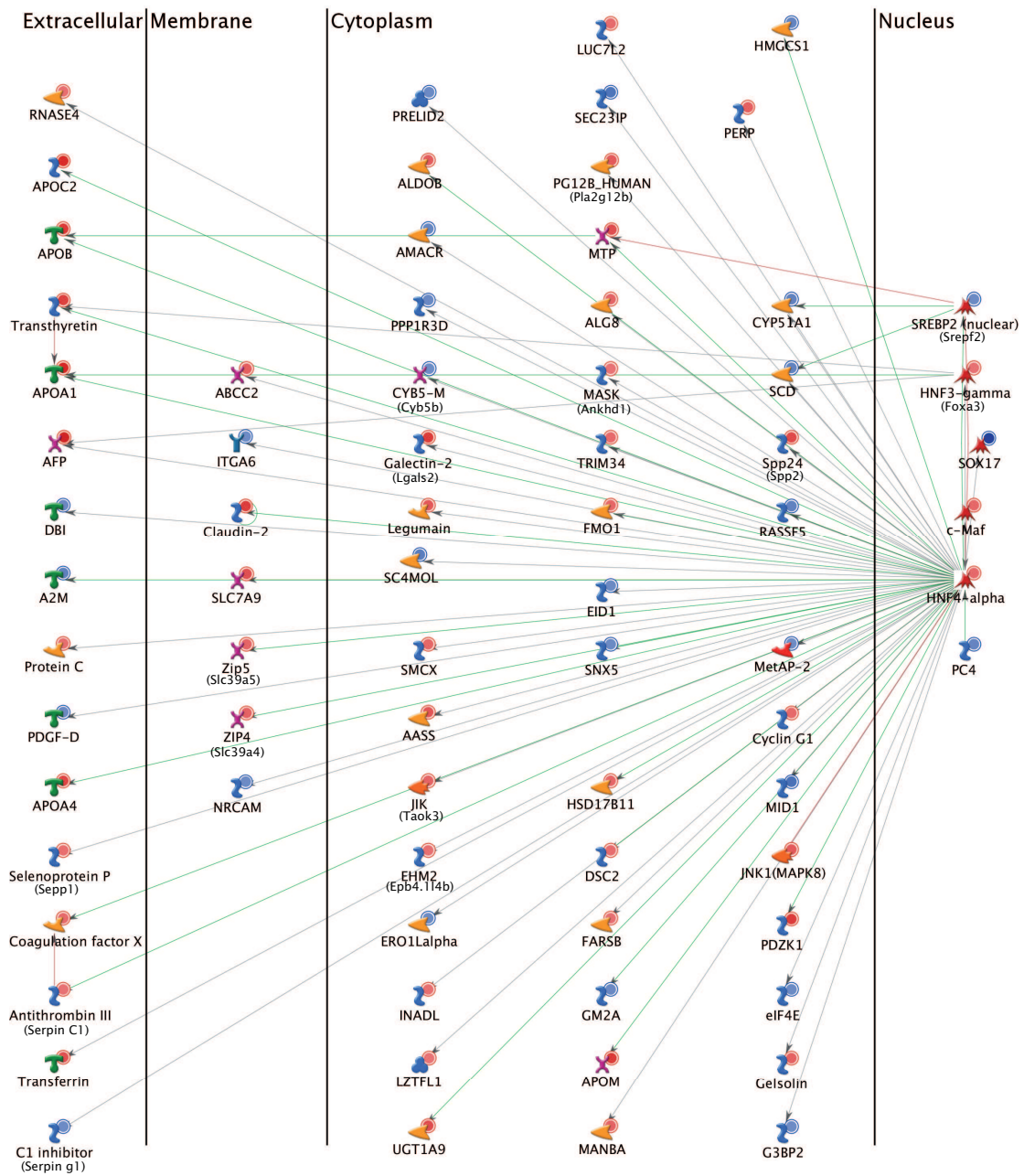


SUPPLEMENTARY MATERIAL

corresponding to:

***Sox17*-dependent gene expression and early heart and gut development in *Sox17*-deficient mouse embryos**

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Supplementary Figure S1. Putative Sox17 transcriptional network. Results of analysis using Metacore (www.genego.com) showing the networks of transcriptional targets of Sox17 activity that may be mediated by Hnf4, based the findings of CHIP studies indicating either a known effect on transcription or evidence for binding of Hnf4 to putative regulatory regions.

Supplementary Table S1: Genes that were significantly up- or down-regulated in *Sox17*^{-/-} embryos compared with wild-type embryos ordered by log₂ fold change

Symbol	Probe	Description	GenBank	Gene Ontology – biological function	Log ₂ FoldChange	P
<i>Sox17</i>	1429177_x_at 1421657_a_at	SRY-box containing gene 17	AK004781	angiogenesis, vasculogenesis, transcription, regulation of transcription, DNA-dependent negative regulation of Wnt receptor signaling pathway	-4.88 -1.24	0 0.000592
<i>Eif2s3y</i>	1417210_at	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	NM_012011	translation	-3.7	0.019055
<i>Ddx3y</i>	1426438_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	AA210261		-3.65	0.015622
<i>Prl8a2</i>	1448608_at	prolactin family 8, subfamily a, member 2	NM_010088	response to hypoxia, maternal process involved in pregnancy	-2.72	2.5e-05
<i>Jarid1d</i>	1424903_at	jumonji, AT rich interactive domain 1D (Rbp2 like)	AF127244	chromatin modification, oxidation reduction	-2.39	0.016077
<i>Uty</i>	1426598_at 1422247_a_at	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	BB742957	chromatin modification, oxidation reduction	-2.33 -1.35	0.016234 0.034294
<i>Mid1</i>	1438239_at	midline 1	BG073178	ubiquitin-dependent protein catabolic process, negative regulation of microtubule depolymerization	-1.99	0.00304
<i>Nepn</i>	1419065_at	nephrocan	NM_025684	negative regulation of specific transcription from RNA polymerase II promoter, extracellular matrix organization, negative regulation of transforming growth factor beta receptor signaling pathway	-1.92	3.2e-05

<i>Myl3</i>	1427768_s_at	myosin, light polypeptide 3	X67685		-1.88	0.024414
<i>Sec23ip</i>	1439882_at	Sec23 interacting protein	BE685845		-1.8	0.005151
<i>Actc1</i>	1415927_at	actin, alpha, cardiac muscle 1	NM_009608	apoptosis, muscle thin filament assembly, actomyosin structure, organization cardiac myofibril assembly, cardiac muscle tissue morphogenesis	-1.58	0.037231
<i>A230083H22Rik</i>	1432198_at	RIKEN cDNA A230083H22 gene	AK018172		-1.53	0.011163
<i>Ctla2a</i>	1416811_s_at	cytotoxic T lymphocyte-associated protein 2 alpha	NM_007796		-1.51 -1.05	2e-06 0.000175
<i>Adm</i>	1447839_x_at	adrenomedullin	AV378441	heart development, positive regulation of cell proliferation	-1.43	0.007703
<i>Myl7</i>	1449071_at	myosin, light polypeptide 7, regulatory	NM_022879		-1.38	0.009943
<i>3110040N11Rik</i>	1450972_at	RIKEN cDNA 3110040N11 gene	AK019261		-1.33	6.7e-05
<i>Myl4</i>	1422580_at	myosin, light polypeptide 4	NM_010858		-1.33	0.030957
<i>Rpl17</i>	1453752_at	ribosomal protein L17	BF453369	translation	-1.28	0.033485
<i>Sc4mol</i>	1423078_a_at	sterol-C4-methyl oxidase-like	AK005441	steroid biosynthetic process, lipid biosynthetic process, sterol biosynthetic process, oxidation reduction	-1.24	5.4e-05
<i>6720422M22Rik</i>	1437798_at	RIKEN cDNA 6720422M22 gene	BB051012		-1.21	0.000251
<i>Sfrp1</i>	1460187_at 1428136_at	secreted frizzled-related protein 1	BI658627	somitogenesis, multicellular organismal development, anterior/posterior pattern formation, Wnt receptor signaling pathway, cell differentiation prostate gland development	-1.21 -0.7	0.012182 0.032311
<i>Fosb</i>	1422134_at	FBJ osteosarcoma oncogene B	NM_008036	regulation of transcription, DNA-dependent	-1.17	0.018573
<i>Idi1</i>	1423804_a_at 1451122_at	isopentenyl-diphosphate delta isomerase	BC004801	steroid biosynthetic process, cholesterol biosynthetic process, isoprenoid biosynthetic process, lipid biosynthetic process, carotenoid	-1.09 -1.02	0.00046 0.000377

				biosynthetic process, sterol biosynthetic process		
<i>Insig1</i>	1454671_at	insulin induced gene 1	BB005488	lipid metabolic process, response to sterol depletion, steroid metabolic process, cholesterol metabolic process	-1.08	0.00383
<i>Ldlr</i>	1421821_at 1459403_at	low density lipoprotein receptor	AF425607	lipid metabolic process, transport, lipid transport. endocytosis. steroid metabolic process. cholesterol metabolic process. cholesterol transport. lipoprotein metabolic process. lipoprotein catabolic process. lipoprotein catabolic process cholesterol homeostasis	-1.07 -0.63	7.7e-05 0.017534
<i>A2m</i>	1434719_at	alpha-2-macroglobulin	BB185854	female pregnancy	-1.06	0.000593
<i>Ctla2b</i>	1452352_at	cytotoxic T lymphocyte-associated protein 2 beta	BG064656		-1.06	0.0039
<i>Cryab</i>	1434369_a_at	crystallin, alpha B	AV016515	transmembrane receptor protein tyrosine kinase signaling pathway muscle development response to heat Z camera-type eye development	-1.04	0.011805
<i>Myocd</i>	1425978_at	myocardin	AF384055	regulation of cell growth by extracellular stimulus, vasculogenesis, nucleic acid binding, transcription, regulation of transcription, DNA-dependent, regulation of transcription from RNA polymerase II promoter, heart development ,positive regulation of cell proliferation, muscle cell differentiation, regulation of myoblast differentiation, positive regulation of transcription,, positive regulation of transcription from RNA polymerase II promoter	-1.02	0.040638
<i>Rassf5</i>	1422638_s_at	Ras association (RalGDS/AF-6) domain family member 5	NM_018750	apoptosis, cell cycle signal transduction ,intracellular signaling cascade, negative regulation of cell cycle	-1.01	0.025531

<i>Trub1</i>	1428281_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	AK011362	pseudouridine synthesis, tRNA processing	-1	0.015486
<i>Myl9</i>	1452670_at	myosin, light polypeptide 9, regulatory	AK007972		-0.98	0.013607
<i>Shisa4</i>	1438426_at	shisa homolog 4 (<i>Xenopus laevis</i>)	BF468228		-0.98	8.3e-05
<i>Cyp51</i>	1422533_at 1450646_at	cytochrome P450, family 51	NM_020010	cholesterol biosynthetic process, methyltransferase activity	-0.96 -0.85	0.004533 0.013608
<i>Fabp4</i>	1451263_a_at 1417023_a_at	fatty acid binding protein 4, adipocyte	BC002148	cytokine production, negative regulation of protein kinase activity, transport, negative regulation of transcription, cholesterol homeostasis, positive regulation of inflammatory response	-0.96 -0.54	0.004028 0.003654
<i>Tnni1</i>	1450813_a_at	troponin I, skeletal, slow 1	NM_021467	ventricular cardiac muscle morphogenesis	-0.95	0.020174
<i>ENSMUSG00000068790</i>	1452731_x_at 1428301_at	predicted gene, ENSMUSG00000068790	BM195235		-0.9 -0.83	0.000401 0.00047
<i>Gprc5b</i>	1451411_at	G protein-coupled receptor, family C, group 5, member B	BC020004	signal transduction, G-protein coupled receptor protein signaling pathway	-0.9	0.008682
<i>Idh1</i>	1422433_s_at	isocitrate dehydrogenase 1 (NADP+), soluble	NM_010497	glyoxylate cycle, tricarboxylic acid cycle, isocitrate metabolic process, glutathione metabolic process, response to oxidative stress, metabolic process, oxidation reduction	-0.89	3.8e-05
<i>Slc30a1</i>	1436164_at	solute carrier family 30 (zinc transporter), member 1	BE685959	in utero embryonic development, transport, ion transport, cation transport zinc, ion transport cellular, zinc ion homeostasis	-0.89	0.004055
	1447096_at		AU042527		-0.89	0.017574
<i>2610528B01Rik</i>	1429232_at	RIKEN cDNA 2610528B01 gene	AK012160		-0.88	0.044927
<i>Scd1</i>	1415964_at 1415965_at	stearoyl-Coenzyme A desaturase 1	NM_009127	lipid metabolic, process fatty acid biosynthetic process, ,oxidation reduction	-0.87 -0.48	0.001857 0.003378
	1442257_at		BI134319		-0.86	0.019898

	1441050_at		BB235490		-0.83	0.013944
<i>D14Ert449e</i>	1428738_a_at	DNA segment, Chr 14, ERATO Doi 449, expressed	BG072279		-0.83	0.006323
<i>Rabif</i>	1457969_at	RAB interacting factor	AI482417	transport, small GTPase mediated signal transduction, protein transport	-0.83	0.003305
<i>LOC100040592</i>	1433445_x_at	similar to Hmgcs1 protein	BB705380		-0.83	0.014569
	1433444_at				-0.78	0.027376
	1433443_a_at				-0.66	0.005753
<i>Duxbl</i>	1445710_x_at	double homeobox B-like	AV321065		-0.82	0.037615
<i>Mef2c</i>	1424852_at	myocyte enhancer factor 2C	BB280300	blood vessel development, osteoblast differentiation, endochondral ossification endochondral ossification, blood vessel remodeling chondrocyte differentiation transcription regulation of transcription, DNA-dependent heart development transcription activator activity sequence-specific DNA binding positive regulation of transcription positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter smooth muscle cell differentiation	-0.79	0.006327
	1451507_at				-0.71	0.044262
	1421028_a_at				-0.44	0.026516
<i>Myl2</i>	1448394_at	myosin, light polypeptide 2, regulatory, cardiac, slow	NM_010861	heart development muscle cell fate specification cardiac myofibril assembly heart contraction	-0.79	0.005975
<i>Sqle</i>	1415993_at	squalene epoxidase	NM_009270	metabolic process, oxidation reduction	-0.79	0.004187
<i>Ryr2</i>	1450123_at	ryanodine receptor 2, cardiac	NM_023868	transport ion transport calcium ion transport calcium ion transport integral to membrane response to caffeine	-0.78	0.046402
<i>Sub1</i>	1422692_at	SUB1 homolog (S. cerevisiae)	BE989104	transcription, regulation of transcription, DNA-dependent	-0.77	0.001453
	1439651_at		AV370006		-0.76	0.017987

<i>3110045C21Rik</i>	1430401_at	RIKEN cDNA 3110045C21 gene	AK014177		-0.76	0.000721
<i>Nppa</i>	1456062_at	natriuretic peptide precursor type A	BM122009	regulation of blood vessel size	-0.76	0.040718
<i>Rnf41</i>	1455763_at	ring finger protein 41	BB753958	ubiquitin-dependent protein catabolic process, biological_process, protein ubiquitination	-0.76	0.001667
<i>Lbh</i>	1429088_at	limb-bud and heart	AK007400	transcription, regulation of transcription, DNA-dependent, regulation of transcription from RNA polymerase II promoter, multicellular organismal development, transcription activator activity	-0.74	0.046309
<i>Rccd1</i>	1456411_at 1424194_at	RCC1 domain containing 1	BM218704		-0.73 -0.47	0.000819 0.02112
<i>Pdk1</i>	1423747_a_at 1423748_at	pyruvate dehydrogenase kinase, isoenzyme 1	BC027196	carbohydrate metabolic process, glucose metabolic process, signal transduction intracellular signaling cascade, peptidyl-histidine phosphorylation	-0.69 -0.62	0.047474 0.020543
<i>3632451O06Rik</i>	1450770_at	RIKEN cDNA 3632451O06 gene	BC023359		-0.69	0.035032
<i>Gas5</i>	1436222_at	growth arrest specific 5	AW547050		-0.68	0.025605
<i>Nexn</i>	1435649_at	nexilin	BM225804		-0.68	0.002487
<i>Prl2c2</i>	1427760_s_at	prolactin family 2, subfamily c, member 2	X75557	sprouting angiogenesis, positive regulation of neuroblast proliferation, positive regulation of cell projection organization, regulation of microvillus assembly, positive regulation of blood vessel, endothelial cell migration, negative regulation of myoblast differentiation, positive regulation of angiogenesis, positive regulation of transcription from RNA polymerase II promoter	-0.68	0.037615
<i>2610204K14Rik</i>	1428966_at	RIKEN cDNA 2610204K14 gene	AK018614		-0.67	0.024392
<i>Amacr</i>	1417208_at	alpha-methylacyl-CoA racemase	NM_008537	metabolic process, isoprenoid catabolic process	-0.67	0.002456

<i>Fdft1</i>	1438322_x_at	farnesyl diphosphate farnesyl transferase 1	BB028312	steroid biosynthetic process, cholesterol biosynthetic process, isoprenoid biosynthetic process, lipid biosynthetic process, biosynthetic process, sterol biosynthetic process, ,oxidation reduction	-0.65	0.004893
<i>Jph2</i>	1455404_at	junctionophilin 2	BG870711	elevation of cytosolic calcium ion concentration, multicellular organismal development	-0.63	0.004503
<i>Neb1</i>	1439897_at	nebulette	BE457796		-0.63	0.019382
<i>Nsdhl</i>	1416222_at	NAD(P) dependent steroid dehydrogenase-like	BC019945	hair follicle development, steroid biosynthetic process, cholesterol biosynthetic process , metabolic process, cholesterol metabolic process, lipid biosynthetic process, sterol biosynthetic process, oxidation reduction	-0.63	0.002874
<i>1700113i22rik</i>	1432073_at	RIKEN cDNA 1700113I22 gene	AK007198		-0.62	0.043633
<i>AI605517</i>	1457797_at	expressed sequence AI605517	AV340788		-0.62	0.039188
<i>Pdhb</i>	1448214_at	pyruvate dehydrogenase (lipoamide) beta	AK011810	glycolysis, metabolic process oxidation reduction	-0.62	0.010268
	1444198_at		BM117570		-0.61	0.011813
<i>ENSMUSG00000074303</i>	1436287_at	predicted gene, ENSMUSG00000074303	BF466943		-0.6	0.029406
<i>Rps24</i>	1455195_at	ribosomal protein S24	BM119287	translation	-0.6	0.028279
<i>Afap111</i>	1454727_at	actin filament associated protein 1-like 1	BB106834		-0.59	0.004788
<i>Dhcr7</i>	1448619_at	7-dehydrocholesterol reductase	NM_007856	blood vessel development, steroid biosynthetic process, cholesterol biosynthetic process, lipid biosynthetic process, post-embryonic development, cell differentiation, lung development, multicellular organism growth	-0.59	0.006907

