Supplimentary Data:
Title: Gene Set Enrichment Analysis Identifies LIF as a Negative Regulator of human Th2 Cell Differentiation
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Supplemenatry Table IA

Symbol	**BKL description**
AIRE	Autoimmune regulator; a transcription regulator; acts in hemopoiesis; downregulated in Omenn syndrome; acts as an autoantigen in Addison disease; thyroiditis; and premature menopause; gene mutations causes alopecia areata and polyendocrinopathies
AK3	Adenylate kinase 3; plays a role in nucleotide phosphorylation
AK3L1	Adenylate kinase 3-like 1; may be involved in energy metabolism and nucleotide phosphorylation
ALOX5AP	Arachidonate 5-lipoxygenase-activating protein; involved in leukotriene synthesis; decreased expression correlates with HIV infections; increased mRNA expression correlates with proteinuria associated with IgA and membranoproliferative glomerulonephritis
ANG	Angiogenin ribonuclease RNase A family 5; an antimicrobial protein that acts in angiogenesis; upregulated in anoxia; synovitis; amyotrophic lateral sclerosis; endometriosis; arterial occlusive diseases; Waldenstrom macroglobulinaemia; and several cancers
ANTXR2	Anthrax toxin receptor 2; binds to antigen moiety of anthrax toxin; may function in blood vessel development and female reproduction; gene mutations are associated with juvenile hyaline fibromatosis and infantile systemic hyalinosis
APOL6	Apolipoprotein L6; a lipid binding protein that induces mitochondria-mediated apoptosis characterized by mitochondrial release of cytochrome c and activation of various caspases; contains a Bcl 2 homology (BH) 3 domain
ARMC9	Armadillo repeat containing 9 (melanomamelanocyte specific protein KU-MEL-1); a tumor antigen in melanoma; Vogt Koyanagi Harada disease; and some cancers including brain; esophageal; colon; and chronic myelogenous leukemia
ASCL2	Achaete-scute complex homolog 2; a putative transcription factor that plays a role in cell proliferation; may play a role in histone H3-K4 methylation and in utero embryonic development
ATP8B4	Protein with high similarity to aminophospholipid ATPase transporter (human ATP8B1); which is a predicted phospholipid-translocating ATPase that is associated with familial intrahepatic cholestasis in which there is impaired bile flow
BACE2	Beta-site APP-cleaving enzyme 2; an aspartic-type protease that acts in APP processing; expression is upregulated in sporadic inclusion-body myositis; Down syndrome; liver-; breast-; and colon neoplasms; expression plays a role in Alzheimer
BFSP1	Beaded filament structural protein 1 (filensin); an intermediate filament protein specific to the lens; associates with phakinin (BFSP2) to form the beaded filament
BSPRY	B-box and SPRY-domain containing (zetin-1); exhibits protein binding activity; a testis-specific member of the Ro-Ret family that contains a B-box and a SPRY domain and a 14-3-3 consensus interaction motif
C1orf21	Protein of unknown function; has very strong similarity to uncharacterized mouse 1700025G04Rik
C6orf173	Chromosome 6 open reading frame 173 (cancer upregulated gene 2); a nuclear protein that may act as a transcption factor; cellular overexpression induces a cancer-specific; tumorigenic phenotype; increased expression is observed in multiple cancer types
C8orf85	Protein of unknown function; has high similarity to uncharacterized A5D3 protein (rat Aard); which may be involved in postnatal lung development and spermatogenesis
CABLES1	Cdk5 and Abl enzyme substrate 1; regulates endometrial cell proliferation; decreased expression is associated with endometrial hyperplasia; loss of expression is associated with head and neck squamous cell carcinoma; lung cancer; and colon adenocarcinoma
CBS	Cystathionine-beta-synthase; binds to pyridoxal phosphate; plays a role in cysteine metabolic process; upregulated in Down syndrome; gene polymorphisms are associated with cardiovascular disease and homocystinuria
CCR1	Chemokine receptor-1; acts in G protein signaling; metastasis; and leukocyte chemotaxis; aberrant expression correlates with multiple sclerosis; hypersensitivity; hepatitis C and HIV infections; granulomatous and Alzheimer diseases; and Hodgkin lymphomas
CCR8	Chemokine receptor 8; a G protein-coupled receptor that elevates intracellular Ca2+ flux; functions in cell adhesion and chemotaxis; may play a role in antiapoptosis; aberrant expression correlates with asthma and pulmonary sarcoidosis
CD1C	CD1c molecule; presents bacterial glycolipid and microbial lipid antigens to T cells; involved in cellular defense responses and cytokine production; decreased expression correlates with non-Hodgkin lymphoma; skin neoplasms; and melanoma
CD86	CD86 antigen; a CD28 and CTLA-4 ligand; promotes IL-2 production and phosphatidylinositol-3-kinase activation; acts in T-cell costimulation; aberrant expression correlates with multiple sclerosis; asthma; Hodgkin disease; and inflammatory bowel disorders
CHDH	Choline dehydrogenase; involved in response to nutrient; may play a role in choline metabolic process; single nucleotide polymorphisms are associated with breast cancer risk
CHST2	Carbohydrate sulfotransferase 2; catalyze the transfer of sulfate from 3-prime-phosphoadenosine 5-prime-phosphosulfate to position 6 of a nonreducing N-acetylglucosamine residue; aberrant mRNA expression correlates with colonic neoplasms and endometriosis
CLGN	Calmegin; a putative testis specific chaperone that may play a role in male infertility; may cause protein folding
CLIC4	Chloride intracellular channel 4; a putative actin binding protein that may play a role in apoptosis and maintenance of apical basal membrane polarity; gene expression is downregulated in ovary; breast; and kidney cancers
CLIC6	Chloride intracellular channel 6; a putative voltage-gated chloride channel protein that may play a role in chloride transport; expressed in the pancreas; placenta; liver and brain
CLU	Clusterin; a cholesterol transporter that acts in antiapoptosis; cytolysis; and cell adhesion; gene mutation causes nephrotic syndrome; mRNA is overexpressed in retinitis pigmentosa; mouse Clu is associated with chronic glomerular kidney disease
CPNE2	Protein with high similarity to copine III (human CPNE3); which is a member of the copine family of phospholipid binding proteins; may play a role in membrane trafficking; displays protein kinase activity; contains two C2 domain
CTNNA1	Catenin alpha 1; an actin binding and bundling protein that binds to CDH1; CTNNB1; and JUP; may act in cell-cell adhesion; mutations in gene causes colon cancer; decreased mRNA level correlates with acute myeloid leukemia and myelodysplastic syndrome
CXCR6	Chemokine (C-X-C motif) receptor 6; a coreceptor that acts in cell-cell adhesion; cytokine production; I-kappaB kinase - NF-kappaB cascade; leukocyte chemotaxis; and regulation of cell adhesion mediated by integrin; upregulated in prostate cancer
CYB5R2	NAD(P)H-dependent cytochrome b5 reductase-like b5R.2; a putative cytochrome b5 reductase which contains consensus motifs for FAD and NAD(P)H binding
DBN1	Drebrin 1; an actin binding protein that may play a role in dendrite development; memory; and neuron differentiation; aberrant expression is associated with basal and squamous cell carcinoma; Alzheimer disease; and Down syndrome
DFNA5	Deafness autosomal dominant 5; may play a role in caspase activation; cell proliferation; and cell cycle arrest; gene mutation causes non syndromic hearing loss; downregulated in breast and colorectal cancers; and melanoma
DNAH14	Dynein axonemal heavy polypeptide 14; a putative microtubule motor protein that may function in the movement of cilia and flagella
DPF3	D4 zinc and double PHD fingers family member 3; a predicted transcription modulator that contains a d4 zinc-finger domain
EAF2	ELL associated factor 2; a transcriptional activator that plays a role in the induction of apoptosis; decreased mRNA expression correlates with prostate cancer
ENTPD1	Ectonucleoside triphosphate diphosphohydrolase 1; an ATPase that acts in cell adhesion; angiogenesis; and leukocyte chemotaxis; aberrant expression is associated with Hodgkin disease; B-cell leukemia; multiple sclerosis; pancreatitis; and HIV infections
FAM110C	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
FAM40B	Member of the N1221-like protein family; has strong similarity to uncharacterized mouse D330017J20RIK
FES	Feline sarcoma oncogene; a protein tyrosine kinase that is involved in cytokine mediated signal transduction; myeloid cell differentiation; and macrophage differentiation; aberrant expression correlates with lung neoplasms and adenocarcinoma
FGFR1	Fibroblast growth factor receptor 1; a putative protein tyrosine kinase that acts in cell proliferation and skeletal development; protein expression is upregulated in Alzheimer disease and lung and various neoplasms; gene mutation causes Pfeiffer syndrome

