

ID REF	SYMBOL	UP/DOWN REGULATED	NAME	Description	Tag	Function
1562659_at	LINC02139			(lincRNA) genes have diverse features that distinguish them from mRNA-encoding genes and exercise functions such as remodelling chromatin and genome architecture, RNA stabilization and transcription regulation, including enhancer-associated activity.	Transcription Regulation	
234666_at		Up	long intergenic non-protein coding RNA 2139			
		Up	unknown		Unknown	
	GLI4					<p>Molecular Function: RNA polymerase II cis-regulatory region sequence-specific DNA binding (GO: 0000978) DNA-binding transcription factor activity, RNA polymerase II-specific (GO: 0000981) molecular_function (GO:0003674) protein binding (GO:0005515) metal ion binding (GO:0046872)</p> <p>Biological Process: regulation of DNA-templated transcription (GO:0006355) regulation of transcription by RNA polymerase II (GO:0006357) biological_process (GO:0008150)</p> <p>Cellular Component: nucleus (GO:0005634)</p>
238364_x_at		Up	GLI family zinc finger 4	Predicted to enable DNA-binding transcription factor activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Predicted to be involved in regulation of transcription, DNA-templated. Predicted to be located in nucleus	Transcription Regulation	
1555262_a_at	MAGI1	Up	membrane associated guanylate kinase, WW and PDZ domain containing 1	ATP, protein and alpha actinin binding protein	Cell Adhesion, Extracellular Matrix and Cytoskeleton Proteins	scaffolding protein at cell-cell junctions and involved in signal transduction to regulateacid-induced sodium ion channel 3 expression at the cell surface
224253_at	EXOC5	Up	exocyst complex component 5	protein component of exocyst transporter complex	Transport	involved in assembly of exocyst complex for targeting exocytic vesicles to specific docking
	FTH1					<p>Molecular Function: ferroxidase activity (GO:0004322) iron ion binding (GO:0005506) protein binding (GO:0005515) ferrous iron binding (GO:0008198) ferrous iron binding (GO:0008198) ferric iron binding (GO:0008199) identical protein binding (GO:0042802) iron ion sequestering activity (GO:0140315)</p> <p>Biological Process: iron ion transport (GO:0006826) intracellular iron ion homeostasis (GO:0006879) intracellular sequestering of iron ion (GO:0006880) immune response (GO:0006955) negative regulation of cell population proliferation (GO:0008285) negative regulation of fibroblast proliferation (GO:0048147)</p> <p>Cellular Component: extracellular region (GO:0005576) nucleus (GO:0005634) cytoplasm (GO:0005737) cytosol (GO:0005829) intracellular ferritin complex (GO:0008043) autolysosome (GO:0044754) extracellular exosome (GO:0070062) tertiary granule lumen (GO:1904724) ficolin-1-rich granule lumen (GO:1904813)</p>
200748_s_at		Up	ferritin heavy chain 1	Encodes ferritin heavy chain a major non-haem iron storage protein	Transport, Immune Response, Cell Proliferation	
	HECW1					<p>Molecular Function: protein binding (GO:0005515) ubiquitin protein ligase activity (GO:0061630) ubiquitin protein ligase activity (GO:0061630)</p> <p>Biological Process: protein ubiquitination (GO:0016567) protein ubiquitination (GO:0016567) regulation of dendrite morphogenesis (GO:0048814) negative regulation of canonical Wnt signaling pathway (GO:0090090) negative regulation of sodium ion transmembrane transporter activity (GO: 2000650)</p> <p>Cellular Component: cytoplasm (GO:0005737) cytosol (GO:0005829)</p>
215584_at		Down	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	Predicted to enable ubiquitin protein ligase activity. Predicted to be involved in several processes, including cellular protein metabolic process; negative regulation of sodium ion transmembrane transporter activity; and regulation of dendrite morphogenesis. Located in cytosol.	Cell Signalling	