<i>Gm2a</i>	1448241_at	GM2 ganglioside activator protein	BC004651	lipid metabolic process, sphingolipid metabolic process, ganglioside catabolic process, learning or memory ,oligosaccharide catabolic process ,lipid storage, neurological system process ,neuromuscular process, controlling balance	-0.58	0.010333
<i>Ppp1r3d</i>	1452922_at	protein phosphatase 1, regulatory subunit 3D	AK011539		-0.58	0.046812
<i>Procr</i>	1420664_s_at	protein C receptor, endothelial	NM_011171	immune response, blood coagulation , antigen processing and presentation, negative regulation of coagulation	-0.57	0.013064
<i>Dbi</i>	1455976_x_at 1433991_x_at	diazepam binding inhibitor	AV019984	transport	-0.57 -0.54	0.032348 0.038575
<i>Rgs5</i>	1420940_x_at 1417466_at	regulator of G-protein signaling 5	BF585144	G-protein coupled receptor protein signaling pathway, negative regulation of signal transduction	-0.56 -0.45	0.008065 0.043235
<i>Anxa1</i>	1448213_at	annexin A1	NM_010730	cell cycle, signal transduction, regulation of cell proliferation, arachidonic acid secretion	-0.56	0.041288
<i>Ceacam15</i>	1456451_at	carcinoembryonic antigen-related cell adhesion molecule 15	BB407699		-0.56	0.017862
<i>Egln1</i>	1423785_at	EGL nine homolog 1 (C. elegans)	BE995700	embryonic placenta development, heart development	-0.56	0.026442
<i>Scin</i>	1450276_a_at	scinderin	NM_009132	barbed-end actin filament capping	-0.56	0.024547
<i>Tnrc6c</i>	1440997_at	trinucleotide repeat containing 6C	AV236734		-0.56	0.005955
<i>6720475J19Rik</i>	1423071_x_at	RIKEN cDNA 6720475J19 gene	AW549928		-0.55	0.044846
<i>Lrp8</i>	1440882_at 1442347_at	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	BB750940	endocytosis, hippocampus development, layer formation in the cerebral cortex	-0.54 -0.46	0.019013 0.04647
<i>Pdgfd</i>	1456532_at	platelet-derived growth factor, D	BB428671	cell proliferation, regulation of peptidyl-tyrosine	-0.53	0.030262

		polypeptide		phosphorylation		
<i>Cdh6</i>	1450288_at	cadherin 6	NM_007666	cell adhesion, homophilic cell adhesion	-0.52	0.028787
<i>Dmrt3</i>	1440707_at	doublesex and mab-3 related transcription factor 3	AV298122	transcription, regulation of transcription, DNA-dependent multicellular organismal development, sex determination, cell differentiation	-0.52	0.028252
<i>Higd1a</i>	1416480_a_at	HIG1 domain family, member 1A	NM_019814	response to stress	-0.52	0.042551
<i>Hmgcs1</i>	1441536_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	AV362707	steroid biosynthetic process, cholesterol biosynthetic process, isoprenoid biosynthetic process, lipid biosynthetic process, sterol biosynthetic process	-0.52	0.012101
<i>Yap1</i>	1416487_a_at	yes-associated protein 1	NM_009534	positive regulation of transcription from RNA polymerase II promoter	-0.52	0.012245
<i>Epb4.1l4a</i>	1449167_at	erythrocyte protein band 4.1-like 4a	NM_013512		-0.51	0.01248
<i>Ly6a</i>	1417185_at	lymphocyte antigen 6 complex, locus A	BC002070		-0.51	0.021608
<i>Preli2</i>	1436194_at	PRELI domain containing 2	BE985366		-0.51	0.041327
<i>Tal2</i>	1450517_at	T-cell acute lymphocytic leukemia 2	NM_009317	transcription, regulation of transcription, DNA-dependent, behavior post-embryonic development, thalamus development, midbrain development, multicellular organism growth regulation of transcription	-0.5	0.021054
<i>Eif4e</i>	1450909_at	eukaryotic translation initiation factor 4E	BB406487	translational initiation, regulation of translation	-0.49	0.017803
<i>Fhod3</i>	1435551_at	formin homology 2 domain containing 3	BG066491	cellular component organization, actin cytoskeleton organization	-0.49	0.01334
<i>Rab33a</i>	1417529_at	RAB33A, member of RAS oncogene family	NM_011228	small GTPase mediated signal transduction, protein transport	-0.48	0.006162

<i>Cxcl12</i>	1448823_at	chemokine (C-X-C motif) ligand 12	BC006640	patterning of blood vessels, ameoboidal cell migration, cchemotaxis, immune response, germ cell development, brain development, cmotor axon guidance, growth factor activity, germ cell migration, regulation of cell migration positive regulation of cell migration, T cell proliferation, induction of positive chemotaxis	-0.47	0.028133
<i>Eid1</i>	1448405_a_at	EP300 interacting inhibitor of differentiation 1	BC010712	negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent, cell cycle, cell differentiation	-0.47	0.047682
<i>Fam162a</i>	1451385_at	family with sequence similarity 162, member A	BC010826		-0.47	0.029832
<i>Mri1</i>	1417146_at	methylthioribose-1-phosphate isomerase homolog (<i>S. cerevisiae</i>)	NM_026423	regulation of transcription, DNA-dependent, cellular metabolic process, cellular biosynthetic process	-0.47	0.012812
<i>Acat2</i>	1435630_s_at	acetyl-Coenzyme A acetyltransferase 2	AV148646	metabolic process	-0.46	0.030595
<i>Dpysl4</i>	1418298_s_at	dihydropyrimidinase-like 4	NM_011993		-0.46	0.043413
<i>Eno3</i>	1417951_at	enolase 3, beta muscle	NM_007933	glycolysis	-0.46	0.039877
<i>Pcsk9</i>	1437453_s_at	proprotein convertase subtilisin/kexin type 9	AV010795	kidney development, liver development, proteolysis, lipid metabolic process, triglyceride metabolic process, phospholipid metabolic process, steroid metabolic process, cholesterol metabolic process, cellular response to starvation, protein autoprocessing, neurogenesis, neuron differentiation, low-density lipoprotein receptor metabolic process, regulation of low-density lipoprotein receptor catabolic process, cellular response to insulin stimulus, lipoprotein metabolic process ,cholesterol homeostasis, positive regulation of neuron apoptosis	-0.46	0.023829

<i>Srebf2</i>	1426744_at	sterol regulatory element binding factor 2	BM123132	transcription regulation of transcription, DNA-dependent lipid metabolic process steroid metabolic process cholesterol metabolic process regulation of transcription	-0.46	0.010795
<i>Xpnp1</i>	1422443_at	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	NM_133216	proteolysis	-0.46	0.039717
<i>Pxmp2</i>	1417841_at	peroxisomal membrane protein 2	AF309644		-0.45	0.009917
<i>Tspan18</i>	1429856_at	tetraspanin 18	AK011742		-0.45	0.010117
<i>Acp5</i>	1453257_at	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	BB758649	metabolic process phospholipid biosynthetic process	-0.44	0.016934
<i>Gpr116</i>	1440830_at	G protein-coupled receptor 116	AW547876		-0.44	0.01918
<i>Tm2d2</i>	1456663_x_at	TM2 domain containing 2	BB718785		-0.44	0.019305
<i>Nrcam</i>	1434709_at	neuron-glia-CAM-related cell adhesion molecule	BB202655	cell adhesion axon guidance central nervous system development protein localization cell-cell adhesion action potential propagation	-0.43	0.022227
<i>Rcan2</i>	1421425_a_at	regulator of calcineurin 2	NM_030598	calcium-mediated signaling	-0.43	0.042972
	1459497_at		AU019852		-0.42	0.038961
<i>Esam</i>	1460356_at	endothelial cell-specific adhesion molecule	AF361882	cell adhesion homophilic cell adhesion	-0.42	0.040415
<i>Csgalnact1</i>	1452366_at	chondroitin sulfate N-acetylgalactosaminyltransferase 1	AV371987		-0.41	0.037915
<i>Lats2</i>	1439441_x_at	large tumor suppressor 2	BB134767	G1/S transition of mitotic cell cycle protein amino acid phosphorylation cell cycle mitosis negative regulation of cell cycle cell division	-0.41	0.039409
<i>Pcyt1b</i>	1436124_at	phosphate cytidyltransferase 1, choline, beta isoform	BE996519	ovarian follicle development spermatogenesis phospholipid biosynthetic process biosynthetic process	-0.41	0.012974

<i>Serping1</i>	1416625_at	serine (or cysteine) peptidase inhibitor, clade G, member 1	NM_009776	immune response complement activation, classical pathway blood coagulation innate immune response	-0.41	0.04643
<i>Trmt2a</i>	1457620_at	TRM2 tRNA methyltransferase 2 homolog A (<i>S. cerevisiae</i>)	BB792008	RNA processing	-0.41	0.027383
<i>Gpr182</i>	1418554_at	G protein-coupled receptor 182	NM_007412	signal transduction G-protein coupled receptor protein signaling pathway	-0.4	0.009967
<i>Pgk1</i>	1439435_x_at	phosphoglycerate kinase 1	BB411302	glycolysis	-0.4	0.047801
<i>Sox11</i>	1453002_at	SRY-box containing gene 11	BE825056	transcription regulation of transcription, DNA-dependent transcription activator activity positive regulation of transcription from RNA polymerase II promoter	-0.4	0.022229
<i>Zfp593</i>	1447703_x_at	zinc finger protein 593	AV214133	transcription regulation of transcription, DNA-dependent	-0.4	0.033101
<i>Trappc5</i>	1448999_at	trafficking protein particle complex 5	AV226526	transport vesicle-mediated transport	-0.39	0.034955
<i>4930452B06Rik</i>	1438228_at	RIKEN cDNA 4930452B06 gene	AV302073		-0.38	0.017407
<i>6430514M23Rik</i>	1436492_x_at	RIKEN cDNA 6430514M23 gene	AI842757		-0.38	0.042687
<i>G3bp2</i>	1415697_at	GTPase activating protein (SH3 domain) binding protein 2	BG069656	transport small GTPase mediated signal transduction mRNA transport	-0.38	0.023142
<i>Neurog2</i>	1422839_at	neurogenin 2	NM_009718	neuron migration transcription regulation of transcription, DNA-dependent multicellular organismal development nervous system development axon guidance central nervous system neuron development central nervous system neuron development neurogenesis cell differentiation neuron differentiation forebrain development cell fate commitment regulation of transcription positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA	-0.38	0.026266

				polymerase II promoter		
<i>Tlcd2</i>	1432282_a_at	TLC domain containing 2	AK008522		-0.38	0.014437
<i>Zxdc</i>	1417158_at	ZXD family zinc finger C	BB238025	transcription regulation of transcription, DNA-dependent	-0.38	0.047638
<i>Aacs</i>	1456081_a_at	acetoacetyl-CoA synthetase	AI987654	lipid metabolic process fatty acid metabolic process metabolic process	-0.37	0.043634
<i>Ero1l</i>	1449324_at	ERO1-like (<i>S. cerevisiae</i>)	BM234652	protein folding protein thiol-disulfide exchange transport oxidation reduction	-0.37	0.047264
<i>Anp32e</i>	1420592_a_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	NM_023210		-0.36	0.036021
<i>Itga6</i>	1422445_at	integrin alpha 6	BM935811	cell-matrix adhesion integrin-mediated signaling pathway positive regulation of cell-cell adhesion cellular response to extracellular stimulus cell adhesion mediated by integrin odontogenesis of dentine-containing tooth filopodium formation leukocyte migration leukocyte migration	-0.36	0.045989
<i>Nuf2</i>	1430811_a_at	NUF2, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)	AK010351	cell cycle mitosis attachment of spindle microtubules to kinetochore cell division	-0.36	0.041831
<i>Rab6</i>	1448305_at	RAB6, member RAS oncogene family	NM_024287	transport intracellular protein transport small GTPase mediated signal transduction protein transport vesicle-mediated transport peptidyl-cysteine methylation	-0.36	0.049536
<i>Blm</i>	1448953_at	Bloom syndrome homolog (human)	NM_007550	telomere maintenance DNA replication DNA repair DNA recombination negative regulation of mitotic recombination alpha-beta T cell differentiation positive regulation of alpha-beta T cell proliferation regulation of binding chromosome organization	-0.35	0.03753

<i>Leprel1</i>	1436178_at	leprecan-like 1	AW553532	protein metabolic process oxidation reduction	-0.35	0.038306
<i>Metap2</i>	1436531_at	methionine aminopeptidase 2	BB447764	aminopeptidase activity protein binding proteolysis peptidase activity metalloexopeptidase activity cellular process hydrolase activity metal ion binding cobalt ion binding	-0.35	0.043424
<i>Cbx1</i>	1431773_at	chromobox homolog 1 (Drosophila HP1 beta)	AK017608	chromatin assembly or disassembly	-0.34	0.020956
<i>Hspb2</i>	1429888_a_at	heat shock protein 2	AK012780	response to stress somatic muscle development response to heat	-0.34	0.04899
<i>Mapk12</i>	1449283_a_at	mitogen-activated protein kinase 12	BC021640	protein amino acid phosphorylation cell cycle	-0.34	0.033874
<i>Cyb5b</i>	1417766_at	cytochrome b5 type B	NM_025558	transport	-0.33	0.038435
<i>Dctn6</i>	1416499_a_at	dynactin 6	NM_011722	mitochondrion organization lipid biosynthetic process	-0.33	0.033119
<i>Hgsnat</i>	1450868_at	heparan-alpha-glucosaminide N-acetyltransferase	BF468249		-0.31	0.046666
<i>Egln3</i>	1418649_at	EGL nine homolog 3 (C. elegans)	BB284358	apoptosis	-0.3	0.048309
<i>D930001B02</i>	1442416_at	hypothetical protein D930001B02	BB311940		0.3	0.041607
<i>Tmem144</i>	1452042_a_at	transmembrane protein 144	AV306255		0.3	0.044096
<i>Prkar1b</i>	1434325_x_at	protein kinase, cAMP dependent regulatory, type I beta	BB274009	regulation of protein amino acid phosphorylation protein amino acid phosphorylation signal transduction learning or memory cell proliferation organ morphogenesis	0.31	0.034838
<i>Slc16a10</i>	1434592_at	solute carrier family 16 (monocarboxylic acid transporters), member 10	BB735478	transport	0.31	0.046863
<i>AK220484</i>	1442703_at	cDNA sequence AK220484	BB820231		0.32	0.038644

<i>Ctsb</i>	1417491_at	cathepsin B	M14222	proteolysis regulation of catalytic activity	0.32	0.039867
<i>Fam69a</i>	1429503_at	family with sequence similarity 69, member A	AK013580	biological_process	0.32	0.049513
<i>Lxn</i>	1416503_at	latexin	NM_016753	detection of temperature stimulus involved in sensory perception of pain	0.32	0.046814
<i>Lztf1l</i>	1428974_s_at	leucine zipper transcription factor-like 1	BB161653		0.34	0.041158
<i>Ppig</i>	1434475_at	peptidyl-prolyl isomerase G (cyclophilin G)	BB309731	protein folding	0.34	0.048501
<i>Rc3h2</i>	1426925_at	ring finger and CCCH-type zinc finger domains 2	AA709668		0.34	0.04779
<i>Nrp</i>	1440263_at	neural regeneration protein	BG072413		0.35	0.035699
<i>Gramd1b</i>	1435229_at	GRAM domain containing 1B	BI729743		0.36	0.045839
<i>Stxbp5</i>	1435398_at	syntaxin binding protein 5 (tomosyn)	BQ176171	transport exocytosis protein transport vesicle-mediated transport	0.36	0.04232
<i>Slc25a30</i>	1450018_s_at	solute carrier family 25, member 30	BB032012	transport mitochondrial transport	0.37	0.044286
<i>Ubxn2a</i>	1425019_at	UBX domain protein 2A	AV174556		0.37	0.045725
<i>AI848218</i>	1455612_at	expressed sequence AI848218	AW542748		0.38	0.042352
<i>Ankhd1</i>	1436597_at	ankyrin repeat and KH domain containing 1	BM243710		0.38	0.027447
<i>Slc38a9</i>	1456338_at	solute carrier family 38, member 9	BE647302	transport ion transport sodium ion transport amino acid transport	0.38	0.041335
<i>Grhl3</i>	1436932_at	grainyhead-like 3 (Drosophila)	AV231424	transcription regulation of transcription, DNA-dependent pattern specification process ectoderm development epidermis development wound healing	0.39	0.041545

