

**Table S1**

List of genes specifically upregulated in T cells of patients with CLL (n=107)

Gene Symbol	Gene Name	Fold increase	Description/Function(s)	Probe set ID
<b>Receptors</b>				
CX3CR1	Chemokine (C-X3-C motif) receptor 1	8	chemotaxis, cell adhesion, G-protein coupled receptor	205898_at
CRTAM	Class-I MHC-restricted T cell associated molecule	3.7	CD8 and NKT cell receptor, cell/cell interaction, NCL2 is the ligand.	206914_at
TCRGV9	T cell receptor gamma locus variable 9	3.1	antigen recognition by T cell	211144_x_at
GPR171	G protein-coupled receptor 171	3	G-protein coupled receptor	207651_at
KLRD1(CD94)	Killer cell lectin-like receptor subfamily D, member 1	3	The dimmer CD94/NKG2 exist on NK and a small subset of CD8 T cells. This receptor varies in function as an inhibitor or activator depending on isoform of NKG2	210606_x_at
KLRG1, MAFA	Killer cell lectin-like receptor subfamily G, member 1	2.8	cellular defense response, signaling	210288_at
KLRC3, NKG2C	Killer cell lectin-like receptor subfamily C, member 3	2.5	activating receptor with CD94	206785_s_at
KLRA1, LY49L	Killer cell lectin-like receptor subfamily A, member 1	2.4	signaling, cellular defense	207229_at
KLRC4, NKG2F	Killer cell lectin-like receptor subfamily C, member 4	2.2	signaling, cellular defense	210690_at
LY9, SLAMF3	leukocyte cell surface receptor	2.7	cell adhesion, humoral defense mechanism	215967_s_at
CYSLTR1	G-protein coupled receptor protein signaling pathway	2.7	G-protein coupled receptor	216288_at
TCRD@	T cell receptor delta locus	2.6	Ag recognition by T cell	216191_s_at
DP	Prostaglandin D2 receptor	2.4	G-protein coupled, signaling pathway	215894_at
TGFBR3	TGF-beta receptor III	2.4	TGFbeta signaling pathway, proliferation	204731_at
HCP5	HLA complex P5	2.3	defense response	206082_at
CD122	IL-2 receptor, beta	2.2	part of IL-2 receptor, differentiation and activation of T cells	205291_at
IL12RB2	IL-12 receptor, beta 2	2.2	IL-12 receptor, positive regulation of cell proliferation	206999_at
PROCR, EPCR	Endothelial protein C receptor	2.2	inflammatory response, blood coagulation	203650_at
FHC, LDLR	Low density lipoprotein receptor	2.1	lipid metabolism and transport	202068_s_at
TLR3	Toll-like receptor 3	2.1	cause expression of co-receptor when activated	206271_at
<b>TNF family</b>				
LTA, TNFSF1	Lymphotoxin alpha (TNF superfamily, member 1)	3.4	induction of apoptosis, cytokine activity	206975_at
CD154, CD40L	T cell-B cell activating molecule	3.1	growth factor for T and B cells	207892_at
CD137, TNFRSF9	TNF receptor superfamily, member 9	2.7	prevention of activation-induced death of T cells	211786_at
TNFSF6, FasL	TNF superfamily (ligand), member 6	2.7	apoptosis	211333_s_at
Fas(CD95)	Fas antigen	2.2	apoptosis	204780_s_at
TRAF1	TNF-receptor associated factor 1	2.0	anti-apoptotic agent	205599_at
<b>Cytokines/Chemokines</b>				
XCL2	Chemokine (C motif) ligand 2	29	lymphocyte chemotaxis	214567_s_at
XCL1	Chemokine (C motif) ligand 1	17	lymphocyte chemotaxis	206366_x_at
IFNG	gamma interferon	14.1	immune defense	210354_at

Gene Symbol	Gene Name	Fold increase	Description/Function(s)	Probe set ID
CCL4	Chemokine (C-C motif) ligand 4	5	chemotaxis	204103_at
GZMA	Granzyme A	4	target cell lysis in cell-mediated immune responses	205488_at
GZMB	Granzyme B	3	target cell lysis in cell-mediated immune responses	210164_at
RANTES, CCL5	chemokine ligand 5	2.3	chemoattractant for blood monocytes, memory T helper cells and eosinophils.	204655_at
	<b>Proto/Oncogenes</b>			
GFI1	growth factor independent 1	2.8	Proto-oncogene	206589_at
ENC-1, PIG10	ectodermal-neural cortex	2.7	malignant transformation	201340_s_at
MAF	musculoaponeurotic fibrosarcoma oncogene homolog (avian)	2.5	avian oncogene homolog, cell growth and/or maintenance	209348_s_at
FLI1, SIC-1	Friend leukemia virus integration 1	2.2	may be involved in human sarcomas, leukemias, and lymphomas	204236_at
	<b>Suppressor/Repressor</b>			
KLF12, AP-2REP	repressor of AP-2	2.8	AP-2 is involved in embryonic development and malignant transformation	206965_at
FKBP4	T cell FK506-binding protein 4	2.5	immunosuppressant that blocks distinct steps in intracellular signaling pathways	200895_s_at
GAGE7	G antigen 7	2.3	anti-apoptotic gene that confers resistance to Fas/CD95/APO-1	208235_x_at
FEZ1	Fasciculation and elongation protein zeta 1 (zygin I)	2.4	tumor suppressor	203562_at
SAP30	Sin3A-associated protein, 30kDa	2.3	transcriptional repressor, responds to TGFbeta	204900_x_at
CD152, CTLA4	cytotoxic T-lymphocyte-associated protein 4	2.1	soluble form of CTLA4	221331_x_at
DLEU2, LEU2	deleted in lymphocytic leukemia, 2	2.1	candidate gene causing B-CLL and mantle-cell lymphoma	215629_s_at
ACTN4	Actinin, alpha 4	2.1	suppresses tumorigenicity of human neuroblastoma cells	200601_at
LAG3	lymphocyte-activation gene 3	2.0	regulatory rule in Treg , suppressor in CD4 T-cells	206486_at
	<b>Cell cycle/proliferation control</b>			
CSF1, MCSF	colony stimulating factor 1	3.6	cell proliferation, growth factor	209716_at
IEGF, PDGFD	platelet derived growth factor D	2.6	growth factor	219304_s_at
TBRG4, CPR2	transforming growth factor beta regulator 4	2.2	positive regulation of cell proliferation	220789_s_at
BTG3	BTG family, member 3	2.2	negative regulation of cell proliferation	215425_at
ISG20, HEM45	interferon stimulated exonuclease gene 20kDa	2.2	mediating Estrogen control of cellular proliferation and differentiation	204698_at
MGC2463, STAG3	stromal antigen 3	2.2	chromosome segregation, meiosis	219812_at
CDC14	cell division cycle 14	2.0	controlling cell cycle events	210742_at
	<b>Transcription factor</b>			
