycoprotein catabolism development zinc ion binding		2.85
228723_at	SDFR1	stromal cell derived factor receptor 1	receptor activity mannose binding membrane		1.61
208054_at	HERC4	hect domain and RLD 4	ubiquitin-protein ligase activity intracellular ubiquitin cycle		1.63
238558_at	MBNL1	muscleblind-like	embryonic development (sensu Mammalia)		1.87

		(Drosophila)	nucleic acid binding double-stranded RNA binding nucleus nucleus cytoplasm neurogenesis muscle development embryonic limb morphogenesis myoblast differentiation		
231871_at	ITR		receptor activity		1.74
204012_s_at	LCMT2	leucine carboxyl methyltransferase 2	protein binding methyltransferase activity transferase activity		3.42
224822_at	DLC1	deleted in liver cancer 1	Rho GTPase activator activity protein binding extracellular cytoplasm cytoskeleton organization and biogenesis signal transduction regulation of cell adhesion negative regulation of cell growth		5.21
228993_s_	PDCD4	programmed cell	apoptosis		1.50

at		death 4 (neoplastic transformation inhibitor)			
232865_at	AF5Q31		transcription factor activity transcription from Pol II promoter		2.62
230206_at	DOCK5	dedicator of cytokinesis 5	guanyl-nucleotide exchange factor activity GTP binding GTPase binding		2.90
239731_at					2.39
1558467_a_at	UGCGL2	UDP-glucose ceramide glucosyltransferase-like 2	UDP-glucose:glycoprotein glucosyltransferase activity protein binding endoplasmic reticulum lumen protein amino acid glycosylation transferase activity, transferring glycosyl groups	Fructose and mannose metabolism N-Glycans biosynthesis O-Glycans biosynthesis NA Glycerolipid metabolism Glycosylphosphatidylinositol(GPI)-anchor biosynthesis Glycosphingolipid metabolism Blood group glycolipid biosynthesis-lactoseries	2.38

				Blood group glycolipid biosynthesis-neolactoseries Globoside metabolism Ganglioside biosynthesis	
201865_x_at	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	transcription factor activity glucocorticoid receptor activity steroid binding nucleus cytoplasm mitochondrial matrix regulation of transcription, DNA-dependent transcription from Pol II promoter inflammatory response signal transduction	Neuroactive ligand-receptor interaction	4.11
238549_at	CBFA2T2	core-binding factor, runt domain, alpha subunit 2, translocated to, 2	transcription factor activity transcription cofactor activity nucleus regulation of transcription, DNA-dependent cell proliferation		2.71
226807_at	ZFP1	zinc finger protein 1 homolog (mouse)	DNA binding nucleus transcription		2.45

			regulation of transcription, DNA-dependent zinc ion binding		
240502_at	MGC14161		binding cytoplasm cytoskeleton cytoskeletal protein binding membrane		1.99
219595_at	ZNF26	zinc finger protein 26 (KOX 20)	nucleic acid binding nucleus regulation of transcription, DNA-dependent zinc ion binding		1.86
222313_at	CNOT2	CCR4-NOT transcription complex, subunit 2	nucleus regulation of transcription, DNA-dependent regulation of global transcription from Pol II promoter RNA polymerase II transcription mediator activity transcription regulator activity		2.30
227140_at	INHBA	inhibin, beta A (activin A, activin AB alpha polypeptide)	skeletal development ovarian follicle development cytokine activity transforming growth factor beta receptor binding hormone activity protein binding	Cytokine-cytokine receptor interaction TGF-beta signaling pathway	2.14

			extracellular induction of apoptosis defense response cell cycle arrest cell surface receptor linked signal transduction cell-cell signaling neurogenesis mesoderm development growth factor activity response to external stimulus activin inhibitor activity cell differentiation erythrocyte differentiation growth negative regulation of phosphorylation hemoglobin biosynthesis negative regulation of interferon-gamma biosynthesis negative regulation of B-cell differentiation negative regulation of macrophage differentiation negative regulation of cell cycle positive regulation of follicle-stimulating hormone secretion negative regulation of follicle-stimulating hormone secretion		

237483_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	biological_process unknown phosphatidylinositol binding cellular_component unknown		1.55
230083_at	USP53	ubiquitin specific protease 53	cysteine-type endopeptidase activity ubiquitin thiolesterase activity ubiquitin-dependent protein catabolism ubiquitin cycle		2.77
213913_s_at	KIAA0984				3.20
233369_at	SOS2	son of sevenless homolog 2 (Drosophila)	DNA binding guanyl-nucleotide exchange factor activity small GTPase mediated signal transduction cellular_component unknown	MAPK signaling pathway Integrin-mediated cell adhesion Jak-STAT signaling pathway NA	3.25
218926_at	MYNN	myoneurin	nucleic acid binding transcription factor activity protein binding nucleus		1.80

			transcription, DNA-dependent regulation of transcription, DNA-dependent zinc ion binding zinc ion binding		
229366_at	CRBN	cereblon	ATP-dependent peptidase activity mitochondrion ATP-dependent proteolysis		2.59
229483_at	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	ubiquitin conjugating enzyme activity ubiquitin-protein ligase activity ubiquitin cycle ligase activity		2.29
232778_at	C10orf18	chromosome 10 open reading frame 18			2.04
225956_at	LOC153222		DNA binding nucleus regulation of transcription, DNA-dependent		4.73
235436_at	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	nucleic acid binding ATP binding ATP-dependent helicase activity hydrolase activity		2.15