<i>Lmna</i>	1421654_a_at	lamin A	NM_019390	structural molecule activity protein binding nucleus lamin filament intermediate filament nuclear envelope organization	0.39	0.033659
<i>Meg3</i>	1428765_at	maternally expressed 3	AV015833		0.39	0.045199
<i>4922501C03Rik</i>	1442733_at	RIKEN cDNA 4922501C03 gene	BE848415	protein binding nucleus cell cycle mitosis cell division	0.4	0.048663
<i>E030049G20Rik</i>	1444086_at	RIKEN cDNA E030049G20 gene	BB536333		0.4	0.023663
<i>Kalrn</i>	1457899_at	kalirin, RhoGEF kinase	BG066934	protein amino acid phosphorylation kinase activity transferase activity regulation of Rho protein signal transduction metal ion binding	0.4	0.014265
<i>Ankle2</i>	1453017_at	ankyrin repeat and LEM domain containing 2	BM227962	nuclear envelope membrane integral to membrane	0.41	0.042243
<i>Eda2r</i>	1440085_at	ectodysplasin A2 isoform receptor	AV246296	receptor activity multicellular organismal development programmed cell death cell differentiation	0.41	0.011739
<i>Rasal2</i>	1444671_at	RAS protein activator like 2	BB523168		0.41	0.026207
<i>Rbm4b</i>	1430032_at	RNA binding motif protein 4B	AK019871		0.41	0.033691
<i>Zbtb44</i>	1427271_at	zinc finger and BTB domain containing 44	BC027138	transcription regulation of transcription, DNA- dependent	0.41	0.048303
<i>Gab1</i>	1417693_a_at 1417694_at	growth factor receptor bound protein 2-associated protein 1	NM_021356	activation of MAPK activity response to oxidative stress signal transduction regulation of cell migration	0.4 0.41	0.020322 0.03736
	1459989_at		AV271189		0.42	0.045316
<i>2610019F03Rik</i>	1428357_at	RIKEN cDNA 2610019F03 gene	AK011462		0.42	0.040387
<i>Ddit4l</i>	1444139_at	DNA-damage-inducible transcript 4- like	BG797099	negative regulation of signal transduction	0.42	0.024447
<i>Foxa3</i>	1431900_a_at	forkhead box A3	AK019022	cellular glucose homeostasis transcription	0.42	0.014752

				regulation of transcription, DNA-dependent cellular response to starvation transcription regulator activity		
<i>Serpinc1</i>	1417909_at	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	BC019447		0.42	0.027346
<i>Ugt2b34</i>	1427961_s_at	UDP glucuronosyltransferase 2 family, polypeptide B34	BC028826		0.42	0.048359
<i>Gm879</i>	1455512_at	gene model 879, (NCBI)	AI852151		0.43	0.03678
<i>Rasef</i>	1458591_at	RAS and EF hand domain containing	AV256591	small GTPase mediated signal transduction protein transport	0.43	0.025346
<i>Trpc2</i>	1430485_at	transient receptor potential cation channel, subfamily C, member 2	AW324327	single strand break repair inter-male aggressive behavior territorial aggressive behavior transport ion transport calcium ion transport elevation of cytosolic calcium ion concentration acrosome reaction female courtship behavior response to pheromone mating behavior, sex discrimination	0.43	0.048155
<i>4632427E13Rik</i>	1442155_at	RIKEN cDNA 4632427E13 gene	BB456609		0.44	0.035958
<i>Farsb</i>	1430986_at	phenylalanyl-tRNA synthetase, beta subunit	AK012154	translation phenylalanyl-tRNA aminoacylation	0.44	0.031407
<i>Prkg2</i>	1435162_at	protein kinase, cGMP-dependent, type II	BB823350	regulation of protein amino acid phosphorylation	0.44	0.025575
<i>Epb4.114b</i>	1418294_at	erythrocyte protein band 4.1-like 4b	NM_019427		0.45	0.017642
<i>Ttc14</i>	1437878_s_at	tetratricopeptide repeat domain 14	BB711506		0.45	0.038927
<i>Acadl</i>	1448987_at	acyl-Coenzyme A dehydrogenase, long-chain	BB728073	lipid metabolic process fatty acid metabolic process metabolic process oxidation reduction	0.46	0.04246
<i>Akr1c12</i>	1450455_s_at	aldo-keto reductase family 1, member C12	AF177041	aldo-keto reductase activity xenobiotic metabolic process	0.46	0.017008

<i>Bbx</i>	1425835_a_at	bobby sox homolog (Drosophila)	AF454944	transcription regulation of transcription, DNA-dependent	0.46	0.035918
<i>Gpr177</i>	1437434_a_at	G protein-coupled receptor 177	BM241735		0.46	0.045944
<i>Igf1r</i>	1446303_at	insulin-like growth factor I receptor	AV374369	nucleotide binding protein amino acid phosphorylation transmembrane receptor protein tyrosine kinase signaling pathway brain development organ morphogenesis membrane male sex determination mammary gland development insulin-like growth factor receptor signaling pathway	0.46	0.04904
<i>Lypd6</i>	1456138_at	LY6/PLAUR domain containing 6	BB541620		0.46	0.031879
<i>Slu7</i>	1425488_at	SLU7 splicing factor homolog (S. cerevisiae)	BC025870	mRNA processing RNA splicing	0.46	0.033652
<i>Tex19.1</i>	1417482_at	testis expressed gene 19.1	NM_028602		0.46	0.013604
<i>Bspry</i>	1450131_a_at	B-box and SPRY domain containing	NM_138653	transport ion transport calcium ion transport	0.47	0.041379
<i>Defcr-rs7</i>	1422934_x_at	defensin related cryptdin, related sequence 7	NM_007848	defense response	0.47	0.015404
<i>H13</i>	1438456_at	histocompatibility 13	BB327773		0.47	0.035715
<i>AI662270</i>	1434068_s_at	expressed sequence AI662270	BE688410		0.48	0.029164
<i>Gnpda2</i>	1426523_a_at	glucosamine-6-phosphate deaminase 2	AK014950	carbohydrate metabolic process N-acetylglucosamine metabolic process	0.48	0.040079
<i>Inadl</i>	1418983_at	InaD-like (Drosophila)	AV287690		0.48	0.048338
<i>Pls1</i>	1460406_at	plastin 1 (I-isoform)	BC026410		0.48	0.004216
<i>Rabgap11</i>	1434062_at	RAB GTPase activating protein 1-like	AV226672	regulation of protein localization	0.49	0.040175
<i>Psph</i>	1415673_at	phosphoserine phosphatase	NM_133900	L-serine biosynthetic process metabolic process amino acid biosynthetic process	0.5	0.023359

<i>Rian</i>	1427580_a_at	RNA imprinted and accumulated in nucleus	BB649603		0.5	0.009365
<i>Rnase4</i>	1422603_at	ribonuclease, RNase A family 4	BC005569		0.5	0.012129
<i>Rpl3</i>	1438527_at	ribosomal protein L3	BG073445	translation	0.5	0.032215
<i>1810013L24Rik</i>	1436478_at	RIKEN cDNA 1810013L24 gene	BE651508		0.51	0.017889
<i>2810459M11Rik</i>	1452354_at	RIKEN cDNA 2810459M11 gene	AK013367	protein binding cellular_component extracellular region biological_process	0.51	0.032591
<i>5530601H04Rik</i>	1436347_a_at	RIKEN cDNA 5530601H04 gene	BB501229		0.51	0.027878
<i>Dsg2</i>	1425619_s_at	desmoglein 2	AB072269	cell adhesion	0.52	0.019318
<i>Sepp1</i>	1452141_a_at	selenoprotein P, plasma, 1	BC001991	selenium metabolic process selenium metabolic process brain development locomotory behavior post-embryonic development sexual reproduction growth	0.52	0.032482
<i>BC066028</i>	1458163_at	cDNA sequence BC066028	AV328953		0.53	0.007111
<i>Depdc7</i>	1424303_at	DEP domain containing 7	BC013499	intracellular signaling cascade	0.53	0.004365
<i>Dsc2</i>	1426911_at	desmocollin 2	BC004663	cell adhesion	0.53	0.010887
<i>P2rx4</i>	1425525_a_at	purinergic receptor P2X, ligand-gated ion channel 4	AF089751	nitric oxide biosynthetic process nitric oxide biosynthetic process transport ion transport calcium ion transport metabolic process vasodilation regulation of excitatory postsynaptic membrane potential	0.53	0.008411
<i>Gstm1</i>	1416416_x_at 1448330_at	glutathione S-transferase, mu 1	NM_010358	metabolic process	0.51 0.53	0.01515 0.013719
<i>Abcc4</i>	1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	BB291885	multidrug transport	0.54	0.009661
<i>Gipc2</i>	1417178_at	GIPC PDZ domain containing family, member 2	NM_016867	protein binding	0.54	0.009074

<i>Hpn</i>	1420712_a_at	hepsin	NM_008281	proteolysis cell growth hydrolase activity	0.54	0.01159
<i>Nrp1</i>	1457198_at 1448944_at	neuropilin 1	AV291009	angiogenesis patterning of blood vessels cell adhesion multicellular organismal development nervous system development axon guidance axonal fasciculation heart development membrane dendrite development cell migration cell differentiation negative regulation of axon extension vascular endothelial growth factor receptor signaling pathway negative regulation of axon extension involved in axon guidance	0.53 0.54	0.019106 0.015245
<i>Proc</i>	1418845_at	protein C	NM_008934	serine-type endopeptidase activity calcium ion binding extracellular region proteolysis blood coagulation peptidase activity serine-type peptidase activity hydrolase activity negative regulation of blood coagulation negative regulation of apoptosis	0.55	0.011454
<i>Rpap1</i>	1440986_at	RNA polymerase II associated protein 1	BM197823	transcription	0.55	0.033986
<i>Slc40a1</i>	1417061_at	solute carrier family 40 (iron-regulated transporter), member 1	AF226613	iron ion binding transport ion transport iron ion transport	0.55	0.013053
<i>4732418C07Rik</i>	1427978_at	RIKEN cDNA 4732418C07 gene	BB318254	calcium ion binding	0.56	0.041024
<i>Defcr-rs2</i>	1420598_x_at	defensin related cryptdin, related sequence 2	NM_007847		0.56	0.010415
<i>Dlk1</i>	1449939_s_at	delta-like 1 homolog (Drosophila)	NM_010052		0.56	0.019291
<i>Irf6</i>	1418301_at	interferon regulatory factor 6	NM_016851	transcription regulation of transcription, DNA-dependent negative regulation of cell proliferation keratinocyte differentiation skin development skin development keratinocyte proliferation keratinocyte proliferation cell development	0.56	0.032757

<i>Myo6</i>	1433942_at	myosin VI	BE133806	protein targeting transport endocytosis synaptic transmission synaptogenesis sensory perception of sound locomotory behavior glutamate secretion protein transport dendrite development cytoplasmic vesicle inner ear morphogenesis auditory receptor cell differentiation regulation of synaptic plasticity inner ear development	0.56	0.015647
<i>Nkd1</i>	1429506_at	naked cuticle 1 homolog (Drosophila)	AK020249	multicellular organismal development spermatogenesis Wnt receptor signaling pathway cell differentiation	0.56	0.00161
<i>Pvr</i>	1423904_a_at	poliovirus receptor	BB049138	cell-cell adhesion cell migration	0.56	0.014326
<i>Slc13a3</i>	1438377_x_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	BB497312	transport ion transport sodium ion transport dicarboxylic acid transport	0.56	0.00506
<i>Srbdl</i>	1436375_at	S1 RNA binding domain 1	C85414	biological_process	0.56	0.020712
<i>Efnb1</i>	1418285_at	ephrin B1	NM_010110	neural crest cell migration multicellular organismal development nervous system development axon guidance embryonic pattern specification cell differentiation positive regulation of T cell proliferation	0.57	0.044121
<i>Nxf3</i>	1456035_at	nuclear RNA export factor 3	BM236468	poly(A)+ mRNA export from nucleus	0.57	0.041663
<i>S100a10</i>	1416762_at	S100 calcium binding protein A10 (calpactin)	NM_009112		0.57	0.038543
<i>Enpp3</i>	1439260_a_at	ectonucleotide pyrophosphatase/phosphodiesterase 3	BB039510	metabolic process	0.58	0.023051
<i>2810474O19Rik</i>	1437110_at	RIKEN cDNA 2810474O19 gene	BM232998		0.59	0.027971
<i>Atf7ip2</i>	1427603_at	activating transcription factor 7 interacting protein 2	BC018510	transcription regulation of transcription, DNA-dependent	0.59	0.01669

<i>Bmp4</i>	1422912_at	bone morphogenetic protein 4	NM_007554	<p>skeletal system development ossification angiogenesis osteoblast differentiation metanephros development ureteric bud development ureteric bud branching positive regulation of protein amino acid phosphorylation multicellular organismal development germ cell development mesodermal cell fate determination heart development negative regulation of cell proliferation tissue development dorsoventral neural tube patterning telencephalon regionalization cell differentiation erythrocyte differentiation lung development positive regulation of bone mineralization BMP signaling pathway forebrain development negative regulation of chondrocyte differentiation growth odontogenesis of dentine- containing tooth camera-type eye development cell fate commitment regulation of cell differentiation positive regulation of cell differentiation negative regulation of myoblast differentiation positive regulation of osteoblast differentiation positive regulation of ossification negative regulation of striated muscle development embryonic morphogenesis anatomical structure formation neuron fate commitment smooth muscle cell differentiation cartilage development lens induction in camera- type eye</p>	0.59	0.018206
<i>Icam1</i>	1424067_at	intercellular adhesion molecule 1	BC008626	<p>T cell antigen processing and presentation cell adhesion leukocyte adhesion cell-cell adhesion regulation of cell adhesion cell adhesion mediated by integrin</p>	0.59	0.004935
<i>Luc7l2</i>	1436767_at	LUC7-like 2 (<i>S. cerevisiae</i>)	BB475271		0.59	0.030272

<i>Tmed6</i>	1416490_at	transmembrane emp24 protein transport domain containing 6	NM_025458	transport	0.6	0.001111
<i>H47</i>	1448704_s_at	histocompatibility 47	NM_024439	intracellular protein transport inflammatory response negative regulation of interleukin-6 production negative regulation of tumor necrosis factor production	0.6	0.017081
<i>Zcchc14</i>	1418170_a_at	zinc finger, CCHC domain containing 14	BB223737		0.6	0.019875
<i>Bhmt2</i>	1418913_at	betaine-homocysteine methyltransferase 2	NM_022884	methionine biosynthetic process	0.61	0.027493
<i>Osr1</i>	1449350_at	odd-skipped related 1 (Drosophila)	NM_011859	metanephros development heart development zinc ion binding gonad development intermediate mesoderm development	0.61	0.003197
<i>Rnf128</i>	1418318_at	ring finger protein 128	AK004847	ubiquitin-dependent protein catabolic process negative regulation of cytokine biosynthetic process	0.61	0.002801
<i>Trmt6</i>	1431212_a_at	tRNA methyltransferase 6 homolog (S. cerevisiae)	BG079674	translational initiation regulation of translational initiation tRNA processing	0.61	0.02167
<i>Tsc22d1</i>	1439111_at	TSC22 domain family, member 1	BM230984	transcription regulation of transcription, DNA-dependent	0.61	0.021945
	1437599_at		BM246546		0.62	0.028487
<i>9130023H24Rik</i>	1456331_at	RIKEN cDNA 9130023H24 gene	BB040432		0.62	0.046149
<i>Bub1</i>	1438571_at	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	BB479886	protein kinase activity protein serine/threonine kinase activity ATP binding nucleus protein amino acid phosphorylation cell cycle mitosis cell division	0.62	0.046703
<i>Myo7a</i>	1421385_a_at	myosin VIIA	NM_008663	phagolysosome formation phagocytosis signal transduction sensory perception visual perception sensory perception of sound sensory	0.62	0.032956

				perception of sound apical plasma membrane cell projection organization inner ear morphogenesis auditory receptor cell differentiation synapse post-embryonic organ morphogenesis inner ear development sensory perception of light stimulus pigment granule localization pigment granule transport auditory receptor cell stereocilium organization inner ear receptor cell differentiation		
<i>Odz4</i>	1451888_a_at	odd Oz/ten-m homolog 4 (Drosophila)	AB025413	gastrulation with mouth forming second signal transduction	0.62	0.001014
<i>Pnma5</i>	1439207_at	paraneoplastic antigen family 5	BB698563		0.62	0.009824
<i>Trim34</i>	1424857_a_at	tripartite motif-containing 34	AF220142		0.64	0.020914
<i>F10</i>	1449305_at	coagulation factor X	NM_007972	proteolysis blood coagulation	0.65	0.006358
<i>Mosc1</i>	1428005_at	MOCO sulphurase C-terminal domain containing 1	AA958845	oxidation reduction	0.65	0.002001
<i>Cobll1</i>	1454795_at	Cobl-like 1	AV080881		0.66	0.013717
<i>Klhl24</i>	1438519_at	kelch-like 24 (Drosophila)	BM124262	protein binding cell projection	0.66	0.002815
<i>Hnf4a</i>	1427000_at	hepatic nuclear factor 4, alpha	BF580781	transcription regulation of transcription, DNA-dependent lipid metabolic process positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter metal ion binding	0.67	0.002785
<i>Coch</i>	1423285_at	coagulation factor C homolog (Limulus polyphemus)	BB731671		0.68	0.040711
<i>Ddc</i>	1426215_at	dopa decarboxylase	AF071068	cellular amino acid and derivative metabolic process response to toxin catecholamine biosynthetic process	0.68	0.001121