KLF6, COPEB	Kruppel-like Factor 6	4.5	increases iNOS and NO production	208960_s_at
FOXP1	Forkhead box P1	2.6	transcription regulation	215221_at
TOX	thymus high mobility group box	2.5	transcription regulation	204529_s_at
	<b>Metabolism</b>			
SCD	Stearoyl-CoA desaturase (delta-9-desaturase)	2.7	production of monounsaturated fatty acids, oxidoreductase activity	200832_s_at
CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	2.7	carbohydrate metabolism	218927_s_at
LOC283970	hypothetical protein LOC283970	2.5	carboxylic acid metabolism, lyase activity	221992_at
ACYPE, ACYP1	acylphosphatase 1, erythrocyte (common) type	2.2	Glycolysis/Gluconeogenesis Pyruvate metabolism	205260_s_at
HSD17B7	Hydroxysteroid (17-beta) dehydrogenase 7	2.1	regulates the biologic potency of estrogens and androgens by	220081_x_at

Gene Symbol	Gene Name	Fold increase	Description/Function(s)	Probe set ID
			oxidoreducton	
B4GAL-T1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	2.1	carbohydrate metabolism	201883_s_at
TPST2	Tyrosylprotein sulfotransferase 2	2.1	protein-tyrosine sulfotransferase activity	204079_at
MRPS6	Mitochondrial ribosomal protein S6	2.0	protein biosynthesis	212944_at
CACYBP	calcyclin binding protein	2.0	ubiquitin cycle	210691_s_at
	<b>Transporters</b>			
SLCO4C1	solute carrier organic anion transporter family, member 4C1	2.4	organic anion transporter	222071_s_at
VDP	vesicle docking protein P115	2.4	protein transporter ER-Golgi activity	201831_s_at
C1orf24	chromosome 1 open reading frame 24	2.2	transport, protein folding	217966_s_at
CLTC	Clathrin, heavy polypeptide (Hc)	2.2	intracellular protein transport	220855_at
VAMP4	vesicle-associated membrane protein 4	2.1	vesicle-mediated transport	211760_s_at
STAU2	staufen RNA binding protein, homolog 2	2.0	RNA transport	204226_at
	<b>DNA binding proteins</b>			
H2aa	Histone H2A family	2.8	nucleosome assembly and chromosome organization	214290_s_at
H1.2	H1 histone family, member 2	2.8	chromosome organization	209398_at
HIST2H2AA	H2A histone family	2.3	chromosome organization	218280_x_at
	<b>Heat-shock proteins</b>			
HSPA6	heat shock 70kDa protein 6 (HSP70B')	10.6	protein folding	117_at
HSPB1	heat shock 27kDa protein 1	8.1	regulation of translational initiation, protein folding, anti-apoptosis	201841_s_at
DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	5.1	protein folding	203810_at
STIP1	stress-induced-phosphoprotein 1	2.6	response to stress	213330_s_at
HSPH1	heat shock 105kDa/110kDa protein 1	2.5	protein folding	208744_x_at
HSPE1	heat shock 10kDa protein 1	2.4	protein folding, caspase activation	205133_s_at
HSPD1	heat shock 60kDa protein 1	2.4	protein import into mitochondrial matrix, protein folding	200806_s_at
DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	2.2	protein folding	200666_s_at
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	2.1	positive regulation of nitric oxide biosynthesis, protein folding	211969_at
	<b>Others</b>			
VCAM-1	vascular cell adhesion molecule 1	3.6	cell adhesion molecules	203868_s_at
DOCK9	dedicator of cytokinesis 9	2.8	GTPase binding	215626_at
SNX9	sorting nexin 9	2.6	intracellular signaling cascade	215284_at
APOBEC3G, APOBEC3F	apolipoprotein B mRNA editing enzyme	2.6	innate immune response, negative regulation of retroviral genome replication	214995_s_at
EZH2	enhancer of zeste homolog 2(Drosophila)	2.4	establishment and/or maintenance of chromatin architecture, regulation of transcription	215006_at
TRA2A	Transformer-2 alpha	2.3	pre-mRNA splicing factor activity	213593_s_at
SFRS11	splicing factor, arginine/serine-rich 11	2.3	pre-mRNA splicing factor activity	213742_at
PYHIN1	pyrin and HIN domain family, member 1	2.3	monocyte differentiation	216748_at
TRIM14	tripartite motif-containing 14	2.2	compartment specification	203148_s_at
GVIN1	GTPase very large interferon inducible 1	2.2	soluble, cytosolic and nuclear protein. no record of function	220577_at
PPIA	Peptidylprolyl isomerase A (cyclophilin A)	2.2	Protein folding	217136_at

Gene Symbol	Gene Name	Fold increase	Description/Function(s)	Probe set ID
HCE, HCE1	RNA guanylyltransferase and 5'-phosphatase	2.2	mRNA capping	204208_at
ANX6	annexin A6	2.2	vesicle fusion during exocytosis	200982_s_at
FMOD	fibromodulin	2.1	An extracellular matrix glycoprotein which is overexpressed in B cells of B-CLL. It might be involved in pathology of B-CLL.	202709_at
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	2.1	innate immune response, helicase activity	218943_s_at
MRP-S31	mitochondrial ribosomal protein S31	2.1	structural constituent of ribosome	212604_at
TBCE	tubulin-specific chaperone e	2.1	protein folding	203714_s_at
SF1	splicing factor 1	2.1	mRNA splicing	210172_at
CHPPR	mitochondrial fission regulator 1	2.1	promote mitochondrial fission, secreted by chondrocytes	203208_s_at
	<b>Unknown function</b>			
PMAIP1	PMA-induced protein 1	2.3	protein binding, function unknown	204285_s_at
MGC2463	stromal antigen 3	2.2	hypothetical protein	219812_at
GSDMDC1	gasdermin domain containing 1	2.3	function unknown	218154_at
BTN3A2	butyrophilin, subfamily 3, member A2	2.8	membrane-bound Ig-like protein, function unknown	209846_s_at
BTN3A3	butyrophilin, subfamily 3, member A3	2.1	membrane-bound Ig-like protein, function unknown	204821_at
BTN3A1, BTF5	butyrophilin, subfamily 3, member A1	2.0	membrane-bound Ig-like protein. function unknown	207485_x_at

**Table S2**

List of genes specifically downregulated in T cells of patients with CLL (n=249)

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
	<b>Receptors</b>			
CD87, PLAUR	plasminogen activator urokinase receptor	0.12	chemotaxis, significantly diminished in diffuse type gastric carcinoma	211924_s_at