217626_at	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2, bile acid binding protein, 3-alpha hydroxysteroid dehydrogenase, type III)	binding electron transporter activity lipid metabolism transport digestion steroid metabolism bile acid transporter activity canalicular bile acid transport oxidoreductase activity 3-alpha-hydroxysteroid dehydrogenase (A-specific) activity trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity		2.20
222853_at	FLRT3	fibronectin leucine rich transmembrane protein 3	receptor signaling protein activity extracellular matrix integral to plasma membrane cell adhesion protein binding, bridging		2.23
225731_at	KIAA1223				3.08
243691_at	KIAA0276				2.48
213684_s_at	PDLIM5	PDZ and LIM domain 5	actin binding protein kinase C binding		2.20

			protein binding membrane fraction cytosol heart development zinc ion binding receptor signaling complex scaffold activity actinin binding		
226075_at	SSB1		intracellular signaling cascade		1.87
239862_at	TPD52	tumor protein D52	morphogenesis		2.48
241681_at	MBNL1	muscleblind-like (Drosophila)	embryonic development (sensu Mammalia) nucleic acid binding double-stranded RNA binding nucleus nucleus cytoplasm neurogenesis muscle development embryonic limb morphogenesis myoblast differentiation		2.49
1553994_at	NT5E	5'-nucleotidase, ecto (CD73)	nucleotide binding membrane fraction	Purine metabolism Pyrimidine metabolism	2.77

			DNA metabolism 5'-nucleotidase activity nucleotide catabolism membrane hydrolase activity, acting on ester bonds	Nicotinate and nicotinamide metabolism	
229022_at	ZFX	zinc finger protein, X-linked	DNA binding DNA binding transcription coactivator activity nucleus regulation of transcription, DNA-dependent zinc ion binding transcription regulator activity regulation of transcription metal ion binding		1.72
239476_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	phosphatidylinositol binding phosphoinositide 3-kinase complex intracellular signaling cascade intracellular signaling cascade kinase activity phosphatidylinositol 3-kinase activity phosphatidylinositol 3-kinase activity	Phosphatidylinositol signaling system Apoptosis Integrin-mediated cell adhesion Toll-like receptor signaling pathway Jak-STAT signaling	3.47

				pathway NA	
213065_at	MGC23401		nucleus mRNA processing		2.53
233112_at	C9orf150	chromosome 9 open reading frame 150			2.99
240655_at	ALCAM	activated leukocyte cell adhesion molecule	receptor binding protein binding membrane fraction integral to plasma membrane cell adhesion signal transduction antimicrobial humoral response (sensu Vertebrata)		2.25
41329_at	SCYL3	SCY1-like 3 (S. cerevisiae)	protein serine/threonine kinase activity ATP binding Golgi apparatus protein amino acid phosphorylation		2.10
235757_at	C10orf18	chromosome 10 open reading frame 18			2.36
213743_at	CCNT2	cyclin T2	regulation of cell cycle		3.16

			regulation of cyclin dependent protein kinase activity cytokinesis nucleus transcription regulation of transcription, DNA-dependent transcription from Pol II promoter		
232017_at	TJP2	tight junction protein 2 (zona occludens 2)	guanylate kinase activity protein binding nucleus integral to plasma membrane tight junction membrane	NA	1.90
216022_at	WNK1	WNK lysine deficient protein kinase 1	protein serine/threonine kinase activity protein kinase inhibitor activity ATP binding cytoplasm protein amino acid phosphorylation ion transport protein kinase cascade transferase activity regulation of cellular process		2.30
235648_at	ZNF567	zinc finger	nucleic acid binding		3.43

		protein 567	nucleus regulation of transcription, DNA-dependent zinc ion binding		
226588_at	KIAA1604		RNA binding		2.29
240594_at	CDYL	chromodomain protein, Y-like	chromatin chromatin binding catalytic activity nucleus chromatin assembly/disassembly spermatogenesis metabolism peptidase activity		3.04
222872_x_at	FLJ22833		nucleic acid binding DNA binding		4.61
222728_s_at	MGC5306				1.92
222282_at	PAPD4	PAP associated domain containing 4	nucleic acid binding		1.78
236153_at					1.65
225914_s_	CAB39L	calcium binding	binding		2.14

at		protein 39-like			
218566_s_at	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1	biological_process unknown molecular_function unknown cellular_component unknown		1.49
224831_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	nucleotide binding nucleic acid binding		4.57
1560082_at	FLJ14075				1.97
227038_at	MGC26963		Golgi apparatus integral to plasma membrane lipid metabolism sphingolipid metabolism sphingomyelin biosynthesis kinase activity transferase activity integral to Golgi membrane ceramide cholinephosphotransferase activity	Glycosphingolipid metabolism	2.59