238138_at	CANX	Up	calnexin	Calcium-binding molecular chaperone protein that interacts with newly synthesized N-linked glycoproteins in the endoplasmic reticulum.	Protein Synthesis	facilitate protein folding and assembly in ER has protein folding quality control role to retain wrongly folded proteins in ER for ubiquitin degradation may function as a signaling complex regulating thymocyte maturation play a role in receptor-mediated endocytosis at the synapse
241674_s_at		Up	unknown		Unknown	
210496_at		Down	unknown		Unknown	
	TRIM8		tripartite motif containing 8			<p>Molecular Function: transcription coactivator activity (GO:0003713) protein binding (GO:0005515) zinc ion binding (GO:0008270) identical protein binding (GO:0042802) protein homodimerization activity (GO:0042803) ubiquitin protein ligase activity (GO:0061630)</p> <p>Biological Process: I-kappaB kinase/NF-kappaB signaling (GO:0007249) positive regulation of autophagy (GO:0010508) stem cell population maintenance (GO:0019827) negative regulation of viral transcription (GO:0032897) positive regulation of I-kappaB kinase/NF-kappaB signaling (GO:0043123) suppression of viral release by host (GO:0044790) innate immune response (GO:0045087) positive regulation of DNA-templated transcription (GO:0045893) negative regulation of viral entry into host cell (GO:0046597) positive regulation of DNA-binding transcription factor activity (GO:0051091) positive regulation of NF-kappaB transcription factor activity (GO:0051092) protein K63-linked ubiquitination (GO:0070534) positive regulation of protein localization to nucleus (GO:1900182)</p> <p>Cellular Component: nucleus (GO:0005634) cytoplasm (GO:0005737) cytosol (GO:0005829) PML body (GO:0016605)</p>
221012_s_at		Up		Encodes a member of the tripartite motif (TRIM) protein family. Suspected to be an E3 ubiquitin-protein ligase	Transcription Regulation, Immune Response	
221865_at	TMEM268	Up	transmembrane protein 268	Family of protein with unknown function Predicted to be integral component of membrane.	Unknown	Cellular Component: membrane (GO:0016020)
	PSD4		pleckstrin and Sec7 domain containing 4			regulation of ARF protein signal transduction which regulates actin cytoskeleton reorganisation involved in vesicle transport, membrane recycling and cleavage furrow formation
236616_at		Down		lipid binding guanine nucleotide exchange factor	Cell Signalling	
239656_at	LHFPL3-AS2	Up	LHFPL3 antisense RNA 2	long noncoding RNA tumour suppressor gene	Cell Signalling	inhibit migration and invasion of non-small cell lung cancer cells
	TNFSF8		TNF superfamily member 8			<p>Molecular Function: signaling receptor binding (GO:0005102) cytokine activity (GO:0005125) tumor necrosis factor receptor binding (GO:0005164) protein binding (GO:0005515)</p> <p>Biological Process: immune response (GO:0006955) signal transduction (GO:0007165) cell-cell signaling (GO:0007267) regulation of T cell proliferation (GO:0042129) CD8-positive, alpha-beta T cell differentiation (GO:0043374) positive regulation of transcription by RNA polymerase II (GO:0045944) defense response to Gram-positive bacterium (GO:0050830)</p> <p>Cellular Component: extracellular space (GO:0005615) plasma membrane (GO:0005886)</p>
235735_at		Up		Encodes a cytokine that belongs to the tumor necrosis factor (TNF) ligand family. Inhibitory role in modulating Ig class switch in B cells Induce cell death and regulates cell proliferation in lymphoma cell lines	Cell Signalling	