CLEC7A, CLECSF12	C-type lectin superfamily member 12	0.13	MHC protein binding, phagocytosis, cell recognition, carbohydrate mediated signaling, <b>T-cell activation</b> , defense response to pathogenic protozoa	221698_s_at
DCIR, CLECSF6	C-type lectin superfamily member 6	0.28	May play a role in modulating DC differentiation and/or maturation. May be involved via its ITIM motif in the inhibition of B-cell-receptor-mediated calcium mobilization and protein tyrosine phosphorylation.	219947_at
CD1d	CD1d antigen	0.14	CD1d (MHCI-like) expressed on APCs, recognized by CD1d-restricted NKT cells	205789_at
CCR1	chemokine (C-C motif) receptor 1	0.14	chemotaxis, inflammatory response, immune response, cell adhesion, G-protein signaling, cell-cell signaling. One of the RANTES receptor.	205098_at
TREM1	triggering receptor expressed on myeloid cells 1	0.14	Expressed in monocytes and neutrophils. Stimulates neutrophil and monocyte-mediated inflammatory responses. Triggers release of pro-inflammatory chemokines and cytokines, as well as increased surface expression of cell activation markers.	219434_at
HBEGF	heparin-binding EGF-like growth factor	0.14	positive regulation of cell proliferation, growth factor activity	38037_at
C5R1, CD88	complement component 5 receptor 1	0.16	C5a receptor, activation of MAPK, chemotaxis, cellular defense response	220088_at
FCAR, CD89	receptor for Fc fragment of IgA	0.18	binds to the Fc region of immunoglobulins alpha, induce cytokine production	207674_at
FCGR2A, CD32	receptor for Fc fragment of IgG, low affinity IIa	0.18	low affinity receptor which binds to the Fc region of immunoglobulins gamma	203561_at
TLR4	Toll-like receptor 4	0.19	cause expression of co-receptor, Cooperates with LY96 and CD14 to mediate the innate immune response	221060_s_at
TLR2	Toll-like receptor 2	0.25	cause expression of co-receptor, Cooperates with LY96 to mediate the innate immune response	204924_at
TLR1	Toll-like receptor 1	0.37	cause expression of co-receptor, participates in the innate immune response to microbial agents	210176_at
FPR, FMLP	Formyl peptide receptor 1	0.19	chemotaxis, NO mediated signal transduction	205119_s_at
CSF1R, CD115	Colony stimulating factor 1 receptor	0.22	receptor for CSF-1, protein tyrosine-kinase	203104_at
LILRB7	Leukocyte immunoglobulin-like receptor, subfamily B, member 7	0.22	receptor activity(with TM and ITIM domains), function unknown	215838_at
LILRA2	Leukocyte immunoglobulin-like receptor, subfamily A, member 2	0.23	may act as receptor (with TM domain) for class I MHC antigens	207857_at
LILRB2	Leukocyte immunoglobulin-like receptor, subfamily B, member 2	0.24	receptor (with TM and ITIM domains) for class I MHC antigens, recognizes a broad spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles, involved in the down-regulation of the immune response and the development of tolerance, expressed on monocytes, B cells, DCs and natural killer cells	207697_x_at
LILRB6	Leukocyte immunoglobulin-	0.35	receptor activity (with TM and ITIM	208594_x_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
	like receptor, subfamily B, member 6		domains), function unknown	
PILRA	Paired immunoglobulin-like type 2 receptor alpha	0.25	strongly expressed in peripheral blood-derived monocytes, granulocytes, and particularly dendritic cells, but not in lymphocytes.	219788_at
CD302	CD302 Ag	0.25	receptor activity, function unknown	203799_at
PTGER3	Prostaglandin E receptor 3 (subtype EP3)	0.25	receptor for PGE2, the activity of this receptor can couple to both the inhibition of adenylate cyclase mediated by G-I proteins, and to an elevation of intracellular calcium	213933_at
CD163, M130	CD163 antigen	0.26	scavenger receptor activity, copper ion binding, involved in myeloid specific gene expression including several alternatively spliced isoforms	203645_s_at
TYROBP, DAP12	TYRO protein tyrosine kinase binding protein	0.27	associates with membrane glycoproteins of the KIR family without an ITIM which results in cellular activation	204122_at
FCER1G	Fc receptor of IgE	0.30	IgE high affinity Fc receptor, gamma polypeptide, expressed in most cells	204232_at
IL1R1, IL1RA	Interleukin 1 receptor, type 1	0.31	Binding to the ligand leads to the activation of NFkB	202948_at
FPR2A, FPRH1	Formyl peptide receptor-like 1	0.31	Expressed abundantly in the lung and neutrophils, also found in the spleen and testis	210772_at
EGF-like module EMR2	Egf-like module containing, mucin-like, hormone receptor-like sequence 2 (CD312 antigen)	0.32	probably involved in cell attachment	
LYN	protein tyrosine kinase Lyn , v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.32	physically linked to AMPA receptor and activated following stimulation of the receptor, then activating the MAP Kinase pathway, highly expressed in the central nervous system	202625_at
C1QR1	complement component 1, q subcomponent, receptor 1	0.32	Receptor for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens.	202878_s_at
GEM	GTP-binding protein overexpressed in skeletal muscle	0.32	possibly participating in receptor-mediated signal transduction at the plasma membrane	204472_at
CCRL2, CKRX	Chemokine (C-C motif) receptor-like 2	0.32	G-protein coupled receptor, chemotaxis	211434_s_at
IL13RA1	Interleukin 13 receptor, alpha 1	0.34	binds IL13 with a low affinity	201887_at
APLP2	Amyloid beta (A4) precursor-like protein 2	0.34	G-protein coupled receptor protein signaling pathway, may play a role in the regulation of hemostasis.	208702_x_at