<i>Mcoln2</i>	1431705_a_at	mucolipin 2	AK014467	transport ion transport	0.68	0.001367
<i>Bcmo1</i>	1449907_at	beta-carotene 15,15'-monooxygenase	NM_021486	oxidation reduction	0.69	0.000566
<i>Ccng1</i>	1450016_at	cyclin G1	BG065754	cell cycle mitosis cell division	0.61	0.029938
	1450017_at				0.67	0.04752
	1420827_a_at				0.69	0.022896
<i>Lrrc19</i>	1434915_s_at	leucine rich repeat containing 19	AI267139	protein binding	0.69	0.011681
<i>Pcdh19</i>	1444422_at	protocadherin 19	BB732600	cell adhesion homophilic cell adhesion	0.69	0.03427
<i>Tmem130</i>	1455148_at	transmembrane protein 130	AV173792		0.69	0.036271
<i>1110030E23Rik</i>	1455219_at	RIKEN cDNA 1110030E23 gene	BQ033747		0.7	0.018346
<i>Anxa4</i>	1421223_a_at	annexin A4	NM_013471	kidney development	0.7	0.036552
<i>Hoxd1</i>	1420573_at	homeo box D1	NM_010467	transcription regulation of transcription, DNA-dependent multicellular organismal development regulation of transcription embryonic skeletal system development	0.7	0.007312
	1443913_at		BG071002		0.71	0.008854
	1445600_at		BM219178		0.72	0.027084
<i>Zc3hav1</i>	1436183_at	RIKEN cDNA 9830115L13 gene	BB757349		0.72	0.004324
<i>Rab20</i>	1438097_at	RAB20, member RAS oncogene family	BG066967	transport small GTPase mediated signal transduction protein transport	0.72	0.049929
<i>Maf</i>	1456060_at	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	AV284857	cytokine production lens development in camera-type eye transcription regulation of transcription, DNA-dependent cell cycle regulation of chondrocyte differentiation regulation of transcription negative regulation of cell cycle positive regulation of transcription from RNA polymerase II promoter positive	0.74	0.035513

				regulation of transcription from RNA polymerase II promoter cell development lens fiber cell differentiation		
<i>Nodal</i>	1422058_at	nodal	X70514	negative regulation of transcription from RNA polymerase II promoter in utero embryonic development gastrulation with mouth forming second trophodermal cell differentiation trophodermal cellular morphogenesis embryonic placenta development heart looping repression of premature neural plate formation transforming growth factor beta receptor signaling pathway multicellular organismal development determination of left/right symmetry growth factor activity positive regulation of cell proliferation anterior/posterior pattern formation cell migration stem cell maintenance cell migration involved in gastrulation cell fate commitment negative regulation of cell differentiation positive regulation of transcription from RNA polymerase II promoter anatomical structure formation embryonic process involved in female pregnancy	0.74	0.019165
<i>Vnn1</i>	1418486_at	vanin 1	NM_011704	acute inflammatory response chronic inflammatory response nitrogen compound metabolic process anti-apoptosis cell-cell adhesion positive regulation of T cell differentiation in the thymus innate immune response	0.74	0.016306
<i>Jarid1c</i>	1457930_at	jumonji, AT rich interactive domain 1C (Rbp2 like)	BB165753	transcription regulation of transcription, DNA-dependent chromatin modification oxidation reduction	0.75	0.038484
<i>Fmo1</i>	1417429_at	flavin containing monooxygenase 1	BC011229	oxidation reduction	0.76	0.003412

<i>Hsd17b11</i>	1434642_at	hydroxysteroid (17-beta) dehydrogenase 11	BB546344	catalytic activity estradiol 17-beta-dehydrogenase activity binding steroid biosynthetic process metabolic process lipid biosynthetic process oxidation reduction	0.76	0.012396
<i>Ugt1a9</i>	1424783_a_at	UDP glucuronosyltransferase 1 family, polypeptide A9	BC019434	metabolic process	0.77	9e-04
<i>4832420A03Rik</i>	1457751_at	RIKEN cDNA 4832420A03 gene	BB371102		0.78	0.019795
<i>Alg8</i>	1455887_at	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	BM249614		0.78	0.027388
<i>Slc39a5</i>	1429523_a_at	solute carrier family 39 (metal ion transporter), member 5	AK008448	transport ion transport zinc ion transport cellular zinc ion homeostasis metal ion transport	0.78	0.00263
<i>Eps8</i>	1422823_at 1422824_s_at	epidermal growth factor receptor pathway substrate 8	NM_007945	adult locomotory behavior actin cytoskeleton reorganization behavioral response to ethanol	0.52 0.79	0.033458 0.001872
<i>Mef2a</i>	1427186_a_at 1452347_at	myocyte enhancer factor 2A	AV255689	transcription factor activity transcription regulation of transcription, DNA-dependent multicellular organismal development nervous system development transcription activator activity cell differentiation positive regulation of transcription	0.71 0.79	0.040809 0.009243
<i>Shmt1</i>	1425177_at 1425178_s_at	serine hydroxymethyltransferase 1 (soluble)	AF237702	glycine metabolic process L-serine metabolic process one-carbon compound metabolic process	0.73 0.79	0.00073 0.000899
<i>4833420G17Rik</i>	1430220_at	RIKEN cDNA 4833420G17 gene	AK017802		0.79	0.02252
<i>Skiv2l2</i>	1447517_at	superkiller viralicidic activity 2-like 2 (<i>S. cerevisiae</i>)	BM208991	mRNA processing	0.79	0.007549
<i>1100001H23Rik</i>	1448786_at	RIKEN cDNA 1100001H23 gene	NM_025806	extracellular region lipid catabolic process hydrolase activity	0.81	0.007003
<i>Steap2</i>	1428636_at	six transmembrane epithelial antigen	AK015015	transport ion transport iron ion transport	0.81	0.003697

		of prostate 2		metabolic process oxidation reduction		
<i>Taok3</i>	1435964_a_at	TAO kinase 3	BB194075	protein amino acid phosphorylation	0.81	0.017701
<i>Sord</i>	1426584_a_at 1438183_x_at	sorbitol dehydrogenase	BI143942	sorbitol metabolic process oxidation reduction	0.79 0.82	0.005128 0.00803
<i>Zfp39</i>	1441198_at	zinc finger protein 39	BB311524	transcription regulation of transcription, DNA-dependent multicellular organismal development spermatogenesis cell differentiation	0.82	0.00022
<i>Manba</i>	1450626_at	mannosidase, beta A, lysosomal	NM_027288	carbohydrate metabolic process glycoprotein catabolic process metabolic process	0.84	0.001371
	1427820_at		BC021831		0.85	0.021891
<i>ApoE</i>	1432466_a_at	apolipoprotein E	AK019319	response to dietary excess lipid metabolic process cholesterol catabolic process transport lipid transport cellular calcium ion homeostasis response to oxidative stress protein localization cholesterol metabolic process regulation of gene expression axon regeneration cholesterol efflux lipoprotein metabolic process lipoprotein biosynthetic process lipoprotein catabolic process vasodilation chylomicron cholesterol homeostasis artery morphogenesis maintenance of location in cell lipid homeostasis	0.86	0.014195
<i>Slc39a8</i>	1448482_at 1416832_at	solute carrier family 39 (metal ion transporter), member 8	NM_026228	transport ion transport zinc ion transport zinc ion binding	0.6 0.87	0.005722 0.010475
<i>Slc39a4</i>	1451139_at	solute carrier family 39 (zinc transporter), member 4	BC023498	transport ion transport zinc ion transport cellular zinc ion homeostasis metal ion transport	0.87	0.011224
<i>Trim6</i>	1424448_at	tripartite motif-containing 6	BC026912		0.87	0.003541
<i>Mt1</i>	1422557_s_at	metallothionein 1	NM_013602	cellular metal ion homeostasis cellular zinc ion homeostasis nitric oxide mediated signal	0.88	0.037788

<i>Tbx3</i>	1448029_at 1437479_x_at	T-box 3	AA543734	transduction blood vessel development in utero embryonic development heart looping heart morphogenesis transcription regulation of transcription, DNA-dependent multicellular organismal development cell aging organ morphogenesis negative regulation of transcription limbic system development mammary gland development mammary gland development limb morphogenesis forelimb morphogenesis regulation of cell proliferation negative regulation of transcription, DNA-dependent positive regulation of transcription, DNA-dependent branching morphogenesis of a tube	0.47	0.030654
					0.88	0.007058
<i>Gsn</i>	1415812_at 1456312_x_at 1437171_x_at	gelsolin	NM_010354	vesicle-mediated transport barbed-end actin filament capping	0.73	0.008263
					0.8	0.007652
<i>Lhx1</i>	1450428_at 1421951_at	LIM homeobox protein 1	AV335209	urogenital system development ureteric bud development gastrulation with mouth forming second ectoderm formation endoderm formation kidney development transcription regulation of transcription, DNA-dependent cell-cell signaling multicellular organismal development pattern specification process pattern specification process nervous system development anatomical structure morphogenesis post-embryonic development anterior/posterior pattern formation dorsal/ventral pattern formation regulation of gene expression cerebellum development cerebellar Purkinje cell differentiation Purkinje cell-granule cell precursor cell signaling involved in regulation of granule cell precursor	0.66	0.028072
					0.9	0.017528

				cell proliferation cell differentiation anatomical structure formation anatomical structure formation		
<i>Plg</i>	1416729_at	plasminogen	NM_008877	proteolysis apoptosis induction of apoptosis blood coagulation negative regulation of angiogenesis tissue regeneration fibrinolysis myoblast differentiation muscle maintenance tissue remodeling	0.92	0.000392
<i>Zfp42</i>	1418362_at	zinc finger protein 42	NM_009556	transcription regulation of transcription, DNA-dependent	0.92	0.009366
<i>Ctsc</i>	1416382_at	cathepsin C	NM_009982	proteolysis	0.94	0.003183
<i>Snrpn</i>	1441905_x_at	small nuclear ribonucleoprotein N	BB264453		0.94	0.047906
<i>Tcfcp2l1</i>	1418091_at	transcription factor CP2-like 1	NM_023755	negative regulation of transcription from RNA polymerase II promoter cell morphogenesis epithelial cell maturation transcription regulation of transcription, DNA-dependent cytoplasm organization salivary gland development determination of adult life span membrane general transcriptional repressor activity positive regulation of growth	0.94	0.004336
<i>Perp</i>	1416271_at	PERP, TP53 apoptosis effector	NM_022032	apoptosis induction of apoptosis cell adhesion	0.96	0.001491
<i>Sgk3</i>	1450036_at 1420919_at	serum/glucocorticoid regulated kinase 3	BB768208	protein amino acid phosphorylation anti-apoptosis cell communication	0.47 0.98	0.0445 0.001873
<i>Aadat</i>	1418519_at	aminoadipate aminotransferase	BC012637	biosynthetic process	0.98	0.004775
<i>Slc13a4</i>	1433734_at	solute carrier family 13 (sodium/sulfate symporters), member 4	BB192951		0.99	0.025105
<i>Abcc2</i>	1450109_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	NM_013806	transport	1	4.7e-05
<i>Phf17</i>	1426753_at	PHD finger protein 17	BG065238	transcription regulation of transcription, DNA-	1	0.012456

				dependent apoptosis		
<i>Slc16a9</i>	1429727_at 1429726_at	solute carrier family 16 (monocarboxylic acid transporters), member 9	AK004684	transport	0.64 1.02	0.002342 9e-06
<i>Xlr5c</i>	1422933_at	X-linked lymphocyte-regulated 5C	NM_031493		1.03	0.000125
<i>Rbm47</i>	1423411_at 1438021_at	RNA binding motif protein 47	BI099836		0.71 1.04	0.026081 0.000699
	1456214_at	protocadherin 7	BB197591	cell adhesion	1.04	0.017952
<i>Eomes</i>		eomesodermin homolog (<i>Xenopus</i> <i>laevis</i>)	BB128925	mesoderm formation blastocyst development trophectodermal cell differentiation trophectodermal cell differentiation transcription regulation of transcription, DNA- dependent multicellular organismal development cell differentiation positive regulation of cell differentiation	1.05	0.000654
<i>B4galnt2</i>	1442028_at	beta-1,4-N-acetyl-galactosaminyl transferase 2	AI593864	UDP-N-acetylglucosamine metabolic process protein amino acid glycosylation UDP-N- acetylgalactosamine metabolic process negative regulation of cell-cell adhesion integral to Golgi membrane lipid glycosylation	1.06	8.5e-05
<i>Aldob</i>	1451194_at	aldolase B, fructose-bisphosphate	BC024112	glycolysis metabolic process	1.07	0.000944
<i>Gnb4</i>	1419469_at	guanine nucleotide binding protein (G protein), beta 4	BI713933	signal transduction G-protein coupled receptor protein signaling pathway	1.07	0.004004
<i>AI662270</i>	1434067_at	expressed sequence AI662270	BE688410		1.08	0.003368
<i>Folr1</i>	1450995_at	folate receptor 1 (adult)	BG245669	posttranslational protein targeting to membrane folic acid metabolic process	1.09	0.001148
<i>Mapk8</i>	1457936_at	mitogen-activated protein kinase 8	BB184171	ossification protein amino acid phosphorylation JUN phosphorylation JUN phosphorylation response to UV peptidyl-threonine	1.1	0.016827

				phosphorylation induction of apoptosis in response to chemical stimulus negative regulation of apoptosis response to cadmium ion		
<i>Fmr1nb</i>	1434739_at	fragile X mental retardation 1 neighbor	AW542416		1.11	0.003715
<i>Pla2g12b</i>	1419614_at	phospholipase A2, group XIIB	BC021592	phospholipid metabolic process lipid catabolic process	1.12	6e-04
<i>4933402E13Rik</i>	1429511_at	RIKEN cDNA 4933402E13 gene	AK016614		1.13	0.003075
<i>Gpr155</i>	1452353_at	G protein-coupled receptor 155	BB762731		1.14	0.001286
<i>Dab2</i>	1420498_a_at 1430604_a_at 1423805_at	disabled homolog 2 (Drosophila)	NM_023118	cell morphogenesis involved in differentiation in utero embryonic development protein binding excretion	0.67 0.97 1.14	0.018146
<i>Cfi</i>	1418724_at	complement component factor i	NM_007686	proteolysis immune response complement activation, classical pathway	1.15	0.000877
<i>Adora2b</i>	1434431_x_at 1434430_s_at	adenosine A2b receptor	BB709140	positive regulation of chronic inflammatory response to non-antigenic stimulus signal transduction G-protein coupled receptor protein signaling pathway activation of adenylate cyclase activity by G-protein signaling pathway positive regulation vascular endothelial growth factor production positive regulation of cAMP biosynthetic process positive regulation of cGMP biosynthetic process positive regulation of guanylate cyclase activity cellular response to extracellular stimulus positive regulation of chemokine production positive regulation of interleukin-6 production positive regulation of mast cell degranulation relaxation of vascular smooth muscle	0.78 1.16	0.003153 0.000824

<i>Lgmn</i>	1448883_at	legumain	NM_011175	proteolysis negative regulation of multicellular organism growth	1.16	0.005371
<i>Morc4</i>	1434436_at	microrchidia 4	AV036158		1.18	0.000231
<i>Aass</i>	1423523_at	aminoadipate-semialdehyde synthase	BF687395	generation of precursor metabolites and energy L-lysine catabolic process oxidation reduction	1.22	0.000219
<i>Reep6</i>	1430128_a_at	receptor accessory protein 6	AK002562		1.24	0.002068
<i>Slco4c1</i>	1437870_at 1460616_at	solute carrier organic anion transporter family, member 4C1	AV024403	transport ion transport multicellular organismal development spermatogenesis organic anion transport cell differentiation	1.27 1.29	0.00385 0.002926
<i>Rhox5</i>	1423429_at	reproductive homeobox 5	BM210473	negative regulation of transcription from RNA polymerase II promoter regulation of transcription, DNA-dependent sperm motility germ cell programmed cell death	1.3	0.000802
<i>Fga</i>	1424279_at	fibrinogen, alpha polypeptide	BC005467	blood coagulation	1.31	7.8e-05
<i>Trf</i>	1425546_a_at	transferrin	AF440692	transport ion transport iron ion transport cellular iron ion homeostasis	1.33	2.9e-05
<i>Car7</i>	1443824_s_at	carbonic anhydrase 7	BB193643		1.35	0.000905
<i>Soat2</i>	1460722_at	sterol O-acyltransferase 2	BC025931	lipid metabolic process steroid metabolic process cholesterol metabolic process	1.35	0.00197
<i>Slc7a9</i>	1448783_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	NM_021291	transport amino acid transport amino acid transmembrane transporter activity	1.36	0.000537
<i>Tdh</i>	1449064_at	L-threonine dehydrogenase	NM_021480	cellular metabolic process oxidation reduction	1.36	0.000199
<i>Npl</i>	1424265_at	N-acetylneuraminate pyruvate lyase	BC022734	carbohydrate metabolic process biological_process metabolic process	1.37	0.00026
<i>Mbl2</i>	1418787_at	mannose-binding lectin (protein C) 2	NM_010776	immune response innate immune response	1.38	0.00046
<i>2610528J11Rik</i>	1450947_at	RIKEN cDNA 2610528J11 gene	AK012175	membrane integral to membrane	1.39	7e-05