	ZNF592		zinc finger protein 592			<p>Molecular Function: DNA binding (GO:0003677) protein binding (GO:0005515) PH domain binding (GO:0042731) insulin receptor substrate binding (GO:0043560) metal ion binding (GO:0046872)</p> <p>Biological Process: negative regulation of insulin receptor signaling pathway (GO:0046627) regulation of peptidyl-tyrosine phosphorylation (GO:0050730)</p> <p>Cellular Component: nucleus (GO:0005634)</p>
213389_at		Up		Gene is thought to play a role in a complex developmental pathway and the regulation of genes involved in cerebellar development	Cell Signalling	

1555856_s_at	AKR1C1	Up	aldo-keto reductase family 1 member C1	metabolic oxidoreductase enzyme involved in lipid metabolism involved in cholesterol homeostasis	Metabolism	catalyzes the NADH and NADPH-dependent reduction of aldehyde and ketones to their respective alcohols to regulate the metabolism of hormones (androgens, prostaglandin), vitamin A and steroids binds to bile acids to facilitate bile acid metabolism and transport
235418_at	FAHD2A	Up	fumarylacetoacetate hydrolase domain containing 2A	Predicted to enable hydro-lyase activity. Fumarylacetoacetate hydrolase catalyses the hydrolytic cleavage of a carbon-carbon bond in fumarylacetoacetate to yield fumarate and acetoacetate as the final step in phenylalanine and tyrosine degradation	Metabolism	Molecular Function: protein binding (GO:0005515) hydrolase activity (GO:0016787) metal ion binding (GO:0046872)
236104_at	HNRNPLL	Up	heterogeneous nuclear ribonucleoprotein L like	A master regulator of activation-induced alternative splicing in T cells. Alters splicing of CD45, a tyrosine phosphatase essential for T-cell development and activation	Transcription Regulation	Molecular Function: RNA binding (GO:0003723) mRNA binding (GO:0003729) mRNA binding (GO:0003729) protein binding (GO:0005515) Biological Process: mRNA processing (GO:0006397) positive regulation of RNA splicing (GO:0033120) regulation of RNA splicing (GO:0043484) Cellular Component: nucleus (GO:0005634) membrane (GO:0016020) synapse (GO:0045202) ribonucleoprotein complex (GO:1990904)
1559551_at		Down	unknown		Unknown	

			O-linked N-acetylglucosamine (GlcNAc) transferase			<p>Molecular Function: protein binding (GO:0005515) phosphatidylinositol-3,4,5-trisphosphate binding (GO:0005547) acetylglucosaminyltransferase activity (GO:0008375) chromatin DNA binding (GO:0031490) translation regulator activity (GO:0045182) protein O-acetylglucosaminyltransferase activity (GO:0097363) transcription regulator activator activity (GO:0140537)</p> <p>Biological Process: negative regulation of transcription by RNA polymerase II (GO:0000122) mitophagy (GO:0000423) positive regulation of transcription from RNA polymerase II promoter by glucose (GO:0000432) regulation of glycolytic process (GO:0006110) regulation of gluconeogenesis (GO:0006111) chromatin organization (GO:0006325) regulation of transcription by RNA polymerase II (GO:0006357) protein O-linked glycosylation (GO:0006493) apoptotic process (GO:0006915) signal transduction (GO:0007165) response to nutrient (GO:0007584) protein processing (GO:0016485) hemopoiesis (GO:0030097) negative regulation of cell migration (GO:0030336) negative regulation of transforming growth factor beta receptor signaling pathway (GO:0030512) negative regulation of protein ubiquitination (GO:0031397) negative regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032435) response to insulin (GO:0032868) circadian regulation of gene expression (GO:0032922) regulation of Rac protein signal transduction (GO:0035020) histone H4-K5 acetylation (GO:0043981) histone H4-K8 acetylation (GO:0043982) histone H4-K16 acetylation (GO:0043984) positive regulation of translation (GO:0045727) positive regulation of proteolysis (GO:0045862) positive regulation of DNA-templated