OLR1	Oxidised low density lipoprotein (oxLDL) (lectin-like) receptor 1	0.35	Its association with oxLDL induces the activation of NFkB through an increased production of intracellular reactive oxygen and a variety of pro- atherogenic cellular responses including a reduction of NO release, monocyte adhesion and apoptosis. In addition to binding oxLDL, it acts as a receptor for the HSP70 protein involved in antigen cross-presentation to naive T-cells in dendritic cells.	210004_at
PTPRE	protein tyrosine phosphatase, receptor type, E	0.38	protein tyrosine phosphatase activity	221840_at
CSF2RB	colony stimulating factor 2 receptor, beta	0.39	High affinity receptor for IL-3, IL-5 and GM-CSF	205159_at
NGFRAP1, NADE	nerve growth factor receptor (TNFRSF16) associated protein 1	0.41	may involve in mediated apoptosis induced by NGF	217963_s_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
TNFRSF1A, TNFR1	tumor necrosis factor receptor superfamily, member 1A	0.43	Receptor for TNF-alpha and lymphotoxin-alpha which can trigger apoptosis. TNFR1 activates at least two distinct signaling cascades, apoptosis and NFkB signaling.	207643_s_at
IFNGR2, IFNGT1	interferon gamma receptor 2 (interferon gamma transducer 1)	0.44	part of the receptor for IFN-gamma	201642_at
SORT1	sortilin 1	0.44	receptor activity, protein transporter activity, G-protein coupled	212807_s_at
IFNGR1	interferon gamma receptor 1	0.48	an integral part of the IFN-gamma receptor	211676_s_at
RXRA	Retinoid X receptor alpha	0.48	Nuclear hormone receptor. Involved in the retinoic acid response pathway. ARF6 acts as a key regulator of the tissue-specific adipocyte P2 (aP2) enhancer (By similarity)	202426_s_at
GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1	0.48	glutamate receptor	212090_at
RARA	retinoic acid receptor, alpha	0.49	steroid hormone receptor, transcription factor activity	203749_s_at
JMJD1C, TRIP8	jumonji domain containing 1C	0.49	thyroid hormone receptor binding, regulation of transcription	221763_at
JMJD3	jumonji domain containing 3	0.49	function unknown	213146_at
	<b>Signaling</b>			
JAG1, AGS	Jagged 1 (Alagille syndrome)	0.12	Angiogenesis, cell communication, Notch signaling pathway, hemopoiesis, regulation of cell migration and proliferation, myoblast and endothelial cell differentiation	209099_x_at
ADM	Adrenomedullin	0.19	signal transduction, cell-cell signaling, cAMP biosynthesis, progesterone biosynthesis	202912_at
CD86, B7-2	CD28 Ag ligand 2	0.22	costimulatory signal essential for T lymphocyte proliferation and IL-2 production	205685_at
OSM	Oncostatin M	0.25	cell-cell signaling, immune response, development, negative regulation of proliferation	214637_at
PLK2	polo-like kinase 2 (Drosophila)	0.32	protein serine/threonine kinase activity, signal transducer	201939_at
RAB31	Ras-associated protein RAB31	0.33	RAS oncogene family, small GTPase mediated signal transduction	217762_s_at
PTPNS1	Protein tyrosine phosphatase, non-receptor type substrate 1	0.34	membrane protein, Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin	202897_at
HCK, JTK9	hemopoietic cell kinase	0.35	protein-tyrosine kinase activity	208018_s_at
PECAM1,CD31	platelet/endothelial cell adhesion molecule	0.35	cell motility, signal transduction	208981_at
HMOX1, HO-1	Heme oxygenase (decycling) 1	0.35	heme oxygenase activity, signal transducer activity	203665_at
IRS2	Insulin receptor substrate 2	0.36	signal transduction, glucose metabolism	209185_s_at
NRGN	Neurogranin	0.37	protein kinase C substrate, RC3	204081_at
BASP1	Brain abundant, membrane attached signal protein 1	0.37	Associated with the membranes of "growth cones" that form the tips of elongating axons, expressed in various tissue at nerve endings, also expressed in testis, kidney, lymphoid organs	202391_at
PRKAR2B	Protein kinase, cAMP-dependent regulatory type II beta	0.38	intracellular signaling cascade	203680_at
CTNNB1	Catenin beta 1	0.40	TGF-Beta Signaling Pathway	201533_at
PBEF1	pre-B-cell colony enhancing factor 1	0.40	cell-cell signaling, positive regulation of cell proliferation	217738_at
SOCS1	suppressor of cytokine	0.40	intracellular signaling cascade, regulation	209999_x_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
	signaling 1		of cell growth, ubiquitin cycle, negative regulation of JAK-STAT cascade, protein kinase inhibitor activity, insulin-like growth factor receptor binding	
SOCS2, CIS2	suppressor of cytokine signaling 2	0.45	regulation of cell growth, anti-apoptosis, JAK-STAT cascade, regulation of signal transduction, positive regulation of neuron differentiation	203373_at
MPP1, PEMP	Membrane protein, palmitoylated 1	0.41	signal transduction, guanylate kinase activity	202974_at
CHMP1B	chromatin modifying protein 1B	0.42	G-protein signaling	218177_at
GNG11	Guanine nucleotide binding protein 11	0.44	G-protein coupled receptor protein signaling pathway	204115_at
APP, AAA	Amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	0.44	signal transduction, copper ion homeostasis, apoptosis, cell adhesion	200602_at
LY96	lymphocyte antigen 96	0.44	inflammatory response, cellular defense response, cell surface receptor linked signal transduction	206584_at
SPHK1	Sphingosine kinase 1	0.45	protein kinase C activation, intracellular signaling cascade, sphingoid catabolism	219257_s_at
RAB1A	RAB1	0.46	small GTPase mediated signal transduction, member of RAS oncogene family	207791_s_at
CORO1C	Coronin actin-binding protein 1C	0.47	Phagocytosis, signal transduction	221676_s_at
ZFYVE16	zinc finger FYVE domain containing 16	0.48	signal transduction, protein-lysosome targeting	203651_at
SGK	serum/glucocorticoid regulated kinase	0.48	protein serine/threonine kinase activity	201739_at
RHOQ, TC10	Ras homolog gene family, member Q	0.39	small GTPase mediated signal transduction	212120_at