FGFRL1	Fibroblast growth factor receptor-like 1; exhibits protein homodimerization activity; regulates cell adhesion; may be involved in regulation of cell differentiation and cell proliferation
FREQ	Frequenin homolog; a calcium-binding protein that binds and modulates the activity of KV4 K+ channels and regulates dopamine induced D2 receptor internalization and phosphorylation; overexpressed in schizophrenia and bipolar disorder
FURIN	Furin (paired basic amino acid cleaving enzyme); acts in chemokine metabolism; overexpressed in oral tongue squamous cell carcinoma; increased activity correlates with cystic fibrosis; gene is aberrantly expressed in Alzheimer disease and breast neoplasm
FUT7	Fucosyltransferase 7 (alpha (1;3) fucosyltransferase); forms the sialyl Lewis x moiety and functions in the glycosylation of selectin ligands; increased expression may be associated with adenocarcinoma and lung neoplasms
GALNT3	polypeptide N-acetylgalactosaminyltransferase 3; acts in cell differentiation and is involved in response to chemical stimulus; aberrant expression correlates with several cancers; missense mutations in the gene cause familial tumoral calcinosis
GJB2	Connexin 26; a gap junction channel that acts in apoptosis; cell-cell signaling; and epidermis development; inhibits cell differentiation and growth; gene mutation is associated with deafness; Bart Pumphrey syndrome; and palmoplantar keratoderma
GNG4	Guanine nucleotide binding protein gamma 4; a putative GTPase that plays a role in the regulation of adenylyl cyclase activity; may act in G protein-coupled receptor protein signaling pathway
GPR34	G protein-coupled receptor 34; a GPCR that binds lysophosphatidylserine to inhibit intracellular cAMP levels and stimulate ERK phosphorylation; likely positively regulates mast cell degranulation
GPR56	G protein-coupled receptor 56; a transcription activator that acts in cerebellum development; upregulated in esophageal cancer; gene mutations correlate with polymicrogyria and nervous system disorders; mouse Gpr56 is associated with neuronal ectopia
GPT2	Glutamic pyruvate transaminase 2; catalyzes the reversible transamination between alanine and 2-oxoglutarate to form pyruvate and glutamate; may play a role in gluconeogenesis and fatty acid metabolism
GZMB	Granzyme B; functions in extracellular matrix remodeling via cleavage of vitronectin; fibronectin; and laminin; overexpressed in rheumatoid arthritis; leukemia; melanoma; Hepatitis B and C; Sjogren syndrome; mycosis fungoides; Hodgkin disease; and asthma
HES1	Hairy and enhancer of split 1; a transcriptional repressor that plays a role in Notch signaling pathway; neurogenesis; and organ development; regulates cell fate and apoptosis; gene is upregulated in meningioma; medulloblastoma; and Down syndrome
HIP1	Huntingtin interacting protein 1; acts in androgen receptor signaling; antiapoptosis; and actin cytoskeleton organization and biogenesis; upregulated in non Hodgkin and Hodgkin lymphomas and prostrate and colon cancers
HS6ST1	Heparan sulfate 6-O-sulfotransferase 1; a putative plasma membrane associated protein that is involved in heparan sulfate proteoglycan biosynthetic process
IGKC	
IGKC	Immunoglobulin kappa light chain constant region; a portion of the mature immunoglobulin molecule; likely plays a role in determining antigen binding specificity; associated with B cell chronic lymphocytic leukemia and amyloidosis upon mutation
IL10	Interleukin 10; regulates inflammatory response; aberrant expression is associated with diabetes; rheumatoid arthritis; HIV infections; pelvic inflammatory disease; psoriasis; graft versus host disease; and several neoplasms
IL12RB2	Interleukin 12 receptor beta 2; binds to SOCS3; mediates T cell differentiation; expression is increased in diabetes; multiple sclerosis; and tuberculoid leprosy; increased gene expression correlates with paraparesis; Crohn disease; and tuberculosis
IL2RA	Interleukin 2 receptor alpha; plays a role in regulation of T cell mediated immune response; expression is altered in several neoplasms; immune system and inflammatory diseases; Parkinson disease; asthma; and type I diabetes mellitus
IL3RA	Interleukin 3 receptor alpha; plays a role in cell proliferation and histamine release; may be involved in antiapoptosis and B-cell differentiation; aberrantly expressed in leukemia; HIV infection; atopic dermatitis; breast and skin neoplasms
ITGA1	Integrin alpha 1; binds to cell adhesion molecule; mediates matrix-cell adhesion; angiogenesis; cartilage development; and wound healing; aberrantly expressed in multiple sclerosis; female infertility; psoriasis; and rheumatoid arthritis; and many cancers
ITGAX	Integrin alpha X; plays a role in B cell differentiation; aberrant protein expression is associated with rheumatoid arthritis; Crohn disease; granulomatous disease; leukemia; psoriasis; pyoderma gangrenosum; HIV infections; and multiple sclerosis
ITM2C	Protein with strong similarity to integral membrane protein 2C (mouse Itm2c); which exhibits regulated expression in brain following treatment with the Chinese medicine Huang Lian Jie Du decoction; contains a BRICHOS domain
ITPKA	Inositol 1 4 5 trisphosphate 3 kinase A; plays a role in inositol and derivative phosphorylation; may play a role in cellular calcium ion homeostasis; protein expression is downregulated in oral squamous cell carcinoma
JAKMIP1	Janus kinase and microtubule interacting protein 1; binds RNA; GABA receptors; Janus kinases; and microtubules; regulates microtubule bundle formation; abnormal expression in lymphoblastoid cells may correlate with autism spectrum disorders
KCNK1	Potassium channel subfamily K member 1; a disulfide-linked homodimeric channel that may control background K+-mediated membrane conductance; gene overexpression correlates with dementia associated with acquired immunodeficiency syndrome (AIDS)
KIAA1211	Protein of unknown function; has high similarity to uncharacterized mouse C530008M17Rik
KIF5C	Kinesin family member 5C; interacts with GRIF1 and rat kinesin light chain (KLC); may play a role in microtubule-based movement
LAMB3	Laminin beta 3; plays a role in cell adhesion and in hemidesmosome formation; downregulation correlates with prostatic neoplasms; aberrant expression of mRNA correlates with adenocarcinoma and glioma; gene mutation causes junctional epidermolysis bullosa
LAT2	Linker for activation of T cells family member 2; a signal transducer that binds to GRB2; promotes mast cell degranulation; inhibits ERK phosphorylation and TNF and IL8 production; gene haploinsufficiency correlates with Williams syndrome
LIF	Leukemia inhibitory factor; a transcription coactivator that activates MAPK activity and acts in stem cell expansion; ossification; inflammatory response; and antiapoptosis; upregulated in arthritis; arteriosclerosis; septic shock; and bone neoplasms
LMNB1	Lamin B1; a structural constituent of cytoskeleton that acts in chromosome and nuclear envelope organization; apoptosis; lung development; and ossification; acts as autoantigen in chronic fatigue syndrome; aberrantly expressed in colonic neoplasms
LONRF2	Protein containing four type 2 tetratricopeptide repeats; has moderate similarity to uncharacterized human LONRF3
LRP12	Low density lipoprotein-related protein 12; member of the LDLR superfamily; a putative cell surface receptor that may function in signaling pathways or endocytosis; upregulated expression may have a role in oral squamous cell carcinoma
LTK	Leukocyte tyrosine kinase; binds to p85 subunit of phosphatidylinositol 3-kinase and regulates cell proliferation; mRNA expression is upregulated in acute myeloid leukemia; gene polymorphism is associated with systemic lupus erythematosus
LYN	Homolog of v-yes-1 Yamaguchi sarcoma viral related oncogene; a protein tyrosine kinase that acts in apoptosis; cytokine-mediated signaling pathway; leukocyte chemotaxis; and phagocytosis; upregulated in squamous cell carcinoma and several other neoplasms
MAMLD1	Mastermind-like domain containing 1; exhibits transcription coactivator activity at the HES3 promoter; augments testosterone production; gene mutations cause isolated hypospadias of varying severity
MAP3K8	Mitogen activated protein kinase kinase kinase 8; a protein serine threonine kinase that plays a role in interleukin 1 beta production; regulates protein amino acid autophosphorylation; mRNA expression is upregulated in breast and stomach neoplasms
MCTP2	Multiple C2-domains with two transmembrane regions 2; contains three C2 domains which bind calcium but not phospholipids
MIAT	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
MYB	Homolog of v-myb myeloblastosis viral oncogene; a transcription activator that mediates G1-S mitotic transition; erythrocyte differentiation; and regulation of myeloid cell differentiation; upregulated in breast and several other neoplasms
MYO1E	Myosin IE; an ATPase that associates with actin and calmodulin; binds to rat Dnm1; rat Dnm2; and rat Dnm3; plays a role in receptor-mediated endocytosis; may be involved in actin filament based movement
MYOF	Fer-1-like 3; binds to phospholipids; involved in myoblast fusion; endocytic recycling; and plasma membrane repair; activates protein phosphorylation and vascular permeability; regulates gene expression; mouse Fer1l3 is associated with muscular dystrophy
NANOS3	
NDFIP2	Nedd4 family interacting protein 2; binds to ubiquitin protein ligase NEDD4; may play a role in regulating EGFR trafficking; expression is regulated by a calcineurin-mediated pathway and is induced in activated T cells
NKD2	Naked cuticle homolog 2; a cytokine binding protein that mediates protein targeting to membrane; may inhibit Wnt receptor signaling; may play a role in cell fate determination; gene upregulation is associated with malignant peripheral nerve sheath tumors
NKG7	Natural killer cell group 7 sequence; may play a role in immune response and release of cytoplasmic granules from lymphocytes and neutrophils following target cell recognition; corresponding gene is downregulated in Sezary syndrome and mycosis fungoides
P4HA2	Prolyl 4-hydroxylase alpha polypeptide II; exhibits protein heterodimerization activity; acts in peptidyl-proline hydroxylation; may play a role in blood vessel; cartilage; and kidney development; increased mRNA expression correlates with osteoarthritis
PAICS	AIR carboxylase; a putative phosphoribosylaminoimidazole carboxylase and succinocarboxamide synthase; forms octamers; aberrant gene expression is associated with lung squamous cell carcinoma and acute lymphoblastic leukemia
PCDH8	Protocadherin 8; may play a role in cell-cell signaling and expressed in brain

PDE4A	Phosphodiesterase 4A; an cAMP-specific phosphodiesterase that is sensitive to the antidepressant rolipram; acts in signal transduction; may regulate T cell proliferation
PDGFRB	Platelet-derived growth factor receptor beta polypeptide; a protein-tyrosine kinase that acts in GPCR pathway and induces cell proliferation and metastasis; upregulated in several cancers; translocation correlates with myeloproliferative disorders
PFKFB4	6-phosphofructo-2-kinase-fructose-2-6-biphosphatase 4; synthesizes and degrades fructose-2;6-bisphosphate and may be involved in the regulation of glycolysis; corresponding gene expression is upregulated in breast and colon malignant tumors
PHLDA1	Pleckstrin homology-like domain family A member 1; acts in ribosome biogenesis and apoptosis; downregulated in metastatic melanoma and upregulated in intractable epilepsy; mouse Phlda1 is associated with mouse model of atherosclerosis
PLA2G16	Phospholipase A2 group XVI; induces apoptosis; plays a role in the regulation of Ras GTPase activity; aberrant mRNA expression correlates with non small cell lung carcinoma and psoriasis
PLA2G4A	Phospholipase A2 group IVA; plays a role in platelet activating factor biosynthetic process; gene is upregulated in Alzheimer disease and esophageal squamous cell carcinoma; gene polymorphism is associated with type 2 diabetes mellitus
POU2AF1	POU class 2 associating factor 1; a transcriptional coactivator that plays a role in the regulation of cell proliferation and transcription; decreased expression of mRNA correlates with Hodgkin's disease and lymphoma
PPFIBP1	PTPRF interacting protein binding protein 1; binds to alpha liprins and LAR family transmembrane protein tyrosine phosphatases; may play a role in cell adhesion
PRDM1	PR domain containing 1 with ZNF domain; a transcriptional repressor that acts in myeloid cell differentiation; placenta development; and T cell homeostasis; aberrant expression correlates with multiple myeloma; gene mutation causes B-cell lymphoma
RAB11FIP5	RAB11 family interacting protein 5; binds kinesin II to regulate endocytic protein recycling; also a component of a complex containing gamma SNAP (NAPG) and gamma tubulin; may act as an autoantigen in neonatal lupus erythematosus and Sjogren syndrome
RAB32	RAB32 member RAS oncogene family; a GTPase and an anchor protein that plays a role in mitochondrial membrane organization; hypermethylation of the corresponding gene is associated with colonic neoplasms and gastric and endometrial adenocarcinomas
RCAN2	Regulator of calcineurin 2; a phosphoprotein phosphatase inhibitor that acts in calcineurin-NFAT signaling pathway; learning; locomotory behavior; and cardiac muscle hypertrophy; negatively regulates T cell mediated cytotoxicity
RGS18	Regulator of G protein signaling 18; interacts with heterotrimeric G protein G(i) and G(q) alpha subunits; attenuates signaling through G protein-coupled receptors; may be involved in megakaryocyte differentiation; platelet activation; and chemotaxis
RNF213	Protein containing a C3HC4 type (RING) zinc finger; which may mediate protein-protein interactions
RPL7L1	Protein containing a ribosomal L30p or L7e domain; has moderate similarity to ribosomal protein L7 (mouse RPL7); which is an RNA-binding putative ribosomal structural component that may play a role in protein biosynthesis
RUNX2	Runt-related transcription factor 2; acts in odontogenesis; upregulated in arteriosclerosis and calcinosis; gene mutation causes cleidocranial dysplasia; mouse Runx2 is associated with dysplasia; osteopenia; and diabetes
SETBP1	SET binding protein 1; may play a role in cell proliferation and regulation of protein binding; fusion of the corresponding gene with NUP98 gene correlates with T cell acute lymphoblastic leukemia
SHROOM1	Protein of unknown function; has high similarity to uncharacterized mouse Shroom1
SIGLECP3	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
SLC27A2	Solute carrier family 27 (fatty acid transporter) member 2; a long-chain-fatty-acid-CoA ligase that is involved in peroxisomal beta oxidation; decreased protein activity correlates with X-linked adrenoleukodystrophy
SLC2A8	Solute carrier family 2 member 8; a glucose transporter that interacts with beta2 adaptin subunit of the AP 2 adaptor complex (AP2M1); acts in carbohydrate metabolism
SLC7A5	Solute carrier family 7 (cationic amino acid transporter y+ system) member 5; forms a heterodimer with SLC3A2; involved in leucine; tryptophan; organomercurial; and drug transport; overexpressed in lung carcinoma and in brain and colon neoplasms
SPIRE1	Spire homolog 1; sequesters four G-actin subunits to nucleate; sever; and cap filaments at their barbed ends
SPN	Sialophorin; a transmembrane receptor that acts in MAPK cascade; cell adhesion; apoptosis; immunity; and chemotaxis; abnormally glycosylated in HIV infection; aberrantly expressed in Alzheimer disease; Wiskott-Aldrich syndrome; and several cancers
SPSB1	SplA-ryanodine receptor domain and SOCS box containing 1; binds the receptor tyrosine kinase MET and enhances hepatocyte growth factor (HGF)-induced transcriptional activity; tyrosine phosphorylated form binds p120RasGAP (RASA1)
TERT	Telomerase reverse transcriptase; an RNA-directed DNA polymerase that functions in telomere maintenance; aging; DNA repair; and antiapoptosis; abnormal gene expression correlates with melanoma; neuroblastoma; and breast; lung; and other various cancers
TLX2	T-cell leukemia homeobox 2; a transcription activator that plays a role in peripheral nervous system and mesoderm development; gastrulation; and embryonic development; mouse Tlx2 gene deficiency causes myenteric neuronal hyperplasia and megacolon
TMEM163	Protein of unknown function; has strong similarity to uncharacterized mouse Tmem163
TMEM44	Protein of unknown function; has high similarity to uncharacterized mouse Tmem44
TNFRSF18	Tumor necrosis factor receptor superfamily member 18; plays a role in antiapoptosis; inhibits NK cell activation; and induces NF-kappaB transcription factor activity; increased expression correlates with rheumatoid arthritis and HIV infections
TNFRSF8	Tumor necrosis factor receptor superfamily member 8; acts in cell cycle and apoptosis; aberrantly expressed in arthritisis; colitis; dermatitis; HIV; various cancers; sclerosis; hepatitis; asthma; thyroiditis; and Hodgkin; autoimmune; and celiac diseases
TPO	Thyroid peroxidase; binds to heme; acts in T cell proliferation; increased expression of autoantibodies correlates with Turner syndrome; Hashimoto thyroiditis; depression; and sarcoidosis; abnormally expressed in thyroid cancer and Graves ophthalmopathy
TUBB6	Protein with strong similarity to beta-2 tubulin (rat Rgd1309427); which polymerizes to form microtubules and may act in axonal outgrowth and regeneration; contains a tubulin or FtsZ family GTPase domain and a tubulin or FtsZ family C-terminal domain
VDR	Vitamin D receptor; a transcriptional regulator; upregulated in idiopathic hypercalciuria; gene mutations and polymorphisms are associated with rickets; AIDS; multiple sclerosis; diabetes; several cancers; colitis; Addition; Graves; and Crohn disease
ZBED2	Protein containing a BED zinc finger domain; has high similarity to uncharacterized human ZBED3
ZNF365	Zinc finger protein 365; a putative membrane protein that is expressed as four different alternative forms in various tissues; mutations in the corresponding gene are associated with uric acid nephrolithiasis

