Symbol	(Zratio) biot-miR-519 PD vs biot-Ctrl-miR PD	(Fold) biot-miR-519 PD vs biot-Ctrl-miR PD	ACCESSION	Definition
WDR20	14.69	18.67	NM_181291.1	WD repeat domain 20 (WDR20)
SEC16A	14.05	16.64	NM_014866.1	SEC16 homolog A (S. cerevisiae) (SEC16A)
RAB32	12.81	14.57	NM_006834.2	RAB32
C14orf138	12.39	12.34	NM_024558.2	chromosome 14 open reading frame 138 (C14orf138)
PIGA	11.97	11.57	NM_020473.2	phosphatidylinositol glycan anchor biosynthesis
ORAI1	12.4	11.49	NM_032790.2	ORAI calcium release-activated calcium modulator 1 (ORAI1)
MBNL1	11.71	11.02	NM_207296.1	muscleblind-like (Drosophila) (MBNL1)
REPIN1	11.42	10.97	NM_014374.1	replication initiator 1 (REPIN1)
FBXW11	11.52	10.84	NM_033645.2	F-box and WD repeat domain containing 11 (FBXW11)
APH1A	11.35	10.31	NM_001077628.1	anterior pharynx defective 1 homolog A (C. elegans) (APH1A)
BLCAP	11.41	10.23	NM_006698.2	bladder cancer associated protein (BLCAP)
MBNL1	11.43	10.04	NM_207295.1	muscleblind-like (Drosophila) (MBNL1)
LOC100129668	11.65	10	XM_001713607.1	PREDICTED: hypothetical protein LOC100129668 (LOC100129668)
KIAA1826	11.15	9.83	NM_032424.1	KIAA1826 (KIAA1826)
BTG1	10.49	9.76	NM_001731.1	B-cell translocation gene 1
CDCA7	10.43	9.42	NM_031942.4	cell division cycle associated 7 (CDCA7)
IRF2BP2	10.83	8.94	NM_182972.2	interferon regulatory factor 2 binding protein 2 (IRF2BP2)
HSPBL2	10.58	8.75	NR_024392.1	heat shock 27kDa protein-like 2 pseudogene (HSPBL2)
WDR82	10.57	8.59	NM_025222.3	WD repeat domain 82 (WDR82)
MAPK6	10.19	8.52	NM_002748.2	mitogen-activated protein kinase 6 (MAPK6)
C12orf32	10.57	8.47	NM_031465.2	chromosome 12 open reading frame 32 (C12orf32)
SMYD2	10.38	8.47	NM_020197.1	PREDICTED: SET and MYND domain containing 2 (SMYD2)
COX10	10.53	8.28	NM_001303.2	COX10 homolog
PAFAH1B3	10.14	8.19	NM_002573.2	platelet-activating factor acetylhydrolase
METRNL	10.16	8.06	XM_941466.2	PREDICTED: meteorin
LOC653506	9.95	8.05	XM_927769.1	PREDICTED: similar to meteorin
DAD1	9.43	7.88	NM_001344.1	defender against cell death 1 (DAD1)
CDKN1A	9.57	7.82	NM_000389.2	cyclin-dependent kinase inhibitor 1A (p21
UQCRC1	9.71	7.79	NM_003365.2	ubiquinol-cytochrome c reductase core protein I (UQCRC1)
TUFM	9.57	7.63	NM_003321.3	Tu translation elongation factor
CEP55	9.51	7.5	NM_018131.3	centrosomal protein 55kDa (CEP55)
PDRG1	10.03	7.48	NM_030815.2	p53 and DNA-damage regulated 1 (PDRG1)
PON2	9.42	7.46	NM_000305.2	paraoxonase 2 (PON2)
RBMS1	9.58	7.44	NM_002897.3	RNA binding motif
SLC25A44	9.73	7.32	NM_014655.1	solute carrier family 25
KLHL8	9.92	7.2	NM_020803.3	kelch-like 8 (Drosophila) (KLHL8)
APH1A	9.82	7.2	NM_001077628.1	anterior pharynx defective 1 homolog A (C. elegans) (APH1A)
C14orf138	9.39	7.09	NM_001040662.1	chromosome 14 open reading frame 138 (C14orf138)
PPP1R10	9.76	7.02	NM_002714.2	protein phosphatase 1
PRKAA1	9.29	6.95	NM_206907.3	protein kinase
IER3IP1	9.33	6.93	NM_016097.3	immediate early response 3 interacting protein 1 (IER3IP1)
RAB5C	9.34	6.9	NM_201434.1	RAB5C
LYRM1	9.14	6.85	NM_020424.2	LYR motif containing 1 (LYRM1)
OBFC2A	9.39	6.82	NM_001031716.1	oligonucleotide/oligosaccharide-binding fold containing 2A (OBFC2A)
LOC145853	9.26	6.73	XM_096885.9	PREDICTED: hypothetical LOC145853 (LOC145853)

TMEM50B	9.2	6.72	NM_006134.5	transmembrane protein 50B (TMEM50B)
BRP44L	9.22	6.65	NM_016098.1	brain protein 44-like (BRP44L)
RALGDS	8.82	6.5	NM_006266.2	ral guanine nucleotide dissociation stimulator (RALGDS)
PHACTR4	8.96	6.49	NM_001048183.1	phosphatase and actin regulator 4 (PHACTR4)
TSKU	8.98	6.36	NM_015516.3	tsukushin (TSKU)
CKLF	8.62	6.33	NM_001040139.1	chemokine-like factor (CKLF)
TXNIP	8.34	6.29	NM_006472.2	thioredoxin interacting protein (TXNIP)
CD58	8.98	6.16	NM_001779.1	CD58 molecule (CD58)
C17orf100	9.15	6.15	NM_001105520.1	chromosome 17 open reading frame 100 (C17orf100)
RAB5B	8.62	6.11	NM_002868.2	RAB5B
ERGIC1	9.1	6.06	NM_001031711.1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (ERGIC1)
STX10	8.67	6.06	NM_003765.1	syntaxin 10 (STX10)
SLC25A23	8.62	6.04	NM_024103.2	solute carrier family 25 (mitochondrial carrier; phosphate carrier)
AKIRIN1	8.75	5.99	NM_024595.1	akirin 1 (AKIRIN1)
CAPRIN2	8.82	5.96	NM_001002259.1	caprin family member 2 (CAPRIN2)
PON2	8.47	5.96	NM_000305.2	paraoxonase 2 (PON2)
LRRC61	9.07	5.95	NM_023942.1	leucine rich repeat containing 61 (LRRC61)
CCNG2	8.12	5.92	NM_004354.1	cyclin G2 (CCNG2)
CKLF	8.12	5.92	NM_001040138.1	chemokine-like factor (CKLF)
MTMR4	8.96	5.9	NM_004687.3	myotubularin related protein 4 (MTMR4)
PIGS	8.67	5.84	NM_033198.2	phosphatidylinositol glycan anchor biosynthesis
SLC2A4RG	8.7	5.83	NM_020062.3	SLC2A4 regulator (SLC2A4RG)
LDOC1L	8.51	5.8	NM_032287.2	leucine zipper
TGFBR2	8.13	5.8	NM_001024847.1	transforming growth factor
FBXL11	8.62	5.73	NM_012308.1	F-box and leucine-rich repeat protein 11 (FBXL11)
SNX5	8.62	5.73	NM_014426.2	sorting nexin 5 (SNX5)
FAM13B	8.31	5.7	NM_001101800.1	family with sequence similarity 13
IRF2BP2	8.27	5.6	NM_182972.2	interferon regulatory factor 2 binding protein 2 (IRF2BP2)
RAB11A	8.07	5.59	NM_004663.3	RAB11A
CDK2AP2	8.75	5.54	NM_005851.3	cyclin-dependent kinase 2 associated protein 2 (CDK2AP2)
CDC45L	8.45	5.53	NM_003504.3	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L)
VPS4B	8.2	5.53	NM_004869.3	vacuolar protein sorting 4 homolog B (S. cerevisiae) (VPS4B)
MRRF	8.3	5.52	NM_199177.1	mitochondrial ribosome recycling factor (MRRF)
SLC44A2	8.45	5.51	NM_020428.2	solute carrier family 44
TTL	8.06	5.46	NM_153712.4	tubulin tyrosine ligase (TTL)
TES	8.31	5.45	NM_152829.1	testis derived transcript (3 LIM domains) (TES)
EPHX1	8.67	5.42	NM_000120.2	epoxide hydrolase 1
PLOD2	7.88	5.38	NM_000935.2	procollagen-lysine
HIP2	8.12	5.35	NM_005339.3	huntingtin interacting protein 2 (HIP2)
COMMD6	7.52	5.35	NM_203497.2	COMM domain containing 6 (COMMD6)
LOC100131940	8.18	5.33	XR_037582.1	PREDICTED: misc_RNA (LOC100131940)
ARL6IP1	7.42	5.31	NM_015161.1	ADP-ribosylation factor-like 6 interacting protein 1 (ARL6IP1)
PECI	7.9	5.3	NM_006117.2	peroxisomal D3
STAU1	7.85	5.27	NM_004602.2	staufen
C8orf4	7.88	5.26	NM_020130.3	chromosome 8 open reading frame 4 (C8orf4)
CBFB	7.93	5.24	NM_001755.2	core-binding factor
ZCCHC9	7.79	5.2	NM_032280.1	zinc finger
NDUFAF3	7.13	5.14	NM_199069.1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
ZNF614	8.07	5.12	NM_025040.2	zinc finger protein 614 (ZNF614)

CDC2	7.67	5.1	NM_001786.2	cell division cycle 2
MED6	7.85	5.09	NM_005466.2	mediator complex subunit 6 (MED6)
C13orf27	7.73	5.05	NM_138779.2	chromosome 13 open reading frame 27 (C13orf27)
TIMP2	7.32	5.05	NM_003255.4	PREDICTED: TIMP metallopeptidase inhibitor 2 (TIMP2)
LY6E	7.57	5.03	NM_002346.1	lymphocyte antigen 6 complex
TRIB1	7.96	5.01	NM_025195.2	tribbles homolog 1 (Drosophila) (TRIB1)
TGFBR2	7.56	5.01	NM_001024847.2	transforming growth factor
LDLR	7.89	4.98	NM_000527.2	low density lipoprotein receptor (familial hypercholesterolemia) (LDLR)
TNFRSF10B	7.84	4.98	NM_003842.3	tumor necrosis factor receptor superfamily
LOC387820	7.22	4.98	XR_019393.1	PREDICTED: similar to DnaJ (Hsp40) homolog
ZNF277	7.73	4.97	NM_021994.2	zinc finger protein 277 (ZNF277)
NR2F2	7.72	4.97	NM_021005.2	nuclear receptor subfamily 2
METRNL	8.18	4.94	NM_001004431.1	PREDICTED: meteorin
ABHD10	7.91	4.87	NM_018394.1	abhydrolase domain containing 10 (ABHD10)
DCTPP1	7.41	4.84	NM_024096.1	dCTP pyrophosphatase 1 (DCTPP1)
LOC100132499	6.96	4.84	XM_001725693.1	PREDICTED: similar to mCG7602 (LOC100132499)
RNF14	7.59	4.83	NM_183399.1	ring finger protein 14 (RNF14)
C17orf63	7.63	4.82	NM_001077498.1	chromosome 17 open reading frame 63 (C17orf63)
GALNT11	7.7	4.8	NM_022087.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)
DPY19L1	7.16	4.8	NM_015283.1	dpy-19-like 1 (C. elegans) (DPY19L1)
HNRPUL1	7.35	4.76	NM_144732.1	heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1)
KBTBD2	7.29	4.76	NM_015483.1	kelch repeat and BTB (POZ) domain containing 2 (KBTBD2)
EFR3A	7.21	4.76	NM_015137.3	EFR3 homolog A (S. cerevisiae) (EFR3A)
CLDN12	7.56	4.75	NM_012129.2	claudin 12 (CLDN12)
MORF4L1	6.77	4.75	NM_206839.1	mortality factor 4 like 1 (MORF4L1)
STAU1	7.04	4.74	NM_017454.2	staufen
CD58	7.6	4.73	NM_001779.1	CD58 molecule (CD58)
STK40	7.76	4.7	NM_032017.1	serine/threonine kinase 40 (STK40)
SP3	7.35	4.69	NM_001017371.3	Sp3 transcription factor (SP3)
FAM18B	7.26	4.69	NM_016078.4	family with sequence similarity 18
FJX1	7.58	4.68	NM_014344.2	four jointed box 1 (Drosophila) (FJX1)
TUBB2C	7.25	4.68	NM_006088.5	tubulin
LOC100129599	7.26	4.67	XM_001724539.1	PREDICTED: similar to mCG7602 (LOC100129599)
C5orf28	7.52	4.62	NM_022483.3	chromosome 5 open reading frame 28 (C5orf28)
ZBTB4	7.44	4.61	NM_020899.2	zinc finger and BTB domain containing 4 (ZBTB4)
FAM127B	7.3	4.53	NM_001078172.1	family with sequence similarity 127
LOC654103	7.27	4.51	XM_939368.1	PREDICTED: similar to solute carrier family 25
DPYSL2	6.84	4.46	NM_001386.4	dihydropyrimidinase-like 2 (DPYSL2)
SRXN1	7.1	4.44	NM_080725.1	sulfiredoxin 1 homolog (S. cerevisiae) (SRXN1)
C5orf5	7.09	4.42	NM_016603.1	chromosome 5 open reading frame 5 (C5orf5)
PPARG	6.93	4.41	NM_015869.4	peroxisome proliferator-activated receptor gamma (PPARG)
LOC653778	7.32	4.4	XM_929667.1	PREDICTED: similar to solute carrier family 25
PRKAA1	7.25	4.39	NM_006251.5	protein kinase
HSPB1	5.77	4.39	NM_001540.2	heat shock 27kDa protein 1 (HSPB1)
KIAA0494	7.07	4.37	NM_014774.1	KIAA0494 (KIAA0494)
CTXN1	6.81	4.37	NM_206833.2	cortexin 1 (CTXN1)
UBAC2	7.23	4.34	NM_177967.2	UBA domain containing 2 (UBAC2)
POLE4	6.5	4.33	NM_019896.2	polymerase (DNA-directed)
E2F2	7.22	4.32	NM_004091.2	E2F transcription factor 2 (E2F2)

LMBRD1	7.12	4.3	NM_018368.2	LMBR1 domain containing 1 (LMBRD1)
MAT2B	6.62	4.3	NM_013283.3	methionine adenosyltransferase II
PLIN2	7.21	4.29	NM_001122.2	perilipin 2 (PLIN2)
VPS35	6.95	4.29	NM_018206.3	vacuolar protein sorting 35 homolog (S. cerevisiae) (VPS35)
FOXF2	7.3	4.28	NM_001452.1	forkhead box F2 (FOXF2)
PECI	7.14	4.26	NM_006117.2	peroxisomal D3
RNF38	6.52	4.26	NM_022781.4	ring finger protein 38 (RNF38)
TMEM55B	7.26	4.25	NM_144568.1	transmembrane protein 55B (TMEM55B)
LOC205251	6.9	4.24	XR_017711.1	PREDICTED: misc_RNA (LOC205251)
BECN1	6.75	4.24	NM_003766.2	beclin 1
IRF1	7.4	4.23	NM_002198.1	interferon regulatory factor 1 (IRF1)
PID1	6.94	4.21	NM_017933.3	phosphotyrosine interaction domain containing 1 (PID1)
FABP5	6.79	4.21	NM_001444.1	fatty acid binding protein 5 (psoriasis-associated) (FABP5)
DCTPP1	6.36	4.18	NM_024096.1	dCTP pyrophosphatase 1 (DCTPP1)
CCNH	6.94	4.17	NM_001239.2	cyclin H (CCNH)
FABP5L2	6.55	4.17	XM_001134012.2	PREDICTED: fatty acid binding protein 5-like 2 (FABP5L2)
USP42	7.07	4.14	NM_032172.1	ubiquitin specific peptidase 42 (USP42)
ZNF385A	7.38	4.13	NM_015481.1	zinc finger protein 385A (ZNF385A)
ZNF77	7.2	4.12	NM_021217.1	zinc finger protein 77 (ZNF77)
MCTS1	6.79	4.11	NM_014060.1	malignant T cell amplified sequence 1 (MCTS1)
SP3	6.82	4.08	NM_001017371.3	Sp3 transcription factor (SP3)
CLIP4	6.67	4.07	NM_024692.3	CAP-GLY domain containing linker protein family
H19	7.54	4.06	NR_002196.1	H19
CTSA	7.14	4.06	NM_000308.2	cathepsin A (CTSA)
CDC25A	6.46	4.06	NM_001789.2	cell division cycle 25 homolog A (S. pombe) (CDC25A)
LOC100134273	6.44	4.04	XM_001724343.1	PREDICTED: similar to mCG7602 (LOC100134273)
RAB5C	6.84	4.03	NM_004583.2	RAB5C
FOXJ3	6.5	4.03	NM_014947.3	forkhead box J3 (FOXJ3)
METRNL	6.93	4.02	XM_941466.2	PREDICTED: meteorin
SNRK	6.82	4.02	NM_017719.3	SNF related kinase (SNRK)
KLHL8	7.06	4.01	NM_020803.3	kelch-like 8 (Drosophila) (KLHL8)
MEGF9	6.91	4	NM_001080497.1	multiple EGF-like-domains 9 (MEGF9)
DUSP3	6.19	4	NM_004090.2	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) (DUSP3)
STX6	6.79	3.99	NM_005819.4	syntaxin 6 (STX6)
FAM175B	6.81	3.98	NM_032182.3	family with sequence similarity 175
OXA1L	6.53	3.98	NM_005015.1	oxidase (cytochrome c) assembly 1-like (OXA1L)
HABP4	6.91	3.97	NM_014282.1	hyaluronan binding protein 4 (HABP4)
ZNFX1	6.91	3.97	NM_021035.2	zinc finger
MPV17	6.76	3.97	NM_002437.4	MpV17 mitochondrial inner membrane protein (MPV17)
FARP1	6.64	3.97	NM_005766.2	FERM
DAZAP2	5.93	3.96	NM_014764.2	DAZ associated protein 2 (DAZAP2)
CRTC2	7.01	3.95	NM_181715.1	CREB regulated transcription coactivator 2 (CRTC2)
HDHD1A	6.69	3.94	NM_012080.3	haloacid dehalogenase-like hydrolase domain containing 1A (HDHD1A)
PLOD2	6.64	3.93	NM_000935.2	procollagen-lysine
TIPARP	6.35	3.93	NM_015508.3	TCDD-inducible poly(ADP-ribose) polymerase (TIPARP)
FABP5	6.82	3.92	NM_001444.1	fatty acid binding protein 5 (psoriasis-associated) (FABP5)
FAM102A	6.6	3.89	NM_001035254.1	family with sequence similarity 102
PTK2	6.07	3.89	NM_005607.3	PTK2 protein tyrosine kinase 2 (PTK2)
SS18L2	5.79	3.89	NM_016305.2	synovial sarcoma translocation gene on chromosome 18-like 2 (SS18L2)

NRBP2	6.78	3.88	NM_178564.2	nuclear receptor binding protein 2 (NRBP2)
SLC22A5	6.53	3.88	NM_003060.2	solute carrier family 22 (organic cation transporter)
BIVM	6.56	3.87	NM_017693.2	basic
THG1L	6.94	3.85	NM_017872.3	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae) (THG1L)
MCM6	6.13	3.84	NM_005915.4	minichromosome maintenance complex component 6 (MCM6)
NDUFA2	5.76	3.84	NM_002488.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
CDC42EP4	6.13	3.83	NM_012121.4	CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4)
VAMP7	6.24	3.82	NM_005638.3	Yq12w
LOC644132	6.53	3.78	XR_017532.2	PREDICTED: misc_RNA (LOC644132)
CSTB	5.61	3.77	NM_000100.2	cystatin B (stefin B) (CSTB)
ATP6V1C1	6.75	3.76	NM_001695.4	ATPase
POLQ	6.42	3.76	NM_199420.3	polymerase (DNA directed)
C6orf62	5.94	3.75	NM_030939.3	chromosome 6 open reading frame 62 (C6orf62)
TNFRSF21	5.87	3.75	NM_014452.3	tumor necrosis factor receptor superfamily
TMEM138	6.54	3.74	NM_016464.3	transmembrane protein 138 (TMEM138)
GLCE	6.55	3.73	NM_015554.1	glucuronic acid epimerase (GLCE)
E2F7	6	3.72	NM_203394.2	E2F transcription factor 7 (E2F7)
FAM120A	5.85	3.72	NM_014612.3	family with sequence similarity 120A (FAM120A)
PPARG	6.35	3.71	NM_138712.3	peroxisome proliferator-activated receptor gamma (PPARG)
RAB22A	6.36	3.7	NM_020673.2	RAB22A
MRPL21	6.23	3.7	NM_181514.1	mitochondrial ribosomal protein L21 (MRPL21)
SYDE1	6.42	3.69	NM_033025.4	synapse defective 1
VAMP3	6.06	3.68	NM_004781.3	vesicle-associated membrane protein 3 (cellubrevin) (VAMP3)
SMAD6	5.96	3.68	NM_005585.3	SMAD family member 6 (SMAD6)
ZNF317	6.6	3.67	NM_020933.2	zinc finger protein 317 (ZNF317)
FAM102A	6.56	3.66	NM_001035254.1	family with sequence similarity 102
GADD45B	6.22	3.66	NM_015675.2	growth arrest and DNA-damage-inducible
USP3	6.2	3.66	NM_006537.2	ubiquitin specific peptidase 3 (USP3)
SCRN1	6.15	3.66	NM_014766.3	secernin 1 (SCRN1)
USP1	5.84	3.65	NM_001017416.1	ubiquitin specific peptidase 1 (USP1)
ALCAM	6.22	3.64	NM_001627.2	activated leukocyte cell adhesion molecule (ALCAM)
LOC642956	6.04	3.63	XM_938166.3	PREDICTED: hypothetical LOC642956 (LOC642956)
PSMG2	5.71	3.63	NM_020232.3	proteasome (prosome
ATPAF1	6.07	3.62	NM_022745.3	ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1)
ZMYND11	5.93	3.61	NM_006624.3	zinc finger
TUBB4Q	6.36	3.6	NM_020040.3	tubulin
HBP1	6.29	3.6	NM_012257.3	HMG-box transcription factor 1 (HBP1)
TMEM64	6.1	3.6	NM_001008495.2	transmembrane protein 64 (TMEM64)
DCUN1D4	5.97	3.59	NM_015115.1	DCN1
MRPL21	5.9	3.57	NM_181515.1	mitochondrial ribosomal protein L21 (MRPL21)
ANKIB1	5.76	3.57	NM_019004.1	ankyrin repeat and IBR domain containing 1 (ANKIB1)
FBXW11	6.09	3.56	NM_033645.2	F-box and WD repeat domain containing 11 (FBXW11)
C20orf30	5.75	3.56	NM_001009924.1	chromosome 20 open reading frame 30 (C20orf30)
STRN3	6.02	3.55	NM_014574.3	striatin
HADHB	6.42	3.54	NM_000183.2	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase
STX6	6.25	3.54	NM_005819.4	syntaxin 6 (STX6)
C5orf32	6.04	3.54	NM_032412.3	chromosome 5 open reading frame 32 (C5orf32)
WEE1	5.8	3.54	NM_003390.2	WEE1 homolog (S. pombe) (WEE1)
RECK	6.34	3.53	NM_021111.1	reversion-inducing-cysteine-rich protein with kazal motifs (RECK)

INO80	6.16	3.53	NM_017553.1	INO80 homolog (S. cerevisiae) (INO80)
PSMF1	6.14	3.53	NM_178579.1	proteasome (prosome
MIDN	6.32	3.52	NM_177401.4	midnolin (MIDN)
LOC100132535	6.24	3.52	XR_038625.1	PREDICTED: misc_RNA (LOC100132535)
MED8	6.46	3.51	NM_201542.2	mediator of RNA polymerase II transcription
OXR1	5.93	3.51	NM_181354.3	oxidation resistance 1 (OXR1)
DNAJB6	5.9	3.51	NM_005494.2	DnaJ (Hsp40) homolog
LOC642975	5.76	3.51	XR_036988.1	PREDICTED: misc_RNA (LOC642975)
TARS	5.47	3.51	NM_152295.3	threonyl-tRNA synthetase (TARS)
SH2B3	6.35	3.5	NM_005475.1	SH2B adaptor protein 3 (SH2B3)
IFNAR2	6.26	3.49	NM_207584.1	interferon (alpha
SMARCA2	5.87	3.49	NM_003070.3	SWI/SNF related
SPATA2	6.23	3.48	NM_006038.2	spermatogenesis associated 2 (SPATA2)
CHN1	6.04	3.48	NM_001025201.1	chimerin (chimaerin) 1 (CHN1)
EPDR1	5.92	3.48	NM_017549.3	ependymin related protein 1 (zebrafish) (EPDR1)
SPOP	5.8	3.48	NM_001007230.1	speckle-type POZ protein (SPOP)
FBLN1	5.86	3.47	NM_006486.2	fibulin 1 (FBLN1)
CXCR4	6.05	3.46	NM_001008540.1	chemokine (C-X-C motif) receptor 4 (CXCR4)
PDCD10	5.57	3.46	NM_145859.1	programmed cell death 10 (PDCD10)
WSB2	5.9	3.45	NM_018639.3	WD repeat and SOCS box-containing 2 (WSB2)
FBRS	6.41	3.44	NM_001105079.1	fibrosin (FBRS)
TBC1D2	6.18	3.43	NM_018421.2	TBC1 domain family
SAC3D1	5.77	3.42	NM_013299.3	SAC3 domain containing 1 (SAC3D1)
MAP3K14	6.34	3.41	NM_003954.2	mitogen-activated protein kinase kinase kinase 14 (MAP3K14)
HBP1	5.92	3.4	NM_012257.3	HMG-box transcription factor 1 (HBP1)
C20orf30	5.5	3.4	NM_001009923.1	chromosome 20 open reading frame 30 (C20orf30)
KIAA1737	6.08	3.39	NM_033426.2	KIAA1737 (KIAA1737)
KCTD20	5.81	3.39	NM_173562.3	potassium channel tetramerisation domain containing 20 (KCTD20)
CDC2	5.59	3.38	NM_001786.2	cell division cycle 2
NSMCE2	6.09	3.36	NM_173685.1	non-SMC element 2
C1orf144	5.78	3.36	NM_015609.2	chromosome 1 open reading frame 144 (C1orf144)
FAM89A	6.25	3.35	NM_198552.1	family with sequence similarity 89
TJAP1	5.96	3.35	NM_080604.1	tight junction associated protein 1 (peripheral) (TJAP1)
M6PR	5.89	3.33	NM_002355.2	mannose-6-phosphate receptor (cation dependent) (M6PR)
JOSD1	5.79	3.33	NM_014876.3	Josephin domain containing 1 (JOSD1)
LOC399748	5.62	3.33	XR_018212.1	PREDICTED: misc_RNA (LOC399748)
MNT	5.98	3.32	NM_020310.2	MAX binding protein (MNT)
IGF2BP2	5.9	3.32	NM_006548.4	insulin-like growth factor 2 mRNA binding protein 2 (IGF2BP2)
FABP5L2	5.84	3.32	XM_001721172.1	PREDICTED: fatty acid binding protein 5-like 2 (FABP5L2)
HPS5	6.14	3.31	NM_007216.3	Hermansky-Pudlak syndrome 5 (HPS5)
STARD3NL	5.91	3.31	NM_032016.2	STARD3 N-terminal like (STARD3NL)
BIVM	5.82	3.31	NM_017693.2	basic
ORMDL1	5.5	3.31	NM_016467.3	ORM1-like 1 (S. cerevisiae) (ORMDL1)
INO80	5.92	3.29	NM_017553.1	INO80 homolog (S. cerevisiae) (INO80)
ADIPOR1	5.72	3.29	NM_015999.2	adiponectin receptor 1 (ADIPOR1)
MICA	6.22	3.27	NM_000247.1	MHC class I polypeptide-related sequence A (MICA)
ADIPOR1	5.55	3.27	NM_015999.2	adiponectin receptor 1 (ADIPOR1)
TMEM147	5.3	3.27	NM_032635.2	transmembrane protein 147 (TMEM147)
MRPL54	5.5	3.26	NM_172251.1	mitochondrial ribosomal protein L54 (MRPL54)

SLC10A7	6.05	3.24	NM_001029998.2	solute carrier family 10 (sodium/bile acid cotransporter family)
TFPI	5.66	3.24	NM_006287.4	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI)
CHD9	5.43	3.24	NM_025134.4	chromodomain helicase DNA binding protein 9 (CHD9)
MAP2K4	5.7	3.23	NM_003010.2	mitogen-activated protein kinase kinase 4 (MAP2K4)
LOC100134648	6.02	3.22	XM_001724681.1	PREDICTED: similar to hCG2024106
RBPMS	6.01	3.22	NM_001008712.1	RNA binding protein with multiple splicing (RBPMS)
MICB	5.95	3.22	NM_005931.2	MHC class I polypeptide-related sequence B (MICB)
MYBL1	5.7	3.22	NM_001080416.1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1 (MYBL1)
TERF2IP	5.67	3.22	NM_018975.2	telomeric repeat binding factor 2
SUZ12	5.24	3.21	NM_015355.1	suppressor of zeste 12 homolog (Drosophila) (SUZ12)
RAC2	5.83	3.2	NM_002872.3	ras-related C3 botulinum toxin substrate 2 (rho family
UHRF2	5.72	3.2	NM_152896.1	ubiquitin-like with PHD and ring finger domains 2 (UHRF2)
NBL1	5.66	3.19	NM_182744.1	neuroblastoma
CCNH	5.5	3.19	NM_001239.2	cyclin H (CCNH)
RBM25	5.22	3.18	NM_021239.1	RNA binding motif protein 25 (RBM25)
FOXA1	5.42	3.17	NM_004496.2	forkhead box A1 (FOXA1)
MKNK2	5.24	3.17	NM_017572.2	MAP kinase interacting serine/threonine kinase 2 (MKNK2)
UBE2Q2	5.32	3.16	NM_173469.1	ubiquitin-conjugating enzyme E2Q family member 2 (UBE2Q2)
COMMD3	5.31	3.16	NM_012071.2	COMM domain containing 3 (COMMD3)
PDCD5	5.27	3.16	NM_004708.2	programmed cell death 5 (PDCD5)
CAPRIN2	5.93	3.15	NM_023925.3	caprin family member 2 (CAPRIN2)
TMTC1	5.55	3.15	NM_175861.2	transmembrane and tetratricopeptide repeat containing 1 (TMTC1)
PGRMC2	4.99	3.15	NM_006320.1	progesterone receptor membrane component 2 (PGRMC2)
GANAB	5.74	3.14	NM_198334.1	glucosidase
TPRG1L	5.19	3.14	NM_182752.3	tumor protein p63 regulated 1-like (TPRG1L)
FASTK	5.51	3.13	NM_033015.2	Fas-activated serine/threonine kinase (FASTK)
KIAA0460	6.09	3.12	NM_015203.2	KIAA0460 (KIAA0460)
DEK	4.76	3.11	NM_003472.2	DEK oncogene (DNA binding) (DEK)
SFT2D2	5.96	3.1	NM_199344.2	SFT2 domain containing 2 (SFT2D2)
RPS26	5.78	3.1	NM_001029.3	ribosomal protein S26 (RPS26)
MUTED	5.66	3.1	NM_201280.1	muted homolog (mouse) (MUTED)
SUV39H1	5.64	3.1	NM_003173.2	suppressor of variegation 3-9 homolog 1 (Drosophila) (SUV39H1)
TUSC2	5.54	3.1	NM_007275.1	tumor suppressor candidate 2 (TUSC2)
CA2	5.36	3.1	NM_000067.1	carbonic anhydrase II (CA2)
ADD3	4.93	3.1	NM_001121.2	adducin 3 (gamma) (ADD3)
UBR5	5.52	3.09	NM_015902.4	ubiquitin protein ligase E3 component n-recognin 5 (UBR5)
ANKRA2	5.37	3.09	NM_023039.2	ankyrin repeat
NBL1	5.58	3.08	NM_005380.4	neuroblastoma
ADIPOR2	5.32	3.07	NM_024551.2	adiponectin receptor 2 (ADIPOR2)
STX3	5.3	3.07	NM_004177.3	syntaxin 3 (STX3)
NUFIP2	5.18	3.06	NM_020772.1	nuclear fragile X mental retardation protein interacting protein 2 (NUFIP2)
FAM89A	5.75	3.05	XM_939093.1	family with sequence similarity 89
FAM73B	5.71	3.03	NM_032809.2	family with sequence similarity 73
IRAK2	5.32	3.03	NM_001570.3	interleukin-1 receptor-associated kinase 2 (IRAK2)
PIP5K2B	4.94	3.02	NM_138687.1	phosphatidylinositol-4-phosphate 5-kinase
JUNB	5.31	3.01	NM_002229.2	jun B proto-oncogene (JUNB)
PFKFB3	5.12	3.01	NM_004566.2	6-phosphofructo-2-kinase/fructose-2
TSC22D2	5.07	3.01	NM_014779.2	TSC22 domain family
LOC100132037	4.31	3	XM_001725987.1	PREDICTED: similar to mCG7602 (LOC100132037)

ANKRD57	5.18	2.99	NM_023016.3	ankyrin repeat domain 57 (ANKRD57)
C11orf59	4.81	2.99	NM_017907.1	chromosome 11 open reading frame 59 (C11orf59)
AXUD1	5.5	2.98	NM_033027.2	AXIN1 up-regulated 1 (AXUD1)
BRP44L	5.48	2.98	NM_016098.1	brain protein 44-like (BRP44L)
KIAA1598	5.26	2.98	NM_018330.4	KIAA1598 (KIAA1598)
ADA	5.45	2.97	NM_000022.2	adenosine deaminase (ADA)
TFPI	5.34	2.97	NM_006287.4	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI)
TMEM9B	5.27	2.97	NM_020644.1	TMEM9 domain family
ZHX1	5.19	2.97	NM_007222.3	zinc fingers and homeoboxes 1 (ZHX1)
MGAT4B	5.13	2.97	NM_054013.2	mannosyl (alpha-1
ZFPM1	5.62	2.94	NM_153813.2	zinc finger protein
ABHD14B	5.47	2.94	NM_032750.1	abhydrolase domain containing 14B (ABHD14B)
ZDHHC9	5.31	2.94	NM_016032.2	zinc finger
DNAJC9	4.75	2.94	NM_015190.3	DnaJ (Hsp40) homolog
ADPGK	5.54	2.93	NM_031284.3	ADP-dependent glucokinase (ADPGK)
FAHD1	5.45	2.93	NM_001018104.1	fumarylacetoacetate hydrolase domain containing 1 (FAHD1)
C2orf64	5.35	2.93	NM_001008215.1	chromosome 2 open reading frame 64 (C2orf64)
FAHD1	5.02	2.93	NM_031208.1	fumarylacetoacetate hydrolase domain containing 1 (FAHD1)
ARHGEF10	5.37	2.92	NM_014629.2	Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10)
ADORA2B	5.31	2.91	NM_000676.2	adenosine A2b receptor (ADORA2B)
CYBRD1	5.2	2.91	NM_024843.2	cytochrome b reductase 1 (CYBRD1)
TAF10	5.17	2.91	NM_006284.2	TAF10 RNA polymerase II
SNIP1	4.75	2.91	NM_024700.2	Smad nuclear interacting protein 1 (SNIP1)
KIAA1737	5.2	2.9	NM_033426.2	KIAA1737 (KIAA1737)
KLF11	5.2	2.9	XM_001129527.1	PREDICTED: Kruppel-like factor 11 (KLF11)
PRDM4	5.05	2.9	NM_012406.3	PR domain containing 4 (PRDM4)
C7orf30	4.57	2.9	NM_138446.1	chromosome 7 open reading frame 30 (C7orf30)
ARL4A	5.27	2.89	NM_001037164.1	ADP-ribosylation factor-like 4A (ARL4A)
DNM1L	5.03	2.89	NM_012062.2	dynamin 1-like (DNM1L)
DUT	4.85	2.89	NM_001025249.1	deoxyuridine triphosphatase (DUT)
SLC39A8	4.83	2.89	NM_022154.5	solute carrier family 39 (zinc transporter)
SNX16	5.31	2.88	NM_022133.2	sorting nexin 16 (SNX16)
RC3H2	5.02	2.88	NM_018835.1	ring finger and CCCH-type zinc finger domains 2 (RC3H2)
CDK2	4.86	2.88	NM_001798.2	cyclin-dependent kinase 2 (CDK2)
ASB13	5.52	2.87	NM_024701.2	ankyrin repeat and SOCS box-containing 13 (ASB13)
BRMS1L	5.06	2.87	NM_032352.3	breast cancer metastasis-suppressor 1-like (BRMS1L)
TMEM8	5.52	2.86	NM_021259.1	transmembrane protein 8 (five membrane-spanning domains) (TMEM8)
TFAP4	5.46	2.86	NM_003223.1	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)
CRTC3	4.88	2.86	NM_022769.3	CREB regulated transcription coactivator 3 (CRTC3)
ABTB1	5.52	2.85	NM_032548.2	ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1)
RUNX3	5.35	2.84	NM_004350.2	runt-related transcription factor 3 (RUNX3)
VGLL4	5.17	2.84	NM_014667.1	vestigial like 4 (Drosophila) (VGLL4)
DUT	4.55	2.84	NM_001025248.1	deoxyuridine triphosphatase (DUT)
CMPK1	4.49	2.84	NM_016308.1	cytidine monophosphate (UMP-CMP) kinase 1
METRNL	5.24	2.83	XM_941466.2	PREDICTED: meteorin
MOBKL1B	5.15	2.83	NM_018221.3	MOB1
RNF150	5.11	2.83	NM_020724.1	ring finger protein 150 (RNF150)
JAZF1	5.06	2.82	NM_175061.3	JAZF zinc finger 1 (JAZF1)
CYBRD1	4.95	2.82	NM_024843.2	cytochrome b reductase 1 (CYBRD1)

FKBP9L	4.78	2.82	NM_182827.1	FK506 binding protein 9-like (FKBP9L)
CAP1	4.19	2.82	NM_006367.2	CAP
TSPAN3	4.11	2.82	NM_005724.4	tetraspanin 3 (TSPAN3)
CRMP1	5.22	2.81	NM_001014809.1	collapsin response mediator protein 1 (CRMP1)
TMEM54	5.4	2.8	NM_033504.2	transmembrane protein 54 (TMEM54)
PNKD	5.27	2.8	NM_022572.2	paroxysmal nonkinesiogenic dyskinesia (PNKD)
DEDD	5.11	2.8	NM_001039712.1	death effector domain containing (DEDD)
ICMT	4.93	2.8	NM_012405.3	isoprenylcysteine carboxyl methyltransferase (ICMT)
GART	4.88	2.8	NM_000819.3	phosphoribosylglycinamide formyltransferase
NPAS2	4.8	2.8	NM_002518.3	neuronal PAS domain protein 2 (NPAS2)
LOC440731	5.02	2.79	XM_933693.2	PREDICTED: hypothetical LOC440731
G6PD	4.71	2.79	NM_000402.3	glucose-6-phosphate dehydrogenase (G6PD)
FOXQ1	5.06	2.78	NM_033260.3	forkhead box Q1 (FOXQ1)
RHOC	4.18	2.78	NM_175744.4	ras homolog gene family
TEX2	5.07	2.77	NM_018469.3	testis expressed 2 (TEX2)
CBX6	5.06	2.77	NM_014292.3	chromobox homolog 6 (CBX6)
ASAP2	4.4	2.77	NM_003887.2	ArfGAP with SH3 domain
JDP2	5.4	2.76	NM_130469.2	Jun dimerization protein 2 (JDP2)
TMEM111	4.98	2.76	NM_018447.1	transmembrane protein 111 (TMEM111)
CREB3L2	4.8	2.76	NM_194071.2	cAMP responsive element binding protein 3-like 2 (CREB3L2)
FAM127B	5.25	2.75	NM_001078172.1	family with sequence similarity 127
ECHDC2	5.07	2.74	NM_018281.2	enoyl Coenzyme A hydratase domain containing 2 (ECHDC2)
SACM1L	4.99	2.74	NM_014016.2	SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L)
GHITM	3.86	2.74	NM_014394.2	growth hormone inducible transmembrane protein (GHITM)
LOC649679	5.17	2.73	XM_945045.1	PREDICTED: similar to Tubulin beta-4q chain
CASP2	4.74	2.73	NM_032982.2	caspase 2
DUT	4.43	2.73	NM_001025248.1	deoxyuridine triphosphatase (DUT)
NCOA3	4.99	2.72	NM_181659.1	nuclear receptor coactivator 3 (NCOA3)
HBXIP	4.14	2.72	NM_006402.2	hepatitis B virus x interacting protein (HBXIP)
ASF1B	4.45	2.71	NM_018154.2	ASF1 anti-silencing function 1 homolog B (S. cerevisiae) (ASF1B)
SKA2	4.44	2.71	NM_182620.3	spindle and kinetochore associated complex subunit 2 (SKA2)
TBC1D20	5.15	2.7	NM_144628.2	TBC1 domain family
ZNHIT6	4.91	2.7	NM_017953.2	zinc finger
MTCH2	4.99	2.69	NM_014342.2	mitochondrial carrier homolog 2 (C. elegans) (MTCH2)
SS18L1	4.92	2.69	NM_198935.1	synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1)
API5	4.78	2.68	NM_006595.2	apoptosis inhibitor 5 (API5)
PANK1	4.75	2.68	NM_138316.2	pantothenate kinase 1 (PANK1)
IRF9	4.69	2.68	NM_006084.4	interferon regulatory factor 9 (IRF9)
LOC645058	4.21	2.68	XM_930423.1	PREDICTED: similar to hepatitis B virus x-interacting protein (LOC645058)
SLC29A2	5.33	2.67	NM_001532.2	solute carrier family 29 (nucleoside transporters)
USP24	4.84	2.67	NM_015306.1	ubiquitin specific peptidase 24 (USP24)
MED31	4.8	2.67	NM_016060.2	mediator complex subunit 31 (MED31)
ASAP1	4.5	2.67	NM_018482.2	ArfGAP with SH3 domain
SLC25A39	3.99	2.67	NM_016016.1	solute carrier family 25
PYCARD	4.98	2.66	NM_013258.3	PYD and CARD domain containing (PYCARD)
FNBP1	4.71	2.66	NM_015033.2	formin binding protein 1 (FNBP1)
C14orf100	4.67	2.66	NM_016475.2	chromosome 14 open reading frame 100 (C14orf100)
ZNF217	4.62	2.66	NM_006526.2	zinc finger protein 217 (ZNF217)
NNT	4.39	2.66	NM_012343.3	nicotinamide nucleotide transhydrogenase (NNT)