NCF4, P40PHOX	Neutrophil cytosolic factor 4 (40kD)	0.49	intracellular signaling cascade, electron transport	207677_s_at
ZYX	Zyxin	0.50	signal transduction, cell-cell signaling, cell adhesion	200808_s_at
	<b>Transcription factors</b>			
MAFB, KRML	V-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	0.13	transcription factor	218559_s_at
SPI1, PU.1	Spleen focus forming virus (SFFV) proviral integration oncogene spi1	0.17	transcription factor essential for the development of myeloid and B-lymphoid cells. Unlike complete or 50% loss, <b>80% loss</b> of PU.1 induced a precancerous state characterized by accumulation of an abnormal precursor pool retaining responsiveness to colony-stimulating factor.	205312_at
FOSL1	FOS-like antigen 1	0.21	transcription factor activity, cell proliferation	204420_at
KLF4	Kruppel-like factor 4	0.24	negative regulation of transcription, mesoderm cell fate determination, negative regulation of cell proliferation	221841_s_at
SOX4	SRY (sex determining region Y)-box 4	0.29	Transcriptional activator that binds with high affinity to the T-cell enhancer motif 5'-AACAAAG-3'	201417_at
CEBPD	CCAAT/enhancer binding protein (C/EBP) delta	0.29	transcriptional activator in the regulation of genes involved in immune and inflammatory responses	213006_at
CEBPB	CCAAT/enhancer binding protein beta	0.46	Specifically binds to an IL-1 response element in the IL-6 gene. CEBPB also binds to regulatory regions of several acute-phase and cytokines genes. It probably plays a role in the regulation of acute-phase reaction, inflammation and hemopoiesis.	212501_at



Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
EGR1, TIS8	Early growth response 1	0.33	Activates the transcription of target genes whose products are required for mitogenesis and differentiation	201694_s_at
HHEX	Hematopoietically expressed homeobox	0.36	transcription factor	215933_s_at
EPAS1	Endothelial PAS domain protein 1	0.37	Transcription factor involved in the induction of oxygen regulated genes. Regulates the vascular endothelial growth factor (VEGF) expression. Potent activator of the Tie-2 tyrosine kinase expression.	200878_at
NRIP1	Nuclear receptor interacting protein 1	0.40	Modulates transcriptional activation by steroid receptors such as NR3C1, NR3C2 and ESR1.	202599_s_at
BACH1	BTB and CNC homology 1, basic leucine zipper transcription factor 1	0.41	Play important roles in coordinating transcription activation and repression by MAFK	204194_at
BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	0.48	Play important roles in coordinating transcription activation and repression by MAFK (By similarity)	221234_s_at
CRK	V-crk avian sarcoma virus CT10 oncogene homolog	0.41	Involved in phagocytosis of apoptotic cells and cell motility via its interaction with DOCK1 and DOCK4	202226_s_at
ETS2	V-ets avian erythroblastosis virus E26 oncogene homolog 2	0.44	activating stromelysin-1 (MMP3) and collagenase 1 (MMP8) promoters, required to maintain the transformed state of human prostate cancer cells	201329_s_at
ZBTB1	zinc finger and BTB domain containing 1	0.45	May be involved in transcriptional regulation	205092_x_at
SCML1	Sex comb on midleg (Drosophila)-like 1	0.45	involved in transcriptional repression of HOX genes	218793_s_at
ZNF557	zinc finger protein 557	0.46	May be involved in transcriptional regulation	220444_at
ZNF571	zinc finger protein 571	0.48	May function as a transcription factor	206648_at
RAI17	Retinoic acid induced 17	0.48	Increases ligand-dependent transcriptional activity of Androgen Receptor and promotes Androgen Receptor sumoylation.	212124_at
LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	0.48	May be involved in sphingolipid synthesis or its regulation (By similarity)	212446_s_at
ELL2	elongation factor, RNA polymerase II, 2	0.49	RNA polymerase II transcription factor activity	214446_at
	<b>Cytokines/Chemokines</b>			
CCL2, MCP1	chemokine (C-C motif) ligand 2	0.05	Chemotactic factor that attracts monocytes and basophils	216598_s_at
CCL7, MCP3	chemokine (C-C motif) ligand 7	0.12	calcium ion homeostasis, chemotaxis, inflammatory response, cell-cell signaling, antimicrobial humoral response	208075_s_at
CXCL1, GRO1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	0.19	chemotactic activity for neutrophils, may play a role in inflammation and exerts its effects on endothelial cells in an autocrine fashion	204470_at
CXCL2, GRO2	chemokine (CXC motif) ligand 2, GRO2	0.22	Hematoregulatory chemokine, which in vitro, suppresses hematopoietic progenitor cell proliferation	209774_x_at
GRN	Granulin	0.25	cytokine activity, growth factor activity, cell-cell signaling, cell proliferation	
TNFSF13 (APRIL)	tumor necrosis factor (ligand) superfamily, member 13	0.27	a proliferation-inducing ligand, a cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA, may be implicated in the regulation of tumor cell growth.	210314_x_at
IL8, CXCL8	Interleukin 8	0.29	IL-8 is a chemotactic factor that attracts neutrophils, basophils, and T-cells, but not monocytes. It is also involved in neutrophil activation.	211506_s_at
CXCL3	chemokine (C-X-C motif) ligand 3	0.31	chemotactic activity for neutrophils, may play a role in inflammation and exert its	207850_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
			effects on endothelial cells in an autocrine fashion	
IL1B	Interleukin 1, beta	0.40	regulation of cell cycle, apoptosis, negative regulation of cell proliferation	205067_at
LARC, CCL20	Small inducible cytokine subfamily A (Cys-Cys), member 20	0.42	chemotactic factor that attracts lymphocytes and, slightly neutrophils	205476_at