Supplementary Table IB

Gene symbol	BKL description
AGPAT5	Protein with strong similarity to 1-acylglycerol-3-phosphate O-acyltransferase 5 (mouse Agpat5); which is an acyltransferase that is ubiquitously expressed; member of the phospholipid and glycerol acyltransferase family
AIPL1	Aryl hydrocarbon receptor interacting protein-like 1; interacts with NUB1; plays a role in protein farnesylation and visual perception; may regulate cell cycle; corresponding gene mutations and knock out of the mouse Aipl1 gene correlates with retinopathy
AK5	Adenylate kinase 5; a nucleotide kinase that plays a role in adenosine 5'-diphosphate biosynthetic process
APBA2	Amyloid beta precursor protein binding family A member 2; inhibits translation; may mediate nervous system development; synaptic vesicle docking during exocytosis; and vesicle-mediated transport; aberrantly expressed in Alzheimer disease
ARHGEF10	Rho guanine nucleotide exchange factor 10; a putative Rho-specific guanine-nucleotide exchange factor; may act in peripheral nerve myelination; gene mutation is associated with slowed nerve conductance and thin peripheral nerve myelination
ARID5A	AT rich interactive domain 5A; an RNA polymerase II transcription factor that may regulate DNA dependent transcription
ASXL3	Additional sex combs like 3; a putative transcription regulator that may play a role in embryonic development and regulation of transcription from RNA polymerase II promoter
AXIN2	Axin 2; involved in negative regulation of Wnt receptor signaling pathway; promotes odontogenesis; gene mutations are associated with hepatocellular carcinoma and colorectal and ovarian neoplasms; gene polymorphisms are associate with lung neoplasms
BACH2	BTB and CNC homology 1 basic leucine zipper transcription factor 2; plays a role in the negative regulation of cell proliferation and is involved in response to arsenic and drug; increased mRNA expression is associated with ovarian cancer
BMF	BCL2 modifying factor; plays a role in B-cell homeostasis and in mammary epithelial anoikis and morphogenesis; regulates B-cell and thymocyte apoptosis; inhibits cell proliferation; genetic knockout in mouse Bmf is associated with B-cell hyperplasia
C11orf35	Protein of unknown function; has high similarity to uncharacterized mouse 1600016N20Rik
C18orf55	Protein of unknown function; has high similarity to uncharacterized mouse 1700034H14Rik
C1orf107	Protein with low similarity to rice Os05g0295100; which is involved in response to arsenic and anoxia
C1orf51	Protein of unknown function; has high similarity to uncharacterized mouse Gm129
C1QTNF4	Protein containing two C-terminal C1q domains; has a region of low similarity to a region of adipose most abundant gene transcript 1 (human ADIPOQ); which is involved in adipocyte differentiation and the regulation of energy balance and insulin sensitivity
C20orf165	Protein of unknown function; has high similarity to uncharacterized mouse 1700020C07Rik
C21orf105	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
C2orf15	Protein of unknown function
C3orf48	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
C6orf105	Chromosome 6 open reading frame 105; may play a role in embryonic development; gene SNP analysis suggests a role in non syndromic oral clefts
CA7	Protein with high similarity to carbonic anhydrase 2 (human CA2); which converts CO2 to bicarbonate and is associated with colitis; pancreatitis; biliary cirrhosis and carbonic anhydrase II deficiency; contains a eukaryotic-type carbonic anhydrase domain
CALD1	Caldesmon 1; a calmodulin binding protein that acts in actin cytoskeleton organization and biogenesis and cell growth; regulates cell shape and stress fiber formation; upregulated in glioma; gene polymorphism correlates with type I diabetes mellitus
CAMK1D	Calcium-calmodulin-dependent protein kinase ID; acts in phagocytosis; MAPK activation; and respiratory burst; mediates FMLP-induced reactive oxygen species production; neutrophil migration; and cell adhesion; may play a role in cellular defense response
CAND1	Cullin-associated and neddylation-dissociated 1; mediates cullin deneddylation; regulates protein complex assembly; inhibits ubiquitin ligase; may play a role in muscle development; gene maps to a locus associated with myopathic scapuloperoneal syndrome
CDH23	Cadherin 23; plays a role in auditory receptor cell differentiation; inner ear morphogenesis; sensory perception of sound; and visual perception; gene mutation causes deafness; retinitis pigmentosa; vestibular diseases; and multiple abnormalities
CLEC4C	C-type lectin domain family 4 member C; a sugar binding putative transmembrane receptor that mediates T-helper 1 type immune response; may play a role in antigen processing and presentation
CPEB2	Protein with very strong similarity to cytoplasmic polyadenylation element binding protein 2 (mouse Cpeb2); which is a RNA poly(U) binding protein that may regulate the translation of stored mRNAs during spermiogenesis; contains two RNA recognition motifs
CTSL1	Cathepsin L1; a cysteine type peptidase that plays a role in axonogenesis; B cell proliferation; extracellular matrix organization; steroid biosynthesis; and regulation of leukocyte migration; upregulated in atrophic gastritis; bone and several neoplasms
CTSL3	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
CYP2C18	Cytochrome P450 family 2 subfamily C polypeptide 18; a monooxygenase and retinoic acid 4-hydroxylase that plays a role in retinoid and xenobiotic metabolic process; upregulation of the corresponding gene is associated with sudden infant death syndrome
CYSLTR2	Cysteinyl leukotriene receptor 2; a G protein-coupled receptor that regulates calcium flux; blood pressure; and vascular permeability; overexpressed in colon cancer; gene mutation correlates with asthma; mouse Cysltr2 is associated with atherosclerosis
DACT1	Dapper antagonist of beta catenin homolog 1; a cytoplasmic protein that may play a role in Wnt receptor signaling pathway and in utero embryonic development

DDAH1	Dimethylarginine dimethylaminohydrolase 1; a catalytic enzyme that regulates asymmetric dimethylarginine proteolysis and AKT1 phosphorylation; decreased activity correlates with cytomegalovirus infections; gene polymorphisms correlate with pre-eclampsia
DDR1	Discoidin domain receptor tyrosine kinase 1; a collagen binding protein that plays a role in MAPKKK cascade; cell maturation; and cell motion; upregulated in churg-Strauss syndrome; increased mRNA expression correlates with non small cell lung carcinoma
DENND2A	Protein with high similarity to suppression of tumorigenicity 5 (human ST5); which is involved in the regulation of MAPK and in maintaining contact-dependent growth; member of the DENN (AEX-3) domain family; contains uDENN and dDENN domains
DIO1	Deiodinase iodothyronine type I; acts in thyroid hormone generation; may play a role in maturation of prostate and inflammatory response; decreased activity correlates with euthyroid sick syndrome; mRNA is downregulated in papillary thyroid carcinomas
DLG2	Discs large homolog 2; plays a role in clustering of voltage-gated potassium channels; nitric oxide mediated signal transduction; and protein complex assembly; increased mRNA expression correlates with epilepsy
DLL1	Delta-like 1; mediates Notch signaling; regulates lymphocyte and osteoblast differentiation; inhibits T cell cytokine production and keratinocyte migration; gene upregulation is associated with Alzheimer disease; Down syndrome; and several carcinomas
DNAJA4	Protein with high similarity to dnaJ (Hsp40) homolog subfamily A member 4 (rat Dnaja4); which is a heat shock protein; member of the DnaJ central domain (4 repeats) family and the DnaJ C-terminal region family; contains a DnaJ domain
DNMT3L	DNA (cytosine-5-)-methyltransferase 3-like; interacts and activates the de novo methyltransferases DNMT3A and DNMT3B and plays a role in DNA methylation; stimulates transferase activity; may play a role in genetic imprinting
DOPEY1	Member of the Dopey N-terminal domain containing family; has low similarity to C. elegans PAD-1; which is involved in embryogenesis and morphogenesis
DPEP2	Protein with high similarity to membrane-bound dipeptidase 2 (mouse Dpep2); which is a membrane dipeptidase catalyzing conversion of leukotriene-D4 to leukotriene-E4; member of the membrane dipeptidase (peptidase family M19) family
DSC1	Desmocollin 1; regulates intercellular adhesion; acts as an autoantigen in pemphigus; corresponding gene polymorphism is associated with susceptibility to Alzheimer disease; gene is aberrantly expressed in Netherton syndrome and colorectal adenocarcinoma
EDAR	Ectodysplasin A receptor; plays a role in cell surface receptor linked signal transduction; gene mutation is associated with Hypohidrotic ectodermal dysplasia
EPHA1	EPH receptor A1; a transmembrane receptor protein tyrosine kinase that may play a role in embryonic development and cell proliferation and differentiation; decreased mRNA expression correlates with prostatic neoplasm
EPHX2	Epoxide hydrolase 2 cytoplasmic; a phosphoric ester hydrolase that acts in isoprenoid catabolic process; SNP is used to treat kidney transplantation; SNPs play roles in cardiovascular diseases and hyperlipoproteinemia type II
FAM117B	Protein has high similarity to a region of mouse Glcci1; which is induced by the steroid drug dexamethasone; transfected androgen receptor or glucocorticoid receptor; may play a role in steroid-mediated apoptosis and T cell differentiation
FAM83F	Member of the DUF1669 domain of unknown function family; which may be phospholipases; has high similarity to uncharacterized mouse MGC27770
FCGBP	Fc fragment of IgG binding protein; may act in immune response; expression during rheumatoid arthritis and SLE correlates with the disease; aberrant mRNA expression is associated with anaplastic astrocytoma; and follicular thyroid adenomas and carcinomas
FLT1	Fms-related tyrosine kinase 1; a vascular endothelial growth factor receptor; acts in angiogenesis; ossification; response to hypoxia; cell phosphorylation; and proliferation; aberrantly expressed in menorrhagia; sclerosis; psoriasis; and several cancers
FMN1	Formin 1; a putative alpha-catenin binding protein that may be involved in embryonic limb morphogenesis
FSTL3	Follistatin-like 3; binds and inhibits activin; regulates osteoclast and erythrocyte differentiation; acts in gonadal development and function; aberrantly expressed in breast and endometrial cancers; gene translocation causes B-cell lymphoma and leukemia
FTCD	Formiminotransferase cyclodeaminase; a metabolic bifunctional enzyme that promotes the association of Golgi complex with cytoskeleton; gene deletion causes inborn errors of amino acid metabolism; autoimmune antibody correlates with autoimmune hepatitis A
GDF9	Growth differentiation factor 9; acts in steroid biosynthetic process; female pregnancy; and antiapoptosis; regulates cell differentiation; transcription; and cell proliferation; downregulated in polycystic ovary syndrome
GPA33	Glycoprotein A33; a putative transmembrane receptor that may play a role in in utero embryonic development; antigen processing and presentation; and cell adhesion; gene is upregulated in Barrett metaplasia
hCG_1774568	
HGSNAT	Heparan-alpha-glucosaminide N-acetyltransferase; an enzyme that exhibits heparan-alpha-glucosaminide N-acetyltransferase activity; a wide variety of mutations is associated with mucopolysaccharidosis IIIC; or Sanfilippo disease type C
HIST2H2BE	Histone cluster 2 H2be; may bind to double-stranded DNA; may play a role in nucleosome assembly
HSPA12A	Protein with very strong similarity to heat shock protein 12A (mouse Hspa12a); which exhibits upregulation in atherosclerotic lesions of the thoracic aorta
HSPG2	Heparan sulfate proteoglycan 2; a coreceptor that acts in angiogenesis; cartilage condensation; and ossification; regulates apoptosis and transcription; gene mutation causes Schwartz Jampel syndrome and Silverman-Handmaker type dyssegmental dysplasia
IFI44	Interferon-induced protein 44; an interferon-inducible protein; may mediate antiviral action of interferons; gene SNP correlates with response to therapeutic drugs for chronic hepatitis C; increased monocyte expression correlates with Sjogrens syndrome
IL1RL2	Interleukin 1 receptor-like 2; regulates I-kappaB kinase and NF-kappaB cascade and cell surface receptor linked signaling; may play a role in cellular defense and inflammatory response; gene is upregulated in psoriatic skin
IL7R	Interleukin 7 receptor; acts in B cell differentiation; T cell receptor V(D)J recombination; and multicellular organismal development; single nucleotide polymorphism correlates with early onset form of type I diabetes mellitus and multiple sclerosis
IVNS1ABP	Influenza virus NS1A binding protein; an alpha-enolase binding protein that plays a role in symbiosis; may be involved in transcription and RNA splicing
KDM2A	F-box and leucine-rich repeat protein 11; a putative ubiquitin-protein ligase activity that may act in SCF-dependent proteasomal ubiquitin-dependent protein catabolism and protein modification
KIAA1543	Protein of unknown function; has strong similarity to uncharacterized mouse 2310057J16Rik