transcription (GO:0045893) positive regulation of transcription by RNA polymerase II (GO:0045944) regulation of insulin receptor signaling pathway (GO:0046626) positive regulation of lipid biosynthetic process (GO:0046889) phosphatidylinositol-mediated signaling (GO:0048015) positive regulation of histone H3-K4 methylation (GO:0051571) regulation of synapse assembly (GO:0051963) regulation of necroptotic process (GO:0060544) regulation of neurotransmitter receptor localization to postsynaptic specialization membrane (GO:0098696) positive regulation of cold-induced thermogenesis (GO:0120162) regulation of dosage compensation by inactivation of X chromosome (GO:1900095) negative regulation of stem cell population maintenance (GO:1902455) positive regulation of stem cell population maintenance (GO:1902459)</p> <p>Cellular Component: histone acetyltransferase complex (GO:0000123) nucleus (GO:0005634) nucleus (GO:0005634) nucleoplasm (GO:0005654) nucleoplasm (GO:0005654) cytosol (GO:0005829) cytosol (GO:0005829) plasma membrane (GO:0005886) Sin3 complex (GO:0016580) protein N-acetylglucosaminyltransferase complex (GO:0017122) mitochondrial membrane (GO:0031966) protein-containing complex (GO:0032991) cell projection (GO:0042995) NSL complex (GO:0044545) glutamatergic synapse (GO:0098978)</p>
212307_s_at	OGT	Down		Encodes a glycosyltransferase that catalyzes the addition of a single N-acetylglucosamine in O-glycosidic linkage to serine or threonine residues	Transcription Regulation, Metabolism, Cell Signalling, Protein Synthesis	
222170_at	ZNF213-AS1	Down	ZNF213 antisense RNA 1 (head to head)	long non coding RNA for	Transcription Regulation, Cell Proliferation	regulates transcription factors involved in cell growth, migration, and proliferation

	GABRB3		gamma-aminobutyric acid type A receptor subunit beta3			<p>Molecular Function: GABA-A receptor activity (GO:0004890) GABA-gated chloride ion channel activity (GO:0022851) GABA-gated chloride ion channel activity (GO:0022851) GABA-gated chloride ion channel activity (GO:0022851) neurotransmitter receptor activity (GO:0030594) identical protein binding (GO:0042802)</p> <p>Biological Process: signal transduction (GO:0007165) gamma-aminobutyric acid signaling pathway (GO:0007214) gamma-aminobutyric acid signaling pathway (GO:0007214) chemical synaptic transmission (GO:0007268) monoatomic ion transmembrane transport (GO:0034220) regulation of membrane potential (GO:0042391) nervous system process (GO:0050877) synaptic transmission, GABAergic (GO:0051932) roof of mouth development (GO:0060021) cellular response to histamine (GO:0071420) chloride transmembrane transport (GO:1902476) chloride transmembrane transport (GO:1902476) chloride transmembrane transport (GO:1902476) inhibitory synapse assembly (GO:1904862)</p> <p>Cellular Component: plasma membrane (GO:0005886) plasma membrane (GO:0005886) plasma membrane (GO:0005886) cytoplasmic vesicle membrane (GO:0030659) chloride channel complex (GO:0034707) neuron projection (GO:0043005) synapse (GO:0045202) postsynaptic membrane (GO:0045211) GABA-A receptor complex (GO:1902711) GABA-A receptor complex (GO:1902711) GABA-A receptor complex (GO:1902711) GABA-A receptor complex (GO:1902711) GABA-A receptor complex (GO:1902711)</p>
227830_at		Up		Encoded protein is one the subunits of a multi-subunit chloride channel that serves as the receptor for gamma-aminobutyric acid, a major inhibitory neurotransmitter of the mammalian nervous system	Transport, Cell Signalling	