<i>Rab11fip5</i>	1427405_s_at 1434314_s_at	RAB11 family interacting protein 5 (class I)	BF682225	transport protein transport	0.62 1.4	0.003925 1.4e-05
<i>Vill</i>	1448837_at	villin 1	NM_009509	cytoskeleton organization barbed-end actin filament capping	1.41	0.000335
<i>Ctsh</i>	1418365_at 1443814_x_at	cathepsin H	NM_007801	proteolysis	1.39 1.46	0.000263 0.000185
<i>Mfap3l</i>	1441481_at 1428804_at	microfibrillar-associated protein 3-like	AV262974		0.92 1.46	0.001854 0.000511
<i>Xlr3a</i>	1420357_s_at	X-linked lymphocyte-regulated 3A	NM_011726		1.5	0.000613
<i>Fgb</i>	1428079_at	fibrinogen, B beta polypeptide	AK011118	signal transduction blood coagulation platelet activation protein polymerization	1.53	3.5e-05
<i>Spp2</i>	1418916_a_at	secreted phosphoprotein 2	NM_029269	bone remodeling	1.53	1.2e-05
<i>Amn</i>	1417920_at	amnionless	NM_033603	multicellular organismal development excretion protein localization	1.6	0.001108
<i>Paip1</i>	1441955_s_at 1425521_at	polyadenylate binding protein- interacting protein 1	BB381990	regulation of translation RNA metabolic process	1.49 1.61	0.007797 0.011812
<i>Apoa4</i>	1417761_at	apolipoprotein A-IV	BC010769	innate immune response in mucosa transport lipid transport regulation of cholesterol absorption lipoprotein metabolic process	1.68	0.000298
<i>Trap1a</i>	1460226_at	tumor rejection antigen P1A	NM_011635		1.7	
<i>Sfmbt2</i>	1434353_at	Scm-like with four mbt domains 2	BM200222	nucleus regulation of transcription	1.72	1.5e-05
<i>2410003J06Rik</i>	1429701_at	RIKEN cDNA 2410003J06 gene	AK010362		1.75	0.000137
<i>Ttr</i>	1454608_x_at 1451580_a_at 1459737_s_at 1455913_x_at	transthyretin	BG141874	thyroid hormone generation transport	1.64 1.65 1.71 1.77	
<i>Rbp4</i>	1426225_at	retinol binding protein 4, plasma	U63146	eye development gluconeogenesis transport	1.8	0

				spermatogenesis spermatogonial cell division male gonad development embryonic development lung development response to insulin stimulus retinol transport retinol metabolic process retinal metabolic process embryonic organ morphogenesis embryonic skeletal system development cardiac muscle development female genitalia morphogenesis detection of light stimulus involved in visual perception positive regulation of immunoglobulin secretion retina development in camera-type eye negative regulation of cardiac muscle cell proliferation embryonic retina morphogenesis in camera-type eye uterus development vagina development urinary bladder development heart trabecula formation		
<i>Cldn2</i>	1417231_at	claudin 2	NM_016675	calcium-independent cell-cell adhesion	1.82	0.000475
<i>Pdzk1</i>	1431701_a_at	PDZ domain containing 1	AK006269		1.85	4.4e-05
<i>Lgals2</i>	1417079_s_at	lectin, galactose-binding, soluble 2	NM_025622		1.89	0
<i>Nrk</i>	1450078_at 1450079_at	Nik related kinase	AK012873	protein amino acid phosphorylation	1.65 1.94	1.8e-05 1.2e-05
<i>Cubn</i>	1452270_s_at 1426990_at	cubilin (intrinsic factor-cobalamin receptor)	AF197159	lipid metabolic process transport receptor- mediated endocytosis steroid metabolic process cholesterol metabolic process protein transport lipoprotein transport	1.8 1.94	0.000644 0.000576
<i>Fgg</i>	1416025_at	fibrinogen, gamma polypeptide	NM_133862	signal transduction blood coagulation platelet activation protein polymerization	1.99	1.5e-05
<i>Ccnb1ip1</i>	1435998_at	cyclin B1 interacting protein 1	BG066504	blastocyst formation apoptosis meiotic metaphase I spermatid development organ growth chiasma formation	2.19	0.005788
<i>Apoc2</i>	1418069_at	apolipoprotein C-II	NM_009695	lipid metabolic process transport lipid transport	2.35	4e-06

				biological_process lipid catabolic process		
<i>Xlr4b</i>	1449347_a_at	X-linked lymphocyte-regulated 4B	NM_021365		2.35	2.4e-05
<i>Timd2</i>	1418766_s_at	T-cell immunoglobulin and mucin domain containing 2	BC028829		2.37	1e-06
				regulation of protein amino acid phosphorylation endothelial cell proliferation lipid metabolic process phospholipid metabolic process cholesterol biosynthetic process transport lipid transport protein localization steroid metabolic process cholesterol metabolic process glucocorticoid metabolic process lipid storage regulation of cholesterol absorption cholesterol transport adrenal gland development axon regeneration cholesterol efflux lipoprotein metabolic process lipoprotein biosynthetic process blood vessel endothelial cell migration negative regulation of hydrolase activity positive regulation of transferase activity		
	1419233_x_at				2.28	3e-06
	1455201_x_at				2.34	4e-06
<i>Apoa1</i>	1419232_a_at	apolipoprotein A-I	NM_009692		2.55	1e-06
	1438840_x_at				2.6	2e-06
<i>D7Ertd715e</i>	1436964_at	DNA segment, Chr 7, ERATO Doi 715, expressed	BB314814		2.72	0.023869
<i>Tspan8</i>	1424649_a_at	tetraspanin 8	BC025461		2.77	0
<i>Slc2a2</i>	1449067_at	solute carrier family 2 (facilitated glucose transporter), member 2	NM_031197	transport carbohydrate transport transmembrane transport	2.83	1e-06
	1436879_x_at				2.96	0
<i>Afp</i>	1416645_a_at	alpha fetoprotein	NM_007423	ovulation from ovarian follicle transport sexual reproduction progesterone metabolic process	2.63	0
	1416646_at				3.14	0
<i>Tsix</i>	1436936_s_at	X (inactive)-specific transcript, antisense	BG806300	dosage compensation, by inactivation of X chromosome dosage compensation, by inactivation of X chromosome chromatin-mediated maintenance of transcription	3.27	0.031924

Supplementary Table S2: Genes that were significantly up- or down-regulated and by greater than 2-fold in *Sox17*-IRES-GFP transfected HepG2 cells compared to GFP transfected cells

Symbol	Name	Genbank	TargetID	log ₂ Fold change	GO Biological function
<i>EDNI</i>	endothelin 1	NM_001955.2	ILMN_28724	3.47341634	signal transduction; positive regulation of cell proliferation; regulation of vasoconstriction
<i>IL8</i>	interleukin 8	NM_000584.2	ILMN_2247	3.44418417	G-protein coupled receptor protein signaling pathway; neutrophil chemotaxis; sensory perception; negative regulation of cell proliferation; neutrophil activation; calcium-mediated signaling; angiogenesis; regulation of cell adhesion
	DNA clone IMAGE:5175893	BI821208	ILMN_123426	2.97575505	
<i>CBLB</i>	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	NM_170662.3	ILMN_18286	2.89173999	cell surface receptor linked signal transduction; protein ubiquitination
<i>GALR2</i>	galanin receptor 2	NM_003857.2	ILMN_4188	2.77843919	learning and/or memory; G-protein coupled receptor protein signaling pathway; development; digestion; synaptic transmission; elevation of cytosolic calcium ion concentration; muscle contraction
<i>CXCL10</i>	chemokine (C-X-C motif) ligand 10	NM_001565.1	ILMN_5066	2.75255363	chemotaxis; muscle development; cell surface receptor linked signal transduction; sensory perception ; positive regulation of cell proliferation; inflammatory response; circulation
<i>BAZ2B</i>	bromodomain adjacent to zinc finger domain, 2B (BAZ2B)	NM_013450.1	ILMN_20026	2.68389758	regulation of transcription
<i>FLJ20647</i>	hypothetical protein FLJ20647.	NM_017918.3	ILMN_11144	2.61071252	
<i>GBP2</i>	guanylate binding protein 2, interferon-inducible	NM_004120.3	ILMN_13936	2.58955921	immune response
<i>PEL1I</i>	pellino homolog 1	NM_020651.2	ILMN_11771	2.56821925	
<i>ZNF6</i>	zinc finger protein 6	NM_021998.3	ILMN_2559	2.56744249	regulation of transcription
<i>KPNA5</i>	karyopherin alpha 5	NM_002269.2	ILMN_26154	2.53310959	protein-nucleus import
<i>IFNB1</i>	interferon, beta 1, fibroblast.	NM_002176.2	ILMN_10140	2.52212008	induction of apoptosis; regulation of MHC class I biosynthesis; natural killer cell activation; cell surface receptor linked signal transduction; negative regulation of virion penetration;
<i>C8orf70</i>	chromosome 8 open reading frame 70	NM_016010.1	ILMN_13979	2.46418238	
<i>MEIS1</i>	myeloid ecotropic viral integration site 1	NM_002398.2	ILMN_19382	2.38630154	regulation of transcription,

<i>CHAC2</i>	cation transport regulator-like 2	NM_0010087.1	ILMN_1763	2.36599071	
<i>NEDD9</i>	neural precursor cell expressed, developmentally down-regulated 9 (NEDD9), transcript variant 2	NM_182966.1	ILMN_137978	2.33437741	signal transduction; cytoskeleton organization and biogenesis; actin filament bundle formation; cell adhesion; integrin-mediated signaling pathway; cell division
<i>ITGA2B</i>	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B).	NM_000419.2	ILMN_137597	2.31469958	cell adhesion; integrin-mediated signaling pathway
<i>LACE1</i>	lactation elevated 1	NM_145315.3	ILMN_14055	2.28519913	
<i>TSPAN13</i>	tetraspanin 13	NM_014399.3	ILMN_17008	2.26123889	
<i>POPI</i>	processing of precursor 1, ribonuclease P/MRP subunit	NM_015029.1	ILMN_16011	2.24099386	tRNA 5'-leader removal
<i>LY96</i>	lymphocyte antigen 96	NM_015364.2	ILMN_25195	2.2188182	cell surface receptor linked signal transduction; antibacterial humoral response (sensu Vertebrata); inflammatory response; cellular defense response
<i>FER</i>	fps/fes related tyrosine kinase	NM_005246.1	ILMN_18146	2.14710902	intracellular signaling cascade
<i>TBC1D19</i>	TBC1 domain family, member 19	NM_018317.1	ILMN_3919	2.13686964	
<i>PARP9</i>	poly (ADP-ribose) polymerase family, member 9	NM_031458.1	ILMN_12926	2.12215043	protein amino acid ADP-ribosylation; cell migration
<i>PTD015</i>	PTD015 protein (PTD015)	NM_024684.2	ILMN_26165	2.11821744	
<i>SERPINI1</i>	serpin peptidase inhibitor, clade I (neuroserpin), member 1	NM_005025.2	ILMN_7089	2.10562687	peripheral nervous system development; central nervous system development
<i>KATNA1</i>	katanin p60 (ATPase-containing) subunit A 1.	NM_007044.2	ILMN_9099	2.04502742	cell cycle; cell division ; mitosis
<i>USP33</i>	ubiquitin specific peptidase 33 (USP33), transcript variant 3,	NM_201626.1	ILMN_5402	2.02871424	ubiquitin-dependent protein catabolism; protein deubiquitination
<i>LOC650029</i>	similar to RNA-binding protein 4 (RNA-binding motif protein 4) (Lark homolog) (Hlark) (RNA-binding motif protein 4a), transcript variant 2	XM_945483.1	ILMN_38345	2.01943685	
<i>CD55</i>	CD55 antigen, decay accelerating factor for complement (Cromer blood group) (CD55), mRNA.	NM_000574.2	ILMN_18297	2.01238059	innate immune response; complement activation, classical pathway
<i>CSRP2</i>	cysteine and glycine-rich protein 2 (CSRP2), mRNA.	NM_001321.1	ILMN_3862	2.00634789	cell proliferation organ morphogenesis; muscle development
<i>FLJ45337</i>	FLJ45337 protein (FLJ45337),	NM_207465.1	ILMN_16305	1.9560697	RNA-dependent DNA replication

	mRNA.				
<i>SERPIN8</i>	peptidase inhibitor, clade B (ovalbumin), member 8	NM_001031848.1	ILMN_4190	1.94183145	
<i>CRYAB</i>	crystallin, alpha B	NM_001885.1	ILMN_6827	1.91050692	visual perception; transmembrane receptor protein tyrosine kinase signaling pathway; protein folding; muscle contraction
<i>CCT6B</i>	chaperonin containing TCP1, subunit 6B (zeta 2)	NM_006584.2	ILMN_11269	1.89628791	chaperone-mediated protein complex assembly; spermatogenesis ; protein folding
<i>LOC55565</i>	hypothetical protein LOC55565	NM_017530.1	ILMN_22894	1.88726578	
<i>C12orf61</i>	chromosome 12 open reading frame 6	NM_175895.2	ILMN_10816	1.83773871	
<i>P2RY5</i>	purinergic receptor P2Y, G-protein coupled, 5	NM_005767.3	ILMN_1003	1.81437925	signal transduction; G-protein coupled receptor protein signaling pathway
<i>TFIP11</i>	tuftelin interacting protein 11 (TFIP11), transcript variant 1	NM_001008697.1	ILMN_5509	1.80687414	secretory pathway; cell differentiation; extracellular matrix organization and biogenesis
<i>JMJD1A</i>	jumonji domain containing 1A	NM_018433.3	ILMN_25544	1.80516967	
<i>FLJ32675</i>	hypothetical protein FLJ32675	NM_173811.2	ILMN_26553	1.78703804	
<i>FREMI</i>	FRAS1 related extracellular matrix 1	NM_144966.3	ILMN_30224	1.78449339	cell communication; homophilic cell-cell adhesion; development
<i>LOC643079</i>	hypothetical protein LOC643079	XM_927251.1	ILMN_137060	1.75690787	
<i>LOC644334</i>	similar to Band 4.1-like protein 5	XM_927497.1	ILMN_35465	1.75468641	
<i>KIFAP3</i>	kinesin-associated protein 3	NM_014970.2	ILMN_13775	1.74603019	signal transduction; protein complex assembly
<i>PCAF</i>	p300/CBP-associated factor	NM_003884.3	ILMN_22596	1.73837906	regulation of transcription, DNA-dependent; cell cycle arrest
<i>IL17D</i>	interleukin 17D	NM_138284.1	ILMN_5192	1.73077979	inflammatory response
<i>JMY</i>	junction-mediating and regulatory protein	NM_152405.1	ILMN_18491	1.72628768	
<i>ASAH3L</i>	N-acylsphingosine amidohydrolase 3-like	NM_001010887.2	ILMN_14768	1.71556373	ceramide metabolism
<i>LOC651302</i>	similar to Zinc finger protein 192	XM_940433.1	ILMN_32136	1.70823749	
<i>FLJ20273</i>	RNA-binding protein (FLJ20273)	NM_019027.1	ILMN_29593	1.70807007	
<i>ICK</i>	intestinal cell (MAK-like) kinase	NM_016513.3	ILMN_23886	1.69459281	signal transduction; development; protein amino acid phosphorylation
<i>C1orf162</i>	chromosome 1 open reading frame 162 (C1orf162)	NM_174896.2	ILMN_19455	1.68365276	
<i>C9orf72</i>	chromosome 9 open reading frame 72 (C9orf72)	NM_018325.1	ILMN_7216	1.67920558	
<i>DYNLT3</i>	dynein, light chain, Tctex-type 3 cDNA clone IMAGE:4619364	NM_006520.1 BG484767	ILMN_2720 ILMN_76683	1.65999334 1.63882448	

<i>WDR25</i>	WD repeat domain 25 cDNA clone IMAGp998C074110	NM_024515.3 BX090843	ILMN_25835 ILMN_10291	1.63731142 1.63151716	
<i>SLC12A2</i>	cDNA FLJ26784 fis solute carrier family 12 (sodium/potassium/chloride transporters), member 2	AK130294 NM_001046.2	ILMN_72286 ILMN_14384	1.62121226 1.61497479	chloride transport; potassium ion transport; sodium ion transport; amino acid transport
<i>PIK3CA</i>	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_006218.2	ILMN_26220	1.59911144	signal transduction
<i>GMCL1</i>	germ cell-less homolog 1	NM_178439.3	ILMN_3285	1.59140181	spermatogenesis; cell differentiation
<i>ZNF143</i>	zinc finger protein 143	NM_003442.3	ILMN_3415	1.59132935	regulation of transcription from RNA polymerase III promoter;
<i>MOGAT1</i>	monoacylglycerol O- acyltransferase 1	NM_058165.1	ILMN_14124	1.59089139	
<i>ADAM19</i>	ADAM metallopeptidase domain 19 (meltrin beta)	NM_033274.2	ILMN_12727	1.58672201	proteolysis and peptidolysis
<i>ANAPC10</i>	anaphase promoting complex subunit 10	NM_014885.1	ILMN_2970	1.58436996	regulation of mitotic metaphase/anaphase transition; G2/M transition of mitotic cell cycle
<i>LOC132321</i>	hypothetical protein LOC132321 (LOC132321)	NM_173487.1	ILMN_4988	1.57292722	
<i>RFX3</i>	regulatory factor X, 3	NM_134428.1	ILMN_21620	1.57034757	regulation of transcription, DNA-dependent
<i>C6orf84</i>	chromosome 6 open reading frame 84	NM_014895.1	ILMN_10764	1.5582802	
<i>WBP5</i>	WW domain binding protein 5 (WBP5)	NM_0010066 14.1	ILMN_3272	1.54858398	
<i>LOC144363</i>	hypothetical protein LOC144363	NM_0010016 60.1	ILMN_21147	1.5316323	electron transport
<i>AYTL1</i>	acyltransferase like 1	NM_017839.3	ILMN_11562	1.51020884	metabolism
<i>CDKAL1</i>	CDK5 regulatory subunit associated protein 1-like 1 cDNA FLJ36037 fis, clone	NM_017774.1 AK093356	ILMN_26274 ILMN_12301	1.50543268 1.49429714	
	cDNA clone DKFZp781L12160	BX951899	ILMN_12572	1.48470345	
<i>IPLA2(GAM MA)</i>	intracellular membrane- associated calcium-independent phospholipase A2 gamma	NM_015723.2	ILMN_22860	1.46344117	fatty acid metabolism; lipid metabolism
<i>UBE2H</i>	ubiquitin-conjugating enzyme	NM_003344.2	ILMN_23401	1.46241072	ubiquitin cycle

	E2H				
<i>DMTF1</i>	cyclin D binding myb-like transcription factor 1	NM_021145.2	ILMN_16919	1.46138894	regulation of transcription, DNA-dependent
<i>C12orf26</i>	chromosome 12 open reading frame 26 (C12orf26)	NM_032230.1	ILMN_732	1.46058982	
<i>DPP4</i>	dipeptidyl-peptidase 4	NM_001935.3	ILMN_20248	1.44255881	immune response; proteolysis and peptidolysis
<i>LATS1</i>	large tumor suppressor, homolog 1	NM_004690.2	ILMN_26841	1.42501961	negative regulation of cyclin dependent protein kinase activity; hormone-mediated signaling; regulation of actin filament polymerization; sister chromatid segregation; cell division; mitosis
<i>FOXP1</i>	forkhead box P1	NM_001012505.1	ILMN_21389	1.42319639	regulation of transcription, DNA-dependent;
<i>PHF20L1</i>	PHD finger protein 20-like 1	NM_198513.1	ILMN_1584	1.41572113	regulation of transcription, DNA-dependent
<i>EAF2</i>	ELL associated factor 2	NM_018456.4	ILMN_519	1.41071604	apoptosis; regulation of transcription, DNA-dependent
<i>APAF1</i>	apoptotic peptidase activating factor	NM_181869.1	ILMN_886	1.40586262	neurogenesis; regulation of apoptosis
<i>C14orf125</i>	chromosome 14 open reading frame 125.	XM_113763.7	ILMN_35287	1.40504787	
<i>ARID5B</i>	AT rich interactive domain 5B (MRF1-like	NM_032199.1	ILMN_17477	1.40413038	negative regulation of transcription, DNA-dependent
<i>GLS</i>	glutaminase	NM_014905.2	ILMN_2718	1.4002039	glutamine catabolism
<i>ASB3</i>	ankyrin repeat and SOCS box-containing 3	NM_016115.3	ILMN_25973	1.38358336	intracellular signaling cascade
<i>TXNL4B</i>	thioredoxin-like 4B	NM_017853.1	ILMN_5441	1.37954804	nuclear mRNA splicing, via spliceosome; electron transport; cell cycle
<i>PLSCR1</i>	phospholipid scramblase 1	NM_021105.1	ILMN_4441	1.37423459	response to virus; phospholipid scrambling ; platelet activation
<i>ABCG1</i>	ATP-binding cassette, sub-family G (WHITE), member 1	NM_207629.1	ILMN_8619	1.36619675	cholesterol homeostasis; detection of hormone stimulus; lipid transport; cholesterol metabolism; response to organic substance; nucleotide binding
<i>CDKN2C</i>	cyclin-dependent kinase inhibitor 2C	NM_078626.1	ILMN_138785	1.36472998	cell cycle arrest; negative regulation of cell proliferation
<i>LOC642236</i>	similar to FRG1 protein	XM_943005.1	ILMN_31082	1.36467707	
<i>C14orf145</i>	chromosome 14 open reading frame 145 (C14orf145	NM_152446.2	ILMN_3022	1.36235206	
<i>FLJ22028</i>	hypothetical protein FLJ22028 (FLJ22028).	NM_024854.2	ILMN_27144	1.34908073	electron transport
<i>FAM24B</i>	family with sequence similarity 24, member B	NM_152644.1	ILMN_25126	1.34828828	
<i>ACTA2</i>	actin, alpha 2, smooth muscle,	NM_001613.1	ILMN_6588	1.34481262	muscle development