236472_at	NRD1	nardilysin (N-arginine dibasic convertase)	proteolysis and peptidolysis neuromuscular junction development cellular_component unknown nardilysin activity		2.59
240788_at	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity electron transporter activity cytosol carbohydrate metabolism tricarboxylic acid cycle malate metabolism oxidoreductase activity	Pyruvate metabolism Carbon fixation	2.30
236265_at					2.43
1559401_a_at	ZNF609	zinc finger protein 609	nucleic acid binding nucleus zinc ion binding		2.10
223204_at	DKFZp434L142				2.85
242225_at	KIAA1040		binding mitochondrion mitotic chromosome condensation ATP synthesis coupled proton transport		3.52

			membrane proton-transporting two-sector ATPase complex hydrogen-transporting ATP synthase activity, rotational mechanism hydrogen-transporting ATPase activity, rotational mechanism		
232489_at	FLJ10287		DNA binding		2.01
239561_at	THRAP2	thyroid hormone receptor associated protein 2	receptor activity		3.41
243410_at	PTPN2	protein tyrosine phosphatase, non-receptor type 2	protein tyrosine phosphatase activity protein tyrosine phosphatase activity receptor activity protein amino acid dephosphorylation protein amino acid dephosphorylation hydrolase activity		2.18
230769_at	FLJ37099				2.04
212990_at	SYNJ1	synaptojanin 1	RNA binding inositol/phosphatidylinositol phosphatase activity phosphoinositide 5-phosphatase activity	Inositol phosphate metabolism Phosphatidylinositol	3.13

			inositol-polyphosphate 5-phosphatase activity phosphate metabolism hydrolase activity	signaling system	
236251_at					3.73
242059_at					2.39
1559020_a_at					1.82
242029_at	FNDC3B	fibronectin type III domain containing 3B			2.17
220612_at	MGC4308				2.64
244010_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ubiquitin ligase complex DNA binding ubiquitin-protein ligase activity ATP binding nucleus transcription regulation of transcription, DNA-dependent methyltransferase activity zinc ion binding ATP synthesis coupled proton transport		3.09

			proton-transporting two-sector ATPase complex protein ubiquitination chromatin modification transferase activity histone-lysine N-methyltransferase activity metal ion binding hydrogen-transporting ATP synthase activity, rotational mechanism hydrogen-transporting ATPase activity, rotational mechanism		
230205_at	ZNF561	zinc finger protein 561	nucleic acid binding nucleus zinc ion binding		1.57
218761_at	RNF111	ring finger protein 111	ubiquitin ligase complex ubiquitin-protein ligase activity zinc ion binding protein ubiquitination		2.44
233869_x_at	DKFZP586B0319				1.66
1557238_s_at	FLJ10707				2.41
1565887_at	TRPM7	transient receptor potential cation	protein serine/threonine kinase activity calcium channel activity		2.08

		channel, subfamily M, member 7	ATP binding protein amino acid phosphorylation cation transport calcium ion transport membrane integral to membrane transferase activity		
232297_at					1.92
244015_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	RNA cap binding translation initiation factor activity regulation of translational initiation eukaryotic translation initiation factor 4F complex		1.83
1556543_at					2.28
243046_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	ubiquitin conjugating enzyme activity ubiquitin-protein ligase activity ubiquitin cycle ligase activity	Ubiquitin mediated proteolysis	2.30
235791_x_at	CHD1	chromodomain helicase DNA binding protein 1	chromatin chromatin binding ATP-dependent DNA helicase activity		2.74

			helicase activity ATP binding nucleus chromatin assembly/disassembly regulation of transcription from Pol II promoter chromosome organization and biogenesis (sensu Eukarya) hydrolase activity		
219284_at	HSPBAP 1	HSPB (heat shock 27kDa) associated protein 1			1.78
228336_at	KIAA19 35				1.82
230296_at	C16orf52	chromosome 16 open reading frame 52			1.88
222580_at	ZNF644	zinc finger protein 644	DNA binding nucleus transcription regulation of transcription, DNA-dependent zinc ion binding		2.94
239516_at	LYPLAL	lysophospholipas	lipid metabolism		2.00

	1	e-like 1	fatty acid metabolism hydrolase activity		
206648_at	ZNF571	zinc finger protein 571	DNA binding nucleus regulation of transcription, DNA-dependent zinc ion binding		1.96
219854_at	ZNF14	zinc finger protein 14 (KOX 6)	DNA binding nucleus transcription regulation of transcription, DNA-dependent zinc ion binding		2.20
215083_at	PSPC1	paraspeckle component 1	nucleotide binding nucleic acid binding		2.30
227599_at	LOC151963				3.70
231940_at	ZNF529	zinc finger protein 529	nucleic acid binding nucleus regulation of transcription, DNA-dependent zinc ion binding		3.68