KIF27	Kinesin family member 27; a putative microtubule motor that may play a role in gamete generation and microtubule-based movement; gene haploinsufficiency is associated with myeloid leukemia
KLHL14	Protein containing six kelch 1 motifs and four kelch 2 motifs; has low similarity to human KLHL13; which is an ubiquitin ligase that plays a role in the regulation of cytokinesis and mitosis
KLHL3	Kelch-like 3; putative actin-binding protein that may play a role in cytoskeletal dynamics
KLRB1	Killer cell lectin-like receptor subfamily B member 1; a phospholipase activator that stimulates T cell proliferation; cytokine biosynthesis; and NK cell degranulation; aberrant expression causes Guillain-Barre syndrome; angina; sclerosis; and melanoma
KRT72	Keratin 72; a putative structural constituent of cytoskeleton that may play a role in hair follicle morphogenesis
KRT74	Keratin 74; a putative structural molecule that may play a role in the intermediate filament-based process
LCE1E	Protein of unknown function
LGR4	Leucine-rich repeat-containing G protein-coupled receptor 4; regulates erythropoiesis and acts in eye development; upregulated in lymph node metastasis and colon carcinomas; mouse Lgr4 is associated with ocular anterior segment dysgenesis
LOC100128003	
LOC100128180	
LOC100129038	
LOC100129196	
LOC100130278	
LOC100130924	
LOC100131150	
LOC100131929	
LOC151878	
LOC284454	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
LOC642413	Synthetic high osmolarity-sensitive 1 (by homology to C. albicans Sho1p); a predicted osmosensor in the HOG1 MAP kinase high-osmolarity signal transduction pathway
LOC730257	
LSR	Lipolysis stimulated lipoprotein receptor; a protein targeted by p53 that may be involved in response to stress
LTC4S	Leukotriene C4 synthase; a glutathione transferase that interacts with mGT; acts in leukotriene biosynthesis; upregulated in chronic myeloid leukemia; gene polymorphism correlates with asthma; gene overexpression is associated with sinusitis
LY9	Lymphocyte antigen 9; plays a role in the formation of immunological synapse and homophilic cell adhesion
MBNL3	
MCF2L	MCF.2 cell line derived transforming sequence-like; a guanyl-nucleotide exchange factor that induces JNK cascade; transcription; stress fiber formation; and GTPase activity; mediates protein localization and GPCR signaling
MPL	Myeloproliferative leukemia virus oncogene; a putative transmembrane receptor that acts in JAK-STAT cascade and definitive hemopoiesis; downregulated in thrombocytopenia; polycythemia vera; and myeloproliferative disorders
MRPL43	Mitochondrial ribosomal protein L43; a putative structural constituent of the mitochondrial large ribosomal subunit; may function in protein biosynthesis and oxidative phosphorylation
MYCT1	Myc target 1; promotes apoptosis in gastric carcinoma cell lines; mRNA expression is decreased in gastric carcinoma
MYPN	Myopalladin; an ANKRD1 binding protein that tethers nebulin and nebulette to alpha-actinin; maintains the sarcomere structure; may play a role in Z-line assembly; mutations in the corresponding gene are associated with idiopathic dilated cardiomyopathy
NELL2	NEL-like 2; may play a role in cell proliferation; nervous system development; signal transduction; and regulation of epidermal growth factor receptor activity; gene expression is upregulated in benign prostratic hyperplasia
NFIA	Nuclear factor I-A; a transcriptional regulator that acts in brain development; neuron differentiation; and redox signal response
NLRP3	NLR family pyrin domain containing 3; acts in cell differentiation; regulates inflammatory response; interleukin secretion; caspase activity; and apoptosis; gene mutations is associated with Crohn syndrome; urticaria; and autoinflammatory disorders
NOG	Noggin; inhibits chondrocyte proliferation; neuron differentiation; and ossification; gene mutation causes ankylosis; proximal symphalangism; and multiple synostoses syndrome; gene translocation is associated with myeloproliferative diseases
NPEPL1	Protein containing a cytosol aminopeptidase family catalytic domain; has moderate similarity to leucine aminopeptidase (C. elegans LAP-1); which is a putative aminopeptidase that acts in oviposition and in the regulation of development

NR1D2	Nuclear receptor subfamily 1 group D member 2; a transcriptional regulator that regulates striated muscle development; may be involved in tissue homeostasis and in regulation of neuronal synaptic plasticity
ODZ1	Odz odd Oz ten m homolog 1; a putative heparin binding signal transducer that may play a role in nervous system development and immune response; upregulation of the corresponding gene is associated with papillary thyroid carcinoma
OR51E2	Olfactory receptor family 51 subfamily E member 2; prostate specific GPCR; binds to GNA12 and mediates cytokine and chemokine mediated signaling; mRNA expression is upregulated in prostate intraepithelial neoplasia and early prostate tumors
OR8D1	Olfactory receptor family 8 subfamily D member 1; a putative G protein-coupled receptor that is expressed in the fetal tongue; may function in taste perception
PAX4	Paired box gene 4; a putative RNA polymerase II transcription factor; acts in positive regulation of cell proliferation; gene mutations are associated with ketosis prone diabetes and type 2 diabetes mellitus
PDE6B	Phosphodiesterase 6B cGMP-specific rod beta; a 3'5'-cyclic-GMP phosphodiesterase that plays a role in circadian rhythm; phototransduction visible light; and retinal cell programmed cell death; gene mutations are associated with retinitis pigmentosa
PDZD2	PDZ domain containing 2; stimulates pancreatic progenitor cell proliferation; increased expression correlates with prostate neoplasms
PDZD3	Protein with high similarity to mouse Pdzd3; which binds to mouse Slc34a1 and interacts with Slc34a1 Trpv6 calcium channel to regulate calcium ion transport; contains three PDZ; DHR; or GLGF domains; which are found in signaling proteins
PHC3	Polyhomeotic like 3; associates with polycomb complex PRC-H components and the E2F6 transcription factor; may act in silencing target promoters in G(0); reduced protein expression and gene mutation is associated with osteosarcoma
PIWIL4	Piwi-like 2; a DICER binding protein that may play a role in RNA interference
POU2F1	POU domain class 2 transcription factor 1; a transcriptional regulator that interacts with nuclear hormone receptors; decreased expression correlates with prostatic neoplasms; gene polymorphism is associated with Alzheimer disease
PRKAG2	Protein kinase AMP-activated gamma 2 non-catalytic subunit; plays a role in glycogen metabolism and regulation of fatty acid oxidation and glucose import; gene mutation causes myocardial glycogen storage disease and Wolff-Parkinson-White syndrome
PRKCZ	Protein kinase C zeta; a serine-threonine kinase; acts in hormone secretion; antiapoptosis; and cytokine-mediated signaling; aberrantly expressed in Alzheimer disease; amyotrophic lateral sclerosis; rheumatoid arthritis; psoriasis; and several cancers
RAB25	RAB25 member RAS oncogene family; associates with integrin to induce invasive cell migration; acts in the regulation of cell proliferation and apoptosis in cancer cells; increased expression is observed in breast; liver; and ovarian neoplasms
RBMS3	RNA binding motif single stranded interacting protein; increases the expression of transcription factor PRRX1 by binding and stabilizing its mRNA; increased mRNA expression is associated with liver fibrosis
RIN1	Ras and Rab interactor 1; an enzyme inhibitor that plays a role in endocytosis; DNA synthesis; and cell cell migration; gene amplification is associated with oral squamous cell carcinoma
RIN2	Ras and Rab interactor 2; a small GTPase regulator that is involved in protein homotetramerization; may act as a Ras effector to promote apoptosis and inhibits cell proliferation; decreased mRNA expression correlates with tumors
RIPK2	Receptor-interacting serine-threonine kinase 2; a signal transducer that acts in activation of MAPK activity; inflammatory response; and regulation of NF-kappaB transcription factor activity; increased mRNA expression correlates with multiple sclerosis
SBF2	SET binding factor 2; binds to the coiled coil region of MTMR2; may play a role in peripheral nervous system and eye development; nonsense mutation in the gene causes autosomal recessive form of Charcot-Marie-Tooth disease
SCML1	Sex comb on midleg-like 1 (Drosophila); a member of a family of D. melanogaster Polycomb group transcriptional repressors involved in development
SERPINF2	Serine proteinase inhibitor clade F member 2; inhibits plasmin mediated fibrinolysis; involved in blood coagulation; aberrant expression correlates with arteriosclerosis; coronary diseases; and brain ischemia; gene mutation causes hemorrhagic disorders
SESN1	Sestrin 1; may act in determination of left and right symmetry and regulation of cell proliferation; gene mutation may correlate with situs inversus
SH3PXD2B	Protein containing a phosphoinositide-binding phox protein (PX) domain; a proline-rich peptide-binding Src homology 3 (SH3) domain; and a variant SH3 domain; has moderate similarity to mouse Sh3md1; which is likely involved in tyrosine kinase signaling
SLC22A23	Member of the major facilitator superfamily and sugar (and other) transporter famliy; has low similarity to mouse Slc22a3; which is a monoamine transporter that regulates neurotransmitter levels and behavior
SLC29A3	Solute carrier family 29 member 3; a broadly selective low affinity nucleoside transporter; gene mutation causes autosomal recessive H syndrome; and pigmented hypertrichotic dermatosis with insulin dependent diabetes syndrome
SNAI1	Snail homolog 1; a transcriptional repressor that plays a role in cell adhesion and induction of apoptosis by p53 in response to DNA damage; involved in epithelial to mesenchymal transition; upregulated in breast neoplasms and thyroid carcinoma
SOD2	Superoxide dismutase 2 mitochondrial; acts in superoxide metabolism; aging; antiapoptosis; and DNA double-strand break repair; aberrantly expressed in asthma; atherosclerosis; schizophrenia; pancreatitis; and colorectal and several neoplasms
SOX12	SRY (sex determining region Y)-box 12; a transcriptional activator that forms a ternary complex with Brn2 (POU3F2) and DNA; may play roles in both differentiation and maintenance of several cell types
SPON1	Spondin 1 extracellular matrix protein; binds to and inhibits the processing of beta-amyloid precursor protein; acts in activation of protein kinase activity; regulates angiogenesis; cell migration; neuron differentiation; and transcription
STMN3	Stathmin-like 3; may play a role in nervous system development
SUSD4	Protein containing two sushi or short consensus repeat (SCR) domains; which are found in complement and adhesion proteins
TAS1R1	Taste receptor type 1 member 1; a G protein-coupled receptor that is involved in elevation of cytosolic calcium ion concentration and sensory perception of taste
TBC1D4	TBC1 domain family member 4; a Rab GTPase activator that plays a role in glucose metabolic process; may regulate small GTPase mediated signal transduction; upregulated in atopic dermatitis and impaired phosphorylation correlates with type 2 diabetes
TCP11L2	Protein with moderate similarity to T-complex protein 11 (mouse Tcp11); which is involved in acrosome reaction and may mediate cell surface receptor linked signal transduction