<i>PAQR3</i>	aorta progesterone and adiponectin receptor family member III	NM_177453.2	ILMN_20371	1.34328286	
<i>ETV6</i>	ets variant gene 6	NM_001987.3	ILMN_7247	1.33782124	regulation of transcription, DNA-dependent; transcription
<i>TXNDC13</i>	thioredoxin domain containing 13	NM_021156.2	ILMN_23065	1.33721192	electron transport
<i>ZFYVE1</i>	zinc finger, FYVE domain containing 1	NM_021260.1	ILMN_6420	1.33340812	vesicle-mediated transport; metal ion binding
<i>NLF2</i>	nuclear localized factor 2	NM_0010075 95.1	ILMN_6857	1.3251958	
<i>TAT</i>	tyrosine aminotransferase	NM_000353.1	ILMN_6875	1.32373046	amino acid and derivative metabolism; L-phenylalanine catabolism; tyrosine catabolism
<i>PDZD6</i>	PDZ domain containing 6	NM_015693.2	ILMN_13017	1.32266392	
<i>PLAC8</i>	placenta-specific 8	NM_016619.1	ILMN_17809	1.31964286	
<i>FOS</i>	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM_005252.2	ILMN_27030	1.31955306	inflammatory response; DNA methylation ; regulation of transcription from RNA polymerase II promoter
<i>PIK3C3</i>	phosphoinositide-3-kinase, class 3	NM_002647.2	ILMN_3418	1.3170853	
<i>ARL13B</i>	ADP-ribosylation factor-like 13B	NM_144996.2	ILMN_3311	1.30286396	intracellular protein transport
<i>TUBE1</i>	tubulin, epsilon 1	NM_016262.3	ILMN_7563	1.29860474	microtubule-based movement; centrosome cycle; protein polymerization
<i>CCDC18</i>	coiled-coil domain containing 18	NM_206886.2	ILMN_21161	1.29814195	
<i>FRYL</i>	furry homolog-like	XM_945282.1	ILMN_33777	1.29787166	
<i>RGC32</i>	response gene to complement 32	NM_014059.1	ILMN_14549	1.29758305	
<i>LOC646609</i>	similar to Chloride intracellular channel protein 4	XM_929546.1	ILMN_41265	1.29045708	
<i>SDCBP</i>	syndecan binding protein	NM_0010070 69.1	ILMN_12107	1.2835433	metabolism; intracellular signaling cascade; substrate-bound cell migration, cell extension; synaptic transmission; protein targeting to membrane; actin cytoskeleton organization and biogenesis
<i>C14orf103</i>	chromosome 14 open reading frame 103	NM_018036.4	ILMN_9364	1.28028457	
<i>PMAIP1</i>	phorbol-12-myristate-13-acetate- induced protein 1	NM_021127.1	ILMN_25637	1.27546907	
<i>NPAT</i>	nuclear protein, ataxia- telangiectasia locus	NM_002519.1	ILMN_2928	1.27259227	
<i>KIAA0256</i>	KIAA0256 gene product	NM_014701.2	ILMN_23132	1.27232144	
<i>C10orf87</i>	chromosome 10 open reading	NM_144587.2	ILMN_23857	1.26144149	

	frame 87				
<i>RBJ</i>	Ras-associated protein Rap1	NM_016544.1	ILMN_30155	1.25981123	protein folding ; small GTPase mediated signal transduction
<i>CWF19L2</i>	CWF19-like 2, cell cycle control	NM_152434.1	ILMN_14972	1.25658561	
<i>CCDC77</i>	coiled-coil domain containing 77	NM_032358.2	ILMN_23011	1.2551876	
<i>PHF20L1</i>	PHD finger protein 20-like 1	NM_016018.3	ILMN_14864	1.24463745	regulation of transcription, DNA-dependent
<i>CTH</i>	cystathionase (cystathionine gamma-lyase)	NM_001902.4	ILMN_25752	1.24424688	amino acid biosynthesis; cysteine biosynthesis
<i>SLC7A11</i>	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	NM_014331.2	ILMN_13883 2	1.24219918	protein complex assembly; amino acid transport
		XM_499121	ILMN_12051 0	1.24036989	
<i>CEACAM1</i>	carcinoembryonic antigen-related cell adhesion molecule 1	NM_001712.3	ILMN_21651	1.23846584	pregnancy; cell migration; integrin-mediated signaling pathway; angiogenesis; homophilic cell adhesion
<i>NCOA7</i>	nuclear receptor coactivator 7	NM_181782.2	ILMN_9525	1.23721258	cell wall catabolism
<i>AKAP7</i>	A kinase (PRKA) anchor protein 7	NM_016377.2	ILMN_21017	1.23200503	ion transport; intracellular signaling cascade; protein localization
<i>RPIB9</i>	Rap2-binding protein 9	NM_138290.1	ILMN_28536	1.23033723	
<i>NEDD9</i>	neural precursor cell expressed, developmentally down-regulated	NM_006403.2	ILMN_11885	1.23022777	signal transduction; cytoskeleton organization and biogenesis; cell cycle; actin filament bundle formation; cell adhesion; integrin-mediated signaling pathway; mitosis
<i>FLJ46906</i>	hypothetical gene supported by AK128874	XM_928441.1	ILMN_40537	1.2272131	
	cDNA clone IMAGp998I115625	BX101252	ILMN_75769	1.22642718	
<i>LOC642787</i>	hypothetical protein LOC642787	XM_926202.1	ILMN_44478	1.22429762	
<i>TSPAN8</i>	tetraspanin 8	NM_004616.2	ILMN_578	1.2234739	protein amino acid glycosylation
<i>HLA-B</i>	major histocompatibility complex, class I, B (HLA-B)	NM_005514.5	ILMN_18149	1.22192826	antigen processing, endogenous antigen via MHC class I
<i>PPP2R1B</i>	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	NM_181699.1	ILMN_25422	1.21748885	induction of apoptosis; regulation of Wnt receptor signaling pathway; ceramide metabolism; inactivation of MAPK activity; regulation of translation; regulation of cell differentiation; regulation of transcription; regulation of cell adhesion; regulation of growth; regulation of DNA replication; negative regulation of tyrosine phosphorylation of Stat3 protein; protein amino acid dephosphorylation; response to organic substance; second-messenger-mediated signaling; regulation of cell cycle; RNA splicing; protein complex assembly

<i>NEK1</i>	NIMA (never in mitosis gene a)-related kinase 1	NM_012224.1	ILMN_26831	1.21659952	mitosis; protein amino acid phosphorylation
<i>LOC647743</i>	similar to G protein-coupled receptor 89	XM_936805.1	ILMN_46476	1.21284174	
<i>SERF2</i>	small EDRK-rich factor 2	NM_0010181	ILMN_7601	1.21254154	
<i>CEP76</i>	centrosomal protein 76kDa	NM_024899.2	ILMN_9192	1.21241347	
<i>KIAA1212</i>		NM_018084.3	ILMN_18796	1.20952528	
<i>GPR89A</i>	G protein-coupled receptor 89A	NM_016334.2	ILMN_10695	1.20824057	positive regulation of I-kappaB kinase/NF-kappaB cascade
<i>LOC152485</i>	hypothetical protein LOC152485	NM_178835.2	ILMN_11861	1.20649655	
<i>ZNF439</i>	zinc finger protein 439	NM_152262.1	ILMN_2860	1.20142296	regulation of transcription, DNA-dependent
<i>ZNF548</i>	zinc finger protein 548	NM_152909.2	ILMN_16141	1.19910415	regulation of transcription, DNA-dependent
<i>LPXN</i>	leupaxin	NM_004811.1	ILMN_25554	1.19715038	signal transduction; protein complex assembly; cell adhesion
<i>IFI44</i>	interferon-induced protein 44	NM_006417.2	ILMN_28905	1.19641378	response to virus
<i>LOC554203</i>	hypothetical LOC554203	XR_001081.1	ILMN_31914	1.1956661	
<i>LPHN2</i>	latrophilin 2	NM_012302.2	ILMN_11901	1.19366924	signal transduction; G-protein coupled receptor protein signaling pathway; neuropeptide signaling pathway
<i>CHIC2</i>	cysteine-rich hydrophobic domain 2	NM_012110.2	ILMN_24345	1.19332137	
<i>MNAT1</i>	menage a trois homolog 1, cyclin H assembly factor	NM_002431.2	ILMN_23149	1.18369084	cell cycle; regulation of transcription from RNA polymerase II promoter; regulation of cyclin dependent protein kinase activity; protein complex assembly; DNA repair
<i>SLC2A13</i>	solute carrier family 2 (facilitated glucose transporter), member 13	NM_052885.1	ILMN_26745	1.18298483	carbohydrate transport
<i>IFT74</i>	intraflagellar transport 74 homolog	NM_025103.1	ILMN_20468	1.18187893	
<i>C1orf103</i>	chromosome 1 open reading frame 103 (C1orf103)	NM_018372.3	ILMN_11973	1.18124574	
<i>BRWD3</i>	bromodomain and WD repeat domain containing 3	NM_153252.2	ILMN_6030	1.17894345	
	Soares_NFL_T_GBC_S1 cDNA clone	BX106357	ILMN_93049	1.17870252	
<i>KIAA0103</i>		NM_014673.2	ILMN_16778	1.17853886	
<i>C13orf24</i>	chromosome 13 open reading frame 24 (C13orf24), mRNA.	NM_006346.2	ILMN_23420	1.17648712	
<i>LOC646463</i>	similar to Ubiquitin-conjugating enzyme E2 H (Ubiquitin-protein	XM_929387.1	ILMN_38228	1.17187674	

	ligase H) (Ubiquitin carrier protein H)				
<i>TRIM9</i>	tripartite motif-containing 9	NM_052978.3	ILMN_11039	1.16960098	protein ubiquitination
<i>TAF13</i>	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	NM_005645.3	ILMN_3685	1.16871063	transcription initiation
<i>MGC33648</i>	hypothetical protein MGC33648	NM_153706.2	ILMN_28708	1.16646143	
<i>CCDC25</i>	coiled-coil domain containing 25 (CCDC25)	NM_001031708.1	ILMN_8455	1.16273058	
<i>GJA12</i>	gap junction protein, alpha 12	NM_020435.2	ILMN_6786	1.16082091	cell communication
<i>ZNF419</i>	zinc finger protein 419	NM_024691.2	ILMN_2849	1.1596756	regulation of transcription, DNA-dependent
<i>FAM46A</i>	family with sequence similarity 46, member A	NM_017633.1	ILMN_12554	1.15886191	
<i>DMXL1</i>	Dmx-like 1	NM_005509.3	ILMN_2505	1.15881809	
<i>GIP3</i>	interferon, alpha-inducible protein (clone IFI-6-16)	NM_002038.2	ILMN_9411	1.15477317	immune response; response to pest, pathogen or parasite
	cDNA FLJ41853	AK123847	ILMN_75009	1.14067862	
<i>RNPC2</i>	RNA-binding region (RNP1, RRM) containing 2	NM_184237.1	ILMN_20445	1.13776913	nuclear mRNA splicing, via spliceosome; regulation of transcription, DNA-dependent
<i>OVGP1</i>	oviductal glycoprotein 1,	NM_002557.3	ILMN_7829	1.13463695	chitin catabolism; pregnancy; fertilization; carbohydrate metabolism
<i>FBXL20</i>	F-box and leucine-rich repeat protein 20	NM_032875.1	ILMN_11563	1.13404385	ubiquitin cycle
<i>SGNE1</i>	secretory granule, neuroendocrine protein 1	NM_003020.1	ILMN_6950	1.1297731	intracellular protein transport; peptide hormone processing; protein folding; transport; regulation of hormone secretion; neuropeptide signaling pathway
<i>RAB33B</i>	RAB33B, member RAS oncogene family	NM_031296.1	ILMN_21878	1.12739164	intracellular protein transport; small GTPase mediated signal transduction
<i>KHDRBS3</i>	KH domain containing, RNA binding, signal transduction associated 3	NM_006558.1	ILMN_4679	1.12178929	spermatogenesis
<i>ALCAM</i>	activated leukocyte cell adhesion molecule	NM_001627.2	ILMN_21054	1.12132902	signal transduction; cell adhesion; antimicrobial humoral response (sensu Vertebrata)
<i>SPIN3</i>	spindlin family, member 3	NM_001010862.1	ILMN_26060	1.11933525	gametogenesis
<i>HNRPLL</i>	heterogeneous nuclear ribonucleoprotein L-like	NM_138394.2	ILMN_4564	1.11902438	mRNA processing
<i>C4orf18</i>	chromosome 4 open reading	NM_0010317	ILMN_16219	1.11620208	

<i>KSR1</i>	frame 18 kinase suppressor of ras 1	00.1 NM_014238.1	ILMN_20813	1.11543998	intracellular signaling cascade; protein amino acid phosphorylation; Ras protein signal transduction
<i>FAM103A1</i>	family with sequence similarity 103, member A1	NM_031452.2	ILMN_28104	1.11504363	
<i>CROT</i>	carnitine O-octanoyltransferase	NM_021151.2	ILMN_3745	1.11037889	fatty acid metabolism; generation of precursor metabolites and energy; transport; lipid metabolism
<i>GABARAPL1</i>	GABA(A) receptor-associated protein like 1	NM_031412.2	ILMN_5224	1.10860275	synaptic transmission; protein targeting
<i>RIOK2</i>	RIO kinase 2	NM_018343.1	ILMN_16482	1.10503411	
<i>LOC652349</i>	similar to nodal modulator 2 isoform 2	XM_941777.1	ILMN_43118	1.10057358	
<i>FBXO33</i>	F-box protein 33	NM_203301.1	ILMN_3703	1.10049158	ubiquitin cycle
<i>LIMK2</i>	LIM domain kinase 2	NM_0010318 01.1	ILMN_6284	1.10032393	protein amino acid phosphorylation
<i>SH3BGRL</i>	SH3 domain binding glutamic acid-rich protein like	NM_003022.1	ILMN_16347	1.09634936	
<i>C14orf140</i>	chromosome 14 open reading frame 140	NM_024643.1	ILMN_13200	1.09195795	
<i>WDR54</i>	WD repeat domain 54	NM_032118.2	ILMN_24792	1.0915774	
<i>C5orf21</i>	chromosome 5 open reading frame 21	NM_032042.3	ILMN_1337	1.08853091	
<i>METT5D1</i>	methyltransferase 5 domain containing 1	NM_152636.1	ILMN_21667	1.08816192	
<i>PPME1</i>	protein phosphatase methyltransferase 1	NM_016147.1	ILMN_17607	1.08230547	protein amino acid demethylation; aromatic compound metabolism
<i>SLC12A6</i>	solute carrier family 12 (potassium/chloride transporters), member 6	NM_005135.1	ILMN_2039	1.08205928	chloride transport; potassium ion transport; cell ion homeostasis; regulation of cell volume; ion transport; sodium ion transport; regulation of blood pressure; regulation of cell cycle; amino acid transport
<i>KLHL15</i>	kelch-like 15	NM_030624.1	ILMN_4687	1.08106553	
<i>ZNF222</i>	zinc finger protein 222	NM_013360.1	ILMN_10406	1.08072235	regulation of transcription, DNA-dependent
<i>CALM1</i>	calmodulin 1	NM_006888.2	ILMN_13730 3	1.06736238	G-protein coupled receptor protein signaling pathway
<i>FLJ11155</i>	hypothetical protein FLJ11155	NM_018342.2	ILMN_24245	1.06517426	
<i>C9orf85</i>	chromosome 9 open reading frame 85	NM_182505.3	ILMN_855	1.06265441	