	ANXA7		annexin A7			<p>Molecular Function: RNA binding (GO:0003723) integrin binding (GO:0005178) calcium ion binding (GO:0005509) protein binding (GO:0005515) calcium-dependent phospholipid binding (GO:0005544) calcium-dependent protein binding (GO:0048306)</p> <p>Biological Process: autophagy (GO:0006914) negative regulation of gene expression (GO:0010629) epithelial cell differentiation (GO:0030855)</p> <p>Cellular Component: nucleus (GO:0005634) nucleus (GO:0005634) cytoplasm (GO:0005737) endoplasmic reticulum membrane (GO:0005789) membrane (GO:0016020) chromaffin granule membrane (GO:0042584) collagen-containing extracellular matrix (GO:0062023) extracellular exosome (GO:0070062)</p>
201366_at		Up		A member of the annexin family of calcium-dependent phospholipid binding proteins.	Transcription Regulation, Cell Differentiation	
			inversin			
211054_at	INVS	Up		calmodulin binding renal developmental protein involved in Wnt signaling pathway	Cell Signalling	Inhibits the canonical Wnt pathway by targeting cytoplasmic disheveled (DVL1) for degradation by the ubiquitin-proteasome to oppose the repression of terminal differentiation of tubular epithelial cells Involved in the organization of apical junctions in kidney cells
57082_at	LDLRAP1	Up	low density lipoprotein receptor adaptor protein 1	Cytosolic protein with a phosphotyrosine binding protein that interacts with the cytoplasmic tail of the LDL receptor	Cell Signalling	Essential for LDL receptor function
1563546_at		Up	unknown		Unknown	
	VWA3B		von Willebrand factor A domain containing 3B			encodes an intracellular protein with VWA domains that function in transcription, DNA repair, ribosomal and membrane transport and the proteasome
1562371_s_at		Up		Expression in fallopian tube, respiratory epithelia and testis.	Transport, Transcription Regulation	
			MOS proto-oncogene, serine/threonine kinase			activates the MAP kinase cascade through direct phosphorylation of the MAP kinase activator MEK that promote meiotic division via controlling meiotic spindle and chromatin organisation
221367_at	MOS	Down		proto oncogene for Serine/threonine-protein kinase	Cell Signalling, Cell Proliferation	

238569_at	GABBR1	Up	gamma-aminobutyric acid type B receptor subunit 1	receptor for Gamma-aminobutyric acid (GABA)	Cell Signalling	G protein-coupled GABA receptor activity; GABA is main inhibitory neurotransmitter in the mammalian central nervous system
233491_at			minichromosome maintenance domain containing 2			Molecular Function DNA binding (GO:0003677) protein binding (GO:0005515) ATP binding (GO:0005524)
1552359_at	MCMD2	Down		protein localised to actin	Cell Proliferation	Biological Process double-strand break repair via break-induced replication (GO:0000727) DNA duplex unwinding (GO:0032508) meiotic cell cycle (GO:0051321)
234059_at	RPL26L1-AS1	Down	RPL26L1 antisense RNA 1	long non coding RNA that may encode ribosomal protein	Protein Synthesis, Unknown	
241150_at	SPTAN1	Up	spectrin alpha, non-erythrocytic 1	calmodulin binding actin capping protein	Cell Adhesion, Extracellular Matrix and Cytoskeleton Proteins	involved in calcium-dependent movement and reorganisation of the actin cytoskeleton at the membrane
1569790_at		Up	unknown		Unknown	
201471_s_at	SQSTM1	Up	sequestosome 1	Mainly protein binding	Cell Signalling	Especially ubiquitin-related binding
227673_at	POLR1H	Up	RNA polymerase I subunit H	RNA polymerase 1 transcribes rRNA	Cell Proliferation	Involved mainly in the termination and cleavage of transcripts, The encoded protein contains two potential zinc-binding motifs and may play a role in regulation of cell proliferation
210390_s_at	CCL15	Down	C-C motif chemokine ligand 15	cytokine involved in chemotaxis process	Immune Response	binds to CC chemokine receptor CCR1 and acts as chemotactic factor that attracts T-cells and monocytes, but not neutrophils, eosinophils, or B-cells.