TES	Testis derived transcript (3 LIM domains); plays a role in regulation of cell proliferation and apoptosis; decreased mRNA expression correlates with breast and prostatic neoplasms
TMEM100	Protein of unknown function; has strong similarity to uncharacterized mouse 1810057C19Rik
TNFRSF10B	Death receptor 5; a caspase activator that mediates induction of apoptosis; mitochondrial membrane potential; and NF-kappaB transcription factor activity; aberrant expression correlates with arthritis; HIV infection; pancreatitis; and several neoplasms
TRIM9	Protein with very strong similarity to rat Trim9; which may inhibit calcium ion dependent exocytosis; member of the SPRY domain containing family; contains a C3HC4 type zinc finger; a fibronectin type III; and two B-box zinc finger domains
TSPAN6	Tetraspanin 6; may be involved in cell adhesion; cell migration; and cell proliferation
TTC16	Protein containing seven tetratricopeptide repeats; which may act in protein binding; has a region of weak similarity to a region of S. cerevisiae Srp40p; which is a suppressor of S. cerevisiae Rpc40p and S. cerevisiae Rpb10p mutations
TTC18	Protein containing seven type 2 tetratricopeptide repeats and seven type 1 tetratricopeptide repeats; which may mediate protein-protein interactions
TTN	Titin; an actin filament binding protein that acts in muscle development; regulates autolysis; acts as an autoantigen in melanoma associated retinopathy and myasthenia gravis; gene mutation is associated with dilated cardiomyopathy and muscular dystrophy
UBQLNL	Protein containing a ubiquitin family domain; has moderate similarity to ubiquilin 1 (human UBQLN1); which accumulates PSEN1 and PSEN2 and is associated with neurofibrillary tangles and Lewy bodies observed in Alzheimer and Parkinson disease
ULBP2	UL16 binding protein 2; binds to KLRK1; acts in immune response; regulates T cell proliferation; natural killer cell mediated cytotoxicity; and IFN-gamma production; overexpressed in T-cell non-Hodgkin lymphoma and acute and chronic myelogenous leukemia
UNQ5814	
VIPR1	Vasoactive intestinal peptide receptor 1; a GPCR that activates adenylyl cyclase; acts in cell proliferation and inflammatory response; mRNA is upregulated in prostate neoplasms; map position correlates with small cell carcinoma
YPEL2	Yippee-like 2; a putative zinc binding protein; may be involved in the cell cycle; member of the yippee putative zinc-binding protein family; gene polymorphism correlates with risk associated with breast cancer
ZBTB40	Zinc finger and BTB domain containing 40; a predicted transcription factor; gene locus may be associated with bone mineral density and fractures
ZNF238	Zinc finger protein 238; a transcriptional repressor that may be involved in brain development and function
ZNF415	Zinc finger protein 415; inhibits AP1 and TP53 mediated transcriptional activity; five isoforms are observed which result from alternate mRNA splicing
ZNF540	Zinc finger protein 540; binds the MAP kinase scaffold protein; MVP; likely functions as a transcriptional repressor in the MAPK signaling pathway to mediate cellular functions

Supplementary Table II

JAK_STAT Signaling

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	GPR56	GPR56	G protein-coupled receptor 56	14	1.989099979	0.28498083	Yes
row_1	CCR5	CCR5	chemokine (C-C motif) receptor 5	266	0.76279974	0.36097574	Yes
row_2	LPHN2	LPHN2	latrophilin 2	297	0.732099891	0.46249688	Yes
row_3	CXCR3	CXCR3	chemokine (C-X-C motif) receptor 3	457	0.610599995	0.52901024	Yes
row_4	CCR3	CCR3	chemokine (C-C motif) receptor 3	909	0.411400318	0.52721685	Yes
row_5	LGR6	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	996	0.387300014	0.571419	Yes
row_6	F2R	F2R	coagulation factor II (thrombin) receptor	1543	0.274299979	0.5369762	Yes
row_7	CCR2	CCR2	chemokine (C-C motif) receptor 2	1550	0.27270031	0.5754932	Yes
row_8	GPR17	GPR17	G protein-coupled receptor 17	2226	0.168500066	0.508307	No
row_9	EDG1	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	3332	0.038999915	0.36416218	No
row_10	LTB4R2	LTB4R2	leukotriene B4 receptor 2	3924	-0.023000002	0.28737637	No
row_11	GPR135	GPR135	G protein-coupled receptor 135	4298	-0.0625	0.24583474	No
row_12	EBI2	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	4860	-0.121200085	0.18727799	No
row_13	CIDEB	CIDEB	cell death-inducing DFFA-like effector b	5028	-0.137899876	0.18453176	No
row_14	EMR3	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	5645	-0.217899978	0.13246697	No
row_15	GPR132	GPR132	G protein-coupled receptor 132	5713	-0.227099985	0.15613948	No
row_16	P2RY11	P2RY11	purinergic receptor P2Y, G-protein coupled, 11	5780	-0.234499931	0.18101476	No
row_17	RLN3R1	null	null	5974	-0.261700034	0.19259965	No

PC12 Cell Differentiation

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	EGR1	EGR1	early growth response 1	0	4.485800266	0.41217282	Yes
row_1	EGR2	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	23	1.801800251	0.57474744	Yes
row_2	EGR3	EGR3	early growth response 3	157	0.973499775	0.6461698	Yes
row_3	JUN	JUN	jun oncogene	279	0.751000166	0.6987745	Yes
row_4	FRS2	FRS2	fibroblast growth factor receptor substrate 2	1923	0.212300062	0.49559242	No
row_5	CREB1	CREB1	cAMP responsive element binding protein 1	2029	0.195600033	0.4993334	No
row_6	GNAQ	GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	2044	0.194500029	0.5153073	No
row_7	CREBBP	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	2460	0.137700081	0.4717114	No
row_8	PTPN11	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	3224	0.050500035	0.37293598	No
row_9	MAPK1	MAPK1	mitogen-activated protein kinase 1	3491	0.022300005	0.33893186	No

row_10	TERF2IP	TERF2IP	telomeric repeat binding factor 2, interacting protein	3620	0.00849998	0.322364	No
row_11	MAPK8	MAPK8	mitogen-activated protein kinase 8	4350	-0.067499995	0.2297589	No
row_12	RPS6KA3	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	4428	-0.075500011	0.22625971	No
row_13	TH	TH	tyrosine hydroxylase	4470	-0.07889998	0.22795229	No
row_14	SH2B	null	null	5467	-0.190900087	0.110497005	No
row_15	PIK3CA	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	6124	-0.290400028	0.04826711	No
row_16	MAPK8IP3	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	7146	-0.654299974	-0.029997637	No
row_17	MAP2K7	MAP2K7	mitogen-activated protein kinase kinase 7	7185	-0.692299962	0.028463133	No

Cytokine Cytokine Receptor Interaction

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	PDGFRB	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	2	2.545100212	0.051106997	Yes
row_1	TPO	TPO	thyroid peroxidase	6	2.168400049	0.09447238	Yes
row_2	CCR8	CCR8	chemokine (C-C motif) receptor 8	17	1.955800295	0.13258833	Yes
row_3	IL2RA	IL2RA	interleukin 2 receptor, alpha	28	1.689100266	0.16532013	Yes
row_4	TNFRSF18	TNFRSF18	tumor necrosis factor receptor superfamily, member 18	34	1.622200012	0.19738525	Yes
row_5	IL3RA	IL3RA	interleukin 3 receptor, alpha (low affinity)	36	1.584900141	0.22924449	Yes
row_6	IL12RB2	IL12RB2	interleukin 12 receptor, beta 2	45	1.465599775	0.25773782	Yes
row_7	IL10	IL10	interleukin 10	72	1.297500134	0.2803755	Yes
row_8	TNFRSF8	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	86	1.221700191	0.30326107	Yes
row_9	CCR1	CCR1	chemokine (C-C motif) receptor 1	89	1.211400032	0.3274433	Yes
row_10	CXCL2	CXCL2	chemokine (C-X-C motif) ligand 2	134	1.034999847	0.34231958	Yes
row_11	LIF	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	136	1.028100014	0.3629381	Yes
row_12	OSM	OSM	oncostatin M	151	0.982999802	0.38086802	Yes
row_13	IL26	IL26	interleukin 26	179	0.922600031	0.3958004	Yes
row_14	FLT1	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability	193	0.878499985	0.41175747	Yes
row_15	PRL	PRL	prolactin	226	0.814800024	0.4238297	Yes
row_16	CCR5	CCR5	chemokine (C-C motif) receptor 5	266	0.76279974	0.4338947	Yes
row_17	IFNG	IFNG	interferon, gamma	290	0.740600109	0.44570002	Yes
row_18	IL5	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	323	0.710299969	0.4556626	Yes
row_19	IFNAR2	IFNAR2	interferon (alpha, beta and omega) receptor 2	339	0.698800087	0.4677183	Yes
row_20	CXCR3	CXCR3	chemokine (C-X-C motif) receptor 3	457	0.610599995	0.46404183	Yes
row_21	IL17RB	IL17RB	interleukin 17 receptor B	478	0.592899799	0.4732757	Yes
row_22	IL1RAP	IL1RAP	interleukin 1 receptor accessory protein	484	0.586699963	0.48443612	Yes