<i>NFIB</i>	nuclear factor I/B	NM_005596.1	ILMN_14904	1.06146153	regulation of transcription, DNA-dependent; DNA replication
<i>FRK</i>	fyn-related kinase	NM_002031.2	ILMN_29306	1.06120007	regulation of cell cycle; intracellular signaling cascade; protein amino acid phosphorylation
<i>LOC650737</i>	hypothetical protein LOC650737	XM_944786.1	ILMN_40280	1.06015226	
<i>GNAQ</i>	guanine nucleotide binding protein (G protein), q polypeptide	NM_002072.2	ILMN_18320	1.05771411	protein amino acid ADP-ribosylation; phospholipase C activation; signal transduction; G-protein coupled receptor protein signaling pathway; blood coagulation
<i>FLJ21986</i>	hypothetical protein FLJ21986	NM_024913.3	ILMN_22149	1.05530063	
<i>CP</i>	ceruloplasmin	NM_000096.1	ILMN_24449	1.05415383	iron ion homeostasis; copper ion transport; copper ion homeostasis
	cDNA FLJ13457	AK023519	ILMN_82165	1.05325449	
<i>RNF122</i>	ring finger protein 122	NM_024787.2	ILMN_16492	1.04809637	protein ubiquitination
<i>TP53AP1</i>	TP53 activated protein 1	NM_007233.1	ILMN_684	1.04163786	response to DNA damage stimulus; response to stress
<i>CTHRC1</i>	collagen triple helix repeat containing 1	NM_138455.2	ILMN_7282	1.04055012	phosphate transport
<i>NIP30</i>	NEFA-interacting nuclear protein NIP30	NM_024946.1	ILMN_29588	1.0383417	
<i>CRIPT</i>	postsynaptic protein CRIPT	NM_014171.3	ILMN_12903	1.03688822	
<i>VAMP4</i>	vesicle-associated membrane protein 4	NM_003762.2	ILMN_139375	1.03552315	protein complex assembly; vesicle-mediated transport
<i>LMO4</i>	LIM domain only 4	NM_006769.2	ILMN_5796	1.03358839	regulation of transcription, DNA-dependent; transcription
<i>HIST2H2AA</i>	histone 2, H2aa	NM_003516.2	ILMN_26733	1.03305226	
<i>ISL2</i>	ISL2 transcription factor, LIM/homeodomain,	NM_145805.1	ILMN_22222	1.02641594	regulation of transcription, DNA-dependent; development; metal ion binding; zinc ion binding
<i>C14orf108</i>	chromosome 14 open reading frame 108	NM_018229.2	ILMN_22880	1.0249722	intracellular protein transport
<i>PTS</i>	6-pyruvoyltetrahydropterin synthase	NM_000317.1	ILMN_22962	1.02181493	tetrahydrobiopterin biosynthesis ; central nervous system development; amino acid; L-phenylalanine catabolism
<i>CYorf15B</i>	chromosome Y open reading frame 15B	NM_032576.2	ILMN_15605	1.02161774	
<i>HPS4</i>	Hermansky-Pudlak syndrome 4	NM_152843.1	ILMN_5996	1.02017388	protein targeting; positive regulation of cuticle pigmentation; hemostasis; protein stabilization; lysosome organization and biogenesis; positive regulation of eye pigmentation
<i>C6orf70</i>	chromosome 6 open reading frame 70	NM_018341.1	ILMN_23256	1.01837463	
<i>RCN1</i>	reticulocalbin 1, EF-hand calcium binding domain	NM_002901.1	ILMN_8159	1.01823348	
<i>SUHW1</i>	suppressor of hairy wing	NM_080740.3	ILMN_22120	1.01693224	regulation of transcription, DNA-dependent

<i>NFE2L1</i>	homolog 1 nuclear factor (erythroid-derived 2)-like 1	NM_003204.1	ILMN_13955	1.01584722	regulation of transcription, DNA-dependent; morphogenesis
<i>ZNF306</i>	zinc finger protein 306	NM_024493.1	ILMN_11711	1.01538699	regulation of transcription, DNA-dependent
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3	NM_002491.1	ILMN_22320	1.01356835	mitochondrial electron transport, NADH to ubiquinone
<i>RAB30</i>	RAS oncogene family member 30	NM_014488.3	ILMN_27838	1.01256351	small GTPase mediated signal transduction; protein transport
<i>RUFY2</i>	RUN and FYVE domain containing 2	NM_017987.3	ILMN_16413	1.01209506	
<i>SVIL</i>	supervillin	NM_003174.2	ILMN_6255	1.01061904	cytoskeleton organization and biogenesis; barbed-end actin filament capping; myogenesis
<i>THADA</i>	thyroid adenoma associated mRNA.	NM_198554.1	ILMN_21795	1.00996448	
<i>ANTXR2</i>	anthrax toxin receptor 2	NM_058172.3	ILMN_22521	1.00985858	
<i>ADM</i>	adrenomedullin	NM_001124.1	ILMN_29514	1.00971924	cell-cell signaling; response to wounding ; signal transduction; cAMP biosynthesis; pregnancy; excretion; progesterone biosynthesis; circulation
<i>C3orf38</i>	chromosome 3 open reading frame 38	NM_173824.2	ILMN_20011	1.00391662	metabolism; proteolysis and peptidolysis
<i>RAB3B</i>	RAB3B, member RAS oncogene family	NM_002867.2	ILMN_29025	1.00142507	intracellular protein transport; small GTPase mediated signal transduction
<i>ADH6</i>	alcohol dehydrogenase 6	NM_000672.2	ILMN_29135	-1.00166344	ethanol oxidation
<i>ANKS4B</i>	ankyrin repeat and sterile alpha motif domain containing 4B	NM_145865.1	ILMN_9791	-1.00825472	
<i>HES1</i>	hairy and enhancer of split	NM_005524.2	ILMN_10521	-1.00909724	regulation of transcription, DNA-dependent
<i>ZFPM1</i>	zinc finger protein, multitype 1	NM_153813.1	ILMN_15190	-1.01044915	regulation of transcription, DNA-dependent
<i>BCAR1</i>	breast cancer anti-estrogen resistance 1	NM_014567.2	ILMN_2703	-1.01222198	cell proliferation; epidermal growth factor receptor signaling pathway; positive regulation of cell migration; cell migration; nerve growth factor receptor signaling pathway; cell adhesion; integrin-mediated signaling pathway; B cell receptor signaling pathway; insulin receptor signaling pathway; regulation of apoptosis; platelet-derived growth factor receptor signaling pathway; actin filament organization; cell division; T cell receptor signaling pathway; regulation of cell growth
<i>PIK3AP1</i>	phosphoinositide-3-kinase adaptor protein 1	NM_152309.2	ILMN_8843	-1.01256097	
<i>TMCO3</i>	transmembrane and coiled-coil	NM_017905.3	ILMN_19218	-1.01539669	transport; regulation of pH

	domains 3				
<i>FLJ45244</i>	FLJ45244 protein	NM_207443.1	ILMN_12880	-1.02172385	
<i>PEG3</i>	paternally expressed 3	NM_006210.1	ILMN_27573	-1.0218359	regulation of transcription, DNA-dependent
<i>LGALS2</i>	lectin, galactoside-binding, soluble, 2	NM_006498.2	ILMN_19736	-1.02284478	
<i>FAM109A</i>	family with sequence similarity 109, member A	NM_144671.2	ILMN_26928	-1.03018783	
<i>LAIR2</i>	leukocyte-associated Ig-like receptor 2	NM_002288.3	ILMN_17175	-1.03832246	
<i>SNF1LK</i>	SNF1-like kinase	NM_173354.2	ILMN_23486	-1.04198823	regulation of cell differentiation; cell cycle; protein amino acid phosphorylation ; regulation of progression through mitotic cell cycle; protein kinase cascade
<i>PLEKHA4</i>	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4	NM_020904.1	ILMN_5126	-1.04265951	
<i>AXL</i>	AXL receptor tyrosine kinase	NM_001699.3	ILMN_17320	-1.04600011	signal transduction; regulation of cell cycle; protein amino acid phosphorylation
<i>GYG2</i>	glycogenin 2	NM_003918.1	ILMN_24869	-1.05338525	carbohydrate biosynthesis; glycogen biosynthesis
<i>APOF</i>	apolipoprotein F	NM_001638.2	ILMN_17377	-1.05398085	lipid metabolism; steroid metabolism; lipid transport; cholesterol metabolism
<i>GADD45B</i>	growth arrest and DNA-damage-inducible, beta	NM_015675.1	ILMN_13833 4	-1.05466621	activation of MAPKKK activity; apoptosis; cell differentiation; response to stress
<i>EGFR</i>	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	NM_005228.3	ILMN_15615	-1.05770746	cell proliferation; positive regulation of cell migration; regulation of peptidyl-tyrosine phosphorylation; ossification; epidermal growth factor receptor signaling pathway; calcium-dependent phospholipase A2 activation; cell cycle; positive regulation of nitric oxide biosynthesis; positive regulation of cell proliferation; protein amino acid phosphorylation; cell surface receptor linked signal transduction; protein insertion into membrane; positive regulation of phosphorylation; phospholipase C activation; response to stress; negative regulation of progression through cell cycle; cell-cell adhesion
<i>FABP1</i>	fatty acid binding protein 1	NM_001443.1	ILMN_11988	-1.05771314	fatty acid metabolism; cell-cell signaling; transport; organ morphogenesis
<i>KIAA1543</i>		XM_048362.9	ILMN_31340	-1.05902021	
<i>SOX9</i>	SRY (sex determining region Y)-box 9	NM_000346.2	ILMN_17599	-1.06997607	cartilage condensation; skeletal development; regulation of transcription from RNA polymerase II promoter

<i>ZNF295</i>	zinc finger protein 295	NM_020727.3	ILMN_12236	-1.07124344	regulation of transcription, DNA-dependent
<i>SOAT2</i>	sterol O-acyltransferase 2	NM_003578.2	ILMN_3634	-1.07784109	steroid metabolism ; cholesterol metabolism; lipid metabolism
<i>IRF1</i>	interferon regulatory factor 1	NM_002198.1	ILMN_11739	-1.08792035	immune response; regulation of transcription, DNA-dependent; cell cycle; negative regulation of progression through cell cycle
<i>APOA5</i>	apolipoprotein A-V	NM_052968.3	ILMN_18555	-1.09370108	regulation of lipid biosynthesis; lipoprotein metabolism; lipid transport; tissue regeneration
<i>ZNF297B</i>	zinc finger protein 297B	NM_014007.2	ILMN_17837	-1.0953481	regulation of transcription, DNA-dependent;
<i>BAIAP2L2</i>	BAI1-associated protein 2-like 2	NM_025045.3	ILMN_21982	-1.09555943	
<i>LOC648526</i>	similar to epiplakin 1	XM_937579.1	ILMN_33325	-1.10334299	
<i>NRP1</i>	neuropilin 1	NM_003873.3	ILMN_17483	-1.10432001	cell-cell signaling; signal transduction; axon guidance; cell adhesion; neurogenesis; angiogenesis; positive regulation of cell proliferation; cell differentiation; organ morphogenesis
<i>C18orf19</i>	chromosome 18 open reading frame 19	NM_152352.1	ILMN_17843	-1.10464543	
<i>PAQR9</i>	progesterone and adiponectin receptor family member IX	NM_198504.1	ILMN_22288	-1.10676646	
<i>C12orf46</i>	chromosome 12 open reading frame 46	NM_152321.1	ILMN_26083	-1.13458299	
<i>JUB</i>	jub, ajuba homolog	NM_032876.4	ILMN_21167	-1.13662697	
<i>LOC440925</i>	hypothetical gene supported by AK123485	NM_0010137.12.1	ILMN_19833	-1.14094855	
<i>HGFAC</i>	HGF activator	NM_001528.2	ILMN_25994	-1.14380211	proteolysis and peptidolysis; cell motility
<i>ZNF77</i>	zinc finger protein 77	NM_021217.1	ILMN_29355	-1.1446586	regulation of transcription, DNA-dependent
<i>ART4</i>	ADP-ribosyltransferase 4	NM_021071.2	ILMN_26808	-1.14484059	protein amino acid ADP-ribosylation; arginine metabolism
<i>C3orf32</i>	chromosome 3 open reading frame 32	NM_015931.1	ILMN_10644	-1.16079179	
<i>GJB1</i>	gap junction protein, beta 1 cDNA FLJ26031	NM_000166.2 AK129542	ILMN_8143 ILMN_82560	-1.16686388 -1.17906299	cell-cell signaling; transport; neurogenesis
<i>PRODH2</i>	proline dehydrogenase (oxidase) 2	NM_021232.1	ILMN_22218	-1.18018441	glutamate biosynthesis; proline catabolism
<i>LOC650803</i>	hypothetical protein LOC650803	XM_939893.1	ILMN_37820	-1.18341017	
<i>FOXA3</i>	forkhead box A3	NM_004497.2	ILMN_22171	-1.19300436	regulation of transcription, DNA-dependent
<i>SERPINA6</i>	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 6	NM_001756.3	ILMN_2426	-1.20109381	transport
<i>ELF3</i>	E74-like factor 3	NM_004433.3	ILMN_13615	-1.20196992	regulation of transcription, DNA-dependent; epidermis development;

<i>AGXT</i>	alanine-glyoxylate aminotransferase	NM_000030.1	ILMN_21738	-1.20214755	morphogenesis metabolism
<i>SLC2A2</i>	solute carrier family 2 (facilitated glucose transporter), member 2	NM_000340.1	ILMN_28285	-1.2061059	carbohydrate metabolism; glucose transport
<i>WWC1</i>	WW, C2 and coiled-coil domain containing 1	NM_015238.1	ILMN_28835	-1.2065926	
	full-length cDNA clone CS0DM001YA20	CR601260	ILMN_74924	-1.21358432	
<i>ZSCAN4</i>	zinc finger and SCAN domain containing 4	NM_152677.1	ILMN_21186	-1.21550099	regulation of transcription, DNA-dependent
<i>DIO1</i>	deiodinase, iodothyronine, type I	NM_000792.4	ILMN_13786 3	-1.21752454	thyroid hormone generation
<i>IRSI</i>	insulin receptor substrate 1	NM_005544.1	ILMN_18432	-1.22084617	signal transduction; insulin receptor signaling pathway; insulin-like growth factor receptor signaling pathway
<i>PAH</i>	phenylalanine hydroxylase	NM_000277.1	ILMN_10844	-1.22110133	metabolism; amino acid biosynthesis; aromatic amino acid family metabolism ; L-phenylalanine catabolism
<i>SULT2A1</i>	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	NM_003167.2	ILMN_16119	-1.24184441	steroid metabolism; bile acid catabolism; digestion; lipid metabolism
<i>RHOA</i>	ras homolog gene family, member U	NM_021205.4	ILMN_19658	-1.24639178	small GTPase mediated signal transduction
<i>SMTN</i>	smoothelin	NM_006932.3	ILMN_18885	-1.24805197	smooth muscle contraction; muscle development
<i>ACSS1</i>	acyl-CoA synthetase short-chain family member 1	NM_032501.2	ILMN_23106	-1.26735497	metabolism
<i>AXUD1</i>	AXIN1 up-regulated 1	NM_033027.2	ILMN_6524	-1.26979605	apoptosis
<i>C11orf11</i>	chromosome 11 open reading frame 11	NM_006133.1	ILMN_2615	-1.27859722	lipid metabolism
<i>EPO</i>	erythropoietin	NM_000799.2	ILMN_6125	-1.27977093	cell-cell signaling; signal transduction; erythrocyte maturation; response to stress; circulation; development
<i>VGF</i>	VGF nerve growth factor inducible	NM_003378.2	ILMN_9112	-1.28161397	
<i>SH3TC1</i>	SH3 domain and tetratricopeptide repeats 1	NM_018986.2	ILMN_7001	-1.28823105	
<i>CGN</i>	cingulin	NM_020770.1	ILMN_22926	-1.29873118	
<i>MBP</i>	myelin basic protein	NM_0010251 00.1	ILMN_10370	-1.29999499	immune response; synaptic transmission; nerve ensheathment; central nervous system development

<i>ZC3HAV1</i>	zinc finger CCCH-type, antiviral 1	NM_024625.3	ILMN_13481	-1.30193826	protein amino acid ADP-ribosylation
<i>CEBPA</i>	CCAAT/enhancer binding protein (C/EBP), alpha	NM_004364.2	ILMN_27029	-1.30826654	regulation of transcription, DNA-dependent; generation of precursor metabolites and energy; transcription; transcription from RNA polymerase II promoter; myeloid cell differentiation; cytokine and chemokine mediated signaling pathway
<i>LIN10</i>	lin-10 homolog	NM_025187.3	ILMN_20432	-1.31003446	
<i>KIAA1539</i>	KIAA1539	NM_025182.2	ILMN_29031	-1.32822426	
<i>ERBB3</i>	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3	NM_001982.2	ILMN_8157	-1.33682716	transmembrane receptor protein tyrosine kinase signaling pathway; protein amino acid phosphorylation
<i>ZNF165</i>	zinc finger protein 165	NM_003447.2	ILMN_8007	-1.34293769	regulation of transcription, DNA-dependent
<i>LOC196752</i>	similar to CG32542-PA	NM_0010108	ILMN_1138	-1.35123598	
<i>FSTL3</i>	folliculin-like 3	NM_005860.1	ILMN_13221	-1.35663717	
<i>LOC388814</i>	hypothetical LOC388814	XM_373926.3	ILMN_37880	-1.36466987	
<i>PARD6B</i>	par-6 partitioning defective 6 homolog beta	NM_032521.1	ILMN_13906	-1.38027838	cell cycle; cell division; regulation of cell migration; intercellular junction assembly; establishment and/or maintenance of cell polarity; axonogenesis
<i>ZFP36</i>	zinc finger protein 36, C3H type	NM_003407.1	ILMN_1557	-1.38680182	mRNA catabolism
	Soares_NFL_T_GBC_S1 cDNA clone	BX279683	ILMN_83038	-1.41044546	
<i>HAMP</i>	hepcidin antimicrobial peptide	NM_021175.2	ILMN_25191	-1.45134233	defense response to bacteria; xenobiotic metabolism; iron ion homeostasis; immune response; defense response to fungi ; response to pathogen
<i>WBSCR14</i>	Williams Beuren syndrome chromosome region 14 (WBSCR14)	NM_032994.1	ILMN_13707	-1.45499501	regulation of transcription, DNA-dependent; morphogenesis; transcription regulator activity
<i>DDIT4</i>	DNA-damage-inducible transcript 4	NM_019058.2	ILMN_13176	-1.46631115	
<i>DNAH17</i>	dynein, axonemal, heavy polypeptide 17	NM_003727.1	ILMN_16763	-1.49328818	microtubule-based movement
<i>OTUD1</i>	OTU domain containing 1	XM_939698.1	ILMN_44016	-1.49606872	
<i>GALNAC4S-6ST</i>	B cell RAG associated protein	NM_015892.2	ILMN_8597	-1.51140811	regulation of DNA recombination ; hexose biosynthesis; regulation of B cell differentiation
<i>INHBE</i>	inhibin, beta E	NM_031479.3	ILMN_7067	-1.53396718	
<i>NGEF</i>	neuronal guanine nucleotide exchange factor	NM_019850.1	ILMN_26971	-1.5350758	

<i>MBL2</i>	mannose-binding lectin (protein C) 2	NM_000242.1	ILMN_6942	-1.53863111	innate immune response; complement activation, lectin pathway; complement activation, classical pathway; response to oxidative stress; phosphate transport
<i>TRIM15</i>	tripartite motif-containing 1	NM_033229.1	ILMN_24997	-1.54985627	mesodermal cell fate determination
<i>CDC42EP2</i>	CDC42 effector protein (Rho GTPase binding) 2	NM_006779.2	ILMN_3335	-1.55510832	regulation of cell shape
<i>NR1H4</i>	nuclear receptor subfamily 1, group H, member 4	NM_005123.1	ILMN_25067	-1.5977192	regulation of transcription, DNA-dependent; signal transduction; transcription; bile acid metabolism
<i>LOC55908</i>	hepatocellular carcinoma-associated gene TD26	NM_018687.3	ILMN_19905	-1.61172871	
<i>CIDEB</i>	cell death-inducing DFFA-like effector b	NM_014430.1	ILMN_11569	-1.62178283	apoptosis; DNA damage response, signal transduction resulting in induction of apoptosis
<i>TRIM10</i>	tripartite motif-containing 10	NM_052828.1	ILMN_20158	-1.63515815	protein ubiquitination; hemopoiesis
<i>TRIM15</i>	tripartite motif-containing 15	NM_052812.1	ILMN_18211	-1.64467016	mesodermal cell fate determination; protein ubiquitination
<i>TCF1</i>	transcription factor 1, hepatic nuclear factor (HNF1)	NM_000545.3	ILMN_27901	-1.69153767	positive regulation of transcription
<i>PLEKHG3</i>	pleckstrin homology domain containing, family G	NM_015549.1	ILMN_28109	-1.69697843	
<i>ZNF556</i>	zinc finger protein 556	NM_024967.1	ILMN_9913	-1.70774509	regulation of transcription, DNA-dependent
<i>FLJ45248</i>	FLJ45248 protein	NM_207505.1	ILMN_21467	-1.72388403	
<i>HERC5</i>	hect domain and RLD	NM_016323.1	ILMN_22093	-1.73332362	regulation of cyclin dependent protein kinase activity; ubiquitin cycle
<i>ABCC6</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	XM_936351.1	ILMN_13751 5	-1.7970588	
<i>SLC17A2</i>	solute carrier family 17 (sodium phosphate), member 2	NM_005835.1	ILMN_27529	-1.8209492	ion transport ; phosphate metabolism ; transport; sodium ion transport
<i>HKDC1</i>	hexokinase domain containing 1	NM_025130.2	ILMN_4255	-1.84734256	glycolysis
<i>OTUD1</i>	OTU domain containing 1	XM_166659.6	ILMN_43748	-1.90684556	
<i>SCN9A</i>	sodium channel, voltage-gated, type IX, alpha	NM_002977.1	ILMN_17490	-1.96590682	sodium ion transport; cation transport
<i>FLJ46230</i>	FLJ46230 protein	NM_207463.1	ILMN_15593	-2.03499995	
<i>LOC144501</i>	hypothetical protein LOC144501	NM_182507.1	ILMN_3629	-2.17818257	
<i>EEF1A2</i>	eukaryotic translation elongation factor 1 alpha 2	NM_001958.2	ILMN_2929	-2.18440206	protein biosynthesis; translational elongation
<i>CCL5</i>	chemokine (C-C motif) ligand 5	NM_002985.2	ILMN_22732	-2.63724966	cell-cell signaling; chemotaxis; signal transduction; response to virus ; exocytosis; calcium ion homeostasis; cell adhesion; response to oxidative stress ; sensory perception; inflammatory response; cellular defense response; cell motility

<i>VMD2</i>	vitelliform macular dystrophy 2	NM_004183.1	ILMN_13919 0	-2.7956185	ion transport; visual perception ; sensory perception
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Supplementary Table S3: Genes that were significantly differentially expressed in mouse *Sox17*-null E8.5 embryos compared with those identified in (A) *Sox17* over-expressing mouse ES cells compared to control ES cells (Niakan et al., 2010) and in (B) *Sox17* over-expressing human ES cells compared to control ES cells (Seguin et al., 2008). Genes that were detected by Sox17 ChIP on chip from mouse ES or XEN cells are indicated.

(A) Comparison with *Sox17* overexpressing mouse ES cells

Symbol	E8.5 <i>Sox17</i> ⁻ / <i>Sox17</i> ⁺⁺ Log ₂ fold change	Mouse ES Log ₂ fold change ¹	Mouse ES ChIP (fold change) ¹	Mouse XEN ChIP (fold change) ¹	GO Biological Process
<i>Eno3</i>	-0.46	1.03			Glycolysis
<i>Ero1l</i>	-0.37	0.97			Protein folding, protein thiol-disulfide exchange, transport oxidation reduction
<i>Fgb</i>	1.53	-0.86	6.0		Signal transduction, blood coagulation, platelet activation, protein polymerization
<i>Folr1</i>	1.09	-0.76		2.6	Posttranslational protein targeting to membrane folic acid metabolic process
<i>Manba</i>	0.84	-0.91			Carbohydrate metabolic process glycoprotein catabolic process metabolic process
<i>Myo6</i>	0.56	-0.88			Protein targeting transport endocytosis synaptic transmission synaptogenesis sensory perception of sound locomotory behavior glutamate secretion protein transport dendrite development cytoplasmic vesicle inner ear morphogenesis auditory receptor cell differentiation regulation of synaptic plasticity inner ear development

(B) Comparison with *Sox17* overexpressing human ES cells

Symbol	E8.5 <i>Sox17⁻/Sox17⁺⁺</i> Log ₂ fold change	Human ES Log ₂ fold change ²	Mouse ES ChIP (fold change) ¹	Mouse XEN ChIP (fold change) ¹	GO Biological Process
<i>Adm/ADM</i>	-1.43	3.03	3.0	3.4	Heart development, positive regulation of cell proliferation
<i>Lbh/LBH</i>	-0.74	2.05			Transcription, regulation of transcription, DNA-dependent, regulation of transcription from RNA polymerase II promoter, multicellular organismal development, transcription activator activity
<i>Sord/SORD</i>	0.82	-0.53			Sorbitol metabolic process oxidation reduction
<i>Steap2/STEAP2</i>	0.81	-0.58			Transport ion transport iron ion transport metabolic process oxidation reduction
<i>Vil1/VIL1</i>	1.41	-0.60			Cytoskeleton organization, barbed-end actin filament capping
<i>Zbtb44/ZBTB44</i>	0.41	-0.62			Regulation of transcription, DNA dependent

¹ data from (Niakan et al., 2010)² data from (Seguin et al., 2008)

Supplementary Table S4: Differentially expressed genes in Sox17-GFP over-expressing HepG2 cells that are common to Sox17-overexpressing human ES cells (Seguin et al 2008).

Gene	HepG2 SOX17GFP/GFP Log ₂ fold change	Human ES cells Sox17 Log ₂ fold change ¹	GO Biological Process
<i>ACSL4</i>	-0.72	-0.53	dendrite development; embryonic process involved in female pregnancy; fatty acid metabolic process; fatty acid transport; learning or memory; lipid metabolic process; response to interleukin-15; response to nutrient; triglyceride biosynthetic process
<i>ADM</i>	1.01	3.03	cell-cell signaling; response to wounding ; signal transduction; cAMP biosynthesis; pregnancy; excretion; progesterone biosynthesis; circulation
<i>BPHL</i>	-0.45	-0.32	cellular amino acid and derivative metabolic process; response to toxin
<i>CDC42</i>	0.46	0.98	JNK cascade; actin cytoskeleton organization; actin filament organization; actin filament polymerization; actin filament polymerization; axon guidance; axonogenesis; cell projection assembly; cellularization; cortical actin cytoskeleton organization; cytoskeleton organization; dendrite morphogenesis; dorsal appendage formation; dorsal closure; dorsal closure;; establishment of neuroblast polarity; hemocyte migration; imaginal disc-derived wing hair outgrowth; maintenance of cell polarity; neuron projection development; oogenesis; ovarian follicle cell development; phagocytosis, engulfment; regulation of axonogenesis
<i>CORO2A</i>	-0.64	-0.51	
<i>CPOX</i>	-0.34	-0.97	heme biosynthetic process; oxidation reduction; response to arsenic;
<i>FST</i>	0.73	2.48	response to drug; response to mercury ion BMP signaling pathway; female gonad development; hair follicle morphogenesis; hemopoietic progenitor cell differentiation; keratinocyte proliferation; negative regulation of activin receptor signaling pathway; negative regulation of cell differentiation; negative regulation of follicle-stimulating hormone secretion; negative regulation of transcription from RNA polymerase II promoter; odontogenesis of dentine-containing tooth; pattern specification process; positive regulation of hair follicle development
<i>GNG4</i>	-0.59	-1.79	G-protein coupled receptor protein signaling pathway; GTP catabolic process; hormone-mediated signaling pathway ; negative regulation of cell growth; signal transduction
<i>GPC6</i>	0.56	0.85	
<i>LYAR</i>	-0.34	-0.53	
<i>MAL2</i>	-0.626	-0.90	
<i>PHF20L1</i>	1.42	0.39	regulation of transcription, DNA-dependent
<i>RDX</i>	0.52	0.54	actin filament capping
<i>S100A16</i>	0.36	2.83	response to calcium ion
<i>SERINC3</i>	0.60	1.33	induction of apoptosis

<i>SERPINE2</i>	0.77	1.81	cell differentiation; multicellular organismal development; negative regulation of blood coagulation; negative regulation of blood coagulation; negative regulation of plasminogen activation; negative regulation of platelet aggregation; negative regulation of protein maturation by peptide bond cleavage; negative regulation of proteolysis; nervous system development; positive regulation of astrocyte differentiation; regulation of cell migration
<i>STC2</i>	-0.32	-1.12	cell surface receptor linked signaling pathway; cell-cell signalling; response to nutrient
<i>TMCO1</i>	0.36	0.62	
<i>WDR20</i>	-0.29	-0.22	
<i>ZNF114</i>	0.78	0.85	regulation of transcription, DNA-dependent

¹Data from (Seguin et al. 2008)

Supplementary Table S5: Differentially expressed genes in *Sox17*^{-/-} embryos and in HepG2 cells overexpressing *Sox17*-IRES-GFP that were detected in ChIP-Chip experiments in mouse ES or XEN cells (Niakan et al., 2010).

	E8.5 embryo: Sox17 ^{-/-} vs Sox17 ^{+/+}	HepG2 cells: Sox17-IRES-GFP vs GFP	ES ChIP ¹	XEN ChIP ¹
<i>Adm</i>	-1.43	1.01	8.5	5.7
<i>Fgb</i>	1.53	-0.32	6.0	-
<i>Mbl2</i>	1.38	-1.54	-	4.0
<i>Nrp1</i>	0.54	-1.10	6.3	3.6
<i>Rbm4b</i>	0.41	-0.29	6.0	4.1
<i>Slco4c1</i>	1.29	-0.37	3.9	-

Expression data are presented as log₂ fold change.

¹Data from (Niakan et al., 2010)

Supplementary table S6: Quantitative RT-PCR primers for amplifying transcripts from mouse cDNA.

Primer	5'-3' Sequence	T _m (°C)	Product Size (bp)
<i>Abcc-F</i>	TGGCTCATCTCAAATCCTTTGTGGCT	64	179
<i>Abcc-R</i>	ATCCGTCTCTAGATCCACTGCGGCT	64	
<i>Adm-F</i>	AGGGCCAGATACTCCTTTCGCAGTT	63	220
<i>Adm-R</i>	GGTAGCGTTTGACACGAATGTGGG	63	
<i>Afp-F</i>	CATCTTCCACAAGGATCTGTGCCAA	63	165
<i>Afp-R</i>	TGGGCTTTGCAGCACTTCTCCA	63	
<i>Apoc2-F</i>	ACTGGAGTGAGCCAGGATAGTCCCTT	62	152
<i>Apoc2-R</i>	CTGCCCCGAGTCATCTTCCTGGTT	62	
<i>Cryab-F</i>	AACTCAAAGTCAAGGTTCTGGGGGA	62	151
<i>Cryab-R</i>	CAGGGATGAAGTGATGGTGAGAGGAT	62	
<i>Cyp51-F</i>	GCGCTTGGACTTTAATCCTG	60	240
<i>Cyp51-R</i>	CGGATTACTGGGTTTTCTGG	59	
<i>Fga-F</i>	TCAGAAGACCTGAGGGCGCAGAATT	62	207
<i>Fga-R</i>	TTTATCTCACGGTTTACAGCCCTGCT	62	
<i>Fgb-F</i>	CGGTACAGAACGAGGCCAGCAA	64	221
<i>Fgb-R</i>	ATACCACCAGCCACCACCATCTTCTT	63	
<i>Fgg-F</i>	CACAACGGCATGCAGTTCAGTACCT	63	187
<i>Fgg-R</i>	CAAATAATGCCGTCGTCGAAACCA	63	
<i>Foxa3-F</i>	TGTAGAGAGACCGAAGCACTCGGTTC	62	216
<i>Foxa3-R</i>	AGAGCTGAGTGGGTTCAAGGTCATGT	62	
<i>Gapdh-F</i>	ATGACAACCTTGGCATTGTGGAAGG	60	300
<i>Gapdh-R</i>	CCTGCTTCACCACCTTCTTGATGTC	60	
<i>Idi1-F</i>	ATTGGTGTGAAGCGAGCAG	60	195
<i>Idi1-R</i>	GTTGGGATCTGGATTCAAGG	59	
<i>Insig1-F</i>	GTACACGTCCCCTGATTTCC	59	186
<i>Insig1-R</i>	ACACCAGGACCAGTGTCTC	60	
<i>Ldlr-F</i>	CACTCGCCCAAATTCACC	60	173
<i>Ldlr-R</i>	GCTGAGAGATCCTCACTGTGC	60	
<i>Mbl2-F</i>	TGAATGGCTTCCCAGGCAAAGAT	62	219
<i>Mbl2-R</i>	CGTAGGGCTGCAATTTCTGAATCAA	62	
<i>Myocd-F</i>	ATGCAGTGAAGCAGCAAATG	60	245
<i>Myocd-R</i>	GTGTTCGTCACTGTCGTTGG	60	
<i>Nrp1-F</i>	TTTCTCAGGAAGACTGTGCAAACCA	62	182
<i>Nrp1-R</i>	TCATGGCTATGATGGTGATCAGGATG	62	
<i>Reep6-F</i>	CAAAGCTATCGAGAGCCCAAGCAA	62	203
<i>Reep6-R</i>	ACGCGATGGTATAGTAGTAATGCCCC	61	
<i>Sc4mol-F</i>	CGGAATTGTGCTTTTGTGTG	60	164
<i>Sc4mol-R</i>	TCATGTGGTGGAATCATGG	60	
<i>Slc2a2-F</i>	GTGGGACTTGTGCTGCTGGATAAATT	62	231
<i>Slc2a2-R</i>	CAAGGAAGTCCGCAATGTACTGGAA	62	
<i>Slco4c1-F</i>	ATTGACATCGAGCTTTGCAGCCACT	64	210
<i>Slco4c1-R</i>	CACACCAGCAAATGGCTCATTTTCA	63	

Supplementary table S7: Quantitative RT-PCR primers for amplifying transcripts from human cDNA.

Primer	5'-3' Sequence	T _m (°C)	Product Size (bp)
<i>ABCC-F</i>	TGGTTCCTGTCCCTATTCTGGATTCT	61	217
<i>ABCC-R</i>	CTCAGGAATGAAGCTATGGATGATGG	61	
<i>ADM-F</i>	CGAAAGAAGTGAATAAGTGGGCTCT	61	161
<i>ADM-R</i>	ACTGCTGTCTTCGGGGCTTCGA	64	
<i>AFP-F</i>	TGCGTTTCTCGTTGCTTACACAAAG	61	233
<i>AFP-R</i>	TTGGCATATGAAGAAGTGCAGCACTG	63	
<i>APOC2-F</i>	AAGATGAGATGCCTAGCCCGACCT	62	214
<i>APOC2-R</i>	TCCCTTCAGCACAGAAAGAACTTGGT	62	
<i>CRYAB-F</i>	ATGCGCCTGGAGAAGGACAGGT	63	172
<i>CRYAB-R</i>	GGGATCCGGTATTTCCCTGTGGA ACT	63	
<i>FGA-F</i>	GCATGGACTGCAGATAGTGGTGAAGG	63	169
<i>FGA-R</i>	AACCCTTTCATCCTGCAGCCAGAA	63	
<i>FGB-F</i>	TAATGCCCTCATGGATGGAGCATCT	63	168
<i>FGB-R</i>	TCTATTATACCACCATCCACCACCGT	60	
<i>FGG-F</i>	TGATAAGCACACAGTCTGCCATCCC	63	238
<i>FGG-R</i>	GGTACTGAACTGCATGCCATTATGGG	63	
<i>FOXA3-F</i>	ATGCTGGGCTCAGTGAAGATGGA	61	134
<i>FOXA3-R</i>	AGGATTCAGGGTCATGTAGGAGTTGA	60	
<i>MBL2-F</i>	AAATCCAGGGCCTTCTGGGTCA	62	167
<i>MBL2-R</i>	TTCCCAACTTGTTTGCCAGAGAGA	63	
<i>NRP1-F</i>	TTTGTCCGAATCAAGCCTGCAACT	62	195
<i>NRP1-R</i>	GACTGGTTACCAGGCGGATGTTTT	61	
<i>POLR2A-F</i>	GCACCACGTCCAATGACAT	63	267
<i>POLR2A-R</i>	GTGCGGCTGCTTCCATAA	63	
<i>REEP6-F</i>	TTCCTGTTGTTCTGCATGGCTCC	62	213
<i>REEP6-R</i>	TCAGGGGGCTGCTTCACTTGTC	62	
<i>SLC2A2-F</i>	GTGGGATGTTTGTGTTGTGCCATCTT	62	179
<i>SLC2A2-R</i>	CAGGACGTGGTCCTTGACTGAAAAA	62	
<i>SLCO4C1-F</i>	GATTGACATCCAGCTTCGCAGCTACT	62	209
<i>SLCO4C1-R</i>	CACCAGCAAATGGCTCATTTCACA	63	