214884_at	MCF2	Up	MCF.2 cell line derived transforming sequence	guanyl-nucleotide exchange factor activity	Cell Signalling	exerts control over some members of the Rho family of small GTPases
243530_at		Up	unknown		Unknown	
233114_at		Down	unknown		Unknown	
240406_at		Up	unknown		Unknown	
241317_at		Down	unknown		Unknown	
217614_at	ARHGAP45	Up	Rho GTPase activating protein 45	GTPase activator	Cell Adhesion, Extracellular Matrix and Cytoskeleton Proteins	GTPase activator for the Rho-type GTPases (RhoGAP) domain that would be able to negatively regulate the actin cytoskeleton as well as cell spreading
1555199_at	GOSR1	Down	golgi SNAP receptor complex member 1	essential to SNARE	Transport	trafficking membrane protein receptor involved in transport from the ER to the Golgi apparatus as well as in intra-Golgi transport
215723_s_at	PLD1	Down	phospholipase D1	phospholipase selective for phosphatidylcholine involved in signal transduction, membrane trafficking, and the regulation of mitosis	Cell Signalling	catalyzes the hydrolysis of phosphatidylcholine in order to yield phosphatidic acid and choline
213818_x_at	TMEM223	Up	transmembrane protein 223	Mitochondrial ribosome-associated protein	Metabolism	Molecular Function mitochondrial ribosome binding (GO:0097177) Biological Process nervous system development (GO:0007399) mitochondrial cytochrome c oxidase assembly (GO:0033617)
204106_at	TESK1	Up	testis associated actin remodelling kinase 1	serine/threonine protein kinase	Cell Adhesion, Extracellular Matrix and Cytoskeleton Proteins	preventing microtubule breakdown via inhibition of TAOK1/MARKK kinase activity inhibits podocyte motility, promotes integrin-mediated cell spreading and enhance stress fiber formation via phosphorylation of cofilin to regulate actin cytoskeleton dynamics suppresses ciliogenesis suppression of ciliary vesicle directional trafficking by facilitating YAP1 nuclear localization where it acts as a transcriptional corepressor involved in meiotic spermatogenesis
1557336_at	SUCLG2-DT	Down	SUCLG2 divergent transcript	transcripte variant encodes a GTP-specific beta subunit of succinyl-CoA synthetase with ligase activity	Metabolism	required in assembly of succinyl-CoA synthase that catalyzes the reversible reaction involving the formation of succinyl-CoA and succinate in citric acid cycle for metabolism

213138_at	ARID5A	Up	AT-rich interaction domain 5A	transcription factor that binds to AT rich region	Transcription Regulation, Immune Response, Cell Differentiation, Cell Signalling	<p>Molecular Function transcription cis-regulatory region binding (GO:0000976) DNA binding (GO:0003677) chromatin binding (GO:0003682) transcription corepressor activity (GO:0003714) nuclear estrogen receptor binding (GO:0030331) RNA stem-loop binding (GO:0035613) identical protein binding (GO:0042802) sequence-specific DNA binding (GO:0043565) nuclear retinoid X receptor binding (GO:0046965) nuclear thyroid hormone receptor binding (GO:0046966) nuclear androgen receptor binding (GO:0050681)</p> <p>Biological Process negative regulation of transcription by RNA polymerase II (GO:0000122) chondrocyte differentiation (GO:0002062) regulation of transcription by RNA polymerase II (GO:0006357) positive regulation of type II interferon production (GO:0032729) positive regulation of interleukin-17 production (GO:0032740) positive regulation of interleukin-6 production (GO:0032755) positive regulation of tumor necrosis factor production (GO:0032760) innate immune response (GO:0045087) negative regulation of DNA-templated transcription (GO:0045892) positive regulation of transcription by RNA polymerase II (GO:0045944) cellular response to lipopolysaccharide (GO:0071222) cellular response to estrogen stimulus (GO:0071391) positive regulation of protein acetylation (GO:1901985) positive regulation of T-helper 17 type immune response (GO:2000318) positive regulation of T-helper 1 cell cytokine production (GO:2000556)</p>
-----------	--------	----	-------------------------------	---	---	---