row_23	CSF2	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	532	0.561500072	0.48934302	Yes
row_24	ACVR2B	ACVR2B	activin A receptor, type IIB	574	0.540700018	0.4946507	Yes
row_25	TNFRSF4	TNFRSF4	tumor necrosis factor receptor superfamily, member 4	650	0.506300211	0.49461338	Yes
row_26	CXCL3	CXCL3	chemokine (C-X-C motif) ligand 3	676	0.49029994	0.5010921	Yes
row_27	CCL5	CCL5	chemokine (C-C motif) ligand 5	757	0.455900192	0.49935338	No
row_28	CCR3	CCR3	chemokine (C-C motif) receptor 3	909	0.411400318	0.48700494	No
row_29	TNFSF10	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1025	0.378100157	0.4789083	No
row_30	IL9R	IL9R	interleukin 9 receptor	1026	0.37770009	0.48653334	No
row_31	TNFRSF11A	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	1049	0.373399973	0.49106237	No
row_32	IFNA7	IFNA7	interferon, alpha 7	1073	0.367000103	0.49532545	No
row_33	IL18RAP	IL18RAP	interleukin 18 receptor accessory protein	1329	0.310900211	0.46672297	No
row_34	TNFRSF13C	TNFRSF13C	tumor necrosis factor receptor superfamily, member 13C	1449	0.290199995	0.45630467	No
row_35	CCR2	CCR2	chemokine (C-C motif) receptor 2	1550	0.27270031	0.44813195	No
row_36	CXCL16	CXCL16	chemokine (C-X-C motif) ligand 16	1672	0.251000047	0.43664873	No
row_37	CCL28	CCL28	chemokine (C-C motif) ligand 28	1761	0.237900019	0.4294148	No
row_38	IL2RB	IL2RB	interleukin 2 receptor, beta	1809	0.23029995	0.42763546	No
row_39	IL13	IL13	interleukin 13	2027	0.195899963	0.401909	No
row_40	IL15	IL15	interleukin 15	2493	0.133000135	0.3409912	No
row_41	TNFRSF21	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	2511	0.131299973	0.34131664	No
row_42	EPOR	EPOR	erythropoietin receptor	2519	0.130200028	0.34298766	No
row_43	CXCL12	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	2758	0.102300048	0.3124992	No
row_44	TNFSF11	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	2954	0.078600049	0.28741384	No
row_45	GH1	GH1	growth hormone 1	3054	0.067300081	0.27523127	No
row_46	IL10RB	IL10RB	interleukin 10 receptor, beta	3102	0.06280005	0.2700704	No
row_47	TNFRSF6B	TNFRSF6B	tumor necrosis factor receptor superfamily, member 6b, decoy	3181	0.055199862	0.26051593	No
row_48	IL15RA	IL15RA	interleukin 15 receptor, alpha	3198	0.054199934	0.25942162	No
row_49	CX3CR1	CX3CR1	chemokine (C-X3-C motif) receptor 1	3327	0.039400011	0.24270917	No
row_50	IL28A	IL28A	interleukin 28A (interferon, lambda 2)	3334	0.038800001	0.24267179	No
row_51	TGFBR2	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	3508	0.020799875	0.21942873	No
row_52	IL18R1	IL18R1	interleukin 18 receptor 1	3515	0.019600034	0.21900374	No
row_53	IL21R	IL21R	interleukin 21 receptor	3891	-0.019400001	0.1681028	No
row_54	IL2	IL2	interleukin 2	4049	-0.035700083	0.14734903	No
row_55	IL22	IL22	interleukin 22	4554	-0.087500036	0.08017827	No
row_56	TNFSF9	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	4687	-0.103600025	0.064214766	No

row_57	AMH	AMH	anti-Mullerian hormone	5252	-0.163100004	-0.009636593	No
row_58	ACVR1	ACVR1	activin A receptor, type I	5573	-0.206700087	-0.049233384	No
row_59	IL4	IL4	interleukin 4	5734	-0.229899883	-0.06647699	No
row_60	IL23A	IL23A	interleukin 23, alpha subunit p19	5914	-0.253000021	-0.08585307	No
row_61	TNFRSF1B	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	5958	-0.259200096	-0.08650188	No
row_62	IL2RG	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	6175	-0.299700022	-0.10999605	No
row_63	TGFB3	TGFB3	transforming growth factor, beta 3	6299	-0.32679987	-0.12022257	No
row_64	TNFSF13	TNFSF13	tumor necrosis factor (ligand) superfamily, member 13	6376	-0.341899872	-0.12371558	No
row_65	FAS	FAS	Fas (TNF receptor superfamily, member 6)	6390	-0.345500112	-0.118518755	No
row_66	TNFRSF25	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	6403	-0.348399997	-0.113126606	No
row_67	IL6	IL6	interleukin 6 (interferon, beta 2)	6532	-0.3829	-0.12290447	No
row_68	CCL15	CCL15	chemokine (C-C motif) ligand 15	6646	-0.411800027	-0.1300472	No
row_69	CCL18	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	6719	-0.432299852	-0.1311681	No
row_70	CCL21	CCL21	chemokine (C-C motif) ligand 21	6783	-0.449800014	-0.13070467	No
row_71	IL12RB1	IL12RB1	interleukin 12 receptor, beta 1	6784	-0.449800134	-0.1216241	No
row_72	TNFSF14	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	6894	-0.490799904	-0.12662485	No
row_73	IL6ST	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	6938	-0.507499933	-0.12226097	No
row_74	CCL24	CCL24	chemokine (C-C motif) ligand 24	6964	-0.522700012	-0.1151282	No
row_75	CXCR4	CXCR4	chemokine (C-X-C motif) receptor 4	6967	-0.524100065	-0.10482121	No
row_76	IL24	IL24	interleukin 24	7058	-0.576299906	-0.10549707	No
row_77	IL11RA	IL11RA	interleukin 11 receptor, alpha	7123	-0.63530004	-0.10142554	No
row_78	TNFSF8	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	7198	-0.710200012	-0.09720974	No
row_79	GH2	GH2	growth hormone 2	7234	-0.767799973	-0.08649668	No
row_80	CCR4	CCR4	chemokine (C-C motif) receptor 4	7250	-0.803500056	-0.0723273	No
row_81	IL7R	IL7R	interleukin 7 receptor	7257	-0.814399958	-0.05670685	No
row_82	TNFRSF10B	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	7355	-1.212500095	-0.045496542	No
row_83	CCL25	CCL25	chemokine (C-C motif) ligand 25	7357	-1.236400008	-0.020672845	No
row_84	LTA	LTA	lymphotoxin alpha (TNF superfamily, member 1)	7363	-1.274699926	0.004376934	No

Folate Biosynthesis

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	RAD54L	RAD54L	RAD54-like (S. cerevisiae)	291	0.740299702	0.11139614	Yes
row_1	DHFR	DHFR	dihydrofolate reductase	402	0.651299953	0.22919883	Yes
row_2	GGH	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	559	0.548299789	0.31977546	Yes

row_3	RAD54B	RAD54B	RAD54 homolog B (S. cerevisiae)	806	0.440899968	0.37626344	Yes
row_4	DDX52	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	953	0.397400022	0.4374466	Yes
row_5	ALPP	ALPP	alkaline phosphatase, placental (Regan isozyme)	1273	0.32249999	0.45990944	Yes
row_6	SMARCA5	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	1357	0.307500064	0.5113157	Yes
row_7	DDX4	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	1417	0.295000076	0.563429	Yes
row_8	PTS	PTS	6-pyruvoyltetrahydropterin synthase	1618	0.2597	0.5892305	Yes
row_9	EP400	EP400	E1A binding protein p400	1741	0.240400076	0.6216754	Yes
row_10	RUVBL2	RUVBL2	RuvB-like 2 (E. coli)	1762	0.237900019	0.6674413	Yes
row_11	NUDT5	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	2668	0.111799955	0.5675114	No
row_12	DDX18	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	2791	0.098800063	0.57110184	No
row_13	ENTPD7	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	2982	0.075500011	0.5607241	No
row_14	NUDT8	NUDT8	nudix (nucleoside diphosphate linked moiety X)-type motif 8	3310	0.040900052	0.5247195	No
row_15	ATP13A2	ATP13A2	ATPase type 13A2	3357	0.036000013	0.52581805	No
row_16	SKIV2L2	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	3397	0.031899929	0.5270303	No
row_17	QDPR	QDPR	quinoid dihydropteridine reductase	3599	0.010699987	0.5019564	No
row_18	FPGS	FPGS	folylpolyglutamate synthase	3766	-0.007200003	0.4809151	No
row_19	DDX23	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	3840	-0.015300035	0.47413456	No
row_20	ASCC3	ASCC3	activating signal cointegrator 1 complex subunit 3	4067	-0.038100004	0.45125428	No

Hematopoietic Cell Lineage

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	TPO	TPO	thyroid peroxidase	6	2.168400049	0.110117525	Yes
row_1	IL2RA	IL2RA	interleukin 2 receptor, alpha	28	1.689100266	0.19367692	Yes
row_2	IL3RA	IL3RA	interleukin 3 receptor, alpha (low affinity)	36	1.584900141	0.27380747	Yes
row_3	CD1C	CD1C	CD1c molecule	80	1.249600053	0.33189383	Yes
row_4	ITGA3	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	178	0.925000191	0.36603814	Yes
row_5	ANPEP	ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsoma	265	0.763699889	0.39342487	Yes
row_6	IL5	IL5	interleukin 5 (colony-stimulating factor, eosinophil)	323	0.710299969	0.42201942	Yes
row_7	CD38	CD38	CD38 molecule	391	0.657099962	0.4465338	Yes
row_8	CSF2	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	532	0.561500072	0.4562403	Yes
row_9	CD59	CD59	CD59 molecule, complement regulatory protein	603	0.527500153	0.47371694	Yes
row_10	TFRC	TFRC	transferrin receptor (p90, CD71)	608	0.52579999	0.50007284	Yes
row_11	CD1A	CD1A	CD1a molecule	643	0.510400057	0.5215653	Yes
row_12	ITGA4	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	675	0.491600037	0.5425036	Yes

row_13	CD9	CD9	CD9 molecule	736	0.463400006	0.55805945	Yes
row_14	HLA-DRA	HLA-DRA	major histocompatibility complex, class II, DR alpha	792	0.443900108	0.573297	Yes
row_15	IL9R	IL9R	interleukin 9 receptor	1026	0.37770009	0.5609664	No
row_16	EPOR	EPOR	erythropoietin receptor	2519	0.130200028	0.3649374	No
row_17	CD8A	CD8A	CD8a molecule	2596	0.120700002	0.36078757	No
row_18	CD33	CD33	CD33 molecule	2635	0.116600037	0.36159036	No
row_19	HLA-DRB1	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	3238	0.049399853	0.28233522	No
row_20	ITGAM	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	3427	0.029599667	0.25830948	No
row_21	CD19	CD19	CD19 molecule	4926	-0.128100157	0.06135798	No
row_22	HLA-DRB5	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	5387	-0.180099964	0.008080157	No
row_23	CR2	CR2	complement component (3d/Epstein Barr virus) receptor 2	5395	-0.181999922	0.016440088	No
row_24	CD44	CD44	CD44 molecule (Indian blood group)	5401	-0.182500005	0.025097305	No
row_25	IL4	IL4	interleukin 4	5734	-0.229899883	-0.008243873	No
row_26	ITGA2B	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	5988	-0.264400005	-0.029087828	No
row_27	FCGR1A	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	6462	-0.36259985	-0.074795246	No
row_28	ITGA6	ITGA6	integrin, alpha 6	6499	-0.372299969	-0.06063949	No
row_29	IL6	IL6	interleukin 6 (interferon, beta 2)	6532	-0.3829	-0.04539804	No
row_30	CD3E	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	6538	-0.384499788	-0.026406769	No
row_31	ITGA5	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	7003	-0.547999978	-0.06140669	No
row_32	IL11RA	IL11RA	interleukin 11 receptor, alpha	7123	-0.63530004	-0.045071818	No
row_33	CD37	CD37	CD37 molecule	7241	-0.783599973	-0.020878403	No
row_34	IL7R	IL7R	interleukin 7 receptor	7257	-0.814399958	0.018747514	No