IL1RN, IL1RA	interleukin 1 receptor antagonist	0.44	IL-1 antagonist	212657_s_at
PF4V1	Platelet factor 4 variant 1	0.44	Inhibitor of angiogenesis. Inhibitor of endothelial cell chemotaxis	207815_at
	<b>Cell cyle/Proliferation</b>			
MKP3, PYST1	dual specificity phosphatase 6	0.12	regulation of cell cycle, inactivation of MAPK, protein amino acid dephosphorylation, apoptosis	208891_at
EMP1, TMP	epithelial membrane protein 1	0.12	cell-cell interaction, control of proliferation, not found in leukocytes	201324_at
DIF2, IEX1	Immediate early response 3	0.21	anti-apoptosis, cell growth and/or maintenance, morphogenesis	201631_s_at
DUSP6, MKP3	Dual specificity phosphatase 6	0.21	regulation of cell cycle, inactivation of MAPK, protein dephosphorylation, apoptosis	208892_s_at
LST1	leukocyte specific transcript 1	0.29	negative regulation of lymphocyte proliferation	215633_x_at
G0S2	Putative lymphocyte G0/G1 switch gene	0.31	Potential oncogene and regulator of latent HIV, regulation of progression through cell cycle	213524_s_at
EVI5	Ecotropic viral integration site 5	0.38	development, cell proliferation	209717_at
RBBP6	Retinoblastoma-binding protein 6	0.42	regulation of cell cycle	212783_at
BCL2A1, GRS	BCL2-related protein A1	0.45	anti-apoptosis, regulation of apoptosis	205681_at
RNF125	ring finger protein 125	0.46	T-cell RING activation protein 1 (TRAC-1)	207735_at
GADD45A	Growth arrest and DNA-damage-inducible alpha	0.46	regulation of cyclin	203725_at
CDKN1C	Cyclin-dependent kinase inhibitor 1C	0.47	cyclin-dependent protein kinase inhibitor activity, cell cycle arrest	213348_at
CREG1	Cellular repressor of E1A-stimulated genes	0.47	Transcription regulation, regulation of cell growth	201200_at
	<b>Transporters</b>			
SLC31A2, CTR2	Solute carrier family 31 member 2	0.24	copper ion transporters	204204_at
SLC7A11	Solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	0.28	cystine:glutamate antiporter activity	209921_at
SLC25A37	Solute carrier family 25, member 37 (MSCP)	0.34	mitochondrial carrier family	221920_s_at
SLC11A1	Solute carrier family 11 (proton-coupled divalent metal ion transporters) member 1	0.38	Divalent transition metal (iron and manganese) transporter involved in iron metabolism and host resistance to certain pathogens. Macrophage-specific membrane transport function.	210423_s_at
SLC22A4	Solute carrier family 22, member 4 (OCTN1)	0.42	organic cation transporter	205896_at
SLCO4A1, SLC21A12	Solute carrier organic anion transporter family, member 4A1	0.44	Mediates the Na(+)-independent transport of organic anions such as the thyroid hormones T3 (triiodo-L-thyronine), T4 (thyroxine) and rT3, and of estrone-3-sulfate and taurocholate. Transporter activity	219911_s_at
SLC7A7, LPI	Solute carrier family 7, member 7	0.49	cationic amino acid transporter, y+ system	204588_s_at
KCTD12	voltage-gated potassium channel activity	0.16	voltage-gated potassium channel complex	212192_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	0.35	anion transporter, key gatekeeper influencing intracellular cholesterol transport	203505_at
ATP2A2	ATPase, Ca <sup>++</sup> transporting, cardiac muscle, slow twitch 2	0.42	translocation of calcium from the cytosol to the sarcoplasmic reticulum lumen	212361_s_at
VPS37C	vacuolar protein sorting 37C (yeast)	0.46	function unknown	219053_s_at
PGD	Phosphogluconate dehydrogenase	0.47	electron transporter and oxidoreductase activity	201118_at
	<b>Metabolism</b>			
NCF2	Neutrophil cytosolic factor 2 (chronic granulomatous disease, autosomal 2)	0.17	superoxide metabolism, cellular defense response	209949_at
ANPEP, CD13	Alanyl (membrane) aminopeptidase	0.19	Glutathione metabolism, angiogenesis, cell differentiation, defects in this gene appear to be a cause of various types of <b>leukemia or lymphoma</b> . There are some reports about correlation between CD13 and CLL.	202888_s_at
ALDH2	Aldehyde dehydrogenase 2 family	0.24	mitochiorial oxidative pathway of alcohol metabolism	201425_at
TKT	Transketolase (Wernicke-Korsakoff syndrome)	0.30	Pentose-Phosphate-Pathway	208700_s_at
LACS, FACL1	acyl-CoA synthetase long-chain family member 1	0.31	lipid metabolism	201963_at
WARS	Tryptophanyl-tRNA synthetase	0.33	protein metabolism	200628_s_at
SMPDL3A, ASM3A	sphingomyelin phosphodiesterase acid-like 3A	0.35	carbohydrate metabolism	213624_at
VNN2	Vanin 2	0.37	nitrogen compound metabolism	205922_at
PSAP, GLBA	Prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	0.37	lipid metabolism, activator of degradation of sphingolipids	200866_s_at
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase)	0.37	lipid metabolism, hydrolyzes the sphingolipid ceramide	210980_s_at
PLSCR1	phospholipid scramblase 1	0.38	A protein mediating transbilayer movement of plasma membrane phospholipids.	202446_s_at
CA1	Carbonic anhydrase I	0.38	one-carbon compound metabolism, Nitrogen metabolism	205950_s_at
ALOX5	arachidonate 5-lipoxygenase	0.39	electron transport, inflammatory response, leukotriene biosynthesis	214366_s_at
NP, PNP	Nucleoside phosphorylase	0.39	nucleotide metabolism, PNP deficiency causes SCID disease in childhood	201695_s_at
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	0.40	Lipid metabolism, catalyzes the sulfate conjugation of catecholamines, phenolic drugs and neurotransmitters. Mediates the metabolic activation of carcinogenic N-hydroxyarylamines to DNA binding products and could so participate as modulating factor of cancer risk	215299_x_at
PYGL	phosphorylase, glycogen	0.40	glycogen metabolism	202990_at
GLUL, GLNS	Glutamate-ammonia ligase (glutamine synthase)	0.41	glutamate metabolism, regulation of neurotransmitter levels	200648_s_at