COPS3	4.26	2.66	NM_003653.2	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3)
TMEM158	4.39	2.65	NM_015444.2	transmembrane protein 158 (TMEM158)
FAM60A	4.37	2.65	NM_001135811.1	family with sequence similarity 60
SSBP1	4.24	2.65	NM_003143.1	single-stranded DNA binding protein 1 (SSBP1)
NKIRAS1	5.08	2.64	NM_020345.3	NFKB inhibitor interacting Ras-like 1 (NKIRAS1)
CABLES1	4.74	2.64	NM_138375.1	Cdk5 and Abl enzyme substrate 1 (CABLES1)
HCCS	4.73	2.64	NM_005333.2	holocytochrome c synthase (cytochrome c heme-lyase) (HCCS)
CNIH	4.48	2.64	NM_001009551.1	cornichon homolog (Drosophila) (CNIH)
MBOAT7	4.96	2.63	NM_024298.2	membrane bound O-acyltransferase domain containing 7 (MBOAT7)
EPHB4	4.89	2.63	NM_004444.4	EPH receptor B4 (EPHB4)
LOC401076	4.68	2.63	XR_038201.1	PREDICTED: misc_RNA (LOC401076)
NDEL1	4.49	2.62	NM_030808.3	nudE nuclear distribution gene E homolog (A. nidulans)-like 1 (NDEL1)
MAD2L2	4.31	2.62	NM_006341.2	MAD2 mitotic arrest deficient-like 2 (yeast) (MAD2L2)
DNAJB9	4.99	2.61	NM_012328.1	DnaJ (Hsp40) homolog
C11orf51	4.85	2.61	NM_014042.1	chromosome 11 open reading frame 51 (C11orf51)
KATNAL1	4.85	2.6	NM_001014380.1	katanin p60 subunit A-like 1 (KATNAL1)
ABLIM1	4.08	2.6	NM_006720.3	actin binding LIM protein 1 (ABLIM1)
PPP2R2D	4.67	2.59	NM_001003656.1	protein phosphatase 2
NFIC	4.65	2.59	NM_205843.1	nuclear factor I/C (CCAAT-binding transcription factor) (NFIC)
DNM1L	4.62	2.59	NM_012062.2	dynamin 1-like (DNM1L)
ZNF511	4.62	2.59	NM_145806.2	zinc finger protein 511 (ZNF511)
YOD1	4.47	2.59	NM_018566.3	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae) (YOD1)
SIK3	4.84	2.58	NM_025164.3	SIK family kinase 3 (SIK3)
PARP6	4.82	2.57	NM_020213.1	poly (ADP-ribose) polymerase family
SC4MOL	4.74	2.57	NM_001017369.1	sterol-C4-methyl oxidase-like (SC4MOL)
LCOR	4.52	2.57	NM_032440.1	ligand dependent nuclear receptor corepressor (LCOR)
LOC644563	4	2.57	XR_018203.2	PREDICTED: misc_RNA (LOC644563)
NFX1	4.84	2.56	NM_002504.3	nuclear transcription factor
BMI1	4.23	2.56	NM_005180.5	BMI1 polycomb ring finger oncogene (BMI1)
RABGAP1	4.2	2.56	NM_012197.2	RAB GTPase activating protein 1 (RABGAP1)
ABCE1	4.11	2.56	NM_001040876.1	ATP-binding cassette
LMO4	4.04	2.56	NM_006769.2	LIM domain only 4 (LMO4)
LPCAT1	4.8	2.55	NM_024830.3	lysophosphatidylcholine acyltransferase 1 (LPCAT1)
LOC387934	4.77	2.55	XM_937508.2	PREDICTED: similar to Fatty acid-binding protein
MED8	4.73	2.55	NM_001001651.1	mediator of RNA polymerase II transcription
ZBTB34	3.84	2.55	NM_001099270.1	zinc finger and BTB domain containing 34 (ZBTB34)
BTG2	4.68	2.54	NM_006763.2	BTG family
NPTN	4.07	2.54	NM_012428.2	neuroplastin (NPTN)
TIGA1	3.96	2.54	NM_053000.1	TIGA1 (TIGA1)
STARD7	3.75	2.54	NM_020151.2	START domain containing 7 (STARD7)
PDIA5	4.84	2.53	NM_006810.2	protein disulfide isomerase family A
EIF4EBP2	4.5	2.53	NM_004096.3	eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2)
DDEF2	4.04	2.53	NM_003887.1	development and differentiation enhancing factor 2 (DDEF2)
CNOT6	4.4	2.52	NM_015455.3	CCR4-NOT transcription complex
ATP6V0E1	4.09	2.52	NM_003945.3	ATPase
LOC648742	5.08	2.51	XM_001714210.1	PREDICTED: similar to growth suppressor related (LOC648742)
HPS5	4.7	2.51	NM_007216.3	Hermansky-Pudlak syndrome 5 (HPS5)
GPR180	4.53	2.51	NM_180989.4	G protein-coupled receptor 180 (GPR180)
GLIPR2	4.46	2.51	NM_022343.2	GLI pathogenesis-related 2 (GLIPR2)

SMG7	4.21	2.51	NM_173156.1	Smg-7 homolog
OCIAD1	4.17	2.51	NM_017830.1	OCIA domain containing 1 (OCIAD1)
SDHA	4.04	2.51	NM_004168.1	succinate dehydrogenase complex
CPEB3	4.41	2.5	NM_014912.3	cytoplasmic polyadenylation element binding protein 3 (CPEB3)
MKRN1	4.4	2.5	NM_013446.2	makorin ring finger protein 1 (MKRN1)
DAB2	3.99	2.5	NM_001343.1	disabled homolog 2
UBC	2.96	2.5	NM_021009.3	ubiquitin C (UBC)
GATAD2B	4.98	2.49	NM_020699.1	GATA zinc finger domain containing 2B (GATAD2B)
AIG1	4.87	2.49	NM_016108.2	androgen-induced 1 (AIG1)
TRIM8	4.63	2.49	NM_030912.2	tripartite motif-containing 8 (TRIM8)
BCL6	4.6	2.49	NM_001706.2	B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6)
IGF2R	4.59	2.49	NM_000876.2	insulin-like growth factor 2 receptor (IGF2R)
RPRD2	4.47	2.49	NM_015203.3	regulation of nuclear pre-mRNA domain containing 2 (RPRD2)
NFIA	4.39	2.49	NM_005595.1	nuclear factor I/A (NFIA)
LOC388327	4.85	2.48	XM_371009.4	PREDICTED: hypothetical LOC388327
ATP6V0A2	4.65	2.48	NM_012463.2	ATPase
C11orf82	4.53	2.48	NM_145018.2	chromosome 11 open reading frame 82 (C11orf82)
UBC	3.02	2.48	NM_021009.1	ubiquitin C (UBC)
NR4A2	4.22	2.47	NM_006186.2	nuclear receptor subfamily 4
CENPQ	4.54	2.46	NM_018132.3	centromere protein Q (CENPQ)
SAR1B	4.32	2.46	NM_001033503.1	SAR1 homolog B (S. cerevisiae) (SAR1B)
HDHD2	4.21	2.46	NM_032124.4	haloacid dehalogenase-like hydrolase domain containing 2 (HDHD2)
CD164	4.69	2.45	NM_006016.3	CD164 molecule
RTCD1	4.36	2.45	NM_003729.1	RNA terminal phosphate cyclase domain 1 (RTCD1)
C15orf57	4.31	2.45	NM_052849.2	chromosome 15 open reading frame 57 (C15orf57)
PRKRIR	3.86	2.45	NM_004705.2	protein-kinase
DPP8	4.58	2.44	NM_017743.4	dipeptidyl-peptidase 8 (DPP8)
PER2	4.41	2.44	NM_022817.2	period homolog 2 (Drosophila) (PER2)
FEZ2	4.27	2.44	NM_005102.2	fasciculation and elongation protein zeta 2 (zygin II) (FEZ2)
RFC1	4.27	2.44	NM_002913.3	replication factor C (activator 1) 1
STARD7	4.02	2.44	NM_139267.1	START domain containing 7 (STARD7)
MFF	3.96	2.44	NM_020194.4	mitochondrial fission factor (MFF)
PRPF4	3.95	2.44	NM_004697.3	PRP4 pre-mRNA processing factor 4 homolog (yeast) (PRPF4)
C10orf140	4.67	2.43	NM_207371.3	chromosome 10 open reading frame 140 (C10orf140)
UCHL1	4.45	2.43	NM_004181.3	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1)
CPNE1	4.33	2.43	NM_152931.1	copine I (CPNE1)
PLSCR4	4.32	2.43	NM_020353.1	phospholipid scramblase 4 (PLSCR4)
CA2	4.21	2.43	NM_000067.1	carbonic anhydrase II (CA2)
EIF2AK1	3.62	2.43	NM_014413.2	eukaryotic translation initiation factor 2-alpha kinase 1 (EIF2AK1)
UCP2	4.72	2.42	NM_003355.2	uncoupling protein 2 (mitochondrial
CXCL1	4.56	2.42	NM_001511.1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity
ATMIN	4.49	2.42	NM_015251.2	ATM interactor (ATMIN)
GNPTAB	4.43	2.42	NM_024312.3	N-acetylglucosamine-1-phosphate transferase
ATP6V1B2	4.26	2.42	NM_001693.3	ATPase
LOC650369	3.58	2.42	XR_018848.1	PREDICTED: similar to family with sequence similarity 60
TESK1	4.56	2.41	NM_006285.2	testis-specific kinase 1 (TESK1)
LOC642031	4.51	2.41	XM_936101.2	PREDICTED: hypothetical protein LOC642031 (LOC642031)
C5orf30	4.35	2.41	NM_033211.2	chromosome 5 open reading frame 30 (C5orf30)
TRAPPC4	4.18	2.41	NM_016146.3	trafficking protein particle complex 4 (TRAPPC4)

PRPF38A	4.15	2.41	NM_032864.3	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A (PRPF38A)
DHRS3	4.04	2.41	NM_004753.4	dehydrogenase/reductase (SDR family) member 3 (DHRS3)
RRN3	4	2.41	NM_018427.3	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) (RRN3)
ATG16L1	3.98	2.41	NM_030803.5	ATG16 autophagy related 16-like 1 (S. cerevisiae) (ATG16L1)
UBE2E3	3.67	2.41	NM_006357.2	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog
DKC1	3.64	2.41	NM_001363.2	dyskeratosis congenita 1
GGA2	4.67	2.4	NM_015044.3	golgi associated
ARHGEF3	4.31	2.4	NM_019555.1	Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3)
PBX3	4.14	2.4	NM_006195.4	pre-B-cell leukemia homeobox 3 (PBX3)
ASAP2	3.9	2.4	NM_003887.2	ArfGAP with SH3 domain
ZNF219	4.47	2.39	NM_016423.1	zinc finger protein 219 (ZNF219)
C20orf177	4.25	2.39	NM_022106.1	chromosome 20 open reading frame 177 (C20orf177)
ASF1A	4.14	2.39	NM_014034.1	ASF1 anti-silencing function 1 homolog A (S. cerevisiae) (ASF1A)
KDM5B	4.3	2.38	NM_006618.3	lysine (K)-specific demethylase 5B (KDM5B)
CNIH	3.94	2.38	NM_005776.2	cornichon homolog (Drosophila) (CNIH)
LMO4	3.84	2.38	NM_006769.2	LIM domain only 4 (LMO4)
RHOC	3.8	2.38	NM_001042678.1	ras homolog gene family
NCRNA00219	3.66	2.38	NR_015370.1	non-protein coding RNA 219 (NCRNA00219)
SVIL	4.15	2.37	NM_003174.3	supervillin (SVIL)
ASAP1	4.11	2.37	NM_018482.2	ArfGAP with SH3 domain
PPP1R8	4.17	2.36	NM_014110.3	protein phosphatase 1
MLLT6	4.16	2.36	NM_005937.3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog
HNRPUL1	3.93	2.36	NM_144732.1	heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1)
VIL2	3.8	2.36	NM_003379.3	villin 2 (ezrin) (VIL2)
RSPRY1	3.57	2.36	NM_133368.1	ring finger and SPRY domain containing 1 (RSPRY1)
PI4KB	4.45	2.35	NM_002651.1	phosphatidylinositol 4-kinase
SLC25A28	4.35	2.35	NM_031212.3	solute carrier family 25
SLC35C2	4.22	2.35	NM_015945.10	solute carrier family 35
KLHL5	3.58	2.35	NM_001007075.1	kelch-like 5 (Drosophila) (KLHL5)
LOC642590	3.53	2.35	XR_037021.1	PREDICTED: misc_RNA (LOC642590)
LOC728467	4.44	2.34	XR_039554.1	PREDICTED: misc_RNA (LOC728467)
USP21	4.22	2.34	NM_012475.4	ubiquitin specific peptidase 21 (USP21)
INPP5A	4.2	2.34	XM_001133189.1	PREDICTED: inositol polyphosphate-5-phosphatase
PPTC7	4.2	2.34	NM_139283.1	PTC7 protein phosphatase homolog (S. cerevisiae) (PPTC7)
SLC39A8	4.2	2.34	NM_022154.5	solute carrier family 39 (zinc transporter)
MAP7	4.14	2.34	NM_003980.3	microtubule-associated protein 7 (MAP7)
C18orf25	3.93	2.34	NM_001008239.2	chromosome 18 open reading frame 25 (C18orf25)
ATP6V0E1	3.27	2.34	NM_003945.3	ATPase
PPP3CB	4.13	2.33	NM_021132.1	protein phosphatase 3 (formerly 2B)
FAF2	3.96	2.33	NM_014613.2	Fas associated factor family member 2 (FAF2)
CALM1	3.64	2.33	NM_006888.3	calmodulin 1 (phosphorylase kinase
C5orf35	4.11	2.32	NM_153706.2	chromosome 5 open reading frame 35 (C5orf35)
TBC1D9	4.11	2.32	NM_015130.2	TBC1 domain family
CPOX	4.1	2.32	NM_000097.4	coproporphyrinogen oxidase (CPOX)
TSR2	4.04	2.32	NM_058163.1	TSR2
EZR	3.56	2.32	NM_003379.4	ezrin (EZR)
LOC642590	3.35	2.32	XR_016251.2	PREDICTED: misc_RNA (LOC642590)
ZBTB5	4.3	2.31	NM_014872.1	zinc finger and BTB domain containing 5 (ZBTB5)
ADARB1	4.12	2.31	NM_001112.2	adenosine deaminase

SNRK	4.09	2.31	NM_017719.3	SNF related kinase (SNRK)
MTAP	3.73	2.31	NM_002451.3	methylthioadenosine phosphorylase (MTAP)
EIF2C2	3.69	2.31	NM_012154.2	eukaryotic translation initiation factor 2C
NPTN	3.37	2.31	NM_017455.2	neuroplastin (NPTN)
SRPX	4.5	2.3	NM_006307.3	sushi-repeat-containing protein
MKRN3	4.44	2.3	NM_005664.3	makorin ring finger protein 3 (MKRN3)
LDOC1	4.19	2.3	NM_012317.2	leucine zipper
PLAGL2	4.01	2.3	NM_002657.2	pleiomorphic adenoma gene-like 2 (PLAGL2)
PPP2R4	3.97	2.3	NM_021131.3	protein phosphatase 2A activator
C19orf48	3.93	2.3	NM_199250.1	chromosome 19 open reading frame 48 (C19orf48)
LOC646347	3.41	2.3	XR_017680.1	PREDICTED: misc_RNA (LOC646347)
SMS	3.26	2.3	NM_004595.2	spermine synthase (SMS)
SNORA11D	4.32	2.29	NR_003711.1	small nucleolar RNA
GOLSYN	4.17	2.29	NM_001099743.1	Golgi-localized protein (GOLSYN)
SLC25A37	3.99	2.29	NM_016612.2	solute carrier family 25
TNFRSF10B	4.57	2.28	NM_147187.1	tumor necrosis factor receptor superfamily
FASTK	4.2	2.28	NM_033015.2	Fas-activated serine/threonine kinase (FASTK)
ADNP	4.01	2.28	NM_181442.1	activity-dependent neuroprotector homeobox (ADNP)
MED8	3.95	2.28	NM_001001654.1	mediator of RNA polymerase II transcription
AKT1	3.82	2.28	NM_001014431.1	v-akt murine thymoma viral oncogene homolog 1 (AKT1)
KIF23	3.82	2.28	NM_004856.4	kinesin family member 23 (KIF23)
TOB1	3.79	2.28	NM_005749.2	transducer of ERBB2
RPP40	3.77	2.28	NM_006638.2	ribonuclease P/MRP 40kDa subunit (RPP40)
UBE3C	3.68	2.28	NM_014671.1	ubiquitin protein ligase E3C (UBE3C)
FH	3.66	2.28	NM_000143.2	fumarate hydratase (FH)
ABCE1	3.65	2.28	NM_001040876.1	ATP-binding cassette
DEDD	4.45	2.27	NM_001039712.1	death effector domain containing (DEDD)
PPP1R15A	4.14	2.27	NM_014330.2	protein phosphatase 1
AKT1	3.97	2.27	NM_001014432.1	v-akt murine thymoma viral oncogene homolog 1 (AKT1)
E2F5	3.88	2.27	NM_001951.3	E2F transcription factor 5
TSEN34	3.43	2.27	NM_001077446.1	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (TSEN34)
CERCAM	4.36	2.25	NM_016174.3	cerebral endothelial cell adhesion molecule (CERCAM)
RAB11FIP5	4.35	2.25	NM_015470.2	RAB11 family interacting protein 5 (class I) (RAB11FIP5)
REEP1	4.12	2.25	NM_022912.1	receptor accessory protein 1 (REEP1)
MRPL48	4.02	2.25	NM_016055.4	mitochondrial ribosomal protein L48 (MRPL48)
ANGEL2	3.98	2.25	NM_144567.3	angel homolog 2 (Drosophila) (ANGEL2)
RBMS1	3.7	2.25	NM_002897.3	RNA binding motif
TCEB1	3.26	2.25	NM_005648.2	transcription elongation factor B (SIII)
SH3RF2	4.03	2.24	NM_152550.2	SH3 domain containing ring finger 2 (SH3RF2)
M160	3.89	2.24	NM_174941.3	scavenger receptor cysteine-rich type 1 protein M160 (M160)
AZIN1	3.78	2.24	NM_015878.4	antizyme inhibitor 1 (AZIN1)
NNT	3.74	2.24	NM_012343.3	nicotinamide nucleotide transhydrogenase (NNT)
WDFY1	3.48	2.24	NM_020830.3	WD repeat and FYVE domain containing 1 (WDFY1)
SLC44A1	3.39	2.24	NM_080546.3	solute carrier family 44
FBXO31	4.26	2.23	NM_024735.2	F-box protein 31 (FBXO31)
MASTL	4.17	2.23	NM_032844.1	microtubule associated serine/threonine kinase-like (MASTL)
TXNL1	3.96	2.23	NM_004786.1	thioredoxin-like 1 (TXNL1)
TIMM23	3.88	2.23	NM_006327.2	translocase of inner mitochondrial membrane 23 homolog (yeast) (TIMM23)
LOC644363	3.74	2.23	XR_016912.2	PREDICTED: misc_RNA (LOC644363)

GTF3C6	3.65	2.23	NM_138408.2	general transcription factor IIIC
TGIF1	3.62	2.23	NM_170695.2	TGFB-induced factor homeobox 1 (TGIF1)
DRAM1	3.56	2.23	NM_018370.2	DNA-damage regulated autophagy modulator 1 (DRAM1)
DUSP2	3.76	2.22	NM_004418.2	dual specificity phosphatase 2 (DUSP2)
OSBP2	3.74	2.22	NM_030758.3	oxysterol binding protein 2 (OSBP2)
MRLC2	2.88	2.22	NM_033546.2	myosin regulatory light chain MRLC2 (MRLC2)
AKIRIN1	4.26	2.21	NM_024595.1	akirin 1 (AKIRIN1)
TGFB1I1	4.08	2.21	NM_015927.3	transforming growth factor beta 1 induced transcript 1 (TGFB1I1)
PEPD	3.81	2.21	NM_000285.2	peptidase D (PEPD)
RAB8A	3.54	2.21	NM_005370.4	RAB8A
LIMK1	4.19	2.2	NM_016735.1	LIM domain kinase 1 (LIMK1)
MLL5	4.14	2.2	NM_018682.3	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog
CCNG2	3.86	2.2	NM_004354.1	cyclin G2 (CCNG2)
ARL1	4.12	2.19	NM_001177.3	ADP-ribosylation factor-like 1 (ARL1)
SBF1	4	2.19	NM_002972.1	SET binding factor 1 (SBF1)
VPS24	3.81	2.19	NM_001005753.1	vacuolar protein sorting 24 homolog (S. cerevisiae) (VPS24)
MAP7	3.74	2.19	NM_003980.3	microtubule-associated protein 7 (MAP7)
DCK	3.66	2.19	NM_000788.1	deoxycytidine kinase (DCK)
LEPROTL1	3.65	2.19	NM_015344.1	leptin receptor overlapping transcript-like 1 (LEPROTL1)
WAC	3.47	2.19	NM_016628.2	WW domain containing adaptor with coiled-coil (WAC)
GLTP	3.44	2.19	NM_016433.3	glycolipid transfer protein (GLTP)
SSU72	2.89	2.19	NM_014188.2	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae) (SSU72)
COG5	4.26	2.18	NM_006348.2	component of oligomeric golgi complex 5 (COG5)
PRKAG2	4.21	2.18	NM_024429.1	protein kinase
RNF14	3.88	2.18	NM_183400.1	ring finger protein 14 (RNF14)
SLC35A4	3.59	2.18	NM_080670.2	solute carrier family 35
ATP6V1D	3.14	2.18	NM_015994.2	ATPase
TIMM23	3.12	2.18	NM_006327.2	translocase of inner mitochondrial membrane 23 homolog (yeast) (TIMM23)
MAT2A	2.81	2.18	NM_005911.4	methionine adenosyltransferase II
TMX3	3.94	2.17	NM_019022.3	thioredoxin-related transmembrane protein 3 (TMX3)
DYRK2	3.92	2.17	NM_003583.2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2)
IFNAR1	3.81	2.17	NM_000629.2	interferon (alpha
PKIA	3.81	2.17	NM_181839.1	protein kinase (cAMP-dependent
ARID5B	3.79	2.17	NM_032199.1	AT rich interactive domain 5B (MRF1-like) (ARID5B)
SLAIN1	3.79	2.17	NM_001040153.2	SLAIN motif family
TCEAL1	3.79	2.17	NM_001006639.1	transcription elongation factor A (SII)-like 1 (TCEAL1)
SRPRB	3.77	2.17	NM_021203.2	signal recognition particle receptor
FAM117B	3.52	2.17	NM_173511.2	family with sequence similarity 117
F3	3.76	2.16	NM_001993.2	coagulation factor III (thromboplastin
FAM102B	3.5	2.16	NM_001010883.1	family with sequence similarity 102
SLC7A1	3.5	2.16	NM_003045.3	solute carrier family 7 (cationic amino acid transporter
TNFRSF12A	3.5	2.16	NM_016639.1	tumor necrosis factor receptor superfamily
LOC100131787	3.49	2.16	XR_039693.1	PREDICTED: misc_RNA (LOC100131787)
PEX11B	3.42	2.16	NM_003846.1	peroxisomal biogenesis factor 11 beta (PEX11B)
PAPOLA	3.03	2.16	NM_032632.3	poly(A) polymerase alpha (PAPOLA)
TM2D2	4	2.14	NM_078473.2	TM2 domain containing 2 (TM2D2)
FYCO1	3.92	2.14	NM_024513.1	FYVE and coiled-coil domain containing 1 (FYCO1)
PKIA	3.91	2.14	NM_006823.2	protein kinase (cAMP-dependent
DCTD	3.43	2.14	NM_001921.2	dCMP deaminase (DCTD)

TSEN34	3.42	2.14	NM_001077446.1	tRNA splicing endonuclease 34 homolog (S. cerevisiae) (TSEN34)
CDKN2C	3.3	2.14	NM_078626.2	cyclin-dependent kinase inhibitor 2C (p18
SMS	3.01	2.14	NM_004595.2	spermine synthase (SMS)
PLOD2	4.12	2.13	NM_182943.2	procollagen-lysine
MAFG	3.84	2.13	NM_032711.2	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) (MAFG)
NMB	3.69	2.13	NM_021077.3	neuromedin B (NMB)
PTEN	3.65	2.13	NM_000314.4	phosphatase and tensin homolog (PTEN)
LOC730990	3.55	2.13	XM_001722060.1	PREDICTED: hypothetical LOC730990 (LOC730990)
IMPDH1	3.4	2.13	NM_000883.2	IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1)
NSMCE1	3.39	2.13	NM_145080.3	non-SMC element 1 homolog (S. cerevisiae) (NSMCE1)
LOC399959	3.93	2.12	NR_024430.1	hypothetical LOC399959 (LOC399959)
FAM54A	3.88	2.12	NM_001099286.1	family with sequence similarity 54
RTCD1	3.75	2.12	NM_003729.2	RNA terminal phosphate cyclase domain 1 (RTCD1)
RARS2	3.73	2.12	NM_020320.2	arginyl-tRNA synthetase 2
ATF4	3.5	2.12	NM_182810.1	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4)
CDK6	3.34	2.12	NM_001259.5	cyclin-dependent kinase 6 (CDK6)
BSCL2	3.33	2.12	NM_032667.4	Bernardinelli-Seip congenital lipodystrophy 2 (seipin) (BSCL2)
TBL1X	3.3	2.12	NM_005647.2	transducin (beta)-like 1X-linked (TBL1X)
RBM22	3.15	2.12	NM_018047.1	RNA binding motif protein 22 (RBM22)
JMJD8	3.06	2.12	NM_001005920.2	jumonji domain containing 8 (JMJD8)
EIF4G2	2.63	2.12	NM_001418.3	eukaryotic translation initiation factor 4 gamma
SERTAD2	3.45	2.11	NM_014755.1	SERTA domain containing 2 (SERTAD2)
CTBP1	3.44	2.11	NM_001012614.1	C-terminal binding protein 1 (CTBP1)
TRAPPC1	3.33	2.11	NM_021210.3	trafficking protein particle complex 1 (TRAPPC1)
MCM7	3.11	2.11	NM_182776.1	minichromosome maintenance complex component 7 (MCM7)
CRY2	4.17	2.1	NM_021117.2	cryptochrome 2 (photolyase-like) (CRY2)
DPP8	3.75	2.1	NM_130434.3	dipeptidyl-peptidase 8 (DPP8)
ZFYVE26	3.75	2.1	NM_015346.2	zinc finger
TCEA1	3.67	2.1	NM_201437.1	transcription elongation factor A (SII)
RNF149	3.65	2.1	NM_173647.2	ring finger protein 149 (RNF149)
SMAP2	3.58	2.1	NM_022733.1	small ArfGAP2 (SMAP2)
BMF	3.5	2.1	NM_033503.3	Bcl2 modifying factor (BMF)
WAC	3.45	2.1	NM_100486.1	WW domain containing adaptor with coiled-coil (WAC)
CMPK1	3.37	2.1	NM_016308.1	cytidine monophosphate (UMP-CMP) kinase 1
ATF4	2.37	2.1	NM_001675.2	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4)
URG4	4	2.09	NM_001077664.1	up-regulated gene 4 (URG4)
MPZL1	3.92	2.09	NM_024569.3	myelin protein zero-like 1 (MPZL1)
SYNC1	3.8	2.09	NM_030786.1	syncoilin
HINT3	3.27	2.09	NM_138571.4	histidine triad nucleotide binding protein 3 (HINT3)
MYD88	3.89	2.08	NM_002468.3	myeloid differentiation primary response gene (88) (MYD88)
ARL6IP1	3.86	2.08	NM_015161.1	ADP-ribosylation factor-like 6 interacting protein 1 (ARL6IP1)
PLIN2	3.86	2.08	NM_001122.2	perilipin 2 (PLIN2)
ATMIN	3.82	2.08	NM_015251.2	ATM interactor (ATMIN)
FAM18B	3.72	2.08	NM_016078.4	family with sequence similarity 18
EIF5	3.53	2.08	NM_001969.3	eukaryotic translation initiation factor 5 (EIF5)
TSPAN3	3.36	2.08	NM_005724.4	tetraspanin 3 (TSPAN3)
QDPR	3.23	2.08	NM_000320.1	quinoid dihydropteridine reductase (QDPR)
ZFP91	3	2.08	NM_053023.3	zinc finger protein 91 homolog (mouse) (ZFP91)
ANKFY1	3.72	2.07	NM_016376.3	ankyrin repeat and FYVE domain containing 1 (ANKFY1)

BTBD7	3.66	2.07	NM_001002860.2	BTB (POZ) domain containing 7 (BTBD7)
TOPBP1	3.23	2.07	NM_007027.2	topoisomerase (DNA) II binding protein 1 (TOPBP1)
LSM1	2.73	2.07	NM_014462.1	LSM1 homolog
COL4A2	4.09	2.06	NM_001846.2	collagen
SPTY2D1	3.9	2.06	NM_194285.2	SPT2
DEDD	3.82	2.06	NM_001039712.1	death effector domain containing (DEDD)
TMEM170B	3.72	2.06	NM_001100829.1	transmembrane protein 170B (TMEM170B)
LATS2	3.69	2.06	NM_014572.2	LATS
F3	3.64	2.06	NM_001993.2	coagulation factor III (thromboplastin
ST6GALNAC6	3.6	2.06	NM_013443.3	ST6 (alpha-N-acetyl-neuraminyl-2
LOC100130775	3.57	2.06	XR_042325.1	PREDICTED: misc_RNA (LOC100130775)
MPP5	3.57	2.06	NM_022474.2	membrane protein
MFF	3.53	2.06	NM_020194.4	mitochondrial fission factor (MFF)
ATG16L1	3.33	2.06	NM_017974.3	ATG16 autophagy related 16-like 1 (S. cerevisiae) (ATG16L1)
SNX17	3.24	2.06	NM_014748.2	sorting nexin 17 (SNX17)
NETO2	3.19	2.06	NM_018092.3	neuropilin (NRP) and tolloid (TLL)-like 2 (NETO2)
AP1M1	3.11	2.06	NM_032493.2	adaptor-related protein complex 1
TMEM41A	4.06	2.05	NM_080652.2	transmembrane protein 41A (TMEM41A)
LOC100130008	4.02	2.05	XM_001724677.1	PREDICTED: similar to hCG2024106
FAIM3	3.99	2.05	NM_005449.3	Fas apoptotic inhibitory molecule 3 (FAIM3)
VAMP2	3.9	2.05	NM_014232.1	vesicle-associated membrane protein 2 (synaptobrevin 2) (VAMP2)
ST6GALNAC4	3.35	2.05	NM_175039.3	ST6 (alpha-N-acetyl-neuraminyl-2
JMJD8	3	2.05	NM_001005920.2	jumonji domain containing 8 (JMJD8)
C15orf29	3.77	2.04	NM_024713.1	chromosome 15 open reading frame 29 (C15orf29)
NAGK	3.72	2.04	NM_017567.2	N-acetylglucosamine kinase (NAGK)
ARHGAP12	3.66	2.04	NM_018287.5	Rho GTPase activating protein 12 (ARHGAP12)
LOC646993	3.59	2.04	XM_001717725.1	PREDICTED: similar to high-mobility group box 3 (LOC646993)
SH3PXD2A	3.5	2.04	NM_014631.2	SH3 and PX domains 2A (SH3PXD2A)
WDR59	3.42	2.04	NM_030581.3	WD repeat domain 59 (WDR59)
LOC100130070	2.68	2.04	XM_001723889.1	PREDICTED: similar to metallopanstimulin (LOC100130070)
CXCR4	3.93	2.03	NM_003467.2	chemokine (C-X-C motif) receptor 4 (CXCR4)
RGMB	3.71	2.03	NM_001012761.1	RGM domain family
MAFG	3.65	2.03	NM_002359.2	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) (MAFG)
RCOR3	3.55	2.03	NM_018254.2	REST corepressor 3 (RCOR3)
TANC1	3.55	2.03	NM_033394.1	tetratricopeptide repeat
PPP2CB	3.52	2.03	NM_004156.2	protein phosphatase 2 (formerly 2A)
CPNE1	3.46	2.03	NM_152931.1	copine I (CPNE1)
CA12	3.41	2.03	NM_001218.3	carbonic anhydrase XII (CA12)
ACVR1B	3.66	2.02	NM_004302.3	activin A receptor
DICER1	3.65	2.02	NM_030621.2	Dicer1
TMEM9	3.45	2.02	NM_016456.2	transmembrane protein 9 (TMEM9)
LUM	3.44	2.02	NM_002345.3	lumican (LUM)
C19orf22	3.35	2.02	NM_138774.2	chromosome 19 open reading frame 22 (C19orf22)
ZNF211	3.89	2.01	NM_006385.2	zinc finger protein 211 (ZNF211)
YWHAQ	1.97	2.01	NM_006826.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
TRIM6	3.79	2	NM_058166.3	tripartite motif-containing 6 (TRIM6)
WDR37	3.7	2	NM_014023.3	WD repeat domain 37 (WDR37)
LOC728115	3.5	2	XR_038319.1	PREDICTED: misc_RNA (LOC728115)
SIX4	3.42	2	NM_017420.3	SIX homeobox 4 (SIX4)

PRNP	3.28	2	NM_001080121.1	prion protein (PRNP)
FAM3A	3.17	2	NM_021806.1	family with sequence similarity 3
RAB23	3.12	2	NM_016277.3	RAB23
PLEKHA2	2.99	2	NM_021623.1	pleckstrin homology domain containing
MARCKS	2.62	2	NM_002356.5	myristoylated alanine-rich protein kinase C substrate (MARCKS)
MAPRE3	3.81	1.99	NM_012326.2	microtubule-associated protein
C2orf42	3.48	1.99	NM_017880.1	chromosome 2 open reading frame 42 (C2orf42)
ZFYVE19	3.45	1.99	NM_001077268.1	zinc finger
BRI3BP	3.43	1.99	XM_941876.1	PREDICTED: BRI3 binding protein (BRI3BP)
PPCS	3.33	1.99	NM_001077447.1	phosphopantothenoylcysteine synthetase (PPCS)
URG4	3.69	1.98	NM_017920.3	up-regulated gene 4 (URG4)
G6PD	3.47	1.98	NM_000402.3	glucose-6-phosphate dehydrogenase (G6PD)
RAB6A	3.38	1.98	NM_002869.4	RAB6A
HSD17B11	3.36	1.98	NM_016245.2	hydroxysteroid (17-beta) dehydrogenase 11 (HSD17B11)
CISD2	3.34	1.98	NM_001008388.1	CDGSH iron sulfur domain 2 (CISD2)
ARL8B	3.03	1.98	NM_018184.2	ADP-ribosylation factor-like 8B (ARL8B)
CHES1	3.03	1.98	NM_005197.2	checkpoint suppressor 1 (CHES1)
PRMT6	2.62	1.98	NM_018137.1	protein arginine methyltransferase 6 (PRMT6)
TNFRSF10D	3.8	1.97	NM_003840.3	tumor necrosis factor receptor superfamily
DNAJC27	3.72	1.97	NM_016544.1	DnaJ (Hsp40) homolog
ITGA11	3.56	1.97	NM_001004439.1	integrin
USP21	3.52	1.97	NM_012475.4	ubiquitin specific peptidase 21 (USP21)
CCNE1	3.37	1.97	NM_001238.1	cyclin E1 (CCNE1)
MOCOS	3.37	1.97	NM_017947.1	molybdenum cofactor sulfurase (MOCOS)
DOCK10	3.34	1.97	NM_014689.2	dedicator of cytokinesis 10 (DOCK10)
BTG3	3.31	1.97	NM_006806.3	BTG family
GPT2	3.3	1.97	NM_133443.1	glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2)
PHLDA1	3.26	1.97	NM_007350.3	pleckstrin homology-like domain
HNRPDL	3.21	1.97	NM_031372.1	heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)
ZDHHC6	3.02	1.97	NM_022494.1	zinc finger
KIAA1797	3.5	1.96	NM_017794.2	KIAA1797 (KIAA1797)
ATPAF1	3.49	1.96	NM_001042546.1	ATP synthase mitochondrial F1 complex assembly factor 1 (ATPAF1)
MKRN2	3.27	1.96	NM_014160.3	makorin ring finger protein 2 (MKRN2)
CNIH	3.24	1.96	NM_005776.2	cornichon homolog (Drosophila) (CNIH)
UBE2J1	3.22	1.96	NM_016021.2	ubiquitin-conjugating enzyme E2
NUDT21	3.1	1.96	NM_007006.2	nudix (nucleoside diphosphate linked moiety X)-type motif 21 (NUDT21)
ADAM15	2.98	1.96	NM_207195.1	ADAM metallopeptidase domain 15 (ADAM15)
B4GALT5	2.98	1.96	NM_004776.2	UDP-Gal:betaGlcNAc beta 1
FAM189B	2.98	1.96	NM_006589.2	family with sequence similarity 189
FGF2	2.95	1.96	NM_002006.3	fibroblast growth factor 2 (basic) (FGF2)
UBAP1	2.84	1.96	NM_016525.3	ubiquitin associated protein 1 (UBAP1)
DCBLD2	2.83	1.96	NM_080927.3	discoidin
TBC1D20	3.68	1.95	NM_144628.1	TBC1 domain family
SLC40A1	3.58	1.95	NM_014585.3	solute carrier family 40 (iron-regulated transporter)
HABP4	3.51	1.95	NM_014282.1	hyaluronan binding protein 4 (HABP4)
MRPL10	3.33	1.95	NM_145255.2	mitochondrial ribosomal protein L10 (MRPL10)
FEZ2	3.28	1.95	NM_005102.2	fasciculation and elongation protein zeta 2 (zygin II) (FEZ2)
VPS24	3.23	1.95	NM_001005753.1	vacuolar protein sorting 24 homolog (S. cerevisiae) (VPS24)
LYN	3.12	1.95	NM_002350.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)

LOC645944	3.78	1.94	XR_015802.1	PREDICTED: misc_RNA (LOC645944)
ACD	3.53	1.94	NM_022914.2	adrenocortical dysplasia homolog (mouse) (ACD)
ZFP1	3.49	1.94	NM_153688.2	zinc finger protein 1 homolog (mouse) (ZFP1)
ZNF532	3.42	1.94	NM_018181.4	zinc finger protein 532 (ZNF532)
CNOT4	3.41	1.94	NM_013316.2	CCR4-NOT transcription complex
RAB6A	3.26	1.94	NM_198896.1	RAB6A
TCEB1	3.05	1.94	NM_005648.2	transcription elongation factor B (SIII)
NDUFA9	2.91	1.94	NM_005002.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
BNIP1	3.69	1.93	NM_013979.1	BCL2/adenovirus E1B 19kDa interacting protein 1 (BNIP1)
SIRPA	3.54	1.93	NM_001040023.1	signal-regulatory protein alpha (SIRPA)
KLHL5	3.48	1.93	NM_001007075.1	kelch-like 5 (Drosophila) (KLHL5)
PDGFD	3.39	1.93	NM_033135.3	platelet derived growth factor D (PDGFD)
CD163L1	3.38	1.93	NM_174941.4	CD163 molecule-like 1 (CD163L1)
LOC100131572	3.26	1.93	XM_001725183.1	PREDICTED: similar to hCG1783679 (LOC100131572)
ST6GALNAC4	2.98	1.93	NM_175039.3	ST6 (alpha-N-acetyl-neuraminyl-2
PRMT6	2.71	1.93	NM_018137.1	protein arginine methyltransferase 6 (PRMT6)
TBPL1	2.66	1.93	NM_004865.2	TBP-like 1 (TBPL1)
LAPTM4B	2.47	1.93	NM_018407.4	lysosomal protein transmembrane 4 beta (LAPTM4B)
LOC389641	3.43	1.92	XM_944097.2	PREDICTED: hypothetical gene supported by AK124295 (LOC389641)
ZNF800	3.36	1.92	NM_176814.3	zinc finger protein 800 (ZNF800)
SEC22C	3.25	1.92	NM_004206.2	SEC22 vesicle trafficking protein homolog C (S. cerevisiae) (SEC22C)
NIPA1	3.2	1.92	NM_144599.3	non imprinted in Prader-Willi/Angelman syndrome 1 (NIPA1)
ZC3H12C	3.12	1.92	NM_033390.1	zinc finger CCCH-type containing 12C (ZC3H12C)
LTV1	3.07	1.92	NM_032860.3	LTV1 homolog (S. cerevisiae) (LTV1)
NR4A2	3.07	1.92	NM_006186.2	nuclear receptor subfamily 4
DLEU1	3.04	1.92	NR_002605.1	deleted in lymphocytic leukemia 1 (non-protein coding) (DLEU1)
RHOB	2.88	1.92	NM_004040.2	ras homolog gene family
CST3	2.79	1.92	NM_000099.2	cystatin C (CST3)
SEC22A	3.48	1.91	NM_012430.3	SEC22 vesicle trafficking protein homolog A (S. cerevisiae) (SEC22A)
ZNF280B	3.48	1.91	NM_080764.2	zinc finger protein 280B (ZNF280B)
TRIP10	3.42	1.91	NM_004240.2	thyroid hormone receptor interactor 10 (TRIP10)
ZNHIT6	3.38	1.91	NM_017953.2	zinc finger
GNA11	3.36	1.91	NM_002067.1	guanine nucleotide binding protein (G protein)
UFSP2	3.31	1.91	NM_018359.1	UFM1-specific peptidase 2 (UFSP2)
UBL3	3.12	1.91	NM_007106.2	ubiquitin-like 3 (UBL3)
AMMECR1	2.81	1.91	NM_015365.2	Alport syndrome
HIF1A	2.63	1.91	NM_181054.1	hypoxia-inducible factor 1
BHLHB2	2.32	1.91	NM_003670.1	basic helix-loop-helix domain containing
SLC35B3	3.57	1.9	NM_015948.2	solute carrier family 35
LOC729580	3.56	1.9	XM_001130700.1	PREDICTED: hypothetical LOC729580 (LOC729580)
PDZD8	3.5	1.9	NM_173791.3	PDZ domain containing 8 (PDZD8)
NELL2	3.44	1.9	NM_006159.1	NEL-like 2 (chicken) (NELL2)
C3orf38	3.33	1.9	NM_173824.2	chromosome 3 open reading frame 38 (C3orf38)
CSNK1A1	3.3	1.9	NM_001025105.1	casein kinase 1
ACVR1	3.08	1.9	NM_001105.2	activin A receptor
USP8	2.96	1.9	NM_005154.2	ubiquitin specific peptidase 8 (USP8)
SIK1	2.87	1.9	NM_173354.3	salt-inducible kinase 1 (SIK1)
INO80	3.61	1.89	NM_017553.1	INO80 homolog (S. cerevisiae) (INO80)
ITGA11	3.58	1.89	NM_012211.3	integrin

FAM43A	3.53	1.89	NM_153690.4	family with sequence similarity 43
ASAP1	3.27	1.89	NM_018482.2	ArfGAP with SH3 domain
PHF12	3.24	1.89	NM_001033561.1	PHD finger protein 12 (PHF12)
TOMM70A	3.06	1.89	NM_014820.3	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae) (TOMM70A)
NUFIP2	3.01	1.89	NM_020772.1	nuclear fragile X mental retardation protein interacting protein 2 (NUFIP2)
C8orf76	2.92	1.89	NM_032847.1	chromosome 8 open reading frame 76 (C8orf76)
SHOC2	2.92	1.89	NM_007373.2	soc-2 suppressor of clear homolog (C. elegans) (SHOC2)
ADSS	2.71	1.89	NM_001126.2	adenylosuccinate synthase (ADSS)
FLJ42627	3.51	1.88	NR_024492.1	hypothetical LOC645644 (FLJ42627)
ITGB4	3.43	1.88	NM_001005619.1	integrin
C18orf21	3.23	1.88	NM_031446.3	chromosome 18 open reading frame 21 (C18orf21)
BICD2	3.12	1.88	NM_001003800.1	bicaudal D homolog 2 (Drosophila) (BICD2)
AKTIP	3.11	1.88	NM_001012398.1	AKT interacting protein (AKTIP)
PPCS	3.07	1.88	NM_024664.2	phosphopantothenoylcysteine synthetase (PPCS)
MRPL43	3.06	1.88	NM_032112.2	mitochondrial ribosomal protein L43 (MRPL43)
LOC642755	2.64	1.88	XM_926382.2	PREDICTED: similar to DEXI
EIF3F	2.21	1.88	NM_003754.2	eukaryotic translation initiation factor 3
CASP2	3.55	1.87	NM_032983.2	caspase 2
PANX2	3.34	1.87	NM_052839.2	pannexin 2 (PANX2)
LOC100134108	3.09	1.87	XM_001713975.1	PREDICTED: similar to succinate dehydrogenase complex
ITSN1	2.98	1.87	NM_001001132.1	intersectin 1 (SH3 domain protein) (ITSN1)
PCMTD1	2.95	1.87	NM_052937.1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 (PCMTD1)
TIMM23	2.93	1.87	NM_006327.2	translocase of inner mitochondrial membrane 23 homolog (yeast) (TIMM23)
PTP4A1	2.89	1.87	NM_003463.3	protein tyrosine phosphatase type IVA
ARF5	2.64	1.87	NM_001662.2	ADP-ribosylation factor 5 (ARF5)
ALDH3A2	2.54	1.87	NM_000382.2	aldehyde dehydrogenase 3 family
MGST1	2.31	1.87	NM_145792.1	microsomal glutathione S-transferase 1 (MGST1)
MCART1	3.47	1.86	NM_033412.2	mitochondrial carrier triple repeat 1 (MCART1)
RNF216	3.37	1.86	NM_207111.2	ring finger protein 216 (RNF216)
PURA	3.16	1.86	NM_005859.3	purine-rich element binding protein A (PURA)
DBNDD1	3.11	1.86	NM_001042610.1	dysbindin (dystrobrevin binding protein 1) domain containing 1 (DBNDD1)
TBP	3.02	1.86	NM_003194.3	TATA box binding protein (TBP)
FAM45A	3.01	1.86	NM_207009.2	family with sequence similarity 45
LCMT1	2.95	1.86	NM_001032391.1	leucine carboxyl methyltransferase 1 (LCMT1)
B4GALT3	2.87	1.86	NM_003779.2	UDP-Gal:betaGlcNAc beta 1
SLC35B1	2.59	1.86	NM_005827.1	solute carrier family 35
NFIB	2.37	1.86	NM_005596.2	nuclear factor I/B (NFIB)
MMD	2.3	1.86	NM_012329.2	monocyte to macrophage differentiation-associated (MMD)
NHLRC3	3.42	1.85	NM_001017370.1	NHL repeat containing 3 (NHLRC3)
PIGK	3.35	1.85	NM_005482.2	phosphatidylinositol glycan anchor biosynthesis
AP4B1	3.03	1.85	NM_006594.1	adaptor-related protein complex 4
SLC25A10	3.03	1.85	NM_012140.3	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter)
AURKB	2.79	1.85	NM_004217.2	aurora kinase B (AURKB)
C12orf44	2.79	1.85	NM_001098673.1	chromosome 12 open reading frame 44 (C12orf44)
RPS6KA2	2.69	1.85	NM_001006932.1	ribosomal protein S6 kinase
SMAD5	2.68	1.85	NM_005903.5	SMAD family member 5 (SMAD5)
CDKN2B	2.49	1.85	NM_078487.2	cyclin-dependent kinase inhibitor 2B (p15
LAPTM4B	2.26	1.85	NM_018407.4	lysosomal protein transmembrane 4 beta (LAPTM4B)
CYB5R3	2.13	1.85	NM_007326.2	cytochrome b5 reductase 3 (CYB5R3)