DNA Replication Reactome

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	RFC2	RFC2	replication factor C (activator 1) 2, 40kDa	383	0.663499951	0.027988456	Yes
row_1	CDC6	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	460	0.608300209	0.091015846	Yes
row_2	PRIM2A	PRIM2A	primase, polypeptide 2A, 58kDa	618	0.519799948	0.13237086	Yes
row_3	GMNN	GMNN	geminin, DNA replication inhibitor	654	0.502799988	0.18824534	Yes
row_4	CDC45L	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	720	0.473199844	0.2364762	Yes
row_5	MCM4	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	947	0.39839983	0.25382152	Yes
row_6	ORC6L	ORC6L	origin recognition complex, subunit 6 like (yeast)	955	0.396399975	0.300669	Yes
row_7	POLE2	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	1162	0.346600056	0.31448457	Yes
row_8	RFC3	RFC3	replication factor C (activator 1) 3, 38kDa	1197	0.338000059	0.35062316	Yes

row_9	POLA2	POLA2	polymerase (DNA directed), alpha 2 (70kD subunit)	1280	0.32130003	0.378229	Yes
row_10	RFC4	RFC4	replication factor C (activator 1) 4, 37kDa	1319	0.31280005	0.4107857	Yes
row_11	CDK2	CDK2	cyclin-dependent kinase 2	1387	0.300500035	0.43792066	Yes
row_12	CDC7	CDC7	CDC7 cell division cycle 7 (S. cerevisiae)	1529	0.276799917	0.45214757	Yes
row_13	MCM10	MCM10	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	1612	0.260700226	0.47244623	Yes
row_14	PCNA	PCNA	proliferating cell nuclear antigen	1825	0.227400064	0.4710737	Yes
row_15	MCM2	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	1854	0.222599983	0.49411216	Yes
row_16	RPA2	RPA2	replication protein A2, 32kDa	1879	0.219099879	0.5172718	Yes
row_17	POLD1	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	1936	0.210400105	0.53503644	Yes
row_18	RFC5	RFC5	replication factor C (activator 1) 5, 36.5kDa	2008	0.198600054	0.54934096	Yes
row_19	MCM6	MCM6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cere	2128	0.183300018	0.5552815	Yes
row_20	MCM5	MCM5	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae	2295	0.159100056	0.5519208	Yes
row_21	POLA	null	null	2372	0.150200129	0.5597101	Yes
row_22	ORC1L	ORC1L	origin recognition complex, subunit 1-like (yeast)	2518	0.130399942	0.5557408	No
row_23	CDT1	CDT1	chromatin licensing and DNA replication factor 1	2685	0.110000134	0.5464595	No
row_24	MCM3	MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	2750	0.10289979	0.55017513	No
row_25	PRIM1	PRIM1	primase, polypeptide 1, 49kDa	2895	0.086400032	0.54103607	No
row_26	POLD3	POLD3	polymerase (DNA-directed), delta 3, accessory subunit	2943	0.080300093	0.5443354	No
row_27	POLE	POLE	polymerase (DNA directed), epsilon	3846	-0.015700102	0.42372414	No
row_28	ORC4L	ORC4L	origin recognition complex, subunit 4-like (yeast)	4031	-0.034100056	0.40284616	No
row_29	ORC2L	ORC2L	origin recognition complex, subunit 2-like (yeast)	4497	-0.081200004	0.3494837	No
row_30	POLD2	POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	4635	-0.096599817	0.3425252	No
row_31	RPA1	RPA1	replication protein A1, 70kDa	4927	-0.128200054	0.31846175	No
row_32	UBA52	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	5024	-0.137600005	0.3220155	No

Valine Leucine Isoleucine Degradation

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	ALDH2	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	168	0.944400012	0.15727271	Yes
row_1	BCAT1	BCAT1	branched chain aminotransferase 1, cytosolic	191	0.886600018	0.3233123	Yes
row_2	ACADM	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	482	0.588400006	0.39618394	Yes
row_3	AUH	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase	733	0.465499878	0.4510467	Yes
row_4	OXCT1	OXCT1	3-oxoacid CoA transferase 1	999	0.387199998	0.48894963	Yes
row_5	ACAT2	ACAT2	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	1200	0.337000012	0.5260912	Yes
row_6	ACAA2	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	1613	0.260400057	0.51989967	Yes

row_7	ACAT1	ACAT1	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	1632	0.257800102	0.5666072	Yes
row_8	PCCB	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide	1671	0.251099944	0.609327	Yes
row_9	HMGCS1	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1770	0.235199988	0.6408845	Yes
row_10	HADHA	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coe	2748	0.103199959	0.52815574	No
row_11	HIBCH	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase	3229	0.050300002	0.47269547	No
row_12	ECHS1	ECHS1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	3272	0.044799984	0.47554427	No
row_13	IVD	IVD	isovaleryl Coenzyme A dehydrogenase	3438	0.029000044	0.4587121	No
row_14	BCAT2	BCAT2	branched chain aminotransferase 2, mitochondrial	3440	0.028700113	0.46404794	No
row_15	BCKDHB	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine dise	4697	-0.104199886	0.3136998	No
row_16	HSD17B4	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	6017	-0.271700144	0.1867461	No

Prostaglandin Leukotriene Metabolism

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	TPO	TPO	thyroid peroxidase	6	2.168400049	0.31950608	Yes
row_1	ALOX5	ALOX5	arachidonate 5-lipoxygenase	109	1.093800068	0.46726263	Yes
row_2	PLA2G4A	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	114	1.087199926	0.6273233	Yes
row_3	PGDS	PGDS	-	818	0.437399864	0.5966792	Yes
row_4	CBR1	CBR1	carbonyl reductase 1	923	0.406199932	0.6425915	Yes
row_5	PRDX6	PRDX6	peroxiredoxin 6	1214	0.334999979	0.65278274	Yes
row_6	PRDX2	PRDX2	peroxiredoxin 2	3072	0.065700054	0.41086206	No
row_7	CBR3	CBR3	carbonyl reductase 3	3639	0.006500006	0.3351285	No
row_8	PRDX5	PRDX5	peroxiredoxin 5	3796	-0.011299968	0.3156595	No
row_9	PRDX1	PRDX1	peroxiredoxin 1	4183	-0.049299955	0.27063864	No
row_10	TBXAS1	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamily A)	4363	-0.06889987	0.25656188	No
row_11	LTA4H	LTA4H	leukotriene A4 hydrolase	4634	-0.096500039	0.23423165	No
row_12	PTGES2	PTGES2	prostaglandin E synthase 2	4991	-0.133599997	0.20572874	No
row_13	CYP4F2	CYP4F2	cytochrome P450, family 4, subfamily F, polypeptide 2	5513	-0.19660002	0.16417457	No
row_14	GGT1	GGT1	gamma-glutamyltransferase 1	6142	-0.293400049	0.12242118	No
row_15	PLA2G1B	PLA2G1B	phospholipase A2, group IB (pancreas)	6271	-0.319700003	0.15230355	No

Calcineurine NFAT Signaling

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	EGR2	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	23	1.801800251	0.10368311	Yes
row_1	IL2RA	IL2RA	interleukin 2 receptor, alpha	28	1.689100266	0.20326997	Yes

row_2	IL10	IL10	interleukin 10	72	1.297500134	0.2743371	Yes
row_3	EGR3	EGR3	early growth response 3	157	0.973499775	0.32061982	Yes
row_4	FKBP1B	FKBP1B	FK506 binding protein 1B, 12.6 kDa	181	0.91989994	0.37202328	Yes
row_5	FOSL1	FOSL1	FOS-like antigen 1	218	0.838699996	0.4168447	Yes
row_6	IFNG	IFNG	interferon, gamma	290	0.740600109	0.4510894	Yes
row_7	CD69	CD69	CD69 molecule	330	0.704599857	0.48755315	Yes
row_8	CSF2	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	532	0.561500072	0.49349603	Yes
row_9	FOS	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	980	0.389800072	0.4557956	Yes
row_10	JUNB	JUNB	jun B proto-oncogene	984	0.389300108	0.47846547	Yes
row_11	PPP3CC	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A	1111	0.359199941	0.48261854	Yes
row_12	MAPK14	MAPK14	mitogen-activated protein kinase 14	1152	0.348599911	0.49784234	Yes
row_13	PTPRC	PTPRC	protein tyrosine phosphatase, receptor type, C	1469	0.285300016	0.47176778	No
row_14	PPP3CB	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A bet	1535	0.275099993	0.47923356	No
row_15	IL13	IL13	interleukin 13	2027	0.195899963	0.424053	No
row_16	MEF2B	MEF2B	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2	2189	0.173300028	0.41242456	No
row_17	P2RX7	P2RX7	purinergic receptor P2X, ligand-gated ion channel, 7	2327	0.154700041	0.40295836	No
row_18	VEGF	VEGF	vascular endothelial growth factor	2415	0.144899845	0.399713	No
row_19	PPP3R1	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calc	2448	0.139400005	0.40362358	No
row_20	CREBBP	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	2460	0.137700081	0.41029012	No
row_21	VAV3	VAV3	vav 3 oncogene	2539	0.127500057	0.40723762	No
row_22	CEBPB	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	2822	0.094900131	0.37450123	No
row_23	CSNK2B	CSNK2B	casein kinase 2, beta polypeptide	2898	0.086300135	0.36941448	No
row_24	NFKBIE	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	2974	0.076799989	0.36376452	No
row_25	CSNK2A1	CSNK2A1	casein kinase 2, alpha 1 polypeptide	3202	0.052999973	0.33602625	No
row_26	SP1	SP1	Sp1 transcription factor	3475	0.024500012	0.30047688	No
row_27	NFKBIB	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	3695	0	0.270685	No
row_28	XPO5	XPO5	exportin 5	3853	-0.016000032	0.25027585	No
row_29	IL2	IL2	interleukin 2	4049	-0.035700083	0.22586517	No
row_30	PIN1	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1	4293	-0.062100053	0.19648978	No
row_31	MAPK8	MAPK8	mitogen-activated protein kinase 8	4350	-0.067499995	0.19287321	No
row_32	NFATC2	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	4455	-0.077300072	0.18330787	No
row_33	NFATC3	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	4457	-0.077499986	0.18776609	No
row_34	PPIA	PPIA	peptidylprolyl isomerase A (cyclophilin A)	4606	-0.093400002	0.1731696	No
row_35	CAMK4	CAMK4	calcium/calmodulin-dependent protein kinase IV	4862	-0.121500015	0.14568304	No

row_36	CALM3	CALM3	calmodulin 3 (phosphorylase kinase, delta)	4872	-0.122799993	0.15173838	No
row_37	SP3	SP3	Sp3 transcription factor	4979	-0.132600069	0.1451792	No
row_38	IL4	IL4	interleukin 4	5734	-0.229899883	0.056236733	No
row_39	BCL2	BCL2	B-cell CLL/lymphoma 2	5779	-0.234300137	0.064140625	No
row_40	IL6	IL6	interleukin 6 (interferon, beta 2)	6532	-0.3829	-0.015459816	No
row_41	CD3E	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	6538	-0.384499788	0.006653411	No
row_42	CABIN1	CABIN1	-	6699	-0.425499976	0.01011159	No
row_43	MAP2K7	MAP2K7	mitogen-activated protein kinase kinase 7	7185	-0.692299962	-0.014825823	No
row_44	NFKB2	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	7212	-0.729699969	0.02489435	No