NP-C2, HE1	Niemann-Pick disease, type C2 gene	0.44	lipid metabolism	200701_at
FBP1	Fructose-1,6-bisphosphatase 1	0.45	fructose metabolism, neoglucogenesis, energy pathway	209696_at
GERP, TRIM8	tripartite motif-containing 8	0.45	protein ubiquitination	221012_s_at
GSTO1	glutathione S-transferase omega1	0.48	glutathione-dependent thiol transferase and dehydroascorbate reductase activities	201470_at
RNF184, msl-2	ring finger protein 184	0.48	protein ubiquitination	218733_at
PFKFB3, IPFK2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3	0.48	synthesis and degradation of fructose 2,6-bisphosphate	202464_s_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
TMEM23	transmembrane protein 23	0.48	lipid metabolism, converting phosphatidylcholine (PC) and ceramide to sphingomyelin (SM) and diacylglycerol (DAG) and vice versa	212989_at
LTA4H	Leukotriene A4 hydrolase	0.49	leukotriene biosynthesis, epoxide hydrolase, peptidase, metallopeptidase	208771_s_at
RNMT	RNA (guanine-7-) methyltransferase	0.49	mRNA capping	202684_s_at
GM2A, SAP-3	GM2 ganglioside activator	0.50	lipid metabolism, stimulates ganglioside GM2 degradation	33646_g_at
PISD, PSSC	Phosphatidylserine decarboxylase	0.50	phospholipid biosynthesis	202392_s_at
	<b>Adhesion molecules</b>			
FCNM, FCN1	Ficolin (collagen/fibrinogen domain-containing) 1	0.17	Phosphate transport, heterophilic cell adhesion, opsonization	205237_at
CSPG2	chondroitin sulfate proteoglycan 2	0.18	heterophilic cell adhesion, development, cell recognition	221731_x_at
C1orf38, ICB-1	chromosome 1 open reading frame 38	0.22	function unknown	207571_x_at
TGFBI, CSD	Transforming growth factor, beta-induced, 68kD	0.26	cell adhesion, negative regulation of cell adhesion, visual perception, cell proliferation	201506_at
	<b>Cytoskeletal</b>			
TUBB-5	Tubulin beta-5	0.22	the major constituent of microtubules	209191_at
BANK1	B-cell scaffold protein with ankyrin repeats 1	0.24	BANK regulates BCR-induced calcium mobilization by promoting tyrosine phosphorylation of IP3 receptor.	219667_s_at
EPB41L3	erythrocyte membrane protein band 4.1-like 3	0.28	actin binding structural molecule	212681_at
TPM4	Tropomyosin 4	0.44	In non-muscle cells is implicated in stabilizing cytoskeleton actin filaments	209344_at
CKAP4	cytoskeleton-associated protein 4	0.50	membrane protein	200998_s_at
	<b>Growth factor</b>			
VEGFA	Vascular endothelial growth factor	0.39	Induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels.	210512_s_at
EREG	Epiregulin	0.41	as a mitogen it may stimulate cell proliferation and/or angiogenesis	205767_at
ECGF1	Endothelial cell growth factor 1 (platelet-derived)	0.45	growth promoting activity on endothelial cells, angiogenic activity in vivo and chemotactic activity on endothelial cells in vitro	204858_s_at
	<b>Others</b>			
CD14	CD14 antigen	0.09	Monocyte differentiation Ag	201743_at
PI	protease inhibitor	0.13	deficiency of this gene is associated with emphysema and liver disease	211429_s_at
S100A12	S100 calcium-binding protein A12 (calgranulin C)	0.15	Family of S100 proteins comprises the largest group of calcium-binding proteins. Regulating enzyme activities, the dynamics of cytoskeleton constituents, cell growth and differentiation, and Ca(2+) homeostasis.	205863_at
MIF, NIF	S100 calcium-binding protein A9 (calgranulin B)	0.21	cell-cell signaling, inflammatory response	203535_at
S100C, MLN70	S100 calcium-binding protein A11 (calgizzarin)	0.30	pro-inflammatory molecules	200660_at
S100A8	S100 calcium-binding protein A8 (calgranulin A)	0.45	pro-inflammatory molecules	202917_s_at
THRM, CD141	Thrombomodulin	0.16	blood coagulation	203887_s_at
CYP1B1, CP1B	Cytochrome P450, subfamily I	0.16	monooxygenase activity	202437_s_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
	(dioxin-inducible), polypeptide 1			
IFI30	Interferon gamma-inducible protein 30	0.19	MHC class II-restricted antigen processing (enzyme)	201422_at
CYP3	Peptidylprolyl isomerase F (cyclophilin F)	0.21	protein folding	201489_at
TRIB1	tribbles homolog 1 (Drosophila)	0.22	protein kinase activity, ATP binding, cell proliferation	202241_at
CSPG2	Chondroitin sulfate proteoglycan 2 (versican)	0.23	development, cell recognition	204620_s_at
CYBB, CGD	Cytochrome b-245, beta polypeptide	0.24	Ferric_reduct;oxidoreductase activity, involved in chronic granulomatous disease	203923_s_at
CST3	Cystatin C	0.25	cystatin;cysteine protease inhibitor activity, involved in amyloid angiopathy and cerebral hemorrhage	201360_at
SNCA	synuclein alpha	0.27	anti-apoptosis	204466_s_at
BRAG	B cell RAG-associated protein	0.27	B cell surface signaling receptor molecule	203066_at
CSTA, STFA	Cystatin A (stefin A)	0.28	intracellular cysteine protease inhibitor activity	204971_at
IGHA1, IGH A2	immunoglobulin heavy constant alpha 1 and 2	0.29	MHC-I receptor	217022_s_at
FLJ20273	RNA binding protein	0.29	RNA binding protein	218035_s_at
DMXL2	Dmx-like 2	0.29	function unknown	212820_at
CTSS	Cathepsin S	0.29	protease, specifically involved in MHCII-associated chain processing and peptide loading	202902_s_at
CTSL	Cathepsin L	0.30	protease, important for Ag presentation & the overall degradation of proteins in lysosomes	202087_s_at
CTSB	Cathepsin B	0.35	protease, participate in intracellular degradation and turnover of proteins, also implicated in tumor invasion and metastasis	200838_at
CTSZ	Cathepsin Z	0.43	protease, involved in normal intracellular degradation	210042_s_at
LGALS3, GALIG	Lectin galactoside-binding, soluble, 3 (galectin 3)	0.30	regulating the homeostasis and functions of the immune cells	208949_s_at