MIR98	3.54	1.84	NR_029513.1	microRNA 98 (MIR98)
MAPK1	3.51	1.84	NM_002745.4	mitogen-activated protein kinase 1 (MAPK1)
UVRAG	3.32	1.84	NM_003369.3	UV radiation resistance associated gene (UVRAG)
LOC728457	3.21	1.84	XR_037027.1	PREDICTED: misc_RNA (LOC728457)
MYST3	3.18	1.84	NM_006766.2	MYST histone acetyltransferase (monocytic leukemia) 3 (MYST3)
ARHGAP1	3.07	1.84	NM_004308.2	Rho GTPase activating protein 1 (ARHGAP1)
PPFIA1	2.9	1.84	NM_003626.2	protein tyrosine phosphatase
LARP4	2.89	1.84	NM_052879.3	La ribonucleoprotein domain family
NFATC2IP	2.84	1.84	NM_032815.3	nuclear factor of activated T-cells
MEX3C	2.81	1.84	NM_016626.3	mex-3 homolog C (C. elegans) (MEX3C)
TSG101	2.81	1.84	NM_006292.2	tumor susceptibility gene 101 (TSG101)
ITM2B	2.76	1.84	NM_021999.2	integral membrane protein 2B (ITM2B)
TAOK1	2.73	1.84	NM_020791.1	TAO kinase 1 (TAOK1)
LBH	2.41	1.84	NM_030915.1	PREDICTED: hypothetical protein DKFZp566J091 (LBH)
PIGY	2.34	1.84	NM_001042616.1	phosphatidylinositol glycan anchor biosynthesis
KLHL21	3.37	1.83	NM_014851.2	kelch-like 21 (Drosophila) (KLHL21)
LRRC8D	3.11	1.83	NM_018103.3	leucine rich repeat containing 8 family
FBXL18	3.01	1.83	NM_024963.4	F-box and leucine-rich repeat protein 18 (FBXL18)
NPEPPS	2.92	1.83	NM_006310.2	aminopeptidase puromycin sensitive (NPEPPS)
RAB24	2.89	1.83	NM_001031677.2	RAB24
ARMC10	2.82	1.83	NM_031905.2	armadillo repeat containing 10 (ARMC10)
CCNB1	2.76	1.83	NM_031966.2	cyclin B1 (CCNB1)
PLSCR3	2.67	1.83	NM_020360.2	phospholipid scramblase 3 (PLSCR3)
DNAJC30	3.47	1.82	NM_032317.2	DnaJ (Hsp40) homolog
MASTL	3.43	1.82	NM_032844.1	microtubule associated serine/threonine kinase-like (MASTL)
SNX12	3.3	1.82	NM_013346.2	sorting nexin 12 (SNX12)
LOC100128585	3.25	1.82	XR_039418.1	PREDICTED: misc_RNA (LOC100128585)
SLC38A6	3.25	1.82	NM_153811.1	solute carrier family 38
TES	3.2	1.82	NM_152829.1	testis derived transcript (3 LIM domains) (TES)
AKAP11	3.18	1.82	NM_016248.2	A kinase (PRKA) anchor protein 11 (AKAP11)
C2orf29	2.81	1.82	NM_017546.3	chromosome 2 open reading frame 29 (C2orf29)
DAB2	2.74	1.82	NM_001343.2	disabled homolog 2
UCHL3	2.71	1.82	NM_006002.3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3)
PPP6C	2.43	1.82	NM_002721.3	protein phosphatase 6
AIDA	1.95	1.82	NM_022831.2	axin interactor
ATP2C1	3.34	1.81	NM_014382.2	ATPase
SLC35C2	3.29	1.81	NM_173073.2	solute carrier family 35
MOBK1B	3.23	1.81	NM_018221.1	MOB1
EIF2AK1	3.17	1.81	NM_001134335.1	eukaryotic translation initiation factor 2-alpha kinase 1 (EIF2AK1)
AFG3L1	3.12	1.81	NM_001031805.1	AFG3 ATPase family gene 3-like 1 (S. cerevisiae) (AFG3L1)
DPH5	3.1	1.81	NM_001077394.1	DPH5 homolog (S. cerevisiae) (DPH5)
ZFYVE21	3.09	1.81	NM_024071.2	zinc finger
HES1	3.04	1.81	NM_005524.2	hairy and enhancer of split 1
TRIM4	3.02	1.81	NM_033091.1	tripartite motif-containing 4 (TRIM4)
ANKRD13C	3.01	1.81	NM_030816.2	ankyrin repeat domain 13C (ANKRD13C)
LOC652864	2.97	1.81	XM_942571.1	PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim23 (LOC652864)
FAM50B	2.95	1.81	NM_012135.1	family with sequence similarity 50
GRB10	2.73	1.81	NM_001001555.1	growth factor receptor-bound protein 10 (GRB10)
ITPA	2.69	1.81	NM_033453.2	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) (ITPA)

ACTL6A	2.66	1.81	NM_177989.2	actin-like 6A (ACTL6A)
VPS26A	2.53	1.81	NM_001035260.1	vacuolar protein sorting 26 homolog A (S. pombe) (VPS26A)
RFX5	2.46	1.81	NM_001025603.1	regulatory factor X
STAG3	3.4	1.8	NM_012447.2	stromal antigen 3 (STAG3)
RSC1A1	3.3	1.8	NM_006511.1	regulatory solute carrier protein
C19orf40	3.24	1.8	NM_152266.1	chromosome 19 open reading frame 40 (C19orf40)
DPH5	3.12	1.8	NM_001077395.1	DPH5 homolog (S. cerevisiae) (DPH5)
CUTL1	3.11	1.8	NM_181552.1	cut-like 1
UNKL	3.11	1.8	NM_023076.3	unkempt homolog (Drosophila)-like (UNKL)
TUSC3	2.81	1.8	NM_006765.2	tumor suppressor candidate 3 (TUSC3)
PCID2	2.37	1.8	NM_018386.1	PCI domain containing 2 (PCID2)
EPC2	3.3	1.79	NM_015630.2	enhancer of polycomb homolog 2 (Drosophila) (EPC2)
FAM89A	3.28	1.79	NM_198552.1	family with sequence similarity 89
ABCB9	3.26	1.79	NM_019624.2	ATP-binding cassette
NPHP3	3.2	1.79	NM_153240.3	nephronophthisis 3 (adolescent) (NPHP3)
PLAG1	3.18	1.79	NM_002655.1	pleiomorphic adenoma gene 1 (PLAG1)
SLC39A6	3.16	1.79	NM_012319.2	solute carrier family 39 (zinc transporter)
KCTD10	3.07	1.79	NM_031954.3	potassium channel tetramerisation domain containing 10 (KCTD10)
HIF1AN	3.05	1.79	NM_017902.2	hypoxia inducible factor 1
FAM119A	3.03	1.79	NM_145280.3	family with sequence similarity 119
ATP6V0D1	2.82	1.79	NM_004691.4	ATPase
LOC645381	2.77	1.79	XR_038557.1	PREDICTED: misc_RNA (LOC645381)
LOC728755	2.74	1.79	XM_001128377.2	PREDICTED: similar to hCG1984907 (LOC728755)
BTF3L4	2.66	1.79	NM_152265.2	basic transcription factor 3-like 4 (BTF3L4)
C2orf28	2.49	1.79	NM_080592.2	chromosome 2 open reading frame 28 (C2orf28)
STK4	2.4	1.79	NM_006282.2	serine/threonine kinase 4 (STK4)
LAPTM4A	3.12	1.78	NM_014713.3	lysosomal-associated protein transmembrane 4 alpha (LAPTM4A)
C21orf63	2.94	1.78	NM_058187.3	chromosome 21 open reading frame 63 (C21orf63)
DSCR3	2.91	1.78	NM_006052.1	Down syndrome critical region gene 3 (DSCR3)
ITPA	2.86	1.78	NM_033453.2	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) (ITPA)
C5orf13	1.93	1.78	NM_004772.1	chromosome 5 open reading frame 13 (C5orf13)
TSC22D1	1.62	1.78	NM_006022.2	TSC22 domain family
LOC100130255	3.29	1.77	XM_001726456.1	PREDICTED: hypothetical LOC100130255 (LOC100130255)
OSR2	3.19	1.77	XM_001126824.1	PREDICTED: odd-skipped related 2 (Drosophila) (OSR2)
RUNX2	3.16	1.77	NM_001024630.2	runt-related transcription factor 2 (RUNX2)
C7orf43	3.13	1.77	NM_018275.3	chromosome 7 open reading frame 43 (C7orf43)
SRPK1	2.69	1.77	NM_003137.3	SFRS protein kinase 1 (SRPK1)
DUSP22	2.56	1.77	XM_941691.1	dual specificity phosphatase 22 (DUSP22)
CCM2	2.45	1.77	NM_001029835.1	cerebral cavernous malformation 2 (CCM2)
FADS1	2.39	1.77	NM_013402.3	fatty acid desaturase 1 (FADS1)
NME4	2.3	1.77	NM_005009.2	non-metastatic cells 4
CCDC6	1.97	1.77	NM_005436.2	coiled-coil domain containing 6 (CCDC6)
GPX1	1.81	1.77	NM_201397.1	glutathione peroxidase 1 (GPX1)
SLC25A42	3.32	1.76	NM_178526.1	solute carrier family 25
ARL4A	3.23	1.76	NM_001037164.1	ADP-ribosylation factor-like 4A (ARL4A)
LOC644124	3.22	1.76	XR_017531.2	PREDICTED: misc_RNA (LOC644124)
MED9	3.2	1.76	NM_018019.2	mediator complex subunit 9 (MED9)
MRPL30	3.18	1.76	NM_145212.2	mitochondrial ribosomal protein L30 (MRPL30)
SECISBP2L	2.99	1.76	NM_014701.2	SECIS binding protein 2-like (SECISBP2L)

YDJC	2.99	1.76	NM_001017964.1	YdjC homolog (bacterial) (YDJC)
TMEM48	2.94	1.76	NM_018087.3	transmembrane protein 48 (TMEM48)
CAMSAP1	2.84	1.76	NM_015447.1	calmodulin regulated spectrin-associated protein 1 (CAMSAP1)
RFC5	2.69	1.76	NM_007370.3	replication factor C (activator 1) 5
SLC35B2	2.51	1.76	NM_178148.1	solute carrier family 35
MBNL2	2.47	1.76	NM_207304.1	muscleblind-like 2 (Drosophila) (MBNL2)
ZDHHC6	2.47	1.76	NM_022494.1	zinc finger
ZC3H11B	2.22	1.76	XR_041767.1	PREDICTED: misc_RNA (ZC3H11B)
RNF170	3.18	1.75	NM_030954.2	ring finger protein 170 (RNF170)
MEX3D	3.02	1.75	NM_001085363.1	mex-3 homolog D (C. elegans) (MEX3D)
RRP1B	2.91	1.75	NM_015056.2	ribosomal RNA processing 1 homolog B (S. cerevisiae) (RRP1B)
SERPINB1	2.89	1.75	NM_030666.2	serpin peptidase inhibitor
DCAF7	2.87	1.75	NM_005828.3	DDB1 and CUL4 associated factor 7 (DCAF7)
SLC35E1	2.85	1.75	NM_024881.3	solute carrier family 35
CAPZA1	2.76	1.75	NM_006135.1	capping protein (actin filament) muscle Z-line
PIP4K2A	2.63	1.75	NM_005028.4	phosphatidylinositol-5-phosphate 4-kinase
GRPEL2	2.56	1.75	NM_152407.3	GrpE-like 2
SFXN5	3.26	1.74	NM_144579.1	sideroflexin 5 (SFXN5)
WHSC1L1	3.23	1.74	NM_017778.2	Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1)
METTL3	3.11	1.74	NM_019852.3	methyltransferase like 3 (METTL3)
ZBTB4	3.09	1.74	NM_020899.2	zinc finger and BTB domain containing 4 (ZBTB4)
CENPH	3.05	1.74	NM_022909.3	centromere protein H (CENPH)
LCOR	2.92	1.74	NM_032440.2	ligand dependent nuclear receptor corepressor (LCOR)
SESTD1	2.82	1.74	NM_178123.3	SEC14 and spectrin domains 1 (SESTD1)
PARVB	2.8	1.74	NM_013327.3	parvin
GOPC	2.78	1.74	NM_020399.2	golgi associated PDZ and coiled-coil motif containing (GOPC)
NUP205	2.5	1.74	NM_015135.1	nucleoporin 205kDa (NUP205)
RAB40B	2.44	1.74	NM_006822.1	RAB40B
TNRC6A	2.37	1.74	NM_014494.2	trinucleotide repeat containing 6A (TNRC6A)
CHP	2.35	1.74	NM_007236.3	calcium binding protein P22 (CHP)
GNS	2.33	1.74	NM_002076.2	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS)
TMBIM6	2.04	1.74	NM_003217.2	transmembrane BAX inhibitor motif containing 6 (TMBIM6)
SIVA1	1.72	1.74	NM_021709.2	SIVA1
LOC100130008	3.23	1.73	XM_001724677.1	PREDICTED: similar to hCG2024106
FBXL6	3.11	1.73	NM_024555.3	F-box and leucine-rich repeat protein 6 (FBXL6)
FBXW2	3.06	1.73	NM_012164.2	F-box and WD-40 domain protein 2 (FBXW2)
WDR19	2.97	1.73	NM_025132.3	WD repeat domain 19 (WDR19)
PBK	2.82	1.73	NM_018492.2	PDZ binding kinase (PBK)
IFNAR2	2.78	1.73	NM_207585.1	interferon (alpha
C1orf71	2.66	1.73	NM_152609.1	chromosome 1 open reading frame 71 (C1orf71)
SLC16A5	2.58	1.73	NM_004695.2	PREDICTED: solute carrier family 16 (monocarboxylic acid transporters)
EIF2S1	2.57	1.73	NM_004094.4	eukaryotic translation initiation factor 2
C7orf40	2.49	1.73	NR_003697.1	chromosome 7 open reading frame 40 (C7orf40)
KIAA1267	2.48	1.73	NM_015443.2	KIAA1267 (KIAA1267)
TROVE2	2.37	1.73	NM_001042369.1	TROVE domain family
PXMP2	2.28	1.73	NM_018663.1	PREDICTED: peroxisomal membrane protein 2
LOC374395	2.19	1.73	NM_199337.1	similar to RIKEN cDNA 1810059G22 (LOC374395)
RPA2	2	1.73	NM_002946.3	replication protein A2
PNRC2	1.69	1.73	NM_017761.2	proline-rich nuclear receptor coactivator 2 (PNRC2)

AHCTF1	2.96	1.72	NM_015446.3	PREDICTED: AT hook containing transcription factor 1 (AHCTF1)
ELOVL1	2.92	1.72	NM_022821.2	elongation of very long chain fatty acids (FEN1/Elo2
SFMBT1	2.87	1.72	NM_016329.2	Scm-like with four mbt domains 1 (SFMBT1)
TBC1D14	2.62	1.72	NM_020773.1	TBC1 domain family
UNC50	2.32	1.72	NM_014044.4	unc-50 homolog (C. elegans) (UNC50)
BIRC5	2.23	1.72	NM_001168.2	baculoviral IAP repeat-containing 5 (BIRC5)
TSC22D1	1.94	1.72	NM_183422.1	TSC22 domain family
IL8	1.8	1.72	NM_000584.2	interleukin 8 (IL8)
ABTB1	3.23	1.71	NM_172028.1	ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1)
SMAP1	2.92	1.71	NM_021940.2	small ArfGAP 1 (SMAP1)
CUGBP1	2.78	1.71	NM_198700.1	CUG triplet repeat
SMG1	2.71	1.71	NM_015092.3	PI-3-kinase-related kinase SMG-1 (SMG1)
FAM116A	2.67	1.71	XM_001132771.1	PREDICTED: family with sequence similarity 116
ZFP36	2.65	1.71	NM_003407.2	zinc finger protein 36
ZNF252	2.62	1.71	NR_023392.1	zinc finger protein 252 (ZNF252)
TXNDC12	2.34	1.71	NM_015913.2	thioredoxin domain containing 12 (endoplasmic reticulum) (TXNDC12)
ATG3	2.24	1.71	NM_022488.3	ATG3 autophagy related 3 homolog (S. cerevisiae) (ATG3)
PLEKHA1	2.04	1.71	NM_001001974.1	pleckstrin homology domain containing
MLL4	3.01	1.7	NM_014727.1	myeloid/lymphoid or mixed-lineage leukemia 4 (MLL4)
NR1D2	2.95	1.7	XM_001130839.1	PREDICTED: nuclear receptor subfamily 1
PDLIM3	2.95	1.7	NM_014476.1	PDZ and LIM domain 3 (PDLIM3)
SYNJ1	2.94	1.7	NM_203446.1	synaptojanin 1 (SYNJ1)
FAM126B	2.82	1.7	NM_173822.2	family with sequence similarity 126
BMPR2	2.81	1.7	NM_001204.5	bone morphogenetic protein receptor
TRIOBP	2.78	1.7	NM_001039141.1	TRIO and F-actin binding protein (TRIOBP)
C9orf37	2.66	1.7	NM_032937.3	chromosome 9 open reading frame 37 (C9orf37)
LRP8	2.61	1.7	NM_017522.3	low density lipoprotein receptor-related protein 8
PPP4C	2.41	1.7	NM_002720.1	protein phosphatase 4 (formerly X)
CRIPT	2.34	1.7	NM_014171.3	cysteine-rich PDZ-binding protein (CRIPT)
LCMT1	2.12	1.7	NM_016309.2	leucine carboxyl methyltransferase 1 (LCMT1)
OCIAD2	2.04	1.7	NM_001014446.1	OCIA domain containing 2 (OCIAD2)
ADAMTSL5	3.02	1.69	NM_213604.1	ADAMTS-like 5 (ADAMTSL5)
HCCS	2.86	1.69	NM_005333.2	holocytochrome c synthase (cytochrome c heme-lyase) (HCCS)
SFMBT1	2.81	1.69	NM_001005158.1	Scm-like with four mbt domains 1 (SFMBT1)
LOC441481	2.74	1.69	XR_038228.1	PREDICTED: misc_RNA (LOC441481)
POFUT1	2.74	1.69	NM_015352.1	protein O-fucosyltransferase 1 (POFUT1)
HNRNPC	2.63	1.69	NM_001077442.1	heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRNPC)
SDHA	2.6	1.69	NM_004168.1	succinate dehydrogenase complex
PPP4R1	2.32	1.69	NM_005134.2	protein phosphatase 4
FAM46A	2.04	1.69	NM_017633.2	family with sequence similarity 46
PPT2	2.92	1.68	NM_138717.1	palmitoyl-protein thioesterase 2 (PPT2)
PPP1R8	2.9	1.68	NM_138558.1	protein phosphatase 1
C3orf21	2.76	1.68	NM_152531.3	chromosome 3 open reading frame 21 (C3orf21)
FAM135A	2.75	1.68	NM_020819.2	family with sequence similarity 135
PHF11	2.75	1.68	NM_001040443.1	PHD finger protein 11 (PHF11)
TUB	2.69	1.68	NM_177972.1	tubby homolog (mouse) (TUB)
EXT1	2.55	1.68	NM_000127.2	exostoses (multiple) 1 (EXT1)
NOL6	2.53	1.68	NM_139235.3	nucleolar protein family 6 (RNA-associated) (NOL6)
LSM12	2.5	1.68	NM_152344.1	LSM12 homolog (S. cerevisiae) (LSM12)

GORASP2	2.46	1.68	NM_015530.3	golgi reassembly stacking protein 2
PPIC	2.35	1.68	NM_000943.4	peptidylprolyl isomerase C (cyclophilin C) (PPIC)
TMEM69	2.17	1.68	NM_016486.3	transmembrane protein 69 (TMEM69)
LOC651198	2.08	1.68	XM_001715717.1	PREDICTED: similar to hCG2036706 (LOC651198)
KIAA1468	2.96	1.67	NM_020854.3	KIAA1468 (KIAA1468)
GOLGA1	2.85	1.67	NM_002077.2	golgi autoantigen
UBXN6	2.74	1.67	NM_025241.1	UBX domain protein 6 (UBXN6)
CXorf39	2.61	1.67	NM_207318.1	chromosome X open reading frame 39 (CXorf39)
APPBP2	2.58	1.67	NM_006380.2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2)
EEF1B2	2.39	1.67	NM_021121.2	eukaryotic translation elongation factor 1 beta 2 (EEF1B2)
SNHG9	2.28	1.67	NR_003142.2	small nucleolar RNA host gene 9 (non-protein coding) (SNHG9)
C2orf25	1.74	1.67	NM_015702.1	chromosome 2 open reading frame 25 (C2orf25)
ITPR1	2.87	1.66	NM_002222.4	inositol 1
EIF5A2	2.85	1.66	NM_020390.5	eukaryotic translation initiation factor 5A2 (EIF5A2)
ST3GAL5	2.66	1.66	NM_001042437.1	ST3 beta-galactoside alpha-2
VEGFC	2.66	1.66	NM_005429.2	vascular endothelial growth factor C (VEGFC)
HIAT1	2.63	1.66	NM_033055.2	hippocampus abundant transcript 1 (HIAT1)
CYB5R3	2.57	1.66	NM_000398.4	cytochrome b5 reductase 3 (CYB5R3)
FAM35A	2.53	1.66	NM_019054.2	PREDICTED: family with sequence similarity 35
USP8	2.5	1.66	NM_005154.2	ubiquitin specific peptidase 8 (USP8)
BTF3L4	2.46	1.66	NM_152265.1	basic transcription factor 3-like 4 (BTF3L4)
FLJ20489	2.46	1.66	NM_017842.1	hypothetical protein FLJ20489 (FLJ20489)
TMED5	2.45	1.66	NM_016040.3	transmembrane emp24 protein transport domain containing 5 (TMED5)
C16orf91	2.3	1.66	NM_001010878.1	chromosome 16 open reading frame 91 (C16orf91)
FRAG1	2.28	1.66	NM_014489.1	FGF receptor activating protein 1 (FRAG1)
NSF	1.99	1.66	NM_006178.1	PREDICTED: N-ethylmaleimide-sensitive factor (NSF)
MAPRE1	1.77	1.66	NM_012325.1	microtubule-associated protein
HDDC2	1.76	1.66	NM_016063.2	HD domain containing 2 (HDDC2)
SBF2	2.79	1.65	NM_030962.2	SET binding factor 2 (SBF2)
LYPD6	2.66	1.65	NM_194317.2	LY6/PLAUR domain containing 6 (LYPD6)
PHF11	2.64	1.65	NM_001040443.1	PHD finger protein 11 (PHF11)
C19orf48	2.63	1.65	NM_199250.1	chromosome 19 open reading frame 48 (C19orf48)
C8orf38	2.63	1.65	NM_152416.2	chromosome 8 open reading frame 38 (C8orf38)
LYRM4	2.57	1.65	NM_020408.3	LYR motif containing 4 (LYRM4)
TBRG4	2.57	1.65	NM_030900.2	transforming growth factor beta regulator 4 (TBRG4)
WDR42A	2.55	1.65	NM_015726.2	WD repeat domain 42A (WDR42A)
CDC14B	2.54	1.65	NM_033332.1	CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B)
CSNK1G1	2.51	1.65	NM_022048.3	casein kinase 1
DFFA	2.35	1.65	NM_004401.2	DNA fragmentation factor
CPS1	1.92	1.65	NM_001875.2	carbamoyl-phosphate synthetase 1
YAP1	1.89	1.65	NM_006106.2	Yes-associated protein 1
NDUFB4	2.96	1.64	NM_004547.4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
ATG2A	2.9	1.64	NM_015104.1	ATG2 autophagy related 2 homolog A (S. cerevisiae) (ATG2A)
ORMDL1	2.86	1.64	NM_016467.3	ORM1-like 1 (S. cerevisiae) (ORMDL1)
SRGAP2	2.81	1.64	NM_015326.2	SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2)
PRAF2	2.69	1.64	NM_007213.1	PRA1 domain family
DICER1	2.63	1.64	NM_030621.2	Dicer1
CLEC16A	2.59	1.64	NM_015226.1	C-type lectin domain family 16
DARS2	2.59	1.64	NM_018122.3	aspartyl-tRNA synthetase 2

GTF2IRD1	2.53	1.64	NM_016328.1	GTF2I repeat domain containing 1 (GTF2IRD1)
LAMP2	2.5	1.64	NM_013995.1	lysosomal-associated membrane protein 2 (LAMP2)
GLOD4	2.44	1.64	NM_016080.2	glyoxalase domain containing 4 (GLOD4)
MIER1	2.42	1.64	NM_020948.2	mesoderm induction early response 1 homolog (Xenopus laevis) (MIER1)
RPS29	2.4	1.64	NM_001030001.1	ribosomal protein S29 (RPS29)
C2orf28	2.35	1.64	NM_080592.2	chromosome 2 open reading frame 28 (C2orf28)
BMF	2.33	1.64	NM_001003943.1	Bcl2 modifying factor (BMF)
TBRG4	2.28	1.64	NM_199122.1	transforming growth factor beta regulator 4 (TBRG4)
SIVA	2.16	1.64	NM_006427.2	CD27-binding (Siva) protein (SIVA)
CCNA2	1.96	1.64	NM_001237.2	cyclin A2 (CCNA2)
KLF11	2.69	1.63	XM_001129527.1	PREDICTED: Kruppel-like factor 11 (KLF11)
DCPS	2.66	1.63	NM_014026.3	decapping enzyme
SUMF1	2.63	1.63	NM_182760.2	sulfatase modifying factor 1 (SUMF1)
ANKRD54	2.62	1.63	NM_138797.1	ankyrin repeat domain 54 (ANKRD54)
R3HDM1	2.57	1.63	NM_015361.2	R3H domain containing 1 (R3HDM1)
ABLIM1	2.55	1.63	NM_001003407.1	actin binding LIM protein 1 (ABLIM1)
ADAM15	2.54	1.63	NM_003815.3	ADAM metallopeptidase domain 15 (ADAM15)
PKD2	2.54	1.63	NM_000297.2	polycystic kidney disease 2 (autosomal dominant) (PKD2)
BAMBI	2.47	1.63	NM_012342.2	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) (BAMBI)
FAM82A2	2.31	1.63	NM_018145.1	family with sequence similarity 82
PPP2CB	2.31	1.63	NM_004156.2	protein phosphatase 2 (formerly 2A)
KIAA1267	2.28	1.63	NM_015443.2	KIAA1267 (KIAA1267)
RWDD4A	2.25	1.63	NM_152682.2	RWD domain containing 4A (RWDD4A)
STOM	2.02	1.63	NM_004099.4	stomatin (STOM)
SNF8	1.8	1.63	NM_007241.2	SNF8
CCND3	1.77	1.63	NM_001760.2	cyclin D3 (CCND3)
MMADHC	1.73	1.63	NM_015702.2	methylmalonic aciduria (cobalamin deficiency) cblD type
LOC100131261	1.66	1.63	XM_001723141.1	PREDICTED: similar to hCG1728885 (LOC100131261)
ZNF827	2.81	1.62	NM_178835.3	zinc finger protein 827 (ZNF827)
KIAA1539	2.68	1.62	NM_025182.2	KIAA1539 (KIAA1539)
PIK3CA	2.57	1.62	NM_006218.2	phosphoinositide-3-kinase
C5orf41	2.54	1.62	NM_153607.1	chromosome 5 open reading frame 41 (C5orf41)
SLC35E1	2.51	1.62	NM_024881.4	solute carrier family 35
ZBED4	2.49	1.62	NM_014838.2	zinc finger
TIGD5	2.43	1.62	NM_032862.2	tigger transposable element derived 5 (TIGD5)
DCP2	2.32	1.62	NM_152624.4	DCP2 decapping enzyme homolog (S. cerevisiae) (DCP2)
PHKB	2.28	1.62	NM_001031835.1	phosphorylase kinase
OSBPL2	2.25	1.62	NM_144498.1	oxysterol binding protein-like 2 (OSBPL2)
CMTM3	2.22	1.62	NM_144601.2	CKLF-like MARVEL transmembrane domain containing 3 (CMTM3)
LOC651697	2.11	1.62	XR_039237.1	PREDICTED: misc_RNA (LOC651697)
ANKRD9	2.03	1.62	NM_152326.2	ankyrin repeat domain 9 (ANKRD9)
RNF114	2	1.62	NM_018683.3	ring finger protein 114 (RNF114)
RBBP7	1.8	1.62	NM_002893.2	retinoblastoma binding protein 7 (RBBP7)
TFPI	2.83	1.61	NM_001032281.2	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI)
LIPT1	2.7	1.61	NM_015929.2	lipoyltransferase 1 (LIPT1)
ANKRA2	2.68	1.61	NM_023039.2	ankyrin repeat
C3orf38	2.66	1.61	NM_173824.2	chromosome 3 open reading frame 38 (C3orf38)
MGC3032	2.65	1.61	XM_933539.2	PREDICTED: hypothetical protein MGC3032
LOC92249	2.52	1.61	NR_015353.1	hypothetical LOC92249 (LOC92249)

TMEM5	2.51	1.61	NM_014254.1	transmembrane protein 5 (TMEM5)
ATAD2	2.5	1.61	NM_014109.2	ATPase family
SLC5A6	2.49	1.61	NM_021095.1	solute carrier family 5 (sodium-dependent vitamin transporter)
UBE3C	2.41	1.61	NM_014671.1	ubiquitin protein ligase E3C (UBE3C)
RDH11	2.36	1.61	NM_016026.2	retinol dehydrogenase 11 (all-trans/9-cis/11-cis) (RDH11)
ZFAND6	2.33	1.61	NM_019006.2	zinc finger
MTMR3	2.32	1.61	NM_021090.3	myotubularin related protein 3 (MTMR3)
DNAJC12	2.26	1.61	NM_021800.2	DnaJ (Hsp40) homolog
CMTM7	2.25	1.61	NM_181472.1	CKLF-like MARVEL transmembrane domain containing 7 (CMTM7)
ZMAT3	2.22	1.61	NM_152240.1	zinc finger
CNOT1	2.16	1.61	NM_016284.3	CCR4-NOT transcription complex
LOC729843	2.1	1.61	XR_016056.1	PREDICTED: similar to WW domain binding protein 1 (LOC729843)
MGEA5	2.06	1.61	NM_012215.2	meningioma expressed antigen 5 (hyaluronidase) (MGEA5)
EFHD2	2.04	1.61	NM_024329.4	EF-hand domain family
ZNF148	1.98	1.61	NM_021964.1	zinc finger protein 148 (ZNF148)
TIGD2	2.7	1.6	NM_145715.2	tigger transposable element derived 2 (TIGD2)
UBAP2L	2.68	1.6	NM_014847.2	ubiquitin associated protein 2-like (UBAP2L)
C14orf28	2.62	1.6	NM_001017923.1	chromosome 14 open reading frame 28 (C14orf28)
UBTD2	2.59	1.6	NM_152277.2	ubiquitin domain containing 2 (UBTD2)
ARL13B	2.55	1.6	NM_144996.2	ADP-ribosylation factor-like 13B (ARL13B)
HOXA10	2.5	1.6	NM_018951.3	homeobox A10 (HOXA10)
TMEM150A	2.49	1.6	NM_001031738.1	transmembrane protein 150A (TMEM150A)
DCTD	2.46	1.6	NM_001921.2	dCMP deaminase (DCTD)
OCRL	2.43	1.6	NM_000276.3	oculocerebrorenal syndrome of Lowe (OCRL)
MRPS28	2.38	1.6	NM_014018.2	mitochondrial ribosomal protein S28 (MRPS28)
SNCAIP	2.37	1.6	NM_005460.2	synuclein
TMEM179B	2.33	1.6	NM_199337.2	transmembrane protein 179B (TMEM179B)
PNPO	2.25	1.6	NM_018129.2	pyridoxamine 5'-phosphate oxidase (PNPO)
ARL2BP	2.11	1.6	NM_012106.3	ADP-ribosylation factor-like 2 binding protein (ARL2BP)
NUP155	2.08	1.6	NM_153485.1	nucleoporin 155kDa (NUP155)
FAM57A	2.05	1.6	NM_024792.1	family with sequence similarity 57
CENPB	2.03	1.6	NM_001810.5	centromere protein B
LOC100132535	2.62	1.59	XR_038464.1	PREDICTED: misc_RNA (LOC100132535)
NRBP1	2.52	1.59	NM_013392.2	nuclear receptor binding protein 1 (NRBP1)
ZNF280C	2.48	1.59	NM_017666.2	zinc finger protein 280C (ZNF280C)
STRADB	2.46	1.59	NM_018571.5	STE20-related kinase adaptor beta (STRADB)
NFYC	2.43	1.59	NM_014223.2	nuclear transcription factor Y
TSC1	2.32	1.59	NM_000368.3	tuberous sclerosis 1 (TSC1)
OTUD1	2.21	1.59	XM_001134465.1	PREDICTED: OTU domain containing 1 (OTUD1)
PQLC1	1.94	1.59	NM_025078.3	PQ loop repeat containing 1 (PQLC1)
MED28	1.91	1.59	NM_025205.3	mediator complex subunit 28 (MED28)
NUP88	1.84	1.59	NM_002532.3	nucleoporin 88kDa (NUP88)
HINT2	1.78	1.59	NM_032593.2	histidine triad nucleotide binding protein 2 (HINT2)
VAMP8	1.78	1.59	NM_003761.2	vesicle-associated membrane protein 8 (endobrevin) (VAMP8)
PRDX3	1.61	1.59	NM_006793.2	peroxiredoxin 3 (PRDX3)
PITX1	1.39	1.59	NM_002653.3	paired-like homeodomain transcription factor 1 (PITX1)
LIPT1	2.63	1.58	NM_015929.2	lipoyltransferase 1 (LIPT1)
TP53INP1	2.63	1.58	NM_033285.2	tumor protein p53 inducible nuclear protein 1 (TP53INP1)
H2AFV	2.61	1.58	NM_138635.3	H2A histone family

LOC729941	2.56	1.58	XR_015717.2	PREDICTED: misc_RNA (LOC729941)
LOC728650	2.47	1.58	XR_042473.1	PREDICTED: misc_RNA (LOC728650)
AFF1	2.44	1.58	NM_005935.1	AF4/FMR2 family
CMTM8	2.4	1.58	NM_178868.3	CKLF-like MARVEL transmembrane domain containing 8 (CMTM8)
TCEB3	2.29	1.58	NM_003198.1	transcription elongation factor B (SIII)
ZCCHC24	2.21	1.58	NM_153367.2	zinc finger
ACTL6A	2.14	1.58	NM_004301.3	actin-like 6A (ACTL6A)
AGL	2.1	1.58	NM_000645.2	amylo-1
WWP1	2.03	1.58	NM_007013.3	WW domain containing E3 ubiquitin protein ligase 1 (WWP1)
KLF13	2.02	1.58	NM_015995.2	Kruppel-like factor 13 (KLF13)
C3orf10	1.85	1.58	NM_018462.4	chromosome 3 open reading frame 10 (C3orf10)
GOLGA7	1.67	1.58	NM_001002296.1	golgi autoantigen
LOC401397	1.51	1.58	XM_001132317.1	PREDICTED: hypothetical LOC401397 (LOC401397)
SAR1B	2.64	1.57	NM_001033503.1	SAR1 homolog B (S. cerevisiae) (SAR1B)
RARA	2.5	1.57	NM_000964.2	retinoic acid receptor
DCUN1D4	2.47	1.57	NM_015115.2	DCN1
IDI1	2.41	1.57	NM_004508.2	isopentenyl-diphosphate delta isomerase 1 (IDI1)
CUGBP1	2.36	1.57	NM_001025596.1	CUG triplet repeat
FAM165B	2.2	1.57	NM_058182.4	family with sequence similarity 165
FBXO28	2.18	1.57	NM_015176.1	F-box protein 28 (FBXO28)
MAK16	2.09	1.57	NM_032509.2	MAK16 homolog (S. cerevisiae) (MAK16)
CNOT7	1.99	1.57	NM_013354.5	CCR4-NOT transcription complex
RXRA	1.91	1.57	NM_002957.3	retinoid X receptor
UBE3A	1.91	1.57	NM_000462.2	ubiquitin protein ligase E3A (UBE3A)
SIVA1	1.82	1.57	NM_006427.3	SIVA1
TROVE2	1.81	1.57	NM_001042369.1	TROVE domain family
KLF9	1.75	1.57	NM_001206.2	Kruppel-like factor 9 (KLF9)
SSB	1.7	1.57	NM_003142.3	Sjogren syndrome antigen B (autoantigen La) (SSB)
AHR	1.52	1.57	NM_001621.2	aryl hydrocarbon receptor (AHR)
LIN7B	2.7	1.56	NM_022165.2	lin-7 homolog B (C. elegans) (LIN7B)
RBM12B	2.53	1.56	NM_203390.2	RNA binding motif protein 12B (RBM12B)
C15orf44	2.48	1.56	NM_030800.1	PREDICTED: chromosome 15 open reading frame 44 (C15orf44)
FZD6	2.43	1.56	NM_003506.2	frizzled homolog 6 (Drosophila) (FZD6)
AZIN1	2.42	1.56	NM_148174.2	antizyme inhibitor 1 (AZIN1)
C17orf85	2.42	1.56	NM_018553.1	chromosome 17 open reading frame 85 (C17orf85)
PDIK1L	2.37	1.56	NM_152835.2	PDLIM1 interacting kinase 1 like (PDIK1L)
LOC100130092	2.36	1.56	XR_039545.1	PREDICTED: misc_RNA (LOC100130092)
ZNF362	2.35	1.56	NM_152493.2	zinc finger protein 362 (ZNF362)
HEG1	2.29	1.56	NM_020733.1	HEG homolog 1 (zebrafish) (HEG1)
TM7SF3	2.27	1.56	NM_016551.1	transmembrane 7 superfamily member 3 (TM7SF3)
LYRM2	2.13	1.56	NM_020466.4	LYR motif containing 2 (LYRM2)
LOC440353	2.06	1.56	NR_002603.1	nuclear pore complex interacting protein pseudogene (LOC440353)
ALDH3A2	1.97	1.56	NM_001031806.1	aldehyde dehydrogenase 3 family
ZDHHC8	1.93	1.56	NM_013373.2	zinc finger
PAPPA	1.87	1.56	NM_002581.3	pregnancy-associated plasma protein A
RFX7	1.79	1.56	NM_022841.5	regulatory factor X
MMP23B	2.71	1.55	NM_006983.1	matrix metallopeptidase 23B (MMP23B)
RBMS1	2.63	1.55	NM_002897.3	RNA binding motif
CPA4	2.6	1.55	NM_016352.2	carboxypeptidase A4 (CPA4)

TADA2B	2.42	1.55	NM_152293.2	transcriptional adaptor 2B (TADA2B)
ZNF473	2.37	1.55	NM_015428.1	zinc finger protein 473 (ZNF473)
KIAA1429	2.33	1.55	NM_015496.3	KIAA1429 (KIAA1429)
HOXA5	2.31	1.55	NM_019102.2	homeobox A5 (HOXA5)
TOPORS	2.22	1.55	NM_005802.2	topoisomerase I binding
LCLAT1	2.11	1.55	NM_001002257.1	lysocardiolipin acyltransferase 1 (LCLAT1)
ICAM3	2.09	1.55	NM_002162.2	intercellular adhesion molecule 3 (ICAM3)
LOC100134304	2.07	1.55	XM_001720739.1	PREDICTED: similar to hCG1983233 (LOC100134304)
C14orf142	2.03	1.55	NM_032490.4	chromosome 14 open reading frame 142 (C14orf142)
DCBLD2	2.01	1.55	NM_080927.3	discoidin
AGFG1	1.73	1.55	NM_001135189.1	ArfGAP with FG repeats 1 (AGFG1)
C20orf43	1.52	1.55	NM_016407.2	chromosome 20 open reading frame 43 (C20orf43)
SNN	2.5	1.54	NM_003498.4	stannin (SNN)
SCML1	2.29	1.54	NM_001037540.1	sex comb on midleg-like 1 (Drosophila) (SCML1)
STAT3	2.26	1.54	NM_213662.1	signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3)
ATXN1L	2.23	1.54	NM_001137675.2	ataxin 1-like (ATXN1L)
BCAP29	2.23	1.54	NM_001008406.1	B-cell receptor-associated protein 29 (BCAP29)
FAM173B	2.21	1.54	NM_199133.2	family with sequence similarity 173
CLDN1	2.18	1.54	NM_021101.3	claudin 1 (CLDN1)
VPS37A	2.13	1.54	NM_152415.1	vacuolar protein sorting 37 homolog A (S. cerevisiae) (VPS37A)
E2F4	2.1	1.54	NM_001950.3	E2F transcription factor 4
DEXI	2	1.54	NM_014015.3	Dexi homolog (mouse) (DEXI)
LEPROT	1.97	1.54	NM_017526.2	leptin receptor overlapping transcript (LEPROT)
FNBP1L	1.96	1.54	NM_001024948.1	formin binding protein 1-like (FNBP1L)
LOC728888	1.96	1.54	XR_015889.1	PREDICTED: similar to Protein KIAA0220 (LOC728888)
OSBPL10	1.84	1.54	NM_017784.3	oxysterol binding protein-like 10 (OSBPL10)
SDHD	1.84	1.54	NM_003002.1	succinate dehydrogenase complex
C9orf30	1.77	1.54	NM_080655.1	chromosome 9 open reading frame 30 (C9orf30)
NMRAL1	1.75	1.54	NM_020677.2	NmrA-like family domain containing 1 (NMRAL1)
ZFP36L1	1.7	1.54	NM_004926.2	zinc finger protein 36
PSMC2	1.64	1.54	NM_002803.2	proteasome (prosome
FXR1	1.55	1.54	NM_005087.2	fragile X mental retardation
FOXK2	2.53	1.53	NM_004514.3	forkhead box K2 (FOXK2)
SLC9A1	2.52	1.53	NM_003047.2	solute carrier family 9 (sodium/hydrogen exchanger)
FAM190B	2.48	1.53	NM_018999.2	family with sequence similarity 190
ZNF260	2.46	1.53	NM_001012756.1	zinc finger protein 260 (ZNF260)
KCNK2	2.42	1.53	NM_001017425.2	potassium channel
EIF2C1	2.32	1.53	NM_012199.2	eukaryotic translation initiation factor 2C
RNH1	2.32	1.53	NM_203385.1	ribonuclease/angiogenin inhibitor 1 (RNH1)
TP53INP1	2.31	1.53	NM_033285.2	tumor protein p53 inducible nuclear protein 1 (TP53INP1)
FAM60A	2.27	1.53	NM_021238.2	family with sequence similarity 60
PLD6	2.27	1.53	NM_178836.2	phospholipase D family
LCMT1	2.21	1.53	NM_016309.2	leucine carboxyl methyltransferase 1 (LCMT1)
NUDT22	2.2	1.53	NM_032344.1	nudix (nucleoside diphosphate linked moiety X)-type motif 22 (NUDT22)
TRAPPC2	2.19	1.53	NM_014563.3	trafficking protein particle complex 2 (TRAPPC2)
SPSB3	2.03	1.53	NM_080861.3	splA/ryanodine receptor domain and SOCS box containing 3 (SPSB3)
MYPOP	1.99	1.53	NM_001012643.2	Myb-related transcription factor
SLC4A7	1.99	1.53	NM_003615.2	solute carrier family 4
LOC389137	1.94	1.53	XM_371655.3	PREDICTED: hypothetical LOC389137

NINJ1	1.87	1.53	NM_004148.3	ninjurin 1 (NINJ1)
PPIC	1.83	1.53	NM_000943.4	peptidylprolyl isomerase C (cyclophilin C) (PPIC)
LOC100130511	1.77	1.53	XR_038018.1	PREDICTED: misc_RNA (LOC100130511)
TM2D1	1.57	1.53	NM_032027.2	TM2 domain containing 1 (TM2D1)
UBE2I	1.15	1.53	NM_194260.1	ubiquitin-conjugating enzyme E2I (UBC9 homolog
TFG	2.57	1.52	NM_006070.4	TRK-fused gene (TFG)
FAM18B2	2.5	1.52	NM_145301.1	family with sequence similarity 18
FAM81A	2.46	1.52	NM_152450.2	family with sequence similarity 81
CNNM3	2.44	1.52	NM_017623.4	cyclin M3 (CNNM3)
LRIG1	2.39	1.52	NM_015541.2	leucine-rich repeats and immunoglobulin-like domains 1 (LRIG1)
ZNF543	2.37	1.52	NM_213598.1	zinc finger protein 543 (ZNF543)
GPAA1	2.28	1.52	NM_003801.3	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast) (GPAA1)
RBMS1	2.2	1.52	NM_002897.3	RNA binding motif
TMEM109	2.18	1.52	NM_024092.1	transmembrane protein 109 (TMEM109)
RAB40C	1.95	1.52	NM_021168.2	RAB40C
LOC402538	2.54	1.51	XM_380121.3	PREDICTED: hypothetical LOC402538 (LOC402538)
ACPL2	2.41	1.51	NM_152282.3	acid phosphatase-like 2 (ACPL2)
RNF24	2.33	1.51	NM_007219.2	ring finger protein 24 (RNF24)
BMPR2	2.29	1.51	NM_001204.5	bone morphogenetic protein receptor
SOCS4	2.21	1.51	NM_080867.2	suppressor of cytokine signaling 4 (SOCS4)
HIBCH	2.1	1.51	NM_198047.1	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH)
PTPN4	2.07	1.51	NM_002830.2	protein tyrosine phosphatase
DDHD2	2.06	1.51	NM_015214.1	DDHD domain containing 2 (DDHD2)
LOC644762	2.04	1.51	XR_019423.1	PREDICTED: hypothetical LOC644762 (LOC644762)
RHOT1	1.88	1.51	NM_001033566.1	ras homolog gene family
CTDSPL	1.8	1.51	NM_005808.2	CTD (carboxy-terminal domain
SIGMAR1	1.79	1.51	NM_005866.2	sigma non-opioid intracellular receptor 1 (SIGMAR1)
UBE3A	1.77	1.51	NM_000462.2	ubiquitin protein ligase E3A (UBE3A)
FAM108C1	1.76	1.51	NM_021214.1	family with sequence similarity 108
LOC730417	2.4	1.5	XM_001125098.1	PREDICTED: hypothetical protein LOC730417 (LOC730417)
C10orf76	2.35	1.5	NM_024541.2	chromosome 10 open reading frame 76 (C10orf76)
C14orf45	2.31	1.5	NM_025057.1	chromosome 14 open reading frame 45 (C14orf45)
RELL1	2.25	1.5	NM_001085400.1	RELT-like 1 (RELL1)
MRPS25	2.07	1.5	NM_022497.3	mitochondrial ribosomal protein S25 (MRPS25)
ZNF410	2.05	1.5	NM_021188.1	zinc finger protein 410 (ZNF410)
CD46	2.04	1.5	NM_172358.1	CD46 molecule
FBXO22	2.03	1.5	NM_012170.2	F-box protein 22 (FBXO22)
DYRK2	1.87	1.5	NM_003583.2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2)
RAP2C	1.85	1.5	NM_021183.3	RAP2C
LGTN	1.74	1.5	NM_006893.2	ligatin (LGTN)
LOC493869	1.74	1.5	NM_001008397.1	similar to RIKEN cDNA 2310016C16 (LOC493869)
PPP2CA	1.69	1.5	NM_002715.2	protein phosphatase 2 (formerly 2A)
LAMC1	1.48	1.5	NM_002293.2	laminin
FOXP1	2.44	1.49	NM_032682.4	forkhead box P1 (FOXP1)
RAVER2	2.26	1.49	NM_018211.2	ribonucleoprotein
NPAL3	2.22	1.49	NM_020448.3	NIPA-like domain containing 3 (NPAL3)
REPS2	2.15	1.49	NM_004726.2	RALBP1 associated Eps domain containing 2 (REPS2)
PRRG1	2.12	1.49	NM_000950.1	proline rich Gla (G-carboxyglutamic acid) 1 (PRRG1)
SNAI2	2.07	1.49	NM_003068.3	snail homolog 2 (Drosophila) (SNAI2)

TFAP2A	2.05	1.49	NM_001042425.1	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha) (TFAP2A)
NOP2	2.04	1.49	NM_001033714.1	NOP2 nucleolar protein homolog (yeast) (NOP2)
MTCP1	2	1.49	NM_014221.3	mature T-cell proliferation 1 (MTCP1)
RAB24	1.98	1.49	NM_001031677.2	RAB24
LOC728556	1.9	1.49	XM_001129672.1	PREDICTED: similar to Protein C2orf4 (C21orf19-like protein) (LOC728556)
PTAR1	1.9	1.49	NM_001099666.1	protein prenyltransferase alpha subunit repeat containing 1 (PTAR1)
IFI44	1.85	1.49	NM_006417.3	interferon-induced protein 44 (IFI44)
PPP4R1	1.82	1.49	NM_005134.2	protein phosphatase 4
RBPMS2	1.71	1.49	NM_194272.1	RNA binding protein with multiple splicing 2 (RBPMS2)
CDC16	1.61	1.49	NM_001078645.1	cell division cycle 16 homolog (S. cerevisiae) (CDC16)
RASIP1	1.53	1.49	NM_017805.2	Ras interacting protein 1 (RASIP1)
NDFIP2	1.51	1.49	NM_019080.1	Nedd4 family interacting protein 2 (NDFIP2)
RBPMS	2.43	1.48	NM_001008710.1	RNA binding protein with multiple splicing (RBPMS)
ZFYVE1	2.42	1.48	NM_021260.1	zinc finger
FBXL6	2.36	1.48	NM_012162.1	F-box and leucine-rich repeat protein 6 (FBXL6)
RFC1	2.32	1.48	NM_002913.3	replication factor C (activator 1) 1
SEC23IP	2.31	1.48	NM_007190.2	SEC23 interacting protein (SEC23IP)
MARK2	2.3	1.48	NM_004954.3	MAP/microtubule affinity-regulating kinase 2 (MARK2)
SOCS5	2.3	1.48	NM_014011.4	suppressor of cytokine signaling 5 (SOCS5)
TOB2	2.3	1.48	NM_016272.3	transducer of ERBB2
ATP2B4	2.22	1.48	NM_001684.3	ATPase
KIAA1522	2.2	1.48	NM_020888.2	KIAA1522 (KIAA1522)
STX12	2.16	1.48	NM_177424.2	syntaxin 12 (STX12)
PDE8A	2.14	1.48	NM_173454.1	phosphodiesterase 8A (PDE8A)
ANKRD37	2.09	1.48	NM_181726.2	ankyrin repeat domain 37 (ANKRD37)
MAL2	2.07	1.48	NM_052886.2	mal
MTF1	2.07	1.48	NM_005955.2	metal-regulatory transcription factor 1 (MTF1)
KLHL2	2.06	1.48	NM_007246.2	kelch-like 2
MLLT10	2.03	1.48	NM_004641.2	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog
SIK1	2.01	1.48	NM_173354.3	salt-inducible kinase 1 (SIK1)
GCLC	2	1.48	NM_001498.2	glutamate-cysteine ligase
PABPC4L	1.98	1.48	NM_001114734.1	poly(A) binding protein
MAP3K1	1.97	1.48	NM_005921.1	mitogen-activated protein kinase kinase kinase 1 (MAP3K1)
MRI1	1.92	1.48	NM_001031727.2	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) (MRI1)
RABGGTB	1.88	1.48	NM_004582.2	Rab geranylgeranyltransferase
SDAD1	1.75	1.48	NM_018115.2	SDA1 domain containing 1 (SDAD1)
URB1	2.38	1.47	NM_014825.2	URB1 ribosome biogenesis 1 homolog (S. cerevisiae) (URB1)
FAM54A	2.36	1.47	NM_138419.2	family with sequence similarity 54
MARK1	2.33	1.47	NM_018650.3	MAP/microtubule affinity-regulating kinase 1 (MARK1)
SRGAP2	2.31	1.47	NM_015326.2	SLIT-ROBO Rho GTPase activating protein 2 (SRGAP2)
MICALL1	2.3	1.47	NM_033386.2	MICAL-like 1 (MICALL1)
NR2C2AP	2.2	1.47	NM_176880.4	nuclear receptor 2C2-associated protein (NR2C2AP)
HECA	2.17	1.47	NM_016217.2	headcase homolog (Drosophila) (HECA)
C9orf125	2.16	1.47	NM_032342.1	chromosome 9 open reading frame 125 (C9orf125)
R3HDM1	2.12	1.47	NM_015361.2	R3H domain containing 1 (R3HDM1)
KIAA1644	1.77	1.47	XM_936510.2	PREDICTED: KIAA1644 protein (KIAA1644)
CDKN2B	1.76	1.47	NM_004936.3	cyclin-dependent kinase inhibitor 2B (p15
FAM127C	2.38	1.46	NM_001078173.1	family with sequence similarity 127
DBNDD1	2.26	1.46	NM_001042610.1	dysbindin (dystrobrevin binding protein 1) domain containing 1 (DBNDD1)

GABRE	2.21	1.46	NM_004961.3	gamma-aminobutyric acid (GABA) A receptor
TES	2.21	1.46	NM_015641.2	testis derived transcript (3 LIM domains) (TES)
CMTM7	2.2	1.46	NM_181472.1	CKLF-like MARVEL transmembrane domain containing 7 (CMTM7)
CA12	2.19	1.46	NM_001218.3	carbonic anhydrase XII (CA12)
UBE2E3	2.15	1.46	NM_006357.2	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog
SYT17	2.12	1.46	NM_016524.2	synaptotagmin XVII (SYT17)
MRI1	2.11	1.46	NM_032285.2	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) (MRI1)
ZBTB2	2.09	1.46	NM_020861.1	zinc finger and BTB domain containing 2 (ZBTB2)
MLLT10	2.08	1.46	NM_004641.2	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog
PAPD1	2.01	1.46	NM_018109.2	PAP associated domain containing 1 (PAPD1)
MED4	1.96	1.46	NM_014166.2	mediator complex subunit 4 (MED4)
STXBP5	1.96	1.46	NM_139244.2	syntaxin binding protein 5 (tomosyn) (STXBP5)
MGAT1	1.92	1.46	NM_002406.2	mannosyl (alpha-1
PROSC	1.89	1.46	NM_007198.2	proline synthetase co-transcribed homolog (bacterial) (PROSC)
C2orf47	1.76	1.46	NM_024520.1	chromosome 2 open reading frame 47 (C2orf47)
LOC641844	1.75	1.46	XR_018036.2	PREDICTED: misc_RNA (LOC641844)
RB1CC1	1.74	1.46	NM_001083617.1	RB1-inducible coiled-coil 1 (RB1CC1)
TNFAIP1	1.69	1.46	NM_021137.3	tumor necrosis factor
PTGR1	1.16	1.46	NM_012212.2	prostaglandin reductase 1 (PTGR1)
FOXL2	2.35	1.45	NM_023067.2	forkhead box L2 (FOXL2)
LOC729404	2.35	1.45	XR_015968.1	PREDICTED: misc_RNA (LOC729404)
KIAA1545	2.29	1.45	XM_495939.3	PREDICTED: KIAA1545 protein (KIAA1545)
PRKAG2	2.22	1.45	NM_001040633.1	protein kinase
MAP3K8	2.19	1.45	NM_005204.2	mitogen-activated protein kinase kinase kinase 8 (MAP3K8)
RAPGEF6	2.18	1.45	NM_016340.4	Rap guanine nucleotide exchange factor (GEF) 6 (RAPGEF6)
AKTIP	2.17	1.45	NM_022476.2	AKT interacting protein (AKTIP)
NAGPA	2.15	1.45	NM_016256.2	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (NAGPA)
RNH1	2.09	1.45	NM_203385.1	ribonuclease/angiogenin inhibitor 1 (RNH1)
HNRPDL	2.07	1.45	NR_003249.1	heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)
VEZT	2.06	1.45	NM_017599.2	vezatin
MFSD11	2.02	1.45	NM_024311.2	major facilitator superfamily domain containing 11 (MFSD11)
ODF2	1.96	1.45	NM_002540.3	outer dense fiber of sperm tails 2 (ODF2)
LOC642755	1.95	1.45	XM_926382.2	PREDICTED: similar to DEXI
TGIF1	1.93	1.45	NM_170695.2	TGFB-induced factor homeobox 1 (TGIF1)
RPL37A	1.92	1.45	NM_000998.3	ribosomal protein L37a (RPL37A)
C2CD2	1.83	1.45	NM_015500.1	C2 calcium-dependent domain containing 2 (C2CD2)
PAFAH1B1	1.76	1.45	NM_000430.2	platelet-activating factor acetylhydrolase
FAM162A	1.74	1.45	NM_014367.3	family with sequence similarity 162
RAB2B	1.72	1.45	NM_032846.2	RAB2B
SERP1	1.67	1.45	NM_014445.3	stress-associated endoplasmic reticulum protein 1 (SERP1)
FAM83D	1.17	1.45	NM_030919.2	family with sequence similarity 83
PANK3	2.29	1.44	NM_024594.2	pantothenate kinase 3 (PANK3)
IL28RA	2.23	1.44	NM_170743.2	interleukin 28 receptor
PGBD3	2.21	1.44	NM_170753.1	piggyBac transposable element derived 3 (PGBD3)
TMEM135	2.16	1.44	NM_022918.2	transmembrane protein 135 (TMEM135)
FOXP1	2.14	1.44	NM_032682.4	forkhead box P1 (FOXP1)
ABCC5	2.13	1.44	NM_005688.2	ATP-binding cassette
PSMD11	2.11	1.44	NM_002815.2	proteasome (prosome
TSC22D2	2.11	1.44	NM_014779.2	TSC22 domain family

SLC9A6	2.06	1.44	NM_001042537.1	solute carrier family 9 (sodium/hydrogen exchanger)
SEC22C	2.05	1.44	NM_032970.2	SEC22 vesicle trafficking protein homolog C (S. cerevisiae) (SEC22C)
SDC1	2.02	1.44	NM_001006946.1	syndecan 1 (SDC1)
DPP9	1.99	1.44	NM_139159.3	dipeptidyl-peptidase 9 (DPP9)
STARD10	1.99	1.44	NM_006645.2	StAR-related lipid transfer (START) domain containing 10 (STARD10)
OTUB1	1.98	1.44	NR_003089.1	OTU domain
STK38	1.94	1.44	NM_007271.2	serine/threonine kinase 38 (STK38)
FASTKD3	1.9	1.44	NM_024091.2	FAST kinase domains 3 (FASTKD3)
MED29	1.88	1.44	NM_017592.1	mediator complex subunit 29 (MED29)
ADAM19	1.87	1.44	NM_033274.2	ADAM metallopeptidase domain 19 (meltrin beta) (ADAM19)
PIGF	1.79	1.44	NM_002643.3	phosphatidylinositol glycan anchor biosynthesis
CUL1	1.78	1.44	NM_003592.2	cullin 1 (CUL1)
POLR3E	1.77	1.44	NM_018119.2	polymerase (RNA) III (DNA directed) polypeptide E (80kD) (POLR3E)
TACO1	1.76	1.44	NM_016360.2	translational activator of mitochondrially encoded cytochrome c oxidase I (TACO1)
GMNN	1.75	1.44	NM_015895.3	geminin
MBNL2	1.7	1.44	NM_144778.2	muscleblind-like 2 (Drosophila) (MBNL2)
MGST1	1.7	1.44	NM_020300.3	microsomal glutathione S-transferase 1 (MGST1)
RAD23B	1.65	1.44	NM_002874.3	RAD23 homolog B (S. cerevisiae) (RAD23B)
TXLNA	1.63	1.44	NM_175852.3	taxilin alpha (TXLNA)
FNDC3B	1.39	1.44	NM_001135095.1	fibronectin type III domain containing 3B (FNDC3B)
RNF217	2.21	1.43	NM_152553.2	ring finger protein 217 (RNF217)
TTC13	2.18	1.43	NM_024525.2	tetratricopeptide repeat domain 13 (TTC13)
MTUS1	2.15	1.43	NM_001001924.1	mitochondrial tumor suppressor 1 (MTUS1)
TESC	2.09	1.43	NM_017899.2	tescalcin (TESC)
THBS1	2.04	1.43	NM_003246.2	thrombospondin 1 (THBS1)
TCEAL1	2.03	1.43	NM_001006639.1	transcription elongation factor A (SII)-like 1 (TCEAL1)
TMEM62	1.99	1.43	NM_024956.3	transmembrane protein 62 (TMEM62)
NKTR	1.93	1.43	NM_005385.3	natural killer-tumor recognition sequence (NKTR)
DUSP22	1.83	1.43	NM_020185.3	dual specificity phosphatase 22 (DUSP22)
LYPLA1	1.8	1.43	NM_006330.2	lysophospholipase I (LYPLA1)
CD83	1.79	1.43	NM_001040280.1	CD83 molecule (CD83)
DEDD2	1.74	1.43	NM_133328.2	death effector domain containing 2 (DEDD2)
CCDC25	1.69	1.43	NM_018246.2	coiled-coil domain containing 25 (CCDC25)
ELF2	1.66	1.43	NM_006874.2	E74-like factor 2 (ets domain transcription factor) (ELF2)
MUC1	1.6	1.43	NM_001044391.1	mucin 1
CDC16	1.56	1.43	NM_003903.3	cell division cycle 16 homolog (S. cerevisiae) (CDC16)
C14orf4	1.53	1.43	NM_024496.2	chromosome 14 open reading frame 4 (C14orf4)
TIRAP	2.25	1.42	NM_001039661.1	toll-interleukin 1 receptor (TIR) domain containing adaptor protein (TIRAP)
MAP3K12	2.24	1.42	NM_006301.2	mitogen-activated protein kinase kinase kinase 12 (MAP3K12)
NR2F2	2.08	1.42	NM_021005.2	nuclear receptor subfamily 2
ZNF266	2.07	1.42	NM_006631.2	zinc finger protein 266 (ZNF266)
MSL1	2.06	1.42	NM_001012241.1	male-specific lethal 1 homolog (Drosophila) (MSL1)
C5orf41	2.05	1.42	NM_153607.1	chromosome 5 open reading frame 41 (C5orf41)
USP1	2.05	1.42	NM_003368.4	ubiquitin specific peptidase 1 (USP1)
LOC143666	2.02	1.42	XM_001127524.1	PREDICTED: hypothetical protein LOC143666 (LOC143666)
ZNF706	2.02	1.42	NM_016096.3	zinc finger protein 706 (ZNF706)
STK38L	2.01	1.42	NM_015000.2	serine/threonine kinase 38 like (STK38L)
CHRAC1	1.99	1.42	NM_017444.3	chromatin accessibility complex 1 (CHRAC1)
CHST15	1.99	1.42	NM_015892.2	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 (CHST15)

C18orf32	1.97	1.42	NM_001035005.2	chromosome 18 open reading frame 32 (C18orf32)
FAM117B	1.97	1.42	NM_173511.2	family with sequence similarity 117
SLC2A3	1.97	1.42	NM_006931.1	solute carrier family 2 (facilitated glucose transporter)
RNF103	1.95	1.42	NM_005667.2	ring finger protein 103 (RNF103)
FECH	1.94	1.42	NM_000140.2	ferrochelatase (protoporphyria) (FECH)
CDC40	1.89	1.42	NM_015891.2	cell division cycle 40 homolog (S. cerevisiae) (CDC40)
ITFG1	1.88	1.42	NM_030790.3	integrin alpha FG-GAP repeat containing 1 (ITFG1)
PTP4A1	1.88	1.42	NM_003463.3	protein tyrosine phosphatase type IVA
CMTM4	1.83	1.42	NM_181521.2	CKLF-like MARVEL transmembrane domain containing 4 (CMTM4)
DERL2	1.81	1.42	NM_016041.3	Der1-like domain family
ZCCHC14	1.78	1.42	NM_015144.2	zinc finger
STC2	1.74	1.42	NM_003714.2	stanniocalcin 2 (STC2)
SMEK2	1.69	1.42	NM_020463.1	SMEK homolog 2
DNAJC12	1.62	1.42	NM_021800.2	DnaJ (Hsp40) homolog
CSK	1.59	1.42	NM_004383.1	c-src tyrosine kinase (CSK)
GOLGA8B	1.53	1.42	NM_001023567.2	golgi autoantigen
CMIP	1.5	1.42	NM_030629.1	c-Maf-inducing protein (CMIP)
SLC25A12	2.09	1.41	NM_003705.2	solute carrier family 25 (mitochondrial carrier
ULK3	2.08	1.41	NM_001099436.1	unc-51-like kinase 3 (C. elegans) (ULK3)
EYA4	2.04	1.41	NM_004100.3	eyes absent homolog 4 (Drosophila) (EYA4)
LIAS	2.01	1.41	NM_006859.2	lipoic acid synthetase (LIAS)
PANK1	1.99	1.41	NM_148978.1	pantothenate kinase 1 (PANK1)
IL11RA	1.98	1.41	NM_004512.3	interleukin 11 receptor
PAN3	1.93	1.41	NM_175854.5	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) (PAN3)
TMEM199	1.92	1.41	NM_152464.1	transmembrane protein 199 (TMEM199)
NSF	1.9	1.41	NM_006178.1	PREDICTED: N-ethylmaleimide-sensitive factor (NSF)
NEIL2	1.88	1.41	NM_145043.1	nei like 2 (E. coli) (NEIL2)
C14orf135	1.87	1.41	NM_022495.5	chromosome 14 open reading frame 135 (C14orf135)
PKNOX1	1.87	1.41	NM_004571.3	PBX/knotted 1 homeobox 1 (PKNOX1)
FBXO28	1.8	1.41	NM_015176.1	F-box protein 28 (FBXO28)
LHFPL2	1.78	1.41	NM_005779.1	lipoma HMGIC fusion partner-like 2 (LHFPL2)
PTPN1	1.78	1.41	NM_002827.2	protein tyrosine phosphatase
HIAT1	1.76	1.41	NM_033055.2	hippocampus abundant transcript 1 (HIAT1)
KLF6	1.74	1.41	NM_001300.4	Kruppel-like factor 6 (KLF6)
DULLARD	1.69	1.41	NM_015343.3	dullard homolog (Xenopus laevis) (DULLARD)
C4orf34	1.65	1.41	NM_174921.1	chromosome 4 open reading frame 34 (C4orf34)
NCBP2	1.65	1.41	NM_007362.3	nuclear cap binding protein subunit 2
CDV3	1.59	1.41	NM_017548.3	PREDICTED: CDV3 homolog (mouse)
DHPS	1.52	1.41	NM_013406.1	deoxyhypusine synthase (DHPS)
SEL1L3	1.3	1.41	NM_015187.3	sel-1 suppressor of lin-12-like 3 (C. elegans) (SEL1L3)
DCAF6	1.06	1.41	NM_001017977.1	DDB1 and CUL4 associated factor 6 (DCAF6)
PCNXL2	2.16	1.4	NM_014801.3	pecanex-like 2 (Drosophila) (PCNXL2)
HCG18	2.09	1.4	XM_944855.1	PREDICTED: HLA complex group 18 (HCG18)
LOC100130171	2.04	1.4	XR_038676.1	PREDICTED: misc_RNA (LOC100130171)
LOC92659	2.04	1.4	NR_015454.1	hypothetical LOC92659 (LOC92659)
LPGAT1	2.04	1.4	NM_014873.1	lysophosphatidylglycerol acyltransferase 1 (LPGAT1)
TOPORS	2.04	1.4	NM_005802.2	topoisomerase I binding
PGP	2.03	1.4	NM_001042371.2	phosphoglycolate phosphatase (PGP)
C6orf85	2.01	1.4	NM_021945.4	chromosome 6 open reading frame 85 (C6orf85)

TMEM134	1.98	1.4	NM_001078651.1	transmembrane protein 134 (TMEM134)
ZNF12	1.97	1.4	NM_016265.3	zinc finger protein 12 (ZNF12)
KCTD14	1.96	1.4	NM_023930.3	potassium channel tetramerisation domain containing 14 (KCTD14)
RAN	1.86	1.4	NM_006325.2	RAN
BCL2L2	1.85	1.4	NM_004050.2	BCL2-like 2 (BCL2L2)
SLC43A3	1.83	1.4	NM_014096.2	solute carrier family 43
SLTM	1.79	1.4	NM_024755.2	SAFB-like
IFIT1	1.72	1.4	NM_001548.3	interferon-induced protein with tetratricopeptide repeats 1 (IFIT1)
FOXJ2	1.69	1.4	NM_018416.2	forkhead box J2 (FOXJ2)
NCLN	1.68	1.4	NM_020170.3	nicalin homolog (zebrafish) (NCLN)
KPNA3	1.67	1.4	NM_002267.2	karyopherin alpha 3 (importin alpha 4) (KPNA3)
CALU	1.59	1.4	NM_001219.2	calumenin (CALU)
HNRPH3	1.45	1.4	NM_012207.1	heterogeneous nuclear ribonucleoprotein H3 (2H9) (HNRPH3)
ACSL4	1.25	1.4	NM_004458.1	acyl-CoA synthetase long-chain family member 4 (ACSL4)
OSGEPL1	2.12	1.39	NM_022353.2	O-sialoglycoprotein endopeptidase-like 1 (OSGEPL1)
ZBTB47	2.08	1.39	NM_145166.2	zinc finger and BTB domain containing 47 (ZBTB47)
NR2C2	2.03	1.39	NM_003298.3	nuclear receptor subfamily 2
SMARCC2	2.03	1.39	NM_139067.1	SWI/SNF related
GSTM3	1.97	1.39	NM_000849.3	glutathione S-transferase M3 (brain) (GSTM3)
FAM72D	1.94	1.39	NM_207418.2	PREDICTED: family with sequence similarity 72
SERAC1	1.94	1.39	NM_032861.2	serine active site containing 1 (SERAC1)
NPEPL1	1.93	1.39	NM_024663.3	aminopeptidase-like 1 (NPEPL1)
LOC440030	1.88	1.39	XM_498510.2	PREDICTED: hypothetical LOC440030 (LOC440030)
CLPTM1	1.84	1.39	NM_001294.1	cleft lip and palate associated transmembrane protein 1 (CLPTM1)
LOC645166	1.84	1.39	XM_001129441.2	PREDICTED: similar to lymphocyte-specific protein 1 (LOC645166)
IQCK	1.79	1.39	NM_153208.1	IQ motif containing K (IQCK)
BCAT1	1.75	1.39	NM_005504.4	branched chain aminotransferase 1
CP110	1.73	1.39	NM_014711.3	CP110 protein (CP110)
HS6ST2	1.73	1.39	NM_147175.3	heparan sulfate 6-O-sulfotransferase 2 (HS6ST2)
ERI1	1.71	1.39	NM_153332.3	exoribonuclease 1 (ERI1)
TNFSF9	1.71	1.39	NM_003811.2	tumor necrosis factor (ligand) superfamily
RQCD1	1.69	1.39	NM_005444.1	RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1)
SBDS	1.57	1.39	NM_016038.2	Shwachman-Bodian-Diamond syndrome (SBDS)
JARID2	1.56	1.39	NM_004973.2	jumonji
LRRC58	1.56	1.39	NM_001099678.1	leucine rich repeat containing 58 (LRRC58)
FNDC3B	1.22	1.39	NM_022763.3	fibronectin type III domain containing 3B (FNDC3B)
KIAA1715	2.03	1.38	NM_030650.1	KIAA1715 (KIAA1715)
WDR20	2.01	1.38	NM_181308.1	WD repeat domain 20 (WDR20)
MKNK2	1.95	1.38	NM_199054.2	MAP kinase interacting serine/threonine kinase 2 (MKNK2)
DEF8	1.93	1.38	NM_207514.1	differentially expressed in FDCP 8 homolog (mouse) (DEF8)
GPR137C	1.93	1.38	NM_001099652.1	G protein-coupled receptor 137C (GPR137C)
SPIN3	1.93	1.38	NM_001010862.1	spindlin family
IFI30	1.92	1.38	NM_006332.3	interferon
MXD1	1.92	1.38	NM_002357.2	MAX dimerization protein 1 (MXD1)
LRRC57	1.89	1.38	NM_153260.1	leucine rich repeat containing 57 (LRRC57)
TRIM37	1.88	1.38	NM_015294.2	tripartite motif-containing 37 (TRIM37)
PCGF2	1.87	1.38	NM_007144.2	polycomb group ring finger 2 (PCGF2)
TMEM51	1.87	1.38	NM_018022.1	transmembrane protein 51 (TMEM51)
SLC35F5	1.86	1.38	NM_025181.2	solute carrier family 35

WRN	1.84	1.38	NM_000553.3	Werner syndrome
RGL1	1.82	1.38	NM_015149.3	ral guanine nucleotide dissociation stimulator-like 1 (RGL1)
NMD3	1.76	1.38	NM_015938.3	NMD3 homolog (S. cerevisiae) (NMD3)
CBX1	1.72	1.38	NM_006807.3	chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1)
C14orf135	1.7	1.38	NM_022495.3	chromosome 14 open reading frame 135 (C14orf135)
CENTG2	1.66	1.38	NM_014914.2	centaurin
BAZ1B	1.65	1.38	NM_023005.2	bromodomain adjacent to zinc finger domain
SDHC	1.61	1.38	NM_003001.2	succinate dehydrogenase complex
LOC647081	1.59	1.38	XR_017490.2	PREDICTED: misc_RNA (LOC647081)
TRAK1	1.58	1.38	NM_001042646.1	trafficking protein
RNF114	1.56	1.38	NM_018683.3	ring finger protein 114 (RNF114)
IGF2BP3	1.35	1.38	NM_006547.2	insulin-like growth factor 2 mRNA binding protein 3 (IGF2BP3)
BAG1	1.97	1.37	NM_004323.4	BCL2-associated athanogene (BAG1)
ACTR1B	1.92	1.37	NM_005735.2	ARP1 actin-related protein 1 homolog B
ASB1	1.86	1.37	NM_016114.3	ankyrin repeat and SOCS box-containing 1 (ASB1)
XPO7	1.85	1.37	NM_015024.2	exportin 7 (XPO7)
ANKMY2	1.82	1.37	NM_020319.1	ankyrin repeat and MYND domain containing 2 (ANKMY2)
XRCC1	1.82	1.37	NM_006297.1	X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1)
BTBD10	1.77	1.37	NM_032320.5	BTB (POZ) domain containing 10 (BTBD10)
GTF2H1	1.76	1.37	NM_005316.2	general transcription factor IIH
MEMO1	1.76	1.37	NM_015955.2	mediator of cell motility 1 (MEMO1)
TANC2	1.74	1.37	NM_025185.3	tetratricopeptide repeat
CDKN1B	1.51	1.37	NM_004064.2	cyclin-dependent kinase inhibitor 1B (p27
CUL4A	1.02	1.37	NM_003589.2	cullin 4A (CUL4A)
ABCB9	1.98	1.36	NM_019624.2	ATP-binding cassette
C1orf96	1.97	1.36	NM_145257.2	chromosome 1 open reading frame 96 (C1orf96)
COG5	1.97	1.36	NM_006348.2	component of oligomeric golgi complex 5 (COG5)
RP5-1022P6.2	1.97	1.36	NM_019593.3	hypothetical protein KIAA1434 (RP5-1022P6.2)
BNIP1	1.95	1.36	NM_013980.2	BCL2/adenovirus E1B 19kDa interacting protein 1 (BNIP1)
CICE	1.95	1.36	XR_000206.4	PREDICTED: cell death-inducing CIDE-like effector pseudogene (CICE)
ZNF512B	1.94	1.36	NM_020713.1	zinc finger protein 512B (ZNF512B)
LOC391692	1.93	1.36	XM_373031.3	PREDICTED: similar to tubulin
SHARPIN	1.88	1.36	NM_030974.2	SHANK-associated RH domain interactor (SHARPIN)
B4GALT2	1.86	1.36	NM_003780.3	UDP-Gal:betaGlcNAc beta 1
WDR37	1.86	1.36	NM_014023.3	WD repeat domain 37 (WDR37)
FAM86A	1.85	1.36	NM_201598.1	family with sequence similarity 86
TEX261	1.83	1.36	NM_144582.2	testis expressed 261 (TEX261)
ZFAND6	1.8	1.36	NM_019006.2	zinc finger
BUB1	1.76	1.36	NM_004336.2	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast) (BUB1)
MAP3K2	1.72	1.36	XM_001128799.1	PREDICTED: mitogen-activated protein kinase kinase kinase 2
SPHK2	1.71	1.36	NM_020126.3	sphingosine kinase 2 (SPHK2)
MFSD5	1.7	1.36	NM_032889.3	major facilitator superfamily domain containing 5 (MFSD5)
RBL2	1.68	1.36	NM_005611.2	retinoblastoma-like 2 (p130) (RBL2)
FEM1C	1.65	1.36	NM_020177.2	fem-1 homolog c (C. elegans) (FEM1C)
PLCXD1	1.65	1.36	NM_018390.2	Yp11.32c
ATG5	1.64	1.36	NM_004849.1	ATG5 autophagy related 5 homolog (S. cerevisiae) (ATG5)
LARP4B	1.64	1.36	NM_015155.1	La ribonucleoprotein domain family
LOC100128337	1.62	1.36	XR_037222.1	PREDICTED: misc_RNA (LOC100128337)
SNX4	1.58	1.36	NM_003794.2	sorting nexin 4 (SNX4)

LOC645251	1.56	1.36	XR_037203.1	PREDICTED: misc_RNA (LOC645251)
LOC146517	1.5	1.36	XM_928464.1	PREDICTED: hypothetical protein LOC146517 (LOC146517)
WBSCR22	1.4	1.36	NM_017528.2	Williams Beuren syndrome chromosome region 22 (WBSCR22)
CHCHD10	1.12	1.36	NM_213720.1	coiled-coil-helix-coiled-coil-helix domain containing 10 (CHCHD10)
FBS1	1.91	1.35	NM_022452.1	fibrosin 1 (FBS1)
LOC100134053	1.84	1.35	XM_001717094.1	PREDICTED: similar to POLR2J4 protein (LOC100134053)
NRP1	1.83	1.35	NM_003873.4	neuropilin 1 (NRP1)
PAFAH2	1.82	1.35	NM_000437.3	platelet-activating factor acetylhydrolase 2
RSBN1L	1.81	1.35	NM_198467.1	round spermatid basic protein 1-like (RSBN1L)
ACSS2	1.8	1.35	NM_001076552.1	acyl-CoA synthetase short-chain family member 2 (ACSS2)
DNM1L	1.79	1.35	NM_012063.1	dynamin 1-like (DNM1L)
CHST14	1.78	1.35	NM_130468.2	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14 (CHST14)
PHLDA3	1.78	1.35	NM_012396.3	pleckstrin homology-like domain
TLK1	1.77	1.35	NM_012290.3	tousled-like kinase 1 (TLK1)
DLEU1	1.73	1.35	NR_002605.1	deleted in lymphocytic leukemia 1 (non-protein coding) (DLEU1)
ACSS2	1.72	1.35	NM_018677.2	acyl-CoA synthetase short-chain family member 2 (ACSS2)
HS2ST1	1.72	1.35	NM_012262.2	heparan sulfate 2-O-sulfotransferase 1 (HS2ST1)
NICN1	1.67	1.35	NM_032316.3	nicolin 1 (NICN1)
MBP	1.64	1.35	NM_001025100.1	myelin basic protein (MBP)
TSPAN4	1.6	1.35	NM_001025235.1	tetraspanin 4 (TSPAN4)
C6orf129	1.56	1.35	NM_138493.2	chromosome 6 open reading frame 129 (C6orf129)
PHF15	1.52	1.35	NM_015288.4	PHD finger protein 15 (PHF15)
DEPDC1B	1.51	1.35	NM_018369.1	DEP domain containing 1B (DEPDC1B)
CNOT8	1.31	1.35	NM_004779.4	CCR4-NOT transcription complex
AVPI1	0.57	1.35	NM_021732.1	arginine vasopressin-induced 1 (AVPI1)
SNORD17	1.86	1.34	NR_003045.1	small nucleolar RNA
GRAMD3	1.81	1.34	NM_023927.1	GRAM domain containing 3 (GRAMD3)
IPO5	1.81	1.34	NM_002271.4	importin 5 (IPO5)
HSPC157	1.78	1.34	NR_023919.1	hypothetical LOC29092 (HSPC157)
NIPAL4	1.77	1.34	NM_001099287.1	NIPA-like domain containing 4 (NIPAL4)
PKMYT1	1.76	1.34	NM_182687.1	protein kinase
NPTX1	1.73	1.34	NM_002522.2	PREDICTED: neuronal pentraxin I (NPTX1)
C1orf216	1.69	1.34	NM_152374.1	chromosome 1 open reading frame 216 (C1orf216)
BCL7B	1.63	1.34	NM_138707.1	B-cell CLL/lymphoma 7B (BCL7B)
ELMO2	1.59	1.34	NM_133171.2	engulfment and cell motility 2 (ELMO2)
YPEL3	1.58	1.34	NM_031477.4	yippee-like 3 (Drosophila) (YPEL3)
CCNE1	1.57	1.34	NM_057182.1	cyclin E1 (CCNE1)
KLHL28	1.56	1.34	NM_017658.3	kelch-like 28 (Drosophila) (KLHL28)
TFB1M	1.55	1.34	NM_016020.1	transcription factor B1
ABL1	1.13	1.34	NM_005157.3	c-abl oncogene 1
ASB6	1.87	1.33	NM_177999.1	ankyrin repeat and SOCS box-containing 6 (ASB6)
KIAA1602	1.81	1.33	NM_020941.1	KIAA1602 (KIAA1602)
RMND5B	1.81	1.33	NM_022762.3	required for meiotic nuclear division 5 homolog B (S. cerevisiae) (RMND5B)
KIAA1128	1.78	1.33	NM_018999.1	KIAA1128 (KIAA1128)
RECK	1.76	1.33	NM_021111.1	reversion-inducing-cysteine-rich protein with kazal motifs (RECK)
AZI2	1.73	1.33	NM_022461.2	5-azacytidine induced 2 (AZI2)
BRE	1.67	1.33	NM_199191.1	brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE)
PIGB	1.62	1.33	NM_004855.4	phosphatidylinositol glycan anchor biosynthesis
BRE	1.61	1.33	NM_199192.1	brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE)

OTUD1	1.6	1.33	XM_939698.1	PREDICTED: OTU domain containing 1 (OTUD1)
ARID3A	1.59	1.33	NM_005224.2	AT rich interactive domain 3A (BRIGHT-like) (ARID3A)
MAPK9	1.59	1.33	NM_002752.3	mitogen-activated protein kinase 9 (MAPK9)
RAB23	1.59	1.33	NM_016277.3	RAB23
SLC25A25	1.59	1.33	NM_052901.2	solute carrier family 25 (mitochondrial carrier; phosphate carrier)
RALBP1	1.56	1.33	NM_006788.3	ralA binding protein 1 (RALBP1)
PRAGMIN	1.55	1.33	NM_001080826.1	homolog of rat pragma of Rnd2 (PRAGMIN)
METAP1	1.07	1.33	NM_015143.1	methionyl aminopeptidase 1 (METAP1)
ARF1	0.57	1.33	NM_001024227.1	ADP-ribosylation factor 1 (ARF1)
SLC20A2	1.83	1.32	NM_006749.3	solute carrier family 20 (phosphate transporter)
SOCS5	1.83	1.32	NM_144949.2	suppressor of cytokine signaling 5 (SOCS5)
STRN4	1.77	1.32	NM_001039877.1	striatin
C10orf32	1.76	1.32	NM_144591.1	chromosome 10 open reading frame 32 (C10orf32)
LOC100130746	1.75	1.32	XR_038468.1	PREDICTED: misc_RNA (LOC100130746)
CYB561D1	1.7	1.32	NM_182580.2	cytochrome b-561 domain containing 1 (CYB561D1)
AADACL1	1.65	1.32	NM_020792.3	arylacetamide deacetylase-like 1 (AADACL1)
ENO2	1.65	1.32	NM_001975.2	enolase 2 (gamma
EXOSC5	1.61	1.32	NM_020158.3	exosome component 5 (EXOSC5)
COL4A4	1.59	1.32	NM_000092.4	collagen
EPS8	1.59	1.32	NM_004447.4	epidermal growth factor receptor pathway substrate 8 (EPS8)
LOC100130886	1.54	1.32	XM_001714477.1	PREDICTED: hypothetical protein LOC100130886 (LOC100130886)
CPEB2	1.52	1.32	NM_182646.1	cytoplasmic polyadenylation element binding protein 2 (CPEB2)
CLDND1	1.41	1.32	NM_001040181.1	claudin domain containing 1 (CLDND1)
UBA6	1.33	1.32	NM_018227.5	ubiquitin-like modifier activating enzyme 6 (UBA6)
IL8	1.29	1.32	NM_000584.2	interleukin 8 (IL8)
DPYSL3	0.9	1.32	NM_001387.2	dihydropyrimidinase-like 3 (DPYSL3)
HERC5	0.75	1.32	NM_016323.2	hect domain and RLD 5 (HERC5)
HIST1H2BK	0.15	1.32	NM_080593.1	histone cluster 1
PTP4A2	0.09	1.32	NM_080392.2	PREDICTED: protein tyrosine phosphatase type IVA
CLCN6	1.8	1.31	NM_001286.2	chloride channel 6 (CLCN6)
LOC100133609	1.78	1.31	XM_001720815.1	PREDICTED: similar to membrane-associated ring finger (C3HC4) 3 (LOC100133609)
DHDDS	1.74	1.31	NM_024887.2	dehydrodolichyl diphosphate synthase (DHDDS)
PGP	1.7	1.31	NM_001042371.2	phosphoglycolate phosphatase (PGP)
SLC43A3	1.68	1.31	NM_017611.2	solute carrier family 43
TMEM206	1.68	1.31	NM_018252.2	transmembrane protein 206 (TMEM206)
FAH	1.67	1.31	NM_000137.1	fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH)
GLS	1.67	1.31	NM_014905.2	glutaminase (GLS)
FAM8A1	1.65	1.31	NM_016255.1	family with sequence similarity 8
LNX2	1.64	1.31	NM_153371.3	ligand of numb-protein X 2 (LNX2)
TMEM167B	1.63	1.31	NM_020141.3	transmembrane protein 167B (TMEM167B)
MKNK1	1.62	1.31	NM_003684.3	MAP kinase interacting serine/threonine kinase 1 (MKNK1)
SMAD7	1.62	1.31	NM_005904.2	SMAD family member 7 (SMAD7)
C5orf33	1.6	1.31	NM_153013.3	chromosome 5 open reading frame 33 (C5orf33)
ARRDC3	1.59	1.31	NM_020801.1	arrestin domain containing 3 (ARRDC3)
AMMECR1L	1.54	1.31	NM_031445.2	AMME chromosomal region gene 1-like (AMMECR1L)
KIAA0240	1.53	1.31	NM_015349.1	KIAA0240 (KIAA0240)
AGGF1	1.49	1.31	NM_018046.3	angiogenic factor with G patch and FHA domains 1 (AGGF1)
DHX40	1.11	1.31	NM_024612.3	PREDICTED: DEAH (Asp-Glu-Ala-His) box polypeptide 40
TUBB6	1.03	1.31	XM_940079.1	PREDICTED: tubulin

CHURC1	0.94	1.31	NM_145165.2	churchill domain containing 1 (CHURC1)
LOC442229	1.84	1.3	XM_936681.1	PREDICTED: similar to mitochondrial carrier triple repeat 1 (LOC442229)
JMJD4	1.79	1.3	NM_023007.1	jumonji domain containing 4 (JMJD4)
CDC42BPA	1.71	1.3	NM_003607.3	CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA)
FUT4	1.7	1.3	NM_002033.2	fucosyltransferase 4 (alpha (1
DPY19L4	1.68	1.3	NM_181787.1	dpy-19-like 4 (C. elegans) (DPY19L4)
GCNT2	1.65	1.3	NM_001491.2	glucosaminyl (N-acetyl) transferase 2
THAP1	1.65	1.3	NM_018105.2	THAP domain containing
TMEM19	1.65	1.3	NM_018279.3	transmembrane protein 19 (TMEM19)
ADI1	1.64	1.3	NM_018269.1	acireductone dioxygenase 1 (ADI1)
GLRB	1.63	1.3	NM_000824.2	glycine receptor
ZNF706	1.63	1.3	NM_001042511.1	zinc finger protein 706 (ZNF706)
TP53BP2	1.61	1.3	NM_001031685.2	tumor protein p53 binding protein
MYNN	1.6	1.3	NM_018657.3	myoneurin (MYNN)
SEPN1	1.6	1.3	NM_206926.1	selenoprotein N
GRB10	1.59	1.3	NM_005311.3	growth factor receptor-bound protein 10 (GRB10)
LOC100130707	1.59	1.3	XM_001713657.1	PREDICTED: hypothetical protein LOC100130707 (LOC100130707)
VAV3	1.57	1.3	NM_006113.4	vav 3 guanine nucleotide exchange factor (VAV3)
APPL1	1.56	1.3	NM_012096.2	adaptor protein
C17orf42	1.54	1.3	NM_024683.3	chromosome 17 open reading frame 42 (C17orf42)
MTMR11	1.54	1.3	NM_181873.2	myotubularin related protein 11 (MTMR11)
LOC389599	1.53	1.3	XM_001131588.1	PREDICTED: similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region
LCLAT1	1.52	1.3	NM_182551.3	lysocardiolipin acyltransferase 1 (LCLAT1)
CLDND1	1.24	1.3	NM_001040181.1	claudin domain containing 1 (CLDND1)
DYNC1LI2	0.87	1.3	NM_006141.2	dynein
LHX6	1.7	1.29	NM_199160.2	LIM homeobox 6 (LHX6)
NRP1	1.68	1.29	NM_001024629.1	neuropilin 1 (NRP1)
KIAA0100	1.66	1.29	NM_014680.2	KIAA0100 (KIAA0100)
CNNM3	1.63	1.29	NM_017623.4	cyclin M3 (CNNM3)
LOC100128326	1.62	1.29	XR_038006.1	PREDICTED: misc_RNA (LOC100128326)
SERPINE1	1.62	1.29	NM_000602.1	serpin peptidase inhibitor
LOC645094	1.59	1.29	XR_039085.1	PREDICTED: misc_RNA (LOC645094)
HSPC157	1.56	1.29	NR_023918.1	hypothetical LOC29092 (HSPC157)
LCLAT1	1.55	1.29	NM_182551.3	lysocardiolipin acyltransferase 1 (LCLAT1)
DYRK4	1.51	1.29	NM_003845.1	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4)
HMOX1	1.4	1.29	NM_002133.1	heme oxygenase (decycling) 1 (HMOX1)
CHPF2	1.68	1.28	NM_019015.1	chondroitin polymerizing factor 2 (CHPF2)
STK17B	1.66	1.28	NM_004226.2	serine/threonine kinase 17b (STK17B)
ARHGAP12	1.65	1.28	NM_018287.4	Rho GTPase activating protein 12 (ARHGAP12)
LOC652481	1.65	1.28	XM_941942.1	PREDICTED: similar to Mitochondrial import inner membrane translocase subunit Tim23 (LOC652481)
LARP1B	1.59	1.28	NM_018078.2	La ribonucleoprotein domain family
LRRC45	1.59	1.28	NM_144999.2	leucine rich repeat containing 45 (LRRC45)
ARMC10	1.57	1.28	NM_031905.2	armadillo repeat containing 10 (ARMC10)
C20orf3	1.56	1.28	NM_020531.2	chromosome 20 open reading frame 3 (C20orf3)
PPM1H	1.56	1.28	NM_020700.1	protein phosphatase 1H (PP2C domain containing) (PPM1H)
CIC	1.55	1.28	NM_015125.3	capicua homolog (Drosophila) (CIC)
RDH11	1.54	1.28	NM_016026.2	retinol dehydrogenase 11 (all-trans/9-cis/11-cis) (RDH11)
MED21	1.53	1.28	NM_004264.3	mediator complex subunit 21 (MED21)
INO80D	1.47	1.28	NM_017759.4	INO80 complex subunit D (INO80D)

GOLT1B	1.4	1.28	NM_016072.3	golgi transport 1 homolog B (S. cerevisiae) (GOLT1B)
BAG5	1.04	1.28	NM_004873.2	BCL2-associated athanogene 5 (BAG5)
TTC37	1.04	1.28	NM_014639.2	tetratricopeptide repeat domain 37 (TTC37)
CNN3	0.86	1.28	NM_001839.2	calponin 3
TOMM34	0.51	1.28	NM_006809.4	translocase of outer mitochondrial membrane 34 (TOMM34)
ZNF416	1.69	1.27	NM_017879.1	zinc finger protein 416 (ZNF416)
PKMYT1	1.68	1.27	NM_182687.1	protein kinase
IGHMBP2	1.66	1.27	NM_002180.2	immunoglobulin mu binding protein 2 (IGHMBP2)
PRR5	1.66	1.27	NM_001017529.1	proline rich 5 (renal) (PRR5)
TMEM175	1.65	1.27	NM_032326.2	transmembrane protein 175 (TMEM175)
ACPL2	1.57	1.27	NM_152282.2	acid phosphatase-like 2 (ACPL2)
BAPX1	1.56	1.27	NM_001189.2	bagpipe homeobox homolog 1 (Drosophila) (BAPX1)
LOC647691	1.56	1.27	XM_936748.1	PREDICTED: similar to dicer1 (LOC647691)
MFSD6	1.55	1.27	NM_017694.3	major facilitator superfamily domain containing 6 (MFSD6)
CCNE1	1.54	1.27	NM_057182.1	cyclin E1 (CCNE1)
FAM13A	1.53	1.27	NM_001015045.1	family with sequence similarity 13
SFXN1	1.5	1.27	NM_022754.4	sideroflexin 1 (SFXN1)
ZNF621	1.5	1.27	NM_001098414.1	zinc finger protein 621 (ZNF621)
LOC651198	1.35	1.27	XM_001715717.1	PREDICTED: similar to hCG2036706 (LOC651198)
IFIT2	1.3	1.27	NM_001547.4	interferon-induced protein with tetratricopeptide repeats 2 (IFIT2)
CDC2L6	1.18	1.27	NM_015076.3	cell division cycle 2-like 6 (CDK8-like) (CDC2L6)
INSIG1	1.08	1.27	NM_198336.1	insulin induced gene 1 (INSIG1)
MTPN	0.82	1.27	NM_145808.2	myotrophin (MTPN)
RCCD1	1.65	1.26	NM_001017919.1	RCC1 domain containing 1 (RCCD1)
SCLY	1.65	1.26	NM_016510.3	selenocysteine lyase (SCLY)
ZNF473	1.61	1.26	NM_015428.1	zinc finger protein 473 (ZNF473)
FAM119A	1.6	1.26	NM_001127395.1	family with sequence similarity 119
BIRC6	1.57	1.26	NM_016252.3	baculoviral IAP repeat-containing 6 (BIRC6)
HPS1	1.57	1.26	NM_182639.1	Hermansky-Pudlak syndrome 1 (HPS1)
ATN1	1.51	1.26	NM_001007026.1	atrophin 1 (ATN1)
EPN2	1.51	1.26	NM_014964.3	epsin 2 (EPN2)
FAM119A	1.51	1.26	NM_145280.4	family with sequence similarity 119
SUSD1	1.49	1.26	NM_022486.3	sushi domain containing 1 (SUSD1)
FNDC3A	1.46	1.26	NM_001079673.1	fibronectin type III domain containing 3A (FNDC3A)
LZTFL1	1.46	1.26	NM_020347.2	leucine zipper transcription factor-like 1 (LZTFL1)
LAMP2	1.39	1.26	NM_013995.1	lysosomal-associated membrane protein 2 (LAMP2)
TMEM183A	1.59	1.25	NM_138391.4	transmembrane protein 183A (TMEM183A)
SLC16A9	1.55	1.25	NM_194298.1	solute carrier family 16
SASS6	1.39	1.25	NM_194292.1	spindle assembly 6 homolog (C. elegans) (SASS6)
CCNE2	1.33	1.25	NM_057735.1	cyclin E2 (CCNE2)
PELI2	1.16	1.25	NM_021255.2	pellino homolog 2 (Drosophila) (PELI2)
FVT1	0.89	1.25	NM_002035.1	follicular lymphoma variant translocation 1 (FVT1)
ARL4D	1.55	1.24	NM_001661.3	ADP-ribosylation factor-like 4D (ARL4D)
LOC442421	1.51	1.24	XM_927249.1	PREDICTED: similar to prostaglandin E receptor 4
XKR8	1.5	1.24	NM_018053.2	XK
SLC39A6	1.44	1.24	NM_012319.3	solute carrier family 39 (zinc transporter)
BCAR3	1.09	1.24	NM_003567.2	breast cancer anti-estrogen resistance 3 (BCAR3)
TMEM43	1.07	1.24	NM_024334.1	transmembrane protein 43 (TMEM43)
ZSCAN2	1.62	1.23	NM_181877.3	zinc finger and SCAN domain containing 2 (ZSCAN2)

MMP23A	1.53	1.23	NM_004659.1	matrix metallopeptidase 23A (MMP23A)
C14orf126	1.51	1.23	NM_080664.2	chromosome 14 open reading frame 126 (C14orf126)
NCRNA00081	1.48	1.23	NR_024142.1	non-protein coding RNA 81 (NCRNA00081)
MFAP5	1.31	1.23	NM_003480.2	microfibrillar associated protein 5 (MFAP5)
DCTN4	1.28	1.23	NM_016221.2	dynactin 4 (p62) (DCTN4)
TTC33	1.24	1.23	NM_012382.2	tetratricopeptide repeat domain 33 (TTC33)
XPR1	1.11	1.23	NM_004736.2	xenotropic and polytropic retrovirus receptor (XPR1)
GNG10	0.92	1.23	NM_001017998.2	guanine nucleotide binding protein (G protein)
CMTM3	1.43	1.22	NM_001048251.1	CKLF-like MARVEL transmembrane domain containing 3 (CMTM3)
AKAP11	1.29	1.22	NM_016248.2	A kinase (PRKA) anchor protein 11 (AKAP11)
HIF1A	1.28	1.22	NM_001530.2	hypoxia-inducible factor 1
IKBIP	1.28	1.22	NM_153687.2	IKBKB interacting protein (IKBIP)
PER3	1.28	1.22	NM_016831.1	period homolog 3 (Drosophila) (PER3)
FNDC3A	1.24	1.22	NM_001079673.1	fibronectin type III domain containing 3A (FNDC3A)
SPRYD3	1.24	1.22	NM_032840.1	SPRY domain containing 3 (SPRYD3)
AADAT	1.2	1.22	NM_182662.1	aminoadipate aminotransferase (AADAT)
SEMA4B	1.19	1.22	NM_198925.1	sema domain
GOLM1	1.05	1.22	NM_177937.1	golgi membrane protein 1 (GOLM1)
PEA15	0.82	1.22	NM_003768.2	phosphoprotein enriched in astrocytes 15 (PEA15)
RPN2	0.76	1.22	NM_002951.2	ribophorin II (RPN2)
RIOK1	1.35	1.21	NM_031480.2	RIO kinase 1 (yeast) (RIOK1)
KLHL28	1.3	1.21	NM_017658.3	kelch-like 28 (Drosophila) (KLHL28)
ING1	1.27	1.21	NM_198219.1	inhibitor of growth family
PTGFRN	1.26	1.21	NM_020440.2	prostaglandin F2 receptor negative regulator (PTGFRN)
NAV2	0.85	1.21	NM_145117.3	neuron navigator 2 (NAV2)
SH3BGRL	0.51	1.21	NM_003022.1	SH3 domain binding glutamic acid-rich protein like (SH3BGRL)
ATP2C1	1.37	1.2	NM_001001486.1	ATPase
MAP7D2	1.22	1.2	NM_152780.2	MAP7 domain containing 2 (MAP7D2)
USP37	1.13	1.2	NM_020935.1	ubiquitin specific peptidase 37 (USP37)
HIST1H2BK	0.8	1.2	NM_080593.1	histone cluster 1
GPR56	0.59	1.2	NM_201524.1	G protein-coupled receptor 56 (GPR56)
ATP1B3	0.44	1.2	XM_001133534.1	PREDICTED: ATPase
TOM1L1	1.34	1.19	NM_005486.1	target of myb1 (chicken)-like 1 (TOM1L1)
PDCD10	1.32	1.19	NM_145859.1	programmed cell death 10 (PDCD10)
TWISTNB	1.26	1.19	NM_001002926.1	TWIST neighbor (TWISTNB)
ARSB	1.23	1.19	NM_000046.2	arylsulfatase B (ARSB)
LOC730167	1.23	1.19	XM_001726158.1	PREDICTED: similar to protein tyrosine phosphatase 4a1
PIK3C2B	1.22	1.19	NM_002646.2	phosphoinositide-3-kinase
PIM2	1.22	1.19	NM_006875.2	pim-2 oncogene (PIM2)
OASL	1.14	1.19	NM_198213.1	2'-5'-oligoadenylate synthetase-like (OASL)
SNAPIN	0.94	1.19	NM_012437.3	SNAP-associated protein (SNAPIN)
LOC440595	0.69	1.19	XR_038356.1	PREDICTED: misc_RNA (LOC440595)
TMEM189	0.58	1.19	NM_199129.1	transmembrane protein 189 (TMEM189)
NFE2L2	0.45	1.19	NM_006164.2	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2)
PMP22	0.24	1.19	NM_153321.1	peripheral myelin protein 22 (PMP22)
MIR1978	0.23	1.19	NR_031742.1	microRNA 1978 (MIR1978)
AFTPH	1.31	1.18	NM_203437.2	aftiphilin (AFTPH)
RAB4A	1.27	1.18	NM_004578.2	RAB4A
LOC645175	1.14	1.18	XR_017268.2	PREDICTED: misc_RNA (LOC645175)

CNOT8	1.13	1.18	NM_004779.4	CCR4-NOT transcription complex
KPNA1	0.98	1.18	NM_002264.1	karyopherin alpha 1 (importin alpha 5) (KPNA1)
ZNF275	0.85	1.18	NM_001080485.1	zinc finger protein 275 (ZNF275)
PLEKHA3	1.34	1.17	NM_019091.3	pleckstrin homology domain containing
PPFIA1	1.23	1.17	NM_177423.1	protein tyrosine phosphatase
TULP4	1	1.17	NM_001007466.1	tubby like protein 4 (TULP4)
IMPAD1	0.98	1.17	NM_017813.2	inositol monophosphatase domain containing 1 (IMPAD1)
HNRNPUL2	0.95	1.17	NM_001079559.1	heterogeneous nuclear ribonucleoprotein U-like 2 (HNRNPUL2)
BFAR	0.94	1.17	NM_016561.1	bifunctional apoptosis regulator (BFAR)
CYB5R4	0.88	1.17	NM_016230.3	cytochrome b5 reductase 4 (CYB5R4)
SPPL2A	0.76	1.17	NM_032802.3	signal peptide peptidase-like 2A (SPPL2A)
LOC644033	0.7	1.17	XM_927280.1	PREDICTED: similar to similar to RPL23AP7 protein (LOC644033)
PSMG1	0.5	1.17	NM_003720.2	proteasome (prosome
TBL1XR1	1.19	1.16	NM_024665.3	transducin (beta)-like 1X-linked receptor 1 (TBL1XR1)
NCBP2	1.12	1.16	NM_007362.3	nuclear cap binding protein subunit 2
PRNP	1.1	1.16	NM_183079.2	prion protein (PRNP)
LOC642197	1.05	1.16	XM_936354.2	PREDICTED: similar to Protein FAM82B (LOC642197)
KIF1C	0.97	1.16	NM_006612.4	kinesin family member 1C (KIF1C)
NTN4	0.95	1.16	NM_021229.3	netrin 4 (NTN4)
GCLM	0.57	1.16	NM_002061.2	glutamate-cysteine ligase
ISCA1	0.44	1.16	NM_030940.3	iron-sulfur cluster assembly 1 homolog (S. cerevisiae) (ISCA1)
NT5C3	0.34	1.16	NM_001002010.1	5'-nucleotidase
PITPNC1	1.1	1.15	NM_181671.1	phosphatidylinositol transfer protein
AADACL1	1.09	1.15	NM_020792.3	arylacetamide deacetylase-like 1 (AADACL1)
C15orf57	1.07	1.15	NM_001080791.1	chromosome 15 open reading frame 57 (C15orf57)
RAGE	1.06	1.15	NM_014226.1	renal tumor antigen (RAGE)
C10orf104	1.04	1.15	NM_173473.2	chromosome 10 open reading frame 104 (C10orf104)
MED7	0.89	1.15	NM_001100816.1	mediator complex subunit 7 (MED7)
RANBP6	0.85	1.15	NM_012416.2	RAN binding protein 6 (RANBP6)
COPS2	0.83	1.15	NM_004236.2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis) (COPS2)
IFT20	0.77	1.15	NM_174887.2	intraflagellar transport 20 homolog (Chlamydomonas) (IFT20)
NAT13	0.71	1.15	NM_025146.1	N-acetyltransferase 13 (GCN5-related) (NAT13)
HIST1H2BD	0.6	1.15	NM_138720.1	histone cluster 1
BBX	0.59	1.15	NM_020235.3	bobby sox homolog (Drosophila) (BBX)
TACC1	0.51	1.15	NM_006283.1	transforming
LSM10	0.41	1.15	NM_032881.1	LSM10
ASPM	0.32	1.15	NM_018136.3	asp (abnormal spindle) homolog
PRICKLE4	-0.4	1.15	NM_013397.4	prickle homolog 4 (Drosophila) (PRICKLE4)
STT3B	1.15	1.14	NM_178862.1	STT3
KLRAQ1	1.09	1.14	NM_001135629.1	KLRAQ motif containing 1 (KLRAQ1)
FAM13A	1.04	1.14	NM_014883.2	family with sequence similarity 13
NKX3-1	1.01	1.14	NM_006167.2	NK3 homeobox 1 (NKX3-1)
LOC100131139	0.92	1.14	XR_037336.1	PREDICTED: misc_RNA (LOC100131139)
USP13	0.84	1.14	NM_003940.1	ubiquitin specific peptidase 13 (isopeptidase T-3) (USP13)
CBY1	0.76	1.14	NM_015373.3	chibby homolog 1 (Drosophila) (CBY1)
CCDC16	0.59	1.14	NM_052857.2	coiled-coil domain containing 16 (CCDC16)
TMEM77	1.09	1.13	NM_178454.3	transmembrane protein 77 (TMEM77)
MBD2	1.07	1.13	NM_003927.3	methyl-CpG binding domain protein 2 (MBD2)
DYRK2	0.92	1.13	NM_003583.3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2)

MFN2	0.73	1.13	NM_014874.2	mitofusin 2 (MFN2)
PARP8	0.73	1.13	NM_024615.2	PREDICTED: poly (ADP-ribose) polymerase family
ELOVL5	0.64	1.13	NM_021814.3	ELOVL family member 5
PERP	-0.23	1.13	NM_022121.2	PERP
NDUFS3	-0.56	1.13	NM_004551.1	NADH dehydrogenase (ubiquinone) Fe-S protein 3
C14orf156	-1.01	1.13	NM_031210.3	chromosome 14 open reading frame 156 (C14orf156)
AHI1	1.04	1.12	NM_017651.3	Abelson helper integration site 1 (AHI1)
GNGT1	0.92	1.12	NM_021955.3	guanine nucleotide binding protein (G protein)
CUL5	0.91	1.12	NM_003478.3	cullin 5 (CUL5)
EMP1	0.77	1.12	NM_001423.1	epithelial membrane protein 1 (EMP1)
MTIF2	0.74	1.12	NM_001005369.1	mitochondrial translational initiation factor 2 (MTIF2)
PTGFRN	0.74	1.12	NM_020440.2	prostaglandin F2 receptor negative regulator (PTGFRN)
UBE2D2	0.73	1.12	NM_003339.2	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog
LOC100132658	0.19	1.12	XR_038800.1	PREDICTED: misc_RNA (LOC100132658)
SUMO1P3	-0.23	1.12	NR_002190.1	SUMO1 pseudogene 3 (SUMO1P3)
LOC158345	-1.05	1.12	XR_017130.1	PREDICTED: similar to ribosomal protein L4 (LOC158345)
PPP2R2D	1.03	1.11	NM_018461.2	protein phosphatase 2
SLC41A1	0.94	1.11	NM_173854.4	solute carrier family 41
CASP7	0.91	1.11	NM_033339.3	caspase 7
IER5	0.73	1.11	NM_016545.4	immediate early response 5 (IER5)
LOC642333	0.72	1.11	XR_019071.1	PREDICTED: similar to M-phase phosphoprotein
SDHC	0.7	1.11	NM_001035513.1	succinate dehydrogenase complex
PTPLA	0.59	1.11	NM_014241.3	protein tyrosine phosphatase-like (proline instead of catalytic arginine)
C10orf58	0.53	1.11	NM_032333.4	chromosome 10 open reading frame 58 (C10orf58)
PSIP1	0	1.11	NM_033222.2	PC4 and SFRS1 interacting protein 1 (PSIP1)
ERRFI1	-0.1	1.11	NM_018948.2	ERBB receptor feedback inhibitor 1 (ERRFI1)
CEBPB	-0.65	1.11	NM_005194.2	CCAAT/enhancer binding protein (C/EBP)
STS-1	0.92	1.1	NM_032873.3	Cbl-interacting protein Sts-1 (STS-1)
HSD17B11	0.88	1.1	NM_016245.3	hydroxysteroid (17-beta) dehydrogenase 11 (HSD17B11)
CKAP2	0.84	1.1	NM_001098525.1	cytoskeleton associated protein 2 (CKAP2)
CAND1	0.83	1.1	NM_018448.2	cullin-associated and neddylation-dissociated 1 (CAND1)
BBS2	0.81	1.1	NM_031885.2	Bardet-Biedl syndrome 2 (BBS2)
SEPHS1	0.73	1.1	NM_012247.3	selenophosphate synthetase 1 (SEPHS1)
MAP1B	0.58	1.1	NM_032010.1	microtubule-associated protein 1B (MAP1B)
UBE2L3	0.48	1.1	NM_198157.1	ubiquitin-conjugating enzyme E2L 3 (UBE2L3)
MBD4	0.33	1.1	NM_003925.1	methyl-CpG binding domain protein 4 (MBD4)
PSME4	0.33	1.1	NM_014614.1	proteasome (prosome
SCARB2	0.29	1.1	NM_005506.2	scavenger receptor class B
LOC646527	0.18	1.1	XR_016632.2	PREDICTED: misc_RNA (LOC646527)
MLLT11	0.14	1.1	NM_006818.3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog
ATP6AP2	0.11	1.1	NM_005765.2	ATPase
AK3L1	0.04	1.1	NM_203464.1	adenylate kinase 3-like 1 (AK3L1)
HMGN4	0	1.1	NM_006353.2	high mobility group nucleosomal binding domain 4 (HMGN4)
LOC641848	-0.09	1.1	XM_935588.1	PREDICTED: similar to ribosomal protein S3a (LOC641848)
BIRC5	1.01	1.09	NM_001012271.1	baculoviral IAP repeat-containing 5 (BIRC5)
ERGIC1	0.99	1.09	NM_020462.1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (ERGIC1)
LOC401357	0.77	1.09	NM_001013685.1	hypothetical LOC401357 (LOC401357)
LOC653631	0.75	1.09	XM_930476.2	PREDICTED: hypothetical LOC653631 (LOC653631)
LOC201725	0.57	1.09	NM_001008393.1	hypothetical protein LOC201725 (LOC201725)

LOC440926	0.56	1.09	NR_002315.1	H3 histone
TXNRD1	0.52	1.09	NM_182743.1	thioredoxin reductase 1 (TXNRD1)
ZAK	0.32	1.09	NM_133646.2	sterile alpha motif and leucine zipper containing kinase AZK (ZAK)
IL17RD	0.19	1.09	NM_001080973.1	interleukin 17 receptor D (IL17RD)
TRIP13	-0.7	1.09	NM_004237.2	thyroid hormone receptor interactor 13 (TRIP13)
LOC100134504	-0.83	1.09	XM_001725687.1	PREDICTED: hypothetical protein LOC100134504 (LOC100134504)
EEF1A1	-1.62	1.09	NM_001402.5	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1)
C12orf76	0.89	1.08	NM_207435.1	chromosome 12 open reading frame 76 (C12orf76)
GMCL1	0.8	1.08	NM_178439.3	germ cell-less homolog 1 (Drosophila) (GMCL1)
TMEM170A	0.78	1.08	NM_145254.1	transmembrane protein 170A (TMEM170A)
DSTYK	0.74	1.08	NM_199462.2	dual serine/threonine and tyrosine protein kinase (DSTYK)
GNPDA2	0.71	1.08	NM_138335.1	glucosamine-6-phosphate deaminase 2 (GNPDA2)
KIF11	0.64	1.08	NM_004523.2	kinesin family member 11 (KIF11)
LOC221710	0.62	1.08	XM_927609.1	PREDICTED: hypothetical protein LOC221710 (LOC221710)
C4orf46	0.6	1.08	NM_001008393.2	chromosome 4 open reading frame 46 (C4orf46)
CDC42	0.58	1.08	NM_001039802.1	cell division cycle 42 (GTP binding protein
ALG5	0.52	1.08	NM_013338.3	asparagine-linked glycosylation 5 homolog (S. cerevisiae
TMEM209	0.35	1.08	NM_032842.3	transmembrane protein 209 (TMEM209)
RBBP8	-0.07	1.08	NM_203291.1	retinoblastoma binding protein 8 (RBBP8)
AKR1C4	-0.78	1.08	NM_001818.2	aldo-keto reductase family 1
ORC6L	-1.59	1.08	NM_014321.2	origin recognition complex
GPRC5C	0.84	1.07	NM_018653.3	G protein-coupled receptor
PPFIA1	0.84	1.07	NM_177423.1	protein tyrosine phosphatase
SNX25	0.83	1.07	NM_031953.2	sorting nexin 25 (SNX25)
CRLF3	0.78	1.07	NM_015986.2	cytokine receptor-like factor 3 (CRLF3)
ARID3B	0.74	1.07	NM_006465.2	AT rich interactive domain 3B (BRIGHT-like) (ARID3B)
ATP2C1	0.73	1.07	NM_001001485.1	ATPase
C10orf6	0.72	1.07	NM_018121.2	chromosome 10 open reading frame 6 (C10orf6)
RELA	0.72	1.07	NM_021975.2	v-rel reticuloendotheliosis viral oncogene homolog A (avian) (RELA)
BTN3A2	0.7	1.07	NM_007047.3	butyrophilin
CDKN1C	0.63	1.07	NM_000076.1	cyclin-dependent kinase inhibitor 1C (p57
KIAA0430	0.63	1.07	NM_014647.2	KIAA0430 (KIAA0430)
MN1	0.62	1.07	NM_002430.2	meningioma (disrupted in balanced translocation) 1 (MN1)
FAR1	0.6	1.07	NM_032228.4	fatty acyl CoA reductase 1 (FAR1)
NFIX	0.59	1.07	NM_002501.2	nuclear factor I/X (CCAAT-binding transcription factor) (NFIX)
C17orf58	0.58	1.07	NM_181656.3	chromosome 17 open reading frame 58 (C17orf58)
DNAJB14	0.56	1.07	NM_024920.3	DnaJ (Hsp40) homolog
FRMD6	0.52	1.07	NM_152330.2	FERM domain containing 6 (FRMD6)
LEPR	0.51	1.07	NM_001003679.1	leptin receptor (LEPR)
YEATS4	0.47	1.07	NM_006530.2	YEATS domain containing 4 (YEATS4)
DCUN1D5	0.13	1.07	NM_032299.2	DCN1
UBE2F	-0.08	1.07	NM_080678.1	ubiquitin-conjugating enzyme E2F (putative) (UBE2F)
NQO1	-0.92	1.07	NM_000903.2	NAD(P)H dehydrogenase
UBB	-1.2	1.07	NM_018955.2	ubiquitin B (UBB)
LOC392437	-1.35	1.07	XR_037197.1	PREDICTED: misc_RNA (LOC392437)
GNAS	-1.76	1.07	NM_016592.2	GNAS complex locus (GNAS)
SNX5	0.77	1.06	NM_152227.1	sorting nexin 5 (SNX5)
CYCS	0.76	1.06	NM_018947.4	cytochrome c
LIX1L	0.76	1.06	NM_153713.1	Lix1 homolog (mouse)-like (LIX1L)

C6orf176	0.74	1.06	XR_017929.2	PREDICTED: misc_RNA (C6orf176)
ARID4B	0.66	1.06	NM_016374.5	AT rich interactive domain 4B (RBP1-like) (ARID4B)
TAF1D	0.61	1.06	NM_024116.2	TATA box binding protein (TBP)-associated factor
ITPRIPL2	0.52	1.06	NM_001034841.2	inositol 1
AGPAT9	0.49	1.06	NM_032717.3	1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9)
LARP7	0.49	1.06	NM_015454.1	La ribonucleoprotein domain family
SLC12A8	0.45	1.06	NM_024628.4	solute carrier family 12 (potassium/chloride transporters)
GPSM2	0.36	1.06	NM_013296.3	G-protein signalling modulator 2 (AGS3-like
DNAJB1	0.3	1.06	NM_006145.1	DnaJ (Hsp40) homolog
ITGAV	0.21	1.06	NM_002210.2	integrin
ADO	0.01	1.06	NM_032804.5	2-aminoethanethiol (cysteamine) dioxygenase (ADO)
UAP1	-0.01	1.06	NM_003115.3	UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1)
ATP1B1	-0.06	1.06	NM_001677.3	ATPase
DNAJC8	-0.95	1.06	NM_014280.2	DnaJ (Hsp40) homolog
C19orf31	-1.83	1.06	NM_001014373.1	chromosome 19 open reading frame 31 (C19orf31)
SEPN1	0.77	1.05	NM_020451.2	selenoprotein N
C1orf149	0.75	1.05	NM_022756.3	chromosome 1 open reading frame 149 (C1orf149)
ALDH3A2	0.74	1.05	NM_001031806.1	aldehyde dehydrogenase 3 family
AKR1B10	0.71	1.05	NM_020299.3	aldo-keto reductase family 1
HSPA4L	0.7	1.05	NM_014278.2	heat shock 70kDa protein 4-like (HSPA4L)
LIN52	0.69	1.05	NM_001024674.1	lin-52 homolog (C. elegans) (LIN52)
EPM2AIP1	0.67	1.05	NM_014805.2	EPM2A (laforin) interacting protein 1 (EPM2AIP1)
FLJ14213	0.67	1.05	NM_024841.3	protor-2 (FLJ14213)
OCRL	0.67	1.05	NM_001587.3	oculocerebrorenal syndrome of Lowe (OCRL)
TMEM118	0.56	1.05	NM_032814.2	transmembrane protein 118 (TMEM118)
MED30	0.48	1.05	NM_080651.1	mediator complex subunit 30 (MED30)
AP1S2	0.35	1.05	NM_003916.3	adaptor-related protein complex 1
DEPDC1	0.33	1.05	NM_017779.3	DEP domain containing 1 (DEPDC1)
DPM2	0.29	1.05	NM_003863.2	dolichyl-phosphate mannosyltransferase polypeptide 2
EXOSC9	0.28	1.05	NM_001034194.1	exosome component 9 (EXOSC9)
NTAN1	0.21	1.05	NM_173474.2	N-terminal asparagine amidase (NTAN1)
FRG1	0	1.05	NM_004477.2	FSHD region gene 1 (FRG1)
C12orf48	-0.07	1.05	NM_017915.2	chromosome 12 open reading frame 48 (C12orf48)
UPP1	-0.14	1.05	NM_003364.2	uridine phosphorylase 1 (UPP1)
RPL4	-1.54	1.05	NM_000968.2	ribosomal protein L4 (RPL4)
LOC649150	-1.59	1.05	XR_019269.1	PREDICTED: similar to eukaryotic translation elongation factor 1 alpha 2 (LOC649150)
LOC645715	-1.79	1.05	XR_017484.1	PREDICTED: misc_RNA (LOC645715)
LOC100132593	-1.91	1.05	XM_001719642.1	PREDICTED: hypothetical protein LOC100132593 (LOC100132593)
TWF1	0.87	1.04	NM_002822.3	twinfilin
FAM3C	0.73	1.04	NM_001040020.1	family with sequence similarity 3
FOSL1	0.6	1.04	NM_005438.2	FOS-like antigen 1 (FOSL1)
SNX13	0.54	1.04	NM_015132.3	sorting nexin 13 (SNX13)
HSPB8	0.42	1.04	NM_014365.2	heat shock 22kDa protein 8 (HSPB8)
GNB5	0.35	1.04	NM_006578.3	guanine nucleotide binding protein (G protein)
VTI1B	0.24	1.04	NM_006370.1	vesicle transport through interaction with t-SNAREs homolog 1B (yeast) (VTI1B)
FUNDC1	0.23	1.04	NM_173794.2	FUN14 domain containing 1 (FUNDC1)
BRWD1	0.09	1.04	NM_001007246.1	bromodomain and WD repeat domain containing 1 (BRWD1)
IDH1	-0.04	1.04	NM_005896.2	isocitrate dehydrogenase 1 (NADP+)
IARS2	-0.12	1.04	NM_018060.3	isoleucyl-tRNA synthetase 2

MAGT1	-0.12	1.04	NM_032121.4	magnesium transporter 1 (MAGT1)
MRPS11	-0.23	1.04	NM_176805.1	mitochondrial ribosomal protein S11 (MRPS11)
ITGB5	-0.24	1.04	NM_002213.3	PREDICTED: integrin
LOC642828	-1	1.04	XR_016385.2	PREDICTED: misc_RNA (LOC642828)
LOC730534	-1.12	1.04	XR_015150.1	PREDICTED: similar to D-PCa-2 protein isoform c (LOC730534)
SRP14	-1.64	1.04	NM_003134.2	signal recognition particle 14kDa (homologous Alu RNA binding protein) (SRP14)
RTKN	0.66	1.03	NM_033046.2	rhotekin (RTKN)
TROVE2	0.64	1.03	NM_001042370.1	TROVE domain family
IFIH1	0.61	1.03	NM_022168.2	interferon induced with helicase C domain 1 (IFIH1)
GMCL1	0.58	1.03	NM_178439.3	germ cell-less homolog 1 (Drosophila) (GMCL1)
ZNF765	0.56	1.03	NM_001040185.1	zinc finger protein 765 (ZNF765)
CAPRIN1	0.54	1.03	NM_005898.4	cell cycle associated protein 1 (CAPRIN1)
LGALS8	0.53	1.03	NM_201545.1	lectin
TRIM26	0.49	1.03	NM_003449.3	tripartite motif-containing 26 (TRIM26)
KDELR3	0.48	1.03	NM_006855.2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3)
HERC4	0.45	1.03	NM_022079.2	hect domain and RLD 4 (HERC4)
HIST1H2BD	0.44	1.03	NM_138720.1	histone cluster 1
ING2	0.43	1.03	NM_001564.2	inhibitor of growth family
DNAJA4	0.4	1.03	NM_018602.2	DnaJ (Hsp40) homolog
TM9SF3	0.4	1.03	NM_020123.2	transmembrane 9 superfamily member 3 (TM9SF3)
TLE4	0.39	1.03	NM_007005.3	transducin-like enhancer of split 4 (E(sp1) homolog
MTMR9	0.33	1.03	NM_015458.3	myotubularin related protein 9 (MTMR9)
NUAK1	0.33	1.03	NM_014840.2	NUAK family
TTK	0.22	1.03	NM_003318.3	TTK protein kinase (TTK)
BUB3	0.21	1.03	NM_004725.2	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3)
NT5C3	0.2	1.03	NM_001002010.1	5'-nucleotidase
PICALM	0.16	1.03	NM_007166.2	phosphatidylinositol binding clathrin assembly protein (PICALM)
PSMA2	0.15	1.03	NM_002787.3	proteasome (prosome
LOC644131	0.09	1.03	XR_018325.1	PREDICTED: similar to chaperonin containing TCP1
BNIP3L	0.08	1.03	NM_004331.2	BCL2/adenovirus E1B 19kDa interacting protein 3-like (BNIP3L)
YWHAG	0.02	1.03	NM_012479.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
GALNT1	-0.02	1.03	NM_020474.2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)
NUSAP1	-0.17	1.03	NM_018454.5	nucleolar and spindle associated protein 1 (NUSAP1)
MRPL20	-0.44	1.03	NM_017971.2	mitochondrial ribosomal protein L20 (MRPL20)
PFN2	-0.89	1.03	NM_053024.2	profilin 2 (PFN2)
C9orf80	-0.93	1.03	NM_021218.1	chromosome 9 open reading frame 80 (C9orf80)
SFRS9	-1.09	1.03	NM_003769.2	splicing factor
LOC645387	-1.68	1.03	XR_019447.2	PREDICTED: misc_RNA (LOC645387)
ITIH5	-1.88	1.03	NM_001001851.1	inter-alpha (globulin) inhibitor H5 (ITIH5)
FAM177A1	-1.97	1.03	NM_173607.3	family with sequence similarity 177
TSPAN4	0.62	1.02	NM_001025238.1	tetraspanin 4 (TSPAN4)
MAPK1	0.58	1.02	NM_138957.2	mitogen-activated protein kinase 1 (MAPK1)
MRPL35	0.51	1.02	NM_016622.2	mitochondrial ribosomal protein L35 (MRPL35)
TMEM159	0.49	1.02	NM_020422.3	transmembrane protein 159 (TMEM159)
NUP50	0.45	1.02	NM_007172.3	nucleoporin 50kDa (NUP50)
NEK6	0.38	1.02	NM_014397.3	NIMA (never in mitosis gene a)-related kinase 6 (NEK6)
TFIP11	0.33	1.02	NM_012143.2	tuftelin interacting protein 11 (TFIP11)
MLEC	0.31	1.02	NM_014730.2	malectin (MLEC)
RAPGEF1	0.1	1.02	NM_198679.1	Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1)

ITGB3BP	0.01	1.02	NM_014288.3	integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP)
ARMCX2	-0.01	1.02	NM_177949.1	armadillo repeat containing
IRX3	-0.1	1.02	NM_024336.1	iroquois homeobox 3 (IRX3)
LOC100133185	-0.36	1.02	XR_039407.1	PREDICTED: misc_RNA (LOC100133185)
KTN1	-0.45	1.02	NM_004986.2	kinectin 1 (kinesin receptor) (KTN1)
LOC100128288	-0.45	1.02	NR_024447.1	hypothetical protein LOC100128288 (LOC100128288)
COX17	-0.86	1.02	NM_005694.1	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae) (COX17)
ZNF549	-0.9	1.02	NM_153263.1	zinc finger protein 549 (ZNF549)
LOC100130892	-1.03	1.02	XM_001720172.1	PREDICTED: hypothetical protein LOC100130892 (LOC100130892)
BTF3	-1.62	1.02	NM_001037637.1	basic transcription factor 3 (BTF3)
LOC728590	-1.63	1.02	XM_001131826.2	PREDICTED: similar to rCG23287 (LOC728590)
AKR1C3	-1.68	1.02	NM_003739.4	aldo-keto reductase family 1
LOC729324	-1.74	1.02	XR_041500.1	PREDICTED: misc_RNA (LOC729324)
LOC100128410	-1.82	1.02	XR_037117.1	PREDICTED: misc_RNA (LOC100128410)
AKR1C2	-1.84	1.02	NM_001354.4	aldo-keto reductase family 1
LOC100133465	-2	1.02	XR_037361.1	PREDICTED: misc_RNA (LOC100133465)
IMAA	-2.23	1.02	NR_002594.1	SLC7A5 pseudogene (IMAA)
MAT2B	0.71	1.01	NM_013283.3	methionine adenosyltransferase II
ZFP64	0.57	1.01	NM_199427.1	zinc finger protein 64 homolog (mouse) (ZFP64)
VAMP4	0.55	1.01	NM_003762.3	vesicle-associated membrane protein 4 (VAMP4)
KATNA1	0.48	1.01	NM_007044.2	katanin p60 (ATPase-containing) subunit A 1 (KATNA1)
WWP2	0.47	1.01	NM_199423.1	WW domain containing E3 ubiquitin protein ligase 2 (WWP2)
ARIH1	0.41	1.01	NM_005744.2	ariadne homolog
AGPAT2	0.36	1.01	NM_006412.3	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase
OLR1	0.26	1.01	NM_002543.3	oxidized low density lipoprotein (lectin-like) receptor 1 (OLR1)
AEN	0.25	1.01	NM_022767.3	apoptosis enhancing nuclease (AEN)
KIF5B	0.2	1.01	NM_004521.1	kinesin family member 5B (KIF5B)
PNN	0.18	1.01	NM_002687.3	pinin
CD55	0.16	1.01	NM_000574.2	CD55 molecule
TSEN2	0.15	1.01	NM_025265.2	tRNA splicing endonuclease 2 homolog (S. cerevisiae) (TSEN2)
LMOD3	0.08	1.01	NM_198271.2	leiomodin 3 (fetal) (LMOD3)
KIAA0020	0.07	1.01	NM_014878.4	KIAA0020 (KIAA0020)
PPARBP	0.07	1.01	NM_004774.2	PPAR binding protein (PPARBP)
GAPVD1	0.05	1.01	NM_015635.2	GTPase activating protein and VPS9 domains 1 (GAPVD1)
LOC387882	-0.05	1.01	NM_207376.1	hypothetical protein (LOC387882)
CLCC1	-0.06	1.01	NM_015127.3	chloride channel CLIC-like 1 (CLCC1)
LOC647150	-0.26	1.01	XR_017449.2	PREDICTED: misc_RNA (LOC647150)
TMEM17	-0.55	1.01	NM_198276.1	transmembrane protein 17 (TMEM17)
LOC388076	-1.04	1.01	XM_001722259.1	PREDICTED: hypothetical LOC388076 (LOC388076)
LOC731542	-1.57	1.01	XR_015517.2	PREDICTED: misc_RNA (LOC731542)
LOC645387	-1.72	1.01	XR_016424.2	PREDICTED: misc_RNA (LOC645387)
LOC644039	-2.05	1.01	XM_929431.1	PREDICTED: similar to 60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (LOC644039)
RAB7L1	0.54	1	NM_003929.1	RAB7
UGT8	0.4	1	NM_003360.2	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase) (UGT8)
SPOCD1	0.38	1	NM_144569.4	SPOC domain containing 1 (SPOCD1)
CCDC53	-0.03	1	NM_016053.2	coiled-coil domain containing 53 (CCDC53)
CNIH4	-0.63	1	NM_014184.2	cornichon homolog 4 (Drosophila) (CNIH4)
LOC649946	-1.59	1	NR_003040.1	PREDICTED: similar to 60S ribosomal protein L23a (LOC649946)
RPS6P1	-1.92	1	XR_039076.1	PREDICTED: misc_RNA (RPS6P1)

NOV	0.35	-1	NM_002514.2	nephroblastoma overexpressed gene (NOV)
OKL38	0.28	-1	NM_013370.2	pregnancy-induced growth inhibitor (OKL38)
RNF121	0.24	-1	NM_018320.3	ring finger protein 121 (RNF121)
SCCPDH	0.21	-1	NM_016002.2	saccharopine dehydrogenase (putative) (SCCPDH)
DLGAP5	-0.07	-1	NM_014750.3	discs
SEPX1	-0.23	-1	NM_016332.2	selenoprotein X
HMGB1L1	-0.34	-1	NM_001008735.1	high-mobility group box 1-like 1 (HMGB1L1)
SPTLC1	-0.96	-1	NM_178324.1	serine palmitoyltransferase
SNRPG	-1.57	-1	NM_003096.2	small nuclear ribonucleoprotein polypeptide G (SNRPG)
H2AFY	-1.61	-1	NM_004893.2	H2A histone family
HNRPA2B1	-1.66	-1	NM_031243.1	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1)
RAN	-1.76	-1	NM_006325.3	RAN
NACA	-1.79	-1	NM_005594.2	nascent-polypeptide-associated complex alpha polypeptide (NACA)
EIF2C3	0.51	-1.01	NM_177422.1	eukaryotic translation initiation factor 2C
HIF1A	0.43	-1.01	NM_001530.2	hypoxia-inducible factor 1
TAF5	0.41	-1.01	NM_006951.3	TAF5 RNA polymerase II
GPC6	0.36	-1.01	NM_005708.2	glypican 6 (GPC6)
USP33	0.36	-1.01	NM_015017.3	ubiquitin specific peptidase 33 (USP33)
LIPA	0.31	-1.01	NM_000235.2	lipase A
LOC400061	0.09	-1.01	XR_039516.1	PREDICTED: misc_RNA (LOC400061)
LOC645231	0.07	-1.01	XR_040322.1	PREDICTED: misc_RNA (LOC645231)
USP48	0.07	-1.01	NM_001032730.1	ubiquitin specific peptidase 48 (USP48)
RAB3GAP1	0.05	-1.01	NM_012233.1	RAB3 GTPase activating protein subunit 1 (catalytic) (RAB3GAP1)
RSRC2	0.04	-1.01	NM_023012.4	arginine/serine-rich coiled-coil 2 (RSRC2)
TUFT1	0	-1.01	NM_020127.1	tuftelin 1 (TUFT1)
PRCP	-0.04	-1.01	NM_005040.2	prolylcarboxypeptidase (angiotensinase C) (PRCP)
GGH	-0.06	-1.01	NM_003878.1	gamma-glutamyl hydrolase (conjugase
MYH10	-0.07	-1.01	NM_005964.1	myosin
AP1S2	-0.12	-1.01	NM_003916.3	adaptor-related protein complex 1
HSD17B12	-0.32	-1.01	NM_016142.1	hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12)
MRPL34	-0.65	-1.01	NM_023937.2	mitochondrial ribosomal protein L34 (MRPL34)
NLRP8	-0.72	-1.01	NM_176811.2	NLR family
CKS1B	-1.28	-1.01	NM_001826.1	CDC28 protein kinase regulatory subunit 1B (CKS1B)
PSMB1	-1.5	-1.01	NM_002793.2	proteasome (prosome
ANXA2	-1.87	-1.01	NM_001002858.1	annexin A2 (ANXA2)
NME1	-1.87	-1.01	NM_000269.2	non-metastatic cells 1
LOC653314	-2.11	-1.01	NM_001080544.2	similar to ribosomal protein L19 (LOC653314)
HERC3	0.4	-1.02	NM_014606.1	hect domain and RLD 3 (HERC3)
SNORA6	0.39	-1.02	NR_002325.1	small nucleolar RNA
WASH1	0.38	-1.02	NM_182905.3	WAS protein family homolog 1 (WASH1)
BRI3BP	0.36	-1.02	NM_080626.5	PREDICTED: BRI3 binding protein (BRI3BP)
SEC23A	0.34	-1.02	NM_006364.2	Sec23 homolog A (S. cerevisiae) (SEC23A)
FBXO30	0.32	-1.02	NM_032145.4	F-box protein 30 (FBXO30)
LOC100133600	0.27	-1.02	XM_001713611.1	PREDICTED: hypothetical protein LOC100133600 (LOC100133600)
PCYOX1	0.27	-1.02	NM_016297.2	prenylcysteine oxidase 1 (PCYOX1)
TMEM45A	0.26	-1.02	NM_018004.1	transmembrane protein 45A (TMEM45A)
WNT7B	0.08	-1.02	NM_058238.1	wingless-type MMTV integration site family
KIF11	0.04	-1.02	NM_004523.2	kinesin family member 11 (KIF11)
SNHG7	0.02	-1.02	NR_024542.1	small nucleolar RNA host gene 7 (non-protein coding) (SNHG7)

PRRC1	-0.02	-1.02	NM_130809.2	proline-rich coiled-coil 1 (PRRC1)
MLEC	-0.27	-1.02	NM_014730.2	malectin (MLEC)
MRPS2	-0.33	-1.02	NM_016034.2	mitochondrial ribosomal protein S2 (MRPS2)
LOC387791	-0.35	-1.02	XR_037721.1	PREDICTED: misc_RNA (LOC387791)
RPS7	-0.39	-1.02	NM_001011.3	ribosomal protein S7 (RPS7)
PRCP	-0.56	-1.02	NM_199418.2	prolylcarboxypeptidase (angiotensinase C) (PRCP)
EIF4H	-1.01	-1.02	NM_022170.1	eukaryotic translation initiation factor 4H (EIF4H)
DNCL1	-1.58	-1.02	NM_003746.1	dynein
CSDA	-1.63	-1.02	NM_003651.3	cold shock domain protein A (CSDA)
LDHB	-1.69	-1.02	NM_002300.4	lactate dehydrogenase B (LDHB)
FAM115A	-1.7	-1.02	NM_014719.1	family with sequence similarity 115
LOC643509	-1.84	-1.02	XM_928156.1	PREDICTED: similar to Dihydrofolate reductase
LOC641814	-1.88	-1.02	XM_935998.3	PREDICTED: similar to Ribosomal protein L6
CCR6	-2.06	-1.02	NM_031409.2	chemokine (C-C motif) receptor 6 (CCR6)
CLUAP1	-2.5	-1.02	NM_024793.1	clusterin associated protein 1 (CLUAP1)
VHL	0.5	-1.03	NM_000551.2	von Hippel-Lindau tumor suppressor (VHL)
WASPIP	0.42	-1.03	NM_003387.3	Wiskott-Aldrich syndrome protein interacting protein (WASPIP)
LOC731007	0.37	-1.03	XM_001132080.1	PREDICTED: similar to Adenylate kinase isoenzyme 4
LOC729898	0.36	-1.03	XM_001134101.1	PREDICTED: similar to zinc finger and BTB domain containing 8 opposite strand (LOC729898)
SRFBP1	0.36	-1.03	NM_152546.1	serum response factor binding protein 1 (SRFBP1)
TRIM24	0.36	-1.03	NM_015905.2	tripartite motif-containing 24 (TRIM24)
NR2C2	0.33	-1.03	NM_003298.3	nuclear receptor subfamily 2
PSMC3IP	0.26	-1.03	NM_016556.1	PSMC3 interacting protein (PSMC3IP)
LOC100127922	0.18	-1.03	XR_038410.1	PREDICTED: misc_RNA (LOC100127922)
GGH	0.12	-1.03	NM_003878.1	gamma-glutamyl hydrolase (conjugase
MNAT1	0.07	-1.03	NM_002431.2	menage a trois homolog 1
RAB5A	0	-1.03	NM_004162.3	RAB5A
STAG1	-0.05	-1.03	NM_005862.2	stromal antigen 1 (STAG1)
FKBP4	-0.11	-1.03	NM_002014.2	FK506 binding protein 4
PMEPA1	-0.15	-1.03	NM_199169.1	prostate transmembrane protein
UPF3B	-0.31	-1.03	NM_023010.2	UPF3 regulator of nonsense transcripts homolog B (yeast) (UPF3B)
CCL2	-0.38	-1.03	NM_002982.3	chemokine (C-C motif) ligand 2 (CCL2)
SEC31A	-0.39	-1.03	NM_014933.2	SEC31 homolog A (S. cerevisiae) (SEC31A)
C5orf28	-0.71	-1.03	NM_022483.3	chromosome 5 open reading frame 28 (C5orf28)
CKS2	-1.33	-1.03	NM_001827.1	CDC28 protein kinase regulatory subunit 2 (CKS2)
NDUFA8	-1.34	-1.03	NM_014222.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
LOC650152	-1.5	-1.03	XR_018707.1	PREDICTED: similar to tropomyosin 3 isoform 2 (LOC650152)
MDH2	-1.54	-1.03	NM_005918.2	malate dehydrogenase 2
SLC25A3	-1.54	-1.03	NM_002635.2	solute carrier family 25 (mitochondrial carrier; phosphate carrier)
LOC728620	-1.64	-1.03	XR_037241.1	PREDICTED: misc_RNA (LOC728620)
LOC100129028	-2.03	-1.03	XM_001722134.1	PREDICTED: similar to 60S acidic ribosomal protein P1 (LOC100129028)
RPL19	-2.22	-1.03	NM_000981.3	ribosomal protein L19 (RPL19)
F2R	-2.35	-1.03	NM_001992.2	coagulation factor II (thrombin) receptor (F2R)
LOC100129758	-2.41	-1.03	XR_039411.1	PREDICTED: misc_RNA (LOC100129758)
CBL	0.34	-1.04	NM_005188.2	Cas-Br-M (murine) ecotropic retroviral transforming sequence (CBL)
PRR11	0.3	-1.04	NM_018304.2	proline rich 11 (PRR11)
EZH2	0.29	-1.04	NM_004456.3	enhancer of zeste homolog 2 (Drosophila) (EZH2)
USP48	0.28	-1.04	NM_032236.5	ubiquitin specific peptidase 48 (USP48)
HP1BP3	0.27	-1.04	NM_016287.3	heterochromatin protein 1

LOC100127913	0.26	-1.04	XM_001715054.1	PREDICTED: hypothetical LOC100127913 (LOC100127913)	
TCEA1	0.26	-1.04	NM_006756.2	transcription elongation factor A (SII)	
TMEM45A	0.25	-1.04	NM_018004.1	transmembrane protein 45A (TMEM45A)	
TRIM66	0.25	-1.04	NM_014818.1	tripartite motif-containing 66 (TRIM66)	
PSPC1	0.24	-1.04	NR_003272.1	paraspeckle component 1 (PSPC1)	
ZNF423	0.2	-1.04	NM_015069.2	zinc finger protein 423 (ZNF423)	
IFT52	0.15	-1.04	NM_016004.2	intraflagellar transport 52 homolog (Chlamydomonas) (IFT52)	
YME1L1	0.13	-1.04	NM_139312.1	YME1-like 1 (S. cerevisiae) (YME1L1)	
TTC19	0.05	-1.04	NM_017775.2	tetratricopeptide repeat domain 19 (TTC19)	
NRAS	0.03	-1.04	NM_002524.2	neuroblastoma RAS viral (v-ras) oncogene homolog (NRAS)	
GRB2	-0.01	-1.04	NM_002086.3	growth factor receptor-bound protein 2 (GRB2)	
MCEE	-0.02	-1.04	NM_032601.2	methylmalonyl CoA epimerase (MCEE)	
WTAP	-0.02	-1.04	NM_152858.1	Wilms tumor 1 associated protein (WTAP)	
P4HA1	-0.07	-1.04	NM_000917.2	procollagen-proline	
SRI	-0.13	-1.04	NM_003130.2	sorcin (SRI)	
NUP153	-0.16	-1.04	NM_005124.2	nucleoporin 153kDa (NUP153)	
IDS	-0.18	-1.04	NM_006123.2	iduronate 2-sulfatase (Hunter syndrome) (IDS)	
FYTTD1	-0.22	-1.04	NM_001011537.1	forty-two-three domain containing 1 (FYTTD1)	
CAST	-0.28	-1.04	NM_001042445.1	calpastatin (CAST)	
KPNA2	-0.32	-1.04	NM_002266.2	karyopherin alpha 2 (RAG cohort 1	
NCAPG	-0.4	-1.04	NM_022346.3	non-SMC condensin I complex	
MGC3731	-0.41	-1.04	NM_024313.1	hypothetical protein MGC3731 (MGC3731)	
EIF2AK2	-0.44	-1.04	NM_002759.1	eukaryotic translation initiation factor 2-alpha kinase 2 (EIF2AK2)	
TOMM40	-0.65	-1.04	NM_006114.1	translocase of outer mitochondrial membrane 40 homolog (yeast) (TOMM40)	
C6orf153	-0.68	-1.04	NM_033112.2	chromosome 6 open reading frame 153 (C6orf153)	
KRT10	-0.88	-1.04	NM_000421.2	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) (KRT10)	
PSME1	-0.88	-1.04	NM_006263.2	proteasome (prosome	
LOC728553	-1.61	-1.04	XR_041708.1	PREDICTED: misc_RNA (LOC728553)	
LOC388707	-1.63	-1.04	XR_017679.2	PREDICTED: misc_RNA (LOC388707)	
FKTN	-1.68	-1.04	NM_006731.2	fukutin (FKTN)	
S100A10	-1.68	-1.04	NM_002966.1	S100 calcium binding protein A10 (annexin II ligand	
ATP5A1	-1.7	-1.04	NM_004046.4	ATP synthase	
ISG15	-1.71	-1.04	NM_005101.1	ISG15 ubiquitin-like modifier (ISG15)	
TRMT112	-1.72	-1.04	NM_016404.1	tRNA methyltransferase 11-2 homolog (S. cerevisiae) (TRMT112)	
IL18	-1.76	-1.04	NM_001562.2	interleukin 18 (interferon-gamma-inducing factor) (IL18)	
LOC651202	-1.89	-1.04	XM_940333.2	PREDICTED: similar to large subunit ribosomal protein L36a (LOC651202)	
LOC645317	-1.96	-1.04	XM_934920.2	PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	
NACA	-2.09	-1.04	NM_005594.2	nascent-polypeptide-associated complex alpha polypeptide (NACA)	
LOC284393	-2.39	-1.04	XM_001726716.1	PREDICTED: similar to QM protein	
LOC439953	-2.39	-1.04	XR_017375.2	PREDICTED: misc_RNA (LOC439953)	
LOC728368	-2.48	-1.04	XR_015295.2	PREDICTED: misc_RNA (LOC728368)	
PHF20L1	0.38	-1.05	NM_198513.1	PHD finger protein 20-like 1 (PHF20L1)	
FAM177A1	0.34	-1.05	NM_173607.3	family with sequence similarity 177	
ATPBD4	0.23	-1.05	NM_080650.2	ATP binding domain 4 (ATPBD4)	
CHRNA5	0.23	-1.05	NM_000745.2	cholinergic receptor	
BPGM	0.22	-1.05	NM_001724.3		2
MAMDC2	0.21	-1.05	NM_153267.3	MAM domain containing 2 (MAMDC2)	
KITLG	0.18	-1.05	NM_000899.3	KIT ligand (KITLG)	
PPIG	0.16	-1.05	NM_004792.2	peptidylprolyl isomerase G (cyclophilin G) (PPIG)	

LGALS9B	0.12	-1.05	NM_001042685.1	lectin
NARS2	0.09	-1.05	NM_024678.3	asparaginyl-tRNA synthetase 2
TCEAL8	0.05	-1.05	NM_153333.2	transcription elongation factor A (SII)-like 8 (TCEAL8)
LOC650321	0.02	-1.05	XM_939410.1	PREDICTED: similar to zinc finger and BTB domain containing 8 opposite strand (LOC650321)
NUMB	0	-1.05	NM_001005744.1	numb homolog (Drosophila) (NUMB)
AVEN	-0.03	-1.05	NM_020371.2	apoptosis
CLK1	-0.03	-1.05	NM_001024646.1	CDC-like kinase 1 (CLK1)
LOC647389	-0.04	-1.05	XM_936461.1	PREDICTED: hypothetical protein LOC647389 (LOC647389)
PIGT	-0.05	-1.05	NM_015937.3	phosphatidylinositol glycan anchor biosynthesis
SNAPC5	-0.13	-1.05	NM_006049.2	small nuclear RNA activating complex
ACOT9	-0.17	-1.05	NM_001033583.2	acyl-CoA thioesterase 9 (ACOT9)
RGS2	-0.21	-1.05	NM_002923.1	regulator of G-protein signalling 2
ITPRIP	-0.23	-1.05	NM_033397.2	inositol 1
HNRNPA2B1	-0.34	-1.05	NM_031243.2	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRNPA2B1)
HES4	-0.69	-1.05	NM_021170.2	hairy and enhancer of split 4 (Drosophila) (HES4)
HNRNPD	-1.55	-1.05	NM_031369.2	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1
LSM3	-1.6	-1.05	NM_014463.1	LSM3 homolog
MGC26356	-1.61	-1.05	XR_041102.1	PREDICTED: misc_RNA (MGC26356)
RPL9	-1.67	-1.05	NM_001024921.2	ribosomal protein L9 (RPL9)
LOC440043	-1.72	-1.05	XR_015812.2	PREDICTED: misc_RNA (LOC440043)
PDCD6	-1.75	-1.05	NM_013232.3	programmed cell death 6 (PDCD6)
LOC100128505	-1.85	-1.05	XM_001723239.1	PREDICTED: similar to hCG2021201 (LOC100128505)
LOC645895	-2.15	-1.05	XM_928866.1	PREDICTED: hypothetical protein LOC645895 (LOC645895)
RPS4X	-2.23	-1.05	NM_001007.3	ribosomal protein S4
JAK1	0.33	-1.06	NM_002227.2	Janus kinase 1 (JAK1)
DIAPH3	0.26	-1.06	NM_030932.3	diaphanous homolog 3 (Drosophila) (DIAPH3)
SFRS13A	0.14	-1.06	NM_054016.1	splicing factor
TWF1	0.13	-1.06	NM_002822.3	twinfilin
CCDC74B	0.11	-1.06	NM_207310.1	coiled-coil domain containing 74B (CCDC74B)
ARL15	0.1	-1.06	NM_019087.1	ADP-ribosylation factor-like 15 (ARL15)
G3BP2	0.08	-1.06	NM_203504.1	GTPase activating protein (SH3 domain) binding protein 2 (G3BP2)
ARHGEF16	0.06	-1.06	NM_014448.2	Rho guanine exchange factor (GEF) 16 (ARHGEF16)
GFPT1	0.04	-1.06	NM_002056.1	glutamine-fructose-6-phosphate transaminase 1 (GFPT1)
COL4A3BP	0.02	-1.06	NM_005713.1	collagen
NPR3	0.02	-1.06	NM_000908.2	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C) (NPR3)
C9orf123	0	-1.06	NM_033428.1	chromosome 9 open reading frame 123 (C9orf123)
LOC645236	-0.05	-1.06	XM_928275.1	PREDICTED: similar to similar to RPL23AP7 protein (LOC645236)
ZNF395	-0.06	-1.06	NM_018660.2	zinc finger protein 395 (ZNF395)
ARFIP1	-0.14	-1.06	NM_001025593.1	ADP-ribosylation factor interacting protein 1 (ARFIP1)
XBP1	-0.46	-1.06	NM_001079539.1	X-box binding protein 1 (XBP1)
LOC729208	-1.29	-1.06	XR_039643.1	PREDICTED: misc_RNA (LOC729208)
HNRNPAB	-1.34	-1.06	NM_004499.3	heterogeneous nuclear ribonucleoprotein A/B (HNRNPAB)
TMEM14C	-1.58	-1.06	NM_016462.2	transmembrane protein 14C (TMEM14C)
MRPL51	-1.59	-1.06	NM_016497.2	mitochondrial ribosomal protein L51 (MRPL51)
ATP5H	-1.71	-1.06	NM_006356.2	ATP synthase
AKR1B1	-1.8	-1.06	NM_001628.2	aldo-keto reductase family 1
C17orf45	-1.94	-1.06	NM_152350.2	chromosome 17 open reading frame 45 (C17orf45)
LOC134997	-2.12	-1.06	NR_000030.1	peptidylprolyl isomerase A processed pseudogene (LOC134997) on chromosome 6.
ATP5B	-2.18	-1.06	NM_001686.3	ATP synthase

RPS3A	-2.27	-1.06	NM_001006.3	ribosomal protein S3A (RPS3A)
MGC16703	-2.35	-1.06	NM_145042.2	tubulin
RN7SL1	-2.44	-1.06	NR_002715.1	RNA
MSH3	-2.45	-1.06	NM_002439.2	mutS homolog 3 (E. coli) (MSH3)
DPH2	0.2	-1.07	NM_001384.4	DPH2 homolog (S. cerevisiae) (DPH2)
MYADM	0.18	-1.07	NM_138373.3	myeloid-associated differentiation marker (MYADM)
THOC2	0.18	-1.07	NM_001081550.1	THO complex 2 (THOC2)
LPCAT2	0.17	-1.07	NM_017839.3	lysophosphatidylcholine acyltransferase 2 (LPCAT2)
C3orf23	0.15	-1.07	NM_001029840.2	chromosome 3 open reading frame 23 (C3orf23)
ATL2	0.14	-1.07	NM_022374.1	atlastin GTPase 2 (ATL2)
MAP4K4	0.12	-1.07	NM_145687.2	mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4)
MEX3B	0.12	-1.07	NM_032246.3	mex-3 homolog B (C. elegans) (MEX3B)
CXorf38	0.11	-1.07	NM_144970.1	chromosome X open reading frame 38 (CXorf38)
AMMECR1	0.1	-1.07	NM_001025580.1	Alport syndrome
AVPR2	0.1	-1.07	NM_000054.2	arginine vasopressin receptor 2 (nephrogenic diabetes insipidus) (AVPR2)
RIF1	0.1	-1.07	NM_018151.3	RAP1 interacting factor homolog (yeast) (RIF1)
SDHALP1	0.09	-1.07	NR_003264.1	succinate dehydrogenase complex
ARHGAP19	0.08	-1.07	NM_032900.4	Rho GTPase activating protein 19 (ARHGAP19)
LOC100130289	0.06	-1.07	XR_039781.1	PREDICTED: misc_RNA (LOC100130289)
SYNJ2	0.04	-1.07	NM_003898.2	synaptojanin 2 (SYNJ2)
LOC729687	0.03	-1.07	XM_001725257.1	PREDICTED: hypothetical LOC729687 (LOC729687)
SEC31A	-0.03	-1.07	NM_014933.2	SEC31 homolog A (S. cerevisiae) (SEC31A)
SERF2	-0.07	-1.07	NM_001018108.2	small EDRK-rich factor 2 (SERF2)
RPL32	-0.21	-1.07	NM_001007073.1	ribosomal protein L32 (RPL32)
FANCE	-0.22	-1.07	NM_021922.2	Fanconi anemia
PTGES2	-0.25	-1.07	NM_198938.1	prostaglandin E synthase 2 (PTGES2)
HMBS	-0.3	-1.07	NM_000190.3	hydroxymethylbilane synthase (HMBS)
MRPL1	-0.31	-1.07	NM_020236.2	mitochondrial ribosomal protein L1 (MRPL1)
NME7	-0.37	-1.07	NM_013330.3	non-metastatic cells 7
SAP30	-0.39	-1.07	NM_003864.3	Sin3A-associated protein
PPIL5	-0.53	-1.07	NM_203467.1	peptidylprolyl isomerase (cyclophilin)-like 5 (PPIL5)
STIP1	-0.82	-1.07	NM_006819.1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1)
FAM129B	-1.16	-1.07	NM_022833.2	family with sequence similarity 129
SEC61B	-1.5	-1.07	NM_006808.2	Sec61 beta subunit (SEC61B)
PSMC5	-1.51	-1.07	NM_002805.4	proteasome (prosome
MRPS21	-1.6	-1.07	NM_018997.1	mitochondrial ribosomal protein S21 (MRPS21)
LOC644790	-1.66	-1.07	XM_927887.3	PREDICTED: hypothetical LOC644790 (LOC644790)
EIF4B	-1.68	-1.07	NM_001417.4	eukaryotic translation initiation factor 4B (EIF4B)
LOC100130003	-1.71	-1.07	XR_038699.1	PREDICTED: misc_RNA (LOC100130003)
LOC728820	-1.91	-1.07	XR_038223.1	PREDICTED: misc_RNA (LOC728820)
LOC649821	-1.97	-1.07	XM_942212.1	PREDICTED: similar to 60S ribosomal protein L14 (CAG-ISL 7)
PRDX5	-1.98	-1.07	NM_181652.1	peroxiredoxin 5 (PRDX5)
LOC653314	-2	-1.07	NM_001080544.1	similar to ribosomal protein L19 (LOC653314)
TXN	-2.09	-1.07	NM_003329.2	thioredoxin (TXN)
LOC283412	-2.22	-1.07	XM_938790.2	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP) (LOC283412)
FLJ43681	-2.26	-1.07	XR_015857.2	PREDICTED: similar to 60S ribosomal protein L23a (FLJ43681)
LOC647856	-2.28	-1.07	XR_019580.1	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)
PRDX1	-2.32	-1.07	NM_181696.1	peroxiredoxin 1 (PRDX1)
PDCD7	-2.34	-1.07	NM_005707.1	programmed cell death 7 (PDCD7)

CLEC2D	-2.44	-1.07	NM_013269.3	C-type lectin domain family 2
PPIAL4A	-2.45	-1.07	NM_178230.1	peptidylprolyl isomerase A (cyclophilin A)-like 4A (PPIAL4A)
LOC729439	-2.52	-1.07	XM_001723745.1	PREDICTED: similar to HGC6.4 (LOC729439)
SNRPD3	0.2	-1.08	NM_004175.3	small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3)
ARMCX3	0.18	-1.08	NM_177947.2	armadillo repeat containing
MNS1	0.13	-1.08	NM_018365.1	meiosis-specific nuclear structural 1 (MNS1)
RABGAP1L	0.13	-1.08	NM_001035230.1	RAB GTPase activating protein 1-like (RABGAP1L)
RB1	0.13	-1.08	NM_000321.2	retinoblastoma 1 (RB1)
RPS6KA3	0.12	-1.08	NM_004586.2	ribosomal protein S6 kinase
ZEB2	0.11	-1.08	NM_014795.2	zinc finger E-box binding homeobox 2 (ZEB2)
LOC100131360	0.1	-1.08	XR_037562.1	PREDICTED: misc_RNA (LOC100131360)
FCGR3B	0.09	-1.08	NM_000570.2	Fc fragment of IgG
SIX2	0.09	-1.08	NM_016932.3	SIX homeobox 2 (SIX2)
SRPK2	0.09	-1.08	NM_182691.1	SFRS protein kinase 2 (SRPK2)
SNCA	0.07	-1.08	NM_000345.2	synuclein
WDFY2	0.07	-1.08	NM_052950.2	WD repeat and FYVE domain containing 2 (WDFY2)
ASB7	0.05	-1.08	NM_024708.2	ankyrin repeat and SOCS box-containing 7 (ASB7)
LOC100132973	0.05	-1.08	XM_001726567.1	PREDICTED: similar to elongin C (LOC100132973)
TNFAIP8	0.05	-1.08	NM_001077654.1	tumor necrosis factor
IL1A	0.04	-1.08	NM_000575.3	interleukin 1
WTAP	0.04	-1.08	NM_004906.3	Wilms tumor 1 associated protein (WTAP)
GPC5	-0.02	-1.08	NM_004466.3	glypican 5 (GPC5)
LOC653994	-0.02	-1.08	XM_944429.1	PREDICTED: similar to eukaryotic translation initiation factor 4H isoform 2
FEZ1	-0.04	-1.08	NM_005103.3	fasciculation and elongation protein zeta 1 (zygin I) (FEZ1)
KIAA1618	-0.04	-1.08	NM_020954.2	KIAA1618 (KIAA1618)
SEC24D	-0.04	-1.08	NM_014822.1	SEC24 related gene family
GSR	-0.05	-1.08	NM_000637.2	glutathione reductase (GSR)
MNS1	-0.18	-1.08	NM_018365.1	meiosis-specific nuclear structural 1 (MNS1)
LOC644037	-0.25	-1.08	XR_038280.1	PREDICTED: misc_RNA (LOC644037)
FRMD8	-0.42	-1.08	NM_031904.3	FERM domain containing 8 (FRMD8)
WDR33	-0.5	-1.08	NM_001006622.1	WD repeat domain 33 (WDR33)
LOC442727	-0.62	-1.08	XR_017503.2	PREDICTED: misc_RNA (LOC442727)
XBP1	-0.7	-1.08	NM_005080.2	X-box binding protein 1 (XBP1)
GRIPAP1	-0.87	-1.08	NM_207672.1	GRIP1 associated protein 1 (GRIPAP1)
NDUFB5	-1.55	-1.08	NM_002492.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
POLR1D	-1.58	-1.08	NM_015972.2	polymerase (RNA) I polypeptide D
LOC729340	-1.63	-1.08	XR_039650.1	PREDICTED: misc_RNA (LOC729340)
EIF3L	-1.73	-1.08	NM_016091.2	eukaryotic translation initiation factor 3
MYL12A	-1.73	-1.08	NM_006471.2	myosin
FSCN1	-1.75	-1.08	NM_003088.2	fascin homolog 1
RPL36AL	-1.85	-1.08	NM_001001.3	ribosomal protein L36a-like (RPL36AL)
NDUFA4	-1.89	-1.08	NM_002489.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
ATP5H	-1.91	-1.08	NM_001003785.1	ATP synthase
PSMB7	-1.99	-1.08	NM_002799.2	proteasome (prosome
LOC284821	-2.03	-1.08	XR_016232.1	PREDICTED: similar to ribosomal protein L13a (LOC284821)
CHCHD2	-2.06	-1.08	NM_016139.2	coiled-coil-helix-coiled-coil-helix domain containing 2 (CHCHD2)
TOMM7	-2.09	-1.08	NM_019059.2	translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7)
LOC729090	-2.11	-1.08	XR_015449.2	PREDICTED: similar to Eukaryotic translation elongation factor 1 alpha 1 (LOC729090)
LOC401537	-2.14	-1.08	XR_038712.1	PREDICTED: misc_RNA (LOC401537)

LOC646294	-2.15	-1.08	XR_019565.2	PREDICTED: misc_RNA (LOC646294)
XPNPEP3	-2.19	-1.08	NM_022098.2	X-prolyl aminopeptidase (aminopeptidase P) 3
LOC388654	-2.24	-1.08	XM_371273.3	PREDICTED: similar to laminin receptor 1 (ribosomal protein SA) (LOC388654)
RPL3	-2.28	-1.08	NM_001033853.1	ribosomal protein L3 (RPL3)
RPL5	-2.28	-1.08	NM_000969.3	ribosomal protein L5 (RPL5)
RPS3A	-2.37	-1.08	NM_001006.3	ribosomal protein S3A (RPS3A)
LOC441073	-2.39	-1.08	XR_018937.2	PREDICTED: misc_RNA (LOC441073)
RPL6	-2.4	-1.08	NM_001024662.1	ribosomal protein L6 (RPL6)
LOC389141	-2.44	-1.08	XR_016945.2	PREDICTED: misc_RNA (LOC389141)
IVD	0.14	-1.09	NM_002225.2	isovaleryl Coenzyme A dehydrogenase (IVD)
OSBPL8	0.14	-1.09	NM_020841.4	oxysterol binding protein-like 8 (OSBPL8)
VEGFA	0.13	-1.09	NM_001025367.1	vascular endothelial growth factor A (VEGFA)
MRI1	0.11	-1.09	NM_001031727.2	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae) (MRI1)
RBBP5	0.06	-1.09	NM_005057.2	retinoblastoma binding protein 5 (RBBP5)
DIXDC1	0.02	-1.09	NM_001037954.2	DIX domain containing 1 (DIXDC1)
CCPG1	0	-1.09	NM_020739.2	cell cycle progression 1 (CCPG1)
TMEM22	0	-1.09	NM_001097599.1	transmembrane protein 22 (TMEM22)
CDK5RAP2	-0.04	-1.09	NM_001011649.1	CDK5 regulatory subunit associated protein 2 (CDK5RAP2)
HNMT	-0.04	-1.09	NM_006895.2	histamine N-methyltransferase (HNMT)
SS18	-0.05	-1.09	NM_005637.2	synovial sarcoma translocation
C17orf48	-0.06	-1.09	NM_020233.4	chromosome 17 open reading frame 48 (C17orf48)
KCTD9	-0.16	-1.09	NM_017634.2	potassium channel tetramerisation domain containing 9 (KCTD9)
HSPA1B	-0.22	-1.09	NM_005346.3	heat shock 70kDa protein 1B (HSPA1B)
FBXO11	-0.27	-1.09	NM_025133.3	F-box protein 11 (FBXO11)
TOR1AIP1	-0.3	-1.09	NM_015602.2	torsin A interacting protein 1 (TOR1AIP1)
ITPRIP	-0.34	-1.09	NM_033397.2	inositol 1
ACYP1	-0.38	-1.09	NM_001107.3	acylphosphatase 1
PTPN12	-0.42	-1.09	NM_002835.2	protein tyrosine phosphatase
MMGT1	-0.56	-1.09	NM_173470.1	membrane magnesium transporter 1 (MMGT1)
COASY	-0.93	-1.09	NM_001042532.1	Coenzyme A synthase (COASY)
PTGES2	-0.95	-1.09	NM_198938.1	prostaglandin E synthase 2 (PTGES2)
PARL	-0.96	-1.09	NM_001037639.1	presenilin associated
FAM50A	-1.54	-1.09	NM_004699.1	family with sequence similarity 50
NFKBIA	-1.57	-1.09	NM_020529.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor
NDUFB3	-1.62	-1.09	NM_002491.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
NHP2	-1.67	-1.09	NM_017838.3	NHP2 ribonucleoprotein homolog (yeast) (NHP2)
IFITM3	-1.76	-1.09	NM_021034.2	interferon induced transmembrane protein 3 (1-8U) (IFITM3)
LOC648390	-1.82	-1.09	XR_037845.1	PREDICTED: misc_RNA (LOC648390)
LOC652624	-1.94	-1.09	XM_942165.1	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (LOC652624)
LOC646630	-2.1	-1.09	XM_929572.1	PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 2
HSPD1	-2.18	-1.09	NM_002156.4	heat shock 60kDa protein 1 (chaperonin) (HSPD1)
LOC391126	-2.25	-1.09	XR_017684.2	PREDICTED: misc_RNA (LOC391126)
LOC100132673	-2.36	-1.09	XR_039018.1	PREDICTED: misc_RNA (LOC100132673)
TXN	-2.39	-1.09	NM_003329.2	thioredoxin (TXN)
KIAA0101	-2.43	-1.09	NM_001029989.1	KIAA0101 (KIAA0101)
RPLP1	-2.52	-1.09	NM_213725.1	ribosomal protein
LOC100131387	-2.54	-1.09	XM_001725100.1	PREDICTED: similar to mCG146274 (LOC100131387)
RAB12	0.12	-1.1	NM_001025300.2	RAB12
FUT11	0.09	-1.1	NM_173540.2	fucosyltransferase 11 (alpha (1

LOC728024	0.09	-1.1	NR_003671.1	hCG1640171 (LOC728024)
BMP2K	0.06	-1.1	NM_017593.3	BMP2 inducible kinase (BMP2K)
HNRPK	0.04	-1.1	NM_031263.1	heterogeneous nuclear ribonucleoprotein K (HNRPK)
DNAJB14	0.02	-1.1	NM_001031723.1	DnaJ (Hsp40) homolog
LOC650254	0.01	-1.1	XM_499385.2	PREDICTED: similar to hypothetical protein FLJ40722
SLC47A1	0	-1.1	NM_018242.2	solute carrier family 47
TCTN3	-0.01	-1.1	NM_015631.4	tectonic family member 3 (TCTN3)
LOC642513	-0.02	-1.1	XR_016174.2	PREDICTED: misc_RNA (LOC642513)
PEX11A	-0.03	-1.1	NM_003847.1	peroxisomal biogenesis factor 11 alpha (PEX11A)
PPWD1	-0.05	-1.1	NM_015342.1	peptidylprolyl isomerase domain and WD repeat containing 1 (PPWD1)
PRPF18	-0.05	-1.1	NM_003675.3	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae) (PRPF18)
ZNF326	-0.05	-1.1	NM_182976.1	zinc finger protein 326 (ZNF326)
ZP3	-0.05	-1.1	NM_007155.4	zona pellucida glycoprotein 3 (sperm receptor) (ZP3)
CDC42SE1	-0.06	-1.1	NM_001038707.1	CDC42 small effector 1 (CDC42SE1)
TMX4	-0.06	-1.1	NM_021156.2	thioredoxin-related transmembrane protein 4 (TMX4)
PVRL3	-0.08	-1.1	NM_015480.1	poliovirus receptor-related 3 (PVRL3)
TAF7	-0.16	-1.1	NM_005642.2	TAF7 RNA polymerase II
C19orf6	-0.21	-1.1	NM_001033026.1	chromosome 19 open reading frame 6 (C19orf6)
MSRB3	-0.21	-1.1	NM_198080.2	methionine sulfoxide reductase B3 (MSRB3)
SELS	-0.21	-1.1	NM_018445.4	selenoprotein S (SELS)
MTA2	-0.27	-1.1	NM_004739.2	metastasis associated 1 family
NDC80	-0.28	-1.1	NM_006101.1	NDC80 homolog
DNAJC10	-0.43	-1.1	NM_018981.1	DnaJ (Hsp40) homolog
C7orf11	-0.44	-1.1	NM_138701.1	chromosome 7 open reading frame 11 (C7orf11)
RNGTT	-0.47	-1.1	NM_003800.3	RNA guanylyltransferase and 5'-phosphatase (RNGTT)
TPX2	-0.53	-1.1	NM_012112.4	TPX2
SKA2	-0.56	-1.1	NM_182620.3	spindle and kinetochore associated complex subunit 2 (SKA2)
REXO4	-0.77	-1.1	NM_020385.2	REX4
DDAH1	-0.81	-1.1	NM_012137.2	dimethylarginine dimethylaminohydrolase 1 (DDAH1)
YWHAG	-0.96	-1.1	NM_012479.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
XRCC6	-1.37	-1.1	NM_001469.3	X-ray repair complementing defective repair in Chinese hamster cells 6 (XRCC6)
DMC1	-1.38	-1.1	NM_007068.2	DMC1 dosage suppressor of mck1 homolog
LOC727984	-1.38	-1.1	XR_015259.2	PREDICTED: misc_RNA (LOC727984)
C8orf37	-1.59	-1.1	NM_177965.2	chromosome 8 open reading frame 37 (C8orf37)
SDHB	-1.68	-1.1	NM_003000.2	succinate dehydrogenase complex
LOC389787	-1.84	-1.1	XM_497072.2	PREDICTED: similar to Translationally-controlled tumor protein (TCTP) (p23) (Histamine-releasing factor)
PRDX5	-1.85	-1.1	NM_012094.3	peroxiredoxin 5 (PRDX5)
LOC645173	-2.02	-1.1	XR_017590.2	PREDICTED: misc_RNA (LOC645173)
SHFM1	-2.05	-1.1	NM_006304.1	split hand/foot malformation (ectrodactyly) type 1 (SHFM1)
LOC648249	-2.06	-1.1	XM_944165.1	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)
LOC649049	-2.06	-1.1	XM_945192.1	PREDICTED: similar to acidic ribosomal phosphoprotein P0
LOC100131205	-2.09	-1.1	XM_001720494.1	PREDICTED: hypothetical protein LOC100131205
LOC653232	-2.1	-1.1	XM_944104.2	PREDICTED: hypothetical LOC653232
NOP10	-2.11	-1.1	NM_018648.3	NOP10 ribonucleoprotein homolog (yeast) (NOP10)
LOC652235	-2.12	-1.1	XM_941629.1	PREDICTED: hypothetical protein LOC652235 (LOC652235)
RPL36AL	-2.13	-1.1	NM_001001.3	ribosomal protein L36a-like (RPL36AL)
TOMM7	-2.14	-1.1	NM_019059.2	translocase of outer mitochondrial membrane 7 homolog (yeast) (TOMM7)
COX8A	-2.21	-1.1	NM_004074.2	cytochrome c oxidase subunit 8A (ubiquitous) (COX8A)
HINT1	-2.25	-1.1	NM_005340.3	histidine triad nucleotide binding protein 1 (HINT1)

RPL17	-2.3	-1.1	NM_001035006.1	ribosomal protein L17 (RPL17)
UQCRH	-2.38	-1.1	NM_006004.2	ubiquinol-cytochrome c reductase hinge protein (UQCRH)
RPL3	-2.47	-1.1	NM_001033853.1	ribosomal protein L3 (RPL3)
RPS6	-2.61	-1.1	NM_001010.2	ribosomal protein S6 (RPS6)
TMSB10	-2.62	-1.1	NM_021103.3	thymosin beta 10 (TMSB10)
LOC728553	-2.67	-1.1	XR_015414.2	PREDICTED: misc_RNA (LOC728553)
MAP3K3	0.05	-1.11	NM_203351.1	mitogen-activated protein kinase kinase kinase 3 (MAP3K3)
ZDHHC13	0.04	-1.11	NM_001001483.1	zinc finger
LOC730996	0	-1.11	XM_001128017.1	PREDICTED: similar to chromosome 1 open reading frame 80 (LOC730996)
PIBF1	-0.03	-1.11	NM_006346.2	progesterone immunomodulatory binding factor 1 (PIBF1)
LDHA	-0.05	-1.11	NM_005566.3	lactate dehydrogenase A (LDHA)
TRIM37	-0.05	-1.11	NM_001005207.1	tripartite motif-containing 37 (TRIM37)
GAGE2B	-0.13	-1.11	NM_001098411.3	G antigen 2B (GAGE2B)
FAM54B	-0.15	-1.11	NM_019557.5	family with sequence similarity 54
PARP3	-0.15	-1.11	NM_001003931.1	poly (ADP-ribose) polymerase family
WDR33	-0.16	-1.11	NM_001006622.1	WD repeat domain 33 (WDR33)
ZNF16	-0.16	-1.11	NM_006958.2	zinc finger protein 16 (ZNF16)
ALDH2	-0.19	-1.11	NM_000690.2	aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2)
CORO7	-0.19	-1.11	NM_024535.2	coronin 7 (CORO7)
NUF2	-0.22	-1.11	NM_031423.3	NUF2
C1GALT1C1	-0.29	-1.11	NM_152692.3	C1GALT1-specific chaperone 1 (C1GALT1C1)
MSL3	-0.3	-1.11	NM_078629.2	male-specific lethal 3 homolog (Drosophila) (MSL3)
RAPGEF2	-0.37	-1.11	NM_014247.2	Rap guanine nucleotide exchange factor (GEF) 2 (RAPGEF2)
UBE2H	-0.38	-1.11	NM_003344.2	ubiquitin-conjugating enzyme E2H (UBC8 homolog
EHBP1	-0.42	-1.11	NM_015252.2	EH domain binding protein 1 (EHBP1)
LOC100128771	-0.44	-1.11	XR_037860.1	PREDICTED: misc_RNA (LOC100128771)
LAMP2	-0.47	-1.11	NM_002294.1	lysosomal-associated membrane protein 2 (LAMP2)
LOC728855	-0.49	-1.11	NR_024510.1	hypothetical LOC728855 (LOC728855)
LOC645515	-0.59	-1.11	XR_039410.1	PREDICTED: misc_RNA (LOC645515)
PARL	-1.02	-1.11	NM_018622.5	presenilin associated
PMEPA1	-1.18	-1.11	NM_199169.1	prostate transmembrane protein
ILF2	-1.5	-1.11	NM_004515.2	interleukin enhancer binding factor 2
EIF5A	-1.56	-1.11	NM_001970.3	eukaryotic translation initiation factor 5A (EIF5A)
PTTG3P	-1.57	-1.11	NR_002734.1	pituitary tumor-transforming 3 (pseudogene) (PTTG3P)
TALDO1	-1.57	-1.11	NM_006755.1	PREDICTED: transaldolase 1 (TALDO1)
COX6B1	-1.58	-1.11	NM_001863.3	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous) (COX6B1)
LOC727865	-1.7	-1.11	XR_038568.1	PREDICTED: misc_RNA (LOC727865)
PCBP2	-1.74	-1.11	NM_001098620.1	poly(rC) binding protein 2 (PCBP2)
DDIT4	-1.85	-1.11	NM_019058.2	DNA-damage-inducible transcript 4 (DDIT4)
LOC730255	-1.89	-1.11	XR_039376.1	PREDICTED: misc_RNA (LOC730255)
LOC729236	-1.99	-1.11	XR_016041.2	PREDICTED: misc_RNA (LOC729236)
CHCHD9	-2	-1.11	XM_928381.2	PREDICTED: coiled-coil-helix-coiled-coil-helix domain containing 9 (CHCHD9)
ATP5A1	-2.02	-1.11	NM_004046.4	ATP synthase
COX5B	-2.02	-1.11	NM_001862.2	cytochrome c oxidase subunit Vb (COX5B)
AURKAIP1	-2.04	-1.11	NM_017900.1	aurora kinase A interacting protein 1 (AURKAIP1)
LOC728973	-2.08	-1.11	XR_015809.1	PREDICTED: similar to 40S ribosomal protein S7 (S8) (LOC728973)
LOC646531	-2.09	-1.11	XR_018197.1	PREDICTED: similar to nuclease sensitive element binding protein 1 (LOC646531)
LOC285900	-2.3	-1.11	XM_926623.1	PREDICTED: similar to 60S ribosomal protein L6 (TAX-responsive enhancer element binding protein 107)
LOC646785	-2.42	-1.11	XR_017607.1	PREDICTED: misc_RNA (LOC646785)

POTEF	-2.47	-1.11	NM_001099771.1	POTE ankyrin domain family
UQCRHL	-2.47	-1.11	NM_001089591.1	ubiquinol-cytochrome c reductase hinge protein-like (UQCRHL)
LOC645296	-2.53	-1.11	NM_001093733.2	ribosomal protein L17-like (LOC645296)
LOC391777	-2.63	-1.11	XR_040304.1	PREDICTED: misc_RNA (LOC391777)
CRIM1	-0.02	-1.12	NM_016441.1	cysteine rich transmembrane BMP regulator 1 (chordin-like) (CRIM1)
ABI2	-0.08	-1.12	XM_001126750.1	PREDICTED: abl interactor 2 (ABI2)
UBA3	-0.1	-1.12	NM_198195.1	ubiquitin-like modifier activating enzyme 3 (UBA3)
MAP4	-0.11	-1.12	NM_002375.3	microtubule-associated protein 4 (MAP4)
MIR129-2	-0.14	-1.12	NR_029697.1	microRNA 129-2 (MIR129-2)
CLIC4	-0.16	-1.12	NM_013943.1	chloride intracellular channel 4 (CLIC4)
ZNF280D	-0.19	-1.12	NM_001002843.1	zinc finger protein 280D (ZNF280D)
LOC401152	-0.2	-1.12	NM_001001701.1	HCV F-transactivated protein 1 (LOC401152)
RAP1GAP	-0.2	-1.12	NM_002885.1	RAP1 GTPase activating protein (RAP1GAP)
LYRM7	-0.24	-1.12	NM_181705.2	Lyrm7 homolog (mouse) (LYRM7)
GOLPH4	-0.25	-1.12	NM_014498.2	golgi phosphoprotein 4 (GOLPH4)
C1QTNF1	-0.27	-1.12	NM_198594.1	C1q and tumor necrosis factor related protein 1 (C1QTNF1)
PRKAG1	-0.27	-1.12	NM_002733.3	protein kinase
TOM1	-0.29	-1.12	NM_005488.1	target of myb1 (chicken) (TOM1)
PVRL3	-0.3	-1.12	NM_015480.1	poliovirus receptor-related 3 (PVRL3)
SPAG9	-0.31	-1.12	NM_003971.3	sperm associated antigen 9 (SPAG9)
RIMKLB	-0.32	-1.12	NM_020734.2	ribosomal modification protein rimK-like family member B (RIMKLB)
TTC27	-0.33	-1.12	NM_017735.3	tetratricopeptide repeat domain 27 (TTC27)
CDT1	-0.37	-1.12	NM_030928.2	chromatin licensing and DNA replication factor 1 (CDT1)
CLK1	-0.37	-1.12	NM_004071.2	CDC-like kinase 1 (CLK1)
FAM36A	-0.38	-1.12	NM_198076.4	family with sequence similarity 36
AMD1	-0.4	-1.12	NM_001634.4	adenosylmethionine decarboxylase 1 (AMD1)
LOC440354	-0.47	-1.12	NR_002473.2	PI-3-kinase-related kinase SMG-1 pseudogene (LOC440354)
DLGAP5	-0.49	-1.12	NM_014750.3	discs
EFNA1	-0.77	-1.12	NM_004428.2	ephrin-A1 (EFNA1)
SPOCK1	-0.77	-1.12	NM_004598.3	sparc/osteonectin
RHOQ	-1.05	-1.12	NM_012249.3	ras homolog gene family
RPL29	-1.28	-1.12	NM_000992.2	ribosomal protein L29 (RPL29)
HDAC1	-1.55	-1.12	NM_004964.2	histone deacetylase 1 (HDAC1)
PHPT1	-1.59	-1.12	NM_014172.3	phosphohistidine phosphatase 1 (PHPT1)
POFUT1	-1.67	-1.12	NM_015352.1	protein O-fucosyltransferase 1 (POFUT1)
NUDC	-1.72	-1.12	NM_006600.2	nuclear distribution gene C homolog (A. nidulans) (NUDC)
SSR4	-1.74	-1.12	NM_006280.1	signal sequence receptor
LOC550643	-1.77	-1.12	NR_015367.2	hypothetical LOC550643 (LOC550643)
QARS	-1.8	-1.12	NM_005051.1	glutaminyl-tRNA synthetase (QARS)
SNRPF	-1.92	-1.12	NM_003095.2	small nuclear ribonucleoprotein polypeptide F (SNRPF)
PSMB6	-1.93	-1.12	NM_002798.1	proteasome (prosome
NDUFB2	-1.95	-1.12	NM_004546.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
LOC441506	-2.21	-1.12	XR_019580.2	PREDICTED: misc_RNA (LOC441506)
CFL1	-2.25	-1.12	NM_005507.2	cofilin 1 (non-muscle) (CFL1)
RPL26	-2.26	-1.12	NM_000987.3	ribosomal protein L26 (RPL26)
EIF3L	-2.28	-1.12	NM_016091.2	eukaryotic translation initiation factor 3
LOC644745	-2.38	-1.12	XR_038862.1	PREDICTED: misc_RNA (LOC644745)
RPS2	-2.47	-1.12	NM_002952.3	ribosomal protein S2 (RPS2)
RPL31	-2.51	-1.12	NM_000993.4	ribosomal protein L31 (RPL31)

PRDX1	-2.52	-1.12	NM_181696.1	peroxiredoxin 1 (PRDX1)
RPL14L	-2.56	-1.12	XR_041286.1	PREDICTED: misc_RNA (RPL14L)
RPL24	-2.61	-1.12	NM_000986.3	ribosomal protein L24 (RPL24)
RPS13	-2.66	-1.12	NM_001017.2	ribosomal protein S13 (RPS13)
LOC100133931	-2.68	-1.12	XM_001713654.1	PREDICTED: hypothetical protein LOC100133931 (LOC100133931)
RPS8	-2.7	-1.12	NM_001012.1	ribosomal protein S8 (RPS8)
RPL38	-2.71	-1.12	NM_000999.2	ribosomal protein L38 (RPL38)
RPSA	-2.76	-1.12	NM_002295.4	ribosomal protein SA (RPSA)
LOC440589	-2.77	-1.12	XM_942424.2	PREDICTED: similar to ribosomal protein S2
RPS6	-2.8	-1.12	NM_001010.2	ribosomal protein S6 (RPS6)
ACTB	-2.92	-1.12	NM_001101.2	actin
NEK7	0.02	-1.13	NM_133494.1	NIMA (never in mitosis gene a)-related kinase 7 (NEK7)
TRIM29	-0.01	-1.13	NM_012101.3	tripartite motif-containing 29 (TRIM29)
C6orf72	-0.03	-1.13	NM_138785.1	chromosome 6 open reading frame 72 (C6orf72)
LOC401805	-0.04	-1.13	XR_038835.1	PREDICTED: misc_RNA (LOC401805)
UBE2H	-0.05	-1.13	NM_003344.2	ubiquitin-conjugating enzyme E2H (UBC8 homolog
LOC648509	-0.09	-1.13	XR_018376.1	PREDICTED: similar to plakophilin 4 isoform a (LOC648509)
CDK2	-0.11	-1.13	NM_001798.2	cyclin-dependent kinase 2 (CDK2)
UGP2	-0.12	-1.13	NM_006759.3	UDP-glucose pyrophosphorylase 2 (UGP2)
HOXA13	-0.13	-1.13	NM_000522.3	homeobox A13 (HOXA13)
SCLT1	-0.14	-1.13	NM_144643.2	sodium channel and clathrin linker 1 (SCLT1)
DTNBP1	-0.15	-1.13	NM_032122.3	dystrobrevin binding protein 1 (DTNBP1)
SERF1A	-0.15	-1.13	NM_021967.1	small EDRK-rich factor 1A (telomeric) (SERF1A)
MED26	-0.17	-1.13	NM_004831.3	mediator complex subunit 26 (MED26)
INTS8	-0.18	-1.13	NM_017864.2	integrator complex subunit 8 (INTS8)
LAMP2	-0.18	-1.13	NM_013995.1	lysosomal-associated membrane protein 2 (LAMP2)
LOC654189	-0.19	-1.13	XM_942687.1	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A3
CASP6	-0.2	-1.13	NM_032992.2	caspase 6
LOC653635	-0.21	-1.13	XR_017611.1	PREDICTED: similar to CXYorf1-related protein (LOC653635)
ZNF45	-0.21	-1.13	NM_003425.2	zinc finger protein 45 (ZNF45)
BMP1	-0.22	-1.13	NM_006129.2	bone morphogenetic protein 1 (BMP1)
HSPA12A	-0.23	-1.13	NM_025015.2	PREDICTED: heat shock 70kDa protein 12A
LIMS1	-0.29	-1.13	NM_004987.3	PREDICTED: LIM and senescent cell antigen-like domains 1 (LIMS1)
LOC100130123	-0.39	-1.13	XM_001726844.1	PREDICTED: similar to PRO2870 (LOC100130123)
RNF5	-0.39	-1.13	NM_006913.2	ring finger protein 5 (RNF5)
LOC729629	-0.41	-1.13	XM_001719967.1	Yp11.32a
THOC2	-0.51	-1.13	NM_020449.2	THO complex 2 (THOC2)
PTPRF	-0.62	-1.13	NM_002840.3	protein tyrosine phosphatase
SS18	-0.66	-1.13	NM_005637.2	synovial sarcoma translocation
LOC651064	-1.59	-1.13	XM_944489.1	PREDICTED: hypothetical protein LOC651064 (LOC651064)
LOC728661	-1.63	-1.13	XM_001717735.1	PREDICTED: similar to solute carrier family 35
TUBB	-1.64	-1.13	NM_178014.2	tubulin
ODC1	-1.65	-1.13	NM_002539.1	ornithine decarboxylase 1 (ODC1)
CYC1	-1.68	-1.13	NM_001916.3	cytochrome c-1 (CYC1)
POLR2F	-1.76	-1.13	NM_021974.2	polymerase (RNA) II (DNA directed) polypeptide F (POLR2F)
ALDOA	-1.77	-1.13	NM_184043.1	aldolase A
LOC647285	-1.94	-1.13	XR_019567.2	PREDICTED: misc_RNA (LOC647285)
LOC388339	-1.97	-1.13	XM_942039.3	PREDICTED: similar to ribosomal protein
LOC647000	-1.99	-1.13	XM_929980.2	PREDICTED: similar to tubulin

LOC730004	-2	-1.13	XR_039077.1	PREDICTED: misc_RNA (LOC730004)
RPL14	-2.02	-1.13	NM_001034996.1	ribosomal protein L14 (RPL14)
LOC391833	-2.07	-1.13	XR_038761.1	PREDICTED: misc_RNA (LOC391833)
EIF4A1	-2.15	-1.13	NM_001416.2	eukaryotic translation initiation factor 4A
LOC389168	-2.19	-1.13	XR_019471.2	PREDICTED: misc_RNA (LOC389168)
LOC644511	-2.19	-1.13	XM_941634.2	PREDICTED: similar to ribosomal protein L13a
LOC730740	-2.21	-1.13	XM_001128558.1	PREDICTED: similar to H3 histone
LOC646294	-2.33	-1.13	XR_019565.2	PREDICTED: misc_RNA (LOC646294)
RPS27A	-2.34	-1.13	NM_002954.3	ribosomal protein S27a (RPS27A)
LOC440926	-2.47	-1.13	NR_002315.1	H3 histone
LOC729466	-2.64	-1.13	XR_015916.1	PREDICTED: hypothetical protein LOC729466 (LOC729466)
LOC387841	-2.82	-1.13	XM_370681.4	PREDICTED: similar to ribosomal protein L13a
KLRC2	-0.16	-1.14	NM_002260.3	killer cell lectin-like receptor subfamily C
WFDC1	-0.17	-1.14	NM_021197.2	WAP four-disulfide core domain 1 (WFDC1)
SLC25A40	-0.18	-1.14	NM_018843.2	solute carrier family 25
SLTM	-0.2	-1.14	NM_024755.2	SAFB-like
GOLIM4	-0.21	-1.14	NM_014498.3	golgi integral membrane protein 4 (GOLIM4)
CLUL1	-0.22	-1.14	NM_014410.4	clusterin-like 1 (retinal) (CLUL1)
LOC648581	-0.22	-1.14	XM_937648.2	PREDICTED: similar to alveolar soft part sarcoma chromosome region
GNB4	-0.23	-1.14	NM_021629.3	guanine nucleotide binding protein (G protein)
TBL3	-0.23	-1.14	NM_006453.2	transducin (beta)-like 3 (TBL3)
KIF15	-0.27	-1.14	NM_020242.1	kinesin family member 15 (KIF15)
C17orf81	-0.36	-1.14	NM_015362.3	chromosome 17 open reading frame 81 (C17orf81)
UFM1	-0.41	-1.14	NM_016617.1	ubiquitin-fold modifier 1 (UFM1)
DAG1	-0.42	-1.14	NM_004393.2	dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1)
BARD1	-0.49	-1.14	NM_000465.1	BRCA1 associated RING domain 1 (BARD1)
TIMP4	-0.54	-1.14	NM_003256.2	TIMP metallopeptidase inhibitor 4 (TIMP4)
SNRPN	-0.61	-1.14	NM_022806.2	small nuclear ribonucleoprotein polypeptide N (SNRPN)
LOC652233	-0.72	-1.14	XM_941627.1	PREDICTED: hypothetical protein LOC652233 (LOC652233)
BSG	-0.8	-1.14	NM_198590.1	basigin (Ok blood group) (BSG)
XRCC2	-0.92	-1.14	NM_005431.1	X-ray repair complementing defective repair in Chinese hamster cells 2 (XRCC2)
PSCD1	-1.01	-1.14	NM_017456.1	pleckstrin homology
LOC648210	-1.54	-1.14	XR_018923.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
NDUFB9	-1.55	-1.14	NM_005005.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
CIP29	-1.62	-1.14	NM_033082.2	cytokine induced protein 29 kDa (CIP29)
SFRS6	-1.63	-1.14	NM_006275.4	splicing factor
LOC645385	-1.73	-1.14	XM_928427.1	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A1 (LOC645385)
NDUFA11	-1.75	-1.14	NM_175614.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
UXT	-1.76	-1.14	NM_004182.2	ubiquitously-expressed transcript (UXT)
DDT	-1.95	-1.14	NM_001355.3	D-dopachrome tautomerase (DDT)
CIB1	-1.96	-1.14	NM_006384.2	calcium and integrin binding 1 (calmyrin) (CIB1)
CCDC72	-2.12	-1.14	NM_015933.3	coiled-coil domain containing 72 (CCDC72)
LOC731096	-2.12	-1.14	XM_001129635.1	PREDICTED: similar to Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) (LOC731096)
LOC729926	-2.13	-1.14	XR_038426.1	PREDICTED: misc_RNA (LOC729926)
LOC391075	-2.15	-1.14	XR_016557.2	PREDICTED: misc_RNA (LOC391075)
RPL7A	-2.28	-1.14	NM_000972.2	ribosomal protein L7a (RPL7A)
LOC100132795	-2.31	-1.14	XR_037785.1	PREDICTED: misc_RNA (LOC100132795)
LOC645138	-2.33	-1.14	XM_928168.1	PREDICTED: similar to ribosomal protein S11 (LOC645138)
LOC100132742	-2.36	-1.14	XM_001717156.1	PREDICTED: hypothetical protein LOC100132742

LOC646819	-2.51	-1.14	XR_017610.2	PREDICTED: misc_RNA (LOC646819)
LOC729301	-2.52	-1.14	XR_038738.1	PREDICTED: misc_RNA (LOC729301)
LOC100132795	-2.65	-1.14	XR_037619.1	PREDICTED: misc_RNA (LOC100132795)
LOC728126	-2.66	-1.14	XR_036919.1	PREDICTED: misc_RNA (LOC728126)
LOC728128	-2.71	-1.14	XR_015346.1	PREDICTED: misc_RNA (LOC728128)
LOC728576	-2.75	-1.14	XR_038296.1	PREDICTED: misc_RNA (LOC728576)
LOC728658	-2.91	-1.14	XM_939484.3	PREDICTED: similar to 23 kD highly basic protein
LOC654174	-0.08	-1.15	XM_940438.2	PREDICTED: similar to lethal (2) k00619 CG4775-PA (LOC654174)
TTC8	-0.09	-1.15	NM_144596.2	tetratricopeptide repeat domain 8 (TTC8)
DHX40	-0.1	-1.15	NM_024612.3	PREDICTED: DEAH (Asp-Glu-Ala-His) box polypeptide 40
BP75	-0.13	-1.15	NR_002730.1	bromodomain containing protein 75 kDa pseudogene (BP75) on chromosome 6.
HNRNPA3P1	-0.18	-1.15	NR_002726.1	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1 (HNRNPA3P1) on chromosome 10.
ERP29	-0.19	-1.15	NM_006817.3	endoplasmic reticulum protein 29 (ERP29)
LOC100132418	-0.19	-1.15	XM_001719607.1	PREDICTED: similar to PRO1102 (LOC100132418)
PSMB8	-0.19	-1.15	NM_148919.3	proteasome (prosome
CXorf40B	-0.2	-1.15	NM_001013845.1	chromosome X open reading frame 40B (CXorf40B)
NAV1	-0.2	-1.15	NM_020443.2	neuron navigator 1 (NAV1)
CSTF3	-0.22	-1.15	NM_001033506.1	cleavage stimulation factor
TMED10	-0.23	-1.15	NM_006827.5	transmembrane emp24-like trafficking protein 10 (yeast) (TMED10)
FOXC2	-0.24	-1.15	NM_005251.1	forkhead box C2 (MFH-1
IDH1	-0.26	-1.15	NM_005896.2	isocitrate dehydrogenase 1 (NADP+)
LOC650909	-0.26	-1.15	XM_939995.2	PREDICTED: similar to activating signal cointegrator 1 complex subunit 3-like 1 (LOC650909)
SCAMP1	-0.26	-1.15	NM_004866.4	secretory carrier membrane protein 1 (SCAMP1)
ATG4D	-0.28	-1.15	NM_032885.4	ATG4 autophagy related 4 homolog D (S. cerevisiae) (ATG4D)
PSEN2	-0.29	-1.15	NM_012486.1	presenilin 2 (Alzheimer disease 4) (PSEN2)
LRRC49	-0.31	-1.15	NM_017691.2	leucine rich repeat containing 49 (LRRC49)
TYW3	-0.31	-1.15	NM_138467.1	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae) (TYW3)
CKAP2L	-0.36	-1.15	NM_152515.2	cytoskeleton associated protein 2-like (CKAP2L)
NACC1	-0.37	-1.15	NM_052876.2	nucleus accumbens associated 1
SLC25A22	-0.37	-1.15	NM_024698.4	solute carrier family 25 (mitochondrial carrier: glutamate)
PLD3	-0.38	-1.15	NM_001031696.1	phospholipase D family
SLC15A4	-0.44	-1.15	NM_145648.1	solute carrier family 15
FARSA	-0.49	-1.15	NM_004461.2	phenylalanyl-tRNA synthetase
HNRNPU	-0.6	-1.15	NM_004501.3	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRNPU)
LRPPRC	-0.6	-1.15	NM_133259.2	leucine-rich PPR-motif containing (LRPPRC)
SMOC1	-0.63	-1.15	NM_001034852.1	SPARC related modular calcium binding 1 (SMOC1)
ARL5A	-0.66	-1.15	NM_001037174.1	ADP-ribosylation factor-like 5A (ARL5A)
PHF21A	-0.77	-1.15	NM_016621.2	PHD finger protein 21A (PHF21A)
ERH	-1.31	-1.15	NM_004450.1	enhancer of rudimentary homolog (Drosophila) (ERH)
TRABD	-1.43	-1.15	NM_025204.2	TraB domain containing (TRABD)
C19orf56	-1.5	-1.15	NM_016145.2	chromosome 19 open reading frame 56 (C19orf56)
DGUOK	-1.51	-1.15	NM_080918.1	deoxyguanosine kinase (DGUOK)
LOC645436	-1.52	-1.15	XM_928473.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
TPM1	-1.56	-1.15	NM_001018020.1	tropomyosin 1 (alpha) (TPM1)
LOC440991	-1.67	-1.15	XR_017665.2	PREDICTED: misc_RNA (LOC440991)
FKSG30	-1.72	-1.15	NM_001017421.1	actin-like protein (FKSG30)
IMP3	-1.85	-1.15	NM_018285.2	IMP3
NDUFB10	-1.86	-1.15	NM_004548.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
SNRPF	-1.86	-1.15	NM_003095.1	small nuclear ribonucleoprotein polypeptide F (SNRPF)

GUK1	-1.96	-1.15	NM_000858.4	guanylate kinase 1 (GUK1)
LOC729769	-1.99	-1.15	XM_001131246.2	PREDICTED: similar to Ubiquinol-cytochrome c reductase hinge protein (LOC729769)
RHOA	-1.99	-1.15	NM_001664.2	ras homolog gene family
TPI1	-2.04	-1.15	NM_000365.4	triosephosphate isomerase 1 (TPI1)
EEF2	-2.15	-1.15	NM_001961.3	eukaryotic translation elongation factor 2 (EEF2)
LOC644914	-2.23	-1.15	XM_001128558.2	PREDICTED: similar to H3 histone
YBX1	-2.24	-1.15	NM_004559.3	Y box binding protein 1 (YBX1)
LOC653737	-2.29	-1.15	XM_929340.3	PREDICTED: hypothetical LOC653737 (LOC653737)
GNG11	-2.35	-1.15	NM_004126.3	guanine nucleotide binding protein (G protein)
ATP5G2	-2.39	-1.15	NM_005176.4	ATP synthase
LOC285053	-2.39	-1.15	XM_208281.7	PREDICTED: similar to ribosomal protein L18a
LOC286444	-2.51	-1.15	XR_038693.1	PREDICTED: misc_RNA (LOC286444)
H3F3A	-2.55	-1.15	NM_002107.3	H3 histone
H3F3A	-2.6	-1.15	NM_002107.3	H3 histone
COX7C	-2.65	-1.15	NM_001867.2	cytochrome c oxidase subunit VIIc (COX7C)
LOC643863	-2.66	-1.15	XR_016732.2	PREDICTED: misc_RNA (LOC643863)
RPL17	-2.75	-1.15	NM_001035006.1	ribosomal protein L17 (RPL17)
LOC652071	-2.9	-1.15	XM_941396.2	PREDICTED: similar to 60S ribosomal protein L23a (LOC652071)
LOC387930	-2.91	-1.15	XR_041075.1	PREDICTED: misc_RNA (LOC387930)
LOC389101	-2.96	-1.15	XM_001131315.1	PREDICTED: similar to ribosomal protein L23a (LOC389101)
LOC440589	-2.96	-1.15	XM_942424.2	PREDICTED: similar to ribosomal protein S2
LOC401206	-2.97	-1.15	XM_376420.3	PREDICTED: similar to 40S ribosomal protein S25 (LOC401206)
LOC100129158	-3.01	-1.15	XR_038602.1	PREDICTED: misc_RNA (LOC100129158)
LOC440027	-3.01	-1.15	XR_017407.2	PREDICTED: misc_RNA (LOC440027)
TMSB4X	-3.23	-1.15	NM_021109.2	thymosin
SLC25A24	-0.16	-1.16	NM_013386.3	solute carrier family 25 (mitochondrial carrier; phosphate carrier)
GAS2L3	-0.24	-1.16	NM_174942.1	growth arrest-specific 2 like 3 (GAS2L3)
PANX1	-0.24	-1.16	NM_015368.3	pannexin 1 (PANX1)
RSPH3	-0.26	-1.16	NM_031924.3	radial spoke 3 homolog (Chlamydomonas) (RSPH3)
BACE2	-0.28	-1.16	NM_138991.1	beta-site APP-cleaving enzyme 2 (BACE2)
MYPN	-0.3	-1.16	NM_032578.2	myopalladin (MYPN)
PBRM1	-0.32	-1.16	NM_181042.2	polybromo 1 (PBRM1)
ZNF365	-0.32	-1.16	NM_014951.2	zinc finger protein 365 (ZNF365)
HIST1H2AG	-0.34	-1.16	NM_021064.3	histone cluster 1
IER5L	-0.42	-1.16	NM_203434.2	immediate early response 5-like (IER5L)
C15orf48	-0.44	-1.16	NM_032413.2	chromosome 15 open reading frame 48 (C15orf48)
MSL3L1	-0.46	-1.16	NM_078629.1	male-specific lethal 3-like 1 (Drosophila) (MSL3L1)
MVP	-0.47	-1.16	NM_005115.3	major vault protein (MVP)
PTPRK	-0.52	-1.16	NM_002844.2	protein tyrosine phosphatase
ABCB7	-0.54	-1.16	NM_004299.3	ATP-binding cassette
IDS	-0.55	-1.16	NM_006123.2	iduronate 2-sulfatase (Hunter syndrome) (IDS)
LAMP2	-0.55	-1.16	NM_002294.1	lysosomal-associated membrane protein 2 (LAMP2)
ETF1	-0.98	-1.16	NM_004730.1	eukaryotic translation termination factor 1 (ETF1)
HTRA1	-1.01	-1.16	NM_002775.3	HtrA serine peptidase 1 (HTRA1)
UBL5	-1.51	-1.16	NM_001048241.1	ubiquitin-like 5 (UBL5)
LOC643949	-1.58	-1.16	XR_018645.1	PREDICTED: similar to 60S acidic ribosomal protein P2 (LOC643949)
ATP6V0C	-1.65	-1.16	XM_001130742.1	PREDICTED: ATPase
EDF1	-1.67	-1.16	NM_003792.2	endothelial differentiation-related factor 1 (EDF1)
LOC100131609	-1.74	-1.16	XR_038433.1	PREDICTED: misc_RNA (LOC100131609)

LOC645157	-1.77	-1.16	XR_016770.2	PREDICTED: misc_RNA (LOC645157)
ATP5G1	-1.8	-1.16	NM_001002027.1	ATP synthase
EIF3D	-1.8	-1.16	NM_003753.3	eukaryotic translation initiation factor 3
AMY1C	-1.94	-1.16	NM_001008219.1	amylase
LOC388621	-2.07	-1.16	XM_941195.2	PREDICTED: similar to ribosomal protein L21 (LOC388621)
LOC728139	-2.23	-1.16	XR_015301.2	PREDICTED: misc_RNA (LOC728139)
PRDX5	-2.31	-1.16	NM_181652.1	peroxiredoxin 5 (PRDX5)
COX7A2	-2.39	-1.16	NM_001865.2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2)
LOC648771	-2.42	-1.16	XR_039634.1	PREDICTED: misc_RNA (LOC648771)
SLC25A3	-2.44	-1.16	NM_002635.2	solute carrier family 25 (mitochondrial carrier; phosphate carrier)
LOC387867	-2.51	-1.16	XM_939738.2	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)
LOC100132742	-2.53	-1.16	XM_001717161.1	PREDICTED: hypothetical protein LOC100132742
H3F3A	-2.7	-1.16	NM_002107.3	H3 histone
LOC643531	-2.76	-1.16	XR_019563.2	PREDICTED: misc_RNA (LOC643531)
LOC653881	-2.78	-1.16	XM_001718435.1	PREDICTED: similar to ribosomal protein L3 (LOC653881)
RPL8	-2.78	-1.16	NM_033301.1	ribosomal protein L8 (RPL8)
PFN1	-2.88	-1.16	NM_005022.2	profilin 1 (PFN1)
LOC650276	-2.94	-1.16	XM_939363.1	PREDICTED: similar to 60S ribosomal protein L7 (LOC650276)
LOC728481	-3.02	-1.16	XR_015292.1	PREDICTED: similar to similar to RPL23AP7 protein (LOC728481)
RPS15A	-3.05	-1.16	NM_001030009.1	ribosomal protein S15a (RPS15A)
MCM7	-0.23	-1.17	NM_005916.3	minichromosome maintenance complex component 7 (MCM7)
WIPF1	-0.25	-1.17	NM_001077269.1	WAS/WASL interacting protein family
CAMK2D	-0.28	-1.17	NM_001221.2	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D)
LOC730996	-0.3	-1.17	XM_001128017.1	PREDICTED: similar to chromosome 1 open reading frame 80 (LOC730996)
DCBLD1	-0.31	-1.17	NM_173674.1	discoidin
GSTM4	-0.31	-1.17	NM_000850.3	glutathione S-transferase M4 (GSTM4)
PPIB	-0.32	-1.17	NM_000942.4	peptidylprolyl isomerase B (cyclophilin B) (PPIB)
FIGNL1	-0.34	-1.17	NM_001042762.1	fidgetin-like 1 (FIGNL1)
LOC729985	-0.37	-1.17	XM_001131964.1	PREDICTED: similar to CDC42-binding protein kinase beta (LOC729985)
ABI1	-0.45	-1.17	NM_001012751.1	abl-interactor 1 (ABI1)
C7orf68	-0.46	-1.17	NM_013332.3	chromosome 7 open reading frame 68 (C7orf68)
PUS3	-0.52	-1.17	NM_031307.2	pseudouridylate synthase 3 (PUS3)
CYTH1	-0.55	-1.17	NM_017456.2	cytohesin 1 (CYTH1)
DSN1	-0.66	-1.17	NM_024918.2	DSN1
HNRNPAB	-1	-1.17	NM_004499.3	heterogeneous nuclear ribonucleoprotein A/B (HNRNPAB)
GSTO1	-1.57	-1.17	NM_004832.1	glutathione S-transferase omega 1 (GSTO1)
CD81	-1.58	-1.17	NM_004356.3	CD81 molecule (CD81)
ERP29	-1.62	-1.17	NM_001034025.1	endoplasmic reticulum protein 29 (ERP29)
CSRP1	-1.65	-1.17	NM_004078.1	cysteine and glycine-rich protein 1 (CSRP1)
NDUFA3	-1.76	-1.17	NM_004542.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
PFDN5	-2.01	-1.17	NM_002624.3	prefoldin subunit 5 (PFDN5)
HNRPA1L-2	-2.02	-1.17	NR_002944.2	heterogeneous nuclear ribonucleoprotein A1 pseudogene (HNRPA1L-2)
RPS21	-2.13	-1.17	NM_001024.3	ribosomal protein S21 (RPS21)
NDUFS8	-2.17	-1.17	NM_002496.1	NADH dehydrogenase (ubiquinone) Fe-S protein 8
LOC439953	-2.32	-1.17	XR_017375.2	PREDICTED: misc_RNA (LOC439953)
NOP10	-2.37	-1.17	NM_018648.3	NOP10 ribonucleoprotein homolog (yeast) (NOP10)
LOC338870	-2.47	-1.17	XR_038789.1	PREDICTED: misc_RNA (LOC338870)
RPS18	-2.55	-1.17	NM_022551.2	ribosomal protein S18 (RPS18)
LOC100129141	-2.78	-1.17	XR_039484.1	PREDICTED: misc_RNA (LOC100129141)

LOC728576	-2.92	-1.17	XR_038296.1	PREDICTED: misc_RNA (LOC728576)
LOC653232	-2.97	-1.17	XM_944104.2	PREDICTED: hypothetical LOC653232
ACTG1	-2.99	-1.17	NM_001614.2	actin
LOC402057	-3.13	-1.17	NM_001080499.1	similar to 40S ribosomal protein S17 (LOC402057)
ADAM9	-0.26	-1.18	NM_003816.2	ADAM metallopeptidase domain 9 (meltrin gamma) (ADAM9)
KCNN4	-0.31	-1.18	NM_002250.2	potassium intermediate/small conductance calcium-activated channel
TRIM56	-0.34	-1.18	NM_030961.1	tripartite motif-containing 56 (TRIM56)
LOX	-0.36	-1.18	NM_002317.3	lysyl oxidase (LOX)
ST3GAL2	-0.36	-1.18	NM_006927.3	ST3 beta-galactoside alpha-2
MCTP1	-0.38	-1.18	NM_024717.3	multiple C2 domains
H2AFY	-0.4	-1.18	NM_138609.2	H2A histone family
IFIT3	-0.4	-1.18	NM_001549.2	interferon-induced protein with tetratricopeptide repeats 3 (IFIT3)
WBSCR16	-0.43	-1.18	NM_030798.3	Williams-Beuren syndrome chromosome region 16 (WBSCR16)
TPM4	-0.51	-1.18	NM_003290.1	tropomyosin 4 (TPM4)
GUSB	-0.53	-1.18	NM_000181.2	glucuronidase
LAMB1	-0.65	-1.18	NM_002291.1	laminin
HLA-B	-0.67	-1.18	NM_005514.5	major histocompatibility complex
MT1G	-0.68	-1.18	NM_005950.1	metallothionein 1G (MT1G)
LMNA	-1.07	-1.18	NM_005572.3	lamin A/C (LMNA)
MTE	-1.24	-1.18	NM_175621.2	metallothionein E (MTE)
RPL29	-1.37	-1.18	NM_000992.2	ribosomal protein L29 (RPL29)
PRDX4	-1.57	-1.18	NM_006406.1	peroxiredoxin 4 (PRDX4)
HSPD1	-1.59	-1.18	NM_002156.4	heat shock 60kDa protein 1 (chaperonin) (HSPD1)
LSM7	-1.66	-1.18	NM_016199.1	LSM7 homolog
PTBP1	-1.67	-1.18	NM_002819.3	polypyrimidine tract binding protein 1 (PTBP1)
LOC347376	-1.75	-1.18	XM_937928.1	PREDICTED: similar to H3 histone
LOC729500	-1.8	-1.18	XR_018655.2	PREDICTED: misc_RNA (LOC729500)
NDUFA12	-1.82	-1.18	NM_018838.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
PFDN5	-1.82	-1.18	NM_145897.2	prefoldin subunit 5 (PFDN5)
CCT3	-1.87	-1.18	NM_005998.3	chaperonin containing TCP1
ACTB	-1.95	-1.18	NM_001101.2	actin
LOC391532	-2.03	-1.18	XR_017653.1	PREDICTED: misc_RNA (LOC391532)
PTBP1	-2.04	-1.18	NM_175847.1	polypyrimidine tract binding protein 1 (PTBP1)
NDUFB8	-2.09	-1.18	NM_005004.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
VIM	-2.11	-1.18	NM_003380.2	vimentin (VIM)
TXNDC17	-2.16	-1.18	NM_032731.3	thioredoxin domain containing 17 (TXNDC17)
ATP5J2	-2.26	-1.18	NM_004889.2	ATP synthase
LOC731640	-2.26	-1.18	XM_001133089.1	PREDICTED: similar to 60S ribosomal protein L21
PCBP2	-2.31	-1.18	NM_005016.3	poly(rC) binding protein 2 (PCBP2)
LOC100128936	-2.33	-1.18	XM_001721819.1	PREDICTED: similar to ribosomal protein L10a (LOC100128936)
LOC730246	-2.61	-1.18	XR_016080.2	PREDICTED: misc_RNA (LOC730246)
LOC646200	-2.62	-1.18	XM_930460.1	PREDICTED: similar to 60S ribosomal protein L22 (Heparin binding protein HBp15)
LOC389404	-2.68	-1.18	XR_018133.2	PREDICTED: misc_RNA (LOC389404)
RPL9	-2.73	-1.18	NM_001024921.2	ribosomal protein L9 (RPL9)
LOC729798	-2.77	-1.18	XM_001722176.1	PREDICTED: similar to ribosomal protein L23a (LOC729798)
OAZ1	-2.78	-1.18	NM_004152.2	ornithine decarboxylase antizyme 1 (OAZ1)
RPS14	-3.04	-1.18	NM_001025070.1	ribosomal protein S14 (RPS14)
TPT1	-3.07	-1.18	NM_003295.1	tumor protein
LOC389435	-3.15	-1.18	NM_001089587.1	hCG21078 (LOC389435)

RPL6	-3.15	-1.18	NM_001024662.1	ribosomal protein L6 (RPL6)
LOC728517	-3.19	-1.18	XR_015303.2	PREDICTED: misc_RNA (LOC728517)
GTF2IP1	-0.3	-1.19	NR_002206.1	general transcription factor II
ZAK	-0.37	-1.19	NM_016653.2	sterile alpha motif and leucine zipper containing kinase AZK (ZAK)
KCNG1	-0.42	-1.19	NM_002237.3	potassium voltage-gated channel
LOC644684	-0.44	-1.19	XM_001715037.1	PREDICTED: hypothetical LOC644684 (LOC644684)
HM13	-0.45	-1.19	NM_178580.1	histocompatibility (minor) 13 (HM13)
LOC647150	-0.46	-1.19	XR_017449.2	PREDICTED: misc_RNA (LOC647150)
LOC143543	-0.56	-1.19	NR_002197.1	RNA binding motif protein
ITGB1	-0.77	-1.19	NM_033669.1	integrin
SF3B5	-1.53	-1.19	NM_031287.2	splicing factor 3b
LOC644745	-1.58	-1.19	XR_018757.1	PREDICTED: misc_RNA (LOC644745)
ATP1A1	-1.66	-1.19	NM_001001586.1	ATPase
NHP2	-1.69	-1.19	NM_001034833.1	NHP2 ribonucleoprotein homolog (yeast) (NHP2)
CCT7	-1.76	-1.19	NM_001009570.1	chaperonin containing TCP1
WBP5	-1.83	-1.19	NM_001006612.1	WW domain binding protein 5 (WBP5)
LOC389156	-1.85	-1.19	XR_017589.2	PREDICTED: misc_RNA (LOC389156)
HNRPA1P4	-2.09	-1.19	XM_939887.2	PREDICTED: heterogeneous nuclear ribonucleoprotein A1 pseudogene 4 (HNRPA1P4)
IFITM2	-2.22	-1.19	NM_006435.2	interferon induced transmembrane protein 2 (1-8D) (IFITM2)
LOC645688	-2.27	-1.19	XR_017614.1	PREDICTED: similar to 60S ribosomal protein L12 (LOC645688)
PARK7	-2.44	-1.19	NM_007262.3	Parkinson disease (autosomal recessive
LOC731365	-2.57	-1.19	XR_015917.1	PREDICTED: similar to ribosomal protein L24 (LOC731365)
MGC87895	-2.58	-1.19	XM_942712.3	PREDICTED: similar to ribosomal protein S14 (MGC87895)
RPL14L	-2.62	-1.19	XR_041286.1	PREDICTED: misc_RNA (RPL14L)
LOC651436	-2.69	-1.19	XM_940587.1	PREDICTED: similar to ribosomal protein L9 (LOC651436)
LOC440575	-2.74	-1.19	XM_001732837.1	PREDICTED: hypothetical LOC440575 (LOC440575)
LOC642741	-2.74	-1.19	XR_019077.2	PREDICTED: misc_RNA (LOC642741)
LOC728244	-2.74	-1.19	XR_018431.1	PREDICTED: misc_RNA (LOC728244)
LOC731985	-2.76	-1.19	XR_015987.1	PREDICTED: hypothetical protein LOC731985 (LOC731985)
LOC100131713	-2.81	-1.19	XM_001724272.1	PREDICTED: similar to ribosomal protein L29
LOC391656	-2.81	-1.19	XM_373027.4	PREDICTED: similar to hCG1640454 (LOC391656)
SNRPD2	-2.86	-1.19	NM_004597.4	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa (SNRPD2)
UBB	-2.95	-1.19	NM_018955.2	ubiquitin B (UBB)
LOC729617	-3.02	-1.19	NM_001101668.1	ribosomal protein L23a-like (LOC729617)
LOC100129553	-3.03	-1.19	XR_039577.1	PREDICTED: misc_RNA (LOC100129553)
LOC647099	-3.12	-1.19	NM_001093758.2	similar to ribosomal protein L23A (LOC647099)
RPL38	-3.14	-1.19	NM_001035258.1	ribosomal protein L38 (RPL38)
LOC148430	-3.16	-1.19	XR_018751.2	PREDICTED: misc_RNA (LOC148430)
RPLP2	-3.33	-1.19	NM_001004.2	ribosomal protein
LOC653162	-3.34	-1.19	XR_038820.1	PREDICTED: misc_RNA (LOC653162)
ANXA8	-0.36	-1.2	NM_001040084.1	annexin A8 (ANXA8)
IL11	-0.36	-1.2	NM_000641.2	interleukin 11 (IL11)
EID2	-0.37	-1.2	NM_153232.3	EP300 interacting inhibitor of differentiation 2 (EID2)
STK16	-0.37	-1.2	NM_003691.2	serine/threonine kinase 16 (STK16)
GRN	-0.49	-1.2	NM_002087.2	granulin (GRN)
PTBP2	-0.85	-1.2	NM_021190.1	polypyrimidine tract binding protein 2 (PTBP2)
LOC645691	-1.08	-1.2	XM_928701.3	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein A1 (LOC645691)
MAPKAPK3	-1.39	-1.2	NM_004635.3	mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3)
MYH9	-1.51	-1.2	NM_002473.3	myosin

CDH2	-1.52	-1.2	NM_001792.2	cadherin 2
MRPL11	-1.53	-1.2	NM_170738.1	mitochondrial ribosomal protein L11 (MRPL11)
CCT3	-1.68	-1.2	NM_001008800.1	chaperonin containing TCP1
LOC388275	-1.8	-1.2	XM_928429.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
LOC648210	-1.98	-1.2	XR_018923.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
LOC400948	-2.02	-1.2	XM_940643.1	PREDICTED: similar to CG33774-PA (LOC400948)
LOC388532	-2.19	-1.2	XM_939726.2	PREDICTED: similar to ribosomal protein L21 (LOC388532)
MGC4677	-2.24	-1.2	NM_052871.3	hypothetical protein MGC4677 (MGC4677)
LOC347544	-2.26	-1.2	XM_938382.2	PREDICTED: similar to ribosomal protein L18a (LOC347544)
LOC643433	-2.53	-1.2	XM_928197.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP)
RPL13	-2.54	-1.2	NM_033251.1	ribosomal protein L13 (RPL13)
LOC100127993	-2.64	-1.2	XR_037873.1	PREDICTED: misc_RNA (LOC100127993)
LOC402694	-2.66	-1.2	NM_001089590.1	similar to ribosomal protein L15 (LOC402694)
LOC729679	-2.71	-1.2	XR_015990.2	PREDICTED: misc_RNA (LOC729679)
LOC728782	-2.73	-1.2	XM_001720625.1	PREDICTED: similar to ribosomal protein L21 (LOC728782)
LOC390354	-2.75	-1.2	XR_000900.1	PREDICTED: similar to ribosomal protein L18a; 60S ribosomal protein L18a
RPL23	-2.94	-1.2	NM_000978.3	ribosomal protein L23 (RPL23)
LOC642250	-3.02	-1.2	NM_001089592.1	PREDICTED: similar to 60S ribosomal protein L17 (L23)
LOC341457	-3.09	-1.2	XM_292085.2	PREDICTED: similar to peptidylprolyl isomerase A isoform 1 (LOC341457)
LOC648729	-3.12	-1.2	XR_039144.1	PREDICTED: misc_RNA (LOC648729)
LOC644464	-3.25	-1.2	XR_038490.1	PREDICTED: misc_RNA (LOC644464)
RPS17	-3.3	-1.2	NM_001021.3	ribosomal protein S17 (RPS17)
LOC642210	-3.33	-1.2	XM_936874.1	PREDICTED: similar to 60S ribosomal protein L32 (LOC642210)
LOC649076	-3.41	-1.2	XR_018338.2	PREDICTED: misc_RNA (LOC649076)
FSTL4	-0.47	-1.21	NM_015082.1	follistatin-like 4 (FSTL4)
FOXD1	-0.48	-1.21	NM_004472.2	forkhead box D1 (FOXD1)
LGALS8	-0.48	-1.21	NM_201545.1	lectin
UBE2L6	-0.51	-1.21	NM_004223.3	ubiquitin-conjugating enzyme E2L 6 (UBE2L6)
PPP2R5D	-0.54	-1.21	NM_180976.1	protein phosphatase 2
MAGEE1	-0.59	-1.21	NM_020932.1	melanoma antigen family E
HLA-G	-0.6	-1.21	NM_002127.3	HLA-G histocompatibility antigen
WSB1	-0.93	-1.21	NM_134265.2	WD repeat and SOCS box-containing 1 (WSB1)
NHP2L1	-1.08	-1.21	NM_001003796.1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1)
MRPS35	-1.25	-1.21	NM_021821.2	mitochondrial ribosomal protein S35 (MRPS35)
C19orf70	-1.52	-1.21	NM_205767.1	chromosome 19 open reading frame 70 (C19orf70)
SF3A3	-1.64	-1.21	NM_006802.2	splicing factor 3a
PSMB5	-1.75	-1.21	NM_002797.2	proteasome (prosome
SUMO2	-1.76	-1.21	NM_001005849.1	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) (SUMO2)
LOC389156	-1.78	-1.21	XR_019429.2	PREDICTED: misc_RNA (LOC389156)
CDC20	-1.83	-1.21	NM_001255.2	cell division cycle 20 homolog (S. cerevisiae) (CDC20)
LOC644237	-1.83	-1.21	XR_039184.1	PREDICTED: misc_RNA (LOC644237)
NARS	-1.89	-1.21	NM_004539.3	asparaginyl-tRNA synthetase (NARS)
LOC729406	-2.01	-1.21	XR_037260.1	PREDICTED: misc_RNA (LOC729406)
CD44	-2.07	-1.21	NM_001001391.1	CD44 molecule (Indian blood group) (CD44)
GNPDA1	-2.07	-1.21	NM_005471.3	glucosamine-6-phosphate deaminase 1 (GNPDA1)
CCDC34	-2.1	-1.21	NM_030771.1	coiled-coil domain containing 34 (CCDC34)
NDUFB7	-2.26	-1.21	NM_004146.4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
EDF1	-2.29	-1.21	NM_003792.2	endothelial differentiation-related factor 1 (EDF1)
PSMB3	-2.3	-1.21	NM_002795.2	proteasome (prosome

COX6C	-2.33	-1.21	NM_004374.2	cytochrome c oxidase subunit VIc (COX6C)
NDUFA1	-2.54	-1.21	NM_004541.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
VIM	-2.55	-1.21	NM_003380.2	vimentin (VIM)
LOC100133273	-2.71	-1.21	XR_039238.1	PREDICTED: misc_RNA (LOC100133273)
RPS5	-2.82	-1.21	NM_001009.3	ribosomal protein S5 (RPS5)
RPL12	-2.86	-1.21	NM_000976.2	ribosomal protein L12 (RPL12)
LOC730754	-2.91	-1.21	NM_001093779.2	similar to ribosomal protein S18 (LOC730754)
LOC648294	-2.98	-1.21	XR_018553.2	PREDICTED: misc_RNA (LOC648294)
UQCRQ	-2.99	-1.21	NM_014402.4	ubiquinol-cytochrome c reductase
LOC644029	-3.1	-1.21	XR_017397.1	PREDICTED: similar to 60S ribosomal protein L7a (LOC644029)
LOC441013	-3.11	-1.21	XR_016299.2	PREDICTED: misc_RNA (LOC441013)
LOC100130980	-3.34	-1.21	XR_038930.1	PREDICTED: misc_RNA (LOC100130980)
LOC388524	-3.38	-1.21	NM_001005472.1	ribosomal protein SA pseudogene (LOC388524) on chromosome 19.
LOC732432	-0.41	-1.22	XM_001724189.1	PREDICTED: similar to Rho-associated
ABCG1	-0.54	-1.22	NM_016818.2	ATP-binding cassette
LOC728059	-0.54	-1.22	XR_015606.1	PREDICTED: misc_RNA (LOC728059)
MMACHC	-0.63	-1.22	NM_015506.2	methylmalonic aciduria (cobalamin deficiency) cblC type
LOC100132805	-0.68	-1.22	XM_001719188.1	PREDICTED: similar to predicted protein (LOC100132805)
HLA-A29.1	-0.75	-1.22	NM_001080840.1	major histocompatibility complex class I HLA-A29.1 (HLA-A29.1)
JUN	-0.78	-1.22	NM_002228.3	jun oncogene (JUN)
BAT2D1	-0.81	-1.22	NM_015172.3	BAT2 domain containing 1 (BAT2D1)
LOC650517	-1.02	-1.22	XR_019109.1	PREDICTED: hypothetical LOC650517 (LOC650517)
RTN3	-1.03	-1.22	NM_006054.2	reticulon 3 (RTN3)
DCTN2	-1.52	-1.22	NM_006400.3	dynactin 2 (p50) (DCTN2)
C7orf55	-1.54	-1.22	NM_197964.3	chromosome 7 open reading frame 55 (C7orf55)
LOC647307	-1.54	-1.22	XR_039752.1	PREDICTED: misc_RNA (LOC647307)
PRDX2	-1.56	-1.22	NM_181738.1	peroxiredoxin 2 (PRDX2)
LOC729317	-1.68	-1.22	XM_001133585.1	PREDICTED: similar to voltage-dependent anion channel 2 (LOC729317)
P4HB	-1.69	-1.22	NM_000918.3	prolyl 4-hydroxylase
RPP21	-1.71	-1.22	NM_024839.1	ribonuclease P/MRP 21kDa subunit (RPP21)
MGC71993	-1.79	-1.22	NM_001004333.2	similar to DNA segment
PTTG1IP	-1.8	-1.22	NM_004339.2	pituitary tumor-transforming 1 interacting protein (PTTG1IP)
MGST3	-1.82	-1.22	NM_004528.2	microsomal glutathione S-transferase 3 (MGST3)
NENF	-1.93	-1.22	NM_013349.3	neuron derived neurotrophic factor (NENF)
ITGB1	-2.23	-1.22	NM_002211.2	integrin
C20orf24	-2.27	-1.22	NM_018840.2	chromosome 20 open reading frame 24 (C20orf24)
EIF3B	-2.33	-1.22	NM_001037283.1	eukaryotic translation initiation factor 3
MT1E	-2.34	-1.22	NM_175617.3	metallothionein 1E (functional) (MT1E)
LOC646942	-2.68	-1.22	XR_016892.2	PREDICTED: misc_RNA (LOC646942)
FAU	-2.87	-1.22	NM_001997.3	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (FAU)
LOC729402	-3.12	-1.22	XM_001721328.1	PREDICTED: hypothetical LOC729402 (LOC729402)
RPL10A	-3.14	-1.22	NM_007104.4	ribosomal protein L10a (RPL10A)
RPS25	-3.18	-1.22	NM_001028.2	ribosomal protein S25 (RPS25)
RPL41	-3.59	-1.22	NM_001035267.1	ribosomal protein L41 (RPL41)
LOC91561	-3.6	-1.22	NM_001080822.1	hCG1992539 (LOC91561)
PMP22	-0.54	-1.23	NM_153321.1	peripheral myelin protein 22 (PMP22)
DFFB	-0.64	-1.23	NM_004402.2	DNA fragmentation factor
ITGB1	-0.7	-1.23	NM_033668.1	integrin
ETV5	-0.76	-1.23	NM_004454.1	ets variant gene 5 (ets-related molecule) (ETV5)

TDG	-0.99	-1.23	NM_003211.3	thymine-DNA glycosylase (TDG)
SLPI	-1.14	-1.23	NM_003064.2	secretory leukocyte peptidase inhibitor (SLPI)
UNC84B	-1.18	-1.23	NM_015374.1	unc-84 homolog B (C. elegans) (UNC84B)
TOMM22	-1.57	-1.23	NM_020243.4	translocase of outer mitochondrial membrane 22 homolog (yeast) (TOMM22)
ITPR3	-1.6	-1.23	NM_002224.2	inositol 1
MARCKSL1	-1.74	-1.23	NM_023009.4	MARCKS-like 1 (MARCKSL1)
SUPT16H	-1.82	-1.23	NM_007192.2	suppressor of Ty 16 homolog (S. cerevisiae) (SUPT16H)
GSTO1	-2.08	-1.23	NM_004832.1	glutathione S-transferase omega 1 (GSTO1)
POLR2H	-2.08	-1.23	NM_006232.2	polymerase (RNA) II (DNA directed) polypeptide H (POLR2H)
ANXA5	-2.1	-1.23	NM_001154.2	annexin A5 (ANXA5)
C9orf78	-2.1	-1.23	NM_016520.2	chromosome 9 open reading frame 78 (C9orf78)
ETF1	-2.13	-1.23	NM_004730.1	eukaryotic translation termination factor 1 (ETF1)
GLTSCR2	-2.17	-1.23	NM_015710.3	glioma tumor suppressor candidate region gene 2 (GLTSCR2)
C12orf57	-2.24	-1.23	NM_138425.2	chromosome 12 open reading frame 57 (C12orf57)
PPP1R14B	-2.36	-1.23	NM_138689.2	protein phosphatase 1
ATP5J2	-2.49	-1.23	NM_001003714.1	ATP synthase
TGFBI	-2.73	-1.23	NM_000358.1	transforming growth factor
LOC391370	-3.05	-1.23	XM_372926.5	PREDICTED: similar to hCG1818387 (LOC391370)
RPS15A	-3.21	-1.23	NM_001019.4	ribosomal protein S15a (RPS15A)
GNB2L1	-3.4	-1.23	NM_006098.4	guanine nucleotide binding protein (G protein)
LOC343184	-3.42	-1.23	XR_016832.1	PREDICTED: misc_RNA (LOC343184)
SNAP25	-0.74	-1.24	NM_130811.1	synaptosomal-associated protein
IGSF3	-0.87	-1.24	NM_001542.2	immunoglobulin superfamily
CYFIP2	-0.95	-1.24	NM_014376.2	cytoplasmic FMR1 interacting protein 2 (CYFIP2)
GNL3L	-1.02	-1.24	NM_019067.4	guanine nucleotide binding protein-like 3 (nucleolar)-like (GNL3L)
MYLIP	-1.25	-1.24	NM_013262.3	myosin regulatory light chain interacting protein (MYLIP)
IGFBP7	-1.53	-1.24	NM_001553.1	insulin-like growth factor binding protein 7 (IGFBP7)
RNASEK	-1.75	-1.24	NM_001004333.3	ribonuclease
LOC100131801	-1.95	-1.24	XM_001726504.1	PREDICTED: similar to hCG2036585 (LOC100131801)
URM1	-1.97	-1.24	NM_030914.1	ubiquitin related modifier 1 homolog (S. cerevisiae) (URM1)
PEBP1	-1.98	-1.24	NM_002567.2	phosphatidylethanolamine binding protein 1 (PEBP1)
LOC100133372	-1.99	-1.24	XR_039042.1	PREDICTED: misc_RNA (LOC100133372)
ATPIF1	-2.18	-1.24	NM_178191.1	ATPase inhibitory factor 1 (ATPIF1)
PTTG1	-2.5	-1.24	NM_004219.2	pituitary tumor-transforming 1 (PTTG1)
SERF2	-2.74	-1.24	NM_001018108.2	small EDRK-rich factor 2 (SERF2)
CLPTM1L	-2.86	-1.24	NM_030782.3	CLPTM1-like (CLPTM1L)
LOC649447	-2.86	-1.24	XM_941125.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) (LOC649447)
LOC729102	-2.87	-1.24	XR_015895.2	PREDICTED: misc_RNA (LOC729102)
RPL12	-2.93	-1.24	NM_000976.2	ribosomal protein L12 (RPL12)
LOC651894	-3.34	-1.24	XM_941155.2	PREDICTED: similar to ribosomal protein S12 (LOC651894)
LOC100130553	-3.35	-1.24	XM_001713658.1	PREDICTED: hypothetical protein LOC100130553 (LOC100130553)
RPL11	-3.39	-1.24	NM_000975.2	ribosomal protein L11 (RPL11)
RPS10	-3.41	-1.24	NM_001014.3	ribosomal protein S10 (RPS10)
LOC388474	-3.72	-1.24	XM_938181.2	PREDICTED: similar to 60S ribosomal protein L7a
EXT2	-0.66	-1.25	NM_000401.2	exostoses (multiple) 2 (EXT2)
ARL5A	-0.67	-1.25	NM_012097.3	ADP-ribosylation factor-like 5A (ARL5A)
CDCP1	-0.67	-1.25	NM_178181.1	CUB domain containing protein 1 (CDCP1)
STT3A	-0.75	-1.25	NM_152713.2	STT3
SEMA3E	-1.45	-1.25	NM_012431.1	sema domain

ACTG1	-1.57	-1.25	NM_001614.2	actin
FAM96B	-1.6	-1.25	NM_016062.1	family with sequence similarity 96
LOC286512	-1.66	-1.25	XR_038196.1	PREDICTED: misc_RNA (LOC286512)
CTNNA1	-1.78	-1.25	NM_001903.2	catenin (cadherin-associated protein)
LOC731049	-1.81	-1.25	XM_001129232.1	PREDICTED: similar to Ubiquitin-conjugating enzyme E2S (Ubiquitin-conjugating enzyme E2-24 kDa)
S100A13	-1.81	-1.25	NM_001024211.1	S100 calcium binding protein A13 (S100A13)
C7orf59	-1.85	-1.25	NM_001008395.2	chromosome 7 open reading frame 59 (C7orf59)
LOC286016	-2.02	-1.25	NR_002187.2	triosephosphate isomerase 1 pseudogene (LOC286016)
LOC148430	-2.13	-1.25	XR_038750.1	PREDICTED: misc_RNA (LOC148430)
FBL	-2.18	-1.25	NM_001436.2	fibrillarin (FBL)
TSPO	-2.55	-1.25	NM_000714.4	translocator protein (18kDa) (TSPO)
RAC1	-2.6	-1.25	NM_006908.3	ras-related C3 botulinum toxin substrate 1 (rho family
RPL36	-2.6	-1.25	NM_033643.2	ribosomal protein L36 (RPL36)
LOC644907	-2.71	-1.25	NM_001090027.1	hCG18290 (LOC644907)
TPM2	-2.77	-1.25	NM_213674.1	tropomyosin 2 (beta) (TPM2)
GAPDH	-2.95	-1.25	NM_002046.3	glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
LOC728693	-2.95	-1.25	XR_015773.2	PREDICTED: misc_RNA (LOC728693)
LOC649548	-3.2	-1.25	XM_938623.1	PREDICTED: similar to 60S ribosomal protein L32 (LOC649548)
RPL27	-3.36	-1.25	NM_000988.3	ribosomal protein L27 (RPL27)
LACTB	-0.73	-1.26	NM_171846.1	lactamase
CA9	-0.86	-1.26	NM_001216.1	carbonic anhydrase IX (CA9)
ESYT1	-1.06	-1.26	NM_015292.1	extended synaptotagmin-like protein 1 (ESYT1)
FBLN1	-1.33	-1.26	NM_001996.2	fibulin 1 (FBLN1)
HLA-H	-1.46	-1.26	NR_001434.1	major histocompatibility complex
EIF6	-1.71	-1.26	NM_181466.1	eukaryotic translation initiation factor 6 (EIF6)
LOC651816	-1.75	-1.26	XM_941060.1	PREDICTED: similar to Ubiquitin-conjugating enzyme E2S (Ubiquitin-conjugating enzyme E2-24 kDa)
MSRB2	-1.86	-1.26	NM_012228.2	methionine sulfoxide reductase B2 (MSRB2)
CAPZA2	-1.88	-1.26	NM_006136.2	capping protein (actin filament) muscle Z-line
DDB1	-2.15	-1.26	NM_001923.3	PREDICTED: damage-specific DNA binding protein 1
YWHAB	-2.44	-1.26	NM_139323.2	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
LOC100128731	-2.45	-1.26	NM_001134693.1	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4 (LOC100128731)
NDUFB11	-2.47	-1.26	NM_019056.3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex
ATP5L	-2.76	-1.26	NM_006476.4	ATP synthase
RPS14	-3.06	-1.26	NM_001025071.1	ribosomal protein S14 (RPS14)
LOC645174	-3.13	-1.26	XR_017157.2	PREDICTED: misc_RNA (LOC645174)
LOC730187	-3.13	-1.26	XR_042419.1	PREDICTED: misc_RNA (LOC730187)
RPS20	-3.21	-1.26	NM_001023.2	ribosomal protein S20 (RPS20)
MYL6	-3.28	-1.26	NM_021019.3	myosin
RPS11	-3.29	-1.26	NM_001015.3	ribosomal protein S11 (RPS11)
RPL27A	-3.45	-1.26	NM_000990.2	ribosomal protein L27a (RPL27A)
RPL18A	-3.49	-1.26	NM_000980.2	ribosomal protein L18a (RPL18A)
RPS19	-3.49	-1.26	NM_001022.3	ribosomal protein S19 (RPS19)
LOC644615	-0.81	-1.27	XM_927730.1	PREDICTED: similar to Ras-related protein Rab-13 (LOC644615)
LAMB3	-0.86	-1.27	NM_000228.2	laminin
RAD21	-0.86	-1.27	NM_006265.1	RAD21 homolog (S. pombe) (RAD21)
RAD54L2	-0.87	-1.27	NM_015106.2	RAD54-like 2 (S. cerevisiae) (RAD54L2)
ZSWIM4	-1.07	-1.27	NM_023072.1	zinc finger
TGM2	-1.09	-1.27	NM_004613.2	transglutaminase 2 (C polypeptide
TPD52L2	-1.12	-1.27	NM_199361.1	tumor protein D52-like 2 (TPD52L2)

HLA-F	-1.25	-1.27	NM_018950.1	major histocompatibility complex
C20orf127	-1.63	-1.27	NM_080757.1	chromosome 20 open reading frame 127 (C20orf127)
ATP6AP1	-1.64	-1.27	NM_001183.4	ATPase
C9orf169	-1.64	-1.27	NM_199001.1	chromosome 9 open reading frame 169 (C9orf169)
DYNLT1	-1.71	-1.27	NM_006519.1	dynein
RAD23A	-1.9	-1.27	NM_005053.2	RAD23 homolog A (S. cerevisiae) (RAD23A)
NET1	-1.93	-1.27	NM_001047160.1	neuroepithelial cell transforming 1 (NET1)
TIMP1	-1.93	-1.27	NM_003254.2	TIMP metallopeptidase inhibitor 1 (TIMP1)
UBE2M	-1.93	-1.27	NM_003969.3	ubiquitin-conjugating enzyme E2M (UBC12 homolog
IMPDH2	-2.2	-1.27	NM_000884.2	IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2)
KRTCAP2	-2.27	-1.27	NM_173852.3	keratinocyte associated protein 2 (KRTCAP2)
CRIP1	-2.6	-1.27	NM_001311.3	cysteine-rich protein 1 (intestinal) (CRIP1)
GAPDH	-2.77	-1.27	NM_002046.3	glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
GSTP1	-3.01	-1.27	NM_000852.2	glutathione S-transferase pi (GSTP1)
NEDD8	-3.01	-1.27	NM_006156.1	neural precursor cell expressed
RPL18A	-3.46	-1.27	NM_000980.2	ribosomal protein L18a (RPL18A)
LOC441034	-3.74	-1.27	XR_018917.1	PREDICTED: similar to 60S ribosomal protein L7a (LOC441034)
CCDC58	-0.93	-1.28	NM_001017928.2	coiled-coil domain containing 58 (CCDC58)
UBE1	-1.58	-1.28	NM_003334.2	ubiquitin-activating enzyme E1 (UBE1)
EEF1D	-1.87	-1.28	NM_032378.2	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D)
PPM1G	-2.45	-1.28	NM_002707.3	protein phosphatase 1G (formerly 2C)
LOC653079	-2.6	-1.28	XR_016115.2	PREDICTED: misc_RNA (LOC653079)
TCEB2	-2.81	-1.28	NM_007108.2	transcription elongation factor B (SIII)
COX4I1	-3.11	-1.28	NM_001861.2	cytochrome c oxidase subunit IV isoform 1 (COX4I1)
GAPDH	-3.28	-1.28	NM_002046.3	glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
LOC401019	-3.43	-1.28	NM_001080831.1	hCG1783417 (LOC401019)
MYL6	-3.45	-1.28	NM_021019.3	myosin
RPL11	-3.52	-1.28	NM_000975.2	ribosomal protein L11 (RPL11)
RPL37A	-3.58	-1.28	NM_000998.4	ribosomal protein L37a (RPL37A)
LARP1B	-0.95	-1.29	NM_032239.2	La ribonucleoprotein domain family
ACTN1	-1.51	-1.29	NM_001102.2	actinin
TRAPPC3	-1.67	-1.29	NM_014408.3	trafficking protein particle complex 3 (TRAPPC3)
TDP1	-1.97	-1.29	NM_018319.3	tyrosyl-DNA phosphodiesterase 1 (TDP1)
LOC728782	-2.42	-1.29	XM_001128906.2	PREDICTED: similar to ribosomal protein L21 (LOC728782)
LOC440055	-2.53	-1.29	XM_495885.3	PREDICTED: similar to ribosomal protein S12 (LOC440055)
LOC648210	-2.54	-1.29	XR_018923.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)
RPS9	-2.67	-1.29	NM_001013.3	ribosomal protein S9 (RPS9)
LOC100132564	-2.76	-1.29	XM_001713808.1	PREDICTED: hypothetical protein LOC100132564 (LOC100132564)
LOC440737	-3.05	-1.29	XM_496446.3	PREDICTED: similar to 60S ribosomal protein L35 (LOC440737)
LOC729742	-3.07	-1.29	XM_001722353.1	PREDICTED: similar to hCG1812832 (LOC729742)
RPS15	-3.3	-1.29	NM_001018.3	ribosomal protein S15 (RPS15)
RPS12	-3.62	-1.29	NM_001016.3	ribosomal protein S12 (RPS12)
RPL32	-3.66	-1.29	NM_001007074.1	ribosomal protein L32 (RPL32)
ATAD1	-1.12	-1.3	NM_032810.2	ATPase family
NBPF10	-1.13	-1.3	NM_001039703.1	PREDICTED: neuroblastoma breakpoint family
GOT2	-1.7	-1.3	NM_002080.2	glutamic-oxaloacetic transaminase 2
LOC441743	-1.71	-1.3	NM_001045548.1	similar to C367G8.3 (novel protein similar to RPL23A (60S ribosomal protein L23A)) (LOC441743)
PLOD1	-1.73	-1.3	NM_000302.2	procollagen-lysine 1
LOC149501	-1.79	-1.3	XR_017100.2	PREDICTED: misc_RNA (LOC149501)

FAM160B1	-1.83	-1.3	NM_020940.3	family with sequence similarity 160
BOLA2	-1.85	-1.3	NM_001031827.1	bolA homolog 2 (E. coli) (BOLA2)
KRT8	-1.91	-1.3	NM_002273.2	keratin 8 (KRT8)
CUTA	-2.4	-1.3	NM_001014838.1	cutA divalent cation tolerance homolog (E. coli) (CUTA)
RN7SK	-2.45	-1.3	NR_001445.1	RNA
MT1A	-2.84	-1.3	NM_005946.2	metallothionein 1A (MT1A)
NDUFS5	-3.04	-1.3	NM_004552.1	NADH dehydrogenase (ubiquinone) Fe-S protein 5
LOC388556	-3.05	-1.3	XR_039451.1	PREDICTED: misc_RNA (LOC388556)
C20orf24	-3.11	-1.3	NM_199483.1	chromosome 20 open reading frame 24 (C20orf24)
LOC729789	-3.3	-1.3	XM_001722736.1	PREDICTED: similar to insulinoma protein (rig) (LOC729789)
S100A6	-3.47	-1.3	NM_014624.3	S100 calcium binding protein A6 (S100A6)
LOC440733	-3.52	-1.3	XM_496442.3	PREDICTED: similar to 40S ribosomal protein S15 (RIG protein) (LOC440733)
DVL3	-1.08	-1.31	NM_004423.3	dishevelled
SRD5A1	-1.58	-1.31	NM_001047.2	steroid-5-alpha-reductase
RPUSD4	-1.81	-1.31	NM_032795.1	RNA pseudouridylate synthase domain containing 4 (RPUSD4)
ARMET	-1.95	-1.31	NM_006010.2	arginine-rich
ANAPC11	-2.18	-1.31	NM_001002246.1	PREDICTED: APC11 anaphase promoting complex subunit 11 homolog (yeast)
C19orf53	-2.31	-1.31	NM_014047.2	chromosome 19 open reading frame 53 (C19orf53)
RPL21	-2.83	-1.31	NM_000982.3	ribosomal protein L21 (RPL21)
CD44	-1.13	-1.32	NM_001001392.1	CD44 molecule (Indian blood group) (CD44)
CIRBP	-1.55	-1.32	NM_001280.1	cold inducible RNA binding protein (CIRBP)
ACTR1A	-1.61	-1.32	NM_005736.2	ARP1 actin-related protein 1 homolog A
LOC644743	-1.97	-1.32	XR_016703.1	PREDICTED: hypothetical LOC644743 (LOC644743)
UBA1	-1.99	-1.32	NM_003334.3	ubiquitin-like modifier activating enzyme 1 (UBA1)
BCAP31	-2.07	-1.32	NM_005745.6	B-cell receptor-associated protein 31 (BCAP31)
LOC100130562	-2.15	-1.32	XM_001720379.1	PREDICTED: hypothetical protein LOC100130562
LOC401115	-2.64	-1.32	XM_937968.2	PREDICTED: hypothetical gene supported by BC038466; BC062790 (LOC401115)
C20orf24	-3.14	-1.32	NM_018840.2	chromosome 20 open reading frame 24 (C20orf24)
LOC642357	-3.28	-1.32	XR_018361.2	PREDICTED: misc_RNA (LOC642357)
HSP90AB6P	-1.04	-1.33	NM_001014441.1	heat shock protein 90kDa alpha (cytosolic)
BGN	-1.1	-1.33	NM_001711.3	biglycan (BGN)
NUCKS1	-1.21	-1.33	NM_022731.2	nuclear casein kinase and cyclin-dependent kinase substrate 1 (NUCKS1)
KIF3B	-1.55	-1.33	NM_004798.2	kinesin family member 3B (KIF3B)
PMPCA	-1.71	-1.33	NM_015160.1	peptidase (mitochondrial processing) alpha (PMPCA)
KRT17	-2.63	-1.33	NM_000422.1	keratin 17 (KRT17)
MT2A	-2.93	-1.33	NM_005953.2	metallothionein 2A (MT2A)
LOC651894	-3.06	-1.33	XM_941155.2	PREDICTED: similar to ribosomal protein S12 (LOC651894)
MIF	-3.2	-1.33	NM_002415.1	macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF)
LOC653658	-3.49	-1.33	XM_939687.2	PREDICTED: similar to ribosomal protein S23 (LOC653658)
C9orf114	-1.5	-1.34	NM_016390.2	chromosome 9 open reading frame 114 (C9orf114)
RTN3	-1.98	-1.34	NM_201430.1	reticulon 3 (RTN3)
TIMM22	-1.99	-1.34	NM_013337.2	translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22)
CS	-2.47	-1.34	NM_004077.2	citrate synthase (CS)
EEF1D	-2.51	-1.34	NM_032378.2	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D)
PHGDH	-2.57	-1.34	NM_006623.2	phosphoglycerate dehydrogenase (PHGDH)
ARL5A	-2.78	-1.34	NM_001037174.1	ADP-ribosylation factor-like 5A (ARL5A)
RPS9	-3.15	-1.34	NM_001013.3	ribosomal protein S9 (RPS9)
ENO1	-3.28	-1.34	NM_001428.2	enolase 1
HIST1H4C	-3.52	-1.34	NM_003542.3	histone cluster 1

LOC646766	-3.6	-1.34	XR_017605.1	PREDICTED: similar to 60S ribosomal protein L35 (LOC646766)
RPL18A	-3.81	-1.34	NM_000980.2	ribosomal protein L18a (RPL18A)
LOC729903	-3.91	-1.34	XR_040892.1	PREDICTED: misc_RNA (LOC729903)
MT1X	-1.82	-1.35	NM_005952.2	metallothionein 1X (MT1X)
HMGB2	-1.87	-1.35	NM_002129.2	high-mobility group box 2 (HMGB2)
NAP1L4	-1.99	-1.35	NM_005969.3	nucleosome assembly protein 1-like 4 (NAP1L4)
TFG	-2.04	-1.35	NM_001007565.1	TRK-fused gene (TFG)
BOLA2	-2.58	-1.35	NM_001031827.1	bolA homolog 2 (E. coli) (BOLA2)
MRPS24	-2.78	-1.35	NM_032014.2	mitochondrial ribosomal protein S24 (MRPS24)
LOC100131196	-3.15	-1.35	XR_038314.1	PREDICTED: misc_RNA (LOC100131196)
TPM2	-3.37	-1.35	NM_213674.1	tropomyosin 2 (beta) (TPM2)
RPS16	-4.05	-1.35	NM_001020.4	ribosomal protein S16 (RPS16)
UBE2G1	-1.58	-1.36	NM_003342.4	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog
FLNB	-1.6	-1.36	NM_001457.1	filamin B
SLC3A2	-1.71	-1.36	NM_001013251.1	solute carrier family 3 (activators of dibasic and neutral amino acid transport)
RPL12P6	-2.08	-1.36	XR_016704.2	PREDICTED: misc_RNA (RPL12P6)
NDUFA13	-2.26	-1.36	NM_015965.4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex
LOC100134134	-2.3	-1.36	XM_001720850.1	PREDICTED: similar to peroxidasin homolog (LOC100134134)
ANP32B	-3.2	-1.36	NM_006401.2	acidic (leucine-rich) nuclear phosphoprotein 32 family
SCG5	-1.39	-1.37	NM_003020.1	secretogranin V (7B2 protein) (SCG5)
ZDHHC3	-1.51	-1.37	NM_016598.1	zinc finger
KIF3B	-1.57	-1.37	NM_004798.2	kinesin family member 3B (KIF3B)
LOC440145	-1.64	-1.37	NM_001071775.1	similar to RIKEN cDNA 2410129H14 (LOC440145)
ARHGDIA	-1.98	-1.37	NM_004309.3	Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA)
MRPL41	-2.22	-1.37	NM_032477.1	mitochondrial ribosomal protein L41 (MRPL41)
ARIH2	-2.28	-1.37	NM_006321.2	ariadne homolog 2 (Drosophila) (ARIH2)
HLA-A	-2.7	-1.37	NM_002116.5	major histocompatibility complex
RPL35	-3.87	-1.37	NM_007209.3	ribosomal protein L35 (RPL35)
UBA52	-3.9	-1.37	NM_001033930.1	ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52)
LOC441876	-4	-1.37	XM_934931.2	PREDICTED: similar to 40S ribosomal protein S16
TMED7	-1.84	-1.38	NM_181836.3	transmembrane emp24 protein transport domain containing 7 (TMED7)
MSX1	-1.94	-1.38	NM_002448.3	msh homeobox 1 (MSX1)
HARS	-2.07	-1.38	NM_002109.3	histidyl-tRNA synthetase (HARS)
CCDC99	-2.2	-1.38	NM_017785.3	coiled-coil domain containing 99 (CCDC99)
PTRF	-2.45	-1.38	NM_012232.3	polymerase I and transcript release factor (PTRF)
MSN	-2.58	-1.38	NM_002444.2	moesin (MSN)
BOLA2	-2.97	-1.38	NM_001031827.1	bolA homolog 2 (E. coli) (BOLA2)
RPS3	-3.73	-1.38	NM_001005.3	ribosomal protein S3 (RPS3)
KATNB1	-1.54	-1.39	NM_005886.2	katanin p80 (WD repeat containing) subunit B 1 (KATNB1)
LOC645638	-1.96	-1.39	XR_040455.1	PREDICTED: misc_RNA (LOC645638)
RALA	-2.53	-1.39	NM_005402.2	v-ral simian leukemia viral oncogene homolog A (ras related) (RALA)
LOC100129685	-2.67	-1.39	XM_001723814.1	PREDICTED: hypothetical protein LOC100129685 (LOC100129685)
ERGIC3	-2.78	-1.39	NM_198398.1	ERGIC and golgi 3 (ERGIC3)
HMGB2	-2.79	-1.39	NM_002129.2	high-mobility group box 2 (HMGB2)
EIF4A2	-2.8	-1.39	NM_001967.3	eukaryotic translation initiation factor 4A
RPS28	-3.66	-1.39	NM_001031.4	ribosomal protein S28 (RPS28)
LOC646195	-4.07	-1.39	XM_940585.2	PREDICTED: similar to 40S ribosomal protein S28
PPAP2C	-1.77	-1.4	NM_177526.1	phosphatidic acid phosphatase type 2C (PPAP2C)
LOC100133565	-2.24	-1.4	XM_001724542.1	PREDICTED: similar to hCG23738 (LOC100133565)

SMARCD1	-2.27	-1.4	NM_003076.3	SWI/SNF related
OXSR1	-2.3	-1.4	NM_005109.2	oxidative-stress responsive 1 (OXSR1)
TFG	-2.62	-1.4	NM_006070.4	TRK-fused gene (TFG)
TM9SF1	-1.51	-1.41	NM_006405.5	transmembrane 9 superfamily member 1 (TM9SF1)
COX15	-1.66	-1.41	NM_078470.2	COX15 homolog
KLF2	-1.93	-1.41	NM_016270.2	Kruppel-like factor 2 (lung) (KLF2)
MYH9	-2.28	-1.41	NM_002473.3	myosin
LOC441246	-4.04	-1.41	XM_496890.2	PREDICTED: similar to 60S ribosomal protein L35
LGMN	-1.61	-1.42	NM_001008530.1	legumain (LGMN)
THOC3	-1.76	-1.42	NM_032361.1	THO complex 3 (THOC3)
SEC24C	-1.84	-1.42	NM_198597.1	SEC24 family
CYBA	-2.1	-1.42	NM_000101.2	cytochrome b-245
LOC645899	-4.03	-1.42	XM_941610.2	PREDICTED: similar to 40S ribosomal protein S28 (LOC645899)
RPL18	-4.17	-1.42	NM_000979.2	ribosomal protein L18 (RPL18)
TPMT	-1.71	-1.43	NM_000367.2	thiopurine S-methyltransferase (TPMT)
PRKDC	-1.78	-1.43	NM_001081640.1	protein kinase
HIST2H2AC	-1.89	-1.43	NM_003517.2	histone cluster 2
POP5	-2.37	-1.43	NM_198202.1	processing of precursor 5
CCND1	-2.59	-1.43	NM_053056.2	cyclin D1 (CCND1)
RN5S9	-3.24	-1.43	NR_023371.1	RNA
TMED7	-2.17	-1.44	NM_181836.3	transmembrane emp24 protein transport domain containing 7 (TMED7)
ENO3	-2.37	-1.44	NM_001976.3	enolase 3 (beta
RNF19A	-1.63	-1.45	NM_183419.1	ring finger protein 19A (RNF19A)
TIPRL	-1.69	-1.45	NM_152902.3	TIP41
RRAS2	-1.71	-1.45	NM_012250.3	related RAS viral (r-ras) oncogene homolog 2 (RRAS2)
C20orf108	-1.82	-1.45	NM_080821.2	chromosome 20 open reading frame 108 (C20orf108)
LOC653156	-2.68	-1.45	XM_001718864.1	PREDICTED: similar to hCG1782414 (LOC653156)
LOC730288	-2.77	-1.45	XM_001126276.1	PREDICTED: similar to 40S ribosomal protein S28 (LOC730288)
ATP5I	-3.69	-1.45	NM_007100.2	ATP synthase
LOC441775	-3.88	-1.45	XR_019588.1	PREDICTED: similar to 60S ribosomal protein L18 (LOC441775)
COL16A1	-1.57	-1.46	NM_001856.3	collagen
CLCF1	-1.78	-1.46	NM_013246.2	cardiotrophin-like cytokine factor 1 (CLCF1)
KIAA1666	-2.14	-1.46	XM_942124.2	PREDICTED: KIAA1666 protein (KIAA1666)
RNY3	-1.73	-1.47	NR_004392.1	RNA
GEMIN4	-2.25	-1.47	NM_015721.2	gem (nuclear organelle) associated protein 4 (GEMIN4)
PINK1	-2.15	-1.48	NM_032409.2	PTEN induced putative kinase 1 (PINK1)
SNX11	-2.15	-1.48	NM_152244.1	sorting nexin 11 (SNX11)
NUDT1	-2.27	-1.48	NM_198948.1	nudix (nucleoside diphosphate linked moiety X)-type motif 1 (NUDT1)
ZNHIT1	-2.91	-1.48	NM_006349.2	zinc finger
ROMO1	-3.42	-1.48	NM_080748.2	reactive oxygen species modulator 1 (ROMO1)
TRAFD1	-1.75	-1.49	NM_006700.1	TRAF-type zinc finger domain containing 1 (TRAFD1)
MGMT	-2.03	-1.49	NM_002412.2	O-6-methylguanine-DNA methyltransferase (MGMT)
LOC100131205	-2.94	-1.49	XM_001719439.1	PREDICTED: hypothetical protein LOC100131205
CITED4	-2.03	-1.5	NM_133467.2	Cbp/p300-interacting transactivator
CCDC43	-2.07	-1.5	NM_001099225.1	coiled-coil domain containing 43 (CCDC43)
LSM14A	-2.69	-1.5	NM_015578.1	LSM14A
C17orf61	-3.11	-1.5	NM_152766.2	chromosome 17 open reading frame 61 (C17orf61)
TMEM66	-3.38	-1.5	NM_016127.4	transmembrane protein 66 (TMEM66)
RRAS2	-1.96	-1.51	NM_012250.3	related RAS viral (r-ras) oncogene homolog 2 (RRAS2)

IL13RA1	-2.36	-1.51	NM_001560.2	interleukin 13 receptor
NHP2L1	-2.74	-1.51	NM_005008.2	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1)
C14orf78	-2.1	-1.52	XM_001132404.1	PREDICTED: chromosome 14 open reading frame 78 (C14orf78)
EXOSC3	-2.68	-1.52	NM_016042.2	exosome component 3 (EXOSC3)
LOC728453	-4.09	-1.54	XM_001127303.1	PREDICTED: similar to 40S ribosomal protein S28 (LOC728453)
KDELR1	-2.5	-1.55	NM_006801.2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 (KDELR1)
RCC2	-3.22	-1.55	NM_018715.1	regulator of chromosome condensation 2 (RCC2)
LOC100130919	-3.28	-1.55	XM_001722872.1	PREDICTED: hypothetical protein LOC100130919 (LOC100130919)
ADAR	-2.19	-1.56	NM_015840.2	adenosine deaminase
SNORD3D	-3.13	-1.56	NR_006882.1	small nucleolar RNA
ACTA1	-2	-1.57	NM_001100.3	actin
LOC390298	-2.49	-1.57	XR_019644.1	PREDICTED: similar to translocase of inner mitochondrial membrane 17 homolog B (LOC390298)
RNU4ATAC	-2.09	-1.58	NR_023343.1	RNA
ENO3	-2.23	-1.58	NM_001976.2	enolase 3 (beta
COIL	-2.46	-1.58	NM_004645.2	coilin (COIL)
HMG20B	-2.77	-1.58	NM_006339.1	high-mobility group 20B (HMG20B)
LOC440145	-2.16	-1.59	NM_001071775.1	similar to RIKEN cDNA 2410129H14 (LOC440145)
PFKFB4	-2.19	-1.59	NM_004567.2	6-phosphofructo-2-kinase/fructose-2
RBM14	-2.85	-1.59	NM_006328.2	RNA binding motif protein 14 (RBM14)
TWF2	-2.46	-1.6	NM_007284.3	twinfilin
PPT1	-3.34	-1.6	NM_000310.2	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis
SLN	-2.28	-1.62	NM_003063.2	sarcolipin (SLN)
C16orf52	-2.37	-1.62	NM_173501.1	chromosome 16 open reading frame 52 (C16orf52)
HLTF	-2.26	-1.63	NM_139048.2	helicase-like transcription factor (HLTF)
CREBZF	-2.55	-1.63	NM_001039618.1	CREB/ATF bZIP transcription factor (CREBZF)
NHP2L1	-3.83	-1.63	NM_001003796.1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1)
HBB	-2.35	-1.64	NM_000518.4	hemoglobin
CBX2	-2.75	-1.64	NM_005189.1	chromobox homolog 2 (Pc class homolog
SNORD3A	-3.1	-1.64	NR_006880.1	small nucleolar RNA
LOC728554	-3.67	-1.64	XR_015669.1	PREDICTED: similar to THO complex 3 (LOC728554)
MRPL36	-4.29	-1.64	NM_032479.2	mitochondrial ribosomal protein L36 (MRPL36)
MYLPF	-2.11	-1.65	NM_013292.3	myosin light chain
CD97	-2.85	-1.66	NM_078481.2	CD97 molecule (CD97)
C20orf52	-4.12	-1.67	NM_080748.1	chromosome 20 open reading frame 52 (C20orf52)
GABARAPL1	-2.75	-1.69	NM_031412.2	GABA(A) receptor-associated protein like 1 (GABARAPL1)
TNNT3	-2.47	-1.7	NM_001042780.1	troponin T type 3 (skeletal
MYH2	-2.55	-1.7	NM_017534.5	myosin
TIMM17B	-3.08	-1.7	NM_005834.1	translocase of inner mitochondrial membrane 17 homolog B (yeast) (TIMM17B)
DCUN1D3	-2.95	-1.73	NM_173475.1	DCN1
RAB7A	-3.7	-1.73	NM_004637.5	RAB7A
BRI3	-3.87	-1.74	NM_015379.3	brain protein I3 (BRI3)
MYL1	-2.99	-1.75	NM_079422.1	myosin
LOC100132299	-3.11	-1.75	XM_001717905.1	PREDICTED: similar to MSTP075 (LOC100132299)
EWSR1	-2.67	-1.76	NM_013986.2	Ewing sarcoma breakpoint region 1 (EWSR1)
SYF2	-3.56	-1.76	NM_015484.4	SYF2 homolog
SNRNP27	-3.12	-1.77	NM_006857.1	small nuclear ribonucleoprotein 27kDa (U4/U6.U5) (SNRNP27)
ZNRD1	-2.87	-1.78	NM_170783.1	zinc ribbon domain containing 1 (ZNRD1)
MAP4K2	-3.39	-1.78	NM_004579.2	mitogen-activated protein kinase kinase kinase kinase 2 (MAP4K2)
RAB31	-4.46	-1.78	NM_006868.2	RAB31

TNNI2	-2.77	-1.79	NM_003282.2	troponin I type 2 (skeletal
MYL1	-3.01	-1.79	NM_079422.2	myosin
RPA1	-3.25	-1.79	NM_002945.2	replication protein A1
TPD52L2	-3.96	-1.79	NM_003288.2	tumor protein D52-like 2 (TPD52L2)
YY1	-4.7	-1.79	NM_003403.3	YY1 transcription factor (YY1)
DNAJB5	-2.67	-1.8	NM_012266.3	PREDICTED: DnaJ (Hsp40) homolog
TTF1	-2.93	-1.8	NM_007344.2	transcription termination factor
GAK	-3.11	-1.8	NM_005255.1	cyclin G associated kinase (GAK)
PHTF1	-2.9	-1.81	NM_006608.1	putative homeodomain transcription factor 1 (PHTF1)
CKM	-2.98	-1.82	NM_001824.2	creatine kinase
PIGN	-2.78	-1.83	NM_176787.4	phosphatidylinositol glycan anchor biosynthesis
C1orf86	-3.75	-1.85	NM_182533.2	chromosome 1 open reading frame 86 (C1orf86)
RASA1	-3.5	-1.89	NM_002890.1	RAS p21 protein activator (GTPase activating protein) 1 (RASA1)
RBM18	-3.64	-1.9	NM_033117.2	RNA binding motif protein 18 (RBM18)
TNNC2	-3.3	-1.91	NM_003279.2	troponin C type 2 (fast) (TNNC2)
KIAA0406	-3.05	-1.92	NM_014657.1	KIAA0406 (KIAA0406)
C19orf42	-3.29	-1.92	NM_024104.3	chromosome 19 open reading frame 42 (C19orf42)
EXOSC3	-4.3	-1.92	NM_016042.2	exosome component 3 (EXOSC3)
PLEKHJ1	-3.1	-1.93	NM_018049.1	pleckstrin homology domain containing
PSMB2	-4.63	-1.94	NM_002794.3	proteasome (prosome
BMP2	-3.36	-1.95	NM_001200.2	bone morphogenetic protein 2 (BMP2)
SALL2	-3	-1.98	NM_005407.1	sal-like 2 (Drosophila) (SALL2)
LOC730020	-3.35	-1.99	XR_041245.1	PREDICTED: misc_RNA (LOC730020)
BRI3P1	-4.67	-2	XR_015539.2	PREDICTED: misc_RNA (BRI3P1)
RPL28	-3.7	-2.02	NM_000991.3	ribosomal protein L28 (RPL28)
SYF2	-4.27	-2.02	NM_015484.4	SYF2 homolog
ADAR	-4.36	-2.02	NM_001111.3	adenosine deaminase
SRF	-4.18	-2.03	NM_003131.2	serum response factor (c-fos serum response element-binding transcription factor) (SRF)
NDUFS7	-4.81	-2.03	NM_024407.3	NADH dehydrogenase (ubiquinone) Fe-S protein 7
SMARCE1	-3.63	-2.04	NM_003079.4	SWI/SNF related
SRRM2	-4.19	-2.04	NM_016333.2	serine/arginine repetitive matrix 2 (SRRM2)
GATAD2A	-4.36	-2.05	NM_017660.2	GATA zinc finger domain containing 2A (GATAD2A)
EWSR1	-4.06	-2.06	NM_005243.2	Ewing sarcoma breakpoint region 1 (EWSR1)
RPA1	-4.77	-2.06	NM_002945.2	replication protein A1
ZNRD1	-3.99	-2.07	NM_170783.1	zinc ribbon domain containing 1 (ZNRD1)
C14orf106	-4.08	-2.08	NM_018353.3	chromosome 14 open reading frame 106 (C14orf106)
YTHDF2	-4.6	-2.1	NM_016258.2	YTH domain family
B2M	-5.81	-2.1	NM_004048.2	beta-2-microglobulin (B2M)
DNAJB5	-3.55	-2.11	NM_012266.3	PREDICTED: DnaJ (Hsp40) homolog
TCF12	-4.26	-2.14	NM_207038.1	transcription factor 12 (TCF12)
B2M	-5.73	-2.15	NM_004048.2	beta-2-microglobulin (B2M)
ZNRD1	-3.96	-2.16	NM_014596.4	zinc ribbon domain containing 1 (ZNRD1)
YY1	-4.84	-2.21	NM_003403.3	YY1 transcription factor (YY1)
MRPL33	-5.9	-2.23	NM_145330.2	mitochondrial ribosomal protein L33 (MRPL33)
C19orf12	-4.51	-2.24	NM_001031726.2	chromosome 19 open reading frame 12 (C19orf12)
ISCU	-4.32	-2.25	NM_014301.2	iron-sulfur cluster scaffold homolog (E. coli) (ISCU)
SF3B4	-4.69	-2.25	NM_005850.3	splicing factor 3b
TMEM167A	-5.37	-2.25	NM_174909.3	transmembrane protein 167A (TMEM167A)
TCF12	-4.56	-2.26	NM_207037.1	transcription factor 12 (TCF12)

PIAS3	-4.15	-2.27	NM_006099.2	protein inhibitor of activated STAT
ISCU	-5.19	-2.27	NM_213595.1	iron-sulfur cluster scaffold homolog (E. coli) (ISCU)
C13orf37	-4.46	-2.28	NM_001071775.2	chromosome 13 open reading frame 37 (C13orf37)
FBXO34	-4.49	-2.33	NM_017943.2	F-box protein 34 (FBXO34)
UGCG	-4.52	-2.34	NM_003358.1	UDP-glucose ceramide glucosyltransferase (UGCG)
RPL22	-5.9	-2.34	NM_000983.3	ribosomal protein L22 (RPL22)
STK36	-4.62	-2.36	NM_015690.2	serine/threonine kinase 36
C16orf75	-5.09	-2.47	NM_152308.1	chromosome 16 open reading frame 75 (C16orf75)
LOC644799	-5.77	-2.5	XM_934554.1	PREDICTED: hypothetical protein LOC644799
HIST1H2AH	-4.32	-2.54	NM_080596.1	histone cluster 1
FAM107B	-7.15	-2.57	NM_031453.2	family with sequence similarity 107
CHPT1	-5.74	-2.64	NM_020244.2	choline phosphotransferase 1 (CHPT1)
CHPT1	-5.85	-2.69	NM_020244.2	choline phosphotransferase 1 (CHPT1)
LOC730098	-5.59	-2.72	XR_041280.1	PREDICTED: misc_RNA (LOC730098)
SOCS6	-4.92	-2.73	NM_004232.3	suppressor of cytokine signaling 6 (SOCS6)
NAB1	-6.37	-2.75	NM_005966.3	NGFI-A binding protein 1 (EGR1 binding protein 1) (NAB1)
MRPL33	-6.58	-2.76	NM_004891.2	mitochondrial ribosomal protein L33 (MRPL33)
VEZF1	-6.58	-2.86	NM_007146.2	vascular endothelial zinc finger 1 (VEZF1)
ISL1	-6	-2.9	NM_002202.1	ISL1 transcription factor
SUPT4H1	-6.03	-2.91	NM_003168.1	suppressor of Ty 4 homolog 1 (S. cerevisiae) (SUPT4H1)
LOC730432	-6.57	-3.02	XM_001125680.1	PREDICTED: similar to serine/threonine/tyrosine interacting protein
ARID1A	-6.02	-3.16	NM_139135.2	AT rich interactive domain 1A (SWI-like) (ARID1A)
GOT1	-6.93	-3.41	NM_002079.1	glutamic-oxaloacetic transaminase 1
UBE2T	-7.36	-3.53	NM_014176.2	ubiquitin-conjugating enzyme E2T (putative) (UBE2T)
BTBD2	-7.87	-3.78	NM_017797.3	BTB (POZ) domain containing 2 (BTBD2)
ELF4	-7.42	-3.81	NM_001421.2	E74-like factor 4 (ets domain transcription factor) (ELF4)
N-PAC	-7.14	-3.88	NM_032569.2	cytokine-like nuclear factor n-pac (N-PAC)
LYSMD4	-7.35	-3.93	NM_152449.2	LysM
EWSR1	-8.17	-3.98	NM_005243.2	Ewing sarcoma breakpoint region 1 (EWSR1)
SNHG6	-9.01	-4.22	NR_002599.1	small nucleolar RNA host gene 6 (non-protein coding) (SNHG6)
JUND	-11.71	-6.53	NM_005354.3	jun D proto-oncogene (JUND)
RNY1	-14.92	-13.93	NR_004391.1	RNA