Alanine and Aspartate Metabolism

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	GPT2	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	78	1.266599894	0.21730758	Yes
row_1	GAD1	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	305	0.727699995	0.31759968	Yes
row_2	GOT2	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	566	0.546499968	0.380683	Yes
row_3	PDHA1	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	713	0.474799991	0.4463178	Yes
row_4	DLAT	DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase comp	817	0.4375	0.5110699	Yes
row_5	ASRGL1	ASRGL1	asparaginase like 1	962	0.395099878	0.56263655	Yes
row_6	GOT1	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	1096	0.36349988	0.6100089	Yes
row_7	PDHB	PDHB	pyruvate dehydrogenase (lipoamide) beta	1766	0.237300038	0.5620276	No
row_8	DARS2	DARS2	aspartyl-tRNA synthetase 2 (mitochondrial)	1951	0.208600044	0.57461876	No
row_9	AARS	AARS	alanyl-tRNA synthetase	3176	0.055399895	0.41868737	No
row_10	ADSSL1	ADSSL1	adenylosuccinate synthase like 1	3349	0.03670001	0.4019777	No
row_11	ADSL	ADSL	adenylosuccinate lyase	3922	-0.022600055	0.32851598	No
row_12	PC	PC	pyruvate carboxylase	4338	-0.066399813	0.28421396	No
row_13	ASL	ASL	argininosuccinate lyase	4339	-0.066400051	0.29616028	No
row_14	GPT	GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	4794	-0.114400029	0.2552082	No
row_15	CAD	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	4888	-0.124199986	0.26494852	No
row_16	CRAT	CRAT	carnitine acetyltransferase	5487	-0.193300009	0.2186742	No
row_17	DARS	DARS	aspartyl-tRNA synthetase	5668	-0.221200049	0.23407441	No

ATRBRCA Pathway

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	BRCA1	BRCA1	breast cancer 1, early onset	441	0.621299744	0.06270369	Yes

row_1	BRCA2	BRCA2	breast cancer 2, early onset	585	0.53579998	0.14893456	Yes
row_2	FANCD2	FANCD2	Fanconi anemia, complementation group D2	615	0.521499872	0.24779399	Yes
row_3	FANCA	FANCA	Fanconi anemia, complementation group A	703	0.478200197	0.33025986	Yes
row_4	FANCE	FANCE	Fanconi anemia, complementation group E	824	0.43539989	0.39981815	Yes
row_5	CHEK2	CHEK2	CHK2 checkpoint homolog (S. pombe)	834	0.432800055	0.48390466	Yes
row_6	RAD51	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	950	0.39800024	0.54676884	Yes
row_7	MRE11A	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	1258	0.324900031	0.56920856	Yes
row_8	CHEK1	CHEK1	CHK1 checkpoint homolog (S. pombe)	1320	0.312400103	0.6225179	Yes
row_9	RAD1	RAD1	RAD1 homolog (S. pombe)	2878	0.08889997	0.4290647	No
row_10	NBS1	null	null	3059	0.067000031	0.41788033	No
row_11	FANCC	FANCC	Fanconi anemia, complementation group C	3517	0.019199967	0.35974056	No
row_12	RAD50	RAD50	RAD50 homolog (S. cerevisiae)	4520	-0.083499908	0.24042626	No
row_13	TP53	TP53	tumor protein p53 (Li-Fraumeni syndrome)	5295	-0.168499947	0.16875999	No
row_14	FANCF	FANCF	Fanconi anemia, complementation group F	5322	-0.171399951	0.19902033	No
row_15	ATM	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	6659	-0.414699912	0.09972895	No

Glutamate Metabolism

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	GPT2	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	78	1.266599894	0.2175047	Yes
row_1	GAD1	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	305	0.727699995	0.31792003	Yes
row_2	GMPS	GMPS	guanine monphosphate synthetase	407	0.649100065	0.4211175	Yes
row_3	GOT2	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	566	0.546499968	0.49811763	Yes
row_4	GCLM	GCLM	glutamate-cysteine ligase, modifier subunit	933	0.402199984	0.52095366	Yes
row_5	GCLC	GCLC	glutamate-cysteine ligase, catalytic subunit	1054	0.372400045	0.5717525	Yes
row_6	GOT1	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	1096	0.36349988	0.6316519	Yes
row_7	GSS	GSS	glutathione synthetase	1474	0.284999967	0.63189375	Yes
row_8	PPAT	PPAT	phosphoribosyl pyrophosphate amidotransferase	2413	0.145099998	0.5309384	No
row_9	EPRS	EPRS	glutamyl-prolyl-tRNA synthetase	3048	0.067900181	0.45726871	No
row_10	GLS	GLS	glutaminase	3557	0.014800072	0.39110836	No
row_11	GPT	GPT	glutamic-pyruvate transaminase (alanine aminotransferase)	4794	-0.114400029	0.244251	No
row_12	CAD	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	4888	-0.124199986	0.25401536	No
row_13	ALDH5A1	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenas	5731	-0.229599953	0.18128195	No
row_14	ALDH4A1	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	5855	-0.244499922	0.20864382	No

Cell Cycle KEGG

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	CCND2	CCND2	cyclin D2	253	0.773299932	0.00906201	Yes
row_1	CDC25C	CDC25C	cell division cycle 25C	369	0.673199654	0.031288303	Yes
row_2	CCNB2	CCNB2	cyclin B2	388	0.661200047	0.066052645	Yes
row_3	CDC6	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	460	0.608300209	0.090619735	Yes
row_4	E2F2	E2F2	E2F transcription factor 2	487	0.584899902	0.11999968	Yes
row_5	BUB1	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	499	0.579499722	0.15111898	Yes
row_6	CCNB1	CCNB1	cyclin B1	628	0.516300201	0.16274315	Yes
row_7	CCNA2	CCNA2	cyclin A2	690	0.483500004	0.18164794	Yes
row_8	PTTG2	PTTG2	pituitary tumor-transforming 2	718	0.473399639	0.20461576	Yes
row_9	CDC45L	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	720	0.473199844	0.23111407	Yes
row_10	CCNE1	CCNE1	cyclin E1	732	0.46660006	0.25587872	Yes
row_11	CDC2	CDC2	cell division cycle 2, G1 to S and G2 to M	747	0.459700108	0.2798463	Yes
row_12	BUB1B	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	793	0.443899632	0.29870167	Yes
row_13	CHEK2	CHEK2	CHK2 checkpoint homolog (S. pombe)	834	0.432800055	0.31761342	Yes
row_14	BUB3	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)	846	0.429499984	0.34028986	Yes
row_15	MCM4	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	947	0.39839983	0.34909207	Yes
row_16	PLK1	PLK1	polo-like kinase 1 (Drosophila)	952	0.397500038	0.37092087	Yes
row_17	ORC6L	ORC6L	origin recognition complex, subunit 6 like (yeast)	955	0.396399975	0.39296022	Yes
row_18	CDC20	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	1021	0.379300117	0.40545514	Yes
row_19	E2F1	E2F1	E2F transcription factor 1	1132	0.352799892	0.4103285	Yes
row_20	CDC25A	CDC25A	cell division cycle 25A	1168	0.344900131	0.42497382	Yes
row_21	CHEK1	CHEK1	CHK1 checkpoint homolog (S. pombe)	1320	0.312400103	0.42198816	Yes
row_22	PTTG1	PTTG1	pituitary tumor-transforming 1	1322	0.312299728	0.43943006	Yes
row_23	RB1	RB1	retinoblastoma 1 (including osteosarcoma)	1342	0.310000062	0.45429054	Yes
row_24	CDK2	CDK2	cyclin-dependent kinase 2	1387	0.300500035	0.46521074	Yes
row_25	CDC7	CDC7	CDC7 cell division cycle 7 (S. cerevisiae)	1529	0.276799917	0.46158352	Yes
row_26	MAD2L1	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	1686	0.248500109	0.4543201	Yes
row_27	PCNA	PCNA	proliferating cell nuclear antigen	1825	0.227400064	0.448321	Yes
row_28	MCM2	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	1854	0.222599983	0.45703608	Yes
row_29	MDM2	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	1864	0.22179997	0.46829432	Yes
row_30	MCM6	MCM6	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cere	2128	0.183300018	0.44278538	No
row_31	MCM5	MCM5	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae	2295	0.159100056	0.42912775	No

row_32	ESPL1	ESPL1	extra spindle poles like 1 (S. cerevisiae)	2473	0.136000156	0.4126715	No
row_33	ORC1L	ORC1L	origin recognition complex, subunit 1-like (yeast)	2518	0.130399942	0.41401747	No
row_34	HDAC4	HDAC4	histone deacetylase 4	2561	0.124500036	0.4153038	No
row_35	CDC25B	CDC25B	cell division cycle 25B	2722	0.105400085	0.39944094	No
row_36	E2F6	E2F6	E2F transcription factor 6	2726	0.10529995	0.4049592	No
row_37	MCM3	MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	2750	0.10289979	0.40761796	No
row_38	HDAC5	HDAC5	histone deacetylase 5	3504	0.021100044	0.306231	No
row_39	ORC4L	ORC4L	origin recognition complex, subunit 4-like (yeast)	4031	-0.034100056	0.236498	No
row_40	HDAC8	HDAC8	histone deacetylase 8	4163	-0.047199965	0.2213097	No
row_41	WEE1	WEE1	WEE1 homolog (S. pombe)	4284	-0.061100006	0.20840225	No
row_42	SMC1L1	null	null	4444	-0.076400042	0.19104332	No
row_43	ORC2L	ORC2L	origin recognition complex, subunit 2-like (yeast)	4497	-0.081200004	0.18853025	No
row_44	HDAC1	HDAC1	histone deacetylase 1	4620	-0.095499992	0.17728657	No
row_45	CDK4	CDK4	cyclin-dependent kinase 4	4976	-0.132500172	0.13638595	No
row_46	TFDP1	TFDP1	transcription factor Dp-1	5119	-0.149300098	0.12544604	No
row_47	TP53	TP53	tumor protein p53 (Li-Fraumeni syndrome)	5295	-0.168499947	0.111091524	No
row_48	PRKDC	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	5603	-0.210200071	0.08110293	No
row_49	GADD45A	GADD45A	growth arrest and DNA-damage-inducible, alpha	5608	-0.211300135	0.09245129	No
row_50	CCNE2	CCNE2	cyclin E2	5964	-0.260299921	0.058744006	No
row_51	CDC14A	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	6652	-0.413300037	-0.011576954	No
row_52	ATM	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	6659	-0.414699912	0.010947528	No
row_53	MAD1L1	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	7101	-0.617699981	-0.014358153	No
row_54	CDKN2A	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	7316	-0.96420002	0.010761493	No

GPCR DB

NAME	PROBE	GENE SYMBOL	GENE_TITLE	RANK	METRIC SCORE	RUNNING ES	CORE ENRICH
row_0	GPR56	GPR56	G protein-coupled receptor 56	14	1.989099979	0.28498083	Yes
row_1	CCR5	CCR5	chemokine (C-C motif) receptor 5	266	0.76279974	0.36097574	Yes
row_2	LPHN2	LPHN2	latrophilin 2	297	0.732099891	0.46249688	Yes
row_3	CXCR3	CXCR3	chemokine (C-X-C motif) receptor 3	457	0.610599995	0.52901024	Yes
row_4	CCR3	CCR3	chemokine (C-C motif) receptor 3	909	0.411400318	0.52721685	Yes
row_5	LGR6	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	996	0.387300014	0.571419	Yes
row_6	F2R	F2R	coagulation factor II (thrombin) receptor	1543	0.274299979	0.5369762	Yes
row_7	CCR2	CCR2	chemokine (C-C motif) receptor 2	1550	0.27270031	0.5754932	Yes

row_8	GPR17	GPR17	G protein-coupled receptor 17	2226	0.168500066	0.508307	No
row_9	EDG1	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	3332	0.038999915	0.36416218	No
row_10	LTB4R2	LTB4R2	leukotriene B4 receptor 2	3924	-0.023000002	0.28737637	No
row_11	GPR135	GPR135	G protein-coupled receptor 135	4298	-0.0625	0.24583474	No
row_12	EBI2	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	4860	-0.121200085	0.18727799	No
row_13	CIDEB	CIDEB	cell death-inducing DFFA-like effector b	5028	-0.137899876	0.18453176	No
row_14	EMR3	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	5645	-0.217899978	0.13246697	No
row_15	GPR132	GPR132	G protein-coupled receptor 132	5713	-0.227099985	0.15613948	No
row_16	P2RY11	P2RY11	purinergic receptor P2Y, G-protein coupled, 11	5780	-0.234499931	0.18101476	No
row_17	RLN3R1	null	null	5974	-0.261700034	0.19259965	No