KYNU	Kynureninase (L-kynurenine hydrolase)	0.31	Increased levels in several cerebral and systemic inflammatory conditions	217388_s_at
PHLDA1, TDAG51	pleckstrin homology-like domain family A member 1	0.31	seems to be involved in regulation of apoptosis, former name T-cell death-associated gene 51 protein	217997_at
PHLDA2	pleckstrin homology-like domain, family A, member 2	0.40	imprinting, apoptosis	209803_s_at
RNF130, G1RZFP	ring finger protein 130	0.31	may have a role during the apoptosis of hematopoietic cells (By similarity)	217865_at
SNCA, PD1	Synuclein, alpha	0.32	anti-apoptosis, may be involved in the regulation of dopamine release and transport	207827_x_at
CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	0.32	function unknown	221541_at
PTGS2, COX2	prostaglandin-endoperoxide synthase 2	0.34	may be a major mediator of inflammation and/or a role for prostanoid signaling in activity-dependent plasticity	204748_at
PTGS1, COX1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.50	may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells	205128_x_at
SERPIN2, PAI2	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	0.34	Inhibits urokinase-type plasminogen activator. Monocyte derived.	204614_at
IgJ	immunoglobulin J polypeptide	0.35	linker protein for immunoglobulin alpha and mu polypeptides	212592_at
HBD	Hemoglobin, delta	0.36	O <sub>2</sub> transporter	206834_at
GPX1, GSHPX1	Glutathione peroxidase 1	0.36	free radical detoxification	200736_s_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
GPX3	glutathione peroxidase 3 (plasma)	0.47	protects cells and enzymes from oxidative damage	214091_s_at
TIMP1, EPO	Tissue inhibitor of metalloproteinase 1	0.38	collagenase inhibitor, mediates erythropoiesis in vitro, development, positive regulation of cell proliferation, erythrocyte maturation	201666_at
IGLJ3	Immunoglobulin lambda joining 3	0.39	part of Ig genes	214677_x_at
SCO2	SCO (cytochrome oxidase deficient, yeast) homolog 2	0.40	electron transport	205241_at
SOD2	superoxide dismutase 2 (mitochondrial)	0.41	free radical detoxification	215223_s_at
ABHD5, CGI58	abhydrolase domain containing 5	0.42	aminopeptidase activity, proteolysis	213805_at
IGLC1	immunoglobulin lambda constant 1	0.42	lambda light chain	215121_x_at
RAB11FIP1	RAB11 family interacting protein 1 (class I)	0.42	Rab11 effector protein involved in the endosomal recycling process. Also involved in controlling <b>membrane trafficking</b> along the phagocytic pathway and in phagocytosis	219681_s_at
HBG2	Hemoglobin gamma G	0.43	fetal hemoglobin	204419_x_at
SNN	Stannin	0.43	Plays a role in the toxic effects of organotins	218033_s_at
LMO2, TTG2	LIM domain only 2, T-cell translocation protein 2	0.43	exists in nucleus and involved in association with LMO1 (and others) in the formation of multimeric DNA-binding complex for the generation of hematopoietic lineages and angiogenesis (in mice)	204249_s_at
SCPEP1, HSCP1	serine carboxypeptidase 1	0.44	Proteolysis and peptidolysis. May be involved in vascular wall and kidney homeostasis (By similarity)	218217_at
F13A	coagulation factor XIII, A1 polypeptide	0.45	coagulation	203305_at
FGL2, T49, pT49	Fibrinogen-like 2	0.45	T-cell specific. May play a role in physiologic lymphocyte functions at mucosal sites	204834_at
MMP25	membrane matrix metalloproteinase 25	0.46	proteolysis, exist in extracellular matrix, may activate progelatinase A	207890_s_at
APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A, Phorbol-in-1	0.46	molecular function unknown	210873_x_at
APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	0.50	Binds to apoB and AU-rich RNAs, molecular function unknown	206632_s_at
QKI	QKI protein	0.46	quaking homolog, KH domain RNA binding (mouse)	212636_at
NAGA, GALB	N-acetylgalactosaminidase, alpha-	0.46	lysosomal protein, Hydrolysis of terminal non-reducing N-acetyl- D-galactosamine residues in N-acetyl-alpha-D-galactosaminides	202944_at
CD248, TEM1	CD248 antigen, endosialin	0.46	may play a role in tumor angiogenesis, single-pass type I membrane protein, extracellular matrix complex	219025_at
PTX3	pentaxin-related gene	0.47	regulation of innate resistance to pathogens, inflammatory reactions, induced by IL-1 $\beta$ and TNF- $\alpha$	206157_at
NRIP3	nuclear receptor interacting protein 3	0.47	molecular function unknown	219557_s_at
NAT-1, AAC1	N-acetyltransferase 1	0.48	detoxification of a plethora of hydrazine and arylamine drugs, widely expressed, involved in bladder carcinogenesis	214440_at
RP2	Retinitis pigmentosa 2 (X-linked recessive)	0.48	beta-tubulin folding, visual perception	205191_at
PPP1R10	Protein phosphatase 1,	0.48	Inhibitor of PPP1CA and PPP1CC	201703_s_at

Gene Symbol	Gene Name	Fold decrease	Description/Function(s)	Probe set ID
	regulatory subunit 10		phosphatase activities	
DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	0.50	heat shock protein	209015_s_at
FBN2	Fibrillin 2	0.50	morphogenesis, extracellular matrix Ca <sup>2+</sup> binding, early process of elastic fiber assembly	203184_at
	<b>Unknown</b>			
FLJ22662	Hypothetical protein FLJ22662	0.24	function unknown	218454_at
CEP76	centrosomal protein 76kDa	0.40	function unknown	52285_f_at
FAM49A	Family with sequence similarity 49, member A	0.43	function unknown	209683_at
C15orf39	chromosome 15 open reading frame 39	0.45	function unknown	215087_at
ROGDI	rogdi homolog (Drosophila)	0.45	function unknown	218394_at
C18orf1	Chromosome 18 open reading frame 1	0.46	integral to membrane, function unknown	207996_s_at
MGC14376	Hypothetical protein MGC14376	0.47	function unknown	214696_at
ANKRD12	ankyrin repeat domain 12	0.49	nucleous protein, function unknown	212286_at