Since this is a very extensive table, the format and content has not been edited by ActaDV.

Supplementary Table S1a - Differentially expressed genes (DEGs) between keratinocytes from psoriasis lesional skin (PP) and keratinocytes from healthy skin (H)

GeneName	lin FCH	P-value	FDR	Molecular location	Cytogenic location	Official Full Name
PI3	60.88	8.40E-12	2.18E-09	chr20:43803517-43805185 (+)	20q13.12	peptidase inhibitor 3, skin-derived
DEFB4A	51.45	4.33E-11	7.42E-09	chr8:7752151-7754237 (+)	8p23.1	defensin, beta 4A
SERPINB4	46.33	2.14E-13	1.66E-10	chr18:61304493-61311532 (-)	18q21.3	serpin peptidase inhibitor, clade B (ovalbumin), member 4
TCN1	45.10	2.98E-20	2.10E-15	chr11:59620273-59634048 (-)	11q11-q12	transcobalamin I (vitamin B12 binding protein, R binder family)
DEFB4B	34.09	1.45E-10	1.71E-08	chr8:7272382-7274385 (-)	8p23.1	defensin, beta 4B
S100A9	25.56	2.77E-13	2.03E-10	chr1:153330330-153333503 (+)	1q21	S100 calcium binding protein A9
AKR1B10	22.94	1.84E-16	1.23E-12	chr7:134212344-134226166 (+)	7q33	aldo-keto reductase family 1, member B10 (aldose reductase)
S100A7A	22.07	2.47E-13	1.85E-10	chr1:153388945-153395701 (+)	1q21.3	S100 calcium binding protein A7A
KYNU	21.42	9.86E-20	3.48E-15	chr2:143633067-143799890 (+)	2q22.2	kynureninase
SERPINB3	20.81	3.24E-13	2.36E-10	chr18:61322431-61329197 (-)	18q21.3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
IFI6	20.07	5.88E-09	2.73E-07	chr1:27992572-27998729 (-)	1p35	interferon, alpha-inducible protein 6
SPRR2A	19.12	1.22E-09	8.49E-08	chr1:153028589-153030013 (-)	1q21-q22	small proline-rich protein 2A
IFI27	16.44	2.29E-08	7.84E-07	chr14:94577079-94583033 (+)	14q32	interferon, alpha-inducible protein 27
OAS2	14.49	1.03E-11	2.51E-09	chr12:113416200-113449528 (+)	12q24.2	2-5-oligoadenylate synthetase 2, 69 71kDa
IFI44L	14.17	5.54E-07	8.26E-06	chr1:79085607-79111830 (+)	1p31.1	interferon-induced protein 44-like
C10orf99	13.86	7.16E-13	4.07E-10	chr10:85933494-85945050 (+)	10q23.1	chromosome 10 open reading frame 99
TMPRSS11D	13.74	2.40E-13	1.84E-10	chr4:68686594-68749750 (-)	4q13.2	transmembrane protease, serine 11D
IFI44	13.02	6.17E-10	5.00E-08	chr1:79115477-79129763 (+)	1p31.1	interferon-induced protein 44
HEPHL1	12.59	1.48E-11	3.31E-09	chr11:93754378-93847374 (+)	11q21	hephaestin-like 1
EