Appendix Table A.4.5.1. Vascular target genes found using RPKM of Tumour Huvec and hypoxia liver endothelium versus normal bulk human tissues

Log2((t.huvec + hHsec) /human normal tissues)	Gene	Product	Best TM	Signal peptide
13.37	TMSB4X	thymosin beta 4, X-linked	0	extracellular
9.38	ESM1	endothelial cell-specific molecule 1	0	signal
9.07	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	0	signal
8.00	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	0	signal
7.62	RELL1	RELT-like 1	2	signal
7.50	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	0	extracellular
7.29	CLIC1	chloride intracellular channel 1	0	membrane
7.07	THBS1	thrombospondin 1	0	extracellular
6.98	CLDN11	claudin 11	4	signal
6.96	AXL	AXL receptor tyrosine kinase	1	signal
6.89	EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	0	signal
6.83	NUDT19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	0	signal
6.78	SLC35F2	solute carrier family 35, member F2	9	
6.54	ANGPT2	angiopoietin 2	0	signal
6.38	PTX3	pentraxin 3, long	0	signal
6.32	ANXA1	annexin A1	0	extracellular
6.30	LOXL2	lysyl oxidase-like 2	0	signal
6.23	SEP15	15 kDa selenoprotein	0	signal
6.21	MARCKS	myristoylated alanine-rich protein kinase C substrate	0	membrane
6.20	TFPI2	tissue factor pathway inhibitor 2	0	signal

6.19	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	1	signal
6.12	GDF6	growth differentiation factor 6	0	signal
6.10	ECSCR	endothelial cell-specific chemotaxis regulator	1	signal
6.09	CTGF	connective tissue growth factor	0	signal
6.07	SULF1	sulfatase 1	0	extracellular
6.04	HHIP	hedgehog interacting protein	0	signal
6.04	TM4SF18	transmembrane 4 L six family member 18	4	signal
6.01	MMRN1	multimerin 1	0	membrane
6.01	EDN1	endothelin 1	0	signal
5.97	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	12	
5.95	HSPG2	heparan sulfate proteoglycan 2	0	extracellular
5.89	MGP	matrix Gla protein	1	signal
5.77	MMP10	matrix metallopeptidase 10 (stromelysin 2)	0	signal
5.72	TRIM59	tripartite motif containing 59	1	
5.66	TMTC3	transmembrane and tetratricopeptide repeat containing 3	9	
5.49	ANXA2	annexin A2	0	extracellular
5.47	TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	0	signal
5.43	PDGFA	platelet-derived growth factor alpha polypeptide	0	signal
5.41	ZMYM6NB	ZMYM6 neighbor	4	signal
5.33	HTN3	histatin 3	0	signal
5.32	CCL2	chemokine (C-C motif) ligand 2	0	signal
5.30	EMCN	endomucin	1	signal
5.29	VSIG10	V-set and immunoglobulin domain containing 10	2	signal
5.23	CNIH4	cornichon homolog 4 (Drosophila)	3	signal
5.20	LOX	lysyl oxidase	0	signal
5.17	C2orf18	chromosome 2 open reading frame 18	10	signal
5.14	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	1	signal

5.12	GNG11	guanine nucleotide binding protein (G protein), gamma 11	0	membrane
5.10	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	1	signal
5.07	BACE2	beta-site APP-cleaving enzyme 2	1	signal
5.06	F2R	coagulation factor II (thrombin) receptor	7	signal
5.00	BMP4	bone morphogenetic protein 4	0	signal
4.97	CD59	CD59 molecule, complement regulatory protein	0	signal
4.96	OSTC	oligosaccharyltransferase complex subunit	3	signal
4.94	GDF15	growth differentiation factor 15	0	signal
4.91	PROCR	protein C receptor, endothelial	1	signal
4.84	MYCT1	myc target 1	2	signal
4.80	REEP3	receptor accessory protein 3	3	
4.77	HTN1	histatin 1	0	signal
4.71	PGF	placental growth factor	0	signal
4.71	MAGT1	magnesium transporter 1	5	signal
4.69	PEAR1	platelet endothelial aggregation receptor 1	1	
4.69	BMP6	bone morphogenetic protein 6	0	signal
4.68	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	0	membrane
4.66	DKK1	dickkopf homolog 1 (Xenopus laevis)	0	signal
4.62	C12orf23	chromosome 12 open reading frame 23	2	
4.58	LYPD1	LY6/PLAUR domain containing 1	1	signal
4.56	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0	extracellular
4.56	EFNA5	ephrin-A5	0	signal
4.55	COL5A1	collagen, type V, alpha 1	0	extracellular
4.50	MFAP2	microfibrillar-associated protein 2	0	signal
4.50	GPX8	glutathione peroxidase 8 (putative)	1	signal
4.49	CCNB2	cyclin B2	0	membrane
4.48	FKBP14	FK506 binding protein 14, 22 kDa	0	signal
4.46	SPHK1	sphingosine kinase 1	0	membrane

4.46	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	1	
4.45	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	0	signal
4.45	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	1	
4.44	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	0	extracellular
4.44	CDH5	cadherin 5, type 2 (vascular endothelium)	2	signal
4.44	LRRC70	leucine rich repeat containing 70	1	signal
4.43	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	0	signal
4.41	C4orf49	chromosome 4 open reading frame 49	1	
4.40	APLN	apelin	1	signal
4.39	HMGB1	high mobility group box 1	0	extracellular
4.36	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	0	signal
4.36	LCLAT1	lysocardiolipin acyltransferase 1	3	
4.35	TMEM33	transmembrane protein 33	3	
4.29	LAMB1	laminin, beta 1	0	extracellular
4.26	TMEM41B	transmembrane protein 41B	6	
4.24	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0	extracellular
4.23	FKBP9	FK506 binding protein 9, 63 kDa	0	signal
4.22	PRSS23	protease, serine, 23	0	signal
4.20	C18orf19 FAM210A	chromosome 18 open reading frame 19 or FAM210A	1	
4.17	LAMA4	laminin, alpha 4	0	signal
4.13	ADRB1	adrenergic, beta-1-, receptor	7	
4.13	MRPS18C	mitochondrial ribosomal protein S18C	0	signal
4.13	MAP1LC3C	microtubule-associated protein 1 light chain 3 gamma	0	membrane
4.12	SDHD	succinate dehydrogenase complex, subunit D, integral membrane protein	0	signal
4.12	GLTP	glycolipid transfer protein	0	membrane

4.11	RCN2	reticulocalbin 2, EF-hand calcium binding domain	0	signal
4.10	PXDN	peroxidasin homolog (Drosophila)	1	signal
4.05	PODXL	podocalyxin-like	1	signal
4.03	TXN	thioredoxin	0	extracellular
4.01	SRPX2	sushi-repeat containing protein, X-linked 2	0	signal
4.01	VSIG1	V-set and immunoglobulin domain containing 1	1	signal
3.94	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1	signal
3.94	PECAM1	platelet/endothelial cell adhesion molecule	1	signal
3.93	RNF144B	ring finger protein 144B	1	
3.92	TMEM212	transmembrane protein 212	4	signal
3.92	SYNJ2BP	synaptojanin 2 binding protein	1	
3.92	LDLRAD2	low density lipoprotein receptor class A domain containing 2	0	signal
3.90	ITM2A	integral membrane protein 2A	1	
3.89	HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	7	
3.88	ZPBP2	zona pellucida binding protein 2	0	signal
3.87	COL8A1	collagen, type VIII, alpha 1	0	extracellular
3.85	FN1	fibronectin 1	0	signal
3.85	TM4SF1	transmembrane 4 L six family member 1	4	signal
3.85	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	1	signal
3.85	MEGF6	multiple EGF-like-domains 6	1	
3.84	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	0	membrane
3.84	ETNK1	ethanolamine kinase 1	1	signal
3.84	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene)	1	
3.84	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	7	signal
3.83	OPN1SW	opsin 1 (cone pigments), short-wave-sensitive	7	
3.83	NOX4	NADPH oxidase 4	5	

3.82	NOG	noggin	0	signal
3.82	PAPL	iron/zinc purple acid phosphatase-like protein	0	signal
3.81	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	0	membrane
3.80	ICAM2	intercellular adhesion molecule 2	1	signal
3.80	SERF2	small EDRK-rich factor 2	0	signal
3.80	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1	signal
3.79	ANGPTL4	angiopoietin-like 4	0	signal
3.78	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	0	signal
3.78	NTN4	netrin 4	1	signal
3.77	SLC30A7	solute carrier family 30 (zinc transporter), member 7	6	
3.75	PLSCR4	phospholipid scramblase 4	0	membrane
3.73	ENG	endoglin	1	signal
3.73	PDGFB	platelet-derived growth factor beta polypeptide	0	signal
3.71	KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	0	signal
3.70	CALCRL	calcitonin receptor-like	8	signal
3.67	BGN	biglycan	0	signal
3.67	ADAM17	ADAM metallopeptidase domain 17	1	
3.67	ANXA3	annexin A3	0	membrane
3.64	FAM18B1	family with sequence similarity 18, member B1	3	signal
3.64	LPAR6	lysophosphatidic acid receptor 6	7	
3.63	CALU	calumenin	0	signal
3.63	CYTL1	cytokine-like 1	0	signal
3.57	TMEM167B	transmembrane protein 167B	2	signal
3.57	RIT1	Ras-like without CAAX 1	0	membrane
3.56	CYR61	cysteine-rich, angiogenic inducer, 61	0	signal
3.55	RCN1	reticulocalbin 1, EF-hand calcium binding domain	0	signal
3.55	RNF5	ring finger protein 5	2	

3.54	CAV2	caveolin 2	1	signal
3.54	CAV1	caveolin 1, caveolae protein, 22kDa	1	
3.53	MYOF	myoferlin	1	
3.52	PDGFC	platelet derived growth factor C	0	signal
3.51	PMCH	pro-melanin-concentrating hormone	1	signal
3.50	YIPF5	Yip1 domain family, member 5	4	
3.49	RDH10	retinol dehydrogenase 10 (all-trans)	2	
3.48	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1	signal
3.47	DERL2	Der1-like domain family, member 2	4	signal
3.46	B3GALTL	beta 1,3-galactosyltransferase-like	1	signal
3.44	CLEC14A	C-type lectin domain family 14, member A	1	signal
3.43	FDPS	farnesyl diphosphate synthase	2	signal
3.43	POGLUT1	protein O-glucosyltransferase 1	0	signal
3.42	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	1	signal
3.42	EPHA2	EPH receptor A2	1	signal
3.40	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	1	signal
3.40	GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	1	
3.39	GDF7	growth differentiation factor 7	0	signal
3.39	MBOAT1	membrane bound O-acyltransferase domain containing 1	6	
3.39	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1	signal
3.38	ECE1	endothelin converting enzyme 1	1	
3.38	ORAI2	ORAI calcium release-activated calcium modulator 2	4	signal
3.38	EGFL7	EGF-like-domain, multiple 7	0	signal
3.36	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	0	extracellular
3.36	LY96	lymphocyte antigen 96	0	signal
3.36	PTGIS	prostaglandin I2 (prostacyclin) synthase	1	signal
3.36	GP6	glycoprotein VI (platelet)	1	signal

3.35	KCNJ2	potassium inwardly-rectifying channel, subfamily J, member 2	2	
3.35	MARCH2	membrane-associated ring finger (C3HC4) 2	2	signal
3.34	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1	
3.34	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	3	signal
3.33	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	12	
3.32	FADS3	fatty acid desaturase 3	3	
3.31	C18orf26	chromosome 18 open reading frame 26	1	
3.29	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18	1	signal
3.29	BET1	blocked early in transport 1 homolog (S. cerevisiae)	1	
3.28	TRA2A	transformer 2 alpha homolog (Drosophila)	0	signal
3.27	RRM2	ribonucleotide reductase M2	0	signal
3.27	NT5E	5'-nucleotidase, ecto (CD73)	2	signal
3.27	ZDHHC2	zinc finger, DHHC-type containing 2	4	signal
3.26	SLC38A2	solute carrier family 38, member 2	9	
3.26	TBXA2R	thromboxane A2 receptor	6	signal
3.26	JAG2	jagged 2	1	signal
3.26	C1GALT1C1	C1GALT1-specific chaperone 1	1	
3.25	COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	1	
3.25	TINAGL1	tubulointerstitial nephritis antigen-like 1	0	signal
3.24	P4HA3	prolyl 4-hydroxylase, alpha polypeptide III	0	signal
3.24	FAM69B	family with sequence similarity 69, member B	1	signal
3.23	INHBA	inhibin, beta A	0	signal
3.23	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	12	
3.23	FKBP10	FK506 binding protein 10, 65 kDa	0	signal
3.22	TRIM13	tripartite motif containing 13	1	
3.21	DCBLD2	discoidin, CUB and LCCL domain containing 2	1	signal

3.20	DAD1	defender against cell death 1	3	signal
3.20	PSG4	pregnancy specific beta-1-glycoprotein 4	0	signal
3.18	TMX1	thioredoxin-related transmembrane protein 1	3	signal
3.18	MDK	midkine (neurite growth-promoting factor 2)	1	signal
3.18	TGFB1	transforming growth factor, beta 1	0	signal
3.17	DRAM1	DNA-damage regulated autophagy modulator 1	6	signal
3.17	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	4	signal
3.16	FAM70B	family with sequence similarity 70, member B	4	signal
3.16	VMP1	vacuole membrane protein 1	6	
3.16	BCAP31	B-cell receptor-associated protein 31	3	signal
3.16	TMEM188 CNEP1R1	transmembrane protein 188 or CNEP1R1	2	
3.15	MICA	MHC class I polypeptide-related sequence A	1	signal
3.14	RBM39	RNA binding motif protein 39	0	signal
3.13	TTYH3	tweety homolog 3 (Drosophila)	5	
3.13	B2M	beta-2-microglobulin	0	signal
3.12	NRP2	neuropilin 2	1	signal
3.12	OST4	oligosaccharyltransferase 4 homolog (S. cerevisiae)	1	signal
3.12	NRG1	neuregulin 1	1	signal
3.11	MARCH6	membrane-associated ring finger (C3HC4) 6	14	
3.11	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0	signal
3.11	LOC730268	anaphase-promoting complex subunit 1-like	1	signal
3.11	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	1	signal
3.10	COL13A1	collagen, type XIII, alpha 1	0	membrane
3.09	SRPX	sushi-repeat containing protein, X-linked	0	signal
3.09	PHLDA2	pleckstrin homology-like domain, family A, member 2	0	membrane
3.09	GDF3	growth differentiation factor 3	0	signal
3.08	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	0	signal

3.08	CBX2	chromobox homolog 2	0	signal
3.08	CCDC90B	coiled-coil domain containing 90B	1	
3.07	GPR176	G protein-coupled receptor 176	7	
3.07	ACVRL1	activin A receptor type II-like 1	1	signal
3.07	UPK1B	uroplakin 1B	4	
3.07	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	2	signal
3.06	FAM176B	family with sequence similarity 176, member B	1	signal
3.06	LIMS1	LIM and senescent cell antigen-like domains 1	0	membrane
3.05	DCHS1	dachsous 1 (Drosophila)	2	
3.04	COX16	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	1	signal
3.04	CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1	1	signal
3.03	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	2	signal
3.02	TGFB2	transforming growth factor, beta 2	1	signal
3.02	PRKCH	protein kinase C, eta	0	membrane
3.01	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	1	signal
3.01	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	1	signal
3.01	COL5A2	collagen, type V, alpha 2	0	extracellular
3.00	CD9	CD9 molecule	4	signal
3.00	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	2	signal
8.99	RPL21	ribosomal protein L21	0	intracellular
8.53	NFIB	nuclear factor I/B	0	intracellular
8.11	C6orf62	chromosome 6 open reading frame 62	0	intracellular
7.92	SFRS6	serine/arginine-rich splicing factor 6	0	intracellular
7.61	RPS17	ribosomal protein S17	0	intracellular
7.44	SOX4	SRY (sex determining region Y)-box 4	0	intracellular
6.78	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	0	intracellular
6.64	FABP5	fatty acid binding protein 5 (psoriasis-associated)	0	intracellular

6.38	RAB33B	RAB33B, member RAS oncogene family	0	intracellular
6.24	FABP4	fatty acid binding protein 4, adipocyte	0	intracellular
6.18	CARD16	caspase recruitment domain family, member 16	0	intracellular
6.15	BCL10	B-cell CLL/lymphoma 10	0	intracellular
6.13	GSTO1	glutathione S-transferase omega 1	0	intracellular
6.13	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0	intracellular
5.94	SEPT2	septin 2	0	intracellular
5.90	SEPT7	septin 7	0	intracellular
5.89	TIGD1	tigger transposable element derived 1	0	intracellular
5.85	SET	SET nuclear oncogene	0	intracellular
5.83	LOC494141	mitochondrial carrier triple repeat 1 pseudogene	0	intracellular
5.82	PTTG1	pituitary tumor-transforming 1	0	intracellular
5.80	TUBB	tubulin, beta	0	intracellular
5.66	RPS3A	ribosomal protein S3A	0	intracellular
5.62	RAP2B	RAP2B, member of RAS oncogene family	0	intracellular
5.55	RDX	radixin	0	intracellular
5.48	TLK1	tousled-like kinase 1	0	intracellular
5.46	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0	intracellular
5.45	CHP CHP1	calcium binding protein P22 or CHP1	0	intracellular
5.44	CCNB1	cyclin B1	0	intracellular
5.44	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	0	intracellular
5.42	RIN2	Ras and Rab interactor 2	0	intracellular
5.41	POU5F1	POU class 5 homeobox 1	0	intracellular
5.40	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	0	intracellular
5.40	LXN	latexin	0	intracellular
5.34	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	0	intracellular
5.33	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa	0	intracellular

5.32	H2AFZ	H2A histone family, member Z	0	intracellular
5.30	LOC643733	caspase 4, apoptosis-related cysteine peptidase pseudogene	0	intracellular
5.28	THAP5	THAP domain containing 5	0	intracellular
5.24	NUSAP1	nucleolar and spindle associated protein 1	0	intracellular
5.22	STRN3	striatin, calmodulin binding protein 3	0	intracellular
5.17	VIM	vimentin	0	intracellular
5.13	RN7SL1	RNA, 7SL, cytoplasmic 1	0	intracellular
5.12	CASP2	caspase 2, apoptosis-related cysteine peptidase	0	intracellular
5.11	RPL18A	ribosomal protein L18a	0	intracellular
5.08	SAR1A	SAR1 homolog A (S. cerevisiae)	0	intracellular
5.07	SNORD102	small nucleolar RNA, C/D box 102	0	intracellular
5.06	MIR548D2	microRNA 548d-2	0	intracellular
5.02	PAN3	PAN3 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	0	intracellular
5.01	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0	intracellular
4.99	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0	intracellular
4.94	CASP4	caspase 4, apoptosis-related cysteine peptidase	0	intracellular
4.94	NS3BP	NS3BP	0	intracellular
4.92	SRP9	signal recognition particle 9kDa	0	intracellular
4.90	AKAP12	A kinase (PRKA) anchor protein 12	0	intracellular
4.88	RN7SK	RNA, 7SK small nuclear	0	intracellular
4.87	CKS2	CDC28 protein kinase regulatory subunit 2	0	intracellular
4.86	SEPT11	septin 11	0	intracellular
4.85	MIR126	microRNA 126	0	intracellular
4.83	BCYRN1	brain cytoplasmic RNA 1 (non-protein coding)	0	intracellular
4.83	MRPL42	mitochondrial ribosomal protein L42	0	intracellular
4.81	CDK1	cyclin-dependent kinase 1	0	intracellular
4.80	CSNK1A1	casein kinase 1, alpha 1	0	intracellular

4.80	FOXP1	forkhead box P1	0	intracellular
4.78	C10orf46	chromosome 10 open reading frame 46	0	intracellular
4.75	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	0	intracellular
4.73	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	0	intracellular
4.72	FAM103A1	family with sequence similarity 103, member A1	0	intracellular
4.68	BIRC5	baculoviral IAP repeat containing 5	0	intracellular
4.65	NMT2	N-myristoyltransferase 2	0	intracellular
4.65	FLNB	filamin B, beta	0	intracellular
4.62	TRAPPC2	trafficking protein particle complex 2	0	intracellular
4.62	CENPW	centromere protein W	0	intracellular
4.60	RPS27L	ribosomal protein S27-like	0	intracellular
4.59	ARRDC3	arrestin domain containing 3	0	intracellular
4.59	ZNF716	zinc finger protein 716	0	intracellular
4.59	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0	intracellular
4.58	LOC644173	hypothetical LOC644173	0	intracellular
4.57	SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	0	intracellular
4.56	FBLIM1	filamin binding LIM protein 1	0	intracellular
4.56	RPL7	ribosomal protein L7	0	intracellular
4.54	RPL26L1	ribosomal protein L26-like 1	0	intracellular
4.53	FKBP1A	FK506 binding protein 1A, 12kDa	0	intracellular
4.52	RNU6-21	RNA, U6 small nuclear 21	0	intracellular
4.51	ARF6	ADP-ribosylation factor 6	0	intracellular
4.48	LYPLA1	lysophospholipase I	0	intracellular
4.47	ATG12	ATG12 autophagy related 12 homolog (S. cerevisiae)	0	intracellular
4.46	ING3	inhibitor of growth family, member 3	0	intracellular
4.45	SOX7	SRY (sex determining region Y)-box 7	0	intracellular
4.38	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	0	intracellular
4.38	CRX	cone-rod homeobox	0	intracellular

4.37	NQO1	NAD(P)H dehydrogenase, quinone 1	0	intracellular
4.36	ANXA2P2	annexin A2 pseudogene 2	0	intracellular
4.36	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	0	intracellular
4.33	SEPT10	septin 10	0	intracellular
4.33	BMX	BMX non-receptor tyrosine kinase	0	intracellular
4.32	RHOJ	ras homolog gene family, member J	0	intracellular
4.30	CDK7	cyclin-dependent kinase 7	0	intracellular
4.30	HAUS1	HAUS augmin-like complex, subunit 1	0	intracellular
4.29	C20orf29 AP5S1	chromosome 20 open reading frame 29 or AP5S1	0	intracellular
4.29	SCARNA15	small Cajal body-specific RNA 15	0	intracellular
4.29	LOC339803	hypothetical LOC339803	0	intracellular
4.27	EIF4E	eukaryotic translation initiation factor 4E	0	intracellular
4.27	LOC100130 298	hCG1816373-like	0	intracellular
4.26	SHOX	short stature homeobox	0	intracellular
4.25	ARHGAP18	Rho GTPase activating protein 18	0	intracellular
4.24	FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	0	intracellular
4.23	MIR548H2	microRNA 548h-2	0	intracellular
4.23	GMFG	glia maturation factor, gamma	0	intracellular
4.21	PDCD10	programmed cell death 10	0	intracellular
4.21	LOC100127 904	hypothetical LOC100127904	0	intracellular
4.19	SRSF10	serine/arginine-rich splicing factor 10	0	intracellular
4.17	SENP5	SUMO1/sentrin specific peptidase 5	0	intracellular
4.16	SKA2	spindle and kinetochore associated complex subunit 2	0	intracellular
4.16	MYL12B	myosin, light chain 12B, regulatory	0	intracellular
4.15	POMP	proteasome maturation protein	0	intracellular
4.14	ACTG1	actin, gamma 1	0	intracellular

4.14	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	0	intracellular
4.14	TDP2	tyrosyl-DNA phosphodiesterase 2	0	intracellular
4.12	AEBP2	AE binding protein 2	0	intracellular
4.12	RPL7L1	ribosomal protein L7-like 1	0	intracellular
4.11	LOC440926 H3F3AP4	H3 histone, family 3A pseudogene or H3F3AP4	0	intracellular
4.11	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0	intracellular
4.10	MIR1254	microRNA 1254	0	intracellular
4.10	FNIP1	folliculin interacting protein 1	0	intracellular
4.09	ZNF286A	zinc finger protein 286A	0	intracellular
4.08	CDKN3	cyclin-dependent kinase inhibitor 3	0	intracellular
4.07	TRAPPC2P1	trafficking protein particle complex 2 pseudogene 1	0	intracellular
4.06	BLOC1S3	biogenesis of lysosomal organelles complex-1, subunit 3	0	intracellular
4.05	SEPT6	septin 6	0	intracellular
4.05	SKAP2	src kinase associated phosphoprotein 2	0	intracellular
4.05	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	0	intracellular
4.04	BCAT1	branched chain amino-acid transaminase 1, cytosolic	0	intracellular
4.04	ZC3H12D	zinc finger CCCH-type containing 12D	0	intracellular
4.03	LTBP2	latent transforming growth factor beta binding protein 2	0	intracellular
4.03	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0	intracellular
4.02	SKA1	spindle and kinetochore associated complex subunit 1	0	intracellular
4.02	TMSB15B	thymosin beta 15B	0	intracellular
4.02	SARNP	SAP domain containing ribonucleoprotein	0	intracellular
4.01	SNHG3	small nucleolar RNA host gene 3 (non-protein coding)	0	intracellular
4.00	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	0	intracellular
4.00	LOC100190 986	hypothetical LOC100190986	0	intracellular
4.00	LOC375295	hypothetical LOC375295	0	intracellular
3.99	MDM2	Mdm2 p53 binding protein homolog (mouse)	0	intracellular

3.98	RNU6-1	RNA, U6 small nuclear 1	0	intracellular
3.97	NOP10	NOP10 ribonucleoprotein homolog (yeast)	0	intracellular
3.96	LOC100302401	hypothetical LOC100302401	0	intracellular
3.96	HMGA1	high mobility group AT-hook 1	0	intracellular
3.96	CKS1B	CDC28 protein kinase regulatory subunit 1B	0	intracellular
3.95	LOC645166	lymphocyte-specific protein 1 pseudogene	0	intracellular
3.94	CDC26	cell division cycle 26 homolog (S. cerevisiae)	0	intracellular
3.93	LOC644961	actin, gamma 1 pseudogene	0	intracellular
3.93	PRDM1	PR domain containing 1, with ZNF domain	0	intracellular
3.93	MTPAP	mitochondrial poly(A) polymerase	0	intracellular
3.93	RPS26	ribosomal protein S26	0	intracellular
3.91	SKP1	S-phase kinase-associated protein 1	0	intracellular
3.90	TXNDC9	thioredoxin domain containing 9	0	intracellular
3.90	DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	0	intracellular
3.89	C17orf42 TEFM	chromosome 17 open reading frame 42 or TEFM	0	intracellular
3.89	PPP1CB	protein phosphatase 1, catalytic subunit, beta isozyme	0	intracellular
3.89	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	0	intracellular
3.88	LOC646576	hypothetical LOC646576	0	intracellular
3.88	LOC654342	lymphocyte-specific protein 1 pseudogene	0	intracellular
3.88	SRSF11	serine/arginine-rich splicing factor 11	0	intracellular
3.87	UBA6	ubiquitin-like modifier activating enzyme 6	0	intracellular
3.87	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	0	intracellular
3.87	GAS5	growth arrest-specific 5 (non-protein coding)	0	intracellular
3.86	TXNRD1	thioredoxin reductase 1	0	intracellular
3.86	MORC2-AS1	MORC2 antisense RNA 1 (non-protein coding)	0	intracellular

3.85	RPL34	ribosomal protein L34	0	intracellular
3.85	KIF20A	kinesin family member 20A	0	intracellular
3.85	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	0	intracellular
3.84	TRIM5	tripartite motif containing 5	0	intracellular
3.84	JUB AJUBA	jub, ajuba homolog (Xenopus laevis) or AJUBA	0	intracellular
3.83	SPOCD1	SPOC domain containing 1	0	intracellular
3.83	PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	0	intracellular
3.83	TOP2A	topoisomerase (DNA) II alpha 170kDa	0	intracellular
3.83	MRPL20	mitochondrial ribosomal protein L20	0	intracellular
3.82	RN28S1	RNA, 28S ribosomal 1	0	intracellular
3.80	TPI1	triosephosphate isomerase 1	0	intracellular
3.78	TYMS	thymidylate synthetase	0	intracellular
3.78	ATP5E	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0	intracellular
3.77	RAP1B	RAP1B, member of RAS oncogene family	0	intracellular
3.77	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	0	intracellular
3.75	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	0	intracellular
3.74	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	0	intracellular
3.73	EIF4B	eukaryotic translation initiation factor 4B	0	intracellular
3.73	ATRX	alpha thalassemia/mental retardation syndrome X-linked	0	intracellular
3.73	CDC20	cell division cycle 20 homolog (S. cerevisiae)	0	intracellular
3.72	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0	intracellular
3.71	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1	0	intracellular
3.71	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	0	intracellular
3.70	NCK1	NCK adaptor protein 1	0	intracellular
3.70	SHFM1	split hand/foot malformation (ectrodactyly) type 1	0	intracellular
3.69	RPL10	ribosomal protein L10	0	intracellular
3.69	ZC3HAV1	zinc finger CCCH-type, antiviral 1	0	intracellular

3.68	PBK	PDZ binding kinase	0	intracellular
3.68	DYNLT1	dynein, light chain, Tctex-type 1	0	intracellular
3.67	IPO11	importin 11	0	intracellular
3.67	SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)	0	intracellular
3.67	RAB2B	RAB2B, member RAS oncogene family	0	intracellular
3.65	KIF23	kinesin family member 23	0	intracellular
3.65	PIR	pirin (iron-binding nuclear protein)	0	intracellular
3.64	TPM4	tropomyosin 4	0	intracellular
3.63	RPL6	ribosomal protein L6	0	intracellular
3.63	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	0	intracellular
3.63	RPL9	ribosomal protein L9	0	intracellular
3.62	VWF	von Willebrand factor	0	intracellular
3.62	FOSL1	FOS-like antigen 1	0	intracellular
3.62	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	0	intracellular
3.61	LOC100288366	hypothetical LOC100288366	0	intracellular
3.61	CNN3	calponin 3, acidic	0	intracellular
3.61	PAK1IP1	PAK1 interacting protein 1	0	intracellular
3.61	CARD11	caspase recruitment domain family, member 11	0	intracellular
3.61	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0	intracellular
3.60	WWTR1	WW domain containing transcription regulator 1	0	intracellular
3.60	AK4	adenylate kinase 4	0	intracellular
3.59	LOC728758	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) pseudogene	0	intracellular
3.59	RPS7	ribosomal protein S7	0	intracellular
3.59	RBMS2	RNA binding motif, single stranded interacting protein 2	0	intracellular
3.58	CA5B	carbonic anhydrase VB, mitochondrial	0	intracellular
3.58	MIR1302-1	microRNA 1302-1	0	intracellular

3.58	EXOSC8	exosome component 8	0	intracellular
3.58	PPP6R3	protein phosphatase 6, regulatory subunit 3	0	intracellular
3.57	CENPK	centromere protein K	0	intracellular
3.57	LOC100130764	p150-like	0	intracellular
3.57	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	0	intracellular
3.56	EAF1	ELL associated factor 1	0	intracellular
3.56	MIR210	microRNA 210	0	intracellular
3.55	MIR302B	microRNA 302b	0	intracellular
3.55	ZNF22	zinc finger protein 22 (KOX 15)	0	intracellular
3.54	SNRPG	small nuclear ribonucleoprotein polypeptide G	0	intracellular
3.54	MRPS36	mitochondrial ribosomal protein S36	0	intracellular
3.54	WHAMMP3	WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 3	0	intracellular
3.54	ZNF562	zinc finger protein 562	0	intracellular
3.52	RN7SL2	RNA, 7SL, cytoplasmic 2	0	intracellular
3.52	SF3B14	splicing factor 3B, 14 kDa subunit	0	intracellular
3.51	MED21	mediator complex subunit 21	0	intracellular
3.49	RND3	Rho family GTPase 3	0	intracellular
3.49	VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)	0	intracellular
3.48	SNORD96A	small nucleolar RNA, C/D box 96A	0	intracellular
3.48	RBM8A	RNA binding motif protein 8A	0	intracellular
3.48	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	0	intracellular
3.47	HSPB11	heat shock protein family B (small), member 11	0	intracellular
3.45	GNG12	guanine nucleotide binding protein (G protein), gamma 12	0	intracellular
3.45	NLRP12	NLR family, pyrin domain containing 12	0	intracellular
3.45	LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	intracellular
3.44	S100A16	S100 calcium binding protein A16	0	intracellular
3.44	NCRNA001	non-protein coding RNA 114 or LINC00114	0	intracellular

	14 LINC00114			
3.43	ZNF846	zinc finger protein 846	0	intracellular
3.42	ARF4	ADP-ribosylation factor 4	0	intracellular
3.42	RPL23	ribosomal protein L23	0	intracellular
3.42	MIR29B1	microRNA 29b-1	0	intracellular
3.41	LYL1	lymphoblastic leukemia derived sequence 1	0	intracellular
3.41	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	0	intracellular
3.41	CEACAM22P	carcinoembryonic antigen-related cell adhesion molecule 2, pseudogene	0	intracellular
3.40	HNF1A-AS1	HNF1A antisense RNA 1 (non-protein coding)	0	intracellular
3.40	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0	intracellular
3.40	MEX3D	mex-3 homolog D (C. elegans)	0	intracellular
3.39	DCAF13	DDB1 and CUL4 associated factor 13	0	intracellular
3.39	FOXM1	forkhead box M1	0	intracellular
3.39	CENPN	centromere protein N	0	intracellular
3.39	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	0	intracellular
3.39	NCRNA00083 LINC00083	non-protein coding RNA 83 or LINC00083	0	intracellular
3.39	LOC100129434	hypothetical LOC100129434	0	intracellular
3.38	LOC284551	hypothetical LOC284551	0	intracellular
3.38	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	0	intracellular
3.38	MELK	maternal embryonic leucine zipper kinase	0	intracellular
3.38	S100A11	S100 calcium binding protein A11	0	intracellular
3.38	PAWR	PRKC, apoptosis, WT1, regulator	0	intracellular
3.38	LOC550643	hypothetical LOC550643	0	intracellular

3.37	LOC401098	hypothetical LOC401098	0	intracellular
3.37	COX7B	cytochrome c oxidase subunit VIIb	0	intracellular
3.37	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	0	intracellular
3.36	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	0	intracellular
3.36	MRPL13	mitochondrial ribosomal protein L13	0	intracellular
3.36	PDLIM7	PDZ and LIM domain 7 (enigma)	0	intracellular
3.36	PNRC2	proline-rich nuclear receptor coactivator 2	0	intracellular
3.35	PPIE	peptidylprolyl isomerase E (cyclophilin E)	0	intracellular
3.34	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0	intracellular
3.34	DCLRE1C	DNA cross-link repair 1C	0	intracellular
3.34	LOC100128126	hypothetical LOC100128126	0	intracellular
3.34	PNP	purine nucleoside phosphorylase	0	intracellular
3.34	MIR186	microRNA 186	0	intracellular
3.34	GSDMA	gasdermin A	0	intracellular
3.34	LOC646719	hypothetical LOC646719	0	intracellular
3.34	MEMO1	mediator of cell motility 1	0	intracellular
3.34	ERAP2	endoplasmic reticulum aminopeptidase 2	0	intracellular
3.33	FLNA	filamin A, alpha	0	intracellular
3.32	LRRC37BP1	leucine rich repeat containing 37B pseudogene 1	0	intracellular
3.31	GNRHR2	gonadotropin-releasing hormone (type 2) receptor 2	0	intracellular
3.31	SUMO2	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	0	intracellular
3.31	WSB1	WD repeat and SOCS box containing 1	0	intracellular
3.30	LOC100128288	hypothetical LOC100128288	0	intracellular
3.30	MDFI	MyoD family inhibitor	0	intracellular
3.30	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	0	intracellular
3.29	UBE2C	ubiquitin-conjugating enzyme E2C	0	intracellular
3.28	GSTCD	glutathione S-transferase, C-terminal domain containing	0	intracellular

3.28	LOC729291	hypothetical protein LOC729291	0	intracellular
3.28	PLK1	polo-like kinase 1	0	intracellular
3.28	DNAJC8	DnaJ (Hsp40) homolog, subfamily C, member 8	0	intracellular
3.28	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	0	intracellular
3.28	GINS2	GINS complex subunit 2 (Psf2 homolog)	0	intracellular
3.28	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	0	intracellular
3.28	LOC283788	FSHD region gene 1 pseudogene	0	intracellular
3.28	RPL13A	ribosomal protein L13a	0	intracellular
3.28	DMBX1	diencephalon/mesencephalon homeobox 1	0	intracellular
3.27	LOC647070	hypothetical LOC647070	0	intracellular
3.27	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	0	intracellular
3.27	ZFX	zinc finger protein, X-linked	0	intracellular
3.27	SNORD14B	small nucleolar RNA, C/D box 14B	0	intracellular
3.25	RBM34	RNA binding motif protein 34	0	intracellular
3.25	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	0	intracellular
3.25	SNORD14A	small nucleolar RNA, C/D box 14A	0	intracellular
3.25	RSU1	Ras suppressor protein 1	0	intracellular
3.25	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	0	intracellular
3.25	MOV10L1	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	0	intracellular
3.23	MIS18BP1	MIS18 binding protein 1	0	intracellular
3.23	C11orf44	chromosome 11 open reading frame 44	0	intracellular
3.22	SNX6	sorting nexin 6	0	intracellular
3.22	DKFZP434I0714	hypothetical protein DKFZP434I0714	0	intracellular
3.22	HNRNPK	heterogeneous nuclear ribonucleoprotein K	0	intracellular
3.21	MIR25	microRNA 25	0	intracellular
3.21	ZNF556	zinc finger protein 556	0	intracellular
3.21	UBE2B	ubiquitin-conjugating enzyme E2B	0	intracellular

3.20	PGM3	phosphoglucomutase 3	0	intracellular
3.20	NOL9	nucleolar protein 9	0	intracellular
3.20	RNY4	RNA, Ro-associated Y4	0	intracellular
3.20	ZNF578	zinc finger protein 578	0	intracellular
3.19	LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	intracellular
3.19	SWAP70	SWAP switching B-cell complex 70kDa subunit	0	intracellular
3.19	RPLP0	ribosomal protein, large, P0	0	intracellular
3.18	MIR548C	microRNA 548c	0	intracellular
3.18	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0	intracellular
3.17	PRELID1	PRELI domain containing 1	0	intracellular
3.16	NUP50	nucleoporin 50kDa	0	intracellular
3.16	CCNG1	cyclin G1	0	intracellular
3.15	SMAD1	SMAD family member 1	0	intracellular
3.15	NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	0	intracellular
3.14	TFB1M	transcription factor B1, mitochondrial	0	intracellular
3.14	FLJ31306	hypothetical LOC379025	0	intracellular
3.14	ACTN1	actinin, alpha 1	0	intracellular
3.14	CFL1P1	cofilin 1 (non-muscle) pseudogene 1	0	intracellular
3.13	RBBP5	retinoblastoma binding protein 5	0	intracellular
3.13	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0	intracellular
3.13	MITD1	MIT, microtubule interacting and transport, domain containing 1	0	intracellular
3.12	ATF6	activating transcription factor 6	0	intracellular
3.12	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	0	intracellular
3.12	ORC6	origin recognition complex, subunit 6	0	intracellular
3.12	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	0	intracellular
3.11	PGK1	phosphoglycerate kinase 1	0	intracellular
3.11	CEP55	centrosomal protein 55kDa	0	intracellular

3.11	TGFB1I1	transforming growth factor beta 1 induced transcript 1	0	intracellular
3.10	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0	intracellular
3.09	MRPS14	mitochondrial ribosomal protein S14	0	intracellular
3.08	EEA1	early endosome antigen 1	0	intracellular
3.08	PCNA	proliferating cell nuclear antigen	0	intracellular
3.08	GABPB1	GA binding protein transcription factor, beta subunit 1	0	intracellular
3.08	TK1	thymidine kinase 1, soluble	0	intracellular
3.08	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	0	intracellular
3.07	NME6	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	0	intracellular
3.07	EHD4	EH-domain containing 4	0	intracellular
3.06	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0	intracellular
3.06	HSBP1	heat shock factor binding protein 1	0	intracellular
3.06	DDB2	damage-specific DNA binding protein 2, 48kDa	0	intracellular
3.06	SNAP23	synaptosomal-associated protein, 23kDa	0	intracellular
3.06	S100A6	S100 calcium binding protein A6	0	intracellular
3.05	NR2F2	nuclear receptor subfamily 2, group F, member 2	0	intracellular
3.05	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	0	intracellular
3.05	AURKB	aurora kinase B	0	intracellular
3.05	KRT18	keratin 18	0	intracellular
3.05	INGX	inhibitor of growth family, X-linked, pseudogene	0	intracellular
3.05	ZNF814	zinc finger protein 814	0	intracellular
3.05	BZW1	basic leucine zipper and W2 domains 1	0	intracellular
3.04	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	0	intracellular
3.04	LIMA1	LIM domain and actin binding 1	0	intracellular
3.04	LOC100130938	hypothetical LOC100130938	0	intracellular
3.04	RAD17	RAD17 homolog (S. pombe)	0	intracellular

3.03	CIAPIN1	cytokine induced apoptosis inhibitor 1	0	intracellular
3.02	SNHG7	small nucleolar RNA host gene 7 (non-protein coding)	0	intracellular
3.02	RAN	RAN, member RAS oncogene family	0	intracellular
3.01	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	0	intracellular
3.01	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0	intracellular
3.00	PTMA	prothymosin, alpha	0	intracellular
3.00	RPL36AL	ribosomal protein L36a-like	0	intracellular
3.00	MORF4L1	mortality factor 4 like 1	0	intracellular
3.00	PGBD1	piggyBac transposable element derived 1	0	intracellular
8.93	MTND4P	MT-ND4 pseudogene 12	0	
8.39	RN18S1	RNA, 18S ribosomal 1	0	
7.54	FLJ41200	hypothetical LOC401492	0	
7.49	NCRNA00152 LINC00152	non-protein coding RNA 152 or LINC00152	0	
7.37	LSM12	LSM12 homolog (S. cerevisiae)	0	
7.27	RNY3	RNA, Ro-associated Y3	0	
7.06	LOC541471	hypothetical LOC541471	0	
6.81	RNY1	RNA, Ro-associated Y1	0	
6.80	MTND1P15	MT-ND1 pseudogene 15	0	
6.76	LOC100272146	nuclear factor (erythroid-derived 2)-like 3 pseudogene	0	
6.35	RNU6-15	RNA, U6 small nuclear 15	0	
6.25	PHACTR2	phosphatase and actin regulator 2	0	
6.09	HIST1H4C	histone cluster 1, H4c	0	
6.08	LOC729973	hypothetical LOC729973	0	
5.82	LOC100216001	hypothetical LOC100216001	0	

5.65	SNORD52	small nucleolar RNA, C/D box 52	0
5.28	FAM43A	family with sequence similarity 43, member A	0
5.22	CPNE8	copine VIII	0
5.08	LOC100127894	hypothetical protein LOC100127894	0
5.02	ZMYM5	zinc finger, MYM-type 5	0
4.95	CCDC72	coiled-coil domain containing 72	0
4.95	NHSL1	NHS-like 1	0
4.83	LIMS3	LIM and senescent cell antigen-like domains 3	0
4.67	CD109	CD109 molecule	0
4.51	RAI14	retinoic acid induced 14	0
4.50	DUXA	double homeobox A	0
4.43	C18orf54	chromosome 18 open reading frame 54	0
4.41	TMSL3 TMSB4XP8	thymosin-like 3 or TMSB4XP8	0
4.41	FAM101A	family with sequence similarity 101, member A	0
4.40	WBP5	WW domain binding protein 5	0
4.40	MIR1290	microRNA 1290	0
4.39	EXOC3L2	exocyst complex component 3-like 2	0
4.36	NT5DC2	5'-nucleotidase domain containing 2	0
4.27	LOC651250	leucine rich repeat containing 37, member A3 pseudogene	0
4.21	FAM76A	family with sequence similarity 76, member A	0
4.17	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1-like	0
4.09	FAM114A1	family with sequence similarity 114, member A1	0
4.08	CBWD5	COBW domain containing 5	0
4.08	CHP2	calcineurin B homologous protein 2	0
4.07	C14orf64	chromosome 14 open reading frame 64	0
4.03	C14orf178	chromosome 14 open reading frame 178	0
4.01	MAP7D3	MAP7 domain containing 3	0

4.00	KIAA0101	KIAA0101	0
4.00	CBWD2	COBW domain containing 2	0
3.97	LOC100131031	ankyrin repeat domain 18B pseudogene	0
3.95	METTL21A	methyltransferase like 21A	0
3.93	GIPC2	GIPC PDZ domain containing family, member 2	0
3.93	RAD21-AS1	**RAD21 antisense RNA 1 (non-protein coding)**	0
3.87	FAM124B	family with sequence similarity 124B	0
3.85	LOC729046	ribosomal protein L17 pseudogene	0
3.84	LOC728532	dynein, cytoplasmic 1, intermediate chain 2 pseudogene	0
3.84	FAM60A	family with sequence similarity 60, member A	0
3.84	VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	0
3.82	FRMD6	FERM domain containing 6	0
3.82	CAST	calpastatin	0
3.77	LOC442293	glycine cleavage system protein H pseudogene	0
3.76	CBWD1	COBW domain containing 1	0
3.75	SNORA27	small nucleolar RNA, H/ACA box 27	0
3.73	LOC100131756	hypothetical LOC100131756	0
3.72	C15orf54	chromosome 15 open reading frame 54	0
3.68	C8orf44	chromosome 8 open reading frame 44	0
3.67	MIR1274B	**microRNA 1274b**	0
3.61	IL17RD	interleukin 17 receptor D	0
3.60	OTUD6A	OTU domain containing 6A	0
3.60	C22orf29	chromosome 22 open reading frame 29	0
3.54	C10orf32	chromosome 10 open reading frame 32	0
3.53	THUMPD1	THUMP domain containing 1	0
3.53	SHCBP1	SHC SH2-domain binding protein 1	0
3.53	RTN4IP1	reticulon 4 interacting protein 1	0

3.52	PDE4C	phosphodiesterase 4C, cAMP-specific	0
3.51	COMMD2	COMM domain containing 2	0
3.51	LOC400590	hypothetical LOC400590	0
3.44	C12orf77	chromosome 12 open reading frame 77	0
3.43	FLJ23152	hypothetical protein LOC401236	0
3.42	ANKRD40	ankyrin repeat domain 40	0
3.41	PDLIM4	PDZ and LIM domain 4	0
3.40	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	0
3.38	FAM45A	family with sequence similarity 45, member A	0
3.38	DIAPH3	diaphanous homolog 3 (Drosophila)	0
3.37	GIMAP7	GTPase, IMAP family member 7	0
3.36	PLS3	plastin 3	0
3.35	LOC729317	voltage-dependent anion channel 2 pseudogene	0
3.35	C5orf56	chromosome 5 open reading frame 56	0
3.34	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like	0
3.33	FBXL20	F-box and leucine-rich repeat protein 20	0
3.31	PRR11	proline rich 11	0
3.27	RWDD2B	RWD domain containing 2B	0
3.27	NXNL2	nucleoredoxin-like 2	0
3.26	FAM111A	family with sequence similarity 111, member A	0
3.22	MARCH7	membrane-associated ring finger (C3HC4) 7	0
3.21	LOC643802	u3 small nucleolar ribonucleoprotein protein MPP10-like	0
3.20	C2orf68	chromosome 2 open reading frame 68	0
3.19	C15orf40	chromosome 15 open reading frame 40	0
3.18	NIPSNAP3A	nipsnap homolog 3A (C. elegans)	0
3.17	NUAK2	NUAK family, SNF1-like kinase, 2	0
3.17	AFAP1	actin filament associated protein 1	0
3.17	RPL18AP3	ribosomal protein L18a pseudogene 3	0

3.16	GPN1	GPN-loop GTPase 1	0
3.15	FRA10AC1	fragile site, folic acid type, rare, fra(10)(q23.3) or fra(10)(q24.2) candidate 1	0
3.14	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	0
3.12	LRRC18	leucine rich repeat containing 18	0
3.11	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	0
3.11	METTL21B	methyltransferase like 21B	0
3.11	MIR1273	microRNA 1273	0
3.10	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	0
3.10	SNORD13	small nucleolar RNA, C/D box 13	0
3.09	C1orf31	chromosome 1 open reading frame 31	0
3.08	LOC646851	hypothetical LOC646851	0
3.08	C11orf91	chromosome 11 open reading frame 91	0
3.06	COMMD10	COMM domain containing 10	0
3.04	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0
3.03	C14orf119	chromosome 14 open reading frame 119	0
3.02	TATDN3	TatD DNase domain containing 3	0
3.01	LINC00263	**long intergenic non-protein coding RNA 263**	0
3.00	C20orf177 FAM217B	chromosome 20 open reading frame 177 or FAM217B	0

Appendix Table A.4.5.1. this table shows the results of the RPKM analyses of combined tumour Huvec/hHsec versus normal adult human tissues. 753 genes were found to be log2(FC) >= 3 enriched in hypoxic, tumour conditioned endothelium. 252 of these genes contained either a signal peptide sequence, a transmembrane domain or were classed as extracellular/membrane by the Gene Ontology database (queried through the Entrez Gene database). 4 of these genes have either been subsequently removed from the NCBI or a pseudogenes. They are not included in subsequent analyses: (LOC100127894, LOC100130764, MIR1274B, and MTND4P).

Appendix Table A.4.10.1. Table of tumour endothelial enriched genes from short RNA-seq Cuffdiff analyses

Gene	Solid Lung	Colon	Bladder	T. Huvec	I. Lung	No. of contrasts	Product	Class
TNFRSF10D	1	0	0	1	1	3	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	M
BAMBI	1	0	1	0	1	3	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	M
S1PR3	1	1	0	0	1	3	sphingosine-1-phosphate receptor 3	M
DARC	1	0	1	0	1	3	Duffy blood group, chemokine receptor	M
CD200	1	0	1	0	1	3	CD200 molecule	M
CLDN1	1	1	1	0	0	3	claudin 1	M
FJX1	1	0	1	0	1	3	four jointed box 1 (Drosophila)	M
TMEM27	1	1	1	0	0	3	transmembrane protein 27	M
BIRC6	1	1	1	0	0	3	baculoviral IAP repeat containing 6	M
GALNT14	1	0	1	0	1	3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	M
ERRFI1	1	1	1	0	0	3	ERBB receptor feedback inhibitor 1	M
DLL4	0	0	1	0	1	2	delta-like 4 (Drosophila)	M
F2R	1	0	0	1	0	2	coagulation factor II (thrombin) receptor	M
GP1BB	1	0	0	0	1	2	glycoprotein Ib (platelet), beta polypeptide	M
PROCR	0	0	0	1	1	2	protein C receptor, endothelial	M
ADRA2B	1	0	0	0	1	2	adrenergic, alpha-2B-, receptor	M
GRIN2D	0	1	1	0	0	2	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	M
INSR	1	0	1	0	0	2	insulin receptor	M

ITGB6	1	0	1	0	0	2	integrin, beta 6	M
SLC6A8	1	0	0	1	0	2	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	M
MS4A1	1	0	0	0	1	2	membrane-spanning 4-domains, subfamily A, member 1	M
CLDN4	1	1	0	0	0	2	claudin 4	M
CLDN3	1	1	0	0	0	2	claudin 3	M
DTNA	1	0	1	0	0	2	dystrobrevin, alpha	M
F2RL1	1	1	0	0	0	2	coagulation factor II (thrombin) receptor-like 1	M
FCGR2A	1	1	0	0	0	2	Fc fragment of IgG, low affinity IIa, receptor (CD32)	M
FOLH1	0	1	1	0	0	2	folate hydrolase (prostate-specific membrane antigen) 1	M
TACSTD2	1	0	1	0	0	2	tumor-associated calcium signal transducer 2	M
CXCL9	1	1	0	0	0	2	chemokine (C-X-C motif) ligand 9	M
MUC1	1	0	1	0	0	2	mucin 1, cell surface associated	M
CEACAM6	1	1	0	0	0	2	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	M
GPR143	0	1	1	0	0	2	G protein-coupled receptor 143	M
SDC4	1	1	0	0	0	2	syndecan 4	M
SELE	0	1	1	0	0	2	selectin E	M
SLC16A1	0	0	0	1	1	2	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	M
TSPAN6	0	1	1	0	0	2	tetraspanin 6	M
TPBG	1	0	1	0	0	2	trophoblast glycoprotein	M
UPK1B	1	0	1	0	0	2	uroplakin 1B	M
ADAM12	0	1	1	0	0	2	ADAM metallopeptidase domain 12	M
IER3	1	0	0	0	1	2	immediate early response 3	M
GPRC5A	1	1	0	0	0	2	G protein-coupled receptor, family C, group 5, member A	M
CLDN10	1	0	0	0	1	2	claudin 10	M
ABCG2	1	0	1	0	0	2	ATP-binding cassette, sub-family G (WHITE), member 2	M
CLCA2	1	0	1	0	0	2	chloride channel accessory 2	M

GLCE	1	0	0	1	0	2	glucuronic acid epimerase	M
DNAJA4	0	0	1	0	1	2	DnaJ (Hsp40) homolog, subfamily A, member 4	M
SLC39A4	1	1	0	0	0	2	solute carrier family 39 (zinc transporter), member 4	M
C20orf24	1	1	0	0	0	2	chromosome 20 open reading frame 24	M
CXCR7	1	0	0	0	1	2	chemokine (C-X-C motif) receptor 7	M
RASL11B	1	0	0	0	1	2	RAS-like, family 11, member B	M
NOX5	0	0	1	0	1	2	NADPH oxidase, EF-hand calcium binding domain 5	M
RNF128	0	1	1	0	0	2	ring finger protein 128	M
C3orf52	1	0	1	0	0	2	chromosome 3 open reading frame 52	M
GPR157	0	1	1	0	0	2	G protein-coupled receptor 157	M
MYCT1	1	0	0	1	0	2	myc target 1	M
GDPD5	0	1	0	0	1	2	glycerophosphodiester phosphodiesterase domain containing 5	M
VMP1	1	0	1	0	0	2	vacuole membrane protein 1	M
SLC4A11	0	1	1	0	0	2	solute carrier family 4, sodium borate transporter, member 11	M
TMEM116	1	0	1	0	0	2	transmembrane protein 116	M
TMEM41A	0	1	1	0	0	2	transmembrane protein 41A	M
MAL2	1	1	0	0	0	2	mal, T-cell differentiation protein 2 (gene/pseudogene)	M
KCTD11	1	0	1	0	0	2	potassium channel tetramerisation domain containing 11	M
PROM2	1	0	1	0	0	2	prominin 2	M
PAQR7	1	0	1	0	0	2	progestin and adipoQ receptor family member VII	M
MPZL3	0	1	1	0	0	2	myelin protein zero-like 3	M
MUC20	1	0	1	0	0	2	mucin 20, cell surface associated	M
CXorf61	1	1	0	0	0	2	chromosome X open reading frame 61	M
FAM171A1	0	0	0	1	1	2	family with sequence similarity 171, member A1	M
GPX8	1	0	0	1	0	2	glutathione peroxidase 8 (putative)	M
GPRC5C	1	0	0	0	0	1	G protein-coupled receptor, family C, group 5, member C	M
GPR110	0	0	1	0	0	1	G protein-coupled receptor 110	M
GPR89B	1	0	0	0	0	1	G protein-coupled receptor 89B	M

FZD5	1	0	0	0	0	1	frizzled family receptor 5	M
EPHA4	0	0	1	0	0	1	EPH receptor A4	M
EPHB2	1	0	0	0	0	1	EPH receptor B2	M
GRB10	0	0	0	0	1	1	growth factor receptor-bound protein 10	M
FGFR1	1	0	0	0	0	1	fibroblast growth factor receptor 1	M
FGFR3	0	0	1	0	0	1	fibroblast growth factor receptor 3	M
FGFR2	1	0	0	0	0	1	fibroblast growth factor receptor 2	M
JAG2	0	0	0	0	1	1	jagged 2	M
SPHK1	0	0	0	1	0	1	sphingosine kinase 1	M
SLC6A16	1	0	0	0	0	1	solute carrier family 6, member 16	M
VAMP2	1	0	0	0	0	1	vesicle-associated membrane protein 2 (synaptobrevin 2)	M
CACNB2	0	0	1	0	0	1	calcium channel, voltage-dependent, beta 2 subunit	M
LDLRAD3	1	0	0	0	0	1	low density lipoprotein receptor class A domain containing 3	M
CDH3	0	1	0	0	0	1	cadherin 3, type 1, P-cadherin (placental)	M
TNFRSF10C	1	0	0	0	0	1	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	M
TNFRSF10A	1	0	0	0	0	1	tumor necrosis factor receptor superfamily, member 10a	M
PLXNB1	0	0	1	0	0	1	plexin B1	M
PLXNA4	0	0	0	1	0	1	plexin A4	M
AKAP13	1	0	0	0	0	1	A kinase (PRKA) anchor protein 13	M
SDF2L1	1	0	0	0	0	1	stromal cell-derived factor 2-like 1	M
ROBO1	1	0	0	0	0	1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	M
ROBO3	1	0	0	0	0	1	roundabout, axon guidance receptor, homolog 3 (Drosophila)	M
CD19	0	0	0	0	1	1	CD19 molecule	M
CD79A	0	0	0	0	1	1	CD79a molecule, immunoglobulin-associated alpha	M
BLNK	1	0	0	0	0	1	B-cell linker	M
LYN	1	0	0	0	0	1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	M
BLK	0	0	0	0	1	1	B lymphoid tyrosine kinase	M

ITGB3	0	0	0	1	0	1	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	M
CDH2	0	0	0	1	0	1	cadherin 2, type 1, N-cadherin (neuronal)	M
CDH6	0	0	1	0	0	1	cadherin 6, type 2, K-cadherin (fetal kidney)	M
CDH8	1	0	0	0	0	1	cadherin 8, type 2	M
CDH13	0	0	0	1	0	1	cadherin 13, H-cadherin (heart)	M
FAT2	1	0	0	0	0	1	FAT tumor suppressor homolog 2 (Drosophila)	M
PCDH7	1	0	0	0	0	1	protocadherin 7	M
CELSR1	1	0	0	0	0	1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	M
PCDHA9	1	0	0	0	0	1	protocadherin alpha 9	M
CDHR5	0	0	0	0	1	1	cadherin-related family member 5	M
PCDHB15	0	0	1	0	0	1	protocadherin beta 15	M
PCDHB10	1	0	0	0	0	1	protocadherin beta 10	M
PCDHB4	0	0	1	0	0	1	protocadherin beta 4	M
PCDHA12	1	0	0	0	0	1	protocadherin alpha 12	M
PCDHA11	1	0	0	0	0	1	protocadherin alpha 11	M
PCDHA7	1	0	0	0	0	1	protocadherin alpha 7	M
PCDHA5	1	0	0	0	0	1	protocadherin alpha 5	M
PCDHA3	1	0	0	0	0	1	protocadherin alpha 3	M
PCDHA2	1	0	0	0	0	1	protocadherin alpha 2	M
PCDH10	0	0	0	1	0	1	protocadherin 10	M
CDH26	0	0	1	0	0	1	cadherin 26	M
HTR7	0	0	1	0	0	1	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	M
ADORA2A	0	0	0	0	1	1	adenosine A2a receptor	M
RGS16	0	0	1	0	0	1	regulator of G-protein signaling 16	M
SSTR1	0	0	0	0	1	1	somatostatin receptor 1	M
DRD2	0	1	0	0	0	1	dopamine receptor D2	M
OPRK1	1	0	0	0	0	1	opioid receptor, kappa 1	M

GRK6	1	0	0	0	0	1	G protein-coupled receptor kinase 6	M
HTR1B	0	0	0	1	0	1	5-hydroxytryptamine (serotonin) receptor 1B	M
HTR2B	0	0	1	0	0	1	5-hydroxytryptamine (serotonin) receptor 2B	M
HRH1	1	0	0	0	0	1	histamine receptor H1	M
PACSIN3	1	0	0	0	0	1	protein kinase C and casein kinase substrate in neurons 3	M
GRIK5	0	0	0	1	0	1	glutamate receptor, ionotropic, kainate 5	M
CXCR5	0	0	0	0	1	1	chemokine (C-X-C motif) receptor 5	M
CCR4	0	0	1	0	0	1	chemokine (C-C motif) receptor 4	M
FPR2	0	1	0	0	0	1	formyl peptide receptor 2	M
CXCR6	0	1	0	0	0	1	chemokine (C-X-C motif) receptor 6	M
ITGB1	0	0	0	1	0	1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	M
ROS1	1	0	0	0	0	1	c-ros oncogene 1 , receptor tyrosine kinase	M
ITGA7	0	0	0	0	1	1	integrin, alpha 7	M
ITGAV	0	0	0	1	0	1	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	M
ITGA11	0	0	0	0	1	1	integrin, alpha 11	M
IL2RA	0	1	0	0	0	1	interleukin 2 receptor, alpha	M
IL4R	1	0	0	0	0	1	interleukin 4 receptor	M
IL20RA	0	1	0	0	0	1	interleukin 20 receptor, alpha	M
SLC44A3	0	0	1	0	0	1	solute carrier family 44, member 3	M
RAB28	1	0	0	0	0	1	RAB28, member RAS oncogene family	M
TIAM1	0	0	1	0	0	1	T-cell lymphoma invasion and metastasis 1	M
CD3E	1	0	0	0	0	1	CD3e molecule, epsilon (CD3-TCR complex)	M
IRAK1	1	0	0	0	0	1	interleukin-1 receptor-associated kinase 1	M
TLR2	0	1	0	0	0	1	toll-like receptor 2	M
PERP	0	1	0	0	0	1	PERP, TP53 apoptosis effector	M
ILVBL	1	0	0	0	0	1	ilvB (bacterial acetolactate synthase)-like	M
RYR2	0	0	1	0	0	1	ryanodine receptor 2 (cardiac)	M

RALA	0	0	0	1	0	1	v-ral simian leukemia viral oncogene homolog A (ras related)	M
SYT8	0	0	1	0	0	1	synaptotagmin VIII	M
AGTR1	0	0	1	0	0	1	angiotensin II receptor, type 1	M
FRMD5	0	0	0	1	0	1	FERM domain containing 5	M
ANXA3	0	1	0	0	0	1	annexin A3	M
AQP5	1	0	0	0	0	1	aquaporin 5	M
AQP9	0	1	0	0	0	1	aquaporin 9	M
ABCC6	1	0	0	0	0	1	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	M
ATP1B1	1	0	0	0	0	1	ATPase, Na+/K+ transporting, beta 1 polypeptide	M
C11orf10	1	0	0	0	0	1	chromosome 11 open reading frame 10	M
DDR1	1	0	0	0	0	1	discoidin domain receptor tyrosine kinase 1	M
CD5	1	0	0	0	0	1	CD5 molecule	M
CD9	0	0	1	0	0	1	CD9 molecule	M
CD34	0	0	0	0	1	1	CD34 molecule	M
CD38	1	0	0	0	0	1	CD38 molecule	M
ENTPD1	1	0	0	0	0	1	ectonucleoside triphosphate diphosphohydrolase 1	M
ENTPD3	0	0	1	0	0	1	ectonucleoside triphosphate diphosphohydrolase 3	M
CLDN7	1	0	0	0	0	1	claudin 7	M
CR2	0	0	0	0	1	1	complement component (3d/Epstein Barr virus) receptor 2	M
CXADR	0	1	0	0	0	1	coxsackie virus and adenovirus receptor	M
DIO2	1	0	0	0	0	1	deiodinase, iodothyronine, type II	M
DLG3	1	0	0	0	0	1	discs, large homolog 3 (Drosophila)	M
DSC2	1	0	0	0	0	1	desmocollin 2	M
DSC3	0	1	0	0	0	1	desmocollin 3	M
DSG2	1	0	0	0	0	1	desmoglein 2	M
ENG	0	0	1	0	0	1	endoglin	M
FCER1A	0	0	0	0	1	1	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	M
FCER1G	1	0	0	0	0	1	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	M

FCGR1A	1	0	0	0	0	1	Fc fragment of IgG, high affinity Ia, receptor (CD64)	M
FCGR1B	1	0	0	0	0	1	Fc fragment of IgG, high affinity Ib, receptor (CD64)	M
FCGR3A	0	1	0	0	0	1	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	M
FCGR3B	0	1	0	0	0	1	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	M
GABRD	0	0	0	0	1	1	gamma-aminobutyric acid (GABA) A receptor, delta	M
GAS1	1	0	0	0	0	1	growth arrest-specific 1	M
GCGR	1	0	0	0	0	1	glucagon receptor	M
GGT5	1	0	0	0	0	1	gamma-glutamyltransferase 5	M
GJA4	0	0	0	0	1	1	gap junction protein, alpha 4, 37kDa	M
GJB2	0	0	1	0	0	1	gap junction protein, beta 2, 26kDa	M
GJB5	1	0	0	0	0	1	gap junction protein, beta 5, 31.1kDa	M
GLP1R	0	0	1	0	0	1	glucagon-like peptide 1 receptor	M
GPR35	1	0	0	0	0	1	G protein-coupled receptor 35	M
HAS3	0	0	1	0	0	1	hyaluronan synthase 3	M
NRG1	0	0	0	1	0	1	neuregulin 1	M
HLA-A	0	0	0	0	1	1	major histocompatibility complex, class I, A	M
HLA-DOB	1	0	0	0	0	1	major histocompatibility complex, class II, DO beta	M
HLA-DRB5	0	0	0	0	1	1	major histocompatibility complex, class II, DR beta 5	M
NDST1	1	0	0	0	0	1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	M
IL1RAP	0	1	0	0	0	1	interleukin 1 receptor accessory protein	M
INPP5A	1	0	0	0	0	1	inositol polyphosphate-5-phosphatase, 40kDa	M
IRAK2	1	0	0	0	0	1	interleukin-1 receptor-associated kinase 2	M
KCNC3	0	0	1	0	0	1	potassium voltage-gated channel, Shaw-related subfamily, member 3	M
KCNJ8	0	0	0	0	1	1	potassium inwardly-rectifying channel, subfamily J, member 8	M
KCNJ15	0	0	1	0	0	1	potassium inwardly-rectifying channel, subfamily J, member 15	M
KCNMA1	1	0	0	0	0	1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	M
KCNQ1	1	0	0	0	0	1	potassium voltage-gated channel, KQT-like subfamily, member 1	M

LAIR2	1	0	0	0	0	1	leukocyte-associated immunoglobulin-like receptor 2	M
BCAM	1	0	0	0	0	1	basal cell adhesion molecule (Lutheran blood group)	M
LY6H	0	0	0	0	1	1	lymphocyte antigen 6 complex, locus H	M
EPCAM	1	0	0	0	0	1	epithelial cell adhesion molecule	M
MAG	1	0	0	0	0	1	myelin associated glycoprotein	M
MBP	1	0	0	0	0	1	myelin basic protein	M
MCAM	0	0	0	0	1	1	melanoma cell adhesion molecule	M
MUC4	1	0	0	0	0	1	mucin 4, cell surface associated	M
NCAM2	1	0	0	0	0	1	neural cell adhesion molecule 2	M
NGFR	0	0	0	0	1	1	nerve growth factor receptor	M
NINJ1	1	0	0	0	0	1	ninjurin 1	M
NKG7	1	0	0	0	0	1	natural killer cell group 7 sequence	M
SLC11A2	1	0	0	0	0	1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	M
NRCAM	0	0	0	1	0	1	neuronal cell adhesion molecule	M
CLDN11	0	0	0	1	0	1	claudin 11	M
P2RX7	1	0	0	0	0	1	purinergic receptor P2X, ligand-gated ion channel, 7	M
P2RY11	1	0	0	0	0	1	purinergic receptor P2Y, G-protein coupled, 11	M
SLC26A4	1	0	0	0	0	1	solute carrier family 26, member 4	M
PIGC	0	0	1	0	0	1	phosphatidylinositol glycan anchor biosynthesis, class C	M
PIGH	0	0	1	0	0	1	phosphatidylinositol glycan anchor biosynthesis, class H	M
PIGR	1	0	0	0	0	1	polymeric immunoglobulin receptor	M
PLP2	1	0	0	0	0	1	proteolipid protein 2 (colonic epithelium-enriched)	M
PLXNB3	0	0	1	0	0	1	plexin B3	M
PRNP	1	0	0	0	0	1	prion protein	M
PTGER2	1	0	0	0	0	1	prostaglandin E receptor 2 (subtype EP2), 53kDa	M
PTGFRN	1	0	0	0	0	1	prostaglandin F2 receptor negative regulator	M
PTK7	1	0	0	0	0	1	PTK7 protein tyrosine kinase 7	M

PTPRD	1	0	0	0	0	1	protein tyrosine phosphatase, receptor type, D	M
PVR	0	0	0	1	0	1	poliovirus receptor	M
PVRL2	1	0	0	0	0	1	poliovirus receptor-related 2 (herpesvirus entry mediator B)	M
RARRES3	1	0	0	0	0	1	retinoic acid receptor responder (tazarotene induced) 3	M
RRAD	1	0	0	0	0	1	Ras-related associated with diabetes	M
SCN8A	0	0	0	1	0	1	sodium channel, voltage gated, type VIII, alpha subunit	M
SCNN1A	1	0	0	0	0	1	sodium channel, nonvoltage-gated 1 alpha	M
SCNN1B	1	0	0	0	0	1	sodium channel, nonvoltage-gated 1, beta	M
SCTR	1	0	0	0	0	1	secretin receptor	M
SLC2A1	1	0	0	0	0	1	solute carrier family 2 (facilitated glucose transporter), member 1	M
SLC5A3	1	0	0	0	0	1	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	M
SLC5A4	0	0	1	0	0	1	solute carrier family 5 (low affinity glucose cotransporter), member 4	M
SLC6A1	0	0	1	0	0	1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	M
SLC7A1	1	0	0	0	0	1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	M
SLC11A1	0	1	0	0	0	1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	M
SLC15A1	0	0	1	0	0	1	solute carrier family 15 (oligopeptide transporter), member 1	M
SLC15A2	1	0	0	0	0	1	solute carrier family 15 (H+/peptide transporter), member 2	M
STX4	1	0	0	0	0	1	syntaxin 4	M
TMPRSS2	1	0	0	0	0	1	transmembrane protease, serine 2	M
CLDN5	0	0	0	0	1	1	claudin 5	M
TNFRSF4	0	0	0	0	1	1	tumor necrosis factor receptor superfamily, member 4	M
UGT8	1	0	0	0	0	1	UDP glycosyltransferase 8	M
VCAM1	1	0	0	0	0	1	vascular cell adhesion molecule 1	M
VIPR1	0	0	1	0	0	1	vasoactive intestinal peptide receptor 1	M
TRPV1	1	0	0	0	0	1	transient receptor potential cation channel, subfamily V, member 1	M
WRB	1	0	0	0	0	1	tryptophan rich basic protein	M

SLC30A1	0	0	1	0	0	1	solute carrier family 30 (zinc transporter), member 1	M
SLC30A2	0	0	1	0	0	1	solute carrier family 30 (zinc transporter), member 2	M
REEP5	0	0	1	0	0	1	receptor accessory protein 5	M
ABHD16A	1	0	0	0	0	1	abhydrolase domain containing 16A	M
ST7	1	0	0	0	0	1	suppression of tumorigenicity 7	M
MADCAM1	0	0	0	0	1	1	mucosal vascular addressin cell adhesion molecule 1	M
EPR1	0	0	0	1	0	1	effector cell peptidase receptor 1 (non-protein coding) (note; withdrawn gene, supposed to be antisense of BIRC5)	M
SEMA7A	1	0	0	0	0	1	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	M
KCNAB2	1	0	0	0	0	1	potassium voltage-gated channel, shaker-related subfamily, beta member 2	M
DGKD	1	0	0	0	0	1	diacylglycerol kinase, delta 130kDa	M
LGR5	0	1	0	0	0	1	leucine-rich repeat containing G protein-coupled receptor 5	M
PPAP2A	0	0	0	0	1	1	phosphatidic acid phosphatase type 2A	M
FCGR1C	1	0	0	0	0	1	Fc fragment of IgG, high affinity Ic, receptor (CD64)	M
PPAP2C	0	1	0	0	0	1	phosphatidic acid phosphatase type 2C	M
ABCC3	1	0	0	0	0	1	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	M
TNFRSF25	1	0	0	0	0	1	tumor necrosis factor receptor superfamily, member 25	M
ADAM23	1	0	0	0	0	1	ADAM metallopeptidase domain 23	M
LIN7A	0	1	0	0	0	1	lin-7 homolog A (C. elegans)	M
HCAR3	0	0	1	0	0	1	hydroxycarboxylic acid receptor 3	M
SLC5A6	1	0	0	0	0	1	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	M
CACNA1H	0	0	0	0	1	1	calcium channel, voltage-dependent, T type, alpha 1H subunit	M
MPZL1	1	0	0	0	0	1	myelin protein zero-like 1	M
SLC7A7	1	0	0	0	0	1	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	M
CLDN12	1	0	0	0	0	1	claudin 12	M

CLDN9	0	1	0	0	0	1	claudin 9	M
LPAR2	1	0	0	0	0	1	lysophosphatidic acid receptor 2	M
SLC33A1	1	0	0	0	0	1	solute carrier family 33 (acetyl-CoA transporter), member 1	M
CACNA2D2	1	0	0	0	0	1	calcium channel, voltage-dependent, alpha 2/delta subunit 2	M
SLC9A3R1	1	0	0	0	0	1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	M
STOML1	1	0	0	0	0	1	stomatin (EPB72)-like 1	M
KCNK6	1	0	0	0	0	1	potassium channel, subfamily K, member 6	M
SLC4A7	1	0	0	0	0	1	solute carrier family 4, sodium bicarbonate cotransporter, member 7	M
TP53I11	1	0	0	0	0	1	tumor protein p53 inducible protein 11	M
C20orf3	1	0	0	0	0	1	chromosome 20 open reading frame 3	M
WBP1	1	0	0	0	0	1	WW domain binding protein 1	M
NPIPL3	0	0	0	0	1	1	nuclear pore complex interacting protein-like 3	M
CDKAL1	1	0	0	0	0	1	CDK5 regulatory subunit associated protein 1-like 1	M
TMEM126B	0	0	1	0	0	1	transmembrane protein 126B	M
TMEM120A	1	0	0	0	0	1	transmembrane protein 120A	M
TMEM128	0	0	1	0	0	1	transmembrane protein 128	M
TMEM129	1	0	0	0	0	1	transmembrane protein 129	M
TMEM54	1	0	0	0	0	1	transmembrane protein 54	M
LMTK3	1	0	0	0	0	1	lemur tyrosine kinase 3	M
TMEM125	1	0	0	0	0	1	transmembrane protein 125	M
TMEM119	1	0	0	0	0	1	transmembrane protein 119	M
GDE1	1	0	0	0	0	1	glycerophosphodiester phosphodiesterase 1	M
RTP4	0	0	1	0	0	1	receptor (chemosensory) transporter protein 4	M
RPRML	0	1	0	0	0	1	reprimo-like	M
GCA	1	0	0	0	0	1	grancalcin, EF-hand calcium binding protein	M
YIPF3	1	0	0	0	0	1	Yip1 domain family, member 3	M

STAB2	1	0	0	0	0	1	stabilin 2	M
GPR64	0	1	0	0	0	1	G protein-coupled receptor 64	M
S100A14	1	0	0	0	0	1	S100 calcium binding protein A14	M
SPRED2	1	0	0	0	0	1	sprouty-related, EVH1 domain containing 2	M
MPZL2	1	0	0	0	0	1	myelin protein zero-like 2	M
CNTNAP2	1	0	0	0	0	1	contactin associated protein-like 2	M
CERCAM	0	0	0	0	1	1	cerebral endothelial cell adhesion molecule	M
IER3IP1	1	0	0	0	0	1	immediate early response 3 interacting protein 1	M
CD276	1	0	0	0	0	1	CD276 molecule	M
PVRL4	0	0	1	0	0	1	poliovirus receptor-related 4	M
CRIM1	0	0	0	1	0	1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	M
PCDHA10	1	0	0	0	0	1	protocadherin alpha 10	M
PCDHA6	1	0	0	0	0	1	protocadherin alpha 6	M
PCDHA1	1	0	0	0	0	1	protocadherin alpha 1	M
LILRB2	1	0	0	0	0	1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	M
CMTM7	1	0	0	0	0	1	CKLF-like MARVEL transmembrane domain containing 7	M
CMTM4	1	0	0	0	0	1	CKLF-like MARVEL transmembrane domain containing 4	M
PIGY	0	0	0	0	1	1	phosphatidylinositol glycan anchor biosynthesis, class Y	M
STAB1	0	0	0	0	1	1	stabilin 1	M
PILRB	0	0	1	0	0	1	paired immunoglobin-like type 2 receptor beta	M
PODXL2	1	0	0	0	0	1	podocalyxin-like 2	M
IL1RAPL2	0	0	1	0	0	1	interleukin 1 receptor accessory protein-like 2	M
DLGAP4	1	0	0	0	0	1	discs, large (Drosophila) homolog-associated protein 4	M
SPRED3	1	0	0	0	0	1	sprouty-related, EVH1 domain containing 3	M
HPS4	1	0	0	0	0	1	Hermansky-Pudlak syndrome 4	M
SLC23A2	0	0	1	0	0	1	solute carrier family 23 (nucleobase transporters), member 2	M
MCTP1	0	0	0	1	0	1	multiple C2 domains, transmembrane 1	M

RAPGEF3	0	0	0	0	1	1	Rap guanine nucleotide exchange factor (GEF) 3	M
PCDHAC2	1	0	0	0	0	1	protocadherin alpha subfamily C, 2	M
ABCC5	0	0	1	0	0	1	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	M
MFSD10	1	0	0	0	0	1	major facilitator superfamily domain containing 10	M
SEMA4B	1	0	0	0	0	1	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	M
CNPPD1	1	0	0	0	0	1	cyclin Pas1/PHO80 domain containing 1	M
TAS2R3	1	0	0	0	0	1	taste receptor, type 2, member 3	M
ZDHHC2	1	0	0	0	0	1	zinc finger, DHHC-type containing 2	M
FKBP11	1	0	0	0	0	1	FK506 binding protein 11, 19 kDa	M
TM6SF1	0	0	1	0	0	1	transmembrane 6 superfamily member 1	M
SEMA5B	0	0	0	0	1	1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	M
ST7L	1	0	0	0	0	1	suppression of tumorigenicity 7 like	M
TMEM161A	0	1	0	0	0	1	transmembrane protein 161A	M
SUSD2	1	0	0	0	0	1	sushi domain containing 2	M
TMPRSS4	1	0	0	0	0	1	transmembrane protease, serine 4	M
SLC39A10	1	0	0	0	0	1	solute carrier family 39 (zinc transporter), member 10	M
CACHD1	1	0	0	0	0	1	cache domain containing 1	M
MOSPD3	1	0	0	0	0	1	motile sperm domain containing 3	M
ATP13A4	1	0	0	0	0	1	ATPase type 13A4	M
RFT1	1	0	0	0	0	1	RFT1 homolog (S. cerevisiae)	M
SFT2D1	1	0	0	0	0	1	SFT2 domain containing 1	M
CYYR1	0	0	0	0	1	1	cysteine/tyrosine-rich 1	M
SLC18B1	1	0	0	0	0	1	solute carrier family 18, subfamily B, member 1	M
SLC36A4	1	0	0	0	0	1	solute carrier family 36 (proton/amino acid symporter), member 4	M
SPNS2	1	0	0	0	0	1	spinster homolog 2 (Drosophila)	M

TPRA1	1	0	0	0	0	1	transmembrane protein, adipocyte asscociated 1	M
TMEM37	1	0	0	0	0	1	transmembrane protein 37	M
SLC38A6	1	0	0	0	0	1	solute carrier family 38, member 6	M
SLC22A31	1	0	0	0	0	1	solute carrier family 22, member 31	M
ASPRV1	0	0	1	0	0	1	aspartic peptidase, retroviral-like 1	M
RNF217	1	0	0	0	0	1	ring finger protein 217	M
CYP4Z2P	0	0	1	0	0	1	cytochrome P450, family 4, subfamily Z, polypeptide 2 pseudogene	M
SLC35F1	0	0	1	0	0	1	solute carrier family 35, member F1	M
CYB561D1	0	0	1	0	0	1	cytochrome b-561 domain containing 1	M
SLC35D3	0	1	0	0	0	1	solute carrier family 35, member D3	M
KCNE4	0	0	0	0	1	1	potassium voltage-gated channel, Isk-related family, member 4	M
PKD1L1	1	0	0	0	0	1	polycystic kidney disease 1 like 1	M
PLLP	0	0	1	0	0	1	plasmolipin	M
CATSPERB	0	0	1	0	0	1	cation channel, sperm-associated, beta	M
FAM189B	1	0	0	0	0	1	family with sequence similarity 189, member B	M
TMEM33	1	0	0	0	0	1	transmembrane protein 33	M
ATP6AP1L	1	0	0	0	0	1	ATPase, H+ transporting, lysosomal accessory protein 1-like	M
SCAMP4	1	0	0	0	0	1	secretory carrier membrane protein 4	M
HERC2P3	0	0	1	0	0	1	hect domain and RLD 2 pseudogene 3	M
ABCB9	1	0	0	0	0	1	ATP-binding cassette, sub-family B (MDR/TAP), member 9	M
ATP5L2	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G2	M
ATP5H	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d	M
MERTK	1	0	0	0	0	1	c-mer proto-oncogene tyrosine kinase	M
RASD2	0	0	0	0	1	1	RASD family, member 2	M
RAB40C	1	0	0	0	0	1	RAB40C, member RAS oncogene family	M
MARCKSL1	0	0	0	0	1	1	MARCKS-like 1	M
CD177	1	0	0	0	0	1	CD177 molecule	M
RAET1L	1	0	0	0	0	1	retinoic acid early transcript 1L	M

OSCP1	0	0	1	0	0	1	organic solute carrier partner 1	M
CATSPER3	0	0	1	0	0	1	cation channel, sperm associated 3	M
GJB6	0	0	1	0	0	1	gap junction protein, beta 6, 30kDa	M
GBP5	1	0	0	0	0	1	guanylate binding protein 5	M
NEGR1	0	0	0	1	0	1	neuronal growth regulator 1	M
GPR125	1	0	0	0	0	1	G protein-coupled receptor 125	M
GJB4	0	0	1	0	0	1	gap junction protein, beta 4, 30.3kDa	M
SEMA6C	0	0	0	0	1	1	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	M
SEMA6B	0	0	0	0	1	1	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	M
LILRB4	1	0	0	0	0	1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	M
GPR161	1	0	0	0	0	1	G protein-coupled receptor 161	M
CNNM3	1	0	0	0	0	1	cyclin M3	M
OR7C1	0	0	1	0	0	1	olfactory receptor, family 7, subfamily C, member 1	M
GPR78	0	0	1	0	0	1	G protein-coupled receptor 78	M
GPR84	0	1	0	0	0	1	G protein-coupled receptor 84	M
GPR87	0	0	1	0	0	1	G protein-coupled receptor 87	M
UNC93A	0	1	0	0	0	1	unc-93 homolog A (C. elegans)	M
FLVCR2	0	0	1	0	0	1	feline leukemia virus subgroup C cellular receptor family, member 2	M
PCDHA13	1	0	0	0	0	1	protocadherin alpha 13	M
PMEPA1	0	1	0	0	0	1	prostate transmembrane protein, androgen induced 1	M
GPR126	0	0	0	1	0	1	G protein-coupled receptor 126	M
ELTD1	0	0	0	0	1	1	EGF, latrophilin and seven transmembrane domain containing 1	M
SLC44A4	1	0	0	0	0	1	solute carrier family 44, member 4	M
UPK3B	0	0	1	0	0	1	uroplakin 3B	M
SLC38A1	1	0	0	0	0	1	solute carrier family 38, member 1	M
MFSD9	1	0	0	0	0	1	major facilitator superfamily domain containing 9	M

LINGO1	0	0	0	0	1	1	leucine rich repeat and Ig domain containing 1	M
SLC38A5	1	0	0	0	0	1	solute carrier family 38, member 5	M
OR51E1	0	1	0	0	0	1	olfactory receptor, family 51, subfamily E, member 1	M
SLC16A14	0	0	0	0	1	1	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	M
SLC16A13	0	0	1	0	0	1	solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	M
SLC44A5	0	0	0	1	0	1	solute carrier family 44, member 5	M
GPR115	0	0	1	0	0	1	G protein-coupled receptor 115	M
TMPRSS7	0	0	1	0	0	1	transmembrane protease, serine 7	M
SLC10A6	1	0	0	0	0	1	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	M
IYD	0	1	0	0	0	1	iodotyrosine deiodinase	M
OR2A7	1	0	0	0	0	1	olfactory receptor, family 2, subfamily A, member 7	M
DUOX2	0	0	1	0	0	1	dual oxidase 2	M
DUOX1	0	0	1	0	0	1	dual oxidase 1	M
SLC4A5	1	0	0	0	0	1	solute carrier family 4, sodium bicarbonate cotransporter, member 5	M
KIAA1919	1	0	0	0	0	1	KIAA1919	M
SLC26A9	1	0	0	0	0	1	solute carrier family 26, member 9	M
NPC1L1	0	1	0	0	0	1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	M
SLC39A5	0	1	0	0	0	1	solute carrier family 39 (metal ion transporter), member 5	M
SLC6A14	1	0	0	0	0	1	solute carrier family 6 (amino acid transporter), member 14	M
SLC39A8	1	0	0	0	0	1	solute carrier family 39 (zinc transporter), member 8	M
STRA6	0	1	0	0	0	1	stimulated by retinoic acid gene 6 homolog (mouse)	M
LSR	1	0	0	0	0	1	lipolysis stimulated lipoprotein receptor	M
GPR176	0	0	0	1	0	1	G protein-coupled receptor 176	M
GP6	0	0	1	0	0	1	glycoprotein VI (platelet)	M
CCRL1	0	0	0	1	0	1	chemokine (C-C motif) receptor-like 1	M
TRPV6	0	0	1	0	0	1	transient receptor potential cation channel, subfamily V, member 6	M

PCDHAC1	1	0	0	0	0	1	protocadherin alpha subfamily C, 1	M
PCDHA8	1	0	0	0	0	1	protocadherin alpha 8	M
PCDHA4	1	0	0	0	0	1	protocadherin alpha 4	M
SLC52A2	1	0	0	0	0	1	solute carrier family 52, riboflavin transporter, member 2	M
APCDD1	0	0	1	0	0	1	adenomatosis polyposis coli down-regulated 1	M
CLEC5A	0	1	0	0	0	1	C-type lectin domain family 5, member A	M
SLC34A2	1	0	0	0	0	1	solute carrier family 34 (sodium phosphate), member 2	M
NLGN1	0	0	0	1	0	1	neuroligin 1	M
JAM2	0	0	0	0	1	1	junctional adhesion molecule 2	M
SEMA4A	1	0	0	0	0	1	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	M
KCNK17	0	0	0	0	1	1	potassium channel, subfamily K, member 17	M
LPAR6	0	0	1	0	0	1	lysophosphatidic acid receptor 6	M
HCAR2	0	0	1	0	0	1	hydroxycarboxylic acid receptor 2	M
RHCG	0	0	1	0	0	1	Rh family, C glycoprotein	M
RHBG	0	0	1	0	0	1	Rh family, B glycoprotein (gene/pseudogene)	M
KLHL17	1	0	0	0	0	1	kelch-like 17 (Drosophila)	M
SEMA4C	1	0	0	0	0	1	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	M
MGLL	1	0	0	0	0	1	monoglyceride lipase	M
CLDN18	1	0	0	0	0	1	claudin 18	M
CLDN23	0	0	1	0	0	1	claudin 23	M
FERMT3	1	0	0	0	0	1	fermitin family member 3	M
CD248	0	0	0	0	1	1	CD248 molecule, endosialin	M
FLRT2	0	0	0	1	0	1	fibronectin leucine rich transmembrane protein 2	M
FLRT3	1	0	0	0	0	1	fibronectin leucine rich transmembrane protein 3	M
TFIP11	1	0	0	0	0	1	tuftelin interacting protein 11	M
SLC7A11	0	0	0	1	0	1	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	M

CD2AP	1	0	0	0	0	1	CD2-associated protein	M
TNFRSF12A	0	1	0	0	0	1	tumor necrosis factor receptor superfamily, member 12A	M
PDPN	1	0	0	0	0	1	podoplanin	M
FCRL2	0	0	0	0	1	1	Fc receptor-like 2	M
PARD3B	1	0	0	0	0	1	par-3 partitioning defective 3 homolog B (C. elegans)	M
ATP9B	1	0	0	0	0	1	ATPase, class II, type 9B	M
TSPAN17	1	0	0	0	0	1	tetraspanin 17	M
SLC22A17	1	0	0	0	0	1	solute carrier family 22, member 17	M
KCTD17	1	0	0	0	0	1	potassium channel tetramerisation domain containing 17	M
SHKBP1	1	0	0	0	0	1	SH3KBP1 binding protein 1	M
SERINC2	1	0	0	0	0	1	serine incorporator 2	M
TMEM144	1	0	0	0	0	1	transmembrane protein 144	M
SLC35G1	1	0	0	0	0	1	solute carrier family 35, member G1	M
TMEM175	1	0	0	0	0	1	transmembrane protein 175	M
TMC5	0	1	0	0	0	1	transmembrane channel-like 5	M
SIDT2	1	0	0	0	0	1	SID1 transmembrane family, member 2	M
TMEM39A	1	0	0	0	0	1	transmembrane protein 39A	M
TMEM241	1	0	0	0	0	1	transmembrane protein 241	M
MFSD6L	0	0	1	0	0	1	major facilitator superfamily domain containing 6-like	M
XKRX	1	0	0	0	0	1	XK, Kell blood group complex subunit-related, X-linked	M
GPR137	1	0	0	0	0	1	G protein-coupled receptor 137	M
GPRC5B	1	0	0	0	0	1	G protein-coupled receptor, family C, group 5, member B	M
TMEM45A	1	0	0	0	0	1	transmembrane protein 45A	M
TMBIM1	1	0	0	0	0	1	transmembrane BAX inhibitor motif containing 1	M
TMEM87A	1	0	0	0	0	1	transmembrane protein 87A	M
GPR162	1	0	0	0	0	1	G protein-coupled receptor 162	M
XKR9	1	0	0	0	0	1	XK, Kell blood group complex subunit-related family, member 9	M

TMEM147	1	0	0	0	0	1	transmembrane protein 147	M
TMEM163	1	0	0	0	0	1	transmembrane protein 163	M
YIPF1	1	0	0	0	0	1	Yip1 domain family, member 1	M
ZDHHC11	1	0	0	0	0	1	zinc finger, DHHC-type containing 11	M
GPR89C	1	0	0	0	0	1	G protein-coupled receptor 89C	M
PPAN-P2RY11	1	0	0	0	0	1	PPAN-P2RY11 readthrough	M
YIF1B	1	0	0	0	0	1	Yip1 interacting factor homolog B (S. cerevisiae)	M
ZDHHC24	0	0	1	0	0	1	zinc finger, DHHC-type containing 24	M
TLCD1	0	0	1	0	0	1	TLC domain containing 1	M
TMPPE	1	0	0	0	0	1	transmembrane protein with metallophosphoesterase domain	M
TMEM176A	1	0	0	0	0	1	transmembrane protein 176A	M
FAM18B2	1	0	0	0	0	1	family with sequence similarity 18, member B2	M
TMEM217	0	0	1	0	0	1	transmembrane protein 217	M
TMEM140	1	0	0	0	0	1	transmembrane protein 140	M
ZDHHC12	1	0	0	0	0	1	zinc finger, DHHC-type containing 12	M
FAM70B	1	0	0	0	0	1	family with sequence similarity 70, member B	M
TM4SF18	0	0	0	1	0	1	transmembrane 4 L six family member 18	M
FAM18B2-CDRT4	1	0	0	0	0	1	FAM18B2-CDRT4 readthrough	M
TMEM189	1	0	0	0	0	1	transmembrane protein 189	M
JAGN1	1	0	0	0	0	1	jagunal homolog 1 (Drosophila)	M
ORAI3	1	0	0	0	0	1	ORAI calcium release-activated calcium modulator 3	M
FAM26E	0	0	0	1	0	1	family with sequence similarity 26, member E	M
RNFT2	1	0	0	0	0	1	ring finger protein, transmembrane 2	M
TMEM208	1	0	0	0	0	1	transmembrane protein 208	M
TMEM159	0	0	1	0	0	1	transmembrane protein 159	M
FAM210B	1	0	0	0	0	1	family with sequence similarity 210, member B	M

TMEM218	1	0	0	0	0	1	transmembrane protein 218	M
ARL6IP6	1	0	0	0	0	1	ADP-ribosylation-like factor 6 interacting protein 6	M
KRTCAP3	1	0	0	0	0	1	keratinocyte associated protein 3	M
TMCC1	1	0	0	0	0	1	transmembrane and coiled-coil domain family 1	M
GIMAP2	1	0	0	0	0	1	GTPase, IMAP family member 2	M
RNF186	0	1	0	0	0	1	ring finger protein 186	M
RNF43	0	1	0	0	0	1	ring finger protein 43	M
TMEM40	0	0	1	0	0	1	transmembrane protein 40	M
C12orf23	1	0	0	0	0	1	chromosome 12 open reading frame 23	M
C9orf91	1	0	0	0	0	1	chromosome 9 open reading frame 91	M
TMEM189-UBE2V1	1	0	0	0	0	1	TMEM189-UBE2V1 readthrough	M
TMEM200C	0	1	0	0	0	1	transmembrane protein 200C	M
RNF19B	1	0	0	0	0	1	ring finger protein 19B	M
ASTN2	1	0	0	0	0	1	astrotactin 2	M
PNKD	1	0	0	0	0	1	paroxysmal nonkinesigenic dyskinesia	M
HIGD1B	1	0	0	0	0	1	HIG1 hypoxia inducible domain family, member 1B	M
C19orf24	1	0	0	0	0	1	chromosome 19 open reading frame 24	M
RNF150	1	0	0	0	0	1	ring finger protein 150	M
REEP4	1	0	0	0	0	1	receptor accessory protein 4	M
TMEM199	1	0	0	0	0	1	transmembrane protein 199	M
CYP4Z1	0	0	1	0	0	1	cytochrome P450, family 4, subfamily Z, polypeptide 1	M
TMEM238	1	0	0	0	0	1	transmembrane protein 238	M
MARCH9	1	0	0	0	0	1	membrane-associated ring finger (C3HC4) 9	M
C14orf109	1	0	0	0	0	1	chromosome 14 open reading frame 109	M
TMEM130	1	0	0	0	0	1	transmembrane protein 130	M
TMEM51	0	0	1	0	0	1	transmembrane protein 51	M
RIC3	0	0	1	0	0	1	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	M

PRR24	1	0	0	0	0	1	proline rich 24	M
BTNL8	1	0	0	0	0	1	butyrophilin-like 8	M
MFAP3L	0	0	1	0	0	1	microfibrillar-associated protein 3-like	M
LYPD1	0	0	0	1	0	1	LY6/PLAUR domain containing 1	M
PDZK1IP1	1	0	0	0	0	1	PDZK1 interacting protein 1	M
WSCD1	0	0	0	1	0	1	WSC domain containing 1	M
VSIG2	0	0	1	0	0	1	V-set and immunoglobulin domain containing 2	M
TMEM59L	0	0	0	0	1	1	transmembrane protein 59-like	M
TIMMDC1	1	0	0	0	0	1	translocase of inner mitochondrial membrane domain containing 1	M
C11orf24	1	0	0	0	0	1	chromosome 11 open reading frame 24	M
NPDC1	0	0	0	0	1	1	neural proliferation, differentiation and control, 1	M
SLAMF8	1	0	0	0	0	1	SLAM family member 8	M
NDUFA4L2	0	0	0	0	1	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	M
FNDC4	0	0	0	0	1	1	fibronectin type III domain containing 4	M
IGFLR1	1	0	0	0	0	1	IGF-like family receptor 1	M
LRRC3	0	0	1	0	0	1	leucine rich repeat containing 3	M
PLVAP	0	0	0	0	1	1	plasmalemma vesicle associated protein	M
RNF183	0	1	0	0	0	1	ring finger protein 183	M
CLEC14A	0	0	0	0	1	1	C-type lectin domain family 14, member A	M
LRRN4CL	0	0	1	0	0	1	LRRN4 C-terminal like	M
FAM162B	0	0	0	0	1	1	family with sequence similarity 162, member B	M
EPHX4	0	0	0	0	1	1	epoxide hydrolase 4	M
C19orf38	0	1	0	0	0	1	chromosome 19 open reading frame 38	M
FDCSP	0	0	0	0	1	1	follicular dendritic cell secreted protein	M
B4GALNT3	1	0	0	0	0	1	beta-1,4-N-acetyl-galactosaminyl transferase 3	M
B4GALNT4	0	0	0	0	1	1	beta-1,4-N-acetyl-galactosaminyl transferase 4	M
CD300E	1	0	0	0	0	1	CD300e molecule	M
RNF148	1	0	0	0	0	1	ring finger protein 148	M

C2orf66	0	0	1	0	0	1	chromosome 2 open reading frame 66	M
ASTL	0	0	0	0	1	1	astacin-like metallo-endopeptidase (M12 family)	M
MSMP	0	0	0	1	0	1	microseminoprotein, prostate associated	M
LOC728392	0	0	0	0	1	1	hypothetical protein LOC728392	M
C11orf83	1	0	0	0	0	1	chromosome 11 open reading frame 83	M
LRRC70	0	0	0	1	0	1	leucine rich repeat containing 70	M
C17orf110	0	0	1	0	0	1	chromosome 17 open reading frame 110	M
PET117	1	0	0	0	0	1	cytochrome c oxidase assembly factor-like	M
C17orf62	1	0	0	0	0	1	chromosome 17 open reading frame 62	M
ABHD12	1	0	0	0	0	1	abhydrolase domain containing 12	M
GOLM1	1	0	0	0	0	1	golgi membrane protein 1	M
TTC13	1	0	0	0	0	1	tetratricopeptide repeat domain 13	M
FCRL5	0	0	0	0	1	1	Fc receptor-like 5	M
C15orf48	0	0	1	0	0	1	chromosome 15 open reading frame 48	M
C1QTNF6	0	0	0	0	1	1	C1q and tumor necrosis factor related protein 6	M
C1orf210	1	0	0	0	0	1	chromosome 1 open reading frame 210	M
C19orf63	1	0	0	0	0	1	chromosome 19 open reading frame 63	M
SIRPB2	0	0	1	0	0	1	signal-regulatory protein beta 2	M
C7orf53	0	0	0	0	1	1	chromosome 7 open reading frame 53	M
PRR7	0	0	0	0	1	1	proline rich 7 (synaptic)	M
FCRL1	0	0	0	0	1	1	Fc receptor-like 1	M
TMEM99	1	0	0	0	0	1	transmembrane protein 99	M
PGAM5	1	0	0	0	0	1	phosphoglycerate mutase family member 5	M
GPR89A	1	0	0	0	0	1	G protein-coupled receptor 89A	M
IL8	1	1	1	0	1	4	interleukin 8	E
ESM1	0	1	1	1	1	4	endothelial cell-specific molecule 1	E
ANGPT2	1	0	1	0	1	3	angiopoietin 2	E

MMP1	1	1	0	1	0	3	matrix metallopeptidase 1 (interstitial collagenase)	E
COL10A1	1	1	0	0	1	3	collagen, type X, alpha 1	E
COL11A1	1	1	0	0	1	3	collagen, type XI, alpha 1	E
MMP10	1	0	0	1	1	3	matrix metallopeptidase 10 (stromelysin 2)	E
GDF15	0	1	1	0	1	3	growth differentiation factor 15	E
LOXL2	1	0	0	1	1	3	lysyl oxidase-like 2	E
MMP11	1	1	0	0	1	3	matrix metallopeptidase 11 (stromelysin 3)	E
PGF	0	1	0	1	1	3	placental growth factor	E
SERPINE2	1	0	0	1	1	3	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	E
SPP1	1	1	1	0	0	3	secreted phosphoprotein 1	E
HSPH1	1	1	0	0	1	3	heat shock 105kDa/110kDa protein 1	E
BPIFA1	1	0	1	0	1	3	BPI fold containing family A, member 1	E
C9orf47	1	1	0	0	1	3	chromosome 9 open reading frame 47	E
SAA2-SAA4	1	1	1	0	0	3	SAA2-SAA4 readthrough	E
PDGFD	1	0	0	0	1	2	platelet derived growth factor D	E
SFRP2	1	0	0	0	1	2	secreted frizzled-related protein 2	E
MMP2	1	0	0	1	0	2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	E
MMP12	1	1	0	0	0	2	matrix metallopeptidase 12 (macrophage elastase)	E
TNF	1	0	0	0	1	2	tumor necrosis factor	E
F2RL2	0	1	0	1	0	2	coagulation factor II (thrombin) receptor-like 2	E
SERPINE1	0	0	1	1	0	2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	E
EREG	0	1	0	0	1	2	epiregulin	E
SFN	1	0	0	0	1	2	stratifin	E
CCL20	0	1	0	0	1	2	chemokine (C-C motif) ligand 20	E
COL1A1	1	0	0	0	1	2	collagen, type I, alpha 1	E

COL15A1	1	0	0	0	1	2	collagen, type XV, alpha 1	E
IL23A	0	0	1	0	1	2	interleukin 23, alpha subunit p19	E
INHBA	0	1	1	0	0	2	inhibin, beta A	E
INHBB	1	0	0	0	1	2	inhibin, beta B	E
GDF3	0	0	1	1	0	2	growth differentiation factor 3	E
SFRP4	1	0	0	0	1	2	secreted frizzled-related protein 4	E
IGFBP3	0	0	1	0	1	2	insulin-like growth factor binding protein 3	E
AGT	0	1	0	0	1	2	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	E
ADM	1	0	0	0	1	2	adrenomedullin	E
AZGP1	1	1	0	0	0	2	alpha-2-glycoprotein 1, zinc-binding	E
CEACAM5	1	1	0	0	0	2	carcinoembryonic antigen-related cell adhesion molecule 5	E
CST1	1	1	0	0	0	2	cystatin SN	E
DEFB1	1	1	0	0	0	2	defensin, beta 1	E
EFNA1	0	1	1	0	0	2	ephrin-A1	E
EPOR	1	0	1	0	0	2	erythropoietin receptor	E
CXCL3	1	1	0	0	0	2	chemokine (C-X-C motif) ligand 3	E
HSPD1	1	0	0	0	1	2	heat shock 60kDa protein 1 (chaperonin)	E
HSPG2	0	0	0	1	1	2	heparan sulfate proteoglycan 2	E
IGF2	0	1	1	0	0	2	insulin-like growth factor 2 (somatomedin A)	E
IGFBP7	0	0	1	0	1	2	insulin-like growth factor binding protein 7	E
IL1B	0	1	0	0	1	2	interleukin 1, beta	E
IL1RN	0	1	1	0	0	2	interleukin 1 receptor antagonist	E
IL11	0	1	1	0	0	2	interleukin 11	E
INS	0	1	1	0	0	2	insulin	E
LTF	1	0	1	0	0	2	lactotransferrin	E
NMB	1	0	0	0	1	2	neuromedin B	E
NOV	0	0	1	0	1	2	nephroblastoma overexpressed gene	E
PPIA	0	0	0	1	1	2	peptidylprolyl isomerase A (cyclophilin A)	E

PRG2	0	1	1	0	0	2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	E
HTRA1	1	0	0	0	1	2	HtrA serine peptidase 1	E
PTX3	0	0	0	1	1	2	pentraxin 3, long	E
S100A2	1	0	1	0	0	2	S100 calcium binding protein A2	E
S100A8	0	1	1	0	0	2	S100 calcium binding protein A8	E
S100A9	1	0	1	0	0	2	S100 calcium binding protein A9	E
S100A11	1	0	1	0	0	2	S100 calcium binding protein A11	E
SAA1	1	0	1	0	0	2	serum amyloid A1	E
SAA2	1	0	1	0	0	2	serum amyloid A2	E
SAA4	1	0	1	0	0	2	serum amyloid A4, constitutive	E
STC1	0	1	1	0	0	2	stanniocalcin 1	E
APLN	0	1	0	1	0	2	apelin	E
BAIAP3	1	0	1	0	0	2	BAI1-associated protein 3	E
CRLF1	1	0	0	0	1	2	cytokine receptor-like factor 1	E
ADAMTS6	0	0	1	1	0	2	ADAM metallopeptidase with thrombospondin type 1 motif, 6	E
MMRN1	0	0	0	1	1	2	multimerin 1	E
EGFL6	0	1	1	0	0	2	EGF-like-domain, multiple 6	E
DKK2	0	1	0	0	1	2	dickkopf homolog 2 (Xenopus laevis)	E
KLK12	0	1	0	0	1	2	kallikrein-related peptidase 12	E
SPOCK3	0	1	1	0	0	2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	E
BOLA1	1	0	1	0	0	2	bolA homolog 1 (E. coli)	E
ANGPTL4	0	0	1	1	0	2	angiopoietin-like 4	E
ACP6	1	0	1	0	0	2	acid phosphatase 6, lysophosphatidic	E
FAM3B	0	1	1	0	0	2	family with sequence similarity 3, member B	E
CRTAC1	1	0	1	0	0	2	cartilage acidic protein 1	E
C1orf63	1	0	0	0	1	2	chromosome 1 open reading frame 63	E
PLXDC1	1	0	0	0	1	2	plexin domain containing 1	E

PRSS22	1	0	1	0	0	2	protease, serine, 22	E
VWA1	1	0	0	0	1	2	von Willebrand factor A domain containing 1	E
ULBP2	1	0	0	0	1	2	UL16 binding protein 2	E
HTRA3	1	0	0	0	1	2	HtrA serine peptidase 3	E
LYPD6B	1	0	1	0	0	2	LY6/PLAUR domain containing 6B	E
EGFLAM	1	0	0	0	1	2	EGF-like, fibronectin type III and laminin G domains	E
C2CD4A	1	1	0	0	0	2	C2 calcium-dependent domain containing 4A	E
CILP2	1	0	0	0	1	2	cartilage intermediate layer protein 2	E
ADAMTS18	0	0	0	1	1	2	ADAM metallopeptidase with thrombospondin type 1 motif, 18	E
RNF215	1	0	1	0	0	2	ring finger protein 215	E
SPESP1	0	0	1	0	1	2	sperm equatorial segment protein 1	E
CXCL17	1	0	1	0	0	2	chemokine (C-X-C motif) ligand 17	E
ANXA8	1	0	1	0	0	2	annexin A8	E
INS-IGF2	0	1	1	0	0	2	INS-IGF2 readthrough	E
MAGEA9B	1	0	1	0	0	2	melanoma antigen family A, 9B	E
TGIF2-C20ORF24	1	1	0	0	0	2	TGIF2-C20orf24 readthrough	E
WNT2	0	1	0	0	0	1	wingless-type MMTV integration site family member 2	E
NOTCH3	0	0	0	0	1	1	notch 3	E
PDGFC	0	1	0	0	0	1	platelet derived growth factor C	E
PDGFB	0	0	0	1	0	1	platelet-derived growth factor beta polypeptide	E
VEGFA	1	0	0	0	0	1	vascular endothelial growth factor A	E
MMP14	1	0	0	0	0	1	matrix metallopeptidase 14 (membrane-inserted)	E
MMP28	1	0	0	0	0	1	matrix metallopeptidase 28	E
WNT11	1	0	0	0	0	1	wingless-type MMTV integration site family, member 11	E
MMP9	1	0	0	0	0	1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	E
MMP7	1	0	0	0	0	1	matrix metallopeptidase 7 (matrilysin, uterine)	E

NTN4	0	0	0	1	0	1	netrin 4	E
CALML3	1	0	0	0	0	1	calmodulin-like 3	E
F13A1	1	0	0	0	0	1	coagulation factor XIII, A1 polypeptide	E
SERPINA1	1	0	0	0	0	1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	E
PROC	0	1	0	0	0	1	protein C (inactivator of coagulation factors Va and VIIIa)	E
TFPI2	0	0	0	1	0	1	tissue factor pathway inhibitor 2	E
MST1	0	0	1	0	0	1	macrophage stimulating 1 (hepatocyte growth factor-like)	E
SERPINB2	0	1	0	0	0	1	serpin peptidase inhibitor, clade B (ovalbumin), member 2	E
SERPINF1	1	0	0	0	0	1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	E
PLAU	1	0	0	0	0	1	plasminogen activator, urokinase	E
PLAUR	1	0	0	0	0	1	plasminogen activator, urokinase receptor	E
SERPINF2	1	0	0	0	0	1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2	E
AREG	0	1	0	0	0	1	amphiregulin	E
HBEGF	1	0	0	0	0	1	heparin-binding EGF-like growth factor	E
TGFA	1	0	0	0	0	1	transforming growth factor, alpha	E
C10orf81	0	1	0	0	0	1	chromosome 10 open reading frame 81	E
EPGN	1	0	0	0	0	1	epithelial mitogen homolog (mouse)	E
PEBP4	1	0	0	0	0	1	phosphatidylethanolamine-binding protein 4	E
EDN1	0	0	0	1	0	1	endothelin 1	E
FGF16	0	0	0	1	0	1	fibroblast growth factor 16	E
DHH	0	0	0	0	1	1	desert hedgehog	E
BDNF	0	0	0	1	0	1	brain-derived neurotrophic factor	E
TXN	1	0	0	0	0	1	thioredoxin	E
IFNAR2	1	0	0	0	0	1	interferon (alpha, beta and omega) receptor 2	E
CXCL10	0	1	0	0	0	1	chemokine (C-X-C motif) ligand 10	E
PTGS1	0	0	0	1	0	1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase	E

							and cyclooxygenase)	
CCL4L2	1	0	0	0	0	1	chemokine (C-C motif) ligand 4-like 2	E
COL7A1	0	0	1	0	0	1	collagen, type VII, alpha 1	E
IFNG	0	0	0	0	1	1	interferon, gamma	E
C21orf7	0	0	1	0	0	1	chromosome 21 open reading frame 7	E
IL18	1	0	0	0	0	1	interleukin 18 (interferon-gamma-inducing factor)	E
COL3A1	1	0	0	0	0	1	collagen, type III, alpha 1	E
COL4A1	0	0	0	0	1	1	collagen, type IV, alpha 1	E
COL4A2	0	0	0	0	1	1	collagen, type IV, alpha 2	E
COL4A4	1	0	0	0	0	1	collagen, type IV, alpha 4	E
COL4A5	0	0	1	0	0	1	collagen, type IV, alpha 5	E
COL5A1	1	0	0	0	0	1	collagen, type V, alpha 1	E
COL8A1	1	0	0	0	0	1	collagen, type VIII, alpha 1	E
COL17A1	1	0	0	0	0	1	collagen, type XVII, alpha 1	E
LAMB1	0	0	0	1	0	1	laminin, beta 1	E
LAMB3	1	0	0	0	0	1	laminin, beta 3	E
LAMC2	1	0	0	0	0	1	laminin, gamma 2	E
LAMC3	0	0	1	0	0	1	laminin, gamma 3	E
COL5A3	0	0	0	0	1	1	collagen, type V, alpha 3	E
COL18A1	0	0	0	0	1	1	collagen, type XVIII, alpha 1	E
IL1A	0	0	1	0	0	1	interleukin 1, alpha	E
IL10	0	0	0	0	1	1	interleukin 10	E
C3orf64	1	0	0	0	0	1	chromosome 3 open reading frame 64	E
SNCA	0	0	0	1	0	1	synuclein, alpha (non A4 component of amyloid precursor)	E
MMP3	0	1	0	0	0	1	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	E
BMP1	1	0	0	0	0	1	bone morphogenetic protein 1	E
BMP4	0	0	0	1	0	1	bone morphogenetic protein 4	E
BMP8B	1	0	0	0	0	1	bone morphogenetic protein 8b	E

TGFB1	1	0	0	0	0	1	transforming growth factor, beta 1	E
TLL1	0	0	0	0	1	1	tolloid-like 1	E
GDF6	0	0	0	1	0	1	growth differentiation factor 6	E
LY96	1	0	0	0	0	1	lymphocyte antigen 96	E
THBS1	0	0	0	1	0	1	thrombospondin 1	E
ABP1	1	0	0	0	0	1	amiloride binding protein 1 (amine oxidase (copper-containing))	E
SERPINA3	1	0	0	0	0	1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	E
PLIN2	0	1	0	0	0	1	perilipin 2	E
ACAN	0	1	0	0	0	1	aggrecan	E
ANXA8L2	0	0	1	0	0	1	annexin A8-like 2	E
ALPL	1	0	0	0	0	1	alkaline phosphatase, liver/bone/kidney	E
ANXA2	1	0	0	0	0	1	annexin A2	E
CFB	1	0	0	0	0	1	complement factor B	E
BGN	0	0	0	0	1	1	biglycan	E
BTD	1	0	0	0	0	1	biotinidase	E
C1R	1	0	0	0	0	1	complement component 1, r subcomponent	E
C3	1	0	0	0	0	1	complement component 3	E
C4B	1	0	0	0	0	1	complement component 4B (Chido blood group)	E
C4BPA	1	0	0	0	0	1	complement component 4 binding protein, alpha	E
CA2	1	0	0	0	0	1	carbonic anhydrase II	E
CA11	0	0	1	0	0	1	carbonic anhydrase XI	E
CALCA	0	0	0	0	1	1	calcitonin-related polypeptide alpha	E
CHI3L1	1	0	0	0	0	1	chitinase 3-like 1 (cartilage glycoprotein-39)	E
COMP	0	0	0	0	1	1	cartilage oligomeric matrix protein	E
CP	1	0	0	0	0	1	ceruloplasmin (ferroxidase)	E
CSF1	1	0	0	0	0	1	colony stimulating factor 1 (macrophage)	E
CSF2RA	1	0	0	0	0	1	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	E

CSF3	0	0	1	0	0	1	colony stimulating factor 3 (granulocyte)	E
CST2	0	0	0	0	1	1	cystatin SA	E
CST3	1	0	0	0	0	1	cystatin C	E
CST6	0	0	1	0	0	1	cystatin E/M	E
CTSK	1	0	0	0	0	1	cathepsin K	E
DEFA5	0	1	0	0	0	1	defensin, alpha 5, Paneth cell-specific	E
DEFA6	0	1	0	0	0	1	defensin, alpha 6, Paneth cell-specific	E
DMBT1	1	0	0	0	0	1	deleted in malignant brain tumors 1	E
DPT	1	0	0	0	0	1	dermatopontin	E
EPYC	0	0	0	0	1	1	epiphycan	E
EDA	0	1	0	0	0	1	ectodysplasin A	E
EFNA4	1	0	0	0	0	1	ephrin-A4	E
MEGF6	1	0	0	0	0	1	multiple EGF-like-domains 6	E
CTTN	1	0	0	0	0	1	cortactin	E
FAP	1	0	0	0	0	1	fibroblast activation protein, alpha	E
FBLN2	0	0	0	0	1	1	fibulin 2	E
FBN1	1	0	0	0	0	1	fibrillin 1	E
EFEMP1	0	0	0	1	0	1	EGF containing fibulin-like extracellular matrix protein 1	E
GPC4	0	1	0	0	0	1	glypican 4	E
FOLR1	1	0	0	0	0	1	folate receptor 1 (adult)	E
GLA	1	0	0	0	0	1	galactosidase, alpha	E
CXCL2	0	1	0	0	0	1	chemokine (C-X-C motif) ligand 2	E
GRP	0	0	0	0	1	1	gastrin-releasing peptide	E
GZMA	1	0	0	0	0	1	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	E
GZMK	1	0	0	0	0	1	granzyme K (granzyme 3; tryptase II)	E
HDGF	1	0	0	0	0	1	hepatoma-derived growth factor	E
CFHR2	0	0	0	0	1	1	complement factor H-related 2	E

ZBTB48	1	0	0	0	0	1	zinc finger and BTB domain containing 48	E
HP	1	0	0	0	0	1	haptoglobin	E
HPR	1	0	0	0	0	1	haptoglobin-related protein	E
IGFBP2	0	0	0	0	1	1	insulin-like growth factor binding protein 2, 36kDa	E
IGFBP6	1	0	0	0	0	1	insulin-like growth factor binding protein 6	E
IGLL1	1	0	0	0	0	1	immunoglobulin lambda-like polypeptide 1	E
ITIH3	0	0	1	0	0	1	inter-alpha (globulin) inhibitor H3	E
LCN2	1	0	0	0	0	1	lipocalin 2	E
LGALS1	1	0	0	0	0	1	lectin, galactoside-binding, soluble, 1	E
LGALS3BP	1	0	0	0	0	1	lectin, galactoside-binding, soluble, 3 binding protein	E
LIF	1	0	0	0	0	1	leukemia inhibitory factor (cholinergic differentiation factor)	E
LIPC	0	0	1	0	0	1	lipase, hepatic	E
LOX	0	0	0	1	0	1	lysyl oxidase	E
LOXL1	0	0	0	0	1	1	lysyl oxidase-like 1	E
LUM	0	0	0	0	1	1	lumican	E
MAGEA2	1	0	0	0	0	1	melanoma antigen family A, 2	E
MAGEA3	1	0	0	0	0	1	melanoma antigen family A, 3	E
MAGEA4	1	0	0	0	0	1	melanoma antigen family A, 4	E
MATN3	0	0	1	0	0	1	matrilin 3	E
MDK	1	0	0	0	0	1	midkine (neurite growth-promoting factor 2)	E
KITLG	1	0	0	0	0	1	KIT ligand	E
MSMB	0	0	1	0	0	1	microseminoprotein, beta-	E
NDP	1	0	0	0	0	1	Norrie disease (pseudoglioma)	E
NNAT	0	0	0	1	0	1	neuronatin	E
NTS	1	0	0	0	0	1	neurotensin	E
OLR1	0	1	0	0	0	1	oxidized low density lipoprotein (lectin-like) receptor 1	E
TNFRSF11B	0	0	1	0	0	1	tumor necrosis factor receptor superfamily, member 11b	E

ORM2	1	0	0	0	0	1	orosomucoid 2	E
PAEP	0	0	0	0	1	1	progestagen-associated endometrial protein	E
SERPINA5	1	0	0	0	0	1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5	E
PCOLCE	1	0	0	0	0	1	procollagen C-endopeptidase enhancer	E
ENPP2	0	0	0	0	1	1	ectonucleotide pyrophosphatase/phosphodiesterase 2	E
PGC	1	0	0	0	0	1	progastricsin (pepsinogen C)	E
PI3	1	0	0	0	0	1	peptidase inhibitor 3, skin-derived	E
SERPINI1	0	0	0	0	1	1	serpin peptidase inhibitor, clade I (neuroserpin), member 1	E
PLA2G5	0	0	0	0	1	1	phospholipase A2, group V	E
PLTP	1	0	0	0	0	1	phospholipid transfer protein	E
PON2	0	0	1	0	0	1	paraoxonase 2	E
PON3	1	0	0	0	0	1	paraoxonase 3	E
PRSS1	1	0	0	0	0	1	protease, serine, 1 (trypsin 1)	E
PRSS2	1	0	0	0	0	1	protease, serine, 2 (trypsin 2)	E
PRSS3	1	0	0	0	0	1	protease, serine, 3	E
PRSS8	1	0	0	0	0	1	protease, serine, 8	E
PTHLH	1	0	0	0	0	1	parathyroid hormone-like hormone	E
RBP4	0	1	0	0	0	1	retinol binding protein 4, plasma	E
REN	0	1	0	0	0	1	renin	E
S100A3	0	0	1	0	0	1	S100 calcium binding protein A3	E
S100A7	0	0	1	0	0	1	S100 calcium binding protein A7	E
S100A12	0	0	1	0	0	1	S100 calcium binding protein A12	E
SERPINB3	1	0	0	0	0	1	serpin peptidase inhibitor, clade B (ovalbumin), member 3	E
SERPINB4	1	0	0	0	0	1	serpin peptidase inhibitor, clade B (ovalbumin), member 4	E
CLEC11A	0	0	0	0	1	1	C-type lectin domain family 11, member A	E
CCL14	0	0	0	0	1	1	chemokine (C-C motif) ligand 14	E
CCL15	0	0	0	0	1	1	chemokine (C-C motif) ligand 15	E

CXCL5	0	1	0	0	0	1	chemokine (C-X-C motif) ligand 5	E
SELP	0	0	0	0	1	1	selectin P (granule membrane protein 140kDa, antigen CD62)	E
SEMA3F	0	0	1	0	0	1	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	E
SFTPB	1	0	0	0	0	1	surfactant protein B	E
SFTPD	1	0	0	0	0	1	surfactant protein D	E
SLPI	1	0	0	0	0	1	secretory leukocyte peptidase inhibitor	E
SOD1	1	0	0	0	0	1	superoxide dismutase 1, soluble	E
SOD3	1	0	0	0	0	1	superoxide dismutase 3, extracellular	E
SPINK1	0	0	1	0	0	1	serine peptidase inhibitor, Kazal type 1	E
SPOCK1	0	0	0	1	0	1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1	E
TAC1	1	0	0	0	0	1	tachykinin, precursor 1	E
TCN1	1	0	0	0	0	1	transcobalamin I (vitamin B12 binding protein, R binder family)	E
TDGF1	0	1	0	0	0	1	teratocarcinoma-derived growth factor 1	E
THBS2	1	0	0	0	0	1	thrombospondin 2	E
THBS4	1	0	0	0	0	1	thrombospondin 4	E
THY1	0	0	0	0	1	1	Thy-1 cell surface antigen	E
TIMP1	1	0	0	0	0	1	TIMP metallopeptidase inhibitor 1	E
TNFAIP2	0	0	1	0	0	1	tumor necrosis factor, alpha-induced protein 2	E
TUBA4A	0	0	0	0	1	1	tubulin, alpha 4a	E
TNFSF4	0	0	0	1	0	1	tumor necrosis factor (ligand) superfamily, member 4	E
VEGFB	1	0	0	0	0	1	vascular endothelial growth factor B	E
VEGFC	1	0	0	0	0	1	vascular endothelial growth factor C	E
VIP	1	0	0	0	0	1	vasoactive intestinal peptide	E
HYAL3	1	0	0	0	0	1	hyaluronoglucosaminidase 3	E
PLA2G10	1	0	0	0	0	1	phospholipase A2, group X	E
CILP	1	0	0	0	0	1	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	E

PRSS12	1	0	0	0	0	1	protease, serine, 12 (neurotrypsin, motopsin)	E
MMP23B	1	0	0	0	0	1	matrix metallopeptidase 23B	E
MMP23A	1	0	0	0	0	1	matrix metallopeptidase 23A (pseudogene)	E
STC2	0	1	0	0	0	1	stanniocalcin 2	E
NPFF	1	0	0	0	0	1	neuropeptide FF-amide peptide precursor	E
CHRD	0	0	0	0	1	1	chordin	E
TNFSF9	0	0	0	0	1	1	tumor necrosis factor (ligand) superfamily, member 9	E
GGH	0	1	0	0	0	1	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	E
WISP1	1	0	0	0	0	1	WNT1 inducible signaling pathway protein 1	E
TNFSF18	0	0	0	1	0	1	tumor necrosis factor (ligand) superfamily, member 18	E
ARTN	1	0	0	0	0	1	artemin	E
LIPG	1	0	0	0	0	1	lipase, endothelial	E
NAPSA	1	0	0	0	0	1	napsin A aspartic peptidase	E
SPAG7	1	0	0	0	0	1	sperm associated antigen 7	E
NXPH4	1	0	0	0	0	1	neurexophilin 4	E
EPHX3	0	0	1	0	0	1	epoxide hydrolase 3	E
PSORS1C2	0	0	1	0	0	1	psoriasis susceptibility 1 candidate 2	E
BOLA3	1	0	0	0	0	1	bolA homolog 3 (E. coli)	E
GAL	0	1	0	0	0	1	galanin prepropeptide	E
APOL4	0	0	1	0	0	1	apolipoprotein L, 4	E
FST	1	0	0	0	0	1	follistatin	E
QPCT	1	0	0	0	0	1	glutaminyl-peptide cyclotransferase	E
SPATA6	1	0	0	0	0	1	spermatogenesis associated 6	E
EPDR1	1	0	0	0	0	1	ependymin related protein 1 (zebrafish)	E
PLA2G2F	0	0	1	0	0	1	phospholipase A2, group IIF	E
PLA2G12B	0	1	0	0	0	1	phospholipase A2, group XIIB	E
RNASE7	0	0	1	0	0	1	ribonuclease, RNase A family, 7	E

LCN15	0	1	0	0	0	1	lipocalin 15	E
SMOC2	0	0	0	0	1	1	SPARC related modular calcium binding 2	E
EFEMP2	1	0	0	0	0	1	EGF containing fibulin-like extracellular matrix protein 2	E
COLEC11	0	0	0	0	1	1	collectin sub-family member 11	E
CTHRC1	0	0	0	0	1	1	collagen triple helix repeat containing 1	E
SRPX2	0	0	0	1	0	1	sushi-repeat containing protein, X-linked 2	E
HHIP	0	0	0	1	0	1	hedgehog interacting protein	E
CABP4	1	0	0	0	0	1	calcium binding protein 4	E
OLFML2B	0	0	0	0	1	1	olfactomedin-like 2B	E
SPINK5	0	0	1	0	0	1	serine peptidase inhibitor, Kazal type 5	E
CXCL13	0	0	0	0	1	1	chemokine (C-X-C motif) ligand 13	E
PLA2R1	1	0	0	0	0	1	phospholipase A2 receptor 1, 180kDa	E
LRRC17	0	0	0	1	0	1	leucine rich repeat containing 17	E
WFDC2	1	0	0	0	0	1	WAP four-disulfide core domain 2	E
IL24	0	1	0	0	0	1	interleukin 24	E
ANGPTL2	1	0	0	0	0	1	angiopoietin-like 2	E
IL36RN	0	0	1	0	0	1	interleukin 36 receptor antagonist	E
NENF	1	0	0	0	0	1	neudesin neurotrophic factor	E
IL19	0	0	1	0	0	1	interleukin 19	E
EGFL7	0	0	0	0	1	1	EGF-like-domain, multiple 7	E
CPXM1	1	0	0	0	0	1	carboxypeptidase X (M14 family), member 1	E
SCGB3A1	1	0	0	0	0	1	secretoglobin, family 3A, member 1	E
GREM1	1	0	0	0	0	1	gremlin 1	E
KLK8	0	1	0	0	0	1	kallikrein-related peptidase 8	E
VASH1	1	0	0	0	0	1	vasohibin 1	E
TINAGL1	0	0	0	0	1	1	tubulointerstitial nephritis antigen-like 1	E
PRDX4	1	0	0	0	0	1	peroxiredoxin 4	E
CPXM2	0	0	0	0	1	1	carboxypeptidase X (M14 family), member 2	E

CECR1	1	0	0	0	0	1	cat eye syndrome chromosome region, candidate 1	E
HILPDA	0	0	1	0	0	1	hypoxia inducible lipid droplet-associated	E
LOXL3	1	0	0	0	0	1	lysyl oxidase-like 3	E
OLFM4	1	0	0	0	0	1	olfactomedin 4	E
DKK1	0	0	0	1	0	1	dickkopf homolog 1 (Xenopus laevis)	E
FGFBP1	1	0	0	0	0	1	fibroblast growth factor binding protein 1	E
ACE2	0	1	0	0	0	1	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	E
CYTL1	0	0	0	0	1	1	cytokine-like 1	E
PRRG4	1	0	0	0	0	1	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	E
MSLN	1	0	0	0	0	1	mesothelin	E
MUCL1	1	0	0	0	0	1	mucin-like 1	E
EGFL8	0	0	0	0	1	1	EGF-like-domain, multiple 8	E
NPC2	1	0	0	0	0	1	Niemann-Pick disease, type C2	E
DPP7	1	0	0	0	0	1	dipeptidyl-peptidase 7	E
ADAM32	0	0	1	0	0	1	ADAM metallopeptidase domain 32	E
AGR2	1	0	0	0	0	1	anterior gradient homolog 2 (Xenopus laevis)	E
PRSS23	0	0	0	1	0	1	protease, serine, 23	E
ADAMTSL2	0	0	1	0	0	1	ADAMTS-like 2	E
CRTAP	1	0	0	0	0	1	cartilage associated protein	E
ADAMTS14	0	0	0	0	1	1	ADAM metallopeptidase with thrombospondin type 1 motif, 14	E
ADAMTS16	0	0	0	0	1	1	ADAM metallopeptidase with thrombospondin type 1 motif, 16	E
ADAMTS7	0	0	0	0	1	1	ADAM metallopeptidase with thrombospondin type 1 motif, 7	E
ASPN	0	0	0	0	1	1	asporin	E
PODN	1	0	0	0	0	1	podocan	E
SPINT2	1	0	0	0	0	1	serine peptidase inhibitor, Kunitz type, 2	E
SULF2	1	0	0	0	0	1	sulfatase 2	E
SULF1	0	0	0	1	0	1	sulfatase 1	E

HSD11B1L	1	0	0	0	0	1	hydroxysteroid (11-beta) dehydrogenase 1-like	E
SIAE	1	0	0	0	0	1	sialic acid acetylesterase	E
C3orf58	1	0	0	0	0	1	chromosome 3 open reading frame 58	E
CTRC	0	1	0	0	0	1	chymotrypsin C (caldecrin)	E
ZC3H13	1	0	0	0	0	1	zinc finger CCCH-type containing 13	E
ABHD14A	1	0	0	0	0	1	abhydrolase domain containing 14A	E
POLDIP2	1	0	0	0	0	1	polymerase (DNA-directed), delta interacting protein 2	E
LYPD3	0	0	1	0	0	1	LY6/PLAUR domain containing 3	E
FAM155B	1	0	0	0	0	1	family with sequence similarity 155, member B	E
VPREB3	0	0	0	0	1	1	pre-B lymphocyte 3	E
NRN1	1	0	0	0	0	1	neuritin 1	E
FBXL19	1	0	0	0	0	1	F-box and leucine-rich repeat protein 19	E
RCN3	1	0	0	0	0	1	reticulocalbin 3, EF-hand calcium binding domain	E
LY6G6D	0	1	0	0	0	1	lymphocyte antigen 6 complex, locus G6D	E
C17orf39	1	0	0	0	0	1	chromosome 17 open reading frame 39	E
C1orf54	1	0	0	0	0	1	chromosome 1 open reading frame 54	E
FAM107B	1	0	0	0	0	1	family with sequence similarity 107, member B	E
CCDC3	0	0	1	0	0	1	coiled-coil domain containing 3	E
FCRLB	0	0	1	0	0	1	Fc receptor-like B	E
SOWAHA	0	1	0	0	0	1	sosondowah ankyrin repeat domain family member A	E
AGR3	1	0	0	0	0	1	anterior gradient homolog 3 (Xenopus laevis)	E
C19orf76	0	0	0	0	1	1	chromosome 19 open reading frame 76	E
ADCK5	0	0	1	0	0	1	aarF domain containing kinase 5	E
C2orf69	1	0	0	0	0	1	chromosome 2 open reading frame 69	E
OAF	0	0	0	0	1	1	OAF homolog (Drosophila)	E
NUDT8	0	1	0	0	0	1	nudix (nucleoside diphosphate linked moiety X)-type motif 8	E
P4HA3	1	0	0	0	0	1	prolyl 4-hydroxylase, alpha polypeptide III	E
OLFML1	1	0	0	0	0	1	olfactomedin-like 1	E

EFHA2	0	0	1	0	0	1	EF-hand domain family, member A2	E
JMJD8	1	0	0	0	0	1	jumonji domain containing 8	E
C17orf67	1	0	0	0	0	1	chromosome 17 open reading frame 67	E
SFTA2	1	0	0	0	0	1	surfactant associated 2	E
NUDT19	1	0	0	0	0	1	nudix (nucleoside diphosphate linked moiety X)-type motif 19	E
PAPL	1	0	0	0	0	1	iron/zinc purple acid phosphatase-like protein	E
C10orf114	1	0	0	0	0	1	chromosome 10 open reading frame 114	E
IGIP	0	0	1	0	0	1	IgA-inducing protein homolog (Bos taurus)	E
C15orf62	1	0	0	0	0	1	chromosome 15 open reading frame 62	E
MTRNR2L3	1	0	0	0	0	1	MT-RNR2-like 3	E
MTRNR2L9	1	0	0	0	0	1	MT-RNR2-like 9	E
CES4A	0	0	1	0	0	1	carboxylesterase 4A	E
CRELD2	1	0	0	0	0	1	cysteine-rich with EGF-like domains 2	E
HYI	1	0	0	0	0	1	hydroxypyruvate isomerase (putative)	E
BCL2L12	1	0	0	0	0	1	BCL2-like 12 (proline rich)	E
COQ10A	1	0	0	0	0	1	coenzyme Q10 homolog A (S. cerevisiae)	E
PRAP1	0	1	0	0	0	1	proline-rich acidic protein 1	E
C16orf89	1	0	0	0	0	1	chromosome 16 open reading frame 89	E
TEPP	0	0	1	0	0	1	testis, prostate and placenta expressed	E
PODNL1	0	0	0	0	1	1	podocan-like 1	E
DMKN	1	0	0	0	0	1	dermokine	E
ARG2	1	1	1	0	1	4	arginase, type II	I
UGT1A1	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A1	I
PTGS2	1	1	1	0	0	3	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	I
RPSA	1	0	0	1	1	3	ribosomal protein SA	I
FHL2	1	0	0	1	1	3	four and a half LIM domains 2	I
UGT1A6	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A6	I

CYP24A1	1	0	1	0	1	3	cytochrome P450, family 24, subfamily A, polypeptide 1	I
AKR1C2	1	0	1	0	1	3	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	I
NREP	0	1	1	0	1	3	neuronal regeneration related protein homolog (rat)	I
AKR1C1	1	0	1	0	1	3	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	I
EEF1A2	1	0	1	1	0	3	eukaryotic translation elongation factor 1 alpha 2	I
KRT15	1	1	1	0	0	3	keratin 15	I
HIST2H2BE	1	0	1	0	1	3	histone cluster 2, H2be	I
UCHL1	1	0	0	1	1	3	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	I
OVOL1	0	1	1	0	1	3	ovo-like 1(Drosophila)	I
UGT1A4	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A4	I
TPX2	1	1	0	1	0	3	TPX2, microtubule-associated, homolog (Xenopus laevis)	I
MELK	1	1	0	1	0	3	maternal embryonic leucine zipper kinase	I
DUSP23	1	0	1	0	1	3	dual specificity phosphatase 23	I
UGT1A10	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A10	I
UGT1A8	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A8	I
UGT1A7	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A7	I
UGT1A5	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A5	I
UGT1A3	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A3	I
UGT1A9	1	0	1	0	1	3	UDP glucuronosyltransferase 1 family, polypeptide A9	I
PMAIP1	1	0	1	0	1	3	phorbol-12-myristate-13-acetate-induced protein 1	I
NUP37	1	1	1	0	0	3	nucleoporin 37kDa	I
FAM167B	1	0	1	0	1	3	family with sequence similarity 167, member B	I
CDC42EP5	1	0	1	0	1	3	CDC42 effector protein (Rho GTPase binding) 5	I
KRT13	1	1	1	0	0	3	keratin 13	I
SNORA24	1	1	1	0	0	3	small nucleolar RNA, H/ACA box 24	I
SCARNA7	1	1	1	0	0	3	small Cajal body-specific RNA 7	I

RPSAP58	1	0	0	1	1	3	ribosomal protein SA pseudogene 58	I
LOC550643	1	0	1	0	1	3	hypothetical LOC550643	I
MIR3189	0	1	1	1	0	3	microRNA 3189	I
MEG3	1	0	0	1	1	3	maternally expressed 3 (non-protein coding)	I
IDUA	1	0	0	0	1	2	iduronidase, alpha-L-	I
PNP	0	0	1	0	1	2	purine nucleoside phosphorylase	I
PTS	1	0	1	0	0	2	6-pyruvoyltetrahydropterin synthase	I
SOX9	1	1	0	0	0	2	SRY (sex determining region Y)-box 9	I
KRT17	1	0	1	0	0	2	keratin 17	I
KRT5	1	0	1	0	0	2	keratin 5	I
CYP1A1	0	0	1	1	0	2	cytochrome P450, family 1, subfamily A, polypeptide 1	I
KRT14	1	0	1	0	0	2	keratin 14	I
GSTM1	1	0	1	0	0	2	glutathione S-transferase mu 1	I
AHCY	1	1	0	0	0	2	adenosylhomocysteinase	I
CYP2B6	1	1	0	0	0	2	cytochrome P450, family 2, subfamily B, polypeptide 6	I
GSTT1	0	0	0	1	1	2	glutathione S-transferase theta 1	I
HSD3B1	0	0	0	1	1	2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	I
PIM3	1	0	0	0	1	2	pim-3 oncogene	I
NRARP	1	0	0	0	1	2	NOTCH-regulated ankyrin repeat protein	I
RPS3A	0	0	0	1	1	2	ribosomal protein S3A	I
C4orf46	0	1	1	0	0	2	chromosome 4 open reading frame 46	I
ZNF121	1	0	1	0	0	2	zinc finger protein 121	I
PCGF6	0	1	1	0	0	2	polycomb group ring finger 6	I
C8orf58	1	0	1	0	0	2	chromosome 8 open reading frame 58	I
UFSP1	0	1	1	0	0	2	UFM1-specific peptidase 1 (non-functional)	I
CCDC58	1	1	0	0	0	2	coiled-coil domain containing 58	I
RPS26	0	0	0	1	1	2	ribosomal protein S26	I

ARL4A	1	0	0	0	1	2	ADP-ribosylation factor-like 4A	I
CCNL2	0	0	1	0	1	2	cyclin L2	I
ADAMTSL1	1	0	0	1	0	2	ADAMTS-like 1	I
HIST2H2AA4	1	0	0	0	1	2	histone cluster 2, H2aa4	I
ZC2HC1C	1	0	1	0	0	2	zinc finger, C2HC-type containing 1C	I
GEMIN8	1	0	1	0	0	2	gem (nuclear organelle) associated protein 8	I
TOP2A	0	1	0	1	0	2	topoisomerase (DNA) II alpha 170kDa	I
FAM110C	1	0	1	0	0	2	family with sequence similarity 110, member C	I
PAICS	1	0	0	1	0	2	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	I
JMJD6	1	0	0	0	1	2	jumonji domain containing 6	I
HIC1	1	0	0	0	1	2	hypermethylated in cancer 1	I
RPL22L1	1	0	1	0	0	2	ribosomal protein L22-like 1	I
CCDC64B	1	0	1	0	0	2	coiled-coil domain containing 64B	I
MIR205HG	1	0	1	0	0	2	MIR205 host gene (non-protein coding)	I
FAM118A	1	0	0	0	1	2	family with sequence similarity 118, member A	I
ELF3	1	0	1	0	0	2	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	I
ACCS	1	0	0	0	1	2	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	I
LEF1	0	0	1	0	1	2	lymphoid enhancer-binding factor 1	I
FAM127B	1	0	1	0	0	2	family with sequence similarity 127, member B	I
MFSD2A	1	0	1	0	0	2	major facilitator superfamily domain containing 2A	I
MCTS1	0	1	1	0	0	2	malignant T cell amplified sequence 1	I
LMO2	0	0	1	0	1	2	LIM domain only 2 (rhombotin-like 1)	I
C12orf75	1	1	0	0	0	2	chromosome 12 open reading frame 75	I
PTGR1	1	0	0	1	0	2	prostaglandin reductase 1	I
TIMM17B	0	1	1	0	0	2	translocase of inner mitochondrial membrane 17 homolog B (yeast)	I
SHROOM1	1	0	1	0	0	2	shroom family member 1	I

ZNF692	1	0	1	0	0	2	zinc finger protein 692	I
RGS5	0	0	0	1	1	2	regulator of G-protein signaling 5	I
PHACTR3	0	1	1	0	0	2	phosphatase and actin regulator 3	I
TGIF2	1	1	0	0	0	2	TGFB-induced factor homeobox 2	I
SERPINH1	1	0	0	0	1	2	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	I
GRB7	0	1	1	0	0	2	growth factor receptor-bound protein 7	I
CSE1L	1	1	0	0	0	2	CSE1 chromosome segregation 1-like (yeast)	I
CSRP2	1	0	0	0	1	2	cysteine and glycine-rich protein 2	I
GAS8	1	0	1	0	0	2	growth arrest-specific 8	I
ARL4D	0	0	1	0	1	2	ADP-ribosylation factor-like 4D	I
KLF5	1	1	0	0	0	2	Kruppel-like factor 5 (intestinal)	I
CDK1	0	1	0	1	0	2	cyclin-dependent kinase 1	I
CKS2	0	1	1	0	0	2	CDC28 protein kinase regulatory subunit 2	I
EVPL	1	0	1	0	0	2	envoplakin	I
GPX2	1	0	0	0	1	2	glutathione peroxidase 2 (gastrointestinal)	I
H2AFX	1	0	0	0	1	2	H2A histone family, member X	I
HOXD10	1	0	1	0	0	2	homeobox D10	I
HSPA6	1	0	0	0	1	2	heat shock 70kDa protein 6 (HSP70B')	I
SEPT5	1	0	0	0	1	2	septin 5	I
PPAT	1	1	0	0	0	2	phosphoribosyl pyrophosphate amidotransferase	I
HHEX	0	0	1	0	1	2	hematopoietically expressed homeobox	I
MAPK10	1	0	1	0	0	2	mitogen-activated protein kinase 10	I
RAP2B	1	0	1	0	0	2	RAP2B, member of RAS oncogene family	I
RPS2	1	0	0	0	1	2	ribosomal protein S2	I
FSCN1	1	0	0	0	1	2	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	I
PHLDA2	0	1	0	0	1	2	pleckstrin homology-like domain, family A, member 2	I
ZNF165	0	0	1	0	1	2	zinc finger protein 165	I

SLC7A5	1	0	0	0	1	2	solute carrier family 7 (amino acid transporter light chain, L system), member 5	I
HIST1H2BG	1	0	0	0	1	2	histone cluster 1, H2bg	I
HIST1H3I	0	1	1	0	0	2	histone cluster 1, H3i	I
HIST1H4C	0	1	1	0	0	2	histone cluster 1, H4c	I
PSMG1	1	1	0	0	0	2	proteasome (prosome, macropain) assembly chaperone 1	I
CAPS	1	0	1	0	0	2	calcyphosine	I
FOXS1	0	1	0	0	1	2	forkhead box S1	I
GZMB	0	1	1	0	0	2	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	I
TRIP13	1	1	0	0	0	2	thyroid hormone receptor interactor 13	I
TRIP10	1	0	1	0	0	2	thyroid hormone receptor interactor 10	I
BAG3	1	0	0	0	1	2	BCL2-associated athanogene 3	I
TRAF4	1	0	1	0	0	2	TNF receptor-associated factor 4	I
CEBPA	1	1	0	0	0	2	CCAAT/enhancer binding protein (C/EBP), alpha	I
PPARG	0	1	1	0	0	2	peroxisome proliferator-activated receptor gamma	I
SIM2	0	1	1	0	0	2	single-minded homolog 2 (Drosophila)	I
RND3	0	1	1	0	0	2	Rho family GTPase 3	I
CDKN3	0	1	1	0	0	2	cyclin-dependent kinase inhibitor 3	I
DLX5	0	0	1	0	1	2	distal-less homeobox 5	I
JUND	1	0	0	0	1	2	jun D proto-oncogene	I
MYCN	0	0	1	0	1	2	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	I
NEFM	0	0	1	0	1	2	neurofilament, medium polypeptide	I
PPP1R3C	1	0	1	0	0	2	protein phosphatase 1, regulatory (inhibitor) subunit 3C	I
SPRR3	1	0	1	0	0	2	small proline-rich protein 3	I
HES1	1	0	1	0	0	2	hairy and enhancer of split 1, (Drosophila)	I
KRT6A	1	0	1	0	0	2	keratin 6A	I

KRT16	1	0	1	0	0	2	keratin 16	I
DHRS2	1	0	1	0	0	2	dehydrogenase/reductase (SDR family) member 2	I
MAP1B	1	0	0	1	0	2	microtubule-associated protein 1B	I
MOCS1	1	0	1	0	0	2	molybdenum cofactor synthesis 1	I
S100P	0	1	1	0	0	2	S100 calcium binding protein P	I
SPRR1A	1	0	1	0	0	2	small proline-rich protein 1A	I
TUBB3	0	0	0	1	1	2	tubulin, beta 3	I
DNAJB1	1	0	0	0	1	2	DnaJ (Hsp40) homolog, subfamily B, member 1	I
IRF6	1	0	1	0	0	2	interferon regulatory factor 6	I
NKX3-1	0	0	1	0	1	2	NK3 homeobox 1	I
GLRX3	1	1	0	0	0	2	glutaredoxin 3	I
IGF2BP3	0	1	0	1	0	2	insulin-like growth factor 2 mRNA binding protein 3	I
PLK2	0	0	0	1	1	2	polo-like kinase 2	I
ZNF266	1	0	1	0	0	2	zinc finger protein 266	I
KIF2C	1	0	0	1	0	2	kinesin family member 2C	I
PYCR1	1	0	0	0	1	2	pyrroline-5-carboxylate reductase 1	I
SHC2	1	0	0	0	1	2	SHC (Src homology 2 domain containing) transforming protein 2	I
SERTAD1	1	0	0	0	1	2	SERTA domain containing 1	I
UBE2S	1	0	0	0	1	2	ubiquitin-conjugating enzyme E2S	I
KIAA0101	0	1	0	1	0	2	KIAA0101	I
EIF4A3	1	0	0	0	1	2	eukaryotic translation initiation factor 4A3	I
NCAPD3	1	1	0	0	0	2	non-SMC condensin II complex, subunit D3	I
G0S2	0	1	1	0	0	2	G0/G1switch 2	I
AADAT	1	0	1	0	0	2	aminoadipate aminotransferase	I
ISYNA1	1	0	0	0	1	2	inositol-3-phosphate synthase 1	I
RPP25	1	0	1	0	0	2	ribonuclease P/MRP 25kDa subunit	I
MOCOS	0	1	1	0	0	2	molybdenum cofactor sulfurase	I
PBK	0	1	0	1	0	2	PDZ binding kinase	I

ANLN	0	1	0	1	0	2	anillin, actin binding protein	I
ARL15	1	0	1	0	0	2	ADP-ribosylation factor-like 15	I
AKR1B10	1	0	0	0	1	2	aldo-keto reductase family 1, member B10 (aldose reductase)	I
PDXP	1	0	0	0	1	2	pyridoxal (pyridoxine, vitamin B6) phosphatase	I
RIPK4	0	1	1	0	0	2	receptor-interacting serine-threonine kinase 4	I
PSAT1	1	0	0	1	0	2	phosphoserine aminotransferase 1	I
ZNF77	0	1	1	0	0	2	zinc finger protein 77	I
DNAJC12	0	1	0	0	1	2	DnaJ (Hsp40) homolog, subfamily C, member 12	I
TSPYL2	1	0	0	0	1	2	TSPY-like 2	I
GGCT	1	1	0	0	0	2	gamma-glutamylcyclotransferase	I
DCTPP1	1	1	0	0	0	2	dCTP pyrophosphatase 1	I
KIAA0226L	1	1	0	0	0	2	KIAA0226-like	I
FAM83D	0	1	0	0	1	2	family with sequence similarity 83, member D	I
DIAPH3	0	1	0	1	0	2	diaphanous homolog 3 (Drosophila)	I
PPP1R14C	1	1	0	0	0	2	protein phosphatase 1, regulatory (inhibitor) subunit 14C	I
LONP2	1	0	1	0	0	2	lon peptidase 2, peroxisomal	I
MRPL32	1	0	1	0	0	2	mitochondrial ribosomal protein L32	I
CCNB1	1	0	0	1	0	2	cyclin B1	I
C10orf11	1	0	1	0	0	2	chromosome 10 open reading frame 11	I
ZNF503	1	0	1	0	0	2	zinc finger protein 503	I
CCDC142	1	0	1	0	0	2	coiled-coil domain containing 142	I
SCIN	1	0	1	0	0	2	scinderin	I
FOXQ1	0	1	1	0	0	2	forkhead box Q1	I
FHDC1	1	1	0	0	0	2	FH2 domain containing 1	I
DNTTIP1	1	1	0	0	0	2	deoxynucleotidyltransferase, terminal, interacting protein 1	I
RBP7	1	0	0	0	1	2	retinol binding protein 7, cellular	I
MRPL53	1	0	1	0	0	2	mitochondrial ribosomal protein L53	I
CDKN2D	0	0	1	0	1	2	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	I

SPSB3	1	0	1	0	0	2	splA/ryanodine receptor domain and SOCS box containing 3	I
RHOV	0	1	1	0	0	2	ras homolog gene family, member V	I
BNIPL	1	0	1	0	0	2	BCL2/adenovirus E1B 19kD interacting protein like	I
DUOXA1	1	0	1	0	0	2	dual oxidase maturation factor 1	I
SPOCD1	0	0	1	1	0	2	SPOC domain containing 1	I
STK32A	1	0	1	0	0	2	serine/threonine kinase 32A	I
KIFC2	0	0	1	0	1	2	kinesin family member C2	I
HMGA1	1	0	0	1	0	2	high mobility group AT-hook 1	I
CHMP4C	1	1	0	0	0	2	chromatin modifying protein 4C	I
FAM43A	0	0	0	1	1	2	family with sequence similarity 43, member A	I
MEST	1	1	0	0	0	2	mesoderm specific transcript homolog (mouse)	I
ARL5B	0	1	1	0	0	2	ADP-ribosylation factor-like 5B	I
ANKRD37	1	0	0	0	1	2	ankyrin repeat domain 37	I
UBE2C	1	1	0	0	0	2	ubiquitin-conjugating enzyme E2C	I
ZFAND2A	1	0	0	0	1	2	zinc finger, AN1-type domain 2A	I
KRT80	1	1	0	0	0	2	keratin 80	I
CMC1	0	1	1	0	0	2	COX assembly mitochondrial protein homolog (S. cerevisiae)	I
TMSB15B	0	0	1	1	0	2	thymosin beta 15B	I
AURKA	1	1	0	0	0	2	aurora kinase A	I
GOLT1A	0	1	1	0	0	2	golgi transport 1A	I
NUDT4	1	0	0	0	1	2	nudix (nucleoside diphosphate linked moiety X)-type motif 4	I
MAFA	0	1	0	0	1	2	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	I
ENOSF1	1	0	1	0	0	2	enolase superfamily member 1	I
POLR1C	1	0	1	0	0	2	polymerase (RNA) I polypeptide C, 30kDa	I
CHCHD1	1	1	0	0	0	2	coiled-coil-helix-coiled-coil-helix domain containing 1	I
CCDC64	1	0	0	0	1	2	coiled-coil domain containing 64	I
SNORD32A	1	1	0	0	0	2	small nucleolar RNA, C/D box 32A	I
SNORD15B	1	1	0	0	0	2	small nucleolar RNA, C/D box 15B	I

RNU86	0	1	1	0	0	2	RNA, U86 small nucleolar	I
SNORD35B	0	1	1	0	0	2	small nucleolar RNA, C/D box 35B	I
ANXA2P3	1	0	1	0	0	2	annexin A2 pseudogene 3	I
ATP5EP2	1	0	1	0	0	2	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2	I
NUDT4P1	1	0	0	0	1	2	nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	I
RPPH1	1	1	0	0	0	2	ribonuclease P RNA component H1	I
SNORA10	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 10	I
SNORD12C	0	1	1	0	0	2	small nucleolar RNA, C/D box 12C	I
SNORD100	1	1	0	0	0	2	small nucleolar RNA, C/D box 100	I
SNORD16	0	1	1	0	0	2	small nucleolar RNA, C/D box 16	I
SNORD36A	1	1	0	0	0	2	small nucleolar RNA, C/D box 36A	I
SNORD30	1	1	0	0	0	2	small nucleolar RNA, C/D box 30	I
SNORA72	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 72	I
SNORA52	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 52	I
SNORD87	1	1	0	0	0	2	small nucleolar RNA, C/D box 87	I
SNHG6	1	1	0	0	0	2	small nucleolar RNA host gene 6 (non-protein coding)	I
SNORD60	0	1	1	0	0	2	small nucleolar RNA, C/D box 60	I
SNORD44	1	1	0	0	0	2	small nucleolar RNA, C/D box 44	I
SNORA71A	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 71A	I
SNORA48	1	0	1	0	0	2	small nucleolar RNA, H/ACA box 48	I
GSTM2P1	1	0	1	0	0	2	glutathione S-transferase mu 2 (muscle) pseudogene 1	I
SNORA23	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 23	I
SNORA38	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 38	I
SNORA44	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 44	I
SNORA50	0	1	1	0	0	2	small nucleolar RNA, H/ACA box 50	I
SNORD23	0	1	0	0	1	2	small nucleolar RNA, C/D box 23	I
SNORD62B	0	1	1	0	0	2	small nucleolar RNA, C/D box 62B	I

SNORD110	1	1	0	0	0	2	small nucleolar RNA, C/D box 110	I
H2BFXP	0	0	1	1	0	2	H2B histone family, member X, pseudogene	I
SNORD116-1	0	1	1	0	0	2	small nucleolar RNA, C/D box 116-1	I
SNORD116-16	0	1	1	0	0	2	small nucleolar RNA, C/D box 116-16	I
SNORD116-17	0	1	1	0	0	2	small nucleolar RNA, C/D box 116-17	I
SNORD115-33	0	1	1	0	0	2	small nucleolar RNA, C/D box 115-33	I
ZNFX1-AS1	1	1	0	0	0	2	ZNFX1 antisense RNA 1 (non-protein coding)	I
UBE2Q2P1	1	0	1	0	0	2	ubiquitin-conjugating enzyme E2Q family member 2 pseudogene 1	I
SNORD105B	0	1	1	0	0	2	small nucleolar RNA, C/D box 105B	I
SNORD123	0	1	1	0	0	2	small nucleolar RNA, C/D box 123	I
SNHG15	1	0	0	0	1	2	small nucleolar RNA host gene 15 (non-protein coding)	I
SNORD75	1	1	0	0	0	2	small nucleolar RNA, C/D box 75	I
SNORD76	1	1	0	0	0	2	small nucleolar RNA, C/D box 76	I
UCA1	0	1	1	0	0	2	urothelial cancer associated 1 (non-protein coding)	I
ZSCAN12P1	0	0	1	0	1	2	zinc finger and SCAN domain containing 12 pseudogene 1	I
HSPA7	1	0	0	0	1	2	heat shock 70kDa protein 7 (HSP70B)	I
MGC16121	0	0	1	0	1	2	hypothetical protein MGC16121	I
LINC00240	1	0	1	0	0	2	long intergenic non-protein coding RNA 240	I
LOC100130331	1	0	0	1	0	2	actin, gamma-like	I
LOC96610	1	0	0	0	1	2	BMS1 homolog, ribosome assembly protein (yeast) pseudogene	I
MST1P2	1	0	1	0	0	2	macrophage stimulating 1 (hepatocyte growth factor-like) pseudogene 2	I
MIR21	1	0	1	0	0	2	microRNA 21	I

MIR205	1	0	1	0	0	2	microRNA 205	I
MIR424	0	0	1	0	1	2	microRNA 424	I
MIR503	0	0	1	0	1	2	microRNA 503	I
MIR635	0	1	1	0	0	2	microRNA 635	I
LOC100128338	1	0	1	0	0	2	hypothetical LOC100128338	I
FLJ39639	1	0	1	0	0	2	hypothetical protein FLJ39639	I
KANSL1-AS1	0	0	1	0	1	2	KANSL1 antisense RNA 1 (non-protein coding)	I
MIR3688-2	1	0	1	0	0	2	microRNA 3688-2	I
LOC388796	1	1	0	0	0	2	hypothetical LOC388796	I
CRNDE	0	1	1	0	0	2	colorectal neoplasia differentially expressed (non-protein coding)	I
SEPT5-GP1BB	1	0	0	0	1	2	SEPT5-GP1BB readthrough	I
LOC100506866	1	0	1	0	0	2	hypothetical LOC100506866	I
NAT2	0	1	0	0	0	1	N-acetyltransferase 2 (arylamine N-acetyltransferase)	I
ALAS2	1	0	0	0	0	1	aminolevulinate, delta-, synthase 2	I
ARSE	0	1	0	0	0	1	arylsulfatase E (chondrodysplasia punctata 1)	I
BCKDHB	1	0	0	0	0	1	branched chain keto acid dehydrogenase E1, beta polypeptide	I
CDK4	1	0	0	0	0	1	cyclin-dependent kinase 4	I
CSTB	0	0	1	0	0	1	cystatin B (stefin B)	I
DDB2	1	0	0	0	0	1	damage-specific DNA binding protein 2, 48kDa	I
FAH	1	0	0	0	0	1	fumarylacetoacetate hydrolase (fumarylacetoacetase)	I
FH	1	0	0	0	0	1	fumarate hydratase	I
GALK1	1	0	0	0	0	1	galactokinase 1	I
GSS	1	0	0	0	0	1	glutathione synthetase	I
HBG2	1	0	0	0	0	1	hemoglobin, gamma G	I

HK2	1	0	0	0	0	1	hexokinase 2	I
HPRT1	0	1	0	0	0	1	hypoxanthine phosphoribosyltransferase 1	I
HSD11B2	0	0	0	0	1	1	hydroxysteroid (11-beta) dehydrogenase 2	I
HSD17B3	0	0	1	0	0	1	hydroxysteroid (17-beta) dehydrogenase 3	I
PDX1	0	1	0	0	0	1	pancreatic and duodenal homeobox 1	I
KRT12	0	0	1	0	0	1	keratin 12	I
KRT18	1	0	0	0	0	1	keratin 18	I
NAGA	1	0	0	0	0	1	N-acetylgalactosaminidase, alpha-	I
NME1	1	0	0	0	0	1	non-metastatic cells 1, protein (NM23A) expressed in	I
PEPD	1	0	0	0	0	1	peptidase D	I
PHKG2	1	0	0	0	0	1	phosphorylase kinase, gamma 2 (testis)	I
PKP1	1	0	0	0	0	1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	I
TTPA	0	1	0	0	0	1	tocopherol (alpha) transfer protein	I
BLMH	1	0	0	0	0	1	bleomycin hydrolase	I
GLB1	1	0	0	0	0	1	galactosidase, beta 1	I
NEU1	1	0	0	0	0	1	sialidase 1 (lysosomal sialidase)	I
PAFAH2	1	0	0	0	0	1	platelet-activating factor acetylhydrolase 2, 40kDa	I
NR0B1	0	0	0	0	1	1	nuclear receptor subfamily 0, group B, member 1	I
AK1	1	0	0	0	0	1	adenylate kinase 1	I
ARSA	1	0	0	0	0	1	arylsulfatase A	I
CRYBB2	0	0	1	0	0	1	crystallin, beta B2	I
HBA2	1	0	0	0	0	1	hemoglobin, alpha 2	I
HBB	1	0	0	0	0	1	hemoglobin, beta	I
HBD	1	0	0	0	0	1	hypophosphatemic bone disease	I
HBA1	1	0	0	0	0	1	hemoglobin, alpha 1	I
HBG1	1	0	0	0	0	1	hemoglobin, gamma A	I
SOD2	1	0	0	0	0	1	superoxide dismutase 2, mitochondrial	I
ACY1	1	0	0	0	0	1	aminoacylase 1	I

ALDH1B1	1	0	0	0	0	1	aldehyde dehydrogenase 1 family, member B1	I
ALDH1A3	0	0	1	0	0	1	aldehyde dehydrogenase 1 family, member A3	I
ALDH3B1	1	0	0	0	0	1	aldehyde dehydrogenase 3 family, member B1	I
ALDH3B2	0	0	1	0	0	1	aldehyde dehydrogenase 3 family, member B2	I
BLVRB	1	0	0	0	0	1	biliverdin reductase B (flavin reductase (NADPH))	I
CYP2C8	0	0	1	0	0	1	cytochrome P450, family 2, subfamily C, polypeptide 8	I
GSTA2	1	0	0	0	0	1	glutathione S-transferase alpha 2	I
GSTM2	0	0	1	0	0	1	glutathione S-transferase mu 2 (muscle)	I
GSTT2	0	0	1	0	0	1	glutathione S-transferase theta 2	I
GUCY1A2	1	0	0	0	0	1	guanylate cyclase 1, soluble, alpha 2	I
HPGD	0	0	1	0	0	1	hydroxyprostaglandin dehydrogenase 15-(NAD)	I
IMPDH1	1	0	0	0	0	1	IMP (inosine 5'-monophosphate) dehydrogenase 1	I
PDE3A	0	0	0	1	0	1	phosphodiesterase 3A, cGMP-inhibited	I
POR	1	0	0	0	0	1	P450 (cytochrome) oxidoreductase	I
PPIB	1	0	0	0	0	1	peptidylprolyl isomerase B (cyclophilin B)	I
PPIC	1	0	0	0	0	1	peptidylprolyl isomerase C (cyclophilin C)	I
PPP3R1	1	0	0	0	0	1	protein phosphatase 3, regulatory subunit B, alpha	I
RPL7	0	0	0	1	0	1	ribosomal protein L7	I
RPL24	0	0	1	0	0	1	ribosomal protein L24	I
RPL27	0	1	0	0	0	1	ribosomal protein L27	I
RPL37	0	0	1	0	0	1	ribosomal protein L37	I
RPL37A	1	0	0	0	0	1	ribosomal protein L37a	I
LMO3	1	0	0	0	0	1	LIM domain only 3 (rhombotin-like 2)	I
NCCRP1	0	0	1	0	0	1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	I
HDGFRP2	1	0	0	0	0	1	hepatoma-derived growth factor-related protein 2	I
GGA1	1	0	0	0	0	1	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	I
TIMM50	1	0	0	0	0	1	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	I

SPOPL	1	0	0	0	0	1	speckle-type POZ protein-like	I
MED11	1	0	0	0	0	1	mediator complex subunit 11	I
RUNX1	1	0	0	0	0	1	runt-related transcription factor 1	I
ATP5C1	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	I
EXOSC10	1	0	0	0	0	1	exosome component 10	I
HN1	1	0	0	0	0	1	hematological and neurological expressed 1	I
GATA3	0	0	1	0	0	1	GATA binding protein 3	I
SMC4	1	0	0	0	0	1	structural maintenance of chromosomes 4	I
RAB11FIP1	0	1	0	0	0	1	RAB11 family interacting protein 1 (class I)	I
TWISTNB	1	0	0	0	0	1	TWIST neighbor	I
C11orf49	1	0	0	0	0	1	chromosome 11 open reading frame 49	I
MAD2L1BP	1	0	0	0	0	1	MAD2L1 binding protein	I
ATP5J	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	I
GLE1	1	0	0	0	0	1	GLE1 RNA export mediator homolog (yeast)	I
ERLIN2	1	0	0	0	0	1	ER lipid raft associated 2	I
NHP2L1	1	0	0	0	0	1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	I
SMARCD3	1	0	0	0	0	1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	I
MED15	1	0	0	0	0	1	mediator complex subunit 15	I
RPLP2	1	0	0	0	0	1	ribosomal protein, large, P2	I
AGMO	1	0	0	0	0	1	alkylglycerol monooxygenase	I
PLEKHG7	1	0	0	0	0	1	pleckstrin homology domain containing, family G (with RhoGef domain) member 7	I
RPS3	1	0	0	0	0	1	ribosomal protein S3	I
CHD3	0	0	1	0	0	1	chromodomain helicase DNA binding protein 3	I
MAGED1	1	0	0	0	0	1	melanoma antigen family D, 1	I
AK4	0	0	0	1	0	1	adenylate kinase 4	I
KDM2B	1	0	0	0	0	1	lysine (K)-specific demethylase 2B	I

YPEL2	0	0	1	0	0	1	yippee-like 2 (Drosophila)	I
CHEK2	1	0	0	0	0	1	CHK2 checkpoint homolog (S. pombe)	I
ZNF780B	1	0	0	0	0	1	zinc finger protein 780B	I
FAM149A	1	0	0	0	0	1	family with sequence similarity 149, member A	I
ZNF473	0	0	1	0	0	1	zinc finger protein 473	I
TCEAL4	1	0	0	0	0	1	transcription elongation factor A (SII)-like 4	I
ALG3	1	0	0	0	0	1	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (S. cerevisiae)	I
UHRF1BP1L	1	0	0	0	0	1	UHRF1 binding protein 1-like	I
CARD17	1	0	0	0	0	1	caspase recruitment domain family, member 17	I
ERV3-1	0	0	1	0	0	1	endogenous retrovirus group 3, member 1	I
RASL10A	0	0	1	0	0	1	RAS-like, family 10, member A	I
C2CD4B	0	0	0	0	1	1	C2 calcium-dependent domain containing 4B	I
TTC32	0	1	0	0	0	1	tetratricopeptide repeat domain 32	I
CCDC73	1	0	0	0	0	1	coiled-coil domain containing 73	I
EID3	1	0	0	0	0	1	EP300 interacting inhibitor of differentiation 3	I
ZNF761	1	0	0	0	0	1	zinc finger protein 761	I
STEAP3	1	0	0	0	0	1	STEAP family member 3	I
LGMN	1	0	0	0	0	1	legumain	I
ARHGAP28	1	0	0	0	0	1	Rho GTPase activating protein 28	I
IRAK1BP1	0	0	1	0	0	1	interleukin-1 receptor-associated kinase 1 binding protein 1	I
TTC7B	1	0	0	0	0	1	tetratricopeptide repeat domain 7B	I
ACER2	0	0	1	0	0	1	alkaline ceramidase 2	I
C6orf222	0	1	0	0	0	1	chromosome 6 open reading frame 222	I
HES5	0	0	0	0	1	1	hairy and enhancer of split 5 (Drosophila)	I
HNRNPA1L2	0	0	0	0	1	1	heterogeneous nuclear ribonucleoprotein A1-like 2	I
AKTIP	1	0	0	0	0	1	AKT interacting protein	I

CENPW	0	1	0	0	0	1	centromere protein W	I
CTBP1	1	0	0	0	0	1	C-terminal binding protein 1	I
DPRX	1	0	0	0	0	1	divergent-paired related homeobox	I
C1orf31	0	1	0	0	0	1	chromosome 1 open reading frame 31	I
SNX30	1	0	0	0	0	1	sorting nexin family member 30	I
RPS9	1	0	0	0	0	1	ribosomal protein S9	I
MPST	1	0	0	0	0	1	mercaptopyruvate sulfurtransferase	I
FXR1	1	0	0	0	0	1	fragile X mental retardation, autosomal homolog 1	I
LURAP1	0	0	1	0	0	1	leucine rich adaptor protein 1	I
TRNP1	0	0	1	0	0	1	TMF1-regulated nuclear protein 1	I
C2orf68	1	0	0	0	0	1	chromosome 2 open reading frame 68	I
C17orf97	0	0	1	0	0	1	chromosome 17 open reading frame 97	I
C5orf56	1	0	0	0	0	1	chromosome 5 open reading frame 56	I
EXOC6	0	0	0	1	0	1	exocyst complex component 6	I
KATNAL1	1	0	0	0	0	1	katanin p60 subunit A-like 1	I
NCDN	1	0	0	0	0	1	neurochondrin	I
PAGE2B	1	0	0	0	0	1	P antigen family, member 2B	I
FAM13A	0	1	0	0	0	1	family with sequence similarity 13, member A	I
RUNX2	1	0	0	0	0	1	runt-related transcription factor 2	I
HDAC5	1	0	0	0	0	1	histone deacetylase 5	I
AURKC	0	0	1	0	0	1	aurora kinase C	I
SPRR2B	0	0	1	0	0	1	small proline-rich protein 2B	I
BTBD11	1	0	0	0	0	1	BTB (POZ) domain containing 11	I
SIRT3	1	0	0	0	0	1	sirtuin 3	I
CYB561	1	0	0	0	0	1	cytochrome b-561	I
DAPL1	1	0	0	0	0	1	death associated protein-like 1	I
VMAC	0	0	1	0	0	1	vimentin-type intermediate filament associated coiled-coil protein	I
HSP90AA1	0	0	0	0	1	1	heat shock protein 90kDa alpha (cytosolic), class A member 1	I

YDJC	0	0	1	0	0	1	YdjC homolog (bacterial)	I
SH3PXD2B	1	0	0	0	0	1	SH3 and PX domains 2B	I
KAZN	1	0	0	0	0	1	kazrin, periplakin interacting protein	I
TPM1	0	0	0	1	0	1	tropomyosin 1 (alpha)	I
MTCP1NB	0	0	1	0	0	1	mature T-cell proliferation 1 neighbor	I
MTCP1	0	0	1	0	0	1	mature T-cell proliferation 1	I
POLR3H	1	0	0	0	0	1	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	I
NME1-NME2	1	0	0	0	0	1	NME1-NME2 readthrough	I
NME2	1	0	0	0	0	1	non-metastatic cells 2, protein (NM23B) expressed in	I
RPS16	1	0	0	0	0	1	ribosomal protein S16	I
RPS19	1	0	0	0	0	1	ribosomal protein S19	I
HMBS	1	0	0	0	0	1	hydroxymethylbilane synthase	I
KALRN	1	0	0	0	0	1	kalirin, RhoGEF kinase	I
LIN52	1	0	0	0	0	1	lin-52 homolog (C. elegans)	I
RPS14	1	0	0	0	0	1	ribosomal protein S14	I
RAB12	1	0	0	0	0	1	RAB12, member RAS oncogene family	I
NQO1	1	0	0	0	0	1	NAD(P)H dehydrogenase, quinone 1	I
RFX5	1	0	0	0	0	1	regulatory factor X, 5 (influences HLA class II expression)	I
SOWAHB	0	0	1	0	0	1	sosondowah ankyrin repeat domain family member B	I
METTL17	1	0	0	0	0	1	methyltransferase like 17	I
RPS27	1	0	0	0	0	1	ribosomal protein S27	I
SAMD5	1	0	0	0	0	1	sterile alpha motif domain containing 5	I
ARNTL	1	0	0	0	0	1	aryl hydrocarbon receptor nuclear translocator-like	I
NT5DC3	1	0	0	0	0	1	5'-nucleotidase domain containing 3	I
C3orf75	1	0	0	0	0	1	chromosome 3 open reading frame 75	I
TRMT11	0	0	1	0	0	1	tRNA methyltransferase 11 homolog (S. cerevisiae)	I
OBFC2A	1	0	0	0	0	1	oligonucleotide/oligosaccharide-binding fold containing 2A	I

MRI1	1	0	0	0	0	1	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	I
FDX1L	0	0	1	0	0	1	ferredoxin 1-like	I
ASB9	0	1	0	0	0	1	ankyrin repeat and SOCS box containing 9	I
TIPRL	1	0	0	0	0	1	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	I
UBE2V1	1	0	0	0	0	1	ubiquitin-conjugating enzyme E2 variant 1	I
SUOX	1	0	0	0	0	1	sulfite oxidase	I
PJA1	1	0	0	0	0	1	praja ring finger 1	I
OAS2	0	0	1	0	0	1	2'-5'-oligoadenylate synthetase 2, 69/71kDa	I
RRM1	1	0	0	0	0	1	ribonucleotide reductase M1	I
MYCL1	0	0	1	0	0	1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	I
MACROD2	1	0	0	0	0	1	MACRO domain containing 2	I
SPECC1	1	0	0	0	0	1	sperm antigen with calponin homology and coiled-coil domains 1	I
PHF12	1	0	0	0	0	1	PHD finger protein 12	I
NOP2	1	0	0	0	0	1	NOP2 nucleolar protein homolog (yeast)	I
TRAF5	0	0	0	0	1	1	TNF receptor-associated factor 5	I
ERP29	1	0	0	0	0	1	endoplasmic reticulum protein 29	I
NHP2	1	0	0	0	0	1	NHP2 ribonucleoprotein homolog (yeast)	I
ESRP1	1	0	0	0	0	1	epithelial splicing regulatory protein 1	I
C18orf32	0	1	0	0	0	1	chromosome 18 open reading frame 32	I
RPL17	0	1	0	0	0	1	ribosomal protein L17	I
UFD1L	1	0	0	0	0	1	ubiquitin fusion degradation 1 like (yeast)	I
AGBL5	1	0	0	0	0	1	ATP/GTP binding protein-like 5	I
SDHC	1	0	0	0	0	1	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	I
HHLA3	1	0	0	0	0	1	HERV-H LTR-associating 3	I
CYS1	1	0	0	0	0	1	cystin 1	I
C7orf70	0	0	1	0	0	1	chromosome 7 open reading frame 70	I
SUSD4	1	0	0	0	0	1	sushi domain containing 4	I

ECE2	1	0	0	0	0	1	endothelin converting enzyme 2	I
TRIM16L	0	0	1	0	0	1	tripartite motif containing 16-like	I
USP14	1	0	0	0	0	1	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	I
SCML1	0	1	0	0	0	1	sex comb on midleg-like 1 (Drosophila)	I
SCD5	1	0	0	0	0	1	stearoyl-CoA desaturase 5	I
PARL	1	0	0	0	0	1	presenilin associated, rhomboid-like	I
EEF1B2	0	1	0	0	0	1	eukaryotic translation elongation factor 1 beta 2	I
ZNF630	0	0	1	0	0	1	zinc finger protein 630	I
NCKAP5L	1	0	0	0	0	1	NCK-associated protein 5-like	I
SLC25A29	1	0	0	0	0	1	solute carrier family 25, member 29	I
C20orf7	1	0	0	0	0	1	chromosome 20 open reading frame 7	I
VWA5B1	0	0	1	0	0	1	von Willebrand factor A domain containing 5B1	I
DNAJB2	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily B, member 2	I
AP1S3	1	0	0	0	0	1	adaptor-related protein complex 1, sigma 3 subunit	I
PNCK	0	0	1	0	0	1	pregnancy up-regulated non-ubiquitously expressed CaM kinase	I
DPH2	1	0	0	0	0	1	DPH2 homolog (S. cerevisiae)	I
PRMT5	1	0	0	0	0	1	protein arginine methyltransferase 5	I
ZNF550	1	0	0	0	0	1	zinc finger protein 550	I
TRO	0	0	0	0	1	1	trophinin	I
CHIC1	0	0	1	0	0	1	cysteine-rich hydrophobic domain 1	I
CHN2	0	0	1	0	0	1	chimerin (chimaerin) 2	I
FAM83G	1	0	0	0	0	1	family with sequence similarity 83, member G	I
FAM133B	1	0	0	0	0	1	family with sequence similarity 133, member B	I
C16orf13	1	0	0	0	0	1	chromosome 16 open reading frame 13	I
FAM63A	1	0	0	0	0	1	family with sequence similarity 63, member A	I
U2AF1L4	1	0	0	0	0	1	U2 small nuclear RNA auxiliary factor 1-like 4	I
FABP6	0	1	0	0	0	1	fatty acid binding protein 6, ileal	I
RUFY1	1	0	0	0	0	1	RUN and FYVE domain containing 1	I

ATF3	1	0	0	0	0	1	activating transcription factor 3	I
KIAA0895L	0	0	1	0	0	1	KIAA0895-like	I
CEP63	1	0	0	0	0	1	centrosomal protein 63kDa	I
CRTC3	1	0	0	0	0	1	CREB regulated transcription coactivator 3	I
RRBP1	1	0	0	0	0	1	ribosome binding protein 1 homolog 180kDa (dog)	I
DBNDD1	0	0	0	1	0	1	dysbindin (dystrobrevin binding protein 1) domain containing 1	I
PARP2	1	0	0	0	0	1	poly (ADP-ribose) polymerase 2	I
PLEKHG5	1	0	0	0	0	1	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	I
IQCJ	1	0	0	0	0	1	IQ motif containing J	I
TNNT3	0	0	1	0	0	1	troponin T type 3 (skeletal, fast)	I
RCC1	1	0	0	0	0	1	regulator of chromosome condensation 1	I
TUBB2A	0	0	0	0	1	1	tubulin, beta 2A	I
QSER1	1	0	0	0	0	1	glutamine and serine rich 1	I
MYH14	1	0	0	0	0	1	myosin, heavy chain 14, non-muscle	I
ZNF682	0	0	1	0	0	1	zinc finger protein 682	I
C17orf63	1	0	0	0	0	1	chromosome 17 open reading frame 63	I
VPS37D	0	0	1	0	0	1	vacuolar protein sorting 37 homolog D (S. cerevisiae)	I
URGCP	1	0	0	0	0	1	upregulator of cell proliferation	I
CDC16	1	0	0	0	0	1	cell division cycle 16 homolog (S. cerevisiae)	I
NKX2-1	1	0	0	0	0	1	NK2 homeobox 1	I
BCS1L	1	0	0	0	0	1	BCS1-like (S. cerevisiae)	I
FBXO41	1	0	0	0	0	1	F-box protein 41	I
FTO	1	0	0	0	0	1	fat mass and obesity associated	I
ASPG	1	0	0	0	0	1	asparaginase homolog (S. cerevisiae)	I
RGNEF	0	0	0	1	0	1	190 kDa guanine nucleotide exchange factor	I
CCDC159	1	0	0	0	0	1	coiled-coil domain containing 159	I
BICC1	1	0	0	0	0	1	bicaudal C homolog 1 (Drosophila)	I

ZNF799	0	0	1	0	0	1	zinc finger protein 799	I
CCDC30	1	0	0	0	0	1	coiled-coil domain containing 30	I
ACD	1	0	0	0	0	1	adrenocortical dysplasia homolog (mouse)	I
RBFOX3	0	0	0	0	1	1	RNA binding protein, fox-1 homolog (C. elegans) 3	I
DNAAF2	1	0	0	0	0	1	dynein, axonemal, assembly factor 2	I
ASRGL1	1	0	0	0	0	1	asparaginase like 1	I
DDTL	0	0	1	0	0	1	D-dopachrome tautomerase-like	I
MEX3A	0	0	0	1	0	1	mex-3 homolog A (C. elegans)	I
SMARCD2	1	0	0	0	0	1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	I
FAM129C	0	0	0	0	1	1	family with sequence similarity 129, member C	I
CKAP2	1	0	0	0	0	1	cytoskeleton associated protein 2	I
GNG4	0	1	0	0	0	1	guanine nucleotide binding protein (G protein), gamma 4	I
FAM160A2	1	0	0	0	0	1	family with sequence similarity 160, member A2	I
MORN4	1	0	0	0	0	1	MORN repeat containing 4	I
HEATR7A	1	0	0	0	0	1	HEAT repeat containing 7A	I
PHYHIP	1	0	0	0	0	1	phytanoyl-CoA 2-hydroxylase interacting protein	I
CCNK	1	0	0	0	0	1	cyclin K	I
FAM54B	1	0	0	0	0	1	family with sequence similarity 54, member B	I
FTSJD1	0	0	1	0	0	1	FtsJ methyltransferase domain containing 1	I
TRIM32	1	0	0	0	0	1	tripartite motif containing 32	I
REPIN1	1	0	0	0	0	1	replication initiator 1	I
CYP4B1	0	0	1	0	0	1	cytochrome P450, family 4, subfamily B, polypeptide 1	I
C4orf33	1	0	0	0	0	1	chromosome 4 open reading frame 33	I
DROSHA	1	0	0	0	0	1	drosha, ribonuclease type III	I
C8orf73	0	0	1	0	0	1	chromosome 8 open reading frame 73	I
ST20	1	0	0	0	0	1	suppressor of tumorigenicity 20	I
TMEM176B	1	0	0	0	0	1	transmembrane protein 176B	I

SFTA3	1	0	0	0	0	1	surfactant associated 3	I
FAM183A	1	0	0	0	0	1	family with sequence similarity 183, member A	I
ACOX3	1	0	0	0	0	1	acyl-CoA oxidase 3, pristanoyl	I
IFT43	1	0	0	0	0	1	intraflagellar transport 43 homolog (Chlamydomonas)	I
PCP4L1	0	0	1	0	0	1	Purkinje cell protein 4 like 1	I
PNMAL1	1	0	0	0	0	1	PNMA-like 1	I
SLC25A36	1	0	0	0	0	1	solute carrier family 25, member 36	I
MECOM	1	0	0	0	0	1	MDS1 and EVI1 complex locus	I
FBRS	1	0	0	0	0	1	fibrosin	I
ZNF83	0	0	1	0	0	1	zinc finger protein 83	I
CENPM	1	0	0	0	0	1	centromere protein M	I
ZSCAN30	0	0	1	0	0	1	zinc finger and SCAN domain containing 30	I
TSTD1	1	0	0	0	0	1	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1	I
DEPDC1	1	0	0	0	0	1	DEP domain containing 1	I
MTRF1L	1	0	0	0	0	1	mitochondrial translational release factor 1-like	I
MVK	1	0	0	0	0	1	mevalonate kinase	I
FANCL	1	0	0	0	0	1	Fanconi anemia, complementation group L	I
TP63	1	0	0	0	0	1	tumor protein p63	I
SLC50A1	1	0	0	0	0	1	solute carrier family 50 (sugar transporter), member 1	I
BCKDK	1	0	0	0	0	1	branched chain ketoacid dehydrogenase kinase	I
ADK	1	0	0	0	0	1	adenosine kinase	I
PPIAL4G	0	0	1	0	0	1	peptidylprolyl isomerase A (cyclophilin A)-like 4G	I
PABPC1L	1	0	0	0	0	1	poly(A) binding protein, cytoplasmic 1-like	I
NRGN	1	0	0	0	0	1	neurogranin (protein kinase C substrate, RC3)	I
AURKAIP1	1	0	0	0	0	1	aurora kinase A interacting protein 1	I
AUTS2	1	0	0	0	0	1	autism susceptibility candidate 2	I
BBC3	0	1	0	0	0	1	BCL2 binding component 3	I
MAD2L2	1	0	0	0	0	1	MAD2 mitotic arrest deficient-like 2 (yeast)	I

NR2C1	0	0	1	0	0	1	nuclear receptor subfamily 2, group C, member 1	I
ALS2CR12	1	0	0	0	0	1	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12	I
DFNA5	1	0	0	0	0	1	deafness, autosomal dominant 5	I
CRLS1	1	0	0	0	0	1	cardiolipin synthase 1	I
FLNC	0	0	0	1	0	1	filamin C, gamma	I
PEX26	1	0	0	0	0	1	peroxisomal biogenesis factor 26	I
PCCA	0	0	1	0	0	1	propionyl CoA carboxylase, alpha polypeptide	I
NPHP1	1	0	0	0	0	1	nephronophthisis 1 (juvenile)	I
WDSUB1	1	0	0	0	0	1	WD repeat, sterile alpha motif and U-box domain containing 1	I
FAM198B	0	0	0	1	0	1	family with sequence similarity 198, member B	I
CYP21A2	0	0	1	0	0	1	cytochrome P450, family 21, subfamily A, polypeptide 2	I
PSMG4	1	0	0	0	0	1	proteasome (prosome, macropain) assembly chaperone 4	I
TC2N	1	0	0	0	0	1	tandem C2 domains, nuclear	I
NCS1	0	0	0	1	0	1	neuronal calcium sensor 1	I
ENTPD4	1	0	0	0	0	1	ectonucleoside triphosphate diphosphohydrolase 4	I
NAF1	1	0	0	0	0	1	nuclear assembly factor 1 homolog (S. cerevisiae)	I
CYP4F11	0	0	1	0	0	1	cytochrome P450, family 4, subfamily F, polypeptide 11	I
PLEKHG4	1	0	0	0	0	1	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	I
CSAG3	1	0	0	0	0	1	CSAG family, member 3	I
DNAJC2	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 2	I
EEF1D	1	0	0	0	0	1	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	I
TRIM2	1	0	0	0	0	1	tripartite motif containing 2	I
MOV10	0	0	1	0	0	1	Mov10, Moloney leukemia virus 10, homolog (mouse)	I
ABLIM2	1	0	0	0	0	1	actin binding LIM protein family, member 2	I
C10orf131	0	0	1	0	0	1	chromosome 10 open reading frame 131	I
HMGB2	1	0	0	0	0	1	high mobility group box 2	I

PACRGL	1	0	0	0	0	1	PARK2 co-regulated-like	I
SUPT5H	1	0	0	0	0	1	suppressor of Ty 5 homolog (S. cerevisiae)	I
ERCC2	1	0	0	0	0	1	excision repair cross-complementing rodent repair deficiency, complementation group 2	I
PLCD1	1	0	0	0	0	1	phospholipase C, delta 1	I
ZNF385A	1	0	0	0	0	1	zinc finger protein 385A	I
RBP1	1	0	0	0	0	1	retinol binding protein 1, cellular	I
HMGCR	1	0	0	0	0	1	3-hydroxy-3-methylglutaryl-CoA reductase	I
EIF2AK1	1	0	0	0	0	1	eukaryotic translation initiation factor 2-alpha kinase 1	I
PSMG3	1	0	0	0	0	1	proteasome (prosome, macropain) assembly chaperone 3	I
HS2ST1	1	0	0	0	0	1	heparan sulfate 2-O-sulfotransferase 1	I
TOMM6	0	0	1	0	0	1	translocase of outer mitochondrial membrane 6 homolog (yeast)	I
IPO11	0	0	0	1	0	1	importin 11	I
TRIM17	0	0	1	0	0	1	tripartite motif containing 17	I
FKBP2	1	0	0	0	0	1	FK506 binding protein 2, 13kDa	I
HDHD1	1	0	0	0	0	1	haloacid dehalogenase-like hydrolase domain containing 1	I
FOXI3	1	0	0	0	0	1	forkhead box I3	I
DERL3	1	0	0	0	0	1	Der1-like domain family, member 3	I
FAM60A	0	1	0	0	0	1	family with sequence similarity 60, member A	I
PHPT1	1	0	0	0	0	1	phosphohistidine phosphatase 1	I
LOC100132247	0	0	0	0	1	1	nuclear pore complex interacting protein related gene	I
FXYD3	1	0	0	0	0	1	FXYD domain containing ion transport regulator 3	I
NIF3L1	1	0	0	0	0	1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	I
HDAC11	1	0	0	0	0	1	histone deacetylase 11	I
LRIG3	1	0	0	0	0	1	leucine-rich repeats and immunoglobulin-like domains 3	I
C11orf93	0	0	1	0	0	1	chromosome 11 open reading frame 93	I
TCF3	1	0	0	0	0	1	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	I

HSBP1L1	1	0	0	0	0	1	heat shock factor binding protein 1-like 1	I
GRAMD1A	1	0	0	0	0	1	GRAM domain containing 1A	I
ANP32E	1	0	0	0	0	1	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	I
ZNF844	0	0	0	0	1	1	zinc finger protein 844	I
POLR1B	1	0	0	0	0	1	polymerase (RNA) I polypeptide B, 128kDa	I
TBL1X	1	0	0	0	0	1	transducin (beta)-like 1X-linked	I
DACH2	0	0	1	0	0	1	dachshund homolog 2 (Drosophila)	I
TP53BP1	1	0	0	0	0	1	tumor protein p53 binding protein 1	I
COX4NB	1	0	0	0	0	1	COX4 neighbor	I
HES4	0	0	0	0	1	1	hairy and enhancer of split 4 (Drosophila)	I
RRNAD1	1	0	0	0	0	1	ribosomal RNA adenine dimethylase domain containing 1	I
C1orf106	1	0	0	0	0	1	chromosome 1 open reading frame 106	I
NFYC	1	0	0	0	0	1	nuclear transcription factor Y, gamma	I
EFTUD2	1	0	0	0	0	1	elongation factor Tu GTP binding domain containing 2	I
NEURL1B	0	0	0	0	1	1	neuralized homolog 1B (Drosophila)	I
ARHGAP32	1	0	0	0	0	1	Rho GTPase activating protein 32	I
CHAC1	1	0	0	0	0	1	ChaC, cation transport regulator homolog 1 (E. coli)	I
MAGI3	1	0	0	0	0	1	membrane associated guanylate kinase, WW and PDZ domain containing 3	I
HES6	0	0	0	0	1	1	hairy and enhancer of split 6 (Drosophila)	I
NOX4	0	0	0	1	0	1	NADPH oxidase 4	I
PPIAL4B	1	0	0	0	0	1	peptidylprolyl isomerase A (cyclophilin A)-like 4B	I
CAPN8	1	0	0	0	0	1	calpain 8	I
TBC1D7	1	0	0	0	0	1	TBC1 domain family, member 7	I
WEE1	1	0	0	0	0	1	WEE1 homolog (S. pombe)	I
NDE1	1	0	0	0	0	1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	I
NAT10	1	0	0	0	0	1	N-acetyltransferase 10 (GCN5-related)	I
COPB1	1	0	0	0	0	1	coatomer protein complex, subunit beta 1	I

PHB2	1	0	0	0	0	1	prohibitin 2	I
MBIP	1	0	0	0	0	1	MAP3K12 binding inhibitory protein 1	I
SMCR7	1	0	0	0	0	1	Smith-Magenis syndrome chromosome region, candidate 7	I
ATG7	1	0	0	0	0	1	ATG7 autophagy related 7 homolog (S. cerevisiae)	I
MX1	0	0	1	0	0	1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	I
DTWD1	1	0	0	0	0	1	DTW domain containing 1	I
NEDD4L	1	0	0	0	0	1	neural precursor cell expressed, developmentally down-regulated 4-like	I
FAM190A	0	0	1	0	0	1	family with sequence similarity 190, member A	I
SMAD3	1	0	0	0	0	1	SMAD family member 3	I
RELA	1	0	0	0	0	1	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	I
DEPDC1B	0	1	0	0	0	1	DEP domain containing 1B	I
OTUD1	0	0	0	0	1	1	OTU domain containing 1	I
CHM	1	0	0	0	0	1	choroideremia (Rab escort protein 1)	I
MORN2	1	0	0	0	0	1	MORN repeat containing 2	I
RAI14	0	0	0	1	0	1	retinoic acid induced 14	I
KPNA7	1	0	0	0	0	1	karyopherin alpha 7 (importin alpha 8)	I
HOMER3	1	0	0	0	0	1	homer homolog 3 (Drosophila)	I
TNNI2	0	0	1	0	0	1	troponin I type 2 (skeletal, fast)	I
WFS1	1	0	0	0	0	1	Wolfram syndrome 1 (wolframin)	I
TJAP1	1	0	0	0	0	1	tight junction associated protein 1 (peripheral)	I
JPH4	1	0	0	0	0	1	junctophilin 4	I
FCHO2	1	0	0	0	0	1	FCH domain only 2	I
TOX3	0	1	0	0	0	1	TOX high mobility group box family member 3	I
NCEH1	1	0	0	0	0	1	neutral cholesterol ester hydrolase 1	I
C1orf86	0	1	0	0	0	1	chromosome 1 open reading frame 86	I
SLC25A5	1	0	0	0	0	1	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	I

ANXA4	1	0	0	0	0	1	annexin A4	I
HDAC10	1	0	0	0	0	1	histone deacetylase 10	I
TPI1	1	0	0	0	0	1	triosephosphate isomerase 1	I
ZNF737	0	0	1	0	0	1	zinc finger protein 737	I
POU5F1B	0	1	0	0	0	1	POU class 5 homeobox 1B	I
CD109	0	0	0	1	0	1	CD109 molecule	I
SH3YL1	1	0	0	0	0	1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	I
ACOT13	1	0	0	0	0	1	acyl-CoA thioesterase 13	I
NOS3	0	0	0	0	1	1	nitric oxide synthase 3 (endothelial cell)	I
RPAIN	1	0	0	0	0	1	RPA interacting protein	I
IGF2BP1	0	0	0	1	0	1	insulin-like growth factor 2 mRNA binding protein 1	I
FCHO1	1	0	0	0	0	1	FCH domain only 1	I
RGL3	0	0	1	0	0	1	ral guanine nucleotide dissociation stimulator-like 3	I
FXN	1	0	0	0	0	1	frataxin	I
PPP2R5C	1	0	0	0	0	1	protein phosphatase 2, regulatory subunit B', gamma	I
LOC100128542	1	0	0	0	0	1	hypothetical protein LOC100128542	I
PLK1S1	1	0	0	0	0	1	polo-like kinase 1 substrate 1	I
TBCK	1	0	0	0	0	1	TBC1 domain containing kinase	I
MYO19	1	0	0	0	0	1	myosin XIX	I
COPS7A	1	0	0	0	0	1	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	I
MOV10L1	0	0	0	1	0	1	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	I
DHX16	1	0	0	0	0	1	DEAH (Asp-Glu-Ala-His) box polypeptide 16	I
ZNF415	0	0	1	0	0	1	zinc finger protein 415	I
FLNB	0	0	0	1	0	1	filamin B, beta	I
ZBTB20	1	0	0	0	0	1	zinc finger and BTB domain containing 20	I
THAP4	1	0	0	0	0	1	THAP domain containing 4	I
ARHGAP40	0	0	1	0	0	1	Rho GTPase activating protein 40	I

C6orf132	0	1	0	0	0	1	chromosome 6 open reading frame 132	I
EIF2C2	1	0	0	0	0	1	eukaryotic translation initiation factor 2C, 2	I
RGS9	0	0	1	0	0	1	regulator of G-protein signaling 9	I
STRADA	1	0	0	0	0	1	STE20-related kinase adaptor alpha	I
TADA2A	1	0	0	0	0	1	transcriptional adaptor 2A	I
FHIT	1	0	0	0	0	1	fragile histidine triad gene	I
EHHADH	1	0	0	0	0	1	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	I
HDAC8	1	0	0	0	0	1	histone deacetylase 8	I
MPP1	1	0	0	0	0	1	membrane protein, palmitoylated 1, 55kDa	I
ADH7	1	0	0	0	0	1	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	I
UPK3A	0	0	1	0	0	1	uroplakin 3A	I
VARS2	1	0	0	0	0	1	valyl-tRNA synthetase 2, mitochondrial (putative)	I
NAV1	1	0	0	0	0	1	neuron navigator 1	I
LHPP	1	0	0	0	0	1	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	I
C3orf26	1	0	0	0	0	1	chromosome 3 open reading frame 26	I
ALS2CR11	1	0	0	0	0	1	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	I
KLHL13	0	0	0	1	0	1	kelch-like 13 (Drosophila)	I
BEX2	1	0	0	0	0	1	brain expressed X-linked 2	I
IFT46	1	0	0	0	0	1	intraflagellar transport 46 homolog (Chlamydomonas)	I
SCO2	1	0	0	0	0	1	SCO cytochrome oxidase deficient homolog 2 (yeast)	I
SRPK3	0	1	0	0	0	1	SRSF protein kinase 3	I
ZFAND1	1	0	0	0	0	1	zinc finger, AN1-type domain 1	I
SMG6	1	0	0	0	0	1	smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	I
UBXN6	1	0	0	0	0	1	UBX domain protein 6	I
STRBP	1	0	0	0	0	1	spermatid perinuclear RNA binding protein	I
CAMTA2	1	0	0	0	0	1	calmodulin binding transcription activator 2	I
NOSTRIN	0	0	1	0	0	1	nitric oxide synthase trafficker	I

OAT	1	0	0	0	0	1	ornithine aminotransferase	I
PLS3	0	0	0	1	0	1	plastin 3	I
ZNF559-ZNF177	1	0	0	0	0	1	ZNF559-ZNF177 readthrough	I
ZNF177	1	0	0	0	0	1	zinc finger protein 177	I
ZNF764	0	0	1	0	0	1	zinc finger protein 764	I
PGM1	1	0	0	0	0	1	phosphoglucomutase 1	I
ZNF300	0	0	1	0	0	1	zinc finger protein 300	I
TFCP2	1	0	0	0	0	1	transcription factor CP2	I
OSBPL10	1	0	0	0	0	1	oxysterol binding protein-like 10	I
NLRP2	1	0	0	0	0	1	NLR family, pyrin domain containing 2	I
SGK494	0	0	1	0	0	1	uncharacterized serine/threonine-protein kinase SgK494	I
DMXL2	1	0	0	0	0	1	Dmx-like 2	I
SH2D4A	0	0	1	0	0	1	SH2 domain containing 4A	I
ARL1	1	0	0	0	0	1	ADP-ribosylation factor-like 1	I
ABI1	1	0	0	0	0	1	abl-interactor 1	I
GYG2	1	0	0	0	0	1	glycogenin 2	I
HADH	1	0	0	0	0	1	hydroxyacyl-CoA dehydrogenase	I
CXorf57	0	0	1	0	0	1	chromosome X open reading frame 57	I
KLHDC4	1	0	0	0	0	1	kelch domain containing 4	I
FLAD1	1	0	0	0	0	1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	I
EPB41L5	1	0	0	0	0	1	erythrocyte membrane protein band 4.1 like 5	I
FAM219A	1	0	0	0	0	1	family with sequence similarity 219, member A	I
SH3KBP1	1	0	0	0	0	1	SH3-domain kinase binding protein 1	I
UQCC	1	0	0	0	0	1	ubiquinol-cytochrome c reductase complex chaperone	I
NDUFS5	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)	I
MYNN	1	0	0	0	0	1	myoneurin	I
IP6K2	0	0	1	0	0	1	inositol hexakisphosphate kinase 2	I

DGCR8	1	0	0	0	0	1	DiGeorge syndrome critical region gene 8	I
RPH3AL	1	0	0	0	0	1	rabphilin 3A-like (without C2 domains)	I
MTRNR2L2	1	0	0	0	0	1	MT-RNR2-like 2	I
ZNF317	1	0	0	0	0	1	zinc finger protein 317	I
PLEKHA5	1	0	0	0	0	1	pleckstrin homology domain containing, family A member 5	I
MRPS35	0	1	0	0	0	1	mitochondrial ribosomal protein S35	I
BCL2L1	1	0	0	0	0	1	BCL2-like 1	I
C7orf10	0	0	0	0	1	1	chromosome 7 open reading frame 10	I
ALDH8A1	1	0	0	0	0	1	aldehyde dehydrogenase 8 family, member A1	I
GRHL3	0	0	1	0	0	1	grainyhead-like 3 (Drosophila)	I
DDIT3	0	0	0	0	1	1	DNA-damage-inducible transcript 3	I
GSR	1	0	0	0	0	1	glutathione reductase	I
ZNF783	1	0	0	0	0	1	zinc finger family member 783	I
TLX1	0	1	0	0	0	1	T-cell leukemia homeobox 1	I
VAPB	1	0	0	0	0	1	VAMP (vesicle-associated membrane protein)-associated protein B and C	I
CHPF	1	0	0	0	0	1	chondroitin polymerizing factor	I
SCHIP1	1	0	0	0	0	1	schwannomin interacting protein 1	I
IQCJ-SCHIP1	1	0	0	0	0	1	IQCJ-SCHIP1 readthrough	I
DNAJC27	0	0	1	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 27	I
MAP7	1	0	0	0	0	1	microtubule-associated protein 7	I
CUL2	1	0	0	0	0	1	cullin 2	I
ASCC1	1	0	0	0	0	1	activating signal cointegrator 1 complex subunit 1	I
NFATC4	1	0	0	0	0	1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	I
CYP4F3	1	0	0	0	0	1	cytochrome P450, family 4, subfamily F, polypeptide 3	I
UIMC1	1	0	0	0	0	1	ubiquitin interaction motif containing 1	I
MUTED	0	0	0	1	0	1	muted homolog (mouse)	I

RPL17-C18ORF32	0	1	0	0	0	1	RPL17-C18orf32 readthrough	I
RNF145	1	0	0	0	0	1	ring finger protein 145	I
LETM2	0	0	1	0	0	1	leucine zipper-EF-hand containing transmembrane protein 2	I
MTHFS	1	0	0	0	0	1	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	I
ST20-MTHFS	1	0	0	0	0	1	ST20-MTHFS readthrough	I
MDP1	1	0	0	0	0	1	magnesium-dependent phosphatase 1	I
NEDD8-MDP1	1	0	0	0	0	1	NEDD8-MDP1 readthrough	I
HORMAD1	0	1	0	0	0	1	HORMA domain containing 1	I
DAP3	1	0	0	0	0	1	death associated protein 3	I
RASD1	0	0	0	0	1	1	RAS, dexamethasone-induced 1	I
NPL	1	0	0	0	0	1	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	I
HMGN3	1	0	0	0	0	1	high mobility group nucleosomal binding domain 3	I
C18orf21	0	0	1	0	0	1	chromosome 18 open reading frame 21	I
NUBPL	1	0	0	0	0	1	nucleotide binding protein-like	I
NR4A1	1	0	0	0	0	1	nuclear receptor subfamily 4, group A, member 1	I
WBSCR22	1	0	0	0	0	1	Williams Beuren syndrome chromosome region 22	I
SRP19	1	0	0	0	0	1	signal recognition particle 19kDa	I
CDRT4	1	0	0	0	0	1	CMT1A duplicated region transcript 4	I
DGKH	0	0	1	0	0	1	diacylglycerol kinase, eta	I
SSR4	1	0	0	0	0	1	signal sequence receptor, delta (translocon-associated protein delta)	I
URGCP-MRPS24	1	0	0	0	0	1	URGCP-MRPS24 readthrough	I
GK	0	1	0	0	0	1	glycerol kinase	I
MDM1	1	0	0	0	0	1	Mdm1 nuclear protein homolog (mouse)	I
RAD54B	0	1	0	0	0	1	RAD54 homolog B (S. cerevisiae)	I

KRBOX1	0	0	1	0	0	1	KRAB box domain containing 1	I
EHF	1	0	0	0	0	1	ets homologous factor	I
PLA2G4E	1	0	0	0	0	1	phospholipase A2, group IVE	I
ATF7	1	0	0	0	0	1	activating transcription factor 7	I
ITGB3BP	1	0	0	0	0	1	integrin beta 3 binding protein (beta3-endonexin)	I
ARID4B	1	0	0	0	0	1	AT rich interactive domain 4B (RBP1-like)	I
KAT5	1	0	0	0	0	1	K(lysine) acetyltransferase 5	I
CA9	1	0	0	0	0	1	carbonic anhydrase IX	I
CASP1	1	0	0	0	0	1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	I
CASQ1	0	0	1	0	0	1	calsequestrin 1 (fast-twitch, skeletal muscle)	I
CCNE1	0	0	1	0	0	1	cyclin E1	I
MAP3K13	1	0	0	0	0	1	mitogen-activated protein kinase kinase kinase 13	I
LHX6	0	0	0	0	1	1	LIM homeobox 6	I
PFKP	0	0	0	1	0	1	phosphofructokinase, platelet	I
MAGED4B	1	0	0	0	0	1	melanoma antigen family D, 4B	I
PPP1R1B	1	0	0	0	0	1	protein phosphatase 1, regulatory (inhibitor) subunit 1B	I
LOC100130357	1	0	0	0	0	1	hypothetical LOC100130357	I
ARHGEF38	0	1	0	0	0	1	Rho guanine nucleotide exchange factor (GEF) 38	I
PRMT2	1	0	0	0	0	1	protein arginine methyltransferase 2	I
DDC	0	1	0	0	0	1	dopa decarboxylase (aromatic L-amino acid decarboxylase)	I
ASCC2	1	0	0	0	0	1	activating signal cointegrator 1 complex subunit 2	I
ANKS3	0	0	1	0	0	1	ankyrin repeat and sterile alpha motif domain containing 3	I
PDE8A	1	0	0	0	0	1	phosphodiesterase 8A	I
PIM1	1	0	0	0	0	1	pim-1 oncogene	I
NPRL3	1	0	0	0	0	1	nitrogen permease regulator-like 3 (S. cerevisiae)	I
NARS2	0	1	0	0	0	1	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	I
STK36	0	0	1	0	0	1	serine/threonine kinase 36	I

CDX2	0	1	0	0	0	1	caudal type homeobox 2	I
CHKA	1	0	0	0	0	1	choline kinase alpha	I
TBCB	1	0	0	0	0	1	tubulin folding cofactor B	I
CLIC2	1	0	0	0	0	1	chloride intracellular channel 2	I
CLNS1A	1	0	0	0	0	1	chloride channel, nucleotide-sensitive, 1A	I
CSTF2	1	0	0	0	0	1	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	I
DBP	1	0	0	0	0	1	D site of albumin promoter (albumin D-box) binding protein	I
DECR1	1	0	0	0	0	1	2,4-dienoyl CoA reductase 1, mitochondrial	I
DNASE2	1	0	0	0	0	1	deoxyribonuclease II, lysosomal	I
DRG2	1	0	0	0	0	1	developmentally regulated GTP binding protein 2	I
DUSP4	0	0	0	0	1	1	dual specificity phosphatase 4	I
ECH1	1	0	0	0	0	1	enoyl CoA hydratase 1, peroxisomal	I
EP300	1	0	0	0	0	1	E1A binding protein p300	I
ERN1	1	0	0	0	0	1	endoplasmic reticulum to nucleus signaling 1	I
FBL	1	0	0	0	0	1	fibrillarin	I
EXTL3	1	0	0	0	0	1	exostoses (multiple)-like 3	I
FABP1	0	1	0	0	0	1	fatty acid binding protein 1, liver	I
FOXC1	0	0	0	0	1	1	forkhead box C1	I
GATM	0	0	0	0	1	1	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	I
GCNT2	1	0	0	0	0	1	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	I
GMDS	1	0	0	0	0	1	GDP-mannose 4,6-dehydratase	I
GTF2H4	1	0	0	0	0	1	general transcription factor IIH, polypeptide 4, 52kDa	I
GTF3C2	1	0	0	0	0	1	general transcription factor IIIC, polypeptide 2, beta 110kDa	I
HSPB1	0	0	0	0	1	1	heat shock 27kDa protein 1	I
ID4	0	0	1	0	0	1	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	I
AARS	1	0	0	0	0	1	alanyl-tRNA synthetase	I
ABCA2	1	0	0	0	0	1	ATP-binding cassette, sub-family A (ABC1), member 2	I

ACAA1	1	0	0	0	0	1	acetyl-CoA acyltransferase 1	I
ACADL	1	0	0	0	0	1	acyl-CoA dehydrogenase, long chain	I
ACADSB	1	0	0	0	0	1	acyl-CoA dehydrogenase, short/branched chain	I
ACTA2	0	0	0	0	1	1	actin, alpha 2, smooth muscle, aorta	I
ACTG2	1	0	0	0	0	1	actin, gamma 2, smooth muscle, enteric	I
AMPH	0	0	0	1	0	1	amphiphysin	I
ARF5	1	0	0	0	0	1	ADP-ribosylation factor 5	I
ARSD	1	0	0	0	0	1	arylsulfatase D	I
ATP5O	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	I
BAAT	1	0	0	0	0	1	bile acid CoA: amino acid N-acyltransferase (glycine N-choloyltransferase)	I
BCL7B	1	0	0	0	0	1	B-cell CLL/lymphoma 7B	I
BPGM	0	0	1	0	0	1	2,3-bisphosphoglycerate mutase	I
CAMK4	0	0	1	0	0	1	calcium/calmodulin-dependent protein kinase IV	I
CDC25A	0	1	0	0	0	1	cell division cycle 25 homolog A (S. pombe)	I
CKB	0	1	0	0	0	1	creatine kinase, brain	I
CKS1B	0	1	0	0	0	1	CDC28 protein kinase regulatory subunit 1B	I
CTPS	1	0	0	0	0	1	CTP synthase	I
CYB5A	1	0	0	0	0	1	cytochrome b5 type A (microsomal)	I
CYC1	1	0	0	0	0	1	cytochrome c-1	I
DCTD	1	0	0	0	0	1	dCMP deaminase	I
DUSP7	1	0	0	0	0	1	dual specificity phosphatase 7	I
TYMP	1	0	0	0	0	1	thymidine phosphorylase	I
EGR1	1	0	0	0	0	1	early growth response 1	I
EIF4E	1	0	0	0	0	1	eukaryotic translation initiation factor 4E	I
ENO2	1	0	0	0	0	1	enolase 2 (gamma, neuronal)	I
ETV4	0	1	0	0	0	1	ets variant 4	I
FAU	1	0	0	0	0	1	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed	I

FKBP4	0	0	0	0	1	1	FK506 binding protein 4, 59kDa	I
GALK2	1	0	0	0	0	1	galactokinase 2	I
GFPT1	1	0	0	0	0	1	glutamine--fructose-6-phosphate transaminase 1	I
GOLGA1	1	0	0	0	0	1	golgin A1	I
H2AFZ	0	0	0	0	1	1	H2A histone family, member Z	I
HDC	1	0	0	0	0	1	histidine decarboxylase	I
HLF	1	0	0	0	0	1	hepatic leukemia factor	I
HOXB2	0	0	0	0	1	1	homeobox B2	I
HOXB5	0	0	1	0	0	1	homeobox B5	I
ID2	0	0	0	0	1	1	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	I
ID3	0	0	0	0	1	1	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	I
IDH2	1	0	0	0	0	1	isocitrate dehydrogenase 2 (NADP+), mitochondrial	I
EIF6	1	0	0	0	0	1	eukaryotic translation initiation factor 6	I
JUN	0	0	0	0	1	1	jun proto-oncogene	I
JUNB	1	0	0	0	0	1	jun B proto-oncogene	I
KIF3C	1	0	0	0	0	1	kinesin family member 3C	I
KPNA1	1	0	0	0	0	1	karyopherin alpha 1 (importin alpha 5)	I
KPNA2	0	0	0	1	0	1	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	I
IPO5	0	0	0	1	0	1	importin 5	I
KRT4	1	0	0	0	0	1	keratin 4	I
KRT8	1	0	0	0	0	1	keratin 8	I
KRT19	1	0	0	0	0	1	keratin 19	I
LIMK1	1	0	0	0	0	1	LIM domain kinase 1	I
LRCH4	1	0	0	0	0	1	leucine-rich repeats and calponin homology (CH) domain containing 4	I
MAD2L1	0	1	0	0	0	1	MAD2 mitotic arrest deficient-like 1 (yeast)	I
ME1	1	0	0	0	0	1	malic enzyme 1, NADP(+)-dependent, cytosolic	I
MGMT	1	0	0	0	0	1	O-6-methylguanine-DNA methyltransferase	I
MGST2	0	0	1	0	0	1	microsomal glutathione S-transferase 2	I

MPI	1	0	0	0	0	1	mannose phosphate isomerase	I
MSX1	0	0	0	0	1	1	msh homeobox 1	I
MSX2	0	0	1	0	0	1	msh homeobox 2	I
MYBL2	0	0	0	1	0	1	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	I
NDUFA2	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa	I
NDUFA6	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	I
NFIX	1	0	0	0	0	1	nuclear factor I/X (CCAAT-binding transcription factor)	I
NPAS2	0	0	0	1	0	1	neuronal PAS domain protein 2	I
NPTX2	0	0	0	0	1	1	neuronal pentraxin II	I
TBC1D25	1	0	0	0	0	1	TBC1 domain family, member 25	I
PDE6D	1	0	0	0	0	1	phosphodiesterase 6D, cGMP-specific, rod, delta	I
PDE7A	1	0	0	0	0	1	phosphodiesterase 7A	I
PDK1	1	0	0	0	0	1	pyruvate dehydrogenase kinase, isozyme 1	I
PHB	1	0	0	0	0	1	prohibitin	I
PLAGL2	0	1	0	0	0	1	pleiomorphic adenoma gene-like 2	I
POLB	0	0	1	0	0	1	polymerase (DNA directed), beta	I
POLR2G	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide G	I
PPL	1	0	0	0	0	1	periplakin	I
PPP1R8	1	0	0	0	0	1	protein phosphatase 1, regulatory (inhibitor) subunit 8	I
PRKCB	1	0	0	0	0	1	protein kinase C, beta	I
MAPK11	0	0	0	0	1	1	mitogen-activated protein kinase 11	I
MAP2K3	1	0	0	0	0	1	mitogen-activated protein kinase kinase 3	I
PROX1	1	0	0	0	0	1	prospero homeobox 1	I
PSMA3	1	0	0	0	0	1	proteasome (prosome, macropain) subunit, alpha type, 3	I
PSMA6	1	0	0	0	0	1	proteasome (prosome, macropain) subunit, alpha type, 6	I
PSMB6	1	0	0	0	0	1	proteasome (prosome, macropain) subunit, beta type, 6	I
PSMB9	1	0	0	0	0	1	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	I

PSMC3	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, ATPase, 3	I
PSMD3	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	I
PSMD7	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	I
PSMD8	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	I
PSME2	1	0	0	0	0	1	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	I
TWF1	1	0	0	0	0	1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	I
PTMS	1	0	0	0	0	1	parathymosin	I
PVALB	0	0	1	0	0	1	parvalbumin	I
RAB3B	0	0	0	1	0	1	RAB3B, member RAS oncogene family	I
RAB13	1	0	0	0	0	1	RAB13, member RAS oncogene family	I
RANBP1	1	0	0	0	0	1	RAN binding protein 1	I
RAP1GAP	1	0	0	0	0	1	RAP1 GTPase activating protein	I
RARS	1	0	0	0	0	1	arginyl-tRNA synthetase	I
RBL1	1	0	0	0	0	1	retinoblastoma-like 1 (p107)	I
UPF1	1	0	0	0	0	1	UPF1 regulator of nonsense transcripts homolog (yeast)	I
RGS1	1	0	0	0	0	1	regulator of G-protein signaling 1	I
RPA3	0	1	0	0	0	1	replication protein A3, 14kDa	I
MRPL12	1	0	0	0	0	1	mitochondrial ribosomal protein L12	I
MAPK12	0	0	0	0	1	1	mitogen-activated protein kinase 12	I
SAT1	0	0	1	0	0	1	spermidine/spermine N1-acetyltransferase 1	I
SET	1	0	0	0	0	1	SET nuclear oncogene	I
SRSF2	0	0	0	0	1	1	serine/arginine-rich splicing factor 2	I
SMARCC1	1	0	0	0	0	1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	I
SNCG	0	0	0	0	1	1	synuclein, gamma (breast cancer-specific protein 1)	I
SNRPF	1	0	0	0	0	1	small nuclear ribonucleoprotein polypeptide F	I
SOX4	1	0	0	0	0	1	SRY (sex determining region Y)-box 4	I
SPR	1	0	0	0	0	1	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)	I

SPRR1B	1	0	0	0	0	1	small proline-rich protein 1B	I
SRF	1	0	0	0	0	1	serum response factor (c-fos serum response element-binding transcription factor)	I
SRP54	1	0	0	0	0	1	signal recognition particle 54kDa	I
SSB	1	0	0	0	0	1	Sjogren syndrome antigen B (autoantigen La)	I
SSRP1	1	0	0	0	0	1	structure specific recognition protein 1	I
STAC	1	0	0	0	0	1	SH3 and cysteine rich domain	I
STAT5A	1	0	0	0	0	1	signal transducer and activator of transcription 5A	I
SUPV3L1	1	0	0	0	0	1	suppressor of var1, 3-like 1 (S. cerevisiae)	I
SURF1	1	0	0	0	0	1	surfeit 1	I
TBCC	1	0	0	0	0	1	tubulin folding cofactor C	I
TCEA2	1	0	0	0	0	1	transcription elongation factor A (SII), 2	I
TFAM	1	0	0	0	0	1	transcription factor A, mitochondrial	I
TDG	1	0	0	0	0	1	thymine-DNA glycosylase	I
TEAD3	1	0	0	0	0	1	TEA domain family member 3	I
TFAP2A	0	0	1	0	0	1	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	I
TFAP2C	1	0	0	0	0	1	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	I
TM7SF2	0	0	1	0	0	1	transmembrane 7 superfamily member 2	I
TNNC2	0	1	0	0	0	1	troponin C type 2 (fast)	I
TNNC1	0	0	1	0	0	1	troponin C type 1 (slow)	I
TRIP6	1	0	0	0	0	1	thyroid hormone receptor interactor 6	I
TST	1	0	0	0	0	1	thiosulfate sulfurtransferase (rhodanese)	I
TTK	0	0	0	1	0	1	TTK protein kinase	I
UCP2	1	0	0	0	0	1	uncoupling protein 2 (mitochondrial, proton carrier)	I
UPP1	1	0	0	0	0	1	uridine phosphorylase 1	I
UQCRC1	1	0	0	0	0	1	ubiquinol-cytochrome c reductase core protein I	I
VBP1	1	0	0	0	0	1	von Hippel-Lindau binding protein 1	I

VSNL1	0	0	1	0	0	1	visinin-like 1	I
CLIP2	1	0	0	0	0	1	CAP-GLY domain containing linker protein 2	I
ZNF267	1	0	0	0	0	1	zinc finger protein 267	I
ZNF35	1	0	0	0	0	1	zinc finger protein 35	I
ZNF74	1	0	0	0	0	1	zinc finger protein 74	I
ZNF76	1	0	0	0	0	1	zinc finger protein 76	I
ZNF131	1	0	0	0	0	1	zinc finger protein 131	I
ZNF134	0	0	1	0	0	1	zinc finger protein 134	I
ZNF155	1	0	0	0	0	1	zinc finger protein 155	I
DNALI1	1	0	0	0	0	1	dynein, axonemal, light intermediate chain 1	I
PTP4A1	1	0	0	0	0	1	protein tyrosine phosphatase type IVA, member 1	I
STAM	1	0	0	0	0	1	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	I
HMGA2	0	1	0	0	0	1	high mobility group AT-hook 2	I
AKAP1	1	0	0	0	0	1	A kinase (PRKA) anchor protein 1	I
NAA10	1	0	0	0	0	1	N(alpha)-acetyltransferase 10, NatA catalytic subunit	I
HIST1H2AM	0	0	1	0	0	1	histone cluster 1, H2am	I
HIST2H2AC	0	0	0	0	1	1	histone cluster 2, H2ac	I
HIST1H2BC	0	0	1	0	0	1	histone cluster 1, H2bc	I
HIST1H3A	0	0	1	0	0	1	histone cluster 1, H3a	I
HIST1H3J	0	0	1	0	0	1	histone cluster 1, H3j	I
HIST1H3H	1	0	0	0	0	1	histone cluster 1, H3h	I
HIST1H4K	1	0	0	0	0	1	histone cluster 1, H4k	I
HIST1H4H	1	0	0	0	0	1	histone cluster 1, H4h	I
HIST1H4E	1	0	0	0	0	1	histone cluster 1, H4e	I
OFD1	1	0	0	0	0	1	oral-facial-digital syndrome 1	I
PPFIBP2	0	0	1	0	0	1	PTPRF interacting protein, binding protein 2 (liprin beta 2)	I
ENC1	1	0	0	0	0	1	ectodermal-neural cortex 1 (with BTB-like domain)	I

NDST2	1	0	0	0	0	1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	I
CHST1	0	0	0	0	1	1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	I
CBX4	0	0	0	0	1	1	chromobox homolog 4	I
BLZF1	1	0	0	0	0	1	basic leucine zipper nuclear factor 1	I
YARS	1	0	0	0	0	1	tyrosyl-tRNA synthetase	I
RRP1	1	0	0	0	0	1	ribosomal RNA processing 1 homolog (S. cerevisiae)	I
PDLIM4	1	0	0	0	0	1	PDZ and LIM domain 4	I
NOP14	1	0	0	0	0	1	NOP14 nucleolar protein homolog (yeast)	I
SLC25A12	1	0	0	0	0	1	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	I
PLA2G4C	1	0	0	0	0	1	phospholipase A2, group IVC (cytosolic, calcium-independent)	I
SSNA1	1	0	0	0	0	1	Sjogren syndrome nuclear autoantigen 1	I
OASL	0	0	1	0	0	1	2'-5'-oligoadenylate synthetase-like	I
AKR1C3	0	0	0	0	1	1	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	I
EIF3B	1	0	0	0	0	1	eukaryotic translation initiation factor 3, subunit B	I
B3GALT4	1	0	0	0	0	1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	I
RIPK2	1	0	0	0	0	1	receptor-interacting serine-threonine kinase 2	I
DYRK4	1	0	0	0	0	1	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	I
PEX11B	1	0	0	0	0	1	peroxisomal biogenesis factor 11 beta	I
PEX11A	1	0	0	0	0	1	peroxisomal biogenesis factor 11 alpha	I
DPM1	0	1	0	0	0	1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	I
SAP30	1	0	0	0	0	1	Sin3A-associated protein, 30kDa	I
GMPS	1	0	0	0	0	1	guanine monphosphate synthetase	I
TMEM11	1	0	0	0	0	1	transmembrane protein 11	I
HDAC3	1	0	0	0	0	1	histone deacetylase 3	I
CDK5R1	1	0	0	0	0	1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	I
SYNJ2	0	0	0	1	0	1	synaptojanin 2	I
EIF2S2	1	0	0	0	0	1	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	I

CCNA1	1	0	0	0	0	1	cyclin A1	I
AP1G2	1	0	0	0	0	1	adaptor-related protein complex 1, gamma 2 subunit	I
FUBP3	1	0	0	0	0	1	far upstream element (FUSE) binding protein 3	I
UBE2M	1	0	0	0	0	1	ubiquitin-conjugating enzyme E2M	I
PRC1	0	0	0	1	0	1	protein regulator of cytokinesis 1	I
CLK2	1	0	0	0	0	1	CDC-like kinase 2	I
IRF7	0	0	0	0	1	1	interferon regulatory factor 7	I
RHOB	0	0	0	0	1	1	ras homolog gene family, member B	I
CS	1	0	0	0	0	1	citrate synthase	I
EIF2S1	1	0	0	0	0	1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	I
FASN	1	0	0	0	0	1	fatty acid synthase	I
LLGL1	1	0	0	0	0	1	lethal giant larvae homolog 1 (Drosophila)	I
NDUFB7	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa	I
DRG1	1	0	0	0	0	1	developmentally regulated GTP binding protein 1	I
UXT	1	0	0	0	0	1	ubiquitously-expressed transcript	I
GBF1	1	0	0	0	0	1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	I
FIBP	1	0	0	0	0	1	fibroblast growth factor (acidic) intracellular binding protein	I
AURKB	1	0	0	0	0	1	aurora kinase B	I
PTTG1	1	0	0	0	0	1	pituitary tumor-transforming 1	I
CYTH2	0	0	1	0	0	1	cytohesin 2	I
SOCS6	1	0	0	0	0	1	suppressor of cytokine signaling 6	I
COPS2	1	0	0	0	0	1	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	I
FADS2	1	0	0	0	0	1	fatty acid desaturase 2	I
MED17	1	0	0	0	0	1	mediator complex subunit 17	I
MED7	1	0	0	0	0	1	mediator complex subunit 7	I
PIGL	1	0	0	0	0	1	phosphatidylinositol glycan anchor biosynthesis, class L	I
EEF1E1	0	0	0	1	0	1	eukaryotic translation elongation factor 1 epsilon 1	I

RAB3D	1	0	0	0	0	1	RAB3D, member RAS oncogene family	I
NFE2L3	1	0	0	0	0	1	nuclear factor (erythroid-derived 2)-like 3	I
RIN1	1	0	0	0	0	1	Ras and Rab interactor 1	I
ARL3	1	0	0	0	0	1	ADP-ribosylation factor-like 3	I
KIF1A	1	0	0	0	0	1	kinesin family member 1A	I
BPHL	1	0	0	0	0	1	biphenyl hydrolase-like (serine hydrolase)	I
BRAF	1	0	0	0	0	1	v-raf murine sarcoma viral oncogene homolog B1	I
BUB1	0	0	0	1	0	1	budding uninhibited by benzimidazoles 1 homolog (yeast)	I
CETN2	1	0	0	0	0	1	centrin, EF-hand protein, 2	I
CASP3	1	0	0	0	0	1	caspase 3, apoptosis-related cysteine peptidase	I
CDC34	1	0	0	0	0	1	cell division cycle 34 homolog (S. cerevisiae)	I
CETN3	1	0	0	0	0	1	centrin, EF-hand protein, 3	I
DDX11	1	0	0	0	0	1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	I
DLX2	0	0	0	0	1	1	distal-less homeobox 2	I
DUSP2	0	0	0	0	1	1	dual specificity phosphatase 2	I
DUSP5	0	0	0	0	1	1	dual specificity phosphatase 5	I
ERH	1	0	0	0	0	1	enhancer of rudimentary homolog (Drosophila)	I
ACSL4	1	0	0	0	0	1	acyl-CoA synthetase long-chain family member 4	I
FARSA	1	0	0	0	0	1	phenylalanyl-tRNA synthetase, alpha subunit	I
GPS2	1	0	0	0	0	1	G protein pathway suppressor 2	I
ARHGAP35	1	0	0	0	0	1	Rho GTPase activating protein 35	I
IDI1	1	0	0	0	0	1	isopentenyl-diphosphate delta isomerase 1	I
FOXK2	1	0	0	0	0	1	forkhead box K2	I
ILF2	1	0	0	0	0	1	interleukin enhancer binding factor 2, 45kDa	I
MCM2	1	0	0	0	0	1	minichromosome maintenance complex component 2	I
MYT1	0	0	1	0	0	1	myelin transcription factor 1	I
NDUFA1	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	I
NDUFA3	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa	I

NDUFB2	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	I
NDUFB10	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	I
NDUFS3	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)	I
NDUFS6	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	I
SCO1	1	0	0	0	0	1	SCO cytochrome oxidase deficient homolog 1 (yeast)	I
TBCA	1	0	0	0	0	1	tubulin folding cofactor A	I
TOP3A	1	0	0	0	0	1	topoisomerase (DNA) III alpha	I
CDK2AP1	0	0	1	0	0	1	cyclin-dependent kinase 2 associated protein 1	I
AXIN2	0	1	0	0	0	1	axin 2	I
CLIC3	1	0	0	0	0	1	chloride intracellular channel 3	I
ASH2L	1	0	0	0	0	1	ash2 (absent, small, or homeotic)-like (Drosophila)	I
MTMR4	1	0	0	0	0	1	myotubularin related protein 4	I
NMI	1	0	0	0	0	1	N-myc (and STAT) interactor	I
PRPF4	1	0	0	0	0	1	PRP4 pre-mRNA processing factor 4 homolog (yeast)	I
FAM50A	1	0	0	0	0	1	family with sequence similarity 50, member A	I
CCNB2	0	1	0	0	0	1	cyclin B2	I
PDCD5	1	0	0	0	0	1	programmed cell death 5	I
NEMF	1	0	0	0	0	1	nuclear export mediator factor	I
DGKI	1	0	0	0	0	1	diacylglycerol kinase, iota	I
COX7A2L	1	0	0	0	0	1	cytochrome c oxidase subunit VIIa polypeptide 2 like	I
ZW10	0	1	0	0	0	1	ZW10, kinetochore associated, homolog (Drosophila)	I
DLG5	0	0	1	0	0	1	discs, large homolog 5 (Drosophila)	I
TBRG4	1	0	0	0	0	1	transforming growth factor beta regulator 4	I
ZNHIT3	0	1	0	0	0	1	zinc finger, HIT-type containing 3	I
TXNL1	1	0	0	0	0	1	thioredoxin-like 1	I
LONP1	1	0	0	0	0	1	lon peptidase 1, mitochondrial	I
NMT2	0	0	0	1	0	1	N-myristoyltransferase 2	I

AIM2	0	0	1	0	0	1	absent in melanoma 2	I
EIF4E2	1	0	0	0	0	1	eukaryotic translation initiation factor 4E family member 2	I
ATG5	1	0	0	0	0	1	ATG5 autophagy related 5 homolog (S. cerevisiae)	I
ROCK2	1	0	0	0	0	1	Rho-associated, coiled-coil containing protein kinase 2	I
FXR2	1	0	0	0	0	1	fragile X mental retardation, autosomal homolog 2	I
TP53I3	1	0	0	0	0	1	tumor protein p53 inducible protein 3	I
CIR1	1	0	0	0	0	1	corepressor interacting with RBPJ, 1	I
C14orf2	1	0	0	0	0	1	chromosome 14 open reading frame 2	I
IER2	0	0	0	0	1	1	immediate early response 2	I
CSAG2	1	0	0	0	0	1	CSAG family, member 2	I
C16orf7	1	0	0	0	0	1	chromosome 16 open reading frame 7	I
CDK5	1	0	0	0	0	1	cyclin-dependent kinase 5	I
CDKN2B	1	0	0	0	0	1	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	I
DAPK1	0	0	1	0	0	1	death-associated protein kinase 1	I
DHX8	1	0	0	0	0	1	DEAH (Asp-Glu-Ala-His) box polypeptide 8	I
FPGS	1	0	0	0	0	1	folylpolyglutamate synthase	I
HDAC1	1	0	0	0	0	1	histone deacetylase 1	I
NDUFA7	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	I
NDUFAB1	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	I
NDUFB9	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	I
PIK3R2	1	0	0	0	0	1	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	I
RAD23A	1	0	0	0	0	1	RAD23 homolog A (S. cerevisiae)	I
SCD	0	1	0	0	0	1	stearoyl-CoA desaturase (delta-9-desaturase)	I
TLE3	1	0	0	0	0	1	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	I
TPD52	1	0	0	0	0	1	tumor protein D52	I
SLC27A4	1	0	0	0	0	1	solute carrier family 27 (fatty acid transporter), member 4	I
OXSR1	1	0	0	0	0	1	oxidative-stress responsive 1	I

GFPT2	1	0	0	0	0	1	glutamine-fructose-6-phosphate transaminase 2	I
USP10	1	0	0	0	0	1	ubiquitin specific peptidase 10	I
PPT2	0	0	0	0	1	1	palmitoyl-protein thioesterase 2	I
ABL2	0	0	0	1	0	1	v-abl Abelson murine leukemia viral oncogene homolog 2	I
ALDOC	0	1	0	0	0	1	aldolase C, fructose-bisphosphate	I
ASCL2	0	1	0	0	0	1	achaete-scute complex homolog 2 (Drosophila)	I
CEBPB	1	0	0	0	0	1	CCAAT/enhancer binding protein (C/EBP), beta	I
CRKL	1	0	0	0	0	1	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	I
CSTA	0	0	1	0	0	1	cystatin A (stefin A)	I
ELK1	1	0	0	0	0	1	ELK1, member of ETS oncogene family	I
NR2F6	1	0	0	0	0	1	nuclear receptor subfamily 2, group F, member 6	I
H1F0	1	0	0	0	0	1	H1 histone family, member 0	I
HIST1H1T	0	0	1	0	0	1	histone cluster 1, H1t	I
HBQ1	1	0	0	0	0	1	hemoglobin, theta 1	I
HSPA1A	1	0	0	0	0	1	heat shock 70kDa protein 1A	I
HSPA1B	1	0	0	0	0	1	heat shock 70kDa protein 1B	I
PDK3	0	0	1	0	0	1	pyruvate dehydrogenase kinase, isozyme 3	I
SULT1E1	0	0	0	1	0	1	sulfotransferase family 1E, estrogen-preferring, member 1	I
VAV1	1	0	0	0	0	1	vav 1 guanine nucleotide exchange factor	I
ARHGEF5	1	0	0	0	0	1	Rho guanine nucleotide exchange factor (GEF) 5	I
MLF2	1	0	0	0	0	1	myeloid leukemia factor 2	I
RASSF9	1	0	0	0	0	1	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	I
WDR46	1	0	0	0	0	1	WD repeat domain 46	I
MAFB	1	0	0	0	0	1	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	I
TROAP	1	0	0	0	0	1	trophinin associated protein (tastin)	I
TOM1L1	1	0	0	0	0	1	target of myb1 (chicken)-like 1	I
SH2D3A	0	0	1	0	0	1	SH2 domain containing 3A	I
RANBP9	1	0	0	0	0	1	RAN binding protein 9	I

AP1M2	1	0	0	0	0	1	adaptor-related protein complex 1, mu 2 subunit	I
SAE1	1	0	0	0	0	1	SUMO1 activating enzyme subunit 1	I
ABCA1	1	0	0	0	0	1	ATP-binding cassette, sub-family A (ABC1), member 1	I
BCAT1	1	0	0	0	0	1	branched chain amino-acid transaminase 1, cytosolic	I
DOM3Z	1	0	0	0	0	1	dom-3 homolog Z (C. elegans)	I
HOXA1	0	0	1	0	0	1	homeobox A1	I
IVL	0	0	1	0	0	1	involucrin	I
KRTAP5-9	0	0	1	0	0	1	keratin associated protein 5-9	I
KRT6B	1	0	0	0	0	1	keratin 6B	I
KRT7	0	0	1	0	0	1	keratin 7	I
LAD1	1	0	0	0	0	1	ladinin 1	I
ALDH6A1	1	0	0	0	0	1	aldehyde dehydrogenase 6 family, member A1	I
NHLH2	0	0	1	0	0	1	nescient helix loop helix 2	I
RGS4	0	0	0	1	0	1	regulator of G-protein signaling 4	I
RHEB	1	0	0	0	0	1	Ras homolog enriched in brain	I
ACSM3	1	0	0	0	0	1	acyl-CoA synthetase medium-chain family member 3	I
TAF13	1	0	0	0	0	1	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	I
TCF20	1	0	0	0	0	1	transcription factor 20 (AR1)	I
TDO2	0	1	0	0	0	1	tryptophan 2,3-dioxygenase	I
NR2F1	1	0	0	0	0	1	nuclear receptor subfamily 2, group F, member 1	I
WHSC2	1	0	0	0	0	1	Wolf-Hirschhorn syndrome candidate 2	I
TSSC4	1	0	0	0	0	1	tumor suppressing subtransferable candidate 4	I
ARPC3	1	0	0	0	0	1	actin related protein 2/3 complex, subunit 3, 21kDa	I
PPIF	1	0	0	0	0	1	peptidylprolyl isomerase F	I
KIF20A	0	0	0	1	0	1	kinesin family member 20A	I
ARL4C	1	0	0	0	0	1	ADP-ribosylation factor-like 4C	I
BCAP31	1	0	0	0	0	1	B-cell receptor-associated protein 31	I

TOB1	1	0	0	0	0	1	transducer of ERBB2, 1	I
LPCAT3	1	0	0	0	0	1	lysophosphatidylcholine acyltransferase 3	I
RCL1	1	0	0	0	0	1	RNA terminal phosphate cyclase-like 1	I
CNIH	1	0	0	0	0	1	cornichon homolog (Drosophila)	I
PSME3	1	0	0	0	0	1	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	I
NUTF2	1	0	0	0	0	1	nuclear transport factor 2	I
DDX39A	1	0	0	0	0	1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	I
SLC35B1	1	0	0	0	0	1	solute carrier family 35, member B1	I
MRPS31	1	0	0	0	0	1	mitochondrial ribosomal protein S31	I
HRSP12	0	1	0	0	0	1	heat-responsive protein 12	I
SPRY1	0	0	0	0	1	1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	I
CDK2AP2	0	0	0	0	1	1	cyclin-dependent kinase 2 associated protein 2	I
PRSS16	1	0	0	0	0	1	protease, serine, 16 (thymus)	I
BCAS2	1	0	0	0	0	1	breast carcinoma amplified sequence 2	I
SF3A1	1	0	0	0	0	1	splicing factor 3a, subunit 1, 120kDa	I
SMAD1	1	0	0	0	0	1	SMAD family member 1	I
MCM4	1	0	0	0	0	1	minichromosome maintenance complex component 4	I
MDH2	0	1	0	0	0	1	malate dehydrogenase 2, NAD (mitochondrial)	I
MIPEP	1	0	0	0	0	1	mitochondrial intermediate peptidase	I
FOXO4	1	0	0	0	0	1	forkhead box O4	I
MT1A	0	0	1	0	0	1	metallothionein 1A	I
PRCC	1	0	0	0	0	1	papillary renal cell carcinoma (translocation-associated)	I
PTK6	0	0	1	0	0	1	PTK6 protein tyrosine kinase 6	I
SKP2	0	1	0	0	0	1	S-phase kinase-associated protein 2 (p45)	I
SNAI1	0	0	0	0	1	1	snail homolog 1 (Drosophila)	I
SPRR2A	0	0	1	0	0	1	small proline-rich protein 2A	I
TBX3	0	0	1	0	0	1	T-box 3	I

VPS72	1	0	0	0	0	1	vacuolar protein sorting 72 homolog (S. cerevisiae)	I
SNAPC5	1	0	0	0	0	1	small nuclear RNA activating complex, polypeptide 5, 19kDa	I
SMYD5	1	0	0	0	0	1	SMYD family member 5	I
NOD1	1	0	0	0	0	1	nucleotide-binding oligomerization domain containing 1	I
PIAS3	0	0	1	0	0	1	protein inhibitor of activated STAT, 3	I
NDC80	0	0	0	1	0	1	NDC80 homolog, kinetochore complex component (S. cerevisiae)	I
PRICKLE3	1	0	0	0	0	1	prickle homolog 3 (Drosophila)	I
NEDD8	1	0	0	0	0	1	neural precursor cell expressed, developmentally down-regulated 8	I
NR4A2	0	0	0	0	1	1	nuclear receptor subfamily 4, group A, member 2	I
OAS3	0	0	1	0	0	1	2'-5'-oligoadenylate synthetase 3, 100kDa	I
PA2G4	1	0	0	0	0	1	proliferation-associated 2G4, 38kDa	I
PAX1	1	0	0	0	0	1	paired box 1	I
PCP4	1	0	0	0	0	1	Purkinje cell protein 4	I
PIN1	1	0	0	0	0	1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	I
POLD2	1	0	0	0	0	1	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	I
POLE	1	0	0	0	0	1	polymerase (DNA directed), epsilon	I
POLR2H	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide H	I
POLR2J	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	I
POU2AF1	1	0	0	0	0	1	POU class 2 associating factor 1	I
MOGS	1	0	0	0	0	1	mannosyl-oligosaccharide glucosidase	I
AIMP2	1	0	0	0	0	1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	I
NPEPPS	1	0	0	0	0	1	aminopeptidase puromycin sensitive	I
LYPLA1	0	0	0	1	0	1	lysophospholipase I	I
OLFM1	1	0	0	0	0	1	olfactomedin 1	I
ZER1	1	0	0	0	0	1	zer-1 homolog (C. elegans)	I
PPIH	1	0	0	0	0	1	peptidylprolyl isomerase H (cyclophilin H)	I
COG5	1	0	0	0	0	1	component of oligomeric golgi complex 5	I

ZNHIT1	1	0	0	0	0	1	zinc finger, HIT-type containing 1	I
TIMM44	1	0	0	0	0	1	translocase of inner mitochondrial membrane 44 homolog (yeast)	I
TADA3	1	0	0	0	0	1	transcriptional adaptor 3	I
NXF1	0	0	0	0	1	1	nuclear RNA export factor 1	I
STK25	1	0	0	0	0	1	serine/threonine kinase 25	I
CDRT1	0	0	1	0	0	1	CMT1A duplicated region transcript 1	I
ZNF211	0	0	1	0	0	1	zinc finger protein 211	I
CHERP	1	0	0	0	0	1	calcium homeostasis endoplasmic reticulum protein	I
NOP56	1	0	0	0	0	1	NOP56 ribonucleoprotein homolog (yeast)	I
RNASEH2A	1	0	0	0	0	1	ribonuclease H2, subunit A	I
UBD	1	0	0	0	0	1	ubiquitin D	I
BATF	1	0	0	0	0	1	basic leucine zipper transcription factor, ATF-like	I
DCTN2	1	0	0	0	0	1	dynactin 2 (p50)	I
IFI44	0	0	1	0	0	1	interferon-induced protein 44	I
DPYSL4	0	0	0	1	0	1	dihydropyrimidinase-like 4	I
POLR3C	1	0	0	0	0	1	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	I
SETMAR	0	0	1	0	0	1	SET domain and mariner transposase fusion gene	I
ZNF138	1	0	0	0	0	1	zinc finger protein 138	I
NCOA2	1	0	0	0	0	1	nuclear receptor coactivator 2	I
MTX2	1	0	0	0	0	1	metaxin 2	I
PMVK	1	0	0	0	0	1	phosphomevalonate kinase	I
KHDRBS3	0	0	0	1	0	1	KH domain containing, RNA binding, signal transduction associated 3	I
KLF1	1	0	0	0	0	1	Kruppel-like factor 1 (erythroid)	I
DCTN6	0	0	1	0	0	1	dynactin 6	I
AVIL	1	0	0	0	0	1	advillin	I
CNPY3	1	0	0	0	0	1	canopy 3 homolog (zebrafish)	I
TCFL5	0	0	1	0	0	1	transcription factor-like 5 (basic helix-loop-helix)	I
PHGDH	0	1	0	0	0	1	phosphoglycerate dehydrogenase	I

ARPP19	1	0	0	0	0	1	cAMP-regulated phosphoprotein, 19kDa	I
STARD10	1	0	0	0	0	1	StAR-related lipid transfer (START) domain containing 10	I
CPLX1	0	0	0	0	1	1	complexin 1	I
CLPX	1	0	0	0	0	1	ClpX caseinolytic peptidase X homolog (E. coli)	I
PPP1R13L	1	0	0	0	0	1	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	I
TRAFD1	1	0	0	0	0	1	TRAF-type zinc finger domain containing 1	I
GADD45G	0	0	0	0	1	1	growth arrest and DNA-damage-inducible, gamma	I
EHMT2	1	0	0	0	0	1	euchromatic histone-lysine N-methyltransferase 2	I
COPS8	1	0	0	0	0	1	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	I
CENPI	1	0	0	0	0	1	centromere protein I	I
HOXA2	0	0	1	0	0	1	homeobox A2	I
MCM5	1	0	0	0	0	1	minichromosome maintenance complex component 5	I
UPK2	0	0	1	0	0	1	uroplakin 2	I
TUSC3	0	0	0	0	1	1	tumor suppressor candidate 3	I
LZTR1	1	0	0	0	0	1	leucine-zipper-like transcription regulator 1	I
BRAP	1	0	0	0	0	1	BRCA1 associated protein	I
SYNGAP1	1	0	0	0	0	1	synaptic Ras GTPase activating protein 1	I
CDC42EP2	1	0	0	0	0	1	CDC42 effector protein (Rho GTPase binding) 2	I
WDR3	1	0	0	0	0	1	WD repeat domain 3	I
MSL3	1	0	0	0	0	1	male-specific lethal 3 homolog (Drosophila)	I
AP3M2	0	0	1	0	0	1	adaptor-related protein complex 3, mu 2 subunit	I
BTG3	1	0	0	0	0	1	BTG family, member 3	I
SEC61B	1	0	0	0	0	1	Sec61 beta subunit	I
TOMM34	1	0	0	0	0	1	translocase of outer mitochondrial membrane 34	I
TMED2	1	0	0	0	0	1	transmembrane emp24 domain trafficking protein 2	I
IFI44L	0	0	1	0	0	1	interferon-induced protein 44-like	I
EBNA1BP2	1	0	0	0	0	1	EBNA1 binding protein 2	I

CKAP4	1	0	0	0	0	1	cytoskeleton-associated protein 4	I
YWHAQ	1	0	0	0	0	1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	I
ASCC3	1	0	0	0	0	1	activating signal cointegrator 1 complex subunit 3	I
SDS	0	1	0	0	0	1	serine dehydratase	I
CCDC85B	0	0	0	0	1	1	coiled-coil domain containing 85B	I
PIM2	1	0	0	0	0	1	pim-2 oncogene	I
HOXD3	0	0	1	0	0	1	homeobox D3	I
RASGRF2	0	0	0	0	1	1	Ras protein-specific guanine nucleotide-releasing factor 2	I
SOX15	0	0	1	0	0	1	SRY (sex determining region Y)-box 15	I
SPRR2D	0	0	1	0	0	1	small proline-rich protein 2D	I
SPTBN2	1	0	0	0	0	1	spectrin, beta, non-erythrocytic 2	I
ZNF19	1	0	0	0	0	1	zinc finger protein 19	I
ZNF32	1	0	0	0	0	1	zinc finger protein 32	I
MTERF	0	0	1	0	0	1	mitochondrial transcription termination factor	I
PAPD7	1	0	0	0	0	1	PAP associated domain containing 7	I
UPK1A	0	0	1	0	0	1	uroplakin 1A	I
SLC35D2	1	0	0	0	0	1	solute carrier family 35, member D2	I
TLE4	1	0	0	0	0	1	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	I
C10orf10	0	0	0	0	1	1	chromosome 10 open reading frame 10	I
TMEM115	1	0	0	0	0	1	transmembrane protein 115	I
DUSP14	1	0	0	0	0	1	dual specificity phosphatase 14	I
TRIM31	1	0	0	0	0	1	tripartite motif containing 31	I
RER1	1	0	0	0	0	1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	I
DNAJB4	0	0	0	0	1	1	DnaJ (Hsp40) homolog, subfamily B, member 4	I
KRR1	1	0	0	0	0	1	KRR1, small subunit (SSU) processome component, homolog (yeast)	I
FAF1	1	0	0	0	0	1	Fas (TNFRSF6) associated factor 1	I
KPTN	0	0	1	0	0	1	kaptin (actin binding protein)	I

PTP4A3	0	0	0	0	1	1	protein tyrosine phosphatase type IVA, member 3	I
TMF1	1	0	0	0	0	1	TATA element modulatory factor 1	I
C14orf1	1	0	0	0	0	1	chromosome 14 open reading frame 1	I
WBP4	1	0	0	0	0	1	WW domain binding protein 4 (formin binding protein 21)	I
ANXA10	0	0	1	0	0	1	annexin A10	I
MRPL3	1	0	0	0	0	1	mitochondrial ribosomal protein L3	I
RNF2	1	0	0	0	0	1	ring finger protein 2	I
XPOT	1	0	0	0	0	1	exportin, tRNA (nuclear export receptor for tRNAs)	I
SNF8	1	0	0	0	0	1	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	I
KLHL2	1	0	0	0	0	1	kelch-like 2, Mayven (Drosophila)	I
LYPLA2	1	0	0	0	0	1	lysophospholipase II	I
PARK7	1	0	0	0	0	1	parkinson protein 7	I
GPN1	1	0	0	0	0	1	GPN-loop GTPase 1	I
DIAPH2	1	0	0	0	0	1	diaphanous homolog 2 (Drosophila)	I
TMED3	1	0	0	0	0	1	transmembrane emp24 protein transport domain containing 3	I
PADI2	1	0	0	0	0	1	peptidyl arginine deiminase, type II	I
ELL2	1	0	0	0	0	1	elongation factor, RNA polymerase II, 2	I
FRAT2	1	0	0	0	0	1	frequently rearranged in advanced T-cell lymphomas 2	I
PGLS	1	0	0	0	0	1	6-phosphogluconolactonase	I
PRDX5	1	0	0	0	0	1	peroxiredoxin 5	I
CHIC2	1	0	0	0	0	1	cysteine-rich hydrophobic domain 2	I
AHSA1	1	0	0	0	0	1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	I
CHORDC1	0	0	0	0	1	1	cysteine and histidine-rich domain (CHORD) containing 1	I
DDAH1	1	0	0	0	0	1	dimethylarginine dimethylaminohydrolase 1	I
AATF	1	0	0	0	0	1	apoptosis antagonizing transcription factor	I
SERGEF	0	0	1	0	0	1	secretion regulating guanine nucleotide exchange factor	I
FBXO10	1	0	0	0	0	1	F-box protein 10	I

FBXO4	1	0	0	0	0	1	F-box protein 4	I
FKBP8	1	0	0	0	0	1	FK506 binding protein 8, 38kDa	I
CABYR	1	0	0	0	0	1	calcium binding tyrosine-(Y)-phosphorylation regulated	I
NAT6	1	0	0	0	0	1	N-acetyltransferase 6 (GCN5-related)	I
SCAP	1	0	0	0	0	1	SREBF chaperone	I
SIRT4	0	0	1	0	0	1	sirtuin 4	I
SLC27A5	1	0	0	0	0	1	solute carrier family 27 (fatty acid transporter), member 5	I
HEY1	0	0	0	0	1	1	hairy/enhancer-of-split related with YRPW motif 1	I
LAMP5	0	0	0	0	1	1	lysosomal-associated membrane protein family, member 5	I
SLC39A6	1	0	0	0	0	1	solute carrier family 39 (zinc transporter), member 6	I
LSM4	1	0	0	0	0	1	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	I
MAPRE3	1	0	0	0	0	1	microtubule-associated protein, RP/EB family, member 3	I
DNAJB9	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily B, member 9	I
CCDC19	1	0	0	0	0	1	coiled-coil domain containing 19	I
GTPBP4	0	1	0	0	0	1	GTP binding protein 4	I
GMEB2	0	1	0	0	0	1	glucocorticoid modulatory element binding protein 2	I
PFDN2	1	0	0	0	0	1	prefoldin subunit 2	I
STEAP1	1	0	0	0	0	1	six transmembrane epithelial antigen of the prostate 1	I
TIMM8B	1	0	0	0	0	1	translocase of inner mitochondrial membrane 8 homolog B (yeast)	I
TIMM9	1	0	0	0	0	1	translocase of inner mitochondrial membrane 9 homolog (yeast)	I
UCK2	1	0	0	0	0	1	uridine-cytidine kinase 2	I
PRELID1	1	0	0	0	0	1	PRELI domain containing 1	I
DNAJC15	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 15	I
FHOD1	1	0	0	0	0	1	formin homology 2 domain containing 1	I
C16orf80	0	0	1	0	0	1	chromosome 16 open reading frame 80	I
ZNF180	1	0	0	0	0	1	zinc finger protein 180	I
GLS2	0	1	0	0	0	1	glutaminase 2 (liver, mitochondrial)	I
SHPK	1	0	0	0	0	1	sedoheptulokinase	I

GPSM2	0	1	0	0	0	1	G-protein signaling modulator 2	I
FAM216A	1	0	0	0	0	1	family with sequence similarity 216, member A	I
C2orf27A	0	0	1	0	0	1	chromosome 2 open reading frame 27A	I
PYCR2	1	0	0	0	0	1	pyrroline-5-carboxylate reductase family, member 2	I
OLA1	1	0	0	0	0	1	Obg-like ATPase 1	I
DSE	1	0	0	0	0	1	dermatan sulfate epimerase	I
ANAPC4	1	0	0	0	0	1	anaphase promoting complex subunit 4	I
SERTAD3	1	0	0	0	0	1	SERTA domain containing 3	I
OSGIN1	1	0	0	0	0	1	oxidative stress induced growth inhibitor 1	I
POMT2	1	0	0	0	0	1	protein-O-mannosyltransferase 2	I
PREB	1	0	0	0	0	1	prolactin regulatory element binding	I
PRICKLE4	0	0	1	0	0	1	prickle homolog 4 (Drosophila)	I
LIG3	1	0	0	0	0	1	ligase III, DNA, ATP-dependent	I
BZW2	1	0	0	0	0	1	basic leucine zipper and W2 domains 2	I
SPCS1	1	0	0	0	0	1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	I
C19orf53	1	0	0	0	0	1	chromosome 19 open reading frame 53	I
COMMD5	1	0	0	0	0	1	COMM domain containing 5	I
PSORS1C1	1	0	0	0	0	1	psoriasis susceptibility 1 candidate 1	I
MRPL13	0	1	0	0	0	1	mitochondrial ribosomal protein L13	I
ZNF770	1	0	0	0	0	1	zinc finger protein 770	I
C16orf72	1	0	0	0	0	1	chromosome 16 open reading frame 72	I
MRPL18	0	0	1	0	0	1	mitochondrial ribosomal protein L18	I
CRIPT	1	0	0	0	0	1	cysteine-rich PDZ-binding protein	I
TIMM21	1	0	0	0	0	1	translocase of inner mitochondrial membrane 21 homolog (yeast)	I
HOXD9	0	0	1	0	0	1	homeobox D9	I
SRP68	1	0	0	0	0	1	signal recognition particle 68kDa	I
PTPLA	1	0	0	0	0	1	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	I

YME1L1	1	0	0	0	0	1	YME1-like 1 (S. cerevisiae)	I
PLK4	1	0	0	0	0	1	polo-like kinase 4	I
ETHE1	1	0	0	0	0	1	ethylmalonic encephalopathy 1	I
C22orf28	1	0	0	0	0	1	chromosome 22 open reading frame 28	I
HEBP2	0	0	1	0	0	1	heme binding protein 2	I
TBC1D22A	0	0	1	0	0	1	TBC1 domain family, member 22A	I
SACS	0	0	0	1	0	1	spastic ataxia of Charlevoix-Saguenay (sacsin)	I
PELP1	1	0	0	0	0	1	proline, glutamate and leucine rich protein 1	I
SND1	1	0	0	0	0	1	staphylococcal nuclease and tudor domain containing 1	I
ANKRD1	0	0	0	1	0	1	ankyrin repeat domain 1 (cardiac muscle)	I
GHITM	1	0	0	0	0	1	growth hormone inducible transmembrane protein	I
LAMP3	0	0	1	0	0	1	lysosomal-associated membrane protein 3	I
UQCRQ	1	0	0	0	0	1	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	I
ZBTB11	1	0	0	0	0	1	zinc finger and BTB domain containing 11	I
CPNE7	0	0	1	0	0	1	copine VII	I
LSM1	1	0	0	0	0	1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	I
SULT1B1	0	0	0	1	0	1	sulfotransferase family, cytosolic, 1B, member 1	I
RND1	0	0	1	0	0	1	Rho family GTPase 1	I
DIMT1	1	0	0	0	0	1	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae)	I
FOXP2	1	0	0	0	0	1	forkhead box P2	I
PRPF19	1	0	0	0	0	1	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	I
TOR1B	1	0	0	0	0	1	torsin family 1, member B (torsin B)	I
CNOT3	1	0	0	0	0	1	CCR4-NOT transcription complex, subunit 3	I
ZNF232	1	0	0	0	0	1	zinc finger protein 232	I
NCAPH2	1	0	0	0	0	1	non-SMC condensin II complex, subunit H2	I
TFCP2L1	1	0	0	0	0	1	transcription factor CP2-like 1	I
HEYL	1	0	0	0	0	1	hairy/enhancer-of-split related with YRPW motif-like	I
TMEM97	0	1	0	0	0	1	transmembrane protein 97	I

RHOD	1	0	0	0	0	1	ras homolog gene family, member D	I
ZNRD1	1	0	0	0	0	1	zinc ribbon domain containing 1	I
SOCS7	1	0	0	0	0	1	suppressor of cytokine signaling 7	I
PSME4	1	0	0	0	0	1	proteasome (prosome, macropain) activator subunit 4	I
HOXD4	0	0	1	0	0	1	homeobox D4	I
MICAL2	1	0	0	0	0	1	microtubule associated monoxygenase, calponin and LIM domain containing 2	I
PLCH2	0	0	1	0	0	1	phospholipase C, eta 2	I
TTLL4	1	0	0	0	0	1	tubulin tyrosine ligase-like family, member 4	I
TTI1	1	0	0	0	0	1	Tel2 interacting protein 1 homolog (S. pombe)	I
TTC35	1	0	0	0	0	1	tetratricopeptide repeat domain 35	I
CCP110	1	0	0	0	0	1	centriolar coiled coil protein 110kDa	I
ACAP1	1	0	0	0	0	1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	I
CLSTN3	1	0	0	0	0	1	calsyntenin 3	I
TBKBP1	1	0	0	0	0	1	TBK1 binding protein 1	I
MLEC	1	0	0	0	0	1	malectin	I
ProSAPiP1	1	0	0	0	0	1	ProSAPiP1 protein	I
DLGAP5	0	0	0	1	0	1	discs, large (Drosophila) homolog-associated protein 5	I
ARHGAP11A	1	0	0	0	0	1	Rho GTPase activating protein 11A	I
PLEKHM1	0	0	1	0	0	1	pleckstrin homology domain containing, family M (with RUN domain) member 1	I
LRIG2	1	0	0	0	0	1	leucine-rich repeats and immunoglobulin-like domains 2	I
PSMD6	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	I
TBC1D4	1	0	0	0	0	1	TBC1 domain family, member 4	I
NUAK1	0	0	0	0	1	1	NUAK family, SNF1-like kinase, 1	I
SGSM2	0	0	1	0	0	1	small G protein signaling modulator 2	I
ATP2C2	1	0	0	0	0	1	ATPase, Ca++ transporting, type 2C, member 2	I
KIAA0020	1	0	0	0	0	1	KIAA0020	I

ADNP2	1	0	0	0	0	1	ADNP homeobox 2	I
FNDC3A	0	1	0	0	0	1	fibronectin type III domain containing 3A	I
PLEKHA6	1	0	0	0	0	1	pleckstrin homology domain containing, family A member 6	I
MLXIP	1	0	0	0	0	1	MLX interacting protein	I
KIAA0907	0	0	1	0	0	1	KIAA0907	I
BAHD1	1	0	0	0	0	1	bromo adjacent homology domain containing 1	I
METTL13	1	0	0	0	0	1	methyltransferase like 13	I
EFR3B	0	0	1	0	0	1	EFR3 homolog B (S. cerevisiae)	I
MAPKBP1	1	0	0	0	0	1	mitogen-activated protein kinase binding protein 1	I
USP33	0	0	1	0	0	1	ubiquitin specific peptidase 33	I
PDXDC1	1	0	0	0	0	1	pyridoxal-dependent decarboxylase domain containing 1	I
KIAA0090	1	0	0	0	0	1	KIAA0090	I
RRP1B	1	0	0	0	0	1	ribosomal RNA processing 1 homolog B (S. cerevisiae)	I
PEG10	1	0	0	0	0	1	paternally expressed 10	I
SIPA1L3	1	0	0	0	0	1	signal-induced proliferation-associated 1 like 3	I
MRPS27	1	0	0	0	0	1	mitochondrial ribosomal protein S27	I
CUL9	1	0	0	0	0	1	cullin 9	I
RGL1	1	0	0	0	0	1	ral guanine nucleotide dissociation stimulator-like 1	I
RFTN1	1	0	0	0	0	1	raftlin, lipid raft linker 1	I
PMPCA	1	0	0	0	0	1	peptidase (mitochondrial processing) alpha	I
RRS1	1	0	0	0	0	1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	I
PRRC2C	1	0	0	0	0	1	proline-rich coiled-coil 2C	I
TBC1D12	0	0	1	0	0	1	TBC1 domain family, member 12	I
DNAJC9	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 9	I
ARC	0	0	0	0	1	1	activity-regulated cytoskeleton-associated protein	I
ANKRD28	1	0	0	0	0	1	ankyrin repeat domain 28	I
THSD7A	0	0	1	0	0	1	thrombospondin, type I, domain containing 7A	I
OTUD3	1	0	0	0	0	1	OTU domain containing 3	I

DNMBP	0	0	0	1	0	1	dynamin binding protein	I
CLEC16A	1	0	0	0	0	1	C-type lectin domain family 16, member A	I
ARAP2	1	0	0	0	0	1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	I
ARAP1	1	0	0	0	0	1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	I
CUX2	1	0	0	0	0	1	cut-like homeobox 2	I
DNAJC13	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 13	I
RPGRIP1L	0	0	1	0	0	1	RPGRIP1-like	I
USP22	1	0	0	0	0	1	ubiquitin specific peptidase 22	I
CLASP1	1	0	0	0	0	1	cytoplasmic linker associated protein 1	I
HAUS5	1	0	0	0	0	1	HAUS augmin-like complex, subunit 5	I
KIAA0947	1	0	0	0	0	1	KIAA0947	I
SMG5	1	0	0	0	0	1	smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	I
MED13L	1	0	0	0	0	1	mediator complex subunit 13-like	I
PPWD1	1	0	0	0	0	1	peptidylprolyl isomerase domain and WD repeat containing 1	I
NUP188	1	0	0	0	0	1	nucleoporin 188kDa	I
R3HDM1	1	0	0	0	0	1	R3H domain containing 1	I
SAMM50	1	0	0	0	0	1	sorting and assembly machinery component 50 homolog (S. cerevisiae)	I
ANAPC13	1	0	0	0	0	1	anaphase promoting complex subunit 13	I
RPL36	1	0	0	0	0	1	ribosomal protein L36	I
SPEF1	0	1	0	0	0	1	sperm flagellar 1	I
MXRA5	1	0	0	0	0	1	matrix-remodelling associated 5	I
AASDHPPT	1	0	0	0	0	1	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	I
POLR1A	1	0	0	0	0	1	polymerase (RNA) I polypeptide A, 194kDa	I
MTHFD1L	1	0	0	0	0	1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	I
ZNF521	0	0	0	1	0	1	zinc finger protein 521	I
FAM98A	1	0	0	0	0	1	family with sequence similarity 98, member A	I
TPGS2	1	0	0	0	0	1	tubulin polyglutamylase complex subunit 2	I

KRT23	0	1	0	0	0	1	keratin 23 (histone deacetylase inducible)	I
DYNC2LI1	1	0	0	0	0	1	dynein, cytoplasmic 2, light intermediate chain 1	I
RNF167	1	0	0	0	0	1	ring finger protein 167	I
OSBPL3	1	0	0	0	0	1	oxysterol binding protein-like 3	I
ZNF451	1	0	0	0	0	1	zinc finger protein 451	I
CCDC9	1	0	0	0	0	1	coiled-coil domain containing 9	I
EIF2B4	1	0	0	0	0	1	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	I
IRF2BP1	1	0	0	0	0	1	interferon regulatory factor 2 binding protein 1	I
IFT172	1	0	0	0	0	1	intraflagellar transport 172 homolog (Chlamydomonas)	I
COQ2	1	0	0	0	0	1	coenzyme Q2 homolog, prenyltransferase (yeast)	I
GPKOW	1	0	0	0	0	1	G patch domain and KOW motifs	I
GLTSCR2	1	0	0	0	0	1	glioma tumor suppressor candidate region gene 2	I
GLTSCR1	1	0	0	0	0	1	glioma tumor suppressor candidate region gene 1	I
DCAF8	1	0	0	0	0	1	DDB1 and CUL4 associated factor 8	I
ZNF117	0	0	1	0	0	1	zinc finger protein 117	I
UBXN1	1	0	0	0	0	1	UBX domain protein 1	I
STMN3	1	0	0	0	0	1	stathmin-like 3	I
GMNN	1	0	0	0	0	1	geminin, DNA replication inhibitor	I
WDPCP	1	0	0	0	0	1	WD repeat containing planar cell polarity effector	I
RPS27L	1	0	0	0	0	1	ribosomal protein S27-like	I
NMD3	1	0	0	0	0	1	NMD3 homolog (S. cerevisiae)	I
AMDHD2	1	0	0	0	0	1	amidohydrolase domain containing 2	I
SLC35B3	1	0	0	0	0	1	solute carrier family 35, member B3	I
GET4	0	0	1	0	0	1	golgi to ER traffic protein 4 homolog (S. cerevisiae)	I
FCF1	1	0	0	0	0	1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	I
TPPP3	1	0	0	0	0	1	tubulin polymerization-promoting protein family member 3	I
NDUFA13	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	I

MRPS7	1	0	0	0	0	1	mitochondrial ribosomal protein S7	I
ATP6V1D	0	0	1	0	0	1	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	I
WIPI2	1	0	0	0	0	1	WD repeat domain, phosphoinositide interacting 2	I
ZC2HC1A	1	0	0	0	0	1	zinc finger, C2HC-type containing 1A	I
MECR	1	0	0	0	0	1	mitochondrial trans-2-enoyl-CoA reductase	I
LUC7L2	1	0	0	0	0	1	LUC7-like 2 (S. cerevisiae)	I
TFB1M	1	0	0	0	0	1	transcription factor B1, mitochondrial	I
APH1A	1	0	0	0	0	1	anterior pharynx defective 1 homolog A (C. elegans)	I
LACTB2	1	0	0	0	0	1	lactamase, beta 2	I
FAM82B	1	0	0	0	0	1	family with sequence similarity 82, member B	I
MRPS2	1	0	0	0	0	1	mitochondrial ribosomal protein S2	I
COQ4	1	0	0	0	0	1	coenzyme Q4 homolog (S. cerevisiae)	I
EXOSC1	1	0	0	0	0	1	exosome component 1	I
FAM158A	0	0	1	0	0	1	family with sequence similarity 158, member A	I
RRP15	1	0	0	0	0	1	ribosomal RNA processing 15 homolog (S. cerevisiae)	I
CCDC53	1	0	0	0	0	1	coiled-coil domain containing 53	I
PPIL1	1	0	0	0	0	1	peptidylprolyl isomerase (cyclophilin)-like 1	I
FIS1	1	0	0	0	0	1	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	I
MRPS23	1	0	0	0	0	1	mitochondrial ribosomal protein S23	I
PTRH2	1	0	0	0	0	1	peptidyl-tRNA hydrolase 2	I
RPL26L1	1	0	0	0	0	1	ribosomal protein L26-like 1	I
BRP44L	1	0	0	0	0	1	brain protein 44-like	I
WDR83OS	1	0	0	0	0	1	WD repeat domain 83 opposite strand	I
PPME1	1	0	0	0	0	1	protein phosphatase methylesterase 1	I
PADI3	0	0	1	0	0	1	peptidyl arginine deiminase, type III	I
CYB5R1	0	0	1	0	0	1	cytochrome b5 reductase 1	I
HSD17B14	0	0	1	0	0	1	hydroxysteroid (17-beta) dehydrogenase 14	I
NAGPA	1	0	0	0	0	1	N-acetylglucosamine-1-phosphodiester alpha-N-	I

							acetylglucosaminidase	
VGLL1	0	0	1	0	0	1	vestigial like 1 (Drosophila)	I
TOB2	1	0	0	0	0	1	transducer of ERBB2, 2	I
HSPA14	1	0	0	0	0	1	heat shock 70kDa protein 14	I
SS18L2	1	0	0	0	0	1	synovial sarcoma translocation gene on chromosome 18-like 2	I
MSRB1	0	0	1	0	0	1	methionine sulfoxide reductase B1	I
PLCE1	1	0	0	0	0	1	phospholipase C, epsilon 1	I
CENPF	0	0	0	1	0	1	centromere protein F, 350/400kDa (mitosin)	I
HSD17B7	1	0	0	0	0	1	hydroxysteroid (17-beta) dehydrogenase 7	I
TRMT112	1	0	0	0	0	1	tRNA methyltransferase 11-2 homolog (S. cerevisiae)	I
GLTP	1	0	0	0	0	1	glycolipid transfer protein	I
TUBG2	1	0	0	0	0	1	tubulin, gamma 2	I
PLEK2	1	0	0	0	0	1	pleckstrin 2	I
TMEM9	1	0	0	0	0	1	transmembrane protein 9	I
MZB1	1	0	0	0	0	1	marginal zone B and B1 cell-specific protein	I
C3orf19	1	0	0	0	0	1	chromosome 3 open reading frame 19	I
PDZD11	1	0	0	0	0	1	PDZ domain containing 11	I
RNF181	1	0	0	0	0	1	ring finger protein 181	I
ICK	1	0	0	0	0	1	intestinal cell (MAK-like) kinase	I
IER5	0	0	0	0	1	1	immediate early response 5	I
GMIP	1	0	0	0	0	1	GEM interacting protein	I
CYP39A1	1	0	0	0	0	1	cytochrome P450, family 39, subfamily A, polypeptide 1	I
FAM53C	1	0	0	0	0	1	family with sequence similarity 53, member C	I
SLC25A37	1	0	0	0	0	1	solute carrier family 25, member 37	I
ZNF644	1	0	0	0	0	1	zinc finger protein 644	I
MEX3C	1	0	0	0	0	1	mex-3 homolog C (C. elegans)	I
OAS1	0	0	1	0	0	1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	I
UBN1	1	0	0	0	0	1	ubinuclein 1	I

HOXC10	1	0	0	0	0	1	homeobox C10	I
HOXC13	0	0	1	0	0	1	homeobox C13	I
SIX4	1	0	0	0	0	1	SIX homeobox 4	I
COQ3	0	1	0	0	0	1	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	I
GALNT7	1	0	0	0	0	1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	I
CPSF2	1	0	0	0	0	1	cleavage and polyadenylation specific factor 2, 100kDa	I
TMED9	1	0	0	0	0	1	transmembrane emp24 protein transport domain containing 9	I
HAUS7	1	0	0	0	0	1	HAUS augmin-like complex, subunit 7	I
XAF1	0	0	1	0	0	1	XIAP associated factor 1	I
CRYGS	0	0	0	0	1	1	crystallin, gamma S	I
C2orf29	1	0	0	0	0	1	chromosome 2 open reading frame 29	I
FBLIM1	0	0	0	1	0	1	filamin binding LIM protein 1	I
NAGK	1	0	0	0	0	1	N-acetylglucosamine kinase	I
MKNK2	1	0	0	0	0	1	MAP kinase interacting serine/threonine kinase 2	I
GRAMD1C	1	0	0	0	0	1	GRAM domain containing 1C	I
ZRANB1	1	0	0	0	0	1	zinc finger, RAN-binding domain containing 1	I
UBE2Q1	1	0	0	0	0	1	ubiquitin-conjugating enzyme E2Q family member 1	I
TRIT1	1	0	0	0	0	1	tRNA isopentenyltransferase 1	I
DYM	1	0	0	0	0	1	dymeclin	I
GIPC2	1	0	0	0	0	1	GIPC PDZ domain containing family, member 2	I
QPCTL	1	0	0	0	0	1	glutaminyl-peptide cyclotransferase-like	I
CCDC132	0	0	1	0	0	1	coiled-coil domain containing 132	I
OTUB1	1	0	0	0	0	1	OTU domain, ubiquitin aldehyde binding 1	I
FAM83E	1	0	0	0	0	1	family with sequence similarity 83, member E	I
FAM46C	1	0	0	0	0	1	family with sequence similarity 46, member C	I
TRMT1	1	0	0	0	0	1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	I
TMEM214	1	0	0	0	0	1	transmembrane protein 214	I

WHSC1L1	1	0	0	0	0	1	Wolf-Hirschhorn syndrome candidate 1-like 1	I
CYP2W1	0	1	0	0	0	1	cytochrome P450, family 2, subfamily W, polypeptide 1	I
OSGEP	1	0	0	0	0	1	O-sialoglycoprotein endopeptidase	I
CHCHD3	1	0	0	0	0	1	coiled-coil-helix-coiled-coil-helix domain containing 3	I
KANSL2	1	0	0	0	0	1	KAT8 regulatory NSL complex subunit 2	I
COMMD4	1	0	0	0	0	1	COMM domain containing 4	I
CECR5	1	0	0	0	0	1	cat eye syndrome chromosome region, candidate 5	I
LPCAT2	1	0	0	0	0	1	lysophosphatidylcholine acyltransferase 2	I
SSH3	0	0	1	0	0	1	slingshot homolog 3 (Drosophila)	I
CLN6	1	0	0	0	0	1	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	I
ULK4	0	0	1	0	0	1	unc-51-like kinase 4 (C. elegans)	I
DDX27	1	0	0	0	0	1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	I
TTC22	1	0	0	0	0	1	tetratricopeptide repeat domain 22	I
IWS1	1	0	0	0	0	1	IWS1 homolog (S. cerevisiae)	I
WIPI1	1	0	0	0	0	1	WD repeat domain, phosphoinositide interacting 1	I
DET1	0	0	1	0	0	1	de-etiolated homolog 1 (Arabidopsis)	I
GPATCH1	1	0	0	0	0	1	G patch domain containing 1	I
VAC14	1	0	0	0	0	1	Vac14 homolog (S. cerevisiae)	I
AKIRIN2	1	0	0	0	0	1	akirin 2	I
MAP7D1	1	0	0	0	0	1	MAP7 domain containing 1	I
TRIM68	1	0	0	0	0	1	tripartite motif containing 68	I
RBM28	1	0	0	0	0	1	RNA binding motif protein 28	I
SRBD1	1	0	0	0	0	1	S1 RNA binding domain 1	I
IPO9	1	0	0	0	0	1	importin 9	I
WDR74	0	1	0	0	0	1	WD repeat domain 74	I
PNPO	1	0	0	0	0	1	pyridoxamine 5'-phosphate oxidase	I
CEP55	0	1	0	0	0	1	centrosomal protein 55kDa	I
MRPS10	1	0	0	0	0	1	mitochondrial ribosomal protein S10	I

FAM82A2	1	0	0	0	0	1	family with sequence similarity 82, member A2	I
RNF220	1	0	0	0	0	1	ring finger protein 220	I
RIC8B	1	0	0	0	0	1	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	I
NADSYN1	0	0	1	0	0	1	NAD synthetase 1	I
PLEKHG6	0	1	0	0	0	1	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	I
C1orf112	0	0	1	0	0	1	chromosome 1 open reading frame 112	I
FANCI	1	0	0	0	0	1	Fanconi anemia, complementation group I	I
TBC1D13	1	0	0	0	0	1	TBC1 domain family, member 13	I
PANK4	0	0	1	0	0	1	pantothenate kinase 4	I
RNPEPL1	1	0	0	0	0	1	arginyl aminopeptidase (aminopeptidase B)-like 1	I
OGDHL	1	0	0	0	0	1	oxoglutarate dehydrogenase-like	I
INTS9	1	0	0	0	0	1	integrator complex subunit 9	I
TMEM206	1	0	0	0	0	1	transmembrane protein 206	I
ELP2	1	0	0	0	0	1	elongation protein 2 homolog (S. cerevisiae)	I
TYW1	1	0	0	0	0	1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	I
C7orf43	1	0	0	0	0	1	chromosome 7 open reading frame 43	I
ARHGAP12	1	0	0	0	0	1	Rho GTPase activating protein 12	I
PGM2	0	0	1	0	0	1	phosphoglucomutase 2	I
TBC1D19	0	0	1	0	0	1	TBC1 domain family, member 19	I
RFK	1	0	0	0	0	1	riboflavin kinase	I
C6orf70	1	0	0	0	0	1	chromosome 6 open reading frame 70	I
RSAD1	1	0	0	0	0	1	radical S-adenosyl methionine domain containing 1	I
C5orf22	1	0	0	0	0	1	chromosome 5 open reading frame 22	I
LARP6	1	0	0	0	0	1	La ribonucleoprotein domain family, member 6	I
ABCF3	1	0	0	0	0	1	ATP-binding cassette, sub-family F (GCN20), member 3	I
CNO	1	0	0	0	0	1	cappuccino homolog (mouse)	I
C19orf66	1	0	0	0	0	1	chromosome 19 open reading frame 66	I

LSG1	1	0	0	0	0	1	large subunit GTPase 1 homolog (S. cerevisiae)	I
ABHD10	1	0	0	0	0	1	abhydrolase domain containing 10	I
ADAP2	1	0	0	0	0	1	ArfGAP with dual PH domains 2	I
LAPTM4B	0	1	0	0	0	1	lysosomal protein transmembrane 4 beta	I
SOX18	0	0	0	0	1	1	SRY (sex determining region Y)-box 18	I
FBXO6	1	0	0	0	0	1	F-box protein 6	I
PDP1	1	0	0	0	0	1	pyruvate dehyrogenase phosphatase catalytic subunit 1	I
BRK1	1	0	0	0	0	1	BRICK1, SCAR/WAVE actin-nucleating complex subunit	I
USE1	1	0	0	0	0	1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	I
YOD1	0	0	1	0	0	1	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	I
WSB2	1	0	0	0	0	1	WD repeat and SOCS box containing 2	I
VPS33B	1	0	0	0	0	1	vacuolar protein sorting 33 homolog B (yeast)	I
THSD1	0	0	1	0	0	1	thrombospondin, type I, domain containing 1	I
KIAA1199	0	1	0	0	0	1	KIAA1199	I
FAM114A2	1	0	0	0	0	1	family with sequence similarity 114, member A2	I
COG1	1	0	0	0	0	1	component of oligomeric golgi complex 1	I
BAIAP2L1	1	0	0	0	0	1	BAI1-associated protein 2-like 1	I
CLN8	1	0	0	0	0	1	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	I
HOXA10	0	0	0	1	0	1	homeobox A10	I
HOXB6	0	0	1	0	0	1	homeobox B6	I
GNMT	0	0	1	0	0	1	glycine N-methyltransferase	I
GAR1	0	1	0	0	0	1	GAR1 ribonucleoprotein homolog (yeast)	I
ANKIB1	1	0	0	0	0	1	ankyrin repeat and IBR domain containing 1	I
EXOSC4	1	0	0	0	0	1	exosome component 4	I
ELP4	1	0	0	0	0	1	elongation protein 4 homolog (S. cerevisiae)	I
USP53	1	0	0	0	0	1	ubiquitin specific peptidase 53	I
DDIT4	0	0	0	0	1	1	DNA-damage-inducible transcript 4	I

CCNJ	0	1	0	0	0	1	cyclin J	I
PAF1	1	0	0	0	0	1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	I
ZMAT5	1	0	0	0	0	1	zinc finger, matrin-type 5	I
ALG1	1	0	0	0	0	1	asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)	I
UBFD1	1	0	0	0	0	1	ubiquitin family domain containing 1	I
KLHL4	0	0	0	1	0	1	kelch-like 4 (Drosophila)	I
FAM214A	1	0	0	0	0	1	family with sequence similarity 214, member A	I
METTL3	1	0	0	0	0	1	methyltransferase like 3	I
CYP26B1	0	0	1	0	0	1	cytochrome P450, family 26, subfamily B, polypeptide 1	I
CHST7	0	0	0	0	1	1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	I
INPP5E	1	0	0	0	0	1	inositol polyphosphate-5-phosphatase, 72 kDa	I
SLC2A4RG	1	0	0	0	0	1	SLC2A4 regulator	I
SH3GLB2	1	0	0	0	0	1	SH3-domain GRB2-like endophilin B2	I
RAD18	0	0	1	0	0	1	RAD18 homolog (S. cerevisiae)	I
MCCC1	1	0	0	0	0	1	methylcrotonoyl-CoA carboxylase 1 (alpha)	I
C11orf30	1	0	0	0	0	1	chromosome 11 open reading frame 30	I
MFF	1	0	0	0	0	1	mitochondrial fission factor	I
SDR39U1	1	0	0	0	0	1	short chain dehydrogenase/reductase family 39U, member 1	I
NIT2	1	0	0	0	0	1	nitrilase family, member 2	I
PPAN	1	0	0	0	0	1	peter pan homolog (Drosophila)	I
C17orf48	1	0	0	0	0	1	chromosome 17 open reading frame 48	I
CDC42SE2	1	0	0	0	0	1	CDC42 small effector 2	I
COQ9	1	0	0	0	0	1	coenzyme Q9 homolog (S. cerevisiae)	I
CIAPIN1	1	0	0	0	0	1	cytokine induced apoptosis inhibitor 1	I
RALGAPA2	0	0	1	0	0	1	Ral GTPase activating protein, alpha subunit 2 (catalytic)	I
LZTFL1	1	0	0	0	0	1	leucine zipper transcription factor-like 1	I
PCNP	0	0	0	0	1	1	PEST proteolytic signal containing nuclear protein	I

SETD8	1	0	0	0	0	1	SET domain containing (lysine methyltransferase) 8	I
RAB25	1	0	0	0	0	1	RAB25, member RAS oncogene family	I
CAMK1D	1	0	0	0	0	1	calcium/calmodulin-dependent protein kinase ID	I
MRPL47	1	0	0	0	0	1	mitochondrial ribosomal protein L47	I
SALL4	1	0	0	0	0	1	sal-like 4 (Drosophila)	I
YIF1A	1	0	0	0	0	1	Yip1 interacting factor homolog A (S. cerevisiae)	I
GALNT1	0	0	0	1	0	1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	I
DCUN1D1	1	0	0	0	0	1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	I
JPH1	1	0	0	0	0	1	junctophilin 1	I
ZNF304	0	0	1	0	0	1	zinc finger protein 304	I
RHOJ	0	0	0	1	0	1	ras homolog gene family, member J	I
DECR2	1	0	0	0	0	1	2,4-dienoyl CoA reductase 2, peroxisomal	I
SPC25	0	1	0	0	0	1	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	I
NMRAL1	1	0	0	0	0	1	NmrA-like family domain containing 1	I
REXO1	1	0	0	0	0	1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	I
ZNF512B	1	0	0	0	0	1	zinc finger protein 512B	I
GRAMD1B	0	0	1	0	0	1	GRAM domain containing 1B	I
PRR12	1	0	0	0	0	1	proline rich 12	I
KIAA1257	0	1	0	0	0	1	KIAA1257	I
AARS2	1	0	0	0	0	1	alanyl-tRNA synthetase 2, mitochondrial (putative)	I
KIAA1328	1	0	0	0	0	1	KIAA1328	I
CC2D2A	1	0	0	0	0	1	coiled-coil and C2 domain containing 2A	I
USP35	1	0	0	0	0	1	ubiquitin specific peptidase 35	I
MARCH4	0	0	0	1	0	1	membrane-associated ring finger (C3HC4) 4	I
CRAMP1L	1	0	0	0	0	1	Crm, cramped-like (Drosophila)	I
TSHZ3	1	0	0	0	0	1	teashirt zinc finger homeobox 3	I

RNF213	0	0	1	0	0	1	ring finger protein 213	I
GPAM	1	0	0	0	0	1	glycerol-3-phosphate acyltransferase, mitochondrial	I
KIAA1586	1	0	0	0	0	1	KIAA1586	I
CPNE5	0	0	0	0	1	1	copine V	I
MIER1	1	0	0	0	0	1	mesoderm induction early response 1 homolog (Xenopus laevis)	I
NCOA5	1	0	0	0	0	1	nuclear receptor coactivator 5	I
UBC	0	0	0	0	1	1	ubiquitin C	I
SNTB1	1	0	0	0	0	1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	I
HIST1H2AG	0	1	0	0	0	1	histone cluster 1, H2ag	I
NDUFV2	1	0	0	0	0	1	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	I
KAT2A	0	0	0	0	1	1	K(lysine) acetyltransferase 2A	I
NMT1	1	0	0	0	0	1	N-myristoyltransferase 1	I
RPL41	1	0	0	0	0	1	ribosomal protein L41	I
RGS3	1	0	0	0	0	1	regulator of G-protein signaling 3	I
POLR2L	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	I
KDM6A	1	0	0	0	0	1	lysine (K)-specific demethylase 6A	I
CCNO	0	1	0	0	0	1	cyclin O	I
CROT	0	0	1	0	0	1	carnitine O-octanoyltransferase	I
TRIB3	0	1	0	0	0	1	tribbles homolog 3 (Drosophila)	I
GATAD1	1	0	0	0	0	1	GATA zinc finger domain containing 1	I
SRPRB	1	0	0	0	0	1	signal recognition particle receptor, B subunit	I
PCTP	0	0	1	0	0	1	phosphatidylcholine transfer protein	I
AP2S1	1	0	0	0	0	1	adaptor-related protein complex 2, sigma 1 subunit	I
TSPYL4	0	0	1	0	0	1	TSPY-like 4	I
SIVA1	1	0	0	0	0	1	SIVA1, apoptosis-inducing factor	I
AVPI1	1	0	0	0	0	1	arginine vasopressin-induced 1	I
C2orf43	1	0	0	0	0	1	chromosome 2 open reading frame 43	I

FKBP10	1	0	0	0	0	1	FK506 binding protein 10, 65 kDa	I
ZFAND3	1	0	0	0	0	1	zinc finger, AN1-type domain 3	I
NR0B2	1	0	0	0	0	1	nuclear receptor subfamily 0, group B, member 2	I
POLR2F	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide F	I
HSPA2	0	0	0	0	1	1	heat shock 70kDa protein 2	I
JUP	1	0	0	0	0	1	junction plakoglobin	I
NR1I2	0	1	0	0	0	1	nuclear receptor subfamily 1, group I, member 2	I
MRPL17	1	0	0	0	0	1	mitochondrial ribosomal protein L17	I
UBE2O	1	0	0	0	0	1	ubiquitin-conjugating enzyme E2O	I
ZNF667	0	0	1	0	0	1	zinc finger protein 667	I
PRDM15	1	0	0	0	0	1	PR domain containing 15	I
RBKS	0	0	0	0	1	1	ribokinase	I
MCCC2	1	0	0	0	0	1	methylcrotonoyl-CoA carboxylase 2 (beta)	I
MAGEF1	1	0	0	0	0	1	melanoma antigen family F, 1	I
MOAP1	0	0	1	0	0	1	modulator of apoptosis 1	I
DUS1L	1	0	0	0	0	1	dihydrouridine synthase 1-like (S. cerevisiae)	I
FN3K	1	0	0	0	0	1	fructosamine 3 kinase	I
MRPL46	1	0	0	0	0	1	mitochondrial ribosomal protein L46	I
PDF	1	0	0	0	0	1	peptide deformylase (mitochondrial)	I
C17orf75	0	0	1	0	0	1	chromosome 17 open reading frame 75	I
ERAP2	0	0	1	0	0	1	endoplasmic reticulum aminopeptidase 2	I
PDE4DIP	1	0	0	0	0	1	phosphodiesterase 4D interacting protein	I
MMS19	1	0	0	0	0	1	MMS19 nucleotide excision repair homolog (S. cerevisiae)	I
RHBDF1	1	0	0	0	0	1	rhomboid 5 homolog 1 (Drosophila)	I
SOX17	0	0	0	0	1	1	SRY (sex determining region Y)-box 17	I
HS1BP3	1	0	0	0	0	1	HCLS1 binding protein 3	I
ATG3	1	0	0	0	0	1	ATG3 autophagy related 3 homolog (S. cerevisiae)	I
SUDS3	1	0	0	0	0	1	suppressor of defective silencing 3 homolog (S. cerevisiae)	I

MRPS25	0	0	1	0	0	1	mitochondrial ribosomal protein S25	I
RPS18	1	0	0	0	0	1	ribosomal protein S18	I
ANAPC1	0	1	0	0	0	1	anaphase promoting complex subunit 1	I
ACBD3	1	0	0	0	0	1	acyl-CoA binding domain containing 3	I
PARP12	1	0	0	0	0	1	poly (ADP-ribose) polymerase family, member 12	I
MEAF6	1	0	0	0	0	1	MYST/Esa1-associated factor 6	I
CCDC14	1	0	0	0	0	1	coiled-coil domain containing 14	I
CERK	1	0	0	0	0	1	ceramide kinase	I
AEN	1	0	0	0	0	1	apoptosis enhancing nuclease	I
RMND5A	1	0	0	0	0	1	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	I
SLC25A14	1	0	0	0	0	1	solute carrier family 25 (mitochondrial carrier, brain), member 14	I
CBFB	1	0	0	0	0	1	core-binding factor, beta subunit	I
IFI6	0	0	1	0	0	1	interferon, alpha-inducible protein 6	I
PAPOLG	1	0	0	0	0	1	poly(A) polymerase gamma	I
LPIN3	1	0	0	0	0	1	lipin 3	I
NT5DC2	0	0	0	1	0	1	5'-nucleotidase domain containing 2	I
CENPH	0	1	0	0	0	1	centromere protein H	I
GPBP1	1	0	0	0	0	1	GC-rich promoter binding protein 1	I
NOL6	1	0	0	0	0	1	nucleolar protein family 6 (RNA-associated)	I
KRI1	1	0	0	0	0	1	KRI1 homolog (S. cerevisiae)	I
METTL1	1	0	0	0	0	1	methyltransferase like 1	I
SPATS2	1	0	0	0	0	1	spermatogenesis associated, serine-rich 2	I
ZSWIM4	1	0	0	0	0	1	zinc finger, SWIM-type containing 4	I
CAPN10	1	0	0	0	0	1	calpain 10	I
FUNDC2	1	0	0	0	0	1	FUN14 domain containing 2	I
MRPS34	1	0	0	0	0	1	mitochondrial ribosomal protein S34	I
C1orf116	0	0	1	0	0	1	chromosome 1 open reading frame 116	I
MTRR	1	0	0	0	0	1	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	I

HOXB8	0	0	1	0	0	1	homeobox B8	I
C17orf53	1	0	0	0	0	1	chromosome 17 open reading frame 53	I
C19orf43	1	0	0	0	0	1	chromosome 19 open reading frame 43	I
PDCL3	1	0	0	0	0	1	phosducin-like 3	I
OBFC2B	1	0	0	0	0	1	oligonucleotide/oligosaccharide-binding fold containing 2B	I
DDX54	1	0	0	0	0	1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	I
TMEM38A	1	0	0	0	0	1	transmembrane protein 38A	I
ELOVL6	1	0	0	0	0	1	ELOVL fatty acid elongase 6	I
WDR18	1	0	0	0	0	1	WD repeat domain 18	I
SLC25A23	1	0	0	0	0	1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	I
ALG12	1	0	0	0	0	1	asparagine-linked glycosylation 12, alpha-1,6-mannosyltransferase homolog (S. cerevisiae)	I
ZNF426	1	0	0	0	0	1	zinc finger protein 426	I
TRAPPC6A	1	0	0	0	0	1	trafficking protein particle complex 6A	I
C9orf16	1	0	0	0	0	1	chromosome 9 open reading frame 16	I
TAF1D	0	1	0	0	0	1	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	I
FA2H	1	0	0	0	0	1	fatty acid 2-hydroxylase	I
C1orf35	1	0	0	0	0	1	chromosome 1 open reading frame 35	I
PRR15L	0	1	0	0	0	1	proline rich 15-like	I
IRX3	0	0	1	0	0	1	iroquois homeobox 3	I
THOC6	1	0	0	0	0	1	THO complex 6 homolog (Drosophila)	I
DCTN3	1	0	0	0	0	1	dynactin 3 (p22)	I
PLA2G4A	1	0	0	0	0	1	phospholipase A2, group IVA (cytosolic, calcium-dependent)	I
HOXD1	0	0	0	0	1	1	homeobox D1	I
HAUS3	1	0	0	0	0	1	HAUS augmin-like complex, subunit 3	I
NKAP	1	0	0	0	0	1	NFKB activating protein	I
FAM118B	1	0	0	0	0	1	family with sequence similarity 118, member B	I

ARSJ	0	0	0	1	0	1	arylsulfatase family, member J	I
C16orf57	1	0	0	0	0	1	chromosome 16 open reading frame 57	I
RHBDF2	1	0	0	0	0	1	rhomboid 5 homolog 2 (Drosophila)	I
PPP1R3B	1	0	0	0	0	1	protein phosphatase 1, regulatory (inhibitor) subunit 3B	I
FN3KRP	1	0	0	0	0	1	fructosamine 3 kinase related protein	I
GAL3ST4	1	0	0	0	0	1	galactose-3-O-sulfotransferase 4	I
YRDC	1	0	0	0	0	1	yrdC domain containing (E. coli)	I
MANEA	1	0	0	0	0	1	mannosidase, endo-alpha	I
GLT25D1	1	0	0	0	0	1	glycosyltransferase 25 domain containing 1	I
GTDC1	1	0	0	0	0	1	glycosyltransferase-like domain containing 1	I
SH3D21	0	1	0	0	0	1	SH3 domain containing 21	I
C11orf67	1	0	0	0	0	1	chromosome 11 open reading frame 67	I
ECHDC3	1	0	0	0	0	1	enoyl CoA hydratase domain containing 3	I
ZNF385D	0	0	0	0	1	1	zinc finger protein 385D	I
ZNF750	0	0	1	0	0	1	zinc finger protein 750	I
ZNF668	1	0	0	0	0	1	zinc finger protein 668	I
ELMO3	1	0	0	0	0	1	engulfment and cell motility 3	I
IQCA1	0	0	1	0	0	1	IQ motif containing with AAA domain 1	I
MMRN2	0	0	0	0	1	1	multimerin 2	I
AGMAT	0	1	0	0	0	1	agmatine ureohydrolase (agmatinase)	I
CAMKMT	0	0	1	0	0	1	calmodulin-lysine N-methyltransferase	I
GEMIN6	0	0	1	0	0	1	gem (nuclear organelle) associated protein 6	I
AGBL2	0	0	1	0	0	1	ATP/GTP binding protein-like 2	I
BORA	0	1	0	0	0	1	bora, aurora kinase A activator	I
RPAP2	1	0	0	0	0	1	RNA polymerase II associated protein 2	I
LPCAT1	1	0	0	0	0	1	lysophosphatidylcholine acyltransferase 1	I
MCMBP	1	0	0	0	0	1	minichromosome maintenance complex binding protein	I
ZNF672	1	0	0	0	0	1	zinc finger protein 672	I

PREX2	0	0	1	0	0	1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	I
KIAA0319L	1	0	0	0	0	1	KIAA0319-like	I
DHDDS	1	0	0	0	0	1	dehydrodolichyl diphosphate synthase	I
CEP76	1	0	0	0	0	1	centrosomal protein 76kDa	I
DENND2D	1	0	0	0	0	1	DENN/MADD domain containing 2D	I
WDR76	1	0	0	0	0	1	WD repeat domain 76	I
ATAT1	0	0	1	0	0	1	alpha tubulin acetyltransferase 1	I
GRHL2	1	0	0	0	0	1	grainyhead-like 2 (Drosophila)	I
OBFC1	1	0	0	0	0	1	oligonucleotide/oligosaccharide-binding fold containing 1	I
UBTD1	1	0	0	0	0	1	ubiquitin domain containing 1	I
ZNF703	0	1	0	0	0	1	zinc finger protein 703	I
TOE1	1	0	0	0	0	1	target of EGR1, member 1 (nuclear)	I
ZC3H12A	0	0	0	0	1	1	zinc finger CCCH-type containing 12A	I
USP36	1	0	0	0	0	1	ubiquitin specific peptidase 36	I
ATHL1	0	0	0	0	1	1	ATH1, acid trehalase-like 1 (yeast)	I
HKDC1	0	1	0	0	0	1	hexokinase domain containing 1	I
ALPK1	1	0	0	0	0	1	alpha-kinase 1	I
NINL	1	0	0	0	0	1	ninein-like	I
TANC2	0	0	1	0	0	1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	I
TRABD	1	0	0	0	0	1	TraB domain containing	I
ULBP1	1	0	0	0	0	1	UL16 binding protein 1	I
CYB5B	1	0	0	0	0	1	cytochrome b5 type B (outer mitochondrial membrane)	I
WDR59	1	0	0	0	0	1	WD repeat domain 59	I
CYP2S1	1	0	0	0	0	1	cytochrome P450, family 2, subfamily S, polypeptide 1	I
KLHL15	1	0	0	0	0	1	kelch-like 15 (Drosophila)	I
C17orf28	1	0	0	0	0	1	chromosome 17 open reading frame 28	I
DUSP16	1	0	0	0	0	1	dual specificity phosphatase 16	I

SETD7	1	0	0	0	0	1	SET domain containing (lysine methyltransferase) 7	I
MAP2K2	1	0	0	0	0	1	mitogen-activated protein kinase kinase 2	I
ILKAP	1	0	0	0	0	1	integrin-linked kinase-associated serine/threonine phosphatase	I
CCDC34	1	0	0	0	0	1	coiled-coil domain containing 34	I
PTDSS2	1	0	0	0	0	1	phosphatidylserine synthase 2	I
WBSCR16	1	0	0	0	0	1	Williams-Beuren syndrome chromosome region 16	I
C15orf44	1	0	0	0	0	1	chromosome 15 open reading frame 44	I
TXNDC5	0	0	0	1	0	1	thioredoxin domain containing 5 (endoplasmic reticulum)	I
MRPS26	1	0	0	0	0	1	mitochondrial ribosomal protein S26	I
PDRG1	0	1	0	0	0	1	p53 and DNA-damage regulated 1	I
STK33	1	0	0	0	0	1	serine/threonine kinase 33	I
LBH	1	0	0	0	0	1	limb bud and heart development homolog (mouse)	I
MED25	1	0	0	0	0	1	mediator complex subunit 25	I
FAM108A1	0	0	0	0	1	1	family with sequence similarity 108, member A1	I
RBCK1	1	0	0	0	0	1	RanBP-type and C3HC4-type zinc finger containing 1	I
SF3B5	1	0	0	0	0	1	splicing factor 3b, subunit 5, 10kDa	I
INO80B	1	0	0	0	0	1	INO80 complex subunit B	I
LRRC48	1	0	0	0	0	1	leucine rich repeat containing 48	I
CDCA3	0	1	0	0	0	1	cell division cycle associated 3	I
CECR2	1	0	0	0	0	1	cat eye syndrome chromosome region, candidate 2	I
THAP2	0	0	0	0	1	1	THAP domain containing, apoptosis associated protein 2	I
C22orf13	1	0	0	0	0	1	chromosome 22 open reading frame 13	I
FBXW10	0	0	1	0	0	1	F-box and WD repeat domain containing 10	I
ESPN	0	1	0	0	0	1	espin	I
SLC25A18	1	0	0	0	0	1	solute carrier family 25 (mitochondrial carrier), member 18	I
MARVELD 1	0	0	0	0	1	1	MARVEL domain containing 1	I
GRWD1	1	0	0	0	0	1	glutamate-rich WD repeat containing 1	I

L3MBTL2	1	0	0	0	0	1	l(3)mbt-like 2 (Drosophila)	I
GORASP1	1	0	0	0	0	1	golgi reassembly stacking protein 1, 65kDa	I
ESYT3	1	0	0	0	0	1	extended synaptotagmin-like protein 3	I
TAF3	1	0	0	0	0	1	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa	I
RAB34	1	0	0	0	0	1	RAB34, member RAS oncogene family	I
USHBP1	1	0	0	0	0	1	Usher syndrome 1C binding protein 1	I
SNX25	0	0	1	0	0	1	sorting nexin 25	I
KRTAP3-1	0	0	0	0	1	1	keratin associated protein 3-1	I
MRPS24	1	0	0	0	0	1	mitochondrial ribosomal protein S24	I
TATDN1	1	0	0	0	0	1	TatD DNase domain containing 1	I
B3GNT5	1	0	0	0	0	1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	I
MRPL43	1	0	0	0	0	1	mitochondrial ribosomal protein L43	I
PLEKHN1	0	0	1	0	0	1	pleckstrin homology domain containing, family N member 1	I
KBTBD7	0	0	1	0	0	1	kelch repeat and BTB (POZ) domain containing 7	I
PRAM1	1	0	0	0	0	1	PML-RARA regulated adaptor molecule 1	I
ZNF394	0	0	1	0	0	1	zinc finger protein 394	I
ATRIP	0	0	1	0	0	1	ATR interacting protein	I
TOMM40L	1	0	0	0	0	1	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	I
UTP15	1	0	0	0	0	1	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	I
C12orf26	0	0	0	1	0	1	chromosome 12 open reading frame 26	I
SETD3	1	0	0	0	0	1	SET domain containing 3	I
LARP1B	1	0	0	0	0	1	La ribonucleoprotein domain family, member 1B	I
MEX3B	0	0	0	0	1	1	mex-3 homolog B (C. elegans)	I
ZNRF1	1	0	0	0	0	1	zinc and ring finger 1	I
POLR3GL	1	0	0	0	0	1	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	I
CHCHD5	1	0	0	0	0	1	coiled-coil-helix-coiled-coil-helix domain containing 5	I
C9orf89	1	0	0	0	0	1	chromosome 9 open reading frame 89	I

ZDHHC16	1	0	0	0	0	1	zinc finger, DHHC-type containing 16	I
ING5	1	0	0	0	0	1	inhibitor of growth family, member 5	I
CAPNS2	0	0	1	0	0	1	calpain, small subunit 2	I
MNF1	1	0	0	0	0	1	mitochondrial nucleoid factor 1	I
NUDT22	1	0	0	0	0	1	nudix (nucleoside diphosphate linked moiety X)-type motif 22	I
PDCD2L	0	0	1	0	0	1	programmed cell death 2-like	I
VPS25	1	0	0	0	0	1	vacuolar protein sorting 25 homolog (S. cerevisiae)	I
DNAJC14	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 14	I
ELOF1	1	0	0	0	0	1	elongation factor 1 homolog (S. cerevisiae)	I
COG8	1	0	0	0	0	1	component of oligomeric golgi complex 8	I
PINK1	1	0	0	0	0	1	PTEN induced putative kinase 1	I
LZTS2	1	0	0	0	0	1	leucine zipper, putative tumor suppressor 2	I
ASPH	1	0	0	0	0	1	aspartate beta-hydroxylase	I
MRPS6	1	0	0	0	0	1	mitochondrial ribosomal protein S6	I
DOT1L	1	0	0	0	0	1	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	I
AP1M1	1	0	0	0	0	1	adaptor-related protein complex 1, mu 1 subunit	I
ZNF559	1	0	0	0	0	1	zinc finger protein 559	I
MAK16	1	0	0	0	0	1	MAK16 homolog (S. cerevisiae)	I
PARD6B	0	1	0	0	0	1	par-6 partitioning defective 6 homolog beta (C. elegans)	I
HINT2	1	0	0	0	0	1	histidine triad nucleotide binding protein 2	I
C4orf49	0	0	0	1	0	1	chromosome 4 open reading frame 49	I
CINP	1	0	0	0	0	1	cyclin-dependent kinase 2 interacting protein	I
PCGF1	1	0	0	0	0	1	polycomb group ring finger 1	I
TXNDC17	1	0	0	0	0	1	thioredoxin domain containing 17	I
ZNF496	1	0	0	0	0	1	zinc finger protein 496	I
PHF5A	1	0	0	0	0	1	PHD finger protein 5A	I
LRCH3	1	0	0	0	0	1	leucine-rich repeats and calponin homology (CH) domain containing 3	I
ZNF514	0	0	1	0	0	1	zinc finger protein 514	I

FBXO18	1	0	0	0	0	1	F-box protein, helicase, 18	I
FAM73B	1	0	0	0	0	1	family with sequence similarity 73, member B	I
FAM136A	1	0	0	0	0	1	family with sequence similarity 136, member A	I
CIRH1A	1	0	0	0	0	1	cirrhosis, autosomal recessive 1A (cirhin)	I
SPRYD3	1	0	0	0	0	1	SPRY domain containing 3	I
C12orf52	1	0	0	0	0	1	chromosome 12 open reading frame 52	I
HSH2D	1	0	0	0	0	1	hematopoietic SH2 domain containing	I
TNS4	0	0	1	0	0	1	tensin 4	I
AJUBA	0	0	0	1	0	1	ajuba LIM protein	I
LSM10	1	0	0	0	0	1	LSM10, U7 small nuclear RNA associated	I
RERG	0	1	0	0	0	1	RAS-like, estrogen-regulated, growth inhibitor	I
TCEAL3	1	0	0	0	0	1	transcription elongation factor A (SII)-like 3	I
POLR2C	1	0	0	0	0	1	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	I
MLXIPL	1	0	0	0	0	1	MLX interacting protein-like	I
MAPKAPK 2	1	0	0	0	0	1	mitogen-activated protein kinase-activated protein kinase 2	I
CDK16	1	0	0	0	0	1	cyclin-dependent kinase 16	I
TRIM5	1	0	0	0	0	1	tripartite motif containing 5	I
MYO1G	1	0	0	0	0	1	myosin IG	I
EAF1	1	0	0	0	0	1	ELL associated factor 1	I
ZCCHC3	1	0	0	0	0	1	zinc finger, CCHC domain containing 3	I
RHPN2	1	0	0	0	0	1	rhophilin, Rho GTPase binding protein 2	I
ZCRB1	1	0	0	0	0	1	zinc finger CCHC-type and RNA binding motif 1	I
SEC16B	1	0	0	0	0	1	SEC16 homolog B (S. cerevisiae)	I
CNP	1	0	0	0	0	1	2',3'-cyclic nucleotide 3' phosphodiesterase	I
PIGS	1	0	0	0	0	1	phosphatidylinositol glycan anchor biosynthesis, class S	I
TRIM15	0	1	0	0	0	1	tripartite motif containing 15	I
PPP1R14A	1	0	0	0	0	1	protein phosphatase 1, regulatory (inhibitor) subunit 14A	I

BTBD6	1	0	0	0	0	1	BTB (POZ) domain containing 6	I
XRCC6BP1	1	0	0	0	0	1	XRCC6 binding protein 1	I
DCLK3	1	0	0	0	0	1	doublecortin-like kinase 3	I
HIST3H2A	0	0	0	0	1	1	histone cluster 3, H2a	I
FCHSD1	0	0	1	0	0	1	FCH and double SH3 domains 1	I
C19orf33	1	0	0	0	0	1	chromosome 19 open reading frame 33	I
MFN1	1	0	0	0	0	1	mitofusin 1	I
INTS4	1	0	0	0	0	1	integrator complex subunit 4	I
WDR4	1	0	0	0	0	1	WD repeat domain 4	I
CARD14	0	0	1	0	0	1	caspase recruitment domain family, member 14	I
SCAMP3	1	0	0	0	0	1	secretory carrier membrane protein 3	I
CREB3L1	1	0	0	0	0	1	cAMP responsive element binding protein 3-like 1	I
VPS26B	1	0	0	0	0	1	vacuolar protein sorting 26 homolog B (S. pombe)	I
NACC1	1	0	0	0	0	1	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	I
STK11IP	1	0	0	0	0	1	serine/threonine kinase 11 interacting protein	I
RHPN1	0	0	0	0	1	1	rhophilin, Rho GTPase binding protein 1	I
NT5C3L	1	0	0	0	0	1	5'-nucleotidase, cytosolic III-like	I
RPL39L	1	0	0	0	0	1	ribosomal protein L39-like	I
ADC	1	0	0	0	0	1	arginine decarboxylase	I
PFN2	1	0	0	0	0	1	profilin 2	I
SNAP47	1	0	0	0	0	1	synaptosomal-associated protein, 47kDa	I
GLMN	1	0	0	0	0	1	glomulin, FKBP associated protein	I
FKBP1A	0	0	0	1	0	1	FK506 binding protein 1A, 12kDa	I
GALNTL2	0	0	0	0	1	1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	I
RAD51C	1	0	0	0	0	1	RAD51 homolog C (S. cerevisiae)	I
CDKN1A	0	0	0	0	1	1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	I
SLC36A1	1	0	0	0	0	1	solute carrier family 36 (proton/amino acid symporter), member 1	I

S100A16	0	0	0	1	0	1	S100 calcium binding protein A16	I
TCEAL2	1	0	0	0	0	1	transcription elongation factor A (SII)-like 2	I
SDCBP2	0	0	0	1	0	1	syndecan binding protein (syntenin) 2	I
HIST1H2BK	0	0	0	0	1	1	histone cluster 1, H2bk	I
CDKN2AIPNL	1	0	0	0	0	1	CDKN2A interacting protein N-terminal like	I
RSAD2	0	0	1	0	0	1	radical S-adenosyl methionine domain containing 2	I
WDR89	1	0	0	0	0	1	WD repeat domain 89	I
PTPN13	1	0	0	0	0	1	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	I
SRXN1	1	0	0	0	0	1	sulfiredoxin 1	I
EDARADD	1	0	0	0	0	1	EDAR-associated death domain	I
C20orf151	0	0	1	0	0	1	chromosome 20 open reading frame 151	I
SOCS4	0	1	0	0	0	1	suppressor of cytokine signaling 4	I
MEN1	1	0	0	0	0	1	multiple endocrine neoplasia I	I
PRRC1	1	0	0	0	0	1	proline-rich coiled-coil 1	I
CREB3L4	1	0	0	0	0	1	cAMP responsive element binding protein 3-like 4	I
PPIL3	0	0	1	0	0	1	peptidylprolyl isomerase (cyclophilin)-like 3	I
ELMO2	1	0	0	0	0	1	engulfment and cell motility 2	I
EPS8L1	0	0	1	0	0	1	EPS8-like 1	I
GIPC3	1	0	0	0	0	1	GIPC PDZ domain containing family, member 3	I
DEDD2	1	0	0	0	0	1	death effector domain containing 2	I
ZNF618	1	0	0	0	0	1	zinc finger protein 618	I
DIS3L	1	0	0	0	0	1	DIS3 mitotic control homolog (S. cerevisiae)-like	I
ZNF483	1	0	0	0	0	1	zinc finger protein 483	I
CITED4	1	0	0	0	0	1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	I
SAT2	1	0	0	0	0	1	spermidine/spermine N1-acetyltransferase family member 2	I
SYN3	0	1	0	0	0	1	synapsin III	I

RFXANK	1	0	0	0	0	1	regulatory factor X-associated ankyrin-containing protein	I
SPTSSA	1	0	0	0	0	1	serine palmitoyltransferase, small subunit A	I
FAM181A	1	0	0	0	0	1	family with sequence similarity 181, member A	I
DCAF15	1	0	0	0	0	1	DDB1 and CUL4 associated factor 15	I
MCU	1	0	0	0	0	1	mitochondrial calcium uniporter	I
TTC5	1	0	0	0	0	1	tetratricopeptide repeat domain 5	I
RDH13	1	0	0	0	0	1	retinol dehydrogenase 13 (all-trans/9-cis)	I
AHNAK2	0	0	0	1	0	1	AHNAK nucleoprotein 2	I
ADAT3	1	0	0	0	0	1	adenosine deaminase, tRNA-specific 3	I
SDSL	1	0	0	0	0	1	serine dehydratase-like	I
ACYP2	0	0	1	0	0	1	acylphosphatase 2, muscle type	I
RAB3C	0	0	0	0	1	1	RAB3C, member RAS oncogene family	I
ZMYND19	1	0	0	0	0	1	zinc finger, MYND-type containing 19	I
TECR	1	0	0	0	0	1	trans-2,3-enoyl-CoA reductase	I
EXOC3L2	0	0	0	0	1	1	exocyst complex component 3-like 2	I
ZNF653	1	0	0	0	0	1	zinc finger protein 653	I
MITD1	1	0	0	0	0	1	MIT, microtubule interacting and transport, domain containing 1	I
TAF1	1	0	0	0	0	1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	I
GAMT	0	0	0	0	1	1	guanidinoacetate N-methyltransferase	I
MSI2	1	0	0	0	0	1	musashi homolog 2 (Drosophila)	I
SCAMP5	1	0	0	0	0	1	secretory carrier membrane protein 5	I
BACE1	1	0	0	0	0	1	beta-site APP-cleaving enzyme 1	I
BACE2	0	0	0	0	1	1	beta-site APP-cleaving enzyme 2	I
TPCN2	1	0	0	0	0	1	two pore segment channel 2	I
PPIL4	1	0	0	0	0	1	peptidylprolyl isomerase (cyclophilin)-like 4	I
DEPDC7	0	1	0	0	0	1	DEP domain containing 7	I
HOPX	0	0	1	0	0	1	HOP homeobox	I

ORMDL3	1	0	0	0	0	1	ORM1-like 3 (S. cerevisiae)	I
BIN1	1	0	0	0	0	1	bridging integrator 1	I
AKAP12	0	0	0	1	0	1	A kinase (PRKA) anchor protein 12	I
RPIA	1	0	0	0	0	1	ribose 5-phosphate isomerase A	I
CAPN13	1	0	0	0	0	1	calpain 13	I
BTBD16	0	0	1	0	0	1	BTB (POZ) domain containing 16	I
ANKRD22	0	1	0	0	0	1	ankyrin repeat domain 22	I
CYB5D1	1	0	0	0	0	1	cytochrome b5 domain containing 1	I
C1orf182	1	0	0	0	0	1	chromosome 1 open reading frame 182	I
FAM131A	1	0	0	0	0	1	family with sequence similarity 131, member A	I
ZNF420	0	0	1	0	0	1	zinc finger protein 420	I
CAPN12	1	0	0	0	0	1	calpain 12	I
ZNF558	1	0	0	0	0	1	zinc finger protein 558	I
C1orf51	0	0	1	0	0	1	chromosome 1 open reading frame 51	I
C2orf15	0	1	0	0	0	1	chromosome 2 open reading frame 15	I
FAM124A	1	0	0	0	0	1	family with sequence similarity 124A	I
PRKCDBP	0	0	0	0	1	1	protein kinase C, delta binding protein	I
ZNF501	0	0	1	0	0	1	zinc finger protein 501	I
UBLCP1	1	0	0	0	0	1	ubiquitin-like domain containing CTD phosphatase 1	I
FUK	1	0	0	0	0	1	fucokinase	I
FAM200A	0	0	1	0	0	1	family with sequence similarity 200, member A	I
TTC18	0	0	1	0	0	1	tetratricopeptide repeat domain 18	I
FAM84A	0	0	0	0	1	1	family with sequence similarity 84, member A	I
PYCARD	1	0	0	0	0	1	PYD and CARD domain containing	I
TRIM11	1	0	0	0	0	1	tripartite motif containing 11	I
B3GNT7	1	0	0	0	0	1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	I
DDIT4L	0	0	0	0	1	1	DNA-damage-inducible transcript 4-like	I
METTL21A	1	0	0	0	0	1	methyltransferase like 21A	I

ZNF296	0	0	0	0	1	1	zinc finger protein 296	I
WDR90	1	0	0	0	0	1	WD repeat domain 90	I
MRPL33	1	0	0	0	0	1	mitochondrial ribosomal protein L33	I
ATPAF2	1	0	0	0	0	1	ATP synthase mitochondrial F1 complex assembly factor 2	I
ZNF23	1	0	0	0	0	1	zinc finger protein 23 (KOX 16)	I
FBXO22	0	0	1	0	0	1	F-box protein 22	I
CERS5	1	0	0	0	0	1	ceramide synthase 5	I
FBXO17	0	0	1	0	0	1	F-box protein 17	I
RPP25L	1	0	0	0	0	1	ribonuclease P/MRP 25kDa subunit-like	I
ABHD11	0	0	1	0	0	1	abhydrolase domain containing 11	I
CTSE	1	0	0	0	0	1	cathepsin E	I
IPMK	1	0	0	0	0	1	inositol polyphosphate multikinase	I
CDC42EP1	1	0	0	0	0	1	CDC42 effector protein (Rho GTPase binding) 1	I
C15orf42	1	0	0	0	0	1	chromosome 15 open reading frame 42	I
C19orf40	1	0	0	0	0	1	chromosome 19 open reading frame 40	I
FAM58A	1	0	0	0	0	1	family with sequence similarity 58, member A	I
ZFP62	0	0	1	0	0	1	zinc finger protein 62 homolog (mouse)	I
TARS	1	0	0	0	0	1	threonyl-tRNA synthetase	I
ELOVL3	0	0	1	0	0	1	ELOVL fatty acid elongase 3	I
GYLTL1B	0	1	0	0	0	1	glycosyltransferase-like 1B	I
C11orf46	1	0	0	0	0	1	chromosome 11 open reading frame 46	I
C12orf45	1	0	0	0	0	1	chromosome 12 open reading frame 45	I
FRMD6	0	0	0	1	0	1	FERM domain containing 6	I
FAM213B	1	0	0	0	0	1	family with sequence similarity 213, member B	I
MYOM3	0	0	1	0	0	1	myomesin family, member 3	I
C1orf216	1	0	0	0	0	1	chromosome 1 open reading frame 216	I
SGPP2	1	0	0	0	0	1	sphingosine-1-phosphate phosphatase 2	I
AHSA2	0	0	1	0	0	1	AHA1, activator of heat shock 90kDa protein ATPase homolog 2	I

							(yeast)	
OCIAD2	0	0	1	0	0	1	OCIA domain containing 2	I
PACRG	1	0	0	0	0	1	PARK2 co-regulated	I
C8orf38	1	0	0	0	0	1	chromosome 8 open reading frame 38	I
CEP128	1	0	0	0	0	1	centrosomal protein 128kDa	I
ZNF597	1	0	0	0	0	1	zinc finger protein 597	I
C1orf74	0	0	1	0	0	1	chromosome 1 open reading frame 74	I
COMMD1	1	0	0	0	0	1	copper metabolism (Murr1) domain containing 1	I
ZNF385B	1	0	0	0	0	1	zinc finger protein 385B	I
SCFD2	1	0	0	0	0	1	sec1 family domain containing 2	I
ZNF567	1	0	0	0	0	1	zinc finger protein 567	I
SNX31	0	0	1	0	0	1	sorting nexin 31	I
NANP	1	0	0	0	0	1	N-acetylneuraminic acid phosphatase	I
ZNF449	1	0	0	0	0	1	zinc finger protein 449	I
DOK6	0	0	1	0	0	1	docking protein 6	I
NT5DC1	1	0	0	0	0	1	5'-nucleotidase domain containing 1	I
HOXA9	0	0	0	1	0	1	homeobox A9	I
RGN	0	0	1	0	0	1	regucalcin (senescence marker protein-30)	I
C22orf25	1	0	0	0	0	1	chromosome 22 open reading frame 25	I
RBM45	1	0	0	0	0	1	RNA binding motif protein 45	I
NFXL1	1	0	0	0	0	1	nuclear transcription factor, X-box binding-like 1	I
ST6GALNAC3	1	0	0	0	0	1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	I
HSPA8	0	0	0	0	1	1	heat shock 70kDa protein 8	I
ZNF524	1	0	0	0	0	1	zinc finger protein 524	I
C10orf47	1	0	0	0	0	1	chromosome 10 open reading frame 47	I
SNX33	1	0	0	0	0	1	sorting nexin 33	I
FBXL16	1	0	0	0	0	1	F-box and leucine-rich repeat protein 16	I

CCDC96	0	0	1	0	0	1	coiled-coil domain containing 96	I
ODF2	0	1	0	0	0	1	outer dense fiber of sperm tails 2	I
ORAOV1	1	0	0	0	0	1	oral cancer overexpressed 1	I
MAGEA2B	1	0	0	0	0	1	melanoma antigen family A, 2B	I
COG7	1	0	0	0	0	1	component of oligomeric golgi complex 7	I
PANK2	1	0	0	0	0	1	pantothenate kinase 2	I
FOLH1B	0	0	1	0	0	1	folate hydrolase 1B	I
AAED1	1	0	0	0	0	1	AhpC/TSA antioxidant enzyme domain containing 1	I
PHF13	1	0	0	0	0	1	PHD finger protein 13	I
PGBD2	0	0	1	0	0	1	piggyBac transposable element derived 2	I
ALDH5A1	1	0	0	0	0	1	aldehyde dehydrogenase 5 family, member A1	I
C11orf31	1	0	0	0	0	1	chromosome 11 open reading frame 31	I
PSMD10	1	0	0	0	0	1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	I
RNF39	0	0	1	0	0	1	ring finger protein 39	I
HSCB	1	0	0	0	0	1	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	I
RDH10	1	0	0	0	0	1	retinol dehydrogenase 10 (all-trans)	I
EYA1	1	0	0	0	0	1	eyes absent homolog 1 (Drosophila)	I
CAMK2G	0	0	1	0	0	1	calcium/calmodulin-dependent protein kinase II gamma	I
MRPL54	0	0	1	0	0	1	mitochondrial ribosomal protein L54	I
PSENEN	1	0	0	0	0	1	presenilin enhancer 2 homolog (C. elegans)	I
PPP1R36	0	0	0	0	1	1	protein phosphatase 1, regulatory subunit 36	I
RUNDC1	1	0	0	0	0	1	RUN domain containing 1	I
KRT6C	1	0	0	0	0	1	keratin 6C	I
NFATC2	1	0	0	0	0	1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	I
TGIF1	1	0	0	0	0	1	TGFB-induced factor homeobox 1	I
L3MBTL4	1	0	0	0	0	1	l(3)mbt-like 4 (Drosophila)	I
ANKRD29	1	0	0	0	0	1	ankyrin repeat domain 29	I

FAM117B	1	0	0	0	0	1	family with sequence similarity 117, member B	I
CNKSR3	0	0	0	0	1	1	CNKSR family member 3	I
ZNF610	0	0	1	0	0	1	zinc finger protein 610	I
KLHDC8B	1	0	0	0	0	1	kelch domain containing 8B	I
PGM2L1	1	0	0	0	0	1	phosphoglucomutase 2-like 1	I
FAM98B	1	0	0	0	0	1	family with sequence similarity 98, member B	I
ZNF547	0	0	1	0	0	1	zinc finger protein 547	I
RPUSD3	1	0	0	0	0	1	RNA pseudouridylate synthase domain containing 3	I
ARL10	0	0	1	0	0	1	ADP-ribosylation factor-like 10	I
MORN3	1	0	0	0	0	1	MORN repeat containing 3	I
IDH3G	1	0	0	0	0	1	isocitrate dehydrogenase 3 (NAD+) gamma	I
IFT20	1	0	0	0	0	1	intraflagellar transport 20 homolog (Chlamydomonas)	I
FAM84B	1	0	0	0	0	1	family with sequence similarity 84, member B	I
GAS2L3	0	1	0	0	0	1	growth arrest-specific 2 like 3	I
SMOX	1	0	0	0	0	1	spermine oxidase	I
PRR15	0	1	0	0	0	1	proline rich 15	I
S100A7A	0	0	1	0	0	1	S100 calcium binding protein A7A	I
NR2C2AP	0	0	1	0	0	1	nuclear receptor 2C2-associated protein	I
SNRPD2	1	0	0	0	0	1	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	I
P4HTM	1	0	0	0	0	1	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	I
TUBB2B	0	0	0	0	1	1	tubulin, beta 2B	I
PLA2G4D	0	0	1	0	0	1	phospholipase A2, group IVD (cytosolic)	I
SESTD1	1	0	0	0	0	1	SEC14 and spectrin domains 1	I
ATPIF1	1	0	0	0	0	1	ATPase inhibitory factor 1	I
RILPL1	1	0	0	0	0	1	Rab interacting lysosomal protein-like 1	I
ZFYVE1	1	0	0	0	0	1	zinc finger, FYVE domain containing 1	I
EXOC3L1	0	0	1	0	0	1	exocyst complex component 3-like 1	I
TFAP2E	0	0	1	0	0	1	transcription factor AP-2 epsilon (activating enhancer binding protein	I

							2 epsilon)	
HM13	1	0	0	0	0	1	histocompatibility (minor) 13	I
FBXO27	1	0	0	0	0	1	F-box protein 27	I
C19orf47	1	0	0	0	0	1	chromosome 19 open reading frame 47	I
GATS	1	0	0	0	0	1	GATS, stromal antigen 3 opposite strand	I
KCTD13	1	0	0	0	0	1	potassium channel tetramerisation domain containing 13	I
HIF1A	1	0	0	0	0	1	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	I
MRPL52	1	0	0	0	0	1	mitochondrial ribosomal protein L52	I
ID1	0	0	0	0	1	1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	I
ITPA	1	0	0	0	0	1	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	I
EXOSC8	1	0	0	0	0	1	exosome component 8	I
RFC4	1	0	0	0	0	1	replication factor C (activator 1) 4, 37kDa	I
C1orf88	0	0	1	0	0	1	chromosome 1 open reading frame 88	I
C17orf58	1	0	0	0	0	1	chromosome 17 open reading frame 58	I
GEM	1	0	0	0	0	1	GTP binding protein overexpressed in skeletal muscle	I
ORC5	1	0	0	0	0	1	origin recognition complex, subunit 5	I
HSD11B1	1	0	0	0	0	1	hydroxysteroid (11-beta) dehydrogenase 1	I
POLN	1	0	0	0	0	1	polymerase (DNA directed) nu	I
BCL6B	1	0	0	0	0	1	B-cell CLL/lymphoma 6, member B	I
AMIGO2	0	0	1	0	0	1	adhesion molecule with Ig-like domain 2	I
PKM2	1	0	0	0	0	1	pyruvate kinase, muscle	I
ADAT2	1	0	0	0	0	1	adenosine deaminase, tRNA-specific 2	I
SPC24	1	0	0	0	0	1	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	I
NSUN6	1	0	0	0	0	1	NOP2/Sun domain family, member 6	I
SLC25A45	1	0	0	0	0	1	solute carrier family 25, member 45	I
SKA2	1	0	0	0	0	1	spindle and kinetochore associated complex subunit 2	I
CREM	0	0	0	0	1	1	cAMP responsive element modulator	I

TXNRD1	0	0	0	1	0	1	thioredoxin reductase 1	I
N6AMT1	1	0	0	0	0	1	N-6 adenine-specific DNA methyltransferase 1 (putative)	I
TPRG1L	1	0	0	0	0	1	tumor protein p63 regulated 1-like	I
MACC1	0	1	0	0	0	1	metastasis associated in colon cancer 1	I
MCM7	1	0	0	0	0	1	minichromosome maintenance complex component 7	I
SCARA3	1	0	0	0	0	1	scavenger receptor class A, member 3	I
SYNE2	1	0	0	0	0	1	spectrin repeat containing, nuclear envelope 2	I
NAV2	1	0	0	0	0	1	neuron navigator 2	I
RNF8	1	0	0	0	0	1	ring finger protein 8	I
SEC13	1	0	0	0	0	1	SEC13 homolog (S. cerevisiae)	I
RBM38	1	0	0	0	0	1	RNA binding motif protein 38	I
CREB3L2	1	0	0	0	0	1	cAMP responsive element binding protein 3-like 2	I
INO80C	1	0	0	0	0	1	INO80 complex subunit C	I
DNAJC21	1	0	0	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 21	I
B3GALTL	1	0	0	0	0	1	beta 1,3-galactosyltransferase-like	I
LDHD	1	0	0	0	0	1	lactate dehydrogenase D	I
PHLPP1	1	0	0	0	0	1	PH domain and leucine rich repeat protein phosphatase 1	I
RNF126	1	0	0	0	0	1	ring finger protein 126	I
GRHL1	0	0	1	0	0	1	grainyhead-like 1 (Drosophila)	I
SNRPB2	1	0	0	0	0	1	small nuclear ribonucleoprotein polypeptide B	I
SRC	1	0	0	0	0	1	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	I
TTC8	1	0	0	0	0	1	tetratricopeptide repeat domain 8	I
GALNT10	1	0	0	0	0	1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	I
ZNF600	1	0	0	0	0	1	zinc finger protein 600	I
C19orf54	1	0	0	0	0	1	chromosome 19 open reading frame 54	I
FAM83H	1	0	0	0	0	1	family with sequence similarity 83, member H	I
GALNTL4	0	0	1	0	0	1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	I

TEX9	1	0	0	0	0	1	testis expressed 9	I
HDDC3	0	0	1	0	0	1	HD domain containing 3	I
CA13	1	0	0	0	0	1	carbonic anhydrase XIII	I
ACACA	1	0	0	0	0	1	acetyl-CoA carboxylase alpha	I
QRICH1	0	0	1	0	0	1	glutamine-rich 1	I
GGTLC2	1	0	0	0	0	1	gamma-glutamyltransferase light chain 2	I
FAM173B	1	0	0	0	0	1	family with sequence similarity 173, member B	I
LARP4	1	0	0	0	0	1	La ribonucleoprotein domain family, member 4	I
DHRS9	1	0	0	0	0	1	dehydrogenase/reductase (SDR family) member 9	I
RPE	1	0	0	0	0	1	ribulose-5-phosphate-3-epimerase	I
CCDC23	1	0	0	0	0	1	coiled-coil domain containing 23	I
SPG7	1	0	0	0	0	1	spastic paraplegia 7 (pure and complicated autosomal recessive)	I
WARS2	1	0	0	0	0	1	tryptophanyl tRNA synthetase 2, mitochondrial	I
LUC7L	1	0	0	0	0	1	LUC7-like (S. cerevisiae)	I
TEAD4	1	0	0	0	0	1	TEA domain family member 4	I
NDRG2	0	0	1	0	0	1	NDRG family member 2	I
DGKA	1	0	0	0	0	1	diacylglycerol kinase, alpha 80kDa	I
ZMYM3	1	0	0	0	0	1	zinc finger, MYM-type 3	I
ELF2	1	0	0	0	0	1	E74-like factor 2 (ets domain transcription factor)	I
BMX	0	0	0	1	0	1	BMX non-receptor tyrosine kinase	I
BDH1	1	0	0	0	0	1	3-hydroxybutyrate dehydrogenase, type 1	I
ZRANB2	1	0	0	0	0	1	zinc finger, RAN-binding domain containing 2	I
STMN1	0	0	0	1	0	1	stathmin 1	I
C17orf81	1	0	0	0	0	1	chromosome 17 open reading frame 81	I
IER5L	0	0	0	0	1	1	immediate early response 5-like	I
VKORC1	1	0	0	0	0	1	vitamin K epoxide reductase complex, subunit 1	I
RASL11A	0	0	0	0	1	1	RAS-like, family 11, member A	I
METTL21B	1	0	0	0	0	1	methyltransferase like 21B	I

PRAME	1	0	0	0	0	1	preferentially expressed antigen in melanoma	I
SPAG17	0	0	1	0	0	1	sperm associated antigen 17	I
USF1	1	0	0	0	0	1	upstream transcription factor 1	I
TCEB2	1	0	0	0	0	1	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	I
C3orf25	0	1	0	0	0	1	chromosome 3 open reading frame 25	I
CMPK2	0	0	1	0	0	1	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	I
C10orf129	0	0	1	0	0	1	chromosome 10 open reading frame 129	I
ERICH1	1	0	0	0	0	1	glutamate-rich 1	I
KBTBD12	0	0	1	0	0	1	kelch repeat and BTB (POZ) domain containing 12	I
ZNF467	0	0	0	0	1	1	zinc finger protein 467	I
PAGE2	1	0	0	0	0	1	P antigen family, member 2 (prostate associated)	I
TSEN54	1	0	0	0	0	1	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	I
ANKRD13D	1	0	0	0	0	1	ankyrin repeat domain 13 family, member D	I
ZNF662	0	0	1	0	0	1	zinc finger protein 662	I
C12orf76	1	0	0	0	0	1	chromosome 12 open reading frame 76	I
C15orf54	0	0	0	1	0	1	chromosome 15 open reading frame 54	I
DUOXA2	0	0	1	0	0	1	dual oxidase maturation factor 2	I
FAM211B	1	0	0	0	0	1	family with sequence similarity 211, member B	I
NEBL	0	1	0	0	0	1	nebulette	I
ATP6V1H	1	0	0	0	0	1	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	I
PDLIM7	0	0	0	0	1	1	PDZ and LIM domain 7 (enigma)	I
SNORD15A	0	1	0	0	0	1	small nucleolar RNA, C/D box 15A	I
SNORD21	0	1	0	0	0	1	small nucleolar RNA, C/D box 21	I
SNORD22	0	1	0	0	0	1	small nucleolar RNA, C/D box 22	I
SNORD4B	0	1	0	0	0	1	small nucleolar RNA, C/D box 4B	I
SNORD4A	0	1	0	0	0	1	small nucleolar RNA, C/D box 4A	I
SNORD42B	0	1	0	0	0	1	small nucleolar RNA, C/D box 42B	I

SNORD55	0	1	0	0	0	1	small nucleolar RNA, C/D box 55	I
SNORD36C	0	1	0	0	0	1	small nucleolar RNA, C/D box 36C	I
SNORD36B	0	1	0	0	0	1	small nucleolar RNA, C/D box 36B	I
SNORD35A	0	1	0	0	0	1	small nucleolar RNA, C/D box 35A	I
SNORD34	0	1	0	0	0	1	small nucleolar RNA, C/D box 34	I
SNORD33	0	1	0	0	0	1	small nucleolar RNA, C/D box 33	I
SNORD46	0	1	0	0	0	1	small nucleolar RNA, C/D box 46	I
SNORD83A	0	1	0	0	0	1	small nucleolar RNA, C/D box 83A	I
CELP	0	1	0	0	0	1	carboxyl ester lipase pseudogene	I
SNORD109A	0	1	0	0	0	1	small nucleolar RNA, C/D box 109A	I
PRSS3P2	1	0	0	0	0	1	protease, serine, 3 pseudogene 2	I
HCG4B	0	0	1	0	0	1	HLA complex group 4B (non-protein coding)	I
SNORD38A	0	1	0	0	0	1	small nucleolar RNA, C/D box 38A	I
SNORD38B	0	1	0	0	0	1	small nucleolar RNA, C/D box 38B	I
XIST	0	0	0	1	0	1	X (inactive)-specific transcript (non-protein coding)	I
TPTEP1	1	0	0	0	0	1	transmembrane phosphatase with tensin homology pseudogene 1	I
LOC407835	1	0	0	0	0	1	mitogen-activated protein kinase kinase 2 pseudogene	I
TRAPPC2P1	0	0	1	0	0	1	trafficking protein particle complex 2 pseudogene 1	I
OR7E91P	0	0	1	0	0	1	olfactory receptor, family 7, subfamily E, member 91 pseudogene	I
SUMO1P3	1	0	0	0	0	1	SUMO1 pseudogene 3	I
H19	1	0	0	0	0	1	H19, imprinted maternally expressed transcript (non-protein coding)	I
FTH1P3	1	0	0	0	0	1	ferritin, heavy polypeptide 1 pseudogene 3	I
CSNK2A1P	1	0	0	0	0	1	casein kinase 2, alpha 1 polypeptide pseudogene	I
PDIA3P	0	0	0	0	1	1	protein disulfide isomerase family A, member 3 pseudogene	I
RPS26P11	0	0	0	1	0	1	ribosomal protein S26 pseudogene 11	I
PIPSL	0	0	0	0	1	1	PIP5K1A and PSMD4-like, pseudogene	I

SNORA62	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 62	I
ST7-OT3	1	0	0	0	0	1	ST7 overlapping transcript 3	I
SNORD101	0	1	0	0	0	1	small nucleolar RNA, C/D box 101	I
SNORA33	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 33	I
SNORD54	0	1	0	0	0	1	small nucleolar RNA, C/D box 54	I
SNORD43	0	1	0	0	0	1	small nucleolar RNA, C/D box 43	I
SNORD18A	0	1	0	0	0	1	small nucleolar RNA, C/D box 18A	I
SNORD18B	0	1	0	0	0	1	small nucleolar RNA, C/D box 18B	I
SNORD24	0	1	0	0	0	1	small nucleolar RNA, C/D box 24	I
SNORD68	0	1	0	0	0	1	small nucleolar RNA, C/D box 68	I
LOC440354	0	0	1	0	0	1	PI-3-kinase-related kinase SMG-1 pseudogene	I
LOC613037	0	0	0	0	1	1	nuclear pore complex interacting protein pseudogene	I
SNORD29	0	1	0	0	0	1	small nucleolar RNA, C/D box 29	I
SNORD31	0	1	0	0	0	1	small nucleolar RNA, C/D box 31	I
SNORD28	0	1	0	0	0	1	small nucleolar RNA, C/D box 28	I
SNORD27	0	1	0	0	0	1	small nucleolar RNA, C/D box 27	I
SNORD26	0	1	0	0	0	1	small nucleolar RNA, C/D box 26	I
SNORD25	0	1	0	0	0	1	small nucleolar RNA, C/D box 25	I
CYP2D7P1	0	0	1	0	0	1	cytochrome P450, family 2, subfamily D, polypeptide 7 pseudogene 1	I
SNORD58A	0	1	0	0	0	1	small nucleolar RNA, C/D box 58A	I
SNORD58B	0	1	0	0	0	1	small nucleolar RNA, C/D box 58B	I
SNORD74	0	1	0	0	0	1	small nucleolar RNA, C/D box 74	I
SNORA3	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 3	I
SNORD2	0	1	0	0	0	1	small nucleolar RNA, C/D box 2	I
SNORA4	1	0	0	0	0	1	small nucleolar RNA, H/ACA box 4	I
SNORD51	0	1	0	0	0	1	small nucleolar RNA, C/D box 51	I
SNORA41	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 41	I

SNORD96A	0	1	0	0	0	1	small nucleolar RNA, C/D box 96A	I
SNORD37	0	1	0	0	0	1	small nucleolar RNA, C/D box 37	I
SNORD10	1	0	0	0	0	1	small nucleolar RNA, C/D box 10	I
DLEU1	1	0	0	0	0	1	deleted in lymphocytic leukemia 1 (non-protein coding)	I
ALOX12P2	0	0	1	0	0	1	arachidonate 12-lipoxygenase pseudogene 2	I
MST1P9	1	0	0	0	0	1	macrophage stimulating 1 (hepatocyte growth factor-like) pseudogene 9	I
SNORD61	0	1	0	0	0	1	small nucleolar RNA, C/D box 61	I
SNORD59A	0	1	0	0	0	1	small nucleolar RNA, C/D box 59A	I
SNORD57	0	1	0	0	0	1	small nucleolar RNA, C/D box 57	I
SNORD56	0	1	0	0	0	1	small nucleolar RNA, C/D box 56	I
SNORD53	0	1	0	0	0	1	small nucleolar RNA, C/D box 53	I
SNORD52	0	1	0	0	0	1	small nucleolar RNA, C/D box 52	I
SNORD50A	0	1	0	0	0	1	small nucleolar RNA, C/D box 50A	I
SNORD49A	0	1	0	0	0	1	small nucleolar RNA, C/D box 49A	I
SNORD48	0	1	0	0	0	1	small nucleolar RNA, C/D box 48	I
SNORD47	0	1	0	0	0	1	small nucleolar RNA, C/D box 47	I
SNORD45B	0	1	0	0	0	1	small nucleolar RNA, C/D box 45B	I
SNORD45A	0	1	0	0	0	1	small nucleolar RNA, C/D box 45A	I
SNORD41	0	1	0	0	0	1	small nucleolar RNA, C/D box 41	I
AKIRIN2-AS1	1	0	0	0	0	1	AKIRIN2 antisense RNA 1 (non-protein coding)	I
DLEU2L	0	0	1	0	0	1	deleted in lymphocytic leukemia 2-like	I
RPLP0P2	1	0	0	0	0	1	ribosomal protein, large, P0 pseudogene 2	I
NUDT9P1	1	0	0	0	0	1	nudix (nucleoside diphosphate linked moiety X)-type motif 9 pseudogene 1	I
AKR7A2P1	0	0	0	0	1	1	aldo-keto reductase family 7, member A2 pseudogene 1	I
NAPSB	1	0	0	0	0	1	napsin B aspartic peptidase pseudogene	I
RPL13P5	1	0	0	0	0	1	ribosomal protein L13 pseudogene 5	I

TMED10P1	1	0	0	0	0	1	transmembrane emp24-like trafficking protein 10 (yeast) pseudogene 1	I
LOC400927	1	0	0	0	0	1	TPTE and PTEN homologous inositol lipid phosphatase pseudogene	I
UBE2MP1	1	0	0	0	0	1	ubiquitin-conjugating enzyme E2M pseudogene 1	I
SNORD20	0	1	0	0	0	1	small nucleolar RNA, C/D box 20	I
SNHG3	1	0	0	0	0	1	small nucleolar RNA host gene 3 (non-protein coding)	I
SNORA71B	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 71B	I
SNORA67	1	0	0	0	0	1	small nucleolar RNA, H/ACA box 67	I
SNORD8	0	1	0	0	0	1	small nucleolar RNA, C/D box 8	I
SNORA5A	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 5A	I
SNORA8	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 8	I
SNORA75	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 75	I
SNORA13	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 13	I
FMO9P	0	0	1	0	0	1	flavin containing monooxygenase 9 pseudogene	I
LOC493754	1	0	0	0	0	1	RAB guanine nucleotide exchange factor (GEF) 1 pseudogene	I
SNORA9	0	0	1	0	0	1	small nucleolar RNA, H/ACA box 9	I
SNORA11	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 11	I
SNORA14A	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 14A	I
SNORA14B	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 14B	I
SNORA17	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 17	I
SNORA18	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 18	I
SNORA20	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 20	I
SNORA22	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 22	I
SNORA28	0	0	1	0	0	1	small nucleolar RNA, H/ACA box 28	I
SNORA29	0	0	0	0	1	1	small nucleolar RNA, H/ACA box 29	I
SNORA30	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 30	I
SNORA31	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 31	I

SNORA34	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 34	I
SNORA36A	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 36A	I
SNORA40	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 40	I
SNORA42	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 42	I
SNORA43	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 43	I
SNORA45	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 45	I
SNORA46	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 46	I
SNORA49	0	0	1	0	0	1	small nucleolar RNA, H/ACA box 49	I
SNORA51	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 51	I
SNORA54	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 54	I
SNORA56	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 56	I
SNORA5B	0	0	1	0	0	1	small nucleolar RNA, H/ACA box 5B	I
SNORA76	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 76	I
SNORA80	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 80	I
SCARNA20	0	1	0	0	0	1	small Cajal body-specific RNA 20	I
SCARNA22	0	1	0	0	0	1	small Cajal body-specific RNA 22	I
SCARNA4	0	1	0	0	0	1	small Cajal body-specific RNA 4	I
SCARNA23	0	1	0	0	0	1	small Cajal body-specific RNA 23	I
SCARNA12	0	1	0	0	0	1	small Cajal body-specific RNA 12	I
SCARNA15	0	0	1	0	0	1	small Cajal body-specific RNA 15	I
SCARNA16	0	1	0	0	0	1	small Cajal body-specific RNA 16	I
SNORA53	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 53	I
SNORA26	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 26	I
SNORA71D	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 71D	I
SNORA79	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 79	I
SNORA1	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 1	I
SNORA25	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 25	I
SNORD12	0	1	0	0	0	1	small nucleolar RNA, C/D box 12	I

SNORD11	0	1	0	0	0	1	small nucleolar RNA, C/D box 11	I
SNORA32	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 32	I
SNORD5	0	1	0	0	0	1	small nucleolar RNA, C/D box 5	I
SNORA16A	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 16A	I
SNORD6	0	1	0	0	0	1	small nucleolar RNA, C/D box 6	I
SNORD7	0	1	0	0	0	1	small nucleolar RNA, C/D box 7	I
SNHG5	0	0	0	1	0	1	small nucleolar RNA host gene 5 (non-protein coding)	I
SNORD45C	0	1	0	0	0	1	small nucleolar RNA, C/D box 45C	I
SNORD50B	0	1	0	0	0	1	small nucleolar RNA, C/D box 50B	I
SNORD17	0	1	0	0	0	1	small nucleolar RNA, C/D box 17	I
SNORD59B	0	1	0	0	0	1	small nucleolar RNA, C/D box 59B	I
RMRP	0	1	0	0	0	1	RNA component of mitochondrial RNA processing endoribonuclease	I
SNORD65	0	1	0	0	0	1	small nucleolar RNA, C/D box 65	I
SNORD66	0	1	0	0	0	1	small nucleolar RNA, C/D box 66	I
SNORD67	0	1	0	0	0	1	small nucleolar RNA, C/D box 67	I
SNORD70	0	1	0	0	0	1	small nucleolar RNA, C/D box 70	I
SNORD71	0	1	0	0	0	1	small nucleolar RNA, C/D box 71	I
SNORD84	0	1	0	0	0	1	small nucleolar RNA, C/D box 84	I
SNORD85	0	1	0	0	0	1	small nucleolar RNA, C/D box 85	I
SNORD88A	0	1	0	0	0	1	small nucleolar RNA, C/D box 88A	I
SNORD88B	0	1	0	0	0	1	small nucleolar RNA, C/D box 88B	I
SNORD89	0	1	0	0	0	1	small nucleolar RNA, C/D box 89	I
SNORD90	0	1	0	0	0	1	small nucleolar RNA, C/D box 90	I
SNORD91A	0	1	0	0	0	1	small nucleolar RNA, C/D box 91A	I
SNORD91B	0	1	0	0	0	1	small nucleolar RNA, C/D box 91B	I
SNORD92	0	1	0	0	0	1	small nucleolar RNA, C/D box 92	I
SNORD93	0	1	0	0	0	1	small nucleolar RNA, C/D box 93	I
SNORD98	0	1	0	0	0	1	small nucleolar RNA, C/D box 98	I

SNORD99	0	1	0	0	0	1	small nucleolar RNA, C/D box 99	I
SNORD111	0	1	0	0	0	1	small nucleolar RNA, C/D box 111	I
E2F6	0	0	1	0	0	1	E2F transcription factor 6	I
SNHG1	0	1	0	0	0	1	small nucleolar RNA host gene 1 (non-protein coding)	I
CCT6P1	0	1	0	0	0	1	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1	I
HSP90B3P	0	0	0	1	0	1	heat shock protein 90kDa beta (Grp94), member 3, pseudogene	I
GBP1P1	1	0	0	0	0	1	guanylate binding protein 1, interferon-inducible pseudogene 1	I
CEP170P1	0	0	0	1	0	1	centrosomal protein 170kDa pseudogene 1	I
SCARNA18	0	1	0	0	0	1	small Cajal body-specific RNA 18	I
SNORD117	0	1	0	0	0	1	small nucleolar RNA, C/D box 117	I
SNHG9	1	0	0	0	0	1	small nucleolar RNA host gene 9 (non-protein coding)	I
LOC147804	1	0	0	0	0	1	tropomyosin 3 pseudogene	I
SNORD114-9	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-9	I
SNORD114-10	0	0	1	0	0	1	small nucleolar RNA, C/D box 114-10	I
SNORD114-12	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-12	I
SNORD114-14	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-14	I
SNORD114-17	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-17	I
SNORD114-23	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-23	I
SNORD114-25	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-25	I
SNORD114-26	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-26	I
SNORD114	0	1	0	0	0	1	small nucleolar RNA, C/D box 114-28	I

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SNORD113-4	0	1	0	0	0	1	small nucleolar RNA, C/D box 113-4	I
SNORD113-5	0	1	0	0	0	1	small nucleolar RNA, C/D box 113-5	I
SNORD113-6	0	1	0	0	0	1	small nucleolar RNA, C/D box 113-6	I
SNORD113-7	0	1	0	0	0	1	small nucleolar RNA, C/D box 113-7	I
SNORD113-9	0	1	0	0	0	1	small nucleolar RNA, C/D box 113-9	I
GOLGA6L5	0	0	1	0	0	1	golgin A6 family-like 5 (pseudogene)	I
PA2G4P4	1	0	0	0	0	1	proliferation-associated 2G4 pseudogene 4	I
EP400NL	1	0	0	0	0	1	EP400 N-terminal like	I
SNORD116-2	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-2	I
SNORD116-8	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-8	I
SNORD116-12	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-12	I
SNORD116-14	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-14	I
SNORD116-18	0	0	1	0	0	1	small nucleolar RNA, C/D box 116-18	I
SNORD116-24	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-24	I
SNORD116-25	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-25	I
SNORD116-26	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-26	I
SNORD116	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-27	I

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SNORD116-29	0	1	0	0	0	1	small nucleolar RNA, C/D box 116-29	I
SLED1	0	0	1	0	0	1	proteoglycan 3 pseudogene	I
GUSBP4	1	0	0	0	0	1	glucuronidase, beta pseudogene 4	I
SNORD119	0	1	0	0	0	1	small nucleolar RNA, C/D box 119	I
SNORD121A	0	1	0	0	0	1	small nucleolar RNA, C/D box 121A	I
SNORD19B	0	1	0	0	0	1	small nucleolar RNA, C/D box 19B	I
SNORD11B	0	1	0	0	0	1	small nucleolar RNA, C/D box 11B	I
SNORD12B	0	1	0	0	0	1	small nucleolar RNA, C/D box 12B	I
SNORD58C	0	1	0	0	0	1	small nucleolar RNA, C/D box 58C	I
SNORA84	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 84	I
SNORA38B	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 38B (retrotransposed)	I
H3F3AP5	0	0	1	0	0	1	H3 histone, family 3A, pseudogene 5	I
SNORD79	0	1	0	0	0	1	small nucleolar RNA, C/D box 79	I
SNORD78	0	1	0	0	0	1	small nucleolar RNA, C/D box 78	I
SNORD94	0	1	0	0	0	1	small nucleolar RNA, C/D box 94	I
SNORD104	0	1	0	0	0	1	small nucleolar RNA, C/D box 104	I
SNORD105	0	1	0	0	0	1	small nucleolar RNA, C/D box 105	I
SCARNA10	0	1	0	0	0	1	small Cajal body-specific RNA 10	I
SCARNA14	0	1	0	0	0	1	small Cajal body-specific RNA 14	I
SNORD1A	0	1	0	0	0	1	small nucleolar RNA, C/D box 1A	I
SNORD1B	0	1	0	0	0	1	small nucleolar RNA, C/D box 1B	I
SNORD1C	0	1	0	0	0	1	small nucleolar RNA, C/D box 1C	I
SNORD82	0	1	0	0	0	1	small nucleolar RNA, C/D box 82	I
SNORD86	1	0	0	0	0	1	small nucleolar RNA, C/D box 86	I
EGOT	0	0	1	0	0	1	eosinophil granule ontogeny transcript (non-protein coding)	I
HULC	0	1	0	0	0	1	highly up-regulated in liver cancer (non-protein coding)	I

LOC643837	1	0	0	0	0	1	hypothetical LOC643837	I
C12orf47	1	0	0	0	0	1	chromosome 12 open reading frame 47	I
LOC339535	1	0	0	0	0	1	hypothetical LOC339535	I
LOC284276	1	0	0	0	0	1	hypothetical LOC284276	I
LOC149134	0	0	1	0	0	1	hypothetical LOC149134	I
LOC93622	0	0	1	0	0	1	hypothetical LOC93622	I
BREA2	0	0	1	0	0	1	breast cancer estrogen-induced apoptosis 2	I
LOC100144604	0	0	1	0	0	1	hypothetical LOC100144604	I
PMS2P4	0	0	1	0	0	1	postmeiotic segregation increased 2 pseudogene 4	I
RNU4ATAC	0	1	0	0	0	1	RNA, U4atac small nuclear (U12-dependent splicing)	I
RNU6ATAC	0	1	0	0	0	1	RNA, U6atac small nuclear (U12-dependent splicing)	I
SCARNA9L	0	1	0	0	0	1	small Cajal body-specific RNA 9-like (retrotransposed)	I
ABCC6P2	1	0	0	0	0	1	ATP-binding cassette, sub-family C, member 6 pseudogene 2	I
LINC00312	1	0	0	0	0	1	long intergenic non-protein coding RNA 312	I
GOLGA8IP	1	0	0	0	0	1	golgin A8 family, member I, pseudogene	I
FLJ35776	0	0	1	0	0	1	hypothetical LOC649446	I
DBIL5P	0	0	1	0	0	1	diazepam binding inhibitor-like 5, pseudogene	I
FKBP1AP1	0	0	1	0	0	1	FK506 binding protein 1A, 12kDa pseudogene 1	I
SNAR-C4	0	1	0	0	0	1	small ILF3/NF90-associated RNA C4	I
SNAR-C3	0	1	0	0	0	1	small ILF3/NF90-associated RNA C3	I
SNAR-B1	0	1	0	0	0	1	small ILF3/NF90-associated RNA B1	I
LOC100132111	1	0	0	0	0	1	hypothetical LOC100132111	I
SNAR-E	0	1	0	0	0	1	small ILF3/NF90-associated RNA E	I

LINC00085	0	0	1	0	0	1	long intergenic non-protein coding RNA 85	I
FER1L4	0	0	1	0	0	1	fer-1-like 4 (C. elegans) pseudogene	I
LOC728190	1	0	0	0	0	1	hypothetical LOC728190	I
LOC283663	0	0	0	0	1	1	hypothetical LOC283663	I
GUSBP11	1	0	0	0	0	1	glucuronidase, beta pseudogene 11	I
LOC100190940	0	1	0	0	0	1	hypothetical LOC100190940	I
TPT1-AS1	1	0	0	0	0	1	TPT1 antisense RNA 1	I
LOC100188947	0	0	1	0	0	1	hypothetical LOC100188947	I
BCRP3	1	0	0	0	0	1	breakpoint cluster region pseudogene 3	I
LOC442459	0	0	1	0	0	1	X-ray repair complementing defective repair pseudogene	I
RPL23P8	1	0	0	0	0	1	ribosomal protein L23 pseudogene 8	I
MIR600HG	1	0	0	0	0	1	MIR600 host gene (non-protein coding)	I
VTRNA1-3	0	1	0	0	0	1	vault RNA 1-3	I
HNRNPU-AS1	1	0	0	0	0	1	HNRNPU antisense RNA 1 (non-protein coding)	I
FLJ13197	0	0	1	0	0	1	hypothetical FLJ13197	I
AGSK1	1	0	0	0	0	1	golgin subfamily A member 2-like	I
LOC84856	0	0	1	0	0	1	hypothetical LOC84856	I
GHRLOS2	1	0	0	0	0	1	ghrelin opposite strand RNA 2 (non-protein coding)	I
C21orf119	1	0	0	0	0	1	chromosome 21 open reading frame 119	I
MTMR9LP	0	0	0	0	1	1	myotubularin related protein 9-like, pseudogene	I
RPSAP9	1	0	0	0	0	1	ribosomal protein SA pseudogene 9	I
LOC644172	0	0	1	0	0	1	mitogen-activated protein kinase 8 interacting protein 1 pseudogene	I
AMZ2P1	1	0	0	0	0	1	archaelysin family metallopeptidase 2 pseudogene 1	I

LOC388152	1	0	0	0	0	1	hypothetical LOC388152	I
LOC127841	0	1	0	0	0	1	hypothetical LOC127841	I
LOC100130776	0	0	0	0	1	1	hypothetical LOC100130776	I
LOC646214	1	0	0	0	0	1	p21 protein (Cdc42/Rac)-activated kinase 2 pseudogene	I
MIR31HG	0	0	1	0	0	1	MIR31 host gene (non-protein coding)	I
FLJ34503	1	0	0	0	0	1	hypothetical FLJ34503	I
SFTA1P	1	0	0	0	0	1	surfactant associated 1, pseudogene	I
C1orf126	0	0	1	0	0	1	chromosome 1 open reading frame 126	I
RPL21P44	0	0	1	0	0	1	ribosomal protein L21 pseudogene 44	I
LOC654342	1	0	0	0	0	1	lymphocyte-specific protein 1 pseudogene	I
LOC283070	1	0	0	0	0	1	hypothetical LOC283070	I
LOC100128822	0	0	1	0	0	1	hypothetical LOC100128822	I
INTS4L2	1	0	0	0	0	1	integrator complex subunit 4-like 2	I
FAM223B	1	0	0	0	0	1	family with sequence similarity 223, member B (non-protein coding)	I
SERHL	0	0	1	0	0	1	serine hydrolase-like	I
COL6A4P1	0	0	1	0	0	1	collagen, type VI, alpha 4 pseudogene 1	I
LOC202781	1	0	0	0	0	1	hypothetical LOC202781	I
NEAT1	0	0	1	0	0	1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	I
LOC100302650	0	0	0	0	1	1	hypothetical LOC100302650	I
LOC100133161	1	0	0	0	0	1	hypothetical LOC100133161	I

SNORA80B	0	1	0	0	0	1	small nucleolar RNA, H/ACA box 80B	I
LOC375196	1	0	0	0	0	1	hypothetical LOC375196	I
LOC400027	0	0	1	0	0	1	hypothetical LOC400027	I
KRT16P2	1	0	0	0	0	1	keratin 16 pseudogene 2	I
KRT16P3	1	0	0	0	0	1	keratin 16 pseudogene 3	I
PGCP1	0	1	0	0	0	1	progastricsin (pepsinogen C) pseudogene 1	I
MIR22	1	0	0	0	0	1	microRNA 22	I
MIR29B2	0	0	1	0	0	1	microRNA 29b-2	I
MIR210	0	0	0	1	0	1	microRNA 210	I
MIR217	0	0	0	1	0	1	microRNA 217	I
MIR221	1	0	0	0	0	1	microRNA 221	I
MIRLET7I	0	0	1	0	0	1	microRNA let-7i	I
MIR132	0	0	1	0	0	1	microRNA 132	I
MIR125A	0	0	1	0	0	1	microRNA 125a	I
MIR126	0	0	0	1	0	1	microRNA 126	I
MIR146A	0	0	1	0	0	1	microRNA 146a	I
MIR29C	0	0	1	0	0	1	microRNA 29c	I
MIR429	0	1	0	0	0	1	microRNA 429	I
MIR484	1	0	0	0	0	1	microRNA 484	I
MIR611	1	0	0	0	0	1	microRNA 611	I
MIR612	0	0	1	0	0	1	microRNA 612	I
MIR614	0	1	0	0	0	1	microRNA 614	I
MIR636	0	0	0	0	1	1	microRNA 636	I
MIR639	1	0	0	0	0	1	microRNA 639	I
MIR765	0	0	1	0	0	1	microRNA 765	I
MIR675	1	0	0	0	0	1	microRNA 675	I
MIR147B	0	0	1	0	0	1	microRNA 147b	I

MIR943	1	0	0	0	0	1	microRNA 943	I
LOC645638	1	0	0	0	0	1	WDNM1-like pseudogene	I
MIR622	0	0	0	1	0	1	microRNA 622	I
MIR650	1	0	0	0	0	1	microRNA 650	I
MIR936	1	0	0	0	0	1	microRNA 936	I
MIR1179	0	1	0	0	0	1	microRNA 1179	I
MIR1291	0	1	0	0	0	1	microRNA 1291	I
MIR1304	0	1	0	0	0	1	microRNA 1304	I
MIR1281	1	0	0	0	0	1	microRNA 1281	I
MIR1292	1	0	0	0	0	1	microRNA 1292	I
MIR1306	1	0	0	0	0	1	microRNA 1306	I
MIR1909	1	0	0	0	0	1	microRNA 1909	I
MIR711	0	0	1	0	0	1	microRNA 711	I
LOC729080	0	1	0	0	0	1	glycine cleavage system H pseudogene	I
SNORD103B	0	1	0	0	0	1	small nucleolar RNA, C/D box 103B	I
NSUN5P2	1	0	0	0	0	1	NOP2/Sun domain family, member 5 pseudogene 2	I
LOC100289019	1	0	0	0	0	1	hypothetical LOC100289019	I
MKRN9P	1	0	0	0	0	1	makorin ring finger protein 9, pseudogene	I
DSTNP2	1	0	0	0	0	1	destrin (actin depolymerizing factor) pseudogene 2	I
FLJ31485	1	0	0	0	0	1	hypothetical LOC440119	I
LOC283177	0	0	1	0	0	1	hypothetical LOC283177	I
FLJ41200	1	0	0	0	0	1	hypothetical LOC401492	I
PCBP1-AS1	0	0	1	0	0	1	PCBP1 antisense RNA 1 (non-protein coding)	I
LOC10028	1	0	0	0	0	1	hypothetical LOC100288069	I

8069								
LOC644961	0	0	0	1	0	1	actin, gamma 1 pseudogene	I
FLJ34208	0	0	1	0	0	1	hypothetical LOC401106	I
MRPL45P2	0	1	0	0	0	1	mitochondrial ribosomal protein L45 pseudogene 2	I
LOC727849	1	0	0	0	0	1	golgin A2 pseudogene	I
LOC728377	1	0	0	0	0	1	Rho guanine nucleotide exchange factor (GEF) 5 pseudogene	I
LOC643650	0	0	1	0	0	1	hypothetical LOC643650	I
HOXD-AS1	1	0	0	0	0	1	HOXD cluster antisense RNA 1	I
LOC400456	1	0	0	0	0	1	hypothetical LOC400456	I
LOC100132356	0	0	1	0	0	1	hypothetical LOC100132356	I
LOC440900	0	0	1	0	0	1	hypothetical LOC440900	I
LOC283143	0	0	1	0	0	1	hypothetical LOC283143	I
C11orf92	0	0	1	0	0	1	chromosome 11 open reading frame 92	I
LOC728066	1	0	0	0	0	1	family with sequence similarity 133, member B pseudogene	I
MIR1260B	0	0	0	1	0	1	microRNA 1260b	I
MIR3190	0	0	1	0	0	1	microRNA 3190	I
MIR4260	1	0	0	0	0	1	microRNA 4260	I
MIR4315-2	0	0	1	0	0	1	microRNA 4315-2	I
HERC2P9	0	0	1	0	0	1	hect domain and RLD 2 pseudogene 9	I
LOC100289656	0	0	1	0	0	1	Dexi homolog (mouse) pseudogene	I

LPP-AS2	0	0	1	0	0	1	LPP antisense RNA 2 (non-protein coding)	I
LOC400236	0	0	1	0	0	1	hypothetical LOC400236	I
LOC401321	1	0	0	0	0	1	hypothetical LOC401321	I
C12orf36	0	1	0	0	0	1	chromosome 12 open reading frame 36	I
LOC648809	0	0	1	0	0	1	elongation factor Tu GTP-binding domain-containing protein 1 pseudogene	I
LOC100129518	1	0	0	0	0	1	hypothetical LOC100129518	I
ABHD14A-ACY1	1	0	0	0	0	1	ABHD14A-ACY1 readthrough (non-protein coding)	I
LOC646324	0	0	0	1	0	1	hypothetical LOC646324	I
MIR3606	1	0	0	0	0	1	microRNA 3606	I
MIR3615	1	0	0	0	0	1	microRNA 3615	I
MIR3618	1	0	0	0	0	1	microRNA 3618	I
SNORD111B	0	1	0	0	0	1	small nucleolar RNA, C/D box 111B	I
MIR3651	0	1	0	0	0	1	microRNA 3651	I
MIR3653	0	1	0	0	0	1	microRNA 3653	I
MIR3658	1	0	0	0	0	1	microRNA 3658	I
MIR3662	0	1	0	0	0	1	microRNA 3662	I
MIR3917	0	0	0	1	0	1	microRNA 3917	I
MUTED-TXNDC5	0	0	0	1	0	1	MUTED-TXNDC5 readthrough (non-protein coding)	I
EEF1E1-MUTED	0	0	0	1	0	1	EEF1E1-MUTED readthrough	I
LOC100527964	1	0	0	0	0	1	hypothetical LOC100527964	I

FKBP1A-SDCBP2	0	0	0	1	0	1	FKBP1A-SDCBP2 readthrough (non-protein coding)	I
INO80B-WBP1	1	0	0	0	0	1	INO80B-WBP1 readthrough	I
PPT2-EGFL8	0	0	0	0	1	1	PPT2-EGFL8 readthrough	I
LOC100131825	0	0	1	0	0	1	hypothetical LOC100131825	I
LOC100507053	0	0	1	0	0	1	hypothetical LOC100507053	I
HOXA10-HOXA9	0	0	0	1	0	1	HOXA10-HOXA9 readthrough	I
LOC100506462	0	0	1	0	0	1	hypothetical LOC100506462	I
LOC284998	1	0	0	0	0	1	hypothetical LOC284998	I
LOC100506963	1	0	0	0	0	1	hypothetical LOC100506963	I
C10orf103	1	0	0	0	0	1	chromosome 10 open reading frame 103	I
LOC554206	0	0	1	0	0	1	leucine carboxyl methyltransferase 1 pseudogene	I
LOC100506178	0	0	0	1	0	1	hypothetical LOC100506178	I
CHEK2P2	1	0	0	0	0	1	checkpoint kinase 2 pseudogene 2	I
LOC401320	0	0	1	0	0	1	hypothetical LOC401320	I
LOC100506305	1	0	0	0	0	1	hypothetical LOC100506305	I
LOC100630918	0	0	1	0	0	1	hypothetical LOC100630918	I
LOC10050	0	0	0	1	0	1	hypothetical LOC100507254	I

7254								
MIR550A3	0	1	0	0	0	1	microRNA 550a-3	I
MIR4517	0	0	1	0	0	1	microRNA 4517	I
MIR4654	0	0	1	0	0	1	microRNA 4654	I
MIR4658	1	0	0	0	0	1	microRNA 4658	I
MIR4709	1	0	0	0	0	1	microRNA 4709	I
MIR4723	1	0	0	0	0	1	microRNA 4723	I
MIR4784	0	0	0	1	0	1	microRNA 4784	I
FLJ22447	0	0	1	0	0	1	hypothetical LOC400221	I
LOC375295	0	0	0	1	0	1	hypothetical LOC375295	I
LOC644554	0	0	1	0	0	1	hypothetical LOC644554	I
LOC541471	1	0	0	0	0	1	hypothetical LOC541471	I
LINC00339	1	0	0	0	0	1	long intergenic non-protein coding RNA 339	I
FLJ45983	0	0	1	0	0	1	hypothetical LOC399717	I
FLJ42875	1	0	0	0	0	1	hypothetical LOC440556	I
ZNF503-AS2	0	0	1	0	0	1	ZNF503 antisense RNA 2 (non-protein coding)	I
CECR5-AS1	0	0	1	0	0	1	CECR5 antisense RNA 1 (non-protein coding)	I
LINC00473	0	1	0	0	0	1	long intergenic non-protein coding RNA 473	I
HLA-F-AS1	0	0	0	0	1	1	HLA-F antisense RNA 1 (non-protein coding)	I
LOC145820	1	0	0	0	0	1	hypothetical LOC145820	I
ZNF767	1	0	0	0	0	1	zinc finger family member 767	I
CCL14-CCL15	0	0	0	0	1	1	CCL14-CCL15 readthrough	I
LOC100129917	1	0	0	0	0	1	hypothetical LOC100129917	I

LOC100506930	0	0	1	0	0	1	hypothetical LOC100506930	I
HOTAIRM1	0	0	1	0	0	1	HOXA transcript antisense RNA, myeloid-specific 1 (non-protein coding)	I
LOC100505761	0	0	1	0	0	1	hypothetical LOC100505761	I
LOC100506207	0	0	1	0	0	1	hypothetical LOC100506207	I
CYP21A1P	0	0	1	0	0	1	cytochrome P450, family 21, subfamily A, polypeptide 1 pseudogene	I
LINC00152	1	0	0	0	0	1	long intergenic non-protein coding RNA 152	I
SNHG7	0	1	0	0	0	1	small nucleolar RNA host gene 7 (non-protein coding)	I
GUSBP1	1	0	0	0	0	1	glucuronidase, beta pseudogene 1	I
LOC645166	1	0	0	0	0	1	lymphocyte-specific protein 1 pseudogene	I
C12orf32	1	0	0	0	0	1	chromosome 12 open reading frame 32	I
LOC440335	0	1	0	0	0	1	hypothetical LOC440335	I
LOC100499177	1	0	0	0	0	1	hypothetical LOC100499177	I
CBR3-AS1	1	0	0	0	0	1	CBR3 antisense RNA 1 (non-protein coding)	I
C17orf69	0	0	1	0	0	1	chromosome 17 open reading frame 69	I
MIR22HG	1	0	0	0	0	1	MIR22 host gene (non-protein coding)	I
LOC100506686	1	0	0	0	0	1	hypothetical LOC100506686	I
CASP12	1	0	0	0	0	1	caspase 12 (gene/pseudogene)	I
CYP3A5	0	0	1	0	0	1	cytochrome P450, family 3, subfamily A, polypeptide 5	I
MTERFD2	1	0	0	0	0	1	MTERF domain containing 2	I
G6PC3	1	0	0	0	0	1	glucose 6 phosphatase, catalytic, 3	I
VDAC1	1	0	0	0	0	1	voltage-dependent anion channel 1	I
C11orf73	1	0	0	0	0	1	chromosome 11 open reading frame 73	I

ECSIT	1	0	0	0	0	1	ECSIT homolog (Drosophila)	I
POMGNT1	1	0	0	0	0	1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	I
GSTM3	0	0	1	0	0	1	glutathione S-transferase mu 3 (brain)	I
ZCCHC18	0	0	1	0	0	1	zinc finger, CCHC domain containing 18	I
RPL10	1	0	0	0	0	1	ribosomal protein L10	I
UGGT1	1	0	0	0	0	1	UDP-glucose glycoprotein glucosyltransferase 1	I
THUMPD2	0	0	1	0	0	1	THUMP domain containing 2	I
CSRP2BP	1	0	0	0	0	1	CSRP2 binding protein	I
FAM114A1	1	0	0	0	0	1	family with sequence similarity 114, member A1	I
RAB17	1	0	0	0	0	1	RAB17, member RAS oncogene family	I
IGLL5	1	0	0	0	0	1	immunoglobulin lambda-like polypeptide 5	I
ZNF85	0	0	1	0	0	1	zinc finger protein 85	I
RUFY4	0	0	1	0	0	1	RUN and FYVE domain containing 4	I
C21orf59	1	0	0	0	0	1	chromosome 21 open reading frame 59	I
ORC6	0	1	0	0	0	1	origin recognition complex, subunit 6	I
PDIK1L	0	0	1	0	0	1	PDLIM1 interacting kinase 1 like	I
DNAJC19	0	0	1	0	0	1	DnaJ (Hsp40) homolog, subfamily C, member 19	I
TRAPPC1	1	0	0	0	0	1	trafficking protein particle complex 1	I
ACSF3	1	0	0	0	0	1	acyl-CoA synthetase family member 3	I
KBTBD4	0	0	1	0	0	1	kelch repeat and BTB (POZ) domain containing 4	I
GSTM4	0	0	1	0	0	1	glutathione S-transferase mu 4	I
AFMID	1	0	0	0	0	1	arylformamidase	I
GYS1	1	0	0	0	0	1	glycogen synthase 1 (muscle)	I
FUZ	1	0	0	0	0	1	fuzzy homolog (Drosophila)	I
CCNT2	0	0	1	0	0	1	cyclin T2	I
BCAT2	1	0	0	0	0	1	branched chain amino-acid transaminase 2, mitochondrial	I
IQSEC2	1	0	0	0	0	1	IQ motif and Sec7 domain 2	I
ACP1	1	0	0	0	0	1	acid phosphatase 1, soluble	I

PPP1R21	1	0	0	0	0	1	protein phosphatase 1, regulatory subunit 21	I
ECI2	1	0	0	0	0	1	enoyl-CoA delta isomerase 2	I
PRMT1	1	0	0	0	0	1	protein arginine methyltransferase 1	I
ATP5S	1	0	0	0	0	1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B)	I
SIRT2	1	0	0	0	0	1	sirtuin 2	I
CHN1	1	0	0	0	0	1	chimerin (chimaerin) 1	I
INTS7	1	0	0	0	0	1	integrator complex subunit 7	I
ATP5SL	1	0	0	0	0	1	ATP5S-like	I
FAM213A	1	0	0	0	0	1	family with sequence similarity 213, member A	I
FAM20A	1	0	0	0	0	1	family with sequence similarity 20, member A	I
GCSH	0	1	0	0	0	1	glycine cleavage system protein H (aminomethyl carrier)	I
PSCA	0	0	1	0	0	1	prostate stem cell antigen	I
HCP5	1	0	0	0	0	1	HLA complex P5 (non-protein coding)	I
BCAP29	1	0	0	0	0	1	B-cell receptor-associated protein 29	I
POFUT2	1	0	0	0	0	1	protein O-fucosyltransferase 2	I
MFNG	1	0	0	0	0	1	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	I
ZNF626	0	0	1	0	0	1	zinc finger protein 626	I
MED18	1	0	0	0	0	1	mediator complex subunit 18	I
MALL	1	0	0	0	0	1	mal, T-cell differentiation protein-like	I

Appendix Table A.4.10.1. This tables lists the significantly differentially expressed genes with a log2(fold change) >= 2 enriched in tumour endothelial cells versus normal cells for all 5 contrasts. 2,477 genes were enriched in tumour lung (Solid4), 409 in another tumour lung sequenced with Illumina, 768 genes enriched in bladder ECs (Solid4), 570 enriched in colon tumour endothelium (Solid4) and 215 differentially enriched genes in tumour conditioned HUVEC (Illumina). A non-redundant number of 3,922 genes were enriched in tumour ECs of multiple organs in these 5 contrasts.

Appendix Table A.4.13.1. Full AngioScore results for all 3,922 genes found using Cuffdiff

Gene	Abstracts from gene search	Abstracts matching keywords	Angio Score	Endo log2(FC)	Angio log2(FC)
DLEU2L	1	1	100	-4.03	-0.23
LOC613037	1	1	100	-4.14	-1.2
CHEK2P2	2	2	100		
VEGFA	2373	2257	95	-2.79	1.43
VEGFC	231	215	93	-1.68	0.61
HIF1A	1367	1237	90	1.49	1.12
EDN1	517	451	87	4.05	-0.8
PROCR	114	91	80	-0.36	0.4
HIC1	38	30	79		-2.24
VEGFB	42	32	76	-2.64	-0.15
IRAK1BP1	4	3	75		0.84
NOS3	1302	962	74	-0.17	1.12
CA9	145	107	74		2.04
VASH1	26	19	73	4.78	0.66
COL18A1	124	87	70	-2.13	0.92
VCAM1	345	242	70	-0.35	-0.98
CD248	23	16	70	-3.57	0.07
PTTG1	127	88	69	3.21	0.67
PGF	129	88	68	-3.57	3.08
ESM1	25	17	68	8.35	0.26
ANGPT2	225	148	66	10.68	2.32
PDPN	96	63	66	1.75	1.86
MCAM	81	53	65	1.95	-0.7
LIPG	86	56	65	-0.35	-0.7
TNFRSF12A	51	33	65	-3.61	-0.29
MIR210	31	20	65		
PTK6	58	37	64	3.29	-1.18
NUAK1	22	14	64	2.3	-0.53
IGFBP7	63	40	63	0.17	0.64
TRAF5	63	40	63	-0.88	-0.34
MAGEA4	38	24	63		-1.64
MIR126	35	22	63		
MEN1	196	121	62	-3.2	-0.4
TNF	3633	2180	60		3.69
EGFL7	25	15	60	-3.57	-0.7
MAGEA2	20	12	60		4.25

CCDC34	5	3	**60**	-2.06	-0.58
MIR650	5	3	**60**		1
DLL4	52	31	**60**	3.7	0.39
MYCN	192	113	**59**	2.31	1.86
ENG	242	142	**59**	3.63	1.11
TYMP	123	72	**59**	-8.57	0.37
MAGEA2B	12	7	**58**		
SLC4A11	28	16	**57**	0.82	-0.44
MUCL1	14	8	**57**		
PLVAP	14	8	**57**	-6.1	1.28
SNAI1	157	89	**57**	-1.71	0.85
ORAOV1	9	5	**56**	1.75	0.02
ZNF703	9	5	**56**		-1.64
OLR1	158	87	**55**	-7.03	-0.29
DMBT1	75	41	**55**		0.39
THBS1	319	174	**55**	3.24	-0.84
FGFBP1	22	12	**55**	-8.79	-0.57
CLDN9	22	12	**55**		1.51
TNFRSF10A	149	81	**54**	-0.24	0.23
HMGA2	161	87	**54**	-2.64	-0.38
FHIT	219	118	**54**	-7.03	-0.55
NME1-NME2	13	7	**54**	-1.36	3.69
PRAME	56	30	**54**	-7.59	-0.53
PLXDC1	15	8	**53**	-3.2	1.79
STAB1	30	16	**53**	0.41	1.61
SELE	321	171	**53**	6.08	0.02
OSGIN1	17	9	**53**	-6.1	-1.81
TPD52	42	22	**52**	-2.83	0.04
IL24	90	47	**52**		0.79
SERPINF1	150	78	**52**	-9.3	-0.98
ETV4	62	32	**52**	-5.98	7.15
PDGFC	37	19	**51**	1.67	-0.8
TNFRSF25	39	20	**51**	3.29	1.91
TFPI2	88	45	**51**	0.86	-2.58
ENPP2	75	38	**51**	2.65	-3.44
FJX1	4	2	**50**	-0.43	2.04
TMSB15B	6	3	**50**	4.94	0.29
TRAF4	34	17	**50**	-5.11	0.94
MIR205	30	15	**50**		
MIR3688-2	2	1	**50**		
NTN4	16	8	**50**	3.73	-2.11
HILPDA	14	7	**50**	-0.73	1.77
MMP14	290	145	**50**	-1.36	0.1

LYPD3	20	10	**50**	-6.1	-0.46
GRP	50	25	**50**		2.76
AKR7A2P1	2	1	**50**	2.31	2.76
HOXD-AS1	2	1	**50**	2.31	-0.5
LOC645166	2	1	**50**	0.76	0.28
ECE2	16	8	**50**	0.69	-0.19
STRADA	22	11	**50**	-1.09	-0.56
ST20	2	1	**50**	-3.57	-0.04
MYOM3	4	2	**50**	-3.57	-2.65
MIR622	4	2	**50**		
MIR3917	2	1	**50**		
MIR4784	2	1	**50**		
PAGE2B	2	1	**50**		3.69
PPIAL4B	2	1	**50**		
MIR943	2	1	**50**		
MIR936	2	1	**50**		
MIR1179	2	1	**50**		
MIR3606	2	1	**50**		
MIR3615	2	1	**50**		
MIR3618	2	1	**50**		
MIR3651	2	1	**50**		
MIR3653	2	1	**50**		
MIR3658	2	1	**50**		
LOC100131825	2	1	**50**		-1.02
MIR4654	2	1	**50**		
MIR4658	2	1	**50**		
MIR4709	2	1	**50**		
MIR4723	2	1	**50**		
IGFLR1	2	1	**50**	2.31	1.84
PMEPA1	16	8	**50**	-5.11	0.06
PDZK1IP1	20	10	**50**	-9.3	-1.65
NOX4	115	57	**50**	2.25	-2.07
PTP4A3	77	38	**49**		-0.26
NKX3-1	67	33	**49**	4.94	-0.92
CXCR7	57	28	**49**	-1.68	-0.04
MAGEA3	57	28	**49**	2.31	-0.14
CLDN5	57	28	**49**	1.75	-0.5
TNFSF9	51	25	**49**	-6.1	0.23
CLDN7	62	30	**48**	-2.64	-0.2
MIR22	27	13	**48**		
SEMA3F	42	20	**48**		-0.94
FH	61	29	**48**	-1.09	-0.98

PROX1	59	28	**47**	-2.64	1.2
KLF5	76	36	**47**	-3.84	0.19
TNFRSF10C	57	27	**47**	3.03	-4.16
NME1	199	94	**47**	-0.25	0.82
SERPINB4	32	15	**47**	-7.03	-2.6
BMX	47	22	**47**	7.02	-4.16
ID1	171	80	**47**	-4.59	1.34
F2R	244	114	**47**	0.65	-0.16
ST7	28	13	**46**	2.57	-0.49
MADCAM1	28	13	**46**	-6.1	4.97
PCDH10	24	11	**46**	0.82	-0.25
TNFSF18	35	16	**46**	4.6	
ADM	221	101	**46**	-1.3	-0.37
LOXL2	33	15	**45**	-1.8	2.15
MIR21	187	85	**45**	-2.64	
ITGAV	356	161	**45**	1.5	-0.26
CST6	31	14	**45**		1.99
PLAUR	332	149	**45**	-2.64	0.88
KCTD11	9	4	**44**	-2.64	-0.44
CYP2W1	9	4	**44**	2.31	-2.6
DLEU1	9	4	**44**	-6.1	-0.84
MIR125A	18	8	**44**		
LGALS3BP	50	22	**44**	-6.28	0.82
TNS4	25	11	**44**	2.31	-0.7
LLGL1	25	11	**44**	-0.24	1.22
XAF1	41	18	**44**	-0.49	-0.07
ADAMTS18	16	7	**44**	4.5	6.22
ANGPTL2	16	7	**44**	0.05	1.36
TNFAIP2	16	7	**44**	-0.9	0.11
CLDN3	62	27	**44**		1.3
AXIN2	69	30	**43**		2.47
JAM2	23	10	**43**	3.29	-0.19
TNFRSF10D	51	22	**43**	-1.87	3.17
NME2	58	25	**43**	-0.42	-0.26
NDRG2	65	28	**43**	-7.03	-0.2
LZTFL1	7	3	**43**	3.03	-0.26
STEAP1	21	9	**43**	4.02	-2.67
CCDC19	7	3	**43**	-2.64	-3.39
NOV	61	26	**43**	-8.31	1.44
CDH13	113	48	**42**	4.35	-0.92
DAPK1	132	56	**42**	4.28	1.91
STC1	52	22	**42**	-0.08	-1.82
WNT2	52	22	**42**		3.26

MDK	97	41	**42**	-5.98	1.04
THBS2	57	24	**42**	-8.98	0.55
EXTL3	19	8	**42**	-5.33	-0.65
SCGB3A1	31	13	**42**	-2.64	-1.14
DDAH1	43	18	**42**	3.58	-0.42
S100A2	55	23	**42**	-7.03	-0.91
MMRN1	24	10	**42**	9.54	0.97
CSRP2	12	5	**42**	-3.62	2.78
PTPN13	72	30	**42**	-6.1	-0.95
GBP5	12	5	**42**	-2.64	-0.83
TPBG	17	7	**41**	-2.42	-0.05
CLDN10	22	9	**41**	-0.42	-1.44
PHLPP1	37	15	**41**	-2.64	-0.41
CUL2	79	32	**41**	-0.99	-0.36
TP63	415	168	**40**	0.82	-0.98
CDKN2D	42	17	**40**	0.82	1.54
AURKA	315	127	**40**	-0.2	3.08
NOTCH3	167	67	**40**	-8	0.35
ULBP2	35	14	**40**	0.05	1.51
CXCL17	10	4	**40**		-0.7
ZNFX1-AS1	5	2	**40**	1.34	0.13
NRARP	5	2	**40**		2.13
ADAMTS7	10	4	**40**	0.82	1.58
PEBP4	15	6	**40**		-2.04
CHKA	30	12	**40**	-1.44	0.29
P4HTM	10	4	**40**	-7.03	0.74
EGR1	255	102	**40**	-8.79	0.03
SNORD50A	5	2	**40**		2.76
AGSK1	5	2	**40**		3.69
ENTPD1	60	24	**40**	-0.33	-0.51
ANGPTL4	78	31	**40**	-0.74	0.38
BRAF	751	296	**39**	2.31	0.61
EPHB2	107	42	**39**	0.69	1.76
CLCA2	23	9	**39**	-7.03	-1.02
AKR1B10	46	18	**39**	-7.59	0.66
MGMT	364	142	**39**	-7.59	0.53
PDGFB	203	79	**39**	2.44	2.31
SELP	279	108	**39**		-1.67
CD34	205	79	**39**	5.73	-0.91
PLAU	408	157	**38**	-3.4	0.33
ING5	26	10	**38**	-1.25	1.18
TP53I11	13	5	**38**	-0.52	0.44
STAB2	26	10	**38**	-7.03	-0.7

GDF15	133	51	**38**	-9.3	0.38
CD200	34	13	**38**	-2.64	0.29
APLN	89	34	**38**	7.75	0.78
MUC4	89	34	**38**	-8.31	0.05
MUC1	397	151	**38**	-9.56	0.72
EPCAM	108	41	**38**	-8.57	0.6
GLTSCR2	29	11	**38**	-6.5	0.67
MMP2	921	348	**38**	-1.02	1.41
S100P	56	21	**38**	1.75	-0.94
TDGF1	56	21	**38**	-9.67	0.18
NAPSA	24	9	**38**		-0.32
PODN	8	3	**38**		-0.19
FCRLB	8	3	**38**		-0.7
BTG3	16	6	**38**	1.48	0.06
ID4	40	15	**38**	-6.1	1.18
FXYD3	24	9	**38**	-7.59	-0.89
BEX2	16	6	**38**	-7.59	0.87
MIR217	8	3	**38**		
CLEC14A	8	3	**38**	6.18	-0.98
CLDN1	105	39	**37**	-8.23	-0.78
S1PR3	49	18	**37**	-1.66	0.76
FSCN1	98	36	**37**	-3.1	3.47
GRB7	60	22	**37**	-6.1	0.66
PTGS2	1443	529	**37**	-0.88	-2.1
SDHC	41	15	**37**	-1.7	0.32
GJA4	63	23	**37**	3.7	-1.02
MIR424	11	4	**36**		
COL8A1	22	8	**36**	0.54	-0.92
AGR3	11	4	**36**		-1.41
SOX18	22	8	**36**	5.69	-1.02
NAT6	11	4	**36**	-7.03	0.66
CDH2	165	60	**36**	-3	-0.49
MMP7	270	98	**36**	-10.22	-1.82
CDH3	80	29	**36**	-8.98	-0.31
NDUFA13	47	17	**36**	0.53	0.12
CCNE1	224	81	**36**	2.72	3.32
RARRES3	36	13	**36**		-0.01
PTHLH	147	53	**36**	-8.31	0.86
MMP11	50	18	**36**	-7.03	2.66
FAP	50	18	**36**	-2.08	2.5
DDIT4	50	18	**36**	-6.1	0.76
AIM2	25	9	**36**		2.76
PRKCDBP	14	5	**36**	-3.2	0.6

TSTD1	14	5	**36**		-0.19
MIR29C	14	5	**36**		-1.54
PTX3	121	43	**36**	1.98	6.33
SSTR1	48	17	**35**		1.41
UPK2	17	6	**35**	-7.03	
PLXNB1	51	18	**35**	-5.52	-0.98
PMAIP1	71	25	**35**	-1.66	-0.7
MIR221	71	25	**35**		0.23
CDK4	265	93	**35**	-3	0.46
EFNA1	60	21	**35**	0.26	0.27
CDX2	158	55	**35**		2.4
SFN	138	48	**35**	-9.56	0.67
MSLN	69	24	**35**		1.26
SNCG	69	24	**35**	-2.64	-1.54
CD276	46	16	**35**	-2.64	0.9
BBC3	95	33	**35**	-1.71	0.54
NAA10	49	17	**35**	-1.15	0.63
RELA	724	251	**35**	-2.06	0.32
IER3	52	18	**35**	-3.37	-0.19
CKS2	26	9	**35**	2.52	0.85
ULBP1	26	9	**35**	4.6	-1.67
NACC1	26	9	**35**	-7.03	0.57
CDKN1A	948	328	**35**	-3.53	-0.67
CEACAM5	87	30	**34**	0.82	0.45
MMP9	1400	482	**34**	-3.21	7.48
SIM2	32	11	**34**	-6.1	-0.44
ARG2	38	13	**34**	-2.5	-1.83
PDGFD	38	13	**34**	-2.24	-0.23
CTTN	152	52	**34**	1.53	-0.28
TCEB2	79	27	**34**	2.2	0.2
LOX	88	30	**34**	0.07	-0.41
PHB	121	41	**34**	-2.25	0.06
IGF2BP3	62	21	**34**	-0.56	2.98
SPHK1	124	42	**34**	0.05	2.63
AREG	92	31	**34**	-7.03	-2.6
MIR3189	3	1	**33**		
CXorf61	3	1	**33**	0.82	
F2RL2	54	18	**33**	1.75	-2.45
SPOCK3	9	3	**33**	-7.59	-4.38
C12orf75	3	1	**33**	-1.87	-1.06
ELF3	42	14	**33**	-4.54	-0.29
GAS8	9	3	**33**	-6.1	1.15
BCL2L12	24	8	**33**	-3.2	2.58

ZNF134	3	1	**33**	2.31	5.81
HEY1	42	14	**33**	3.51	1.86
ZNF420	6	2	**33**	2.31	1.51
XRCC6BP1	3	1	**33**	2.31	-0.52
AFMID	3	1	**33**	1.05	-1.08
RPS26P11	3	1	**33**	0.82	1.2
TPGS2	6	2	**33**	-0.3	0.17
VBP1	27	9	**33**	-0.9	0.21
TMEM97	12	4	**33**	-1.98	0.37
LRIG3	15	5	**33**	-2.64	-0.7
ALOX12P2	3	1	**33**	-2.64	0.27
EHF	33	11	**33**	-3.36	-1.1
TCEAL3	6	2	**33**	-3.61	0.73
DSE	12	4	**33**	-3.89	0.29
RBM38	15	5	**33**	-4.52	-0.58
ARHGEF38	6	2	**33**	-6.1	-1.64
ZCCHC18	3	1	**33**	-6.1	6.54
DEPDC7	3	1	**33**	-7.03	-1.47
MAGEF1	9	3	**33**	-9.56	0.29
HSP90B3P	3	1	**33**		
TFAP2A	135	45	**33**		-1.28
TFAP2C	42	14	**33**		-0.85
AGBL2	9	3	**33**		-0.7
RASL11A	3	1	**33**		-1.49
H3F3AP5	3	1	**33**		
SNAR-E	3	1	**33**		-4.16
MIR675	6	2	**33**		
MIR1909	3	1	**33**		
ADAM23	18	6	**33**	0.82	-0.7
SLC35F1	9	3	**33**	0.39	0.35
PVRL4	18	6	**33**	-1.44	-0.51
TMEM120A	3	1	**33**	-2.64	-0.7
MSMP	3	1	**33**	-4.14	0.27
TMPRSS2	78	26	**33**	-6.1	-0.21
CACNA2D2	12	4	**33**		1.44
XKRX	3	1	**33**		1.2
ABCC6	85	28	**33**		-1.23
CXCL5	70	23	**33**	-6.1	0.58
AGR2	46	15	**33**	-7.03	-0.06
LAMC2	86	28	**33**	-3.54	0.63
SLC7A5	77	25	**32**	-10.29	-0.33
HSPG2	87	28	**32**	-1.28	0.15
CLDN4	84	27	**32**	-9.3	-0.92

SOX17	28	9	**32**	4.78	-0.48
CLDN12	28	9	**32**	-0.37	-0.53
CEACAM6	53	17	**32**	-7.59	0.97
PERP	25	8	**32**	-2.16	0.09
HAS3	25	8	**32**	-7.03	3.34
SDC4	91	29	**32**	-0.96	-1.65
ITGB1	747	238	**32**	0.63	-0.17
SLC39A6	22	7	**32**	-1.17	-0.15
FOXO4	66	21	**32**	-6.1	-0.3
ROBO1	63	20	**32**	-3.2	-1.38
TNFRSF11B	353	112	**32**	-0.8	-1.28
SPP1	498	158	**32**	-9.16	-1.19
SKP2	246	78	**32**	4.5	-0.26
THY1	60	19	**32**	-9.43	0.67
SPOCK1	19	6	**32**	0.14	-1.45
GLMN	19	6	**32**	-1.1	0.58
ATF3	114	36	**32**	-3.61	-0.93
HPGD	76	24	**32**	-7.59	-2.48
JAG2	38	12	**32**	1.75	1.33
RPSA	80	25	**31**	-3.32	0.18
NOSTRIN	16	5	**31**	4.86	0.24
HRSP12	16	5	**31**	-2.23	-1.58
UPK1A	16	5	**31**		-4.16
LGALS1	205	64	**31**	0.07	-0.13
SPINT2	45	14	**31**	-5.04	0.25
MEG3	29	9	**31**	-3.5	0.65
RHOD	29	9	**31**	-6.1	-1.02
IL8	1271	394	**31**	-1.71	-0.23
SERPINB2	81	25	**31**	-8.31	-4.28
DKK1	175	54	**31**	-2.19	-0.7
LOXL3	13	4	**31**	-6.1	1.2
STARD10	13	4	**31**	-7.03	0.72
THOC6	13	4	**31**	-8.79	0.8
KRT19	124	38	**31**	-13.06	1.68
FOLH1	111	34	**31**		-1.18
ERRFI1	36	11	**31**	-2.06	-1.47
RBL1	95	29	**31**	0.76	-0.26
EREG	23	7	**30**	3.29	-1.23
CKAP2	23	7	**30**	0.94	1.14
TEAD4	23	7	**30**	-2.64	0.45
HDGF	43	13	**30**	-1.36	0.43
SERPINB3	53	16	**30**	-6.1	-8.03
AKAP12	53	16	**30**	4.93	-0.44

COL4A2	73	22	**30**	-3.29	1.06
SERPINE1	950	286	**30**	2.83	-1.05
EEF1A2	50	15	**30**	-10.36	2.47
COL15A1	20	6	**30**	4.15	1.2
TXNDC17	10	3	**30**	0.98	-0.65
ZRANB1	10	3	**30**	-1.65	-0.32
LRIG2	10	3	**30**	-1.71	2.24
CSAG2	20	6	**30**	-6.1	
GLS2	20	6	**30**	-6.1	-1.61
C19orf33	10	3	**30**	-6.1	-0.7
MIR29B2	10	3	**30**		
MIRLET7I	10	3	**30**		
SLC2A1	280	84	**30**	-0.11	1.28
GPR87	10	3	**30**	-6.1	-0.39
CLDN23	10	3	**30**	-7.03	1.92
PODXL2	10	3	**30**		2.18
IDH2	107	32	**30**	-4.68	0.04
TIAM1	77	23	**30**	-6.1	1.34
CLDN11	27	8	**30**	10.65	0.86
KRT7	71	21	**30**	-4.38	-0.78
MMP10	61	18	**30**	7.45	1.14
RHEB	78	23	**29**	-2.35	-0.07
UGT1A5	17	5	**29**		
SRPX2	17	5	**29**	2.1	-0.44
SULF1	34	10	**29**	-2.14	-0.19
RAP1GAP	51	15	**29**		-0.14
MIR132	17	5	**29**		
ROCK2	75	22	**29**	-0.8	-0.32
HBEGF	133	39	**29**	0.65	1
WFDC2	41	12	**29**	-8.79	-0.7
THBS4	41	12	**29**		2.17
OLFM4	24	7	**29**	-7.03	0.9
UCK2	24	7	**29**	-1.97	1.37
LIMK1	72	21	**29**	-2.64	0.4
CLDN18	24	7	**29**	3.29	-0.06
SOX4	55	16	**29**	5.98	1.37
PELP1	55	16	**29**	-4.54	0.06
FHL2	86	25	**29**	-1.07	-0.85
JUP	124	36	**29**	-2.03	0.93
WISP1	45	13	**29**		1.77
LPAR2	45	13	**29**		0.16
VWA1	7	2	**29**	-7.03	0.65
MAGEA9B	7	2	**29**		

RND3	35	10	**29**	1.36	-1.4
SULF2	28	8	**29**	2	1.76
GPC4	14	4	**29**	-6.1	-0.96
LY6G6D	7	2	**29**		-0.7
RASL10A	7	2	**29**	0.82	1.56
MARVELD1	7	2	**29**	-0.46	0.45
BRK1	14	4	**29**	-1.57	-0.73
TMEM115	7	2	**29**	-2.64	0.79
AGBL5	7	2	**29**	-2.83	-0.33
CINP	7	2	**29**	-3.04	-0.12
ID2	98	28	**29**	-3.22	0.22
DUSP4	28	8	**29**	-3.8	-0.33
MAGED4B	14	4	**29**	-9.43	2.47
FOLH1B	7	2	**29**		
PSCA	63	18	**29**		-4.5
ST7L	7	2	**29**	0.82	-0.2
CDH6	21	6	**29**	-1.44	-0.76
GAS1	28	8	**29**	-8	-1.01
CYP4Z1	7	2	**29**		2.76
PROC	267	76	**28**	-7.03	-0.81
HK2	60	17	**28**	-3.36	1.09
HMGA1	152	43	**28**	-5.08	1.66
CD9	131	37	**28**	2.56	-0.89
SOD3	124	35	**28**		-1.44
PBK	32	9	**28**	0.94	0.94
UBE2C	64	18	**28**	-1.2	3.62
CDKN3	25	7	**28**	0.49	3.49
HSD3B1	75	21	**28**		-4.16
FERMT3	25	7	**28**	-6.33	1.41
COL4A1	122	34	**28**	2.09	1.47
IGFBP2	133	37	**28**	-9.3	1.1
UPK1B	18	5	**28**	1.55	-0.8
RIPK4	18	5	**28**	-7.03	-1.28
DNAJB4	18	5	**28**	1.53	-0.62
CSAG3	18	5	**28**		
SRC	821	228	**28**	1.75	-0.15
PIM1	119	33	**28**	-3.63	0.91
TNFRSF4	65	18	**28**		4.97
PVR	58	16	**28**	-0.57	-0.04
WDR76	11	3	**27**	-0.24	2.26
RERG	11	3	**27**	-6.1	-1.16
RAB25	22	6	**27**	-8	1.15
EDARADD	11	3	**27**		3.69

PPAP2A	22	6	**27**	1.09	-0.83
PPAP2C	11	3	**27**	-9.43	0.4
ITGB3	778	209	**27**	-2.24	-1.95
IGF2	378	101	**27**	-3.92	2.86
FASN	146	39	**27**	-10.22	-1.22
ANXA2	221	59	**27**	0.79	-0.37
SPRR3	30	8	**27**	1.32	-6.85
TP53I3	30	8	**27**	-0.24	-1.19
LZTS2	15	4	**27**	-5.11	-0.35
TMPRSS4	15	4	**27**		0.03
TIMP1	363	96	**26**	-2.52	0.32
NKX2-1	140	37	**26**		1.44
TUBB3	72	19	**26**	-6.57	4.3
FGFR1	262	69	**26**	-2.13	0.16
VMP1	19	5	**26**	2.64	0
MAL2	19	5	**26**	-3.61	1.49
HTRA3	19	5	**26**		-0.06
GGCT	19	5	**26**	-2.1	-1.4
DHH	19	5	**26**	-6.1	-1.98
ENC1	19	5	**26**	-2.03	0.61
TRIB3	57	15	**26**	-6.42	3.09
ADC	19	5	**26**		-0.78
MAD2L1	137	36	**26**	-2.44	-1.16
CHEK2	358	94	**26**	0.69	1.12
SFRP2	61	16	**26**		1.14
LGR5	42	11	**26**		-5.09
TGFA	157	41	**26**	1.86	-0.19
TGFB1	2231	582	**26**	-5.49	-0.53
TTK	69	18	**26**	0.69	4.97
PIN1	200	52	**26**	-9.3	0.65
TACSTD2	54	14	**26**	-9.67	-0.83
JUNB	85	22	**26**	-8	0.26
PLK4	35	9	**26**	1.75	2.5
RALA	74	19	**26**	3.2	0.72
CSF1	157	40	**25**	-7.59	0.4
F2RL1	216	55	**25**	-1.8	-0.17
TP53BP1	139	35	**25**	-2.38	0.44
KITLG	155	39	**25**	-0.5	-0.53
HDAC1	669	168	**25**	-0.76	0.92
ADAMTS6	8	2	**25**	5.01	6.22
LYPD6B	4	1	**25**		1.77
SHROOM1	4	1	**25**	1.23	-1.32
MCTS1	20	5	**25**	-0.06	0.52

PIM3	20	5	**25**	-2.33	-0.03
KIAA0101	24	6	**25**	-3.89	0.99
DNAJC12	8	2	**25**		0.86
FOXQ1	12	3	**25**		-1.37
GOLT1A	8	2	**25**		-0.04
STC2	28	7	**25**	-4.72	0.51
LOC654342	4	1	**25**	1.81	2.87
DEPDC1B	4	1	**25**	3.29	0.84
OCIAD2	4	1	**25**	1.04	0.51
CREB3L4	12	3	**25**	3.7	-0.88
DLGAP5	28	7	**25**	0.98	5.81
CITED4	8	2	**25**	0.82	-1.49
PDRG1	12	3	**25**	-0.16	-0.57
DGKA	32	8	**25**	-1.07	0.47
POLR3GL	4	1	**25**	-1.65	-0.46
IP6K2	24	6	**25**	-1.93	1.94
ERP29	32	8	**25**	-2.1	0.46
RRNAD1	4	1	**25**	-2.33	0.82
PYCARD	80	20	**25**	-2.33	0.76
TATDN1	4	1	**25**	-2.85	-1.94
PLEKHG5	12	3	**25**	-3.04	1.27
RBP1	44	11	**25**	-3.61	0.58
NAPSB	4	1	**25**	-4	1.09
SNORA42	4	1	**25**	-6.1	
ANXA10	12	3	**25**	-7.03	-5.09
PDCD2L	8	2	**25**	-7.03	-0.32
DUSP2	24	6	**25**	-7.59	-1.28
SIVA1	36	9	**25**	-8.98	1.64
HOPX	32	8	**25**	-9.3	0.55
CCDC73	4	1	**25**		-1.67
AURKC	32	8	**25**		3.69
SFTA3	4	1	**25**		1.14
GRHL3	8	2	**25**		0.79
VGLL1	4	1	**25**		-1.26
STK33	12	3	**25**		1.14
SGPP2	4	1	**25**		-1.68
ARL10	4	1	**25**		-0.7
PAGE2	4	1	**25**		2.76
ST7-OT3	4	1	**25**		3.69
RNU6ATAC	4	1	**25**		
MIR484	4	1	**25**		
SNORD111B	4	1	**25**		
SLC36A4	4	1	**25**	3.03	1.67

SPNS2	4	1	**25**	2.31	-0.12
SIRPB2	4	1	**25**	2.72	-1.26
GDE1	12	3	**25**	0.19	-0.29
TMBIM1	12	3	**25**	-1.03	-0.31
Mar-09	8	2	**25**	-2.64	1.52
TMEM54	4	1	**25**	-6.1	1.24
CDH8	16	4	**25**		
CYP4Z2P	4	1	**25**		-5.66
ASTL	4	1	**25**		
CDKN2B	261	65	**25**	-4.18	-0.29
SOX9	153	38	**25**	-4.32	0.35
EPOR	174	43	**25**	-7.03	0.68
JUND	85	21	**25**	-0.44	-0.12
H19	69	17	**25**	-2.64	2.12
RAD51C	49	12	**24**	1.16	-0.9
MIR146A	98	24	**24**		
MAGED1	45	11	**24**	-1.99	1.29
NPAS2	41	10	**24**	-3.57	0.26
BCAM	41	10	**24**		0.9
AURKB	201	49	**24**	-4.14	6.72
PSMD10	78	19	**24**	3.31	0.98
PTP4A1	37	9	**24**	0.28	-0.12
CHN2	37	9	**24**		-1.34
TOP2A	251	61	**24**	0.3	3.78
MMP1	597	145	**24**	12.12	1.38
CD109	33	8	**24**	4.16	-1.76
ACTA2	95	23	**24**	-3.52	-0.87
PHLDA2	29	7	**24**	-6.1	0.92
KLK8	29	7	**24**	-7.03	0.26
SPRY1	29	7	**24**	2.31	1.46
PLS3	29	7	**24**	1.74	0.92
GNMT	29	7	**24**		0.73
ACE2	158	38	**24**		-2
CXADR	96	23	**24**	3.08	-0.01
ADAM12	92	22	**24**	-1.71	1.82
PDCD5	46	11	**24**	0.13	0.94
PTGER2	92	22	**24**	-6.1	4.97
S100A9	155	37	**24**	-6.1	0.8
TGIF2	21	5	**24**	0.33	1.44
RGS5	42	10	**24**	-1.97	-0.03
TNFSF4	84	20	**24**	6.01	1.77
CHST1	21	5	**24**	0.82	1.9
CUL9	21	5	**24**	-0.88	0.38

DDIT3	126	30	**24**	-1.19	-0.89
MAPRE3	21	5	**24**		1.09
FGFR3	311	74	**24**	0.82	0
CHI3L1	135	32	**24**	-8	1.11
CCL20	114	27	**24**	4.15	3.4
BUB1	76	18	**24**	-0.88	1.41
IRAK2	38	9	**24**	3.7	0.85
TXN	178	42	**24**	3.2	-0.16
DDR1	89	21	**24**	-5.69	0.78
DUSP7	17	4	**24**	-1.15	-0.18
PRCC	17	4	**24**	-1.16	1.06
IGF2BP1	68	16	**24**	-2.64	2.35
SAT2	17	4	**24**	-2.96	0.36
PPP1R13L	51	12	**24**	-7.59	0.61
NGFR	187	44	**24**		1.92
AGTR1	661	155	**23**		-2.1
PRSS2	47	11	**23**		1.99
CEP55	30	7	**23**	0.47	2.14
LAPTM4B	30	7	**23**	-3.37	0.93
ANXA3	30	7	**23**	1.26	-1.23
JUN	683	159	**23**	-3.22	1.28
S100A8	138	32	**23**	2.84	-0.26
TXNRD1	82	19	**23**	2.4	-0.42
SFRP4	39	9	**23**		0.15
PTGR1	13	3	**23**	2.05	0.09
PPP1R14C	13	3	**23**		-0.13
LAMC3	13	3	**23**		2.35
CSF3	143	33	**23**		-0.3
CDK2AP1	26	6	**23**	3.44	-0.47
RHOJ	13	3	**23**	7.74	-1.18
URGCP	13	3	**23**	-4.85	-0.38
ZDHHC2	13	3	**23**	2.69	-0.22
FLVCR2	13	3	**23**		0.2
UBC	1728	398	**23**	-1.23	0.83
CCNB1	244	56	**23**	0.33	1.45
ID3	61	14	**23**	-1.65	1.06
RHOB	83	19	**23**	1.87	-0.85
BIN1	101	23	**23**	-9.88	-0.35
SERTAD1	22	5	**23**	-8	-1.43
STMN1	110	25	**23**	-0.59	0.75
PPP1R14A	22	5	**23**		0.03
SAA1	137	31	**23**	-6.1	-3
S100A7	84	19	**23**		5.45

RRM1	71	16	**23**	-1.1	0.15
ASPH	40	9	**23**	-0.48	-0.74
MAPKAPK2	80	18	**23**	-5.83	0.33
ARHGAP35	40	9	**23**	-6.21	0.19
ROS1	40	9	**23**		4.25
ERN1	49	11	**22**		0.84
BCL2L1	431	96	**22**	-6.43	0.54
HSP90AA1	485	108	**22**	-1.2	-0.24
CASP3	741	165	**22**	-2.96	0.21
PHACTR3	18	4	**22**	0.05	1.92
USP22	27	6	**22**	1.02	-1.04
ACER2	9	2	**22**	3.51	
FAM173B	9	2	**22**	0.21	-0.34
FAM53C	9	2	**22**	-0.03	-0.06
PREX2	9	2	**22**	-0.17	-4.16
SHPK	9	2	**22**	-0.26	-1.06
MAGI3	18	4	**22**	-0.5	-0.42
SERTAD3	9	2	**22**	-2.64	-0.51
HES4	9	2	**22**	-6.1	1.38
CAMTA2	9	2	**22**	-6.1	-1
TCEAL2	9	2	**22**	-6.1	0.13
PRICKLE4	9	2	**22**		-0.14
CYYR1	9	2	**22**	1.62	0.93
OR51E1	9	2	**22**		0.4
ANXA4	50	11	**22**	-0.63	0.52
IGFBP3	460	101	**22**	-6.13	0.31
BAG3	82	18	**22**	-0.66	-0.41
CXCL3	32	7	**22**	-6.1	-1.85
DNAJB9	32	7	**22**	0.88	-0.75
PIM2	32	7	**22**	-4.4	2.43
COL11A1	46	10	**22**		1.48
GREM1	46	10	**22**	-4.54	0.1
AJUBA	23	5	**22**	-0.18	0.39
SOCS6	23	5	**22**	-1.52	-0.7
NDP	60	13	**22**	-2.64	-1.69
ITGB6	65	14	**22**	-7.59	0.79
GATA3	158	34	**22**	3.03	-2.67
CDC25A	121	26	**21**	-6.1	5.23
MAP2K2	135	29	**21**	-4.61	1.34
MFSD2A	14	3	**21**		-0.17
SMOX	28	6	**21**	1.75	1.77
FAM84B	14	3	**21**	-1.91	-0.3
MIR429	14	3	**21**		3.69

AGT	788	168	**21**		-0.11
HSPD1	230	49	**21**	-1.9	0.84
SLC7A1	33	7	**21**	-4.04	2.04
PLCD1	52	11	**21**	-1.15	0.46
GPX2	38	8	**21**	-7.03	1.11
CALML3	19	4	**21**	-6.1	-2.58
MIER1	19	4	**21**	6.08	-1.25
FBLIM1	19	4	**21**	-0.01	0.3
RPL10	57	12	**21**	-0.77	0.52
STEAP3	19	4	**21**	-2.64	-0.57
ARHGEF5	19	4	**21**	-7.59	1.27
HES5	19	4	**21**		4.97
IFNG	1165	245	**21**		4.25
CTBP1	124	26	**21**	-0.46	0.15
HSPB1	248	52	**21**	-2.6	1.12
RAPGEF3	91	19	**21**	4.02	-1.18
SAA2	48	10	**21**	-6.1	-0.62
EEF1E1	24	5	**21**	2.84	0.36
TBX3	48	10	**21**	2.72	-0.97
FAU	24	5	**21**	-2.3	0.82
AQP5	48	10	**21**		-2.11
BMP4	231	48	**21**	0.32	2.26
EPHA4	53	11	**21**	-2.64	-0.78
ABCG2	391	81	**21**	-3.61	0.39
IL18	580	120	**21**	-1.71	-2.09
IRF7	92	19	**21**	-4.54	1.01
NOP2	34	7	**21**	-1.66	1.76
NR4A1	112	23	**21**		-0.19
IL10	1786	366	**20**	-1.44	-1.23
CSE1L	49	10	**20**	-0.83	0.75
CCR4	59	12	**20**		
LAMB1	64	13	**20**	1.98	0.41
KCNMA1	128	26	**20**	-7.59	-0.51
GP6	138	28	**20**	-0.18	0.11
FOLR1	74	15	**20**		-1.65
PRMT5	84	17	**20**	-1.39	0.5
MMP3	465	94	**20**	-7.03	1.77
EIF4E	194	39	**20**	0.63	-0.61
CXCL10	269	54	**20**	-1.71	-0.26
FAM167B	5	1	**20**		-6.85
C3orf52	5	1	**20**	-7.03	-0.29
EGFL6	10	2	**20**	-7.03	2.98
FAM3B	10	2	**20**		1.94

ANKRD37	5	1	**20**	4.69	-0.7
ENOSF1	15	3	**20**	-0.02	-0.8
ZNF121	5	1	**20**	-7.03	0.23
TSPYL2	25	5	**20**	-9.3	0.01
RPPH1	5	1	**20**		2.76
NRN1	10	2	**20**	0.24	1.69
P4HA3	5	1	**20**	-1.36	-1.11
ZBTB48	10	2	**20**	-3.92	0.57
LUM	55	11	**20**	-9.3	-1.06
ADAMTS14	10	2	**20**		1.2
CCDC23	5	1	**20**	5.01	1.36
SCML1	5	1	**20**	3.29	0.72
WDPCP	10	2	**20**	2.31	0.28
TTC7B	5	1	**20**	3.03	0.22
TYW1	10	2	**20**	3.7	0.19
LPIN3	5	1	**20**	1.91	0.05
FAM83E	5	1	**20**	2.31	-0.44
NEMF	10	2	**20**	1.52	-1.16
CCNA1	75	15	**20**	3.87	-1.68
GLTSCR1	10	2	**20**	0.82	1.82
PRR15	5	1	**20**	0.82	-0.54
UQCC	30	6	**20**	-0.52	0.46
SETD7	40	8	**20**	-0.61	0.29
MOAP1	20	4	**20**	-0.98	0.68
TPTEP1	5	1	**20**	-1.1	-1.02
GMIP	10	2	**20**	-1.36	0.97
MACC1	20	4	**20**	-2.42	0.26
NEAT1	10	2	**20**	-2.85	-0.57
DPH2	10	2	**20**	-2.86	0.09
C16orf7	5	1	**20**	-3.57	1.09
ZNF668	5	1	**20**	-3.57	1.33
THSD1	10	2	**20**	-4.14	1.82
UPP1	15	3	**20**	-4.3	-0.37
NADSYN1	20	4	**20**	-4.59	0.41
BCKDK	15	3	**20**	-5.98	1.05
BTBD11	5	1	**20**	-7.03	-0.92
STK11IP	10	2	**20**	-7.03	0.1
HES6	20	4	**20**	-8.57	2.57
ZNF296	5	1	**20**		0.58
GUSBP4	5	1	**20**		-5.09
FUZ	5	1	**20**		0.08
INPP5A	15	3	**20**	2.72	0.4
REEP5	20	4	**20**	0.72	-0.49

ABCC5	40	8	**20**	0.3	0.72
PRR7	5	1	**20**	-1.09	0.6
LYPD1	10	2	**20**	-3.22	3.34
TMEM129	5	1	**20**	-3.57	0.18
CERCAM	5	1	**20**	-8	0.43
CDHR5	15	3	**20**		-0.57
KCNJ8	35	7	**20**		-0.89
PCDHA1	10	2	**20**		2.76
PTGS1	191	38	**20**	0.38	0.13
FGFR2	333	66	**20**	3.7	-0.39
LCN2	207	41	**20**	-9.3	0.9
INHBA	167	33	**20**	-1.23	0.29
EP300	659	130	**20**	-1.43	0.91
SALL4	51	10	**20**		2.76
NFATC4	46	9	**20**	0	1.56
NOX5	41	8	**20**		0.79
BLMH	41	8	**20**	-1.51	0.01
MMP12	118	23	**19**	-11.05	2.63
ACY1	36	7	**19**	-2.64	-1.7
GADD45G	36	7	**19**	-2.64	-0.01
KRT8	144	28	**19**	-5.03	1.08
TLX1	36	7	**19**		5.23
EDA	67	13	**19**		-0.3
IRAK1	160	31	**19**	-3.02	0.82
NMI	31	6	**19**	0.13	-1.7
HOXD3	31	6	**19**		-4.28
IL1A	694	134	**19**		4.97
BAMBI	26	5	**19**	-1.68	0.29
SERPINE2	63	12	**19**	-2.03	0.53
BGN	84	16	**19**	0.99	1.52
MMP28	21	4	**19**		-1.02
S100A14	21	4	**19**	-6.1	0.29
FBN1	237	45	**19**	0.89	0.42
IGFBP6	58	11	**19**	-8.31	-0.31
S100A12	58	11	**19**		-2.6
LEF1	132	25	**19**		0.29
PDK1	37	7	**19**	0.41	-0.53
SMAD3	409	77	**19**	-0.91	0.5
LMO2	85	16	**19**	5.08	0.45
TPX2	48	9	**19**	-0.86	2.31
CILP2	16	3	**19**		
NNAT	16	3	**19**	-7.03	3.79
ANXA8L2	16	3	**19**	-8.31	-1.21

NFE2L3	16	3	**19**	0.82	0.65
SMARCC1	96	18	**19**	0.23	0.99
HDAC3	240	45	**19**	-0.89	1.14
DNAJC2	16	3	**19**	-1.97	-1.55
KLHL13	16	3	**19**	-2.64	-0.7
C20orf3	16	3	**19**	-0.95	0.01
H2AFX	215	40	**19**	-4.56	1.54
SAP30	43	8	**19**	-6.1	2.5
PTPRD	43	8	**19**	-3.57	-0.51
WNT11	27	5	**19**		3.81
SOD2	519	96	**18**	-0.95	0.4
MCM7	119	22	**18**	-2.3	1.71
CXCL9	92	17	**18**		0.2
CKAP4	38	7	**18**	-1.45	0.17
MAD2L2	38	7	**18**	-8	0.03
CEBPB	272	50	**18**	-2.96	-0.15
UBD	49	9	**18**	-0.43	0.86
PLCE1	60	11	**18**	0.82	2.48
MAP2K3	60	11	**18**	-2	-1.15
FPR2	71	13	**18**		-4.16
HTRA1	137	25	**18**	-0.51	0.27
PRSS3	33	6	**18**	4.15	0.16
HYAL3	22	4	**18**	-7.03	-0.39
CALCA	209	38	**18**		-1.49
ZNF23	11	2	**18**	3.87	1
SKA2	11	2	**18**	2.24	0.03
NCEH1	11	2	**18**	4.02	0
POFUT2	11	2	**18**	3.29	-0.01
RPS27L	11	2	**18**	3.95	-0.12
DNAJC15	11	2	**18**	2.52	-0.2
WIPI1	11	2	**18**	4.13	-0.59
CHST7	11	2	**18**	0.82	0.27
DMXL2	11	2	**18**	0.05	-0.44
PRRC2C	11	2	**18**	-0.68	0.48
TAF1D	11	2	**18**	-1.17	-0.92
AKIRIN2	11	2	**18**	-1.81	0.53
SCARA3	11	2	**18**	-3.2	0.2
PJA1	22	4	**18**	-3.62	1.29
MYBL2	77	14	**18**	-6.16	4.37
CREB3L1	11	2	**18**	-7.59	1.57
TOX3	33	6	**18**	-8	0.8
LARP6	11	2	**18**	-8.57	0.22
CYP4B1	33	6	**18**		-4.66

TNNI2	33	6	**18**		-0.7
PDF	11	2	**18**		
FNDC4	11	2	**18**	-0.74	0.29
RNF43	11	2	**18**		1.43
ACACA	61	11	**18**	-1.54	0.5
FAF1	61	11	**18**	-4.61	0.56
CXCL2	50	9	**18**	-7.03	-1.75
CXCR6	50	9	**18**		3.69
HMGCR	128	23	**18**	0.5	-0.7
HES1	78	14	**18**	-1.25	0.17
HDAC8	39	7	**18**	-0.28	-0.05
SLC7A11	39	7	**18**	1.3	-0.62
SAA4	28	5	**18**	-7.03	-2.36
EFNA4	28	5	**18**	-3.57	-0.85
ITIH3	28	5	**18**	-7.03	-1.39
ADK	28	5	**18**	2.47	-0.36
ITGB3BP	28	5	**18**	0.49	-1.11
UBE2V1	28	5	**18**	0.34	0.84
PLA2R1	17	3	**18**	1.75	-1.95
COL4A4	68	12	**18**		-3.25
DPT	17	3	**18**		-0.92
GZMK	17	3	**18**		4.97
CKS1B	51	9	**18**	1.02	1.08
UXT	34	6	**18**	-0.88	0.53
OTUB1	34	6	**18**	-0.95	-0.16
FIBP	17	3	**18**	-2.23	-0.25
RRP1	17	3	**18**	-3.36	0.87
HEYL	17	3	**18**	-6.1	0.08
HP	216	38	**18**	-10.43	-5.13
PPARG	1314	231	**18**	1.32	-1.43
AZGP1	57	10	**18**	-8.79	-1.58
IL1B	1677	294	**18**	-2.64	5.45
MEST	40	7	**18**	-9.56	1.14
GPRC5A	23	4	**17**	-3.88	1.07
DKK2	23	4	**17**		4.97
GZMB	184	32	**17**	-8.57	1.05
LY96	92	16	**17**	5.73	4.25
GZMA	46	8	**17**	-1.84	0.03
RASGRF2	23	4	**17**	0.26	-0.55
USP33	23	4	**17**	0.1	-0.77
NINL	23	4	**17**	-0.88	1.04
RUNX2	242	42	**17**		2.24
SCD	75	13	**17**	-1.93	-0.03

CTSK	104	18	**17**	0.06	0.49
HSD11B2	104	18	**17**	-1.71	-1.13
POLB	133	23	**17**	0.56	-0.45
CXCL13	81	14	**17**		1.41
EFEMP1	58	10	**17**	4.46	0.26
PVRL2	58	10	**17**	-3.62	0.32
MYCL1	35	6	**17**	1.75	4.65
YARS	35	6	**17**	-2.13	1.24
MSX2	70	12	**17**		-0.14
SRF	146	25	**17**	-2.45	-0.12
AATF	41	7	**17**	-1.97	-0.03
SMAD1	170	29	**17**	1.35	-0.07
S100A11	53	9	**17**	1.47	0.41
PPP2R5C	53	9	**17**	1.08	-0.19
HSPA1A	321	54	**17**	-1.57	0.98
DARC	96	16	**17**		-0.03
MUC20	12	2	**17**	-2.24	0.26
RASL11B	6	1	**17**	-7.03	0.61
C2CD4A	6	1	**17**	-0.17	1.41
ANXA8	12	2	**17**	-6.1	-1.26
SEPT5-GP1BB	6	1	**17**		2.5
CA11	12	2	**17**		-1.01
NUDT8	6	1	**17**		-1.26
ZNF618	6	1	**17**	1.62	1.29
ZNF521	12	2	**17**	6.61	0.66
SLC35D2	6	1	**17**	4.86	0.46
PMS2P4	6	1	**17**	4.28	-0.13
NT5DC3	6	1	**17**	2.38	-0.16
RNF145	6	1	**17**	1.98	-0.35
ULK4	12	2	**17**	3.7	-0.7
IPMK	12	2	**17**	1.98	-1.06
GTDC1	6	1	**17**	3.87	-1.85
LAMP3	24	4	**17**	6.57	-1.86
RHBDF2	12	2	**17**	0.82	1.82
MEAF6	24	4	**17**	0.47	0.53
OTUD1	6	1	**17**	0.21	-0.05
TMEM38A	6	1	**17**	-0.37	-0.7
SETD8	36	6	**17**	-0.52	0.79
FAM82B	12	2	**17**	-0.98	-0.08
MPP1	24	4	**17**	-2.16	-1.66
SIRT3	48	8	**17**	-3.04	-0.17
PLAGL2	18	3	**17**	-3.36	2.56
DOM3Z	12	2	**17**	-3.57	-0.44

ZC3H12A	18	3	**17**	-3.84	0.87
DACH2	12	2	**17**	-6.1	0.79
ESRP1	12	2	**17**	-7.03	0.19
MXRA5	6	1	**17**	-7.03	1.24
CCDC85B	12	2	**17**	-8	1.09
ALS2CR12	12	2	**17**		-1.9
ABLIM2	12	2	**17**		1.66
RGL3	6	1	**17**		1.48
HORMAD1	12	2	**17**		-6.06
PLXNA4	18	3	**17**	4.15	2.02
TMEM217	6	1	**17**	-1.44	-1.64
C15orf48	6	1	**17**	-1.68	0.7
DUOX2	48	8	**17**	-2.64	0.29
GPR162	6	1	**17**	-3.57	-0.29
SLC6A14	18	3	**17**	-3.76	-3.17
WBP1	12	2	**17**	-5.84	0.95
LMTK3	6	1	**17**	-6.1	0.27
KRTCAP3	6	1	**17**	-6.1	-1.18
ZDHHC24	6	1	**17**	-7.59	-0.48
RRAD	24	4	**17**	-9.67	0.64
SEMA6B	6	1	**17**		1.05
LILRB4	36	6	**17**		0.7
PON2	151	25	**17**	2.68	-0.39
SLPI	85	14	**16**	-6.1	-0.59
PPP1R1B	73	12	**16**	4.28	0.21
NCOA2	128	21	**16**	1.75	1.56
MAPK11	61	10	**16**	0.82	0.86
CASP1	171	28	**16**	2.13	-0.12
AKR1C3	104	17	**16**	0.38	-0.97
PPP3R1	49	8	**16**	-0.88	-0.8
IL36RN	37	6	**16**		2.76
GSTM4	37	6	**16**	-2.07	0.14
TRIP6	37	6	**16**	-4.93	-0.67
KAT5	142	23	**16**	-6.1	-0.12
MST1	62	10	**16**	-7.03	0.53
DFNA5	31	5	**16**	-3.76	-0.63
CEBPA	249	40	**16**	-6.1	0.8
HPR	25	4	**16**		-3.55
ERAP2	25	4	**16**	1.09	0.15
TFCP2	50	8	**16**	0	-0.1
SRP68	25	4	**16**	-1.95	0.12
HDAC11	25	4	**16**	-7.03	-0.46
ELK1	119	19	**16**	-2.64	0.22

SET	113	18	**16**	3.95	0.25
IL11	88	14	**16**	-1.36	-0.13
GOLM1	44	7	**16**	-1.15	-0.09
CXCR5	44	7	**16**		4.25
COL4A5	107	17	**16**	-1.36	-0.42
F13A1	240	38	**16**		2.08
STAT5A	215	34	**16**	-4.03	0.61
INS-IGF2	19	3	**16**		2.76
DHRS2	19	3	**16**	-7.03	0.45
ELF2	19	3	**16**	3.87	-0.81
ABL2	57	9	**16**	0.9	-0.47
OBFC1	19	3	**16**	0	-0.27
MSI2	19	3	**16**	-0.43	0.22
ACSL4	38	6	**16**	-0.58	-1.48
FKBP10	19	3	**16**	-2.02	1.41
PIAS3	57	9	**16**	-2.16	0.15
UPK3A	19	3	**16**		-7.04
GMDS	19	3	**16**		2.27
NEDD8	102	16	**16**	3.12	0.3
NTS	64	10	**16**	-10.72	3.69
PLA2G4C	32	5	**16**	5.93	-1.11
FZD5	32	5	**16**	-2.19	0.18
HDAC5	109	17	**16**	-7.03	1.29
LIPC	264	41	**16**	-6.1	-1.11
HOXA9	84	13	**15**	-0.69	0.7
GLCE	13	2	**15**	6.73	0.61
SMOC2	13	2	**15**		-0.55
ZNF267	13	2	**15**	4.5	2.35
RNF181	13	2	**15**	2.5	-0.1
LPCAT2	13	2	**15**	0.86	-0.5
DPYSL4	13	2	**15**	0.82	1.37
PLEKHA6	13	2	**15**	0.82	0
WARS2	13	2	**15**	0.05	-1.6
DNAJC9	13	2	**15**	-0.88	0.54
RIPK2	78	12	**15**	-1.06	0.61
ZNF131	13	2	**15**	-1.36	0.39
ARNTL	65	10	**15**	-1.68	-0.53
PDE3A	39	6	**15**	-3.2	-1.69
RGS3	39	6	**15**	-3.48	-0.26
ALDH1A3	13	2	**15**	-4.2	-1.88
NHLH2	13	2	**15**	-7.03	5.45
TMEM189-UBE2V1	13	2	**15**	0.82	0.26

SEMA7A	26	4	**15**	-7.03	-5.49
EHMT2	85	13	**15**	-5.33	-0.02
CDK1	478	73	**15**	0.82	2.63
HOXA1	46	7	**15**		
HTR2B	46	7	**15**	3.87	-3.75
PLA2G10	33	5	**15**	1.75	4.65
ATP5J	33	5	**15**	4.25	-0.06
RGS16	33	5	**15**	-5.69	0.58
HSPA8	252	38	**15**	-0.75	1.65
MCM2	126	19	**15**	-4.78	1.04
TPM1	113	17	**15**	0.85	-0.36
PCGF6	20	3	**15**	0.56	0.28
CLEC11A	20	3	**15**	-6.1	1.48
PON3	60	9	**15**	-7.03	-1.38
FBXO4	20	3	**15**	4.15	-0.44
CENPF	60	9	**15**	0	3.69
SLC25A5	40	6	**15**	-0.6	-0.4
GRWD1	20	3	**15**	-1.07	-0.34
MAP7	20	3	**15**	-3.57	-0.65
PHB2	40	6	**15**	-4.09	0.64
RPH3AL	20	3	**15**	-6.1	0.86
FABP1	60	9	**15**	-8.57	-1.27
TUBB2B	20	3	**15**	-8.98	7.58
B3GALT4	20	3	**15**		0.85
NFATC2	128	19	**15**	5.07	0.53
ERV3-1	27	4	**15**	0.41	-1.23
DRG1	27	4	**15**	0.32	-0.9
TAC1	142	21	**15**		-1.64
HOXD10	34	5	**15**	3.03	-6.85
TRO	34	5	**15**	-8.98	-0.18
NQO1	368	54	**15**	1.38	0.42
NR2F1	41	6	**15**	-2.64	-0.46
CAMK2G	103	15	**15**	0.69	-1.11
LTF	180	26	**14**	-8.57	-0.37
NRG1	277	40	**14**	-0.74	-1.17
KRT15	28	4	**14**	-8.79	-0.25
BAIAP3	14	2	**14**		-1.69
PSMG1	21	3	**14**	-3.92	-0.05
FOXS1	7	1	**14**		-1.11
SHC2	14	2	**14**		2.51
PLA2G12B	7	1	**14**	-7.03	-2.54
REN	182	26	**14**		-0.18
ARTN	21	3	**14**		0.45

PLA2G2F	7	1	**14**		
ADAMTS16	7	1	**14**		0.23
C15orf62	7	1	**14**		-2.2
RALGAPA2	7	1	**14**	1.1	0.17
BCL7B	14	2	**14**	2.72	0.03
LURAP1	7	1	**14**	3.03	-0.12
BCAT1	28	4	**14**	2.13	-0.48
PCNP	7	1	**14**	0.76	-0.33
RHBDF1	14	2	**14**	0.69	0.72
YPEL2	7	1	**14**	0.56	0.17
PLA2G4E	7	1	**14**	0.41	2.18
NAGA	28	4	**14**	0.24	0.23
TOB2	14	2	**14**	0	-0.41
DDB2	84	12	**14**	-0.07	1.86
ATG5	56	8	**14**	-0.11	-0.88
CIR1	14	2	**14**	-0.24	-0.6
RGNEF	14	2	**14**	-0.28	-0.89
CTSE	35	5	**14**	-0.74	1.82
E2F6	35	5	**14**	-0.86	1.97
HMGB2	49	7	**14**	-1.02	1.73
HN1	14	2	**14**	-1.24	1.6
SH3PXD2B	14	2	**14**	-1.43	0.78
PCTP	14	2	**14**	-1.44	-0.89
ZNF138	7	1	**14**	-1.66	0.23
ZNF449	7	1	**14**	-1.66	0.26
CDC42EP2	14	2	**14**	-1.71	0.61
HERC2P9	7	1	**14**	-1.85	0.51
XIST	35	5	**14**	-1.92	0.12
PIK3R2	91	13	**14**	-3.04	1.95
NPRL3	14	2	**14**	-3.41	0.8
RNASEH2A	14	2	**14**	-3.89	1.91
DNAJC19	14	2	**14**	-4.05	-1.24
C1orf112	7	1	**14**	-4.14	1.77
CDK2AP2	7	1	**14**	-4.61	-0.16
DUSP5	21	3	**14**	-5.69	0.2
AURKAIP1	21	3	**14**	-5.84	0.93
PHF13	7	1	**14**	-7.03	0.92
SH3D21	7	1	**14**	-7.59	-1.98
DENND2D	7	1	**14**	-8.31	0.54
CENPM	14	2	**14**	-8.57	1.14
GUCY1A2	14	2	**14**		-0.7
ASCL2	14	2	**14**		2.76
SPRR2A	14	2	**14**		-0.7

KIAA1199	14	2	**14**		1.57
PRR12	7	1	**14**		2.13
CAPNS2	7	1	**14**		-0.7
RNU4ATAC	7	1	**14**		
PLXNB3	14	2	**14**	2.31	1.91
LPAR6	28	4	**14**	7.04	0.17
MPZL2	7	1	**14**	1.72	-1.89
TMEM99	7	1	**14**	-0.74	0.07
CYB561D1	7	1	**14**	-1.85	1.12
SPRED2	28	4	**14**	-2.64	0.34
CATSPERB	7	1	**14**	-6.1	-4.16
RAET1L	7	1	**14**	-6.1	
SERINC2	7	1	**14**	-8.57	-0.39
GJB5	7	1	**14**		-0.7
SCTR	35	5	**14**		1.12
PCDHA13	7	1	**14**		-4.16
PCDHAC1	7	1	**14**		
FCRL5	21	3	**14**		2.18
COL3A1	162	23	**14**	-12.44	2.12
TLR2	794	112	**14**	-3.2	0.46
MSMB	71	10	**14**		-6.49
LIF	128	18	**14**	-8.31	1.05
CD5	64	9	**14**		0.23
MT1A	50	7	**14**	2.72	1.51
UGT1A3	43	6	**14**		
KALRN	43	6	**14**	-0.18	-1.48
HDC	43	6	**14**		
VIPR1	79	11	**14**		0.75
PLA2G4A	151	21	**14**	5.21	-2.24
KDM6A	36	5	**14**	-2.96	0.42
VIP	101	14	**14**	-6.1	-1.98
PI3	65	9	**14**		5.12
ZNRD1	29	4	**14**	3.87	1.86
HSD17B7	29	4	**14**	-1.25	1.15
MGLL	29	4	**14**	-0.29	0.13
PARK7	196	27	**14**	0.28	0.31
DROSHA	51	7	**14**	-0.14	1
PRKCB	277	38	**14**	-4.91	-0.53
GLP1R	73	10	**14**		-2.2
NMB	22	3	**14**		0.61
UBE2S	22	3	**14**	-5.1	1.32
SRP19	22	3	**14**	0.2	-0.81
STK25	22	3	**14**	-4.91	0.17

PTK7	22	3	**14**	-1.92	2.56
GRK6	44	6	**14**	-5.98	2.62
KRT5	125	17	**14**	-11.72	1.05
WEE1	81	11	**14**	0.03	-0.49
PA2G4	59	8	**14**	-2.7	0.23
PLA2G5	37	5	**14**		0.42
RGS1	37	5	**14**	2.72	0.4
PEG10	37	5	**14**	-1.65	0.84
MS4A1	82	11	**13**	-6.1	1.26
CYP24A1	97	13	**13**	-6.1	-8.98
TLL1	15	2	**13**	-0.74	-0.14
GLT25D1	15	2	**13**	2.15	2.12
MGST2	15	2	**13**	3.76	1.86
BPHL	15	2	**13**	4.15	0.43
SUDS3	15	2	**13**	1.68	0.13
SOCS4	15	2	**13**	4.5	-0.8
HOXB8	15	2	**13**	0.82	-0.7
SAT1	60	8	**13**	0.69	-1.58
ALPK1	15	2	**13**	0.47	0.87
RFK	15	2	**13**	0.19	-0.47
RPS18	30	4	**13**	-0.35	0.77
ANKRD1	30	4	**13**	-0.9	-1.26
UBN1	15	2	**13**	-1.52	0.63
KCTD13	15	2	**13**	-1.71	1.54
ACAA1	30	4	**13**	-4.03	-0.86
KRT18	150	20	**13**	-5.34	0.74
UBXN6	15	2	**13**	-6.1	0.3
SEMA4A	15	2	**13**	-7.03	0.2
GPR35	15	2	**13**		3.69
KCNC3	15	2	**13**		
ADRA2B	91	12	**13**		-2.6
HSPH1	38	5	**13**	0.23	-0.36
SLC16A1	76	10	**13**	-0.55	-0.01
HHIP	38	5	**13**	9.22	-0.96
SH3KBP1	76	10	**13**	0.82	0.1
NRCAM	38	5	**13**	5.73	0.92
NDC80	61	8	**13**	1.06	-0.53
UCHL1	145	19	**13**	-5.96	0.32
PYCR1	23	3	**13**	-4.86	1.42
EFEMP2	23	3	**13**	-4.4	0.22
FAM82A2	23	3	**13**	-0.26	0.91
PDE7A	23	3	**13**	-0.46	-0.31
RNF213	23	3	**13**	-2.04	0.12

PAF1	23	3	**13**	-3.63	0.97
DGKD	23	3	**13**	-3.84	0.91
SPINK1	131	17	**13**	-6.1	2.06
NR4A2	108	14	**13**	-6.1	0.49
MLXIPL	54	7	**13**		0.82
RANBP9	62	8	**13**	0.28	0.42
RPS27	31	4	**13**	0.15	-0.31
ASH2L	62	8	**13**	-2.86	-0.36
GRB10	62	8	**13**	0.59	0.76
SERPINH1	70	9	**13**	-2.02	1.11
FCGR3A	249	32	**13**	-0.74	0.16
USF1	109	14	**13**	5.21	-0.29
PLK2	39	5	**13**	-1.6	-0.07
SERPINA5	78	10	**13**	-7.59	-2.43
DUOX1	39	5	**13**		-1.06
HSPA1B	141	18	**13**	-1.28	1.72
IL19	55	7	**13**		
CST3	244	31	**13**	-2.9	1.22
DSG2	63	8	**13**	-3.19	0.17
SLC9A3R1	134	17	**13**	-5.02	0.18
EIF2C2	103	13	**13**	-5.11	0.51
DUSP23	16	2	**13**	0.82	-0.57
UGT1A4	48	6	**13**		-5.66
GDF3	16	2	**13**	-3.04	-5.66
KLK12	16	2	**13**		3.69
PRSS22	8	1	**13**		0.13
CCDC58	8	1	**13**	-1.25	-0.04
UCA1	8	1	**13**	-5.11	1.83
SPSB3	8	1	**13**	-8.98	0.8
UFSP1	8	1	**13**		4.97
GGH	48	6	**13**	1.61	-1.07
NENF	8	1	**13**	-2.64	1.52
MMP23A	8	1	**13**		
LHX6	16	2	**13**	1.4	5.64
CENPW	16	2	**13**	5.49	2.18
TOMM6	8	1	**13**	1.4	1.64
MAFB	40	5	**13**	1.75	0.49
C14orf2	8	1	**13**	3.43	0.26
PLEKHG6	8	1	**13**	3.51	0.07
TOB1	40	5	**13**	2.45	-0.09
N6AMT1	8	1	**13**	1.75	-0.13
SCHIP1	16	2	**13**	5.21	-0.33
HIST1H2BC	16	2	**13**	1.75	-0.7

RAB3D	16	2	**13**	3.55	-0.96
MMRN2	8	1	**13**	6.71	-0.97
USHBP1	8	1	**13**	0.82	-2.2
LDHD	8	1	**13**	0.82	-3.25
SCD5	16	2	**13**	-0.07	0.35
NIT2	8	1	**13**	-0.4	-1.37
DDTL	8	1	**13**	-1.71	-1.47
TRMT11	8	1	**13**	-1.92	-0.8
MAPKBP1	8	1	**13**	-2.08	-0.09
ATPIF1	24	3	**13**	-2.44	-0.23
BORA	16	2	**13**	-3.2	1.56
PCGF1	16	2	**13**	-3.2	-0.06
SERGEF	8	1	**13**	-4.85	-0.36
CPNE7	8	1	**13**	-6.1	2.26
NPL	8	1	**13**	-7.03	-1.75
TMEM176B	8	1	**13**	-7.59	-0.66
PDLIM4	24	3	**13**	-8.79	1.73
PNCK	8	1	**13**		-0.57
PHYHIP	8	1	**13**		-1.23
POU5F1B	16	2	**13**		5.45
ZNF32	8	1	**13**		1.45
PRDM15	8	1	**13**		2.24
ESYT3	8	1	**13**		0.02
FBXL16	8	1	**13**		0.35
DUOXA2	8	1	**13**		1.82
TMEM189	8	1	**13**	0.56	-0.09
CACNB2	48	6	**13**	-1.1	-1.5
RNF19B	8	1	**13**	-1.44	0.16
FAM189B	8	1	**13**	-2.07	0.4
NPDC1	16	2	**13**	-4.14	0.41
RHCG	24	3	**13**	-6.1	-1.33
FAT2	8	1	**13**	-7.59	-1.02
TMEM176A	8	1	**13**	-8	-0.55
PCDHB15	8	1	**13**		1.51
PCDHA7	8	1	**13**		2.76
SYT8	8	1	**13**		-0.7
ASPRV1	8	1	**13**		1.38
FDCSP	8	1	**13**		0.27
B4GALNT3	8	1	**13**		-0.38
ADORA2A	177	22	**12**	-2.64	1.59
KIF2C	57	7	**12**	-1.65	1.65
VDAC1	114	14	**12**	-0.97	0.69
PLIN2	49	6	**12**	2.84	-0.6

UIMC1	49	6	**12**	-0.4	-0.26
EIF4A3	41	5	**12**	-3.22	1.2
CRKL	107	13	**12**	1.21	-1.34
PDLIM7	33	4	**12**	-4.48	-0.73
MED15	33	4	**12**	-4.61	0.64
ACTG2	33	4	**12**	-7.59	-2.17
GP1BB	58	7	**12**		7.83
SIRT2	58	7	**12**	-2.33	-0.35
BIRC6	25	3	**12**	-0.21	-0.18
RAP2B	25	3	**12**	5.08	-0.65
ANLN	25	3	**12**	0.53	-0.7
TXNDC5	25	3	**12**	2.53	1.29
DCUN1D1	25	3	**12**	2.78	-0.18
LSM1	25	3	**12**	0.69	-0.93
NOD1	125	15	**12**	-0.96	2.13
RGN	25	3	**12**	-7.03	-2.15
ABHD16A	25	3	**12**	-3.92	-0.24
IL23A	126	15	**12**		-0.44
ABP1	42	5	**12**		-0.92
RPLP2	42	5	**12**	-1.37	1.03
FPGS	42	5	**12**	-1.97	0.37
IL1RN	773	92	**12**	-2.64	-0.06
EEF1D	59	7	**12**	-4.24	1.36
PRSS23	17	2	**12**	3.13	-0.45
ZC3H13	17	2	**12**	-0.09	-1.77
TAF3	17	2	**12**	1.75	2.87
TCEAL4	17	2	**12**	2.99	-0.31
SPECC1	17	2	**12**	-0.42	0.7
BRAP	34	4	**12**	-0.43	-0.7
PREB	17	2	**12**	-2.38	0.97
NDUFB7	17	2	**12**	-2.64	-1.02
MCM5	68	8	**12**	-5.19	2.31
DOT1L	34	4	**12**	-7.59	-0.06
FKBP8	51	6	**12**	-10.36	1.14
ORAI3	17	2	**12**	-0.8	1.04
SLC5A3	17	2	**12**	-1.65	-0.04
ABCA1	461	54	**12**	5.05	-0.29
CD177	43	5	**12**		-0.6
PAEP	95	11	**12**		-3.45
MELK	26	3	**12**	0.03	0.58
UGT1A10	52	6	**12**		1.77
SYNJ2	26	3	**12**	1.38	-0.44
FLNB	52	6	**12**	-0.09	0.26

RAB34	26	3	**12**	-2.46	-0.09
TCF3	156	18	**12**	-3.09	1.56
MPZL1	26	3	**12**	-0.97	1.8
BCAP31	61	7	**11**	1.77	-0.34
DLX5	35	4	**11**		1
SERPINA3	158	18	**11**	-12.68	-1.9
HSPA6	44	5	**11**	-6.1	-0.3
AKR1C1	53	6	**11**	-1.44	-0.26
ABCC3	62	7	**11**	-1.52	0.05
GAL	71	8	**11**	-6.1	-0.7
CDK5	196	22	**11**	-6.1	0.73
PROM2	9	1	**11**	0.82	-0.22
MIR503	9	1	**11**		
CTHRC1	9	1	**11**	-0.09	2.48
APOL4	9	1	**11**	-1.25	-0.85
PLTP	99	11	**11**	-3.57	0.13
EXOC3L2	9	1	**11**	2.07	0.23
CHIC1	9	1	**11**	2.31	0.13
METTL3	9	1	**11**	1.05	-0.15
ZNF35	9	1	**11**	3.29	-0.48
FRMD6	18	2	**11**	1.37	-1.13
MECOM	81	9	**11**	1.51	-1.29
HOXD1	18	2	**11**	3.03	-2.61
PLA2G4D	9	1	**11**	0.82	-6.38
FBXO27	9	1	**11**	0.71	0.68
COQ3	9	1	**11**	0.54	-0.87
CCNK	18	2	**11**	0.41	-0.26
ACBD3	18	2	**11**	0.18	-0.96
SLC35B3	9	1	**11**	0.11	-0.05
SRXN1	27	3	**11**	0.05	0.03
FAM118B	9	1	**11**	0	-0.95
NDST2	9	1	**11**	-0.17	0.51
BCAS2	18	2	**11**	-0.54	-1.74
GALNT7	9	1	**11**	-0.56	0.35
CERS5	9	1	**11**	-0.67	0.61
WHSC1L1	18	2	**11**	-0.81	-0.15
KDM2B	18	2	**11**	-1.1	-0.01
TBC1D7	18	2	**11**	-1.25	0.22
L3MBTL4	9	1	**11**	-1.36	-0.7
YOD1	9	1	**11**	-1.68	-1.9
C17orf28	9	1	**11**	-1.71	0
NHP2	27	3	**11**	-1.87	0.78
TBCC	9	1	**11**	-2.24	-1.04

TOMM34	18	2	**11**	-2.33	-0.47
HSPA14	18	2	**11**	-2.64	0.68
TEAD3	18	2	**11**	-3.57	-0.12
C11orf31	9	1	**11**	-3.63	0.17
VSNL1	36	4	**11**	-4.18	-1.08
C1orf35	9	1	**11**	-5.52	0.87
DEDD2	9	1	**11**	-5.52	0.24
DGKI	9	1	**11**	-6.1	-5.09
DET1	9	1	**11**	-6.1	1.77
CECR2	9	1	**11**	-6.1	5.81
ABCA2	36	4	**11**	-7.03	0.66
NUDT22	9	1	**11**	-7.03	-0.26
CHAC1	9	1	**11**	-7.59	-1.16
ZNF385A	9	1	**11**	-8	-0.44
CXorf57	9	1	**11**	-8.57	1.05
KRT23	18	2	**11**	-10.55	-0.83
C11orf93	9	1	**11**		0.6
CAPN8	9	1	**11**		-0.04
CLIC3	9	1	**11**		2.69
TRIM31	18	2	**11**		-0.06
DCLK3	9	1	**11**		
CAPN13	9	1	**11**		-1.68
LINC00312	9	1	**11**		-0.39
PTGFRN	18	2	**11**	1.62	0.05
ITGA11	18	2	**11**	-0.52	2.4
SLC23A2	54	6	**11**	-2.08	0.74
STRA6	18	2	**11**	-7.03	2.87
SLC5A4	9	1	**11**		
PCDHA10	9	1	**11**		3.69
PCDHAC2	9	1	**11**		1.05
PCDHA8	9	1	**11**		
GSTM3	136	15	**11**	-2.62	-0.46
FADS2	73	8	**11**	-2.28	-2.61
HRH1	73	8	**11**	5.21	1.05
TAF1	138	15	**11**	-1.07	0.87
C11orf30	37	4	**11**	2.72	-1.4
GSR	65	7	**11**	3.29	-0.62
GMNN	65	7	**11**	-1.16	-1.17
FBLN2	28	3	**11**		1.22
SMG6	28	3	**11**	-0.21	0.22
RRP1B	28	3	**11**	-0.96	0.51
RNF2	56	6	**11**	-1.73	-0.7
HLF	28	3	**11**	-6.1	-2.19

HCAR2	28	3	**11**		0.09
PRDX5	47	5	**11**	-2.06	0.39
GSTM2	47	5	**11**	-2.64	-0.57
IFNAR2	85	9	**11**	-4.18	0.61
CRTAC1	19	2	**11**		1.12
TCN1	38	4	**11**	-8.98	-1.18
DEFA6	19	2	**11**		
CREB3L2	19	2	**11**	2.03	0.04
C10orf10	19	2	**11**	3.18	-0.82
CRTC3	19	2	**11**	-0.17	-0.2
AIMP2	38	4	**11**	-0.24	-0.37
BLZF1	19	2	**11**	-0.35	1.4
FAM13A	19	2	**11**	-0.52	-0.65
CLIC2	19	2	**11**	-0.87	-1.4
DUSP16	19	2	**11**	-2.81	0.18
UBXN1	19	2	**11**	-4.13	0.73
PHGDH	38	4	**11**	-4.72	-0.21
AUTS2	19	2	**11**	-8	-0.03
ALAS2	38	4	**11**	-11.96	2.87
CRIM1	19	2	**11**	6.87	-1.9
AKAP13	57	6	**11**	-2.54	0.47
NDST1	19	2	**11**	-2.64	0.39
COMMD1	48	5	**10**	0.76	-0.01
RNF8	48	5	**10**	-1.65	0.74
DSC2	48	5	**10**	-9.88	0.22
YWHAQ	164	17	**10**	-1.91	0.79
USP10	29	3	**10**	-0.65	0.99
HOXB2	29	3	**10**	-1.71	5.96
ATG7	29	3	**10**	-3.62	1.21
IL1RAP	58	6	**10**	2.72	-1.47
DAP3	39	4	**10**	-0.59	0.55
UGT1A8	49	5	**10**		
MTRR	245	25	**10**	-0.58	-0.46
CSTA	59	6	**10**	-0.37	-3.67
ACP1	89	9	**10**	1.88	0.08
FCGR1A	89	9	**10**	0.82	7.09
OVOL1	10	1	**10**		-0.44
HIST1H4C	20	2	**10**	3.77	1.99
LAMB3	60	6	**10**	-7.03	0.62
MMP23B	10	1	**10**		-1.06
TIPRL	10	1	**10**	2.1	2.4
KLHL4	10	1	**10**	2.4	1.2
LIN52	10	1	**10**	3.51	0.84

HSCB	10	1	**10**	5.33	0.39
FAM114A1	10	1	**10**	2.5	-0.4
AKTIP	20	2	**10**	5.64	-0.53
TRIM32	40	4	**10**	1.23	-0.7
DDIT4L	10	1	**10**	3.7	-2.09
RPL41	20	2	**10**	0.98	-0.63
FAM63A	10	1	**10**	0.82	-0.84
ZNF155	10	1	**10**	0.82	0.23
KLHDC8B	10	1	**10**	0.82	0.19
C22orf28	20	2	**10**	0.79	0.29
KPNA2	170	17	**10**	0.45	0.01
CCDC132	10	1	**10**	-0.18	-0.47
FOXK2	20	2	**10**	-0.2	1.66
C12orf32	10	1	**10**	-0.36	0.36
ACADL	20	2	**10**	-0.43	-1.04
CCNB2	50	5	**10**	-0.43	2.12
KLHL2	10	1	**10**	-0.56	-0.81
HAUS3	10	1	**10**	-0.8	0.54
PAFAH2	10	1	**10**	-0.88	-0.48
TOR1B	10	1	**10**	-1.65	-0.18
U2AF1L4	10	1	**10**	-1.68	-0.04
PDIK1L	10	1	**10**	-1.71	0.45
NDUFA3	10	1	**10**	-1.85	-0.36
CHD3	60	6	**10**	-1.92	0.05
COMMD5	10	1	**10**	-3.12	-0.7
MKNK2	20	2	**10**	-3.22	0.5
TBCB	20	2	**10**	-3.89	1.07
PTMS	20	2	**10**	-4.76	1.33
TSSC4	10	1	**10**	-6.1	-0.09
RNPEPL1	10	1	**10**	-6.21	-0.09
TRAPPC1	10	1	**10**	-6.57	0.19
FAM50A	20	2	**10**	-8.57	0.58
BAHD1	10	1	**10**	-8.57	0.84
AMIGO2	10	1	**10**	-8.98	0.13
MTCP1	20	2	**10**		0.79
ZNF19	10	1	**10**		0.54
SLC4A5	10	1	**10**	1.38	-0.13
ELTD1	10	1	**10**	7.99	-0.29
GPR161	10	1	**10**	2.72	-0.7
TIMMDC1	20	2	**10**	-0.04	-0.12
SLC22A17	10	1	**10**	-4.14	0.6
SLC38A5	10	1	**10**	-7.59	1.94
APCDD1	10	1	**10**	-7.59	1.19

SDF2L1	10	1	**10**		-1.09
PCDHA11	10	1	**10**		
PCDHA5	10	1	**10**		
PCDHA3	10	1	**10**		
SLC30A2	10	1	**10**		-4.38
HCAR3	20	2	**10**		-0.7
PCDHA4	10	1	**10**		4.25
MAPK12	61	6	**10**		0.07
GSTA2	51	5	**10**	-6.1	-0.83
RPS2	41	4	**10**	-3.54	1.53
EEF1B2	41	4	**10**	-1.4	0.26
TADA3	41	4	**10**	-3.71	0.64
PKP1	41	4	**10**	-8	0.53
IL4R	339	33	**10**	-2.79	1.12
DEFB1	124	12	**10**	0.82	0.81
AHCY	62	6	**10**	-3.29	0.54
SMC4	31	3	**10**	0.33	0.25
TGIF1	52	5	**10**	-3.15	-0.4
RFC4	52	5	**10**	-4.19	0.87
DLG3	52	5	**10**	-7.03	-0.4
C3	324	31	**10**	-11.96	-0.75
POLDIP2	21	2	**10**	1.4	-0.02
S100A3	21	2	**10**		0.26
NAV2	21	2	**10**	1.37	0.1
NDUFA6	21	2	**10**	2.63	-0.46
UFD1L	42	4	**10**	0.53	0.44
CYP2S1	21	2	**10**	-2.64	2.51
PRAM1	21	2	**10**	-6.1	3.69
HDAC10	21	2	**10**	-7.03	1.33
CELSR1	21	2	**10**		-0.44
CD38	148	14	**9**	-7.59	-1.26
SEPT5	32	3	**9**	-7.03	1.81
CSTB	64	6	**9**	1.26	1.59
PARP2	32	3	**9**	-1.36	-0.12
CDK16	32	3	**9**	-4.3	0.06
PIGR	64	6	**9**	-1.24	-1.04
CSTF2	43	4	**9**	-2.64	-0.12
RPS3A	54	5	**9**	-2.29	1.03
COL5A1	76	7	**9**	-9.43	1.7
TMEM27	11	1	**9**	-7.59	-5.09
BMP1	55	5	**9**	-5.33	-0.01
FGF16	11	1	**9**		
FRAT2	11	1	**9**	3.29	2.4

NDUFA1	22	2	9	2.92	0.52
HS2ST1	11	1	9	2.23	-2.03
GIPC2	11	1	9	7.19	-2.17
DCTN6	11	1	9	0.82	0.82
USP35	11	1	9	0.82	1.51
ASCC3	22	2	9	0.73	1.12
NAV1	11	1	9	0.53	1.19
ECI2	22	2	9	0.36	-0.57
IFT172	11	1	9	0.3	-0.09
ARHGAP12	11	1	9	-0.37	-0.85
WDR59	11	1	9	-0.56	0.29
MLXIP	11	1	9	-1.07	0.09
EFR3B	11	1	9	-1.15	0.15
MTMR4	11	1	9	-1.28	-0.5
FAM60A	11	1	9	-1.35	0.57
SH2D3A	11	1	9	-1.71	-0.23
PARP12	11	1	9	-1.85	0.03
ZBTB20	22	2	9	-2.33	-1.45
HIST1H3H	11	1	9	-2.64	
MED25	33	3	9	-3.57	1.38
RBCK1	33	3	9	-3.62	0.76
FBRS	11	1	9	-4.76	0.29
GYLTL1B	11	1	9	-6.1	-1.06
HINT2	11	1	9	-7.03	0.05
SMARCD2	22	2	9	-8.79	0.65
ALDH3B2	11	1	9		-2.54
HIST1H3J	11	1	9		
PLCH2	11	1	9		1.04
S100A7A	11	1	9		-1.26
SPAG17	11	1	9		-0.7
PCDHA9	11	1	9	1.75	1.51
SLC44A3	11	1	9	2.72	1.08
WRB	11	1	9	-0.91	-0.04
SIDT2	11	1	9	-2.47	0.97
GPR125	11	1	9	-3.21	0.69
PCDHB4	11	1	9		5.81
PCDHA12	11	1	9		
PCDHA2	11	1	9		-4.16
IL20RA	22	2	9		1.41
ENTPD3	11	1	9		-1.11
LIG3	78	7	9	-3.36	0.86
PPIA	212	19	9	-0.92	0.12
MAPK10	67	6	9	-3.57	0.06

CSF2RA	56	5	**9**	4.15	1.82
UCP2	213	19	**9**	-5.34	1.24
ANAPC1	45	4	**9**	-1.15	-0.32
FOXC1	79	7	**9**	2.68	-1.32
MCM4	79	7	**9**	-1.1	1.08
GALNT1	34	3	**9**	2.65	0.44
AKAP1	34	3	**9**	0.19	-0.07
RAD54B	34	3	**9**	-2.96	0.6
HSD11B1	159	14	**9**	-8.31	-2.92
UGT1A6	91	8	**9**		-1.67
C4BPA	57	5	**9**	-3.63	-1.38
EIF2S1	103	9	**9**	1.18	0.09
PCOLCE	23	2	**9**	-8.31	0.81
KIF20A	23	2	**9**	-0.08	6.22
GPSM2	23	2	**9**	-0.17	0.07
PRMT2	23	2	**9**	-1.23	0.33
RAD23A	69	6	**9**	-4.59	-0.05
SLC38A1	23	2	**9**	-0.08	0.58
HIST1H3A	162	14	**9**		2.76
CYP1A1	758	65	**9**	-2.06	-3.39
PFKP	35	3	**9**	-1.7	0.9
DGCR8	35	3	**9**	-1.71	0.2
CBX4	47	4	**9**	-1.68	0.16
KRT17	59	5	**8**	-12.29	1.1
RBP4	189	16	**8**	-8.79	-1.28
INS	533	45	**8**		
INHBB	83	7	**8**	-6.1	1.7
TSPAN6	12	1	**8**	0.21	-0.49
CST1	24	2	**8**		7.43
ARL4A	12	1	**8**	-1.83	0.2
TIMM17B	12	1	**8**	-7.03	-0.7
HIST1H3I	12	1	**8**		3.69
COLEC11	12	1	**8**	-2.64	-2.24
CFHR2	12	1	**8**	-8	-0.7
COL5A3	12	1	**8**		2.13
C2CD4B	12	1	**8**	1.75	3.98
CDC42SE2	12	1	**8**	1.53	0.9
C1orf31	12	1	**8**	1.9	0.87
PTPLA	12	1	**8**	3.7	0.85
MAD2L1BP	24	2	**8**	1.05	0.51
EAF1	12	1	**8**	2.5	0.19
PAPOLG	12	1	**8**	1.15	-0.12
MSL3	12	1	**8**	2.15	-0.44

UBLCP1	12	1	**8**	1.98	-0.48
THSD7A	12	1	**8**	4.28	-1.17
NT5DC1	12	1	**8**	4.02	-1.5
ATP2C2	12	1	**8**	0.82	2
PPIL4	12	1	**8**	0.78	-0.7
SCO2	36	3	**8**	-0.17	0.73
TOE1	12	1	**8**	-1.15	0.07
DHRS9	12	1	**8**	-1.15	-1.69
HSH2D	12	1	**8**	-1.85	-0.19
ZNF300	12	1	**8**	-2.08	1.41
TOP3A	36	3	**8**	-2.42	-0.18
PAPD7	12	1	**8**	-2.64	0.42
ANKRD13D	12	1	**8**	-2.64	-0.18
MALL	12	1	**8**	-2.64	-0.39
RGS9	24	2	**8**	-3.57	-2.6
PARL	24	2	**8**	-4.18	0.45
RNF167	12	1	**8**	-5.52	0.15
DERL3	12	1	**8**	-6.1	1.12
TM7SF2	12	1	**8**	-6.1	-0.12
CNO	12	1	**8**	-6.1	0.73
FCHSD1	12	1	**8**	-6.1	0.28
FBXO10	12	1	**8**	-7.03	2.4
NEBL	24	2	**8**	-7.59	1.1
MZB1	12	1	**8**	-8.31	2.14
VARS2	12	1	**8**	-8.57	1
NCAPH2	12	1	**8**	-8.57	1.18
SSH3	12	1	**8**	-8.79	-1.17
LMO3	12	1	**8**		0.84
HIST1H2AM	24	2	**8**		2.76
HIST1H4K	12	1	**8**		
PCP4	12	1	**8**		-0.89
TBKBP1	12	1	**8**		-0.04
ARC	12	1	**8**		0.29
RHBG	24	2	**8**	0.82	-1.11
ASTN2	12	1	**8**	-0.78	-0.29
GPR126	24	2	**8**	-1.44	-0.34
DSC3	36	3	**8**	-1.49	-0.7
C17orf62	12	1	**8**	-2.32	0.59
FCGR1B	12	1	**8**		-0.14
PCDHA6	12	1	**8**		2.76
SEMA5B	12	1	**8**		7.09
CLEC5A	12	1	**8**		-0.14
VAV1	169	14	**8**	-7.03	1.05

FCGR2A	315	26	**8**	1.75	0.25
ABI1	61	5	**8**	-0.05	-0.44
FBL	61	5	**8**	-2.21	1.07
GSTT1	1302	106	**8**	-8	-1.49
SERPINF2	74	6	**8**	-8	-2.69
CAMK1D	37	3	**8**	0.24	1.79
PPL	37	3	**8**	-10.14	-0.35
CD19	74	6	**8**	-10.06	-0.14
KRT14	99	8	**8**	-9.88	1.32
FLNC	62	5	**8**	-1.25	-0.32
LYN	273	22	**8**	-2.19	1.26
GLB1	87	7	**8**	0.6	0.97
GSTM1	1555	125	**8**	-4.18	-0.85
MAFA	25	2	**8**		3.69
CHRD	25	2	**8**		-2.09
BACE2	50	4	**8**	2.41	-0.23
ANP32E	25	2	**8**	4.76	-0.82
TLE3	25	2	**8**	0.41	0.85
GTPBP4	25	2	**8**	-0.12	0.15
TOM1L1	25	2	**8**	-0.74	-1.09
TBL1X	25	2	**8**	-1.37	1.07
TDO2	25	2	**8**	-7.03	-2.36
CYP2C8	151	12	**8**	-9.15	-0.67
SCNN1A	126	10	**8**	-8	-0.36
NFYC	38	3	**8**	-5.11	0.53
CDK5R1	76	6	**8**		2.08
ERCC2	572	45	**8**	-7.59	1.26
PRMT1	115	9	**8**	-5.04	0.6
SOD1	685	53	**8**	0.1	-0.23
RUNX1	388	30	**8**	-3.79	-0.15
PAQR7	13	1	**8**	1.23	-0.01
G0S2	13	1	**8**	-7.59	0.1
C21orf7	13	1	**8**	1.87	0.94
FAM107B	13	1	**8**	1.97	-0.35
SIAE	13	1	**8**	0.88	0.65
CCL15	39	3	**8**	0.82	-0.92
CECR1	13	1	**8**	-1.37	0.21
NPEPPS	26	2	**8**	1.4	0.07
DUSP14	13	1	**8**	1.25	-0.26
MRI1	13	1	**8**	2.44	-0.65
ST6GALNAC3	13	1	**8**	0.94	-0.3
FA2H	13	1	**8**	0.82	-1.52
RASD1	26	2	**8**	0.24	-0.85

PPIC	13	1	**8**	0	-1.81
SEC61B	26	2	**8**	-0.15	0.17
PDXDC1	13	1	**8**	-0.54	0.22
GPBP1	13	1	**8**	-0.54	0.01
DIMT1	13	1	**8**	-0.66	-0.33
RPIA	13	1	**8**	-0.67	1.53
CRIPT	13	1	**8**	-0.82	-0.21
TXNL1	26	2	**8**	-0.92	-0.29
C15orf44	13	1	**8**	-1.33	0.25
FBXO6	13	1	**8**	-1.36	-0.34
MSRB1	13	1	**8**	-2.07	-0.7
SAMM50	26	2	**8**	-2.49	0.53
RAB11FIP1	26	2	**8**	-2.64	-0.17
CYP4F11	13	1	**8**	-2.64	0.1
ASRGL1	13	1	**8**	-4.18	-1.09
ZNF76	13	1	**8**	-4.18	-0.12
LSM10	13	1	**8**	-4.85	2.27
LRCH4	13	1	**8**	-5.52	-0.7
NR2F6	13	1	**8**	-6.1	0.34
PPFIBP2	13	1	**8**	-7.03	0.96
DNAJB2	26	2	**8**	-8	-0.55
ARAP1	26	2	**8**	-9.43	1
GYG2	13	1	**8**		0.45
PCDH7	13	1	**8**	1.75	-0.05
OSCP1	13	1	**8**	2.72	-1.39
SHKBP1	13	1	**8**	-2.83	1.24
GGT5	13	1	**8**	-3.2	0.03
AQP9	39	3	**8**	-8	1.09
SLC34A2	26	2	**8**	-8.57	-1.28
PDX1	118	9	**8**		4.25
CKB	66	5	**8**	-8.31	0.71
ACAN	93	7	**8**		2.63
PRDX4	40	3	**8**	-1.03	-0.01
COL17A1	80	6	**8**	-6.1	1.35
NMT2	40	3	**8**	2.71	-0.76
PRC1	40	3	**8**	-1.18	2.43
POU2AF1	40	3	**8**	-3.5	0.23
CCL14	27	2	**7**	2.31	-0.44
PHPT1	27	2	**7**	2.68	0.08
ALDH1B1	27	2	**7**	-0.74	-1.59
CBFB	54	4	**7**	-1.1	0.03
TFAM	81	6	**7**	-1.88	-0.38
POLR1A	27	2	**7**	-2.64	0.4

GLA	123	9	**7**	-1.24	0.53
PSMC3	82	6	**7**	-2.32	0.1
FCER1G	41	3	**7**	-6.1	0.69
ITGA7	41	3	**7**		-0.81
IL2RA	302	22	**7**	-1.71	0.49
SULT1E1	55	4	**7**	1.75	1.84
GYS1	55	4	**7**	-2.01	-0.07
CA2	139	10	**7**	-6.53	-1.34
NAT2	517	37	**7**	-7.03	-0.39
BNIPL	14	1	**7**	0.56	-0.7
GLRX3	28	2	**7**	-1.8	0.14
CCNL2	14	1	**7**	-3.76	0.94
EPDR1	14	1	**7**	-7.03	0.55
NAF1	14	1	**7**	2.31	0.79
GMPS	28	2	**7**	3.87	0.72
TNNC2	14	1	**7**	3.51	0.45
PDZD11	14	1	**7**	1.25	0.38
IQSEC2	14	1	**7**	3.03	-0.59
TIMM8B	14	1	**7**	0.92	0.92
MRPL13	14	1	**7**	0.88	-0.05
FAM54B	14	1	**7**	0.58	-0.03
AARS2	14	1	**7**	0.06	-0.18
MED17	42	3	**7**	-0.02	0.29
MRPS27	14	1	**7**	-0.13	1.35
POLR3H	14	1	**7**	-0.17	0.03
POLR1B	28	2	**7**	-0.52	0.29
GNG4	14	1	**7**	-0.92	1.56
PRPF19	42	3	**7**	-1.15	1.53
ZFYVE1	14	1	**7**	-1.44	1.27
HIST1H4E	14	1	**7**	-1.71	-2.6
OGDHL	14	1	**7**	-1.71	-0.7
SLC25A37	14	1	**7**	-1.73	0.79
HIST1H4H	14	1	**7**	-2.08	-1.64
C16orf57	14	1	**7**	-2.16	0.76
ENO2	70	5	**7**	-2.81	0.92
NCOA5	14	1	**7**	-3.36	-0.41
HSPA2	56	4	**7**	-3.61	-0.42
CHERP	14	1	**7**	-7.59	0.27
GATM	28	2	**7**	-8.57	-2.83
RNF126	14	1	**7**	-8.98	-0.01
NR0B1	112	8	**7**		3.56
ESPN	14	1	**7**		-1.11
C11orf10	14	1	**7**	3.53	0.35

PIGC	14	1	**7**	0.93	-0.52
PCDHB10	14	1	**7**		5.64
TRPV6	70	5	**7**		-2.46
MBP	127	9	**7**	-3.2	-2.65
ATP1B1	57	4	**7**	0.72	-0.93
SLC39A4	29	2	**7**		-1.08
C4B	116	8	**7**	-8.79	-1.69
CIAPIN1	29	2	**7**	1.24	0.77
TTPA	29	2	**7**	0.82	-6.38
CREM	87	6	**7**	-0.23	-0.53
PFN2	29	2	**7**	-3.35	-0.22
RPGRIP1L	29	2	**7**		2.98
CACNA1H	58	4	**7**		-1.82
NR1I2	189	13	**7**		1.2
CP	117	8	**7**	-2.81	-1.91
FXN	117	8	**7**	-0.42	-0.45
POLE	44	3	**7**	-8.57	1.07
HTR1B	132	9	**7**		2.76
MVK	59	4	**7**	-4.18	-0.85
HLA-A	1098	74	**7**	-2.55	0.73
P2RX7	193	13	**7**	1.4	-2.21
MX1	104	7	**7**	-4.21	0.26
TRPV1	164	11	**7**	-0.36	-1.97
MAP1B	45	3	**7**	5.55	-1.46
SCIN	15	1	**7**	0.82	-1.28
JMJD6	30	2	**7**	-0.23	0.19
TINAGL1	15	1	**7**	1.71	-1.8
NPTX2	15	1	**7**	2.13	0.57
LSG1	15	1	**7**	1.39	0.23
RDH10	15	1	**7**	1.6	-1.7
SDCBP2	15	1	**7**	0.82	0.05
SLC25A14	15	1	**7**	0.82	-0.96
CC2D2A	15	1	**7**	0.32	-0.25
CYB561	15	1	**7**	0.14	1.54
S100A16	15	1	**7**	0.04	1.01
USP14	30	2	**7**	-0.13	0.8
MOV10	30	2	**7**	-0.52	0.44
RPL37	15	1	**7**	-0.56	0
RPS14	45	3	**7**	-0.79	0.48
PPIL3	15	1	**7**	-0.89	-0.85
ASCC1	15	1	**7**	-1.01	0.34
PPME1	15	1	**7**	-1.74	0.19
SMG5	15	1	**7**	-1.91	0.32

ABHD10	15	1	**7**	-1.92	-0.79
EBNA1BP2	30	2	**7**	-2.15	1.19
ZNRF1	15	1	**7**	-2.24	1.91
SOX15	15	1	**7**	-2.64	1.77
CHN1	30	2	**7**	-2.64	-0.57
SCO1	30	2	**7**	-3.43	0.14
PHF12	15	1	**7**	-3.57	1.28
GPS2	30	2	**7**	-3.84	-0.12
STMN3	15	1	**7**	-4.4	1.59
MRPS34	15	1	**7**	-4.85	0.09
POMGNT1	30	2	**7**	-5.33	-0.23
RIN1	30	2	**7**	-7.59	1.58
TCF20	30	2	**7**	-7.59	1.32
KRT6B	15	1	**7**	-10.22	1.86
MACROD2	15	1	**7**		-1.26
CAMK4	60	4	**7**		-1.64
JPH1	15	1	**7**		0.73
SYN3	30	2	**7**		3.08
POLN	15	1	**7**		-0.7
RASD2	15	1	**7**	4.15	-2.06
FCRL1	15	1	**7**	-2.64	-0.44
SLC30A1	30	2	**7**	-6.1	-0.7
KAT2A	76	5	**7**	-7.59	1.59
SLC11A1	137	9	**7**		0.61
POR	107	7	**7**	-3.61	-0.25
ME1	31	2	**6**	1.55	-0.59
NAT10	31	2	**6**	-1.43	0.4
COPS7A	31	2	**6**	-1.87	0.48
KIF1A	31	2	**6**	-8.31	-0.66
TNNT3	31	2	**6**		-1.28
STX4	62	4	**6**	-2.64	-0.24
UGT1A7	78	5	**6**		
LOXL1	78	5	**6**	-3.92	-0.7
CYTH2	47	3	**6**	-2.64	0.92
PPIB	63	4	**6**	0.14	-2.01
RNF128	16	1	**6**	-11.21	-0.36
ADAMTSL1	16	1	**6**	-6.1	0.03
ARL4D	16	1	**6**	-6.1	-0.33
SPRR1A	16	1	**6**	-7.59	0.79
EXOC6	16	1	**6**	3.27	-0.19
FAM213A	16	1	**6**	2.96	-0.33
PTRH2	16	1	**6**	1.75	-0.33
GPN1	16	1	**6**	1.54	-0.45

ANKRD28	16	1	6	1.28	-0.5
C7orf10	16	1	6	0.82	0.51
ZNF644	16	1	6	0.65	0.01
TRIT1	16	1	6	-0.37	0.14
CROT	16	1	6	-0.43	0.51
AK1	32	2	6	-0.81	0.52
LUC7L2	32	2	6	-1.19	-0.38
ELOVL6	16	1	6	-1.36	1.12
OSGEP	16	1	6	-2	-0.56
IRF2BP1	16	1	6	-2.33	0.96
RNF220	16	1	6	-2.38	0.16
TMEM9	16	1	6	-2.49	0.26
MRPS26	16	1	6	-3.57	0.75
CLIP2	16	1	6	-4.34	1.61
H1F0	32	2	6	-5.04	2.13
HOXC10	16	1	6	-5.52	-1.05
HIST1H2AG	16	1	6	-6.1	
MYO1G	16	1	6	-8.98	0.86
MRPL12	16	1	6	-9.15	1.08
KBTBD7	16	1	6		-0.13
NEGR1	32	2	6	1.75	-1.81
NINJ1	16	1	6	-4.14	-0.18
SEMA4B	16	1	6	-4.54	0.82
DIO2	80	5	6	-8.31	0.24
FCRL2	16	1	6		-0.7
DLG5	65	4	6	-1.81	-0.39
COL7A1	114	7	6	-8	2.17
HIST2H2BE	98	6	6	-8	0.82
CDC16	49	3	6	-1.71	-0.1
IMPDH1	49	3	6	-2.96	1.34
HIST2H2AC	82	5	6		
HIST1H2BG	33	2	6		-0.7
MFN1	33	2	6	0.69	-0.7
FHOD1	33	2	6	-1.34	0.67
NMT1	66	4	6	-1.52	0.16
CD79A	66	4	6	-11.82	1.99
COL10A1	50	3	6		4.97
PSMA6	84	5	6	0.11	0.71
COL1A1	459	27	6	-9.18	1.71
CENPI	17	1	6	2.72	4.25
SURF1	34	2	6	3.29	-0.8
AGMAT	17	1	6	1.32	-2.49
PNPO	17	1	6	0.61	-0.74

TBCA	17	1	6	-0.3	0.91
FKBP2	17	1	6	-1.1	-0.63
METTL1	17	1	6	-1.15	0.09
CYB5R1	17	1	6	-1.66	-0.29
SND1	51	3	6	-1.89	1.03
ECH1	17	1	6	-2	-0.82
NKAP	17	1	6	-2.06	-0.33
CRLS1	17	1	6	-2.27	0.37
ALDH3B1	17	1	6	-2.64	-1.23
MFNG	17	1	6	-2.99	2.08
HOXB6	34	2	6	-3.04	-0.18
PSMB9	85	5	6	-3.57	1.58
ACAP1	17	1	6	-7.59	-0.55
HIST1H2BK	34	2	6	-7.59	0.16
LPCAT1	17	1	6	-8.79	0.53
PADI3	17	1	6		
KCNK6	17	1	6	-0.43	0.6
SLC44A4	17	1	6	-2.64	-0.59
NCAM2	17	1	6	-6.1	0.27
SLC39A8	17	1	6	-6.1	0.76
UGT1A9	120	7	6	-9.78	-2.02
CETN2	52	3	6	0.04	-0.23
CHM	52	3	6	-1.76	-0.94
PEPD	52	3	6	-4.76	-0.26
TRIP10	35	2	6	-7.03	1.32
EIF2S2	35	2	6	1.81	-0.03
ZW10	35	2	6	0.41	-0.92
CLNS1A	35	2	6	-0.41	0.2
LONP1	35	2	6	-7.09	0.35
CFB	123	7	6	-9.78	-0.74
ALPL	142	8	6	-6.1	-0.7
IRF6	89	5	6	-3.79	0.52
PRSS8	36	2	6	-8.79	0.49
SACS	36	2	6	2.51	2.48
RANBP1	36	2	6	2.47	1.4
PEX11B	18	1	6	1.2	-0.41
CABYR	18	1	6	3.03	-0.7
ANAPC4	36	2	6	0.41	-0.29
BCAP29	18	1	6	0.36	-0.25
TWF1	18	1	6	0.28	-0.38
RARS	36	2	6	-0.06	-0.24
PDE8A	18	1	6	-0.34	-0.76
GORASP1	36	2	6	-1.39	0.01

TRAFD1	18	1	**6**	-2.57	0.33
CDC42EP1	18	1	**6**	-3.43	0.43
PMVK	18	1	**6**	-3.57	-0.7
POLD2	36	2	**6**	-4.04	0.37
GCSH	18	1	**6**	-4.34	-1.13
G6PC3	18	1	**6**	-5.04	0.87
RCL1	18	1	**6**	-5.11	-0.38
BAAT	18	1	**6**	-5.33	-1.79
TUBG2	18	1	**6**	-6.1	-0.92
SH3GLB2	18	1	**6**	-7.03	0.45
GEM	18	1	**6**	-7.59	-0.7
PPAN	18	1	**6**	-8.31	0.21
CSNK2A1P	18	1	**6**		
GCA	18	1	**6**	-2.64	-1.28
LSR	18	1	**6**		-0.46
CNTNAP2	55	3	**5**	0.28	-0.36
SERPINI1	37	2	**5**	-1.71	-0.55
PSENEN	37	2	**5**	1.23	0
NDUFV2	37	2	**5**	0.56	-0.78
GFPT1	37	2	**5**	-1.04	-0.13
TUBA4A	93	5	**5**	-7.37	-0.87
SSB	93	5	**5**	-0.11	-0.1
GJB2	505	27	**5**	-6.1	0.29
RPS19	75	4	**5**	-0.9	1.25
SRSF2	94	5	**5**	-0.14	0.4
INSR	434	23	**5**	4.3	-0.57
FTO	303	16	**5**	-0.08	-1.18
NREP	19	1	**5**	-2.44	1.53
PPP1R3C	19	1	**5**	1.75	-0.9
KRT16	38	2	**5**	-9.78	2.41
FANCI	38	2	**5**	1.29	1.7
LUC7L	19	1	**5**	2.31	0.69
MYNN	19	1	**5**	0.15	-0.92
VPS25	19	1	**5**	-0.1	-0.3
TMF1	19	1	**5**	-0.12	-1.26
COPS8	38	2	**5**	-0.46	-0.03
SOCS7	19	1	**5**	-0.46	1.08
FBXO22	19	1	**5**	-0.59	1.04
BZW2	19	1	**5**	-0.66	-1.03
IDI1	19	1	**5**	-1.47	0.62
RPS3	76	4	**5**	-1.49	0.6
WIPI2	19	1	**5**	-2.64	0.08
PMPCA	19	1	**5**	-3.63	0.62

ARHGAP32	19	1	**5**	-4.18	-0.04
TBRG4	19	1	**5**	-4.3	0.69
MRPS6	19	1	**5**	-5.28	-0.56
GSTT2	38	2	**5**		0.42
MYT1	19	1	**5**		1.38
OPRK1	57	3	**5**	0.82	-0.7
IER3IP1	19	1	**5**	-0.82	-1.7
SFTPD	154	8	**5**		-0.12
GBF1	58	3	**5**	-3.85	0.68
HHEX	136	7	**5**	5.21	-0.13
TBC1D4	39	2	**5**	3.55	0.92
CLASP1	39	2	**5**	-1.65	0.71
FCGR3B	137	7	**5**	-6.1	2.14
HOXA10	99	5	**5**	-0.08	0.22
EVPL	20	1	**5**	-6.1	2.14
DPP7	20	1	**5**	-5.69	0.14
DEFA5	40	2	**5**		2.76
DIAPH2	20	1	**5**	1.81	1.41
C14orf1	20	1	**5**	2.93	-0.46
FANCL	40	2	**5**	0.82	0.41
SPRR1B	20	1	**5**	0.82	0.58
PDK3	20	1	**5**	0.06	-0.04
AHSA1	20	1	**5**	-0.08	0.7
CETN3	20	1	**5**	-0.51	-0.04
AARS	20	1	**5**	-1.98	0.84
COQ2	20	1	**5**	-2.08	0.54
PDE4DIP	20	1	**5**	-2.64	0.3
GAMT	20	1	**5**	-2.64	0.1
PCCA	40	2	**5**	-3.61	-0.42
RND1	20	1	**5**	-6.1	-0.19
SMARCD3	20	1	**5**	-8.98	1.5
KCNJ15	20	1	**5**		-1.97
SCNN1B	100	5	**5**		-0.82
PRSS1	121	6	**5**		-0.7
RGS4	101	5	**5**	-0.07	-2.41
PRG2	61	3	**5**	-7.59	4.65
PPP1R8	41	2	**5**	0.49	0.03
OFD1	41	2	**5**	-0.68	1.81
UGT1A1	413	20	**5**		-5.09
PINK1	166	8	**5**	-1.74	-0.22
C1R	42	2	**5**	-5.04	-0.32
CYP21A1P	21	1	**5**	1.04	4.65
PFDN2	21	1	**5**	1.75	0.91

SRP54	21	1	**5**	3.65	-0.75
RAB13	21	1	**5**	0.75	0.01
PPT2	21	1	**5**	0.69	-0.26
ARID4B	21	1	**5**	-0.6	-0.1
CHCHD3	21	1	**5**	-0.89	-0.04
FARSA	21	1	**5**	-1.2	-0.31
VPS33B	21	1	**5**	-1.65	-0.79
OLA1	21	1	**5**	-1.69	0.77
GSS	42	2	**5**	-2.45	1.28
CYP26B1	21	1	**5**		-0.96
RIC3	21	1	**5**	-6.1	-1.91
PACSIN3	21	1	**5**	-7.59	0.46
P2RY11	21	1	**5**		-5.09
LIN7A	21	1	**5**		0.27
SERPINA1	358	17	**5**	-9.43	-1.74
BPIFA1	43	2	**5**		-1.53
MERTK	65	3	**5**	1.32	0.48
DTNA	44	2	**5**	2.72	0.88
NCAPD3	22	1	**5**	3.7	0.73
TRIP13	22	1	**5**	-1.44	1.02
DNAJB1	66	3	**5**	-3.14	-0.89
NPC2	44	2	**5**	0.49	-1.02
CRTAP	22	1	**5**	-2.64	-1.54
ERH	22	1	**5**	1.92	0.76
DGKH	22	1	**5**	2.31	-2.2
NR2C1	22	1	**5**	0.9	-0.87
GHITM	22	1	**5**	0.9	-0.46
PARD6B	22	1	**5**	0.39	-0.62
TDG	66	3	**5**	-0.46	-1.69
WBSCR22	22	1	**5**	-3.08	0.5
RFXANK	22	1	**5**	-3.79	0.54
UPF1	66	3	**5**	-5.33	-0.39
SNTB1	22	1	**5**	-7.03	0.51
PGAM5	22	1	**5**	0.4	-1.37
LILRB2	44	2	**5**		0.61
TPI1	67	3	**4**	0.05	-0.12
PSMD7	67	3	**4**	-1	-0.03
HPRT1	134	6	**4**	-1.95	-0.65
RAD18	68	3	**4**	-2.08	1.59
SLC11A2	68	3	**4**	-1.7	-0.3
WDR3	23	1	**4**	1.75	-1.39
NDUFB9	23	1	**4**	-0.3	-0.06
GAR1	23	1	**4**	-0.74	0.86

LBH	23	1	4	-1.06	1.61
L3MBTL2	23	1	4	-1.34	2.17
APH1A	46	2	4	-1.81	0.3
TUSC3	23	1	4	-2.2	0.25
GCNT2	23	1	4	-2.78	0.42
FABP6	23	1	4		5.96
BDNF	875	38	4	-1.1	-1.28
CYB5A	47	2	4	-1.07	0.27
HMBS	95	4	4	-3.62	-0.35
PTS	48	2	4	5.44	-0.44
CCL4L2	24	1	4	0.82	
POMT2	24	1	4	2.31	0.12
CASP12	24	1	4	1.75	
TLE4	24	1	4	0.41	-0.37
ATP5O	24	1	4	0.21	-0.07
COG5	24	1	4	0.03	0.47
BCKDHB	24	1	4	-0.68	-0.77
ZRANB2	24	1	4	-0.95	-0.34
RPL17	24	1	4	-1.16	0.08
ERLIN2	24	1	4	-1.17	-1.01
GK	24	1	4	-3.62	-1.77
NFIX	24	1	4	-7.03	0.81
SLC7A7	24	1	4	0.56	0.93
NR0B2	97	4	4		-1.11
CR2	97	4	4		-2.38
DDC	73	3	4	0.82	-0.79
PSME2	49	2	4	1.22	0.68
EFTUD2	49	2	4	-1.69	1.51
CD3E	98	4	4	-7.59	0.8
KCNQ1	324	13	4		0
AKR1C2	50	2	4	-0.89	0.05
IGLL1	25	1	4		-4.16
SLC36A1	25	1	4	3.29	1.02
ATP6V1D	25	1	4	-0.46	-0.41
CNP	50	2	4	-1.28	-0.35
TADA2A	25	1	4	-1.44	-0.39
PSMD6	50	2	4	-1.56	-1.28
KRR1	25	1	4	-1.95	-0.16
CENPH	25	1	4	-2.64	1.26
PADI2	25	1	4	-6.1	-0.89
SPTBN2	25	1	4	-7.59	-0.48
HOXC13	25	1	4		-0.7
CYP3A5	457	18	4	-2.24	-0.63

CAPN10	127	5	**4**	-4.14	-0.7
GDF6	26	1	**4**		-2.2
PSMA3	78	3	**4**	1.59	0.25
PACRG	26	1	**4**	2.72	-0.12
NEDD4L	104	4	**4**	1.96	-1.03
RAB3B	26	1	**4**	0.69	-0.29
KIAA0020	26	1	**4**	-0.21	0.75
BAIAP2L1	26	1	**4**	-3.92	0.63
HCP5	26	1	**4**	-6.21	0.03
IVL	52	2	**4**	-7.59	6.22
SLC5A6	26	1	**4**	-2.76	1.86
FCER1A	105	4	**4**		-3.64
PGC	53	2	**4**		-0.33
SPINK5	54	2	**4**	3.03	-0.48
ATF7	27	1	**4**	0.62	-0.78
SSR4	27	1	**4**	-0.5	-0.27
SETMAR	27	1	**4**	-0.8	-0.97
KHDRBS3	27	1	**4**	-1.2	0.87
CLK2	27	1	**4**	-2.38	0.39
UQCRC1	27	1	**4**	-3.54	-0.03
RRBP1	27	1	**4**	-6.1	0.25
TAF13	27	1	**4**	-6.1	-4.16
RYR2	109	4	**4**		-2.05
SLC26A4	138	5	**4**	4.69	-0.7
COMP	83	3	**4**		-0.39
SUOX	28	1	**4**	2.3	-0.58
CCP110	28	1	**4**	0.21	-0.96
COPS2	56	2	**4**	0.03	-0.4
CS	28	1	**4**	-0.72	0.8
HOXB5	28	1	**4**	-1.71	-0.08
SPG7	28	1	**4**	-3.21	0.3
NLRP2	28	1	**4**	-7.03	-0.13
SYNGAP1	28	1	**4**		1.12
SLC4A7	28	1	**4**	-3.76	-0.04
GJB6	112	4	**4**		0.68
CDC34	57	2	**4**	-7.59	0.87
MSX1	86	3	**3**	-0.24	0.43
DECR1	29	1	**3**	2.22	-0.7
LGMN	29	1	**3**	0.28	1.04
NUTF2	29	1	**3**	0.23	1.08
MTHFD1L	29	1	**3**	-0.13	1.74
RPL24	29	1	**3**	-0.44	-0.04
GGA1	58	2	**3**	-2.96	0.23

ACSM3	29	1	**3**	-3.57	-1.04
CLEC16A	58	2	**3**	-4.14	0.19
OASL	29	1	**3**	-4.59	1.7
PRNP	522	18	**3**	-0.59	-0.2
CYP21A2	238	8	**3**		
BTD	30	1	**3**	-0.15	-2.42
TUBB2A	90	3	**3**	-3.48	3.41
SCN8A	30	1	**3**	-6.1	-2.68
KRT13	31	1	**3**		-1.49
RPS26	31	1	**3**	1.3	-0.63
POLR1C	31	1	**3**	1.43	-0.7
ASPN	31	1	**3**	3.03	-1.18
HM13	31	1	**3**	-2.18	0.37
RFX5	31	1	**3**	-2.64	-0.57
WHSC2	31	1	**3**	-8	0.39
FXR2	31	1	**3**	-8.57	1.19
SLC15A1	62	2	**3**	-0.74	-0.89
DRD2	724	23	**3**		2.87
MATN3	32	1	**3**	3.29	-1.11
FKBP1A	96	3	**3**	1.74	0.1
POLR2G	96	3	**3**	1.46	-0.37
SAE1	32	1	**3**	-0.9	0.67
FKBP4	64	2	**3**	-3.98	1.18
GALK1	32	1	**3**	-7.59	1.47
OAS1	65	2	**3**	-2.47	0.5
NOP56	33	1	**3**	-1.52	0.54
CYC1	33	1	**3**	-3.48	-0.46
SLC15A2	33	1	**3**	0.13	-1.56
TNNC1	68	2	**3**	0.82	-0.36
PRPF4	34	1	**3**	-0.29	0.34
NDUFS3	34	1	**3**	-2.64	0.27
ACD	34	1	**3**	-8.31	-0.27
FST	69	2	**3**	-2.33	0.29
ORC5	35	1	**3**	0.56	-0.96
EXOSC10	35	1	**3**	-0.61	-0.4
FOXP2	70	2	**3**	-1.49	-1.24
HBA1	393	11	**3**	-6.1	0.48
CPSF2	36	1	**3**	0.47	-0.46
FIS1	36	1	**3**	-0.58	0.5
NDE1	36	1	**3**	-4.03	2.22
AP1M2	37	1	**3**	-7.59	0.29
SSRP1	75	2	**3**	-1.68	0.86
SYNE2	38	1	**3**	0.69	-0.42

MDH2	38	1	**3**	-3.45	0.26
SLC6A8	39	1	**3**	-3.61	0.26
FAH	39	1	**3**	-10.22	-0.27
GPR143	40	1	**3**	2.31	0.84
CRYBB2	40	1	**3**	0.82	-5.66
OAT	40	1	**3**	-0.79	-0.75
VAMP2	80	2	**3**	-4.14	-0.76
PSME3	81	2	**2**	-1.19	0.6
SCAP	41	1	**2**	-2.16	1.71
ORMDL3	42	1	**2**	0.82	0.84
FXR1	43	1	**2**	1.12	0.84
RPS16	43	1	**2**	-0.15	-0.18
DBP	43	1	**2**		0.17
BACE1	219	5	**2**	0.6	0.55
BLK	44	1	**2**	-8.57	-0.7
EIF3B	45	1	**2**	-3.64	-0.23
HTR7	45	1	**2**		0.02
MAG	45	1	**2**		-1.59
RPA3	46	1	**2**	5.39	0.46
SF3A1	46	1	**2**	-3.44	0.86
VKORC1	233	5	**2**	-0.29	-0.31
AMPH	48	1	**2**		-0.7
ATRIP	48	1	**2**		1.2
CYP2B6	194	4	**2**	2.72	-1.47
DCTN2	49	1	**2**	-0.74	0.31
BLNK	49	1	**2**	-8	0.73
HBB	549	11	**2**	-12.95	-0.2
ILF2	50	1	**2**	0.11	0.63
GRIN2D	51	1	**2**	0.82	0.02
SNRPD2	52	1	**2**	0.43	0.71
POLR2H	104	2	**2**	-0.94	0.43
EYA1	52	1	**2**	-1.71	-0.13
H2AFZ	53	1	**2**	0.9	-0.04
NEU1	54	1	**2**	-3.5	-0.09
CD2AP	54	1	**2**	-0.66	-0.53
NPC1L1	54	1	**2**		-1.26
PSMD3	55	1	**2**	-2.96	0.8
PNP	56	1	**2**	1.58	-0.86
VAPB	58	1	**2**	-3.09	-0.61
KPNA1	118	2	**2**	-0.9	-0.27
CDKAL1	118	2	**2**	2.31	1.08
RCC1	62	1	**2**	-4.2	-1.21
GTF2H4	62	1	**2**	-8.79	-0.05

NXF1	65	1	**2**	-2.9	0.25
IPO5	74	1	**1**	0.21	-0.73
HLA-DRB5	156	2	**1**	-7.59	-1.73
SNCA	788	10	**1**	2.92	0.5
POLR2L	89	1	**1**	0.93	-0.59
POLR2J	91	1	**1**	-1.85	-0.12
HBA2	190	2	**1**	-8.57	0.64
ARSA	97	1	**1**	-0.91	-1.06
POLR2C	107	1	**1**	-0.15	0.13
SFTPB	109	1	**1**	-0.43	-1.19
WFS1	129	1	**1**	0.41	-0.44
HBG2	139	1	**1**	-6.1	4.96
C9orf47	4	0	**0**	-6.1	-2.26
SAA2-SAA4	1	0	**0**		2.76
GALNT14	15	0	**0**	-3.04	-0.89
NUP37	16	0	**0**	0.47	1.48
LOC550643	1	0	**0**	0.36	-0.14
RPSAP58	3	0	**0**	-0.31	0.23
CDC42EP5	5	0	**0**	-6.1	1.04
SNORA24	3	0	**0**		
SCARNA7	1	0	**0**		
MYCT1	8	0	**0**	8.47	4.97
TMEM41A	6	0	**0**	1.98	0.29
FAM171A1	5	0	**0**	1.75	-0.7
GPX8	8	0	**0**	2.04	-0.94
TMEM116	4	0	**0**	0.82	-0.99
C20orf24	10	0	**0**	-1.78	0.35
GDPD5	10	0	**0**	-2.64	-0.25
DNAJA4	7	0	**0**	-3.57	-1.31
GPR157	5	0	**0**		
MPZL3	7	0	**0**		-0.7
C1orf63	6	0	**0**	-2.64	0.03
ACP6	14	0	**0**	-6.1	-0.17
EGFLAM	7	0	**0**	-6.1	-0.63
RNF215	1	0	**0**	-6.1	-2.24
SPESP1	6	0	**0**	-8	0.42
CRLF1	14	0	**0**		6.87
BOLA1	12	0	**0**		-0.13
TGIF2-C20ORF24	1	0	**0**		
SNORA52	4	0	**0**	1.75	2.76
C4orf46	4	0	**0**	1.62	1.48
FAM43A	5	0	**0**	2.56	1.14

DIAPH3	25	0	**0**	5.89	1
LOC100130331	1	0	**0**	2.31	0.79
ARL5B	14	0	**0**	1.75	0.79
NUDT4	10	0	**0**	3.34	0.7
CMC1	4	0	**0**	3.51	0.29
FLJ39639	3	0	**0**	3.03	0.26
GEMIN8	8	0	**0**	1.69	0.21
CRNDE	3	0	**0**	1.75	0.18
MGC16121	2	0	**0**	2.31	0.09
MRPL53	7	0	**0**	3.51	0.08
MRPL32	14	0	**0**	2.2	0.06
CHCHD1	9	0	**0**	2.98	-0.01
ARL15	13	0	**0**	3.7	-1.18
C10orf11	7	0	**0**	2.72	-1.42
CHMP4C	12	0	**0**	2.31	-1.47
ANXA2P3	2	0	**0**	2.72	-4.16
ATP5EP2	0	0	**0**	1.75	
H2BFXP	1	0	**0**	0.82	4.25
UBE2Q2P1	0	0	**0**	0.82	-1.02
RBP7	5	0	**0**	0.82	0.68
SNORD32A	3	0	**0**	0.82	
SNORD35B	2	0	**0**	0.82	
LOC100506866	3	0	**0**	0.82	2.5
ZFAND2A	4	0	**0**	0.41	1.26
PAICS	28	0	**0**	0.23	0.53
ZSCAN12P1	2	0	**0**	0.11	2.63
C8orf58	4	0	**0**	0.05	-0.18
NUDT4P1	2	0	**0**	0.05	-0.48
SNHG15	3	0	**0**	-0.13	0.1
CCDC142	5	0	**0**	-0.41	-0.26
IDUA	53	0	**0**	-0.74	1.37
FHDC1	6	0	**0**	-0.76	-0.35
RPL22L1	7	0	**0**	-1.12	0.57
LOC100128338	2	0	**0**	-1.25	-0.26
PPAT	17	0	**0**	-1.29	0.77
LOC388796	5	0	**0**	-1.39	1.06
ZNF266	10	0	**0**	-1.44	2.03
FAM83D	12	0	**0**	-1.71	6.44
RPP25	9	0	**0**	-2.08	0.87
SNHG6	1	0	**0**	-2.45	-0.38

FAM118A	7	0	**0**	-2.64	-0.42
ZNF165	9	0	**0**	-2.64	
DCTPP1	8	0	**0**	-2.76	1.4
LONP2	7	0	**0**	-2.9	-0.33
PSAT1	16	0	**0**	-3.02	0.36
PDXP	13	0	**0**	-3.2	1.47
ACCS	6	0	**0**	-3.57	-1.15
MOCS1	22	0	**0**	-3.57	-0.44
SPOCD1	3	0	**0**	-3.61	4.25
ISYNA1	10	0	**0**	-3.61	-0.52
ZNF503	7	0	**0**	-3.61	0.38
DNTTIP1	13	0	**0**	-3.62	0.61
LOC96610	5	0	**0**	-3.99	-1.17
FAM127B	10	0	**0**	-4.54	-0.37
FAM110C	3	0	**0**	-6.1	0.07
ZNF692	8	0	**0**	-6.1	0.41
AADAT	14	0	**0**	-6.1	-0.44
DUOXA1	10	0	**0**	-6.1	-1.26
KIFC2	9	0	**0**	-6.1	2.19
CCDC64	3	0	**0**	-6.1	-1.17
SNORD100	2	0	**0**	-6.1	-4.16
SNORD23	2	0	**0**	-6.1	
MIR205HG	2	0	**0**	-7.03	-1.57
SNORA71A	3	0	**0**	-7.03	
KANSL1-AS1	3	0	**0**	-7.03	4.32
NEFM	35	0	**0**	-8.57	-2.02
KIAA0226L	12	0	**0**	-8.57	1.56
KRT80	9	0	**0**	-8.57	0.09
KRT6A	28	0	**0**	-10.92	-0.51
HIST2H2AA4	7	0	**0**		
ZC2HC1C	5	0	**0**		-0.3
CCDC64B	2	0	**0**		4.97
CAPS	15	0	**0**		-1.17
MOCOS	11	0	**0**		0.49
ZNF77	6	0	**0**		-1.42
RHOV	8	0	**0**		0.27
STK32A	8	0	**0**		-4.16
SNORD15B	4	0	**0**		
RNU86	1	0	**0**		
SNORA10	3	0	**0**		
SNORD12C	3	0	**0**		
SNORD16	4	0	**0**		
SNORD36A	3	0	**0**		2.76

SNORD30	3	0	**0**		
SNORA72	4	0	**0**		3.69
SNORD87	4	0	**0**		
SNORD60	2	0	**0**		
SNORD44	2	0	**0**		2.76
SNORA48	4	0	**0**		
GSTM2P1	1	0	**0**		
SNORA23	3	0	**0**		
SNORA38	3	0	**0**		
SNORA44	3	0	**0**		-4.16
SNORA50	3	0	**0**		2.76
SNORD62B	2	0	**0**		
SNORD110	2	0	**0**		
SNORD116-1	3	0	**0**		
SNORD116-16	3	0	**0**		
SNORD116-17	3	0	**0**		
SNORD115-33	7	0	**0**		
SNORD105B	2	0	**0**		
SNORD123	3	0	**0**		
SNORD75	3	0	**0**		
SNORD76	3	0	**0**		
HSPA7	13	0	**0**		1.51
LINC00240	1	0	**0**		-0.7
MST1P2	1	0	**0**		-0.07
MIR635	2	0	**0**		
OLFML1	6	0	**0**	1.75	1.48
CYTL1	9	0	**0**	4.69	0.84
C1orf54	7	0	**0**	1.32	0.7
C3orf58	9	0	**0**	7.13	0.24
EFHA2	3	0	**0**	3.7	-0.14
C17orf39	5	0	**0**	4.15	-0.23
NUDT19	5	0	**0**	7.4	-0.29
ADAMTSL2	8	0	**0**	3.03	-0.53
C2orf69	4	0	**0**	5.27	-0.7
BOLA3	6	0	**0**	1.48	-1.35
C3orf64	0	0	**0**	0.9	-1.47
CPXM2	7	0	**0**	0.82	0.18
COQ10A	9	0	**0**	0.82	-0.77
PRAP1	6	0	**0**	0.82	0.13
C16orf89	5	0	**0**	0.82	-0.7

IGIP	3	0	**0**	0.24	-2.92
QPCT	23	0	**0**	0	-0.86
PAPL	3	0	**0**	-0.72	-0.93
PRRG4	5	0	**0**	-0.8	-1.45
SPATA6	7	0	**0**	-1.15	-0.44
CABP4	11	0	**0**	-1.4	-1.33
PODNL1	1	0	**0**	-1.71	1.36
MEGF6	8	0	**0**	-1.91	0.42
OAF	2	0	**0**	-2.33	0.69
BMP8B	12	0	**0**	-2.64	5.45
MTRNR2L3	4	0	**0**	-2.64	-5.09
ABHD14A	6	0	**0**	-3.57	-0.46
SPAG7	10	0	**0**	-3.92	-0.31
CRELD2	11	0	**0**	-5.11	1
LRRC17	9	0	**0**	-6.1	0.49
CPXM1	10	0	**0**	-6.1	3.17
HSD11B1L	3	0	**0**	-6.1	0.55
FBXL19	8	0	**0**	-6.1	0.86
JMJD8	2	0	**0**	-6.1	-0.46
HYI	9	0	**0**	-6.1	0.76
VPREB3	10	0	**0**	-7.03	0.58
CCDC3	9	0	**0**	-7.03	-0.07
CES4A	8	0	**0**	-7.03	-0.42
PRSS12	7	0	**0**	-7.59	0.29
FAM155B	1	0	**0**	-7.59	1.77
RCN3	8	0	**0**	-8.57	2.14
C10orf81	0	0	**0**		-1.68
EPGN	5	0	**0**		
CST2	32	0	**0**		
EPYC	9	0	**0**		2.76
ORM2	30	0	**0**		-0.86
CILP	23	0	**0**		-6.06
NPFF	17	0	**0**		0.73
NXPH4	6	0	**0**		1.7
EPHX3	7	0	**0**		-1.98
PSORS1C2	7	0	**0**		-4.16
RNASE7	13	0	**0**		-5.09
LCN15	2	0	**0**		4.25
OLFML2B	4	0	**0**		1.54
EGFL8	13	0	**0**		0.39
ADAM32	7	0	**0**		0.26
CTRC	20	0	**0**		
SOWAHA	4	0	**0**		-2.14

C19orf76	1	0	**0**		1.51
ADCK5	5	0	**0**		-0.3
C17orf67	2	0	**0**		1.77
SFTA2	6	0	**0**		-1.11
C10orf114	3	0	**0**		-0.7
MTRNR2L9	4	0	**0**		
TEPP	2	0	**0**		-2.92
DMKN	10	0	**0**		0.76
MARCH4	7	0	**0**	1.75	5.45
ZNF600	4	0	**0**	3.87	4.97
C2orf27A	5	0	**0**	3.7	4.65
MOV10L1	8	0	**0**	4.6	4.25
ZNF630	4	0	**0**	3.51	3.69
LOC100507254	1	0	**0**	6.04	2.76
ZNF304	3	0	**0**	4.02	2.76
KANSL2	12	0	**0**	1.93	2.69
LOC283143	3	0	**0**	3.87	2.18
CEP128	10	0	**0**	2.31	2.18
MTCP1NB	12	0	**0**	1.75	2.06
IPO11	16	0	**0**	3.19	2.04
ZNF610	5	0	**0**	4.02	1.99
ADNP2	9	0	**0**	2.58	1.84
LOC100128822	2	0	**0**	2.72	1.82
ADAP2	20	0	**0**	2.31	1.82
THAP2	11	0	**0**	4.15	1.7
LOC283663	2	0	**0**	2.31	1.7
LOC388152	2	0	**0**	1.75	1.67
GALNT10	8	0	**0**	1.43	1.66
INTS7	19	0	**0**	4.78	1.56
RPSAP9	3	0	**0**	4.28	1.56
CA13	8	0	**0**	2.72	1.56
RPL26L1	8	0	**0**	1.75	1.54
AAED1	5	0	**0**	1.75	1.48
URGCP-MRPS24	2	0	**0**	1.46	1.44
NSUN6	7	0	**0**	3.03	1.38
MED11	7	0	**0**	3.29	1.33
GALNTL2	11	0	**0**	7.01	1.32
ADAT2	6	0	**0**	1.25	1.29
C17orf69	4	0	**0**	1.04	1.28
MRPS24	14	0	**0**	2.09	1.27

NANP	8	0	**0**	4.39	1.24
FLJ41200	2	0	**0**	9.89	1.2
FUK	6	0	**0**	2.31	1.2
GPATCH1	5	0	**0**	2.72	1.14
WDR89	10	0	**0**	4.6	1.08
ZNF83	10	0	**0**	1.72	1.07
STAC	5	0	**0**	3.7	1.05
NDUFB2	11	0	**0**	2.51	1.01
PDCL3	10	0	**0**	3.6	1
GOLGA6L5	4	0	**0**	3.51	1
C2orf68	4	0	**0**	3.31	1
CCDC53	12	0	**0**	1.68	0.98
KIAA0895L	2	0	**0**	2.72	0.97
PDE6D	18	0	**0**	2.31	0.94
RRP15	14	0	**0**	2.27	0.9
UQCRQ	10	0	**0**	4.37	0.88
ZNF626	1	0	**0**	1.62	0.87
ARHGAP11A	10	0	**0**	1.15	0.85
RPAIN	14	0	**0**	1.75	0.84
IFT43	10	0	**0**	4.86	0.83
CCNT2	28	0	**0**	4.94	0.82
MRPL17	14	0	**0**	1.76	0.82
PNMAL1	12	0	**0**	1.75	0.82
LOC283177	2	0	**0**	1.75	0.78
DNMBP	15	0	**0**	1.69	0.76
C19orf53	9	0	**0**	1.53	0.75
C12orf26	6	0	**0**	3.51	0.73
C12orf45	3	0	**0**	1.14	0.73
PDP1	24	0	**0**	1.84	0.64
FBXO17	10	0	**0**	2.25	0.63
UTP15	13	0	**0**	3.87	0.61
TMED10P1	2	0	**0**	3.51	0.58
HOXA2	13	0	**0**	1.75	0.58
PCBP1-AS1	2	0	**0**	1.75	0.58
ZNF662	2	0	**0**	5.27	0.57
CSRP2BP	14	0	**0**	3.51	0.57
AVIL	7	0	**0**	4.14	0.56
PSMB6	47	0	**0**	1.16	0.55
AMZ2P1	3	0	**0**	4.28	0.51
C6orf70	3	0	**0**	4.39	0.49
ARPC3	26	0	**0**	1.81	0.49
C11orf67	6	0	**0**	1.46	0.45
FAM198B	9	0	**0**	2.88	0.42

C17orf58	2	0	**0**	2.31	0.42
FDX1L	4	0	**0**	1.75	0.4
MTERF	24	0	**0**	1.69	0.39
ZNF117	6	0	**0**	1.93	0.37
TFB1M	21	0	**0**	3.13	0.36
RILPL1	5	0	**0**	3.87	0.35
TRIM5	97	0	**0**	3.82	0.29
MRPL33	9	0	**0**	3.08	0.29
EIF4E2	20	0	**0**	1.91	0.29
PIGS	15	0	**0**	1.05	0.29
ARL3	26	0	**0**	1.04	0.29
GALNTL4	11	0	**0**	1.04	0.27
WSB2	12	0	**0**	1.59	0.25
MRPL45P2	1	0	**0**	2.72	0.23
B3GALTL	16	0	**0**	7.57	0.2
MRPL47	8	0	**0**	2.15	0.2
DIS3L	9	0	**0**	1.81	0.2
MCMBP	21	0	**0**	1.68	0.2
WDR83OS	5	0	**0**	1.35	0.2
RPL7	46	0	**0**	1.52	0.19
PPWD1	10	0	**0**	1.59	0.17
PLK1S1	3	0	**0**	7.65	0.16
IFT20	14	0	**0**	4.02	0.12
LOC100289019	0	0	**0**	1.4	0.12
ARSD	10	0	**0**	1.32	0.12
IPO9	19	0	**0**	1.22	0.11
STK36	17	0	**0**	3.29	0.1
BTBD6	6	0	**0**	2.72	0.1
KBTBD4	10	0	**0**	1.75	0.1
THUMPD2	8	0	**0**	1.75	0.09
GATAD1	9	0	**0**	1.67	0.08
ATP6V1H	32	0	**0**	1.05	0.07
ZCRB1	6	0	**0**	1.88	0.03
HMGN3	14	0	**0**	1.53	0.03
LOC541471	2	0	**0**	3.25	0.02
B3GNT7	4	0	**0**	1.4	-0.03
LOC644961	1	0	**0**	3.29	-0.04
RGL1	9	0	**0**	3.29	-0.04
ZFAND1	7	0	**0**	2.18	-0.05
TTC18	3	0	**0**	1.75	-0.06
BCL6B	9	0	**0**	5.77	-0.07
MTHFS	21	0	**0**	1.75	-0.12

LOC100506178	2	0	**0**	4.5	-0.14
FKBP1AP1	1	0	**0**	2.72	-0.14
COG1	14	0	**0**	1.04	-0.14
ZC2HC1A	7	0	**0**	1.55	-0.16
ZNF780B	3	0	**0**	4.6	-0.18
LOC401321	1	0	**0**	4.15	-0.19
PGBD2	3	0	**0**	3.51	-0.19
HHLA3	6	0	**0**	1.75	-0.19
MORN4	6	0	**0**	1.04	-0.2
UGGT1	16	0	**0**	1.12	-0.21
C17orf48	2	0	**0**	5.21	-0.23
FER1L4	9	0	**0**	3.03	-0.23
MTMR9LP	3	0	**0**	3.03	-0.23
CHIC2	14	0	**0**	4.5	-0.25
RAI14	20	0	**0**	2.45	-0.28
LINC00152	2	0	**0**	9.21	-0.29
C8orf38	0	0	**0**	3.03	-0.29
LOC100190940	0	0	**0**	3.03	-0.3
LOC100499177	5	0	**0**	1.09	-0.32
QPCTL	10	0	**0**	5.08	-0.33
DNAJC13	15	0	**0**	2.03	-0.33
C11orf92	6	0	**0**	3.29	-0.36
MAK16	13	0	**0**	1.42	-0.36
GLTP	25	0	**0**	2.56	-0.38
MAP3K13	10	0	**0**	1.54	-0.38
ELP2	12	0	**0**	1.38	-0.38
ZNF559-ZNF177	5	0	**0**	3.7	-0.39
RMND5A	11	0	**0**	3.27	-0.4
QSER1	8	0	**0**	5.08	-0.42
SNX25	6	0	**0**	3.29	-0.42
NDUFA2	15	0	**0**	1.46	-0.43
ALG1	16	0	**0**	1.09	-0.44
B3GNT5	8	0	**0**	4.15	-0.46
TTC5	8	0	**0**	4.28	-0.48
FAM117B	5	0	**0**	1.65	-0.5
MDP1	7	0	**0**	1.75	-0.51
C15orf54	3	0	**0**	5.49	-0.7
HEATR7A	8	0	**0**	5.01	-0.7
SUMO1P3	3	0	**0**	3.87	-0.7

LOC100507053	0	0	**0**	2.31	-0.7
AGMO	9	0	**0**	2.31	-0.7
C11orf73	9	0	**0**	2.07	-0.7
C2orf15	4	0	**0**	1.75	-0.7
EPB41L5	6	0	**0**	3.03	-0.76
DNAJC21	7	0	**0**	2.12	-0.78
COX7A2L	15	0	**0**	2.11	-0.78
MED7	26	0	**0**	1.69	-0.81
ZNF559	7	0	**0**	4.94	-0.82
SETD3	8	0	**0**	1.75	-0.85
NARS2	10	0	**0**	3.29	-0.89
FAM133B	6	0	**0**	2.36	-0.89
SLC25A45	5	0	**0**	3.51	-0.92
CNKSR3	8	0	**0**	1.48	-1.02
TIMM21	6	0	**0**	2.27	-1.05
ELL2	9	0	**0**	2.44	-1.07
ASB9	14	0	**0**	3.51	-1.08
ECHDC3	5	0	**0**	1.75	-1.08
TRAPPC2P1	11	0	**0**	2.62	-1.1
KRT4	25	0	**0**	1.75	-1.11
ZNF547	3	0	**0**	5.15	-1.26
RPL21P44	3	0	**0**	4.6	-1.26
LOC645638	0	0	**0**	3.03	-1.26
FAM200A	6	0	**0**	2.31	-1.28
SRPRB	22	0	**0**	2.29	-1.29
GALK2	11	0	**0**	2.27	-1.39
RBM45	7	0	**0**	1.88	-1.43
MORN2	8	0	**0**	5.15	-1.48
LOC375295	1	0	**0**	5.69	-1.6
INO80C	12	0	**0**	4.15	-1.69
ZNF180	6	0	**0**	1.75	-1.98
ARSJ	7	0	**0**	1.62	-1.98
C10orf47	4	0	**0**	2.31	-2
GEMIN6	17	0	**0**	1.4	-2.09
METTL21B	6	0	**0**	1.37	-2.11
LINC00339	2	0	**0**	3.03	-2.24
CCDC30	1	0	**0**	4.28	-2.26
FAM98B	7	0	**0**	1.75	-2.6
FLJ35776	2	0	**0**	1.75	-2.6
EGOT	2	0	**0**	1.75	-3.1
LOC145820	3	0	**0**	3.03	-3.75
CCT6P1	5	0	**0**	3.7	-4.44

CBR3-AS1	3	0	**0**	1.75	-5.09
GIPC3	14	0	**0**	1.75	-5.66
SNORA25	3	0	**0**	1.75	-6.06
ELOVL3	7	0	**0**	1.75	-8.55
SNORD52	3	0	**0**	3.03	
SNORD99	2	0	**0**	3.03	
LOC646324	0	0	**0**	2.72	
SCARNA15	1	0	**0**	2.31	
MORN3	3	0	**0**	1.75	
ACOT13	17	0	**0**	0.94	-0.31
C3orf26	8	0	**0**	0.94	-0.25
ARL1	26	0	**0**	0.94	-0.04
SS18L2	4	0	**0**	0.94	2.01
CEP63	22	0	**0**	0.93	-0.7
C22orf13	5	0	**0**	0.9	0.74
KATNAL1	9	0	**0**	0.88	-0.26
DHX8	10	0	**0**	0.88	0.55
MRPL18	16	0	**0**	0.86	0.63
OBFC2A	9	0	**0**	0.84	-1.4
SULT1B1	15	0	**0**	0.82	-5.09
SFTA1P	0	0	**0**	0.82	-2.09
NCCRP1	3	0	**0**	0.82	-3.17
PLEKHG7	3	0	**0**	0.82	-5.66
SNX30	4	0	**0**	0.82	0.03
C17orf97	1	0	**0**	0.82	-1.16
C5orf56	10	0	**0**	0.82	3.92
ZSCAN30	3	0	**0**	0.82	0.86
WDSUB1	6	0	**0**	0.82	0.08
LETM2	3	0	**0**	0.82	-0.7
PRICKLE3	10	0	**0**	0.82	0.58
PAX1	20	0	**0**	0.82	4.25
ZNF211	5	0	**0**	0.82	1.77
HOXD9	26	0	**0**	0.82	-1.63
ProSAPiP1	5	0	**0**	0.82	1.84
HSD17B14	10	0	**0**	0.82	-0.01
CECR5	10	0	**0**	0.82	0.54
C9orf16	7	0	**0**	0.82	1.15
IRX3	7	0	**0**	0.82	-0.46
IQCA1	8	0	**0**	0.82	-0.6
MEX3B	18	0	**0**	0.82	1.56
TRIM15	15	0	**0**	0.82	1.38
CARD14	13	0	**0**	0.82	-0.7
RHPN1	7	0	**0**	0.82	0.48

ADAT3	3	0	**0**	0.82	1.59
SNORA4	3	0	**0**	0.82	
SNORD47	2	0	**0**	0.82	
RPL13P5	3	0	**0**	0.82	-4.16
SNORA31	3	0	**0**	0.82	3.69
LOC284276	2	0	**0**	0.82	-1.26
RPL23P8	1	0	**0**	0.82	
FLJ13197	1	0	**0**	0.82	-0.39
LOC727849	3	0	**0**	0.82	1.41
LOC100132356	2	0	**0**	0.82	1.99
PPT2-EGFL8	2	0	**0**	0.82	-4.16
LOC100506462	1	0	**0**	0.82	1.51
LOC100506305	1	0	**0**	0.82	0.4
MIR4517	2	0	**0**	0.82	
HOTAIRM1	1	0	**0**	0.82	0.29
PPP1R21	4	0	**0**	0.82	-0.7
NUBPL	12	0	**0**	0.73	0.24
EXOSC1	19	0	**0**	0.72	-0.34
WBP4	14	0	**0**	0.71	-1.4
MPI	24	0	**0**	0.69	0.91
ICK	16	0	**0**	0.69	-0.09
SESTD1	7	0	**0**	0.69	-0.7
LOC93622	1	0	**0**	0.69	1.09
TARS	27	0	**0**	0.68	-0.08
KIAA0947	5	0	**0**	0.65	-0.62
DHDDS	13	0	**0**	0.62	0.53
KBTBD12	5	0	**0**	0.59	0
SIX4	11	0	**0**	0.57	-0.7
PPP1R3B	15	0	**0**	0.57	-0.38
RPL27	22	0	**0**	0.56	0.5
NDUFS5	22	0	**0**	0.55	1.24
MNF1	7	0	**0**	0.55	1.28
DNAJC14	11	0	**0**	0.54	-0.29
RPLP0P2	5	0	**0**	0.54	0.74
ATP5S	14	0	**0**	0.54	1.12
COPB1	54	0	**0**	0.5	0.77
C1orf86	7	0	**0**	0.5	1.16
FAM136A	15	0	**0**	0.5	0.77
ARPP19	14	0	**0**	0.48	-0.87
ATG3	17	0	**0**	0.48	0.19

SH3YL1	9	0	**0**	0.47	-0.94
LYPLA1	17	0	**0**	0.42	-0.21
CERK	29	0	**0**	0.42	0.03
SNHG3	4	0	**0**	0.42	1.38
PEX26	18	0	**0**	0.41	-0.33
POLR3C	18	0	**0**	0.41	0.01
TIMM9	13	0	**0**	0.41	0.41
TBC1D12	6	0	**0**	0.41	-0.18
MCCC1	21	0	**0**	0.41	-1.53
C19orf40	14	0	**0**	0.41	-0.23
LOC401320	3	0	**0**	0.41	-0.92
MTERFD2	7	0	**0**	0.41	1.03
MUTED	15	0	**0**	0.39	3.34
SGK494	4	0	**0**	0.39	-0.58
KIAA0907	8	0	**0**	0.39	0.88
CYB5B	14	0	**0**	0.38	-0.34
LOC147804	2	0	**0**	0.38	-0.03
QRICH1	12	0	**0**	0.37	-0.26
SPATS2	7	0	**0**	0.34	0.09
EXOSC8	18	0	**0**	0.34	0.26
OTUD3	9	0	**0**	0.32	0
TRMT112	13	0	**0**	0.3	0.46
GRAMD1C	4	0	**0**	0.3	-0.38
KIAA1586	5	0	**0**	0.3	-0.39
RPE	12	0	**0**	0.28	-0.55
ZNHIT3	11	0	**0**	0.26	0.16
CLN8	18	0	**0**	0.26	0.18
HOMER3	20	0	**0**	0.24	0.15
TBC1D13	4	0	**0**	0.24	-0.35
DSTNP2	1	0	**0**	0.24	-0.7
LOC100505761	3	0	**0**	0.24	-0.36
LOC100506686	2	0	**0**	0.24	-0.7
C5orf22	10	0	**0**	0.21	0.1
MITD1	6	0	**0**	0.21	0.13
ZNF597	5	0	**0**	0.21	-1.26
UBFD1	8	0	**0**	0.19	-0.1
HAUS5	10	0	**0**	0.18	1.02
MRPS10	13	0	**0**	0.18	-0.64
TMED2	19	0	**0**	0.17	0
PGM2L1	8	0	**0**	0.15	0.14
OSBPL3	20	0	**0**	0.14	-0.32

FCHO2	13	0	**0**	0.13	-0.51
FAM114A2	8	0	**0**	0.13	-0.01
SPCS1	9	0	**0**	0.12	-0.21
RBM28	20	0	**0**	0.08	0.28
LRRC48	12	0	**0**	0.08	-0.87
MCU	9	0	**0**	0.06	1.23
SCFD2	9	0	**0**	0.06	0.23
PPIH	16	0	**0**	0.05	2.82
UBE2O	19	0	**0**	0.05	0.29
C19orf54	4	0	**0**	0.05	-1.02
GUSBP1	9	0	**0**	0.05	-0.78
FUNDC2	14	0	**0**	0.04	-0.02
GTF3C2	25	0	**0**	0.03	0.95
ZNF232	8	0	**0**	0	-1.47
GAL3ST4	10	0	**0**	0	-0.87
C11orf46	8	0	**0**	0	0.96
TPRG1L	5	0	**0**	-0.01	-0.07
HNRNPA1L2	4	0	**0**	-0.02	2.53
ZDHHC16	8	0	**0**	-0.02	-0.15
MTRF1L	14	0	**0**	-0.03	0.33
ATP5C1	31	0	**0**	-0.04	-1.43
SNRPB2	29	0	**0**	-0.05	-0.23
NDUFA7	15	0	**0**	-0.09	1.6
ORC6	34	0	**0**	-0.09	0.68
NDUFAB1	17	0	**0**	-0.1	0.45
RSAD1	5	0	**0**	-0.11	0.93
LOC84856	3	0	**0**	-0.11	-1.81
PGM2	20	0	**0**	-0.15	-0.7
ZNF761	4	0	**0**	-0.17	-1.35
PSMG3	12	0	**0**	-0.17	-1.25
RASSF9	4	0	**0**	-0.17	-6.06
OAS3	21	0	**0**	-0.17	0.68
C2orf43	9	0	**0**	-0.17	-2.06
SCAMP5	14	0	**0**	-0.17	0.48
FAM124A	6	0	**0**	-0.17	-0.32
METTL21A	2	0	**0**	-0.17	-0.27
GAS2L3	4	0	**0**	-0.17	-1.98
LOC100506930	2	0	**0**	-0.17	0.12
NPHP1	46	0	**0**	-0.18	0.29
AK4	15	0	**0**	-0.2	-2.25
TWISTNB	8	0	**0**	-0.21	0.18
UBE2Q1	13	0	**0**	-0.23	-0.04

PRRC1	7	0	**0**	-0.23	0.15
EIF6	39	0	**0**	-0.24	-0.01
DYM	22	0	**0**	-0.24	-0.18
MMS19	24	0	**0**	-0.24	1.75
FN3KRP	18	0	**0**	-0.24	-0.12
ZBTB11	10	0	**0**	-0.26	-1.28
SNHG7	2	0	**0**	-0.26	1.11
C18orf32	5	0	**0**	-0.33	-0.55
YME1L1	17	0	**0**	-0.33	-1.23
SNRPF	37	0	**0**	-0.35	0.73
CHORDC1	18	0	**0**	-0.35	-0.38
DTWD1	2	0	**0**	-0.37	-1.58
ERICH1	6	0	**0**	-0.37	0.48
TTC35	0	0	**0**	-0.41	-0.38
ZNF317	6	0	**0**	-0.42	0.94
STAM	48	0	**0**	-0.42	-0.58
PACRGL	6	0	**0**	-0.43	-0.87
TBCK	9	0	**0**	-0.43	-0.03
MOGS	42	0	**0**	-0.43	-0.45
IFI44	11	0	**0**	-0.43	-0.26
TMED9	15	0	**0**	-0.43	0.16
TRIM68	17	0	**0**	-0.43	-0.92
C1orf216	3	0	**0**	-0.43	0.29
C1orf74	4	0	**0**	-0.43	-0.44
ZNF567	6	0	**0**	-0.43	-1.64
GOLGA8IP	3	0	**0**	-0.43	-0.96
NHP2L1	29	0	**0**	-0.44	0.26
NFXL1	11	0	**0**	-0.44	0.85
SNHG5	2	0	**0**	-0.46	0.23
C12orf47	0	0	**0**	-0.46	0.76
MTX2	12	0	**0**	-0.46	-1
AP3M2	8	0	**0**	-0.46	-0.7
ZNF770	5	0	**0**	-0.46	-0.26
FCF1	8	0	**0**	-0.46	-1.54
FTSJD1	7	0	**0**	-0.5	-1.37
ENTPD4	13	0	**0**	-0.51	0.99
SNAPC5	8	0	**0**	-0.52	0.49
PLEK2	12	0	**0**	-0.52	-0.25
IER5	10	0	**0**	-0.52	1.09
SLC25A23	9	0	**0**	-0.52	-0.28
RUNDC1	3	0	**0**	-0.55	0.55
MBIP	16	0	**0**	-0.56	-1.44
OSBPL10	14	0	**0**	-0.56	0.8

FUBP3	13	0	**0**	-0.58	1.73
KIAA0319L	6	0	**0**	-0.58	0.3
C16orf72	3	0	**0**	-0.59	-0.06
ANAPC13	13	0	**0**	-0.6	-0.54
AASDHPPT	16	0	**0**	-0.6	-0.17
C3orf19	7	0	**0**	-0.6	1.33
MED13L	10	0	**0**	-0.62	0.26
TRIM16L	2	0	**0**	-0.66	0.02
HDHD1	10	0	**0**	-0.66	-0.8
MED18	12	0	**0**	-0.66	0.87
IFT46	12	0	**0**	-0.67	-1.41
NAGK	20	0	**0**	-0.67	0.33
CCNJ	4	0	**0**	-0.67	-0.25
DHX16	19	0	**0**	-0.68	-0.03
ABHD11	13	0	**0**	-0.68	0.79
SNHG9	0	0	**0**	-0.69	-0.42
POLR2F	91	0	**0**	-0.69	0.73
ALDH5A1	36	0	**0**	-0.69	-0.26
RPL37A	17	0	**0**	-0.71	0.91
RPL36	23	0	**0**	-0.72	0.52
GOLGA1	15	0	**0**	-0.74	-0.24
OLFM1	13	0	**0**	-0.74	0.29
ZNF451	28	0	**0**	-0.74	-0.49
TSPYL4	8	0	**0**	-0.74	-0.26
LOC400456	2	0	**0**	-0.74	0.29
MTRNR2L2	4	0	**0**	-0.79	-1.81
SUPT5H	58	0	**0**	-0.8	0.77
DEPDC1	10	0	**0**	-0.82	2.18
EHHADH	13	0	**0**	-0.85	-1.08
C17orf75	6	0	**0**	-0.85	-0.75
ODF2	20	0	**0**	-0.86	-0.84
AHNAK2	5	0	**0**	-0.87	0.76
LARP4	13	0	**0**	-0.87	-1.39
ZNF74	13	0	**0**	-0.88	0.81
C22orf25	4	0	**0**	-0.9	0.83
KIAA0090	0	0	**0**	-0.91	0.15
ZCCHC3	6	0	**0**	-0.94	0.22
SEC13	29	0	**0**	-0.95	0.29
MRPS35	15	0	**0**	-0.98	-0.38
MRPL3	11	0	**0**	-0.99	0.53
MRPS23	13	0	**0**	-0.99	-0.26
AP1G2	28	0	**0**	-1	0.54
ZNF483	5	0	**0**	-1.02	-0.7

KIF3C	11	0	**0**	-1.08	1.76
ELMO2	18	0	**0**	-1.08	0.99
STRBP	17	0	**0**	-1.09	-0.51
CDRT4	6	0	**0**	-1.09	0.42
ASCC2	16	0	**0**	-1.09	1.25
MRPL52	10	0	**0**	-1.09	1.22
ALG3	13	0	**0**	-1.1	-0.62
TBC1D25	9	0	**0**	-1.1	1.02
MRPL46	11	0	**0**	-1.1	0.29
USP36	24	0	**0**	-1.1	1.02
RAB12	5	0	**0**	-1.15	-0.13
MEX3C	9	0	**0**	-1.15	0.34
CEP76	14	0	**0**	-1.15	-0.44
ZNF496	10	0	**0**	-1.15	1.51
INTS4	10	0	**0**	-1.15	0.29
ZNF385B	9	0	**0**	-1.15	-2.38
COG7	21	0	**0**	-1.15	-1.02
FTH1P3	2	0	**0**	-1.15	4.25
BREA2	1	0	**0**	-1.15	0.02
HLA-F-AS1	4	0	**0**	-1.15	-2.92
PLEKHA5	17	0	**0**	-1.16	-0.87
DYNC2LI1	11	0	**0**	-1.17	-0.57
MRPS25	16	0	**0**	-1.21	0.11
TSHZ3	16	0	**0**	-1.25	1.65
CDKN2AIPNL	2	0	**0**	-1.25	1.48
ARL4C	11	0	**0**	-1.27	0.42
PANK2	44	0	**0**	-1.28	0.84
LOC646214	1	0	**0**	-1.29	-0.07
OXSR1	25	0	**0**	-1.3	0.1
NMD3	12	0	**0**	-1.31	-1.57
SPTSSA	6	0	**0**	-1.32	0.59
PRELID1	11	0	**0**	-1.33	0.71
CCDC14	14	0	**0**	-1.33	1.23
EIF2AK1	27	0	**0**	-1.34	0.88
TMEM11	10	0	**0**	-1.34	-0.1
CPNE5	7	0	**0**	-1.34	1.94
MCCC2	22	0	**0**	-1.34	-0.29
TECR	16	0	**0**	-1.34	-0.07
NCDN	14	0	**0**	-1.36	0.21
C18orf21	5	0	**0**	-1.36	-1.02
MANEA	27	0	**0**	-1.36	0.27
CMPK2	6	0	**0**	-1.36	-0.3
LOC644554	1	0	**0**	-1.36	0.26

IWS1	16	0	**0**	-1.37	0.11
C3orf75	8	0	**0**	-1.39	-0.22
DNASE2	27	0	**0**	-1.39	-0.8
CIRH1A	21	0	**0**	-1.39	-0.04
LARP1B	4	0	**0**	-1.4	-1.06
SCAMP3	23	0	**0**	-1.4	-0.47
ATP5SL	6	0	**0**	-1.43	-0.97
PHKG2	18	0	**0**	-1.44	-0.57
TRNP1	2	0	**0**	-1.44	0.4
BCS1L	27	0	**0**	-1.44	0.55
C2orf29	9	0	**0**	-1.44	0.29
ZNF394	7	0	**0**	-1.46	-0.17
DDX39A	31	0	**0**	-1.47	1.21
PSME4	39	0	**0**	-1.48	0.65
R3HDM1	8	0	**0**	-1.48	-0.41
DDX27	15	0	**0**	-1.48	1.56
DCTN3	19	0	**0**	-1.48	1.28
SAMD5	2	0	**0**	-1.49	-1.7
FAM214A	5	0	**0**	-1.49	-1.88
METTL13	14	0	**0**	-1.5	0.97
ARF5	27	0	**0**	-1.51	0.53
SF3B5	15	0	**0**	-1.52	0.01
MRPS31	12	0	**0**	-1.55	-0.38
SLC35B1	7	0	**0**	-1.59	0
AP1S3	18	0	**0**	-1.6	-0.7
SLC50A1	6	0	**0**	-1.65	-0.38
ANKIB1	10	0	**0**	-1.65	-0.45
COQ9	11	0	**0**	-1.65	0.01
DYRK4	8	0	**0**	-1.66	0.19
SPC25	12	0	**0**	-1.66	0.06
RPAP2	10	0	**0**	-1.66	-0.04
PHF5A	12	0	**0**	-1.66	0.61
UHRF1BP1L	4	0	**0**	-1.68	-0.06
KLHDC4	7	0	**0**	-1.68	0.61
SUPV3L1	19	0	**0**	-1.68	-0.52
CLSTN3	7	0	**0**	-1.68	-0.42
SRBD1	10	0	**0**	-1.68	2.14
PANK4	15	0	**0**	-1.68	-0.12
INTS9	13	0	**0**	-1.68	0.81
ZFAND3	12	0	**0**	-1.68	0.24
C19orf43	6	0	**0**	-1.68	0.36
C4orf33	3	0	**0**	-1.71	1.2
PCP4L1	6	0	**0**	-1.71	0.02

MDM1	8	0	**0**	-1.71	-0.48
TTC22	3	0	**0**	-1.71	-0.92
ABCF3	12	0	**0**	-1.71	0.63
SLC2A4RG	13	0	**0**	-1.71	-0.16
CRAMP1L	4	0	**0**	-1.71	1.46
C9orf89	5	0	**0**	-1.71	1.91
ZNF514	4	0	**0**	-1.71	-0.29
AHSA2	7	0	**0**	-1.71	0.18
BDH1	15	0	**0**	-1.71	-0.22
SNORD96A	2	0	**0**	-1.71	
MIR614	2	0	**0**	-1.71	-2.2
FLAD1	10	0	**0**	-1.74	0.64
SPOPL	7	0	**0**	-1.78	0
ELP4	14	0	**0**	-1.78	-0.55
C17orf81	12	0	**0**	-1.78	0.29
METTL17	10	0	**0**	-1.8	0.47
SLC25A12	39	0	**0**	-1.81	0.06
BPGM	24	0	**0**	-1.82	-0.07
GPKOW	12	0	**0**	-1.87	0.25
TOMM40L	11	0	**0**	-1.87	0.07
DBNDD1	6	0	**0**	-1.92	0.78
SPR	33	0	**0**	-1.92	-0.12
ETHE1	19	0	**0**	-1.92	0.52
CHCHD5	3	0	**0**	-1.92	-0.52
LOC202781	1	0	**0**	-1.92	-1.68
DCTD	12	0	**0**	-1.95	0.18
WDR46	13	0	**0**	-1.95	0.06
NT5DC2	12	0	**0**	-1.97	0.92
HADH	34	0	**0**	-1.97	-0.35
NOL6	16	0	**0**	-1.97	-0.54
COX4NB	0	0	**0**	-2.06	0.86
PSMD8	51	0	**0**	-2.06	0.82
COMMD4	11	0	**0**	-2.06	0.33
MRPL43	14	0	**0**	-2.06	-0.16
DRG2	21	0	**0**	-2.07	0.58
DCAF8	18	0	**0**	-2.07	-0.12
LOC728190	1	0	**0**	-2.07	-0.52
SLC25A29	5	0	**0**	-2.08	1.19
HSBP1L1	3	0	**0**	-2.08	-0.94
ALDH8A1	6	0	**0**	-2.08	-1.69
NDUFS6	20	0	**0**	-2.08	-0.55
ATAT1	7	0	**0**	-2.08	2.3
MRPS7	21	0	**0**	-2.09	-0.31

MFF	6	0	**0**	-2.13	0.1
ACADSB	21	0	**0**	-2.15	-1.27
REPIN1	19	0	**0**	-2.16	0.85
ZNHIT1	11	0	**0**	-2.16	0.2
SPRYD3	9	0	**0**	-2.19	0.06
LOC440354	2	0	**0**	-2.19	-0.82
MYO19	6	0	**0**	-2.23	1.33
TPT1-AS1	0	0	**0**	-2.24	1.2
HDGFRP2	8	0	**0**	-2.24	2.01
TMEM206	6	0	**0**	-2.24	-0.19
ZNF667	8	0	**0**	-2.24	0.29
FAM98A	7	0	**0**	-2.27	0.29
EIF2B4	39	0	**0**	-2.3	-0.1
C6orf132	0	0	**0**	-2.33	-1.28
FAM219A	11	0	**0**	-2.33	0.84
RIC8B	7	0	**0**	-2.33	0.37
RSAD2	21	0	**0**	-2.33	-0.7
FAM213B	12	0	**0**	-2.33	0.06
NCS1	36	0	**0**	-2.38	-0.47
TRIM11	13	0	**0**	-2.4	-0.12
BLVRB	16	0	**0**	-2.42	0.29
LACTB2	7	0	**0**	-2.45	-0.83
FNDC3A	10	0	**0**	-2.47	-0.83
LOC493754	3	0	**0**	-2.47	0.81
MLEC	11	0	**0**	-2.48	0.06
ARSE	15	0	**0**	-2.64	-0.53
GLE1	19	0	**0**	-2.64	0.22
RUFY1	12	0	**0**	-2.64	0.13
ZNF682	4	0	**0**	-2.64	-1.11
ACOX3	14	0	**0**	-2.64	-1.02
ZNF783	5	0	**0**	-2.64	-0.18
TST	28	0	**0**	-2.64	-0.12
PEX11A	10	0	**0**	-2.64	-1.68
DDX11	19	0	**0**	-2.64	2.14
ALDH6A1	13	0	**0**	-2.64	-2.67
IFI44L	5	0	**0**	-2.64	1.91
XPOT	19	0	**0**	-2.64	0.29
FAM216A	5	0	**0**	-2.64	0.42
CNOT3	22	0	**0**	-2.64	1.36
TTLL4	6	0	**0**	-2.64	-0.06
CCDC9	7	0	**0**	-2.64	-0.7
TMEM214	6	0	**0**	-2.64	0.04
USP53	12	0	**0**	-2.64	-1.57

DECR2	12	0	**0**	-2.64	0.57
AVPI1	11	0	**0**	-2.64	-1.02
OBFC2B	8	0	**0**	-2.64	-0.33
ZNF426	9	0	**0**	-2.64	0.28
YRDC	8	0	**0**	-2.64	1.12
UBTD1	10	0	**0**	-2.64	-2.45
TANC2	5	0	**0**	-2.64	0.69
COG8	16	0	**0**	-2.64	-0.04
FBXO18	16	0	**0**	-2.64	0.65
NT5C3L	3	0	**0**	-2.64	0.88
RPL39L	5	0	**0**	-2.64	-0.44
SNAP47	5	0	**0**	-2.64	-0.01
ANKRD22	10	0	**0**	-2.64	-0.12
FAM84A	6	0	**0**	-2.64	0.92
TTC8	12	0	**0**	-2.64	1.02
LOC644172	1	0	**0**	-2.64	-0.7
ZNF767	9	0	**0**	-2.64	0.29
ZNF85	9	0	**0**	-2.64	0.84
DDX54	10	0	**0**	-2.79	0.6
RER1	11	0	**0**	-2.81	0.88
HEBP2	13	0	**0**	-2.83	-0.07
OAS2	23	0	**0**	-2.86	1.53
SLC25A36	10	0	**0**	-2.86	-0.64
TROAP	9	0	**0**	-2.86	6.87
NOP14	11	0	**0**	-2.96	0.15
C16orf80	6	0	**0**	-2.96	0.94
NDUFB10	17	0	**0**	-3	0.75
SLC27A5	10	0	**0**	-3.04	-1.11
MICAL2	12	0	**0**	-3.09	-0.57
CLPX	15	0	**0**	-3.12	0.28
PPIL1	17	0	**0**	-3.12	-0.76
CNIH	8	0	**0**	-3.16	-1.15
DNAAF2	6	0	**0**	-3.2	-0.58
TCFL5	7	0	**0**	-3.2	-0.84
C19orf66	2	0	**0**	-3.2	-0.52
ZSWIM4	2	0	**0**	-3.2	-0.48
WDR4	12	0	**0**	-3.2	1.84
CYB5D1	2	0	**0**	-3.2	-0.83
KRT6C	9	0	**0**	-3.2	2.69
C12orf76	2	0	**0**	-3.2	-1.28
TRIM2	12	0	**0**	-3.26	0.05
PLEKHM1	11	0	**0**	-3.29	0.77
MECR	12	0	**0**	-3.31	-0.33

TBC1D22A	12	0	**0**	-3.36	-0.16
BRP44L	10	0	**0**	-3.37	-1.98
MAP7D1	13	0	**0**	-3.41	0.32
AEN	7	0	**0**	-3.43	1.56
CNPY3	6	0	**0**	-3.48	0.85
NIF3L1	18	0	**0**	-3.55	0.67
C20orf7	0	0	**0**	-3.57	-0.33
LOC100506207	0	0	**0**	-3.57	-2.24
NEURL1B	4	0	**0**	-3.57	4.21
PGLS	7	0	**0**	-3.57	0.7
SIPA1L3	8	0	**0**	-3.57	0.29
RRS1	11	0	**0**	-3.57	0.12
COQ4	11	0	**0**	-3.57	-0.46
TRMT1	9	0	**0**	-3.57	1.08
ZNF385D	7	0	**0**	-3.57	1.77
EPS8L1	8	0	**0**	-3.57	-0.76
FAM131A	5	0	**0**	-3.57	1.15
LOC100129917	1	0	**0**	-3.57	
VMAC	3	0	**0**	-3.61	0.54
LZTR1	15	0	**0**	-3.61	-0.7
WBSCR16	11	0	**0**	-3.61	-0.44
GATS	4	0	**0**	-3.61	1.65
LOC100188947	3	0	**0**	-3.61	-0.19
MIR22HG	6	0	**0**	-3.61	-1.26
ACYP2	21	0	**0**	-3.62	-0.12
PIPSL	7	0	**0**	-3.63	-0.14
PKM2	0	0	**0**	-3.83	1.62
TIMM50	23	0	**0**	-3.84	0.64
C1orf106	7	0	**0**	-3.84	1.5
C21orf59	14	0	**0**	-3.84	-0.31
LPCAT3	22	0	**0**	-3.89	-1
LSM4	22	0	**0**	-3.89	1.44
ALDOC	24	0	**0**	-3.92	-0.62
PYCR2	13	0	**0**	-3.92	0.4
CLN6	27	0	**0**	-3.92	2.26
VPS26B	6	0	**0**	-3.92	1.02
ZFP62	7	0	**0**	-3.92	0.96
KRI1	10	0	**0**	-3.94	1.14
SNHG1	6	0	**0**	-4	0.69
LPP-AS2	1	0	**0**	-4.03	0.66

BCAT2	27	0	**0**	-4.03	-1.74
RPS9	39	0	**0**	-4.07	0.98
SGSM2	8	0	**0**	-4.14	1.41
HAUS7	18	0	**0**	-4.14	-0.31
EXOSC4	20	0	**0**	-4.14	0.29
ZNF672	3	0	**0**	-4.14	0.67
FAM108A1	5	0	**0**	-4.14	-0.43
CDCA3	10	0	**0**	-4.14	4.21
MPST	14	0	**0**	-4.18	-0.35
PGM1	34	0	**0**	-4.3	-0.05
RPUSD3	6	0	**0**	-4.34	0.78
IDH3G	16	0	**0**	-4.34	0.38
TMED3	7	0	**0**	-4.48	0.12
PPIF	21	0	**0**	-4.52	0.38
MEX3A	3	0	**0**	-4.54	3.22
C11orf49	17	0	**0**	-4.54	0.18
BATF	17	0	**0**	-4.54	-0.39
GET4	16	0	**0**	-4.54	0.91
HKDC1	8	0	**0**	-4.54	-0.07
LRCH3	6	0	**0**	-4.54	0.09
FAM73B	3	0	**0**	-4.54	0.05
SDSL	6	0	**0**	-4.54	0.07
NR2C2AP	5	0	**0**	-4.54	0.37
DPM1	21	0	**0**	-4.58	-1.16
RFTN1	13	0	**0**	-4.62	2.4
MLF2	13	0	**0**	-4.76	0.54
AP1M1	53	0	**0**	-4.83	1.25
USE1	16	0	**0**	-4.85	1.02
HS1BP3	9	0	**0**	-4.85	0.65
ACSF3	11	0	**0**	-4.85	1.27
SDR39U1	6	0	**0**	-4.91	0.52
IER2	7	0	**0**	-5.02	0.47
SLC27A4	25	0	**0**	-5.11	-0.12
TIMM44	16	0	**0**	-5.11	-0.33
ITPA	61	0	**0**	-5.11	0.59
TFCP2L1	10	0	**0**	-5.17	-1.6
MRPS2	11	0	**0**	-5.33	0.21
VAC14	14	0	**0**	-5.33	1.43
GPAM	22	0	**0**	-5.33	0.1
ZNF737	5	0	**0**	-5.52	0.07
SNF8	20	0	**0**	-5.52	0.36
VPS72	14	0	**0**	-5.69	0.16
AP2S1	23	0	**0**	-5.69	0.55

ZMYM3	21	0	**0**	-5.78	-0.55
PLEKHG4	19	0	**0**	-5.84	0.26
TCEA2	20	0	**0**	-5.84	-0.14
FAM158A	0	0	**0**	-6.1	-0.19
LOC100506963	0	0	**0**	-6.1	-0.7
FAM149A	3	0	**0**	-6.1	-2.1
ZNF473	11	0	**0**	-6.1	1.2
KAZN	15	0	**0**	-6.1	-0.04
CYS1	3	0	**0**	-6.1	-2.8
NCKAP5L	6	0	**0**	-6.1	5.45
MYH14	26	0	**0**	-6.1	0.02
CCDC159	5	0	**0**	-6.1	0.66
FAM129C	3	0	**0**	-6.1	
FAM160A2	13	0	**0**	-6.1	0.65
PSMG4	6	0	**0**	-6.1	2.48
LOC100132247	3	0	**0**	-6.1	-1.33
FCHO1	9	0	**0**	-6.1	-0.7
ZNF764	4	0	**0**	-6.1	0.03
DNAJC27	9	0	**0**	-6.1	-0.51
RPL17-C18ORF32	1	0	**0**	-6.1	
ANKS3	6	0	**0**	-6.1	-0.01
GFPT2	10	0	**0**	-6.1	0.6
HBQ1	12	0	**0**	-6.1	2.76
SMYD5	5	0	**0**	-6.1	0.87
CDRT1	8	0	**0**	-6.1	-0.7
KLF1	39	0	**0**	-6.1	4.25
ARAP2	10	0	**0**	-6.1	0.6
AMDHD2	5	0	**0**	-6.1	-0.01
FAM46C	6	0	**0**	-6.1	-1.23
REXO1	8	0	**0**	-6.1	0.87
ZNF512B	9	0	**0**	-6.1	-0.17
KIAA1257	6	0	**0**	-6.1	-1.11
C1orf116	7	0	**0**	-6.1	-1.17
ZNF750	8	0	**0**	-6.1	-2.6
INO80B	11	0	**0**	-6.1	-0.12
SLC25A18	9	0	**0**	-6.1	-2.58
ZNF558	4	0	**0**	-6.1	0.13
C1orf51	5	0	**0**	-6.1	-0.51
C15orf42	12	0	**0**	-6.1	2.18
MRPL54	9	0	**0**	-6.1	0.64

TFAP2E	4	0	**0**	-6.1	3.69
C19orf47	6	0	**0**	-6.1	0.85
FAM83H	15	0	**0**	-6.1	0.14
SNORD56	2	0	**0**	-6.1	
SNORA40	3	0	**0**	-6.1	
SNORD17	2	0	**0**	-6.1	
HNRNPU-AS1	3	0	**0**	-6.1	0.07
C21orf119	2	0	**0**	-6.1	0.86
C1orf126	3	0	**0**	-6.1	-5.09
LOC283070	4	0	**0**	-6.1	0.53
INTS4L2	4	0	**0**	-6.1	-5.09
NSUN5P2	7	0	**0**	-6.1	1.81
LOC100288069	1	0	**0**	-6.1	1.77
LOC728377	3	0	**0**	-6.1	0.42
LOC100129518	1	0	**0**	-6.1	-0.7
LOC100527964	3	0	**0**	-6.1	1.24
FLJ42875	2	0	**0**	-6.1	-3.26
ZNF503-AS2	4	0	**0**	-6.1	-0.62
ZNF550	5	0	**0**	-7.03	
C16orf13	6	0	**0**	-7.03	1.79
ZNF799	4	0	**0**	-7.03	-6.38
PABPC1L	8	0	**0**	-7.03	-0.79
TJAP1	11	0	**0**	-7.03	0.86
ZNF415	8	0	**0**	-7.03	1.7
SH2D4A	22	0	**0**	-7.03	-1.08
CYP4F3	22	0	**0**	-7.03	-1.85
ZER1	10	0	**0**	-7.03	0.74
KPTN	11	0	**0**	-7.03	0.4
TTI1	13	0	**0**	-7.03	-0.19
CUX2	11	0	**0**	-7.03	-0.3
TPPP3	11	0	**0**	-7.03	0.56
C7orf43	10	0	**0**	-7.03	0.76
C17orf53	4	0	**0**	-7.03	1.77
TRAPPC6A	7	0	**0**	-7.03	0.61
CAMKMT	8	0	**0**	-7.03	0.08
ATHL1	5	0	**0**	-7.03	0.47
ILKAP	15	0	**0**	-7.03	0.46
RDH13	14	0	**0**	-7.03	0.13
WDR90	4	0	**0**	-7.03	2.13
ATPAF2	14	0	**0**	-7.03	-0.08

RPP25L	8	0	**0**	-7.03	-0.05
ZNF467	5	0	**0**	-7.03	2.77
TSEN54	12	0	**0**	-7.03	0.57
LOC643837	4	0	**0**	-7.03	-1.21
FLJ31485	1	0	**0**	-7.03	-1.42
BICC1	10	0	**0**	-7.59	3.69
THAP4	12	0	**0**	-7.59	0.85
LHPP	9	0	**0**	-7.59	-2.05
MIPEP	12	0	**0**	-7.59	-0.04
SPEF1	8	0	**0**	-7.59	-2.24
WDR74	14	0	**0**	-7.59	0.75
ZMAT5	7	0	**0**	-7.59	0.7
DUS1L	2	0	**0**	-7.59	0.93
DCAF15	4	0	**0**	-7.59	1.54
DOK6	7	0	**0**	-7.59	-0.06
GRHL1	10	0	**0**	-7.59	-2.65
HDDC3	8	0	**0**	-7.59	1.28
LOC339535	2	0	**0**	-7.59	-1.28
FAM20A	7	0	**0**	-7.59	-0.78
TTC32	4	0	**0**	-8	-1.62
NAGPA	16	0	**0**	-8	-0.25
TPCN2	13	0	**0**	-8	0.03
RAB17	19	0	**0**	-8	-2.28
SSNA1	15	0	**0**	-8.31	-0.27
UBE2M	27	0	**0**	-8.31	-0.33
TRABD	10	0	**0**	-8.31	0.75
ELOF1	10	0	**0**	-8.31	0.29
LOC400027	1	0	**0**	-8.31	-0.7
CHPF	14	0	**0**	-8.57	0.36
SDS	13	0	**0**	-8.57	-4.85
GMEB2	10	0	**0**	-8.57	0.82
IFI6	18	0	**0**	-8.57	0.23
WDR18	14	0	**0**	-8.57	-0.64
PTDSS2	8	0	**0**	-8.57	-1.09
C12orf52	8	0	**0**	-8.57	0.92
RHPN2	20	0	**0**	-8.57	0.28
GRAMD1A	7	0	**0**	-8.79	-0.2
FAM58A	6	0	**0**	-8.79	0.1
TC2N	10	0	**0**	-8.98	-0.7
NMRAL1	15	0	**0**	-8.98	-0.03
YIF1A	18	0	**0**	-9.3	1.05
HBD	114	0	**0**	-9.56	
LAD1	11	0	**0**	-9.56	0.38

YDJC	5	0	**0**	-9.67	-0.08
LOC400927	1	0	**0**	-9.97	-0.7
IGLL5	4	0	**0**	-10	0.14
NUP188	16	0	**0**	-10.06	0.61
LYPLA2	9	0	**0**	-10.36	0.16
C4orf49	0	0	**0**		
CEP170P1	3	0	**0**		-5.66
MIR1260B	2	0	**0**		
MUTED-TXNDC5	3	0	**0**		
EEF1E1-MUTED	1	0	**0**		
FKBP1A-SDCBP2	1	0	**0**		-4.16
HOXA10-HOXA9	2	0	**0**		
C7orf70	0	0	**0**		
C17orf63	0	0	**0**		
ARHGAP40	0	0	**0**		2.76
ST20-MTHFS	0	0	**0**		
CTPS	0	0	**0**		
AKIRIN2-AS1	0	0	**0**		5.45
UBE2MP1	0	0	**0**		
SCARNA22	0	0	**0**		
SCARNA4	0	0	**0**		
SCARNA16	0	0	**0**		
GBP1P1	0	0	**0**		0.23
FAM223B	0	0	**0**		
LOC100133161	0	0	**0**		0.79
KRT16P2	0	0	**0**		-4.16
PGCP1	0	0	**0**		
LOC729080	0	0	**0**		
LOC440900	0	0	**0**		-0.7
C10orf103	0	0	**0**		
LOC100630918	0	0	**0**		-1.67
FLJ22447	0	0	**0**		0.23
HSD17B3	32	0	**0**		-1.02
KRT12	18	0	**0**		
HBG1	140	0	**0**		8.21
CARD17	1	0	**0**		
EID3	6	0	**0**		1.2
ARHGAP28	6	0	**0**		0.72

C6orf222	2	0	**0**	4.97
DPRX	1	0	**0**	
SPRR2B	12	0	**0**	-1.64
DAPL1	3	0	**0**	5.45
SOWAHB	2	0	**0**	-1.11
SUSD4	6	0	**0**	0.01
VWA5B1	4	0	**0**	0.23
FAM83G	8	0	**0**	2.76
IQCJ	6	0	**0**	
VPS37D	3	0	**0**	-1.69
FBXO41	7	0	**0**	3.69
ASPG	2	0	**0**	-3.58
RBFOX3	7	0	**0**	-2.14
C8orf73	4	0	**0**	0.28
FAM183A	2	0	**0**	-0.53
PPIAL4G	2	0	**0**	
NRGN	23	0	**0**	-2.86
C10orf131	1	0	**0**	
TRIM17	12	0	**0**	-2.09
FOXI3	2	0	**0**	
ZNF844	2	0	**0**	4.25
SMCR7	11	0	**0**	-0.14
FAM190A	7	0	**0**	-0.7
KPNA7	4	0	**0**	
JPH4	7	0	**0**	1.64
LOC100128542	1	0	**0**	
ADH7	45	0	**0**	-4.38
ALS2CR11	7	0	**0**	-0.7
SRPK3	5	0	**0**	2.5
ZNF177	6	0	**0**	
IQCJ-SCHIP1	4	0	**0**	2.76
NEDD8-MDP1	1	0	**0**	
KRBOX1	6	0	**0**	0.26
CASQ1	13	0	**0**	-0.14
LOC100130357	1	0	**0**	3.69
PVALB	22	0	**0**	-1.17
DNALI1	13	0	**0**	-1.03
PIGL	9	0	**0**	0.02
DLX2	20	0	**0**	5.81
HIST1H1T	20	0	**0**	

KRTAP5-9	8	0	**0**	
PRSS16	10	0	**0**	-0.48
CPLX1	21	0	**0**	1.44
SPRR2D	13	0	**0**	4.97
SIRT4	14	0	**0**	-1.28
LAMP5	4	0	**0**	0.58
PSORS1C1	14	0	**0**	0.23
HOXD4	22	0	**0**	4.25
CYP39A1	7	0	**0**	-0.48
CRYGS	27	0	**0**	
TBC1D19	8	0	**0**	-0.7
INPP5E	12	0	**0**	0.96
GRAMD1B	7	0	**0**	4.97
KIAA1328	8	0	**0**	1.2
CCNO	14	0	**0**	-0.13
RBKS	5	0	**0**	-0.91
FN3K	18	0	**0**	1.28
ALG12	11	0	**0**	0.1
PRR15L	3	0	**0**	-0.7
ELMO3	7	0	**0**	-1.88
GRHL2	15	0	**0**	0.13
KLHL15	8	0	**0**	1.24
FBXW10	5	0	**0**	-1.64
KRTAP3-1	3	0	**0**	
PLEKHN1	5	0	**0**	2.76
SEC16B	21	0	**0**	-0.7
HIST3H2A	19	0	**0**	1.59
C20orf151	5	0	**0**	3.69
FAM181A	5	0	**0**	-2.6
RAB3C	11	0	**0**	1.99
ZMYND19	6	0	**0**	5.64
ZNF653	4	0	**0**	-0.51
BTBD16	8	0	**0**	4.25
C1orf182	6	0	**0**	-1.37
CAPN12	3	0	**0**	-0.48
ZNF501	7	0	**0**	1.51
SNX31	5	0	**0**	3.69
ZNF524	3	0	**0**	-1.26
SNX33	11	0	**0**	0.29
CCDC96	4	0	**0**	2.76
RNF39	15	0	**0**	-0.39
PPP1R36	4	0	**0**	0.84
ANKRD29	5	0	**0**	-0.23

EXOC3L1	5	0	**0**	-0.14
C1orf88	4	0	**0**	-0.84
SPC24	13	0	**0**	2.76
TEX9	3	0	**0**	-0.92
GGTLC2	7	0	**0**	4.25
IER5L	5	0	**0**	-0.32
C3orf25	4	0	**0**	-2.2
C10orf129	2	0	**0**	-5.66
FAM211B	5	0	**0**	-0.84
SNORD15A	3	0	**0**	
SNORD21	2	0	**0**	
SNORD22	4	0	**0**	3.69
SNORD4B	2	0	**0**	
SNORD4A	2	0	**0**	
SNORD42B	2	0	**0**	
SNORD55	3	0	**0**	
SNORD36C	3	0	**0**	
SNORD36B	3	0	**0**	
SNORD35A	3	0	**0**	2.76
SNORD34	3	0	**0**	
SNORD33	3	0	**0**	
SNORD46	3	0	**0**	
SNORD83A	2	0	**0**	
CELP	4	0	**0**	
SNORD109A	2	0	**0**	2.76
PRSS3P2	6	0	**0**	
HCG4B	2	0	**0**	4.25
SNORD38A	2	0	**0**	
SNORD38B	2	0	**0**	-4.16
LOC407835	2	0	**0**	
OR7E91P	2	0	**0**	-2.54
PDIA3P	1	0	**0**	-0.17
SNORA62	4	0	**0**	
SNORD101	2	0	**0**	
SNORA33	4	0	**0**	-0.7
SNORD54	2	0	**0**	
SNORD43	3	0	**0**	2.76
SNORD18A	4	0	**0**	
SNORD18B	4	0	**0**	
SNORD24	5	0	**0**	
SNORD68	3	0	**0**	
SNORD29	3	0	**0**	
SNORD31	3	0	**0**	2.76

SNORD28	3	0	**0**	-4.16
SNORD27	3	0	**0**	
SNORD26	3	0	**0**	
SNORD25	3	0	**0**	2.76
CYP2D7P1	9	0	**0**	-0.7
SNORD58A	2	0	**0**	3.69
SNORD58B	2	0	**0**	
SNORD74	3	0	**0**	
SNORA3	4	0	**0**	
SNORD2	2	0	**0**	
SNORD51	2	0	**0**	
SNORA41	4	0	**0**	
SNORD37	2	0	**0**	
SNORD10	2	0	**0**	
MST1P9	2	0	**0**	1.32
SNORD61	3	0	**0**	
SNORD59A	2	0	**0**	
SNORD57	2	0	**0**	
SNORD53	2	0	**0**	
SNORD49A	2	0	**0**	
SNORD48	2	0	**0**	
SNORD45B	2	0	**0**	
SNORD45A	2	0	**0**	
SNORD41	2	0	**0**	
NUDT9P1	5	0	**0**	
SNORD20	3	0	**0**	
SNORA71B	3	0	**0**	
SNORA67	6	0	**0**	-6.38
SNORD8	2	0	**0**	
SNORA5A	3	0	**0**	
SNORA8	4	0	**0**	-1.64
SNORA75	4	0	**0**	
SNORA13	4	0	**0**	
FMO9P	2	0	**0**	
SNORA9	3	0	**0**	
SNORA11	3	0	**0**	
SNORA14A	3	0	**0**	
SNORA14B	3	0	**0**	
SNORA17	3	0	**0**	
SNORA18	3	0	**0**	-1.64
SNORA20	3	0	**0**	
SNORA22	3	0	**0**	
SNORA28	3	0	**0**	

SNORA29	3	0	**0**	
SNORA30	3	0	**0**	
SNORA34	3	0	**0**	
SNORA36A	3	0	**0**	
SNORA43	4	0	**0**	
SNORA45	3	0	**0**	
SNORA46	3	0	**0**	
SNORA49	3	0	**0**	
SNORA51	3	0	**0**	
SNORA54	4	0	**0**	
SNORA56	3	0	**0**	
SNORA5B	3	0	**0**	
SNORA76	3	0	**0**	0.23
SNORA80	3	0	**0**	
SCARNA20	1	0	**0**	
SCARNA23	3	0	**0**	
SCARNA12	3	0	**0**	3.69
SNORA53	3	0	**0**	
SNORA26	3	0	**0**	
SNORA71D	3	0	**0**	
SNORA79	3	0	**0**	
SNORA1	3	0	**0**	
SNORD12	2	0	**0**	2.76
SNORD11	2	0	**0**	
SNORA32	3	0	**0**	4.25
SNORD5	2	0	**0**	
SNORA16A	3	0	**0**	-4.16
SNORD6	2	0	**0**	
SNORD7	3	0	**0**	2.76
SNORD45C	2	0	**0**	
SNORD50B	2	0	**0**	
SNORD59B	2	0	**0**	
RMRP	24	0	**0**	-2.2
SNORD65	2	0	**0**	2.76
SNORD66	2	0	**0**	
SNORD67	2	0	**0**	
SNORD70	2	0	**0**	
SNORD71	2	0	**0**	
SNORD84	2	0	**0**	-5.09
SNORD85	2	0	**0**	
SNORD88A	2	0	**0**	
SNORD88B	2	0	**0**	
SNORD89	2	0	**0**	2.76

SNORD90	2	0	**0**	
SNORD91A	2	0	**0**	
SNORD91B	2	0	**0**	
SNORD92	2	0	**0**	
SNORD93	2	0	**0**	
SNORD98	2	0	**0**	
SNORD111	2	0	**0**	
SCARNA18	1	0	**0**	
SNORD117	2	0	**0**	
SNORD114-9	2	0	**0**	
SNORD114-10	2	0	**0**	
SNORD114-12	2	0	**0**	
SNORD114-14	2	0	**0**	
SNORD114-17	2	0	**0**	
SNORD114-23	2	0	**0**	
SNORD114-25	2	0	**0**	
SNORD114-26	2	0	**0**	
SNORD114-28	2	0	**0**	
SNORD113-4	2	0	**0**	
SNORD113-5	2	0	**0**	
SNORD113-6	2	0	**0**	
SNORD113-7	2	0	**0**	
SNORD113-9	2	0	**0**	
PA2G4P4	1	0	**0**	
EP400NL	2	0	**0**	0.73
SNORD116-2	3	0	**0**	
SNORD116-8	3	0	**0**	
SNORD116-12	3	0	**0**	
SNORD116-14	3	0	**0**	
SNORD116-18	3	0	**0**	
SNORD116-24	3	0	**0**	
SNORD116-25	3	0	**0**	

SNORD116-26	3	0	**0**	2.76
SNORD116-27	3	0	**0**	
SNORD116-29	3	0	**0**	
SLED1	2	0	**0**	
SNORD119	2	0	**0**	
SNORD121A	2	0	**0**	
SNORD19B	3	0	**0**	
SNORD11B	2	0	**0**	
SNORD12B	2	0	**0**	-4.16
SNORD58C	3	0	**0**	2.76
SNORA84	2	0	**0**	
SNORA38B	2	0	**0**	
SNORD79	3	0	**0**	
SNORD78	3	0	**0**	
SNORD94	2	0	**0**	
SNORD104	2	0	**0**	0.42
SNORD105	2	0	**0**	
SCARNA10	1	0	**0**	
SCARNA14	1	0	**0**	
SNORD1A	2	0	**0**	
SNORD1B	2	0	**0**	
SNORD1C	2	0	**0**	
SNORD82	4	0	**0**	
SNORD86	2	0	**0**	
HULC	1	0	**0**	
LOC149134	2	0	**0**	-0.7
LOC100144604	3	0	**0**	-6.06
SCARNA9L	1	0	**0**	
ABCC6P2	3	0	**0**	-3.39
DBIL5P	1	0	**0**	2.5
SNAR-C4	1	0	**0**	
SNAR-C3	1	0	**0**	
SNAR-B1	1	0	**0**	
LOC100132111	1	0	**0**	
LINC00085	3	0	**0**	1.48
GUSBP11	4	0	**0**	-0.23
BCRP3	3	0	**0**	-4.16
LOC442459	1	0	**0**	
MIR600HG	5	0	**0**	-0.38

VTRNA1-3	3	0	**0**	
GHRLOS2	1	0	**0**	4.25
LOC127841	1	0	**0**	
LOC100130776	3	0	**0**	-0.39
MIR31HG	5	0	**0**	
FLJ34503	2	0	**0**	4.65
SERHL	7	0	**0**	0.79
COL6A4P1	12	0	**0**	
LOC100302650	3	0	**0**	0.58
SNORA80B	1	0	**0**	
LOC375196	1	0	**0**	0.79
KRT16P3	3	0	**0**	0.68
MIR611	2	0	**0**	
MIR612	2	0	**0**	5.64
MIR636	3	0	**0**	
MIR639	2	0	**0**	
MIR765	2	0	**0**	
MIR147B	2	0	**0**	
MIR1291	2	0	**0**	
MIR1304	2	0	**0**	
MIR1281	2	0	**0**	
MIR1292	2	0	**0**	
MIR1306	2	0	**0**	
MIR711	2	0	**0**	
SNORD103B	2	0	**0**	
MKRN9P	1	0	**0**	
FLJ34208	2	0	**0**	
LOC643650	1	0	**0**	-0.7
LOC728066	1	0	**0**	
MIR3190	3	0	**0**	
MIR4260	2	0	**0**	
MIR4315-2	2	0	**0**	
LOC100289656	1	0	**0**	
LOC400236	1	0	**0**	2.25
C12orf36	4	0	**0**	0.27
LOC648809	1	0	**0**	
ABHD14A-ACY1	1	0	**0**	
MIR3662	2	0	**0**	
INO80B-WBP1	3	0	**0**	

LOC284998	1	0	**0**		2.76
LOC554206	3	0	**0**		2.76
MIR550A3	4	0	**0**		
FLJ45983	3	0	**0**		-6.38
CECR5-AS1	1	0	**0**		3.69
LINC00473	3	0	**0**		-7.5
CCL14-CCL15	6	0	**0**		-4.16
LOC440335	1	0	**0**		-1.82
ECSIT	8	0	**0**		-0.04
RUFY4	2	0	**0**		-0.7
TTC13	5	0	**0**	2.72	3.87
TMEM241	4	0	**0**	1.32	1.94
SLC44A5	7	0	**0**	3.03	1.77
FAM26E	4	0	**0**	3.87	1.56
TMEM119	5	0	**0**	3.51	1.36
TMEM59L	5	0	**0**	6.52	1.22
ATP5L2	3	0	**0**	1.75	1.05
ATP5H	21	0	**0**	8.31	0.9
FAM18B2	4	0	**0**	1.14	0.87
CNNM3	13	0	**0**	1.5	0.78
FLRT2	11	0	**0**	2.47	0.28
LRRC70	5	0	**0**	6.93	0.26
SLC38A6	5	0	**0**	1.98	-0.29
MCTP1	6	0	**0**	5.49	-0.3
C9orf91	9	0	**0**	1.43	-0.41
TMEM33	15	0	**0**	2.49	-0.49
C12orf23	5	0	**0**	5.25	-0.53
TM6SF1	4	0	**0**	6.08	-0.55
TMEM144	3	0	**0**	1.23	-0.6
SLC39A10	9	0	**0**	3.44	-0.7
GPR89B	11	0	**0**	1.75	-0.7
RNF217	7	0	**0**	1.75	-0.7
TMEM87A	10	0	**0**	1.65	-0.83
TM4SF18	6	0	**0**	5.43	-0.85
PLLP	6	0	**0**	2.72	-1.45
GIMAP2	8	0	**0**	4.02	-1.9
HERC2P3	5	0	**0**	2.72	-1.9
TMEM140	9	0	**0**	3.7	-2.02
TMEM45A	7	0	**0**	3.16	-2.11
UGT8	19	0	**0**	1.75	-3.1
TMCC1	10	0	**0**	0.91	0.71
GPRC5B	11	0	**0**	0.88	-1.14
RPRML	1	0	**0**	0.82	0.79

CACHD1	6	0	**0**	0.82	0.16
ATP13A4	4	0	**0**	0.82	-1.42
PKD1L1	7	0	**0**	0.82	0.23
ATP6AP1L	2	0	**0**	0.82	-0.34
SEMA6C	10	0	**0**	0.82	0.21
KCNK17	12	0	**0**	0.82	2.76
SLC35G1	5	0	**0**	0.82	4.65
TLCD1	3	0	**0**	0.82	0.6
FAM18B2-CDRT4	3	0	**0**	0.82	2.76
BTNL8	7	0	**0**	0.82	-0.7
MFAP3L	5	0	**0**	0.82	-1.49
NDUFA4L2	5	0	**0**	0.82	1.02
RNF183	4	0	**0**	0.82	-0.39
IYD	16	0	**0**	0.69	-2.18
RNFT2	7	0	**0**	0.56	-0.32
C1QTNF6	13	0	**0**	0.05	1.48
TMEM159	11	0	**0**	0	-0.76
TMEM39A	10	0	**0**	-0.03	-0.32
PLP2	14	0	**0**	-0.2	1.36
ARL6IP6	6	0	**0**	-0.34	0.48
FAM210B	8	0	**0**	-0.45	-0.05
WSCD1	2	0	**0**	-0.52	1.02
LRRC3	6	0	**0**	-0.56	-1.64
TMEM126B	8	0	**0**	-0.65	-0.48
RFT1	7	0	**0**	-0.66	-0.43
SCAMP4	11	0	**0**	-0.67	-0.05
FKBP11	5	0	**0**	-0.69	-0.99
PRR24	2	0	**0**	-0.74	3.08
YIPF1	12	0	**0**	-0.89	-0.6
FRMD5	7	0	**0**	-1.15	1.2
ILVBL	7	0	**0**	-1.15	0.42
KIAA1919	5	0	**0**	-1.15	1.97
HIGD1B	3	0	**0**	-1.15	1.82
PET117	3	0	**0**	-1.15	0.44
SLC18B1	5	0	**0**	-1.25	-0.83
GPR78	8	0	**0**	-1.34	-0.38
C19orf63	0	0	**0**	-1.36	0.27
RAB28	11	0	**0**	-1.36	-0.19
TFIP11	29	0	**0**	-1.39	1.65
LRRN4CL	2	0	**0**	-1.39	-1.42
SLC33A1	11	0	**0**	-1.65	0.68
PNKD	30	0	**0**	-1.65	0.23

TMEM130	12	0	**0**	-1.68	-2.09
C11orf83	8	0	**0**	-1.68	0.39
CCRL1	12	0	**0**	-1.71	-1.26
C14orf109	2	0	**0**	-1.71	-0.46
C1orf210	4	0	**0**	-1.71	1.24
KCNE4	22	0	**0**	-1.85	-0.58
CNPPD1	7	0	**0**	-1.87	-0.29
PIGY	5	0	**0**	-1.88	-0.76
TMEM208	2	0	**0**	-1.97	0.53
HPS4	20	0	**0**	-2.07	0.14
TMEM199	4	0	**0**	-2.33	0.08
TMEM128	3	0	**0**	-2.38	-0.24
TMEM147	8	0	**0**	-2.45	0.5
YIPF3	18	0	**0**	-2.53	0.03
ROBO3	20	0	**0**	-2.64	2.93
DLGAP4	21	0	**0**	-2.64	0.49
KLHL17	3	0	**0**	-2.64	-1.11
FLRT3	12	0	**0**	-2.64	-2.58
TMEM175	5	0	**0**	-2.64	-0.85
TMC5	8	0	**0**	-2.64	1.16
XKR9	1	0	**0**	-2.64	0.86
GPR89C	2	0	**0**	-2.64	-1.02
FAM70B	3	0	**0**	-2.64	1.2
JAGN1	7	0	**0**	-2.64	-0.89
TMEM51	7	0	**0**	-2.64	0.82
VSIG2	8	0	**0**	-2.64	-0.63
GPR89A	13	0	**0**	-2.64	0.51
CMTM4	4	0	**0**	-2.96	-0.93
CMTM7	6	0	**0**	-3.04	0.85
ZDHHC12	7	0	**0**	-3.04	-0.34
PILRB	15	0	**0**	-3.05	-1.07
TMEM37	3	0	**0**	-3.2	-0.82
YIF1B	8	0	**0**	-3.2	-0.08
MARCKSL1	20	0	**0**	-3.38	1.74
NPIPL3	6	0	**0**	-3.57	-0.26
ATP9B	7	0	**0**	-3.57	1.38
PIGH	11	0	**0**	-3.61	-1.38
SEMA4C	14	0	**0**	-4.14	0.18
CD300E	7	0	**0**	-4.4	-0.62
TMEM218	3	0	**0**	-4.54	-0.12
PARD3B	16	0	**0**	-4.61	-1.43
LDLRAD3	5	0	**0**	-4.85	6.44
MOSPD3	5	0	**0**	-5.11	0.87

SFT2D1	4	0	**0**	-5.26	0.48
GPR110	13	0	**0**	-5.52	-1.53
GPR176	6	0	**0**	-6.1	-1.64
NLGN1	27	0	**0**	-6.1	1.05
CDH26	7	0	**0**	-6.1	-0.14
SLC6A1	45	0	**0**	-6.1	0.55
SUSD2	7	0	**0**	-6.1	-1.86
GPR115	8	0	**0**	-6.1	
OR2A7	3	0	**0**	-6.1	-0.7
KCTD17	8	0	**0**	-6.1	-0.96
TMPPE	1	0	**0**	-6.1	-4.16
C17orf110	2	0	**0**	-6.1	-1.67
LOC728392	6	0	**0**	-7.03	1.17
RTP4	5	0	**0**	-7.59	-1.28
TMEM161A	11	0	**0**	-7.59	-0.2
GPR84	7	0	**0**	-7.59	5.64
TSPAN17	7	0	**0**	-7.59	0.87
TMEM40	5	0	**0**	-7.59	-0.13
C19orf24	7	0	**0**	-7.59	0.73
GPRC5C	11	0	**0**	-8	-0.45
RAB40C	9	0	**0**	-8	-0.16
REEP4	10	0	**0**	-8	-0.48
TPRA1	7	0	**0**	-8.57	0.7
SLC52A2	8	0	**0**	-8.57	-0.07
KCNAB2	20	0	**0**	-8.79	-0.2
HLA-DOB	42	0	**0**	-8.98	0.26
C11orf24	5	0	**0**	-9.15	0.43
MFSD10	7	0	**0**	-9.56	0.27
NKG7	4	0	**0**	-10.67	0.6
EPR1	0	0	**0**		
GRIK5	19	0	**0**		2.5
SLC6A16	4	0	**0**		-1.11
GABRD	19	0	**0**		-2.65
GCGR	28	0	**0**		-1.64
LAIR2	13	0	**0**		
LY6H	7	0	**0**		1.59
FCGR1C	8	0	**0**		2.76
STOML1	10	0	**0**		-0.78
TMEM125	3	0	**0**		-1.58
GPR64	7	0	**0**		1.2
IL1RAPL2	10	0	**0**		
SPRED3	6	0	**0**		2.76
TAS2R3	17	0	**0**		

SLC22A31	1	0	**0**	-1.64
SLC35D3	1	0	**0**	7.21
ABCB9	28	0	**0**	-1.42
CATSPER3	6	0	**0**	0.02
GJB4	17	0	**0**	-5.66
OR7C1	6	0	**0**	
UNC93A	4	0	**0**	-1.64
UPK3B	10	0	**0**	0.48
MFSD9	3	0	**0**	-0.3
LINGO1	32	0	**0**	2.07
SLC16A14	4	0	**0**	0.45
SLC16A13	3	0	**0**	-5.09
TMPRSS7	5	0	**0**	2.76
SLC10A6	3	0	**0**	
SLC26A9	15	0	**0**	0.79
SLC39A5	7	0	**0**	-1.11
MFSD6L	3	0	**0**	-2.6
GPR137	5	0	**0**	0.29
TMEM163	5	0	**0**	3.19
ZDHHC11	6	0	**0**	-1.43
PPAN-P2RY11	5	0	**0**	
RNF186	9	0	**0**	-1.15
TMEM200C	2	0	**0**	2.5
RNF150	7	0	**0**	-0.7
TMEM238	1	0	**0**	-1.47
SLAMF8	10	0	**0**	3.69
FAM162B	6	0	**0**	2.63
EPHX4	6	0	**0**	5.45
C19orf38	2	0	**0**	4.25
B4GALNT4	5	0	**0**	3.63
RNF148	5	0	**0**	-1.98
C2orf66	2	0	**0**	4.25
ABHD12	9	0	**0**	0.35
C7orf53	5	0	**0**	2.76

Appendix table 4.13.1; This tables shows the AngioScore (% of abstracts matching an angiogenic related keyword) of all 3,922 genes found to be a log2(FC) >= 2 up-regulated in tumour endothelial cells versus normal endothelial cells. Also reported in blue is a cDNA library endothelial screen (as log2(FC)) and in green, a cDNA library angiogenic screen (foetal/tumour bulk libraries contrasted with bulk normal libraries), also as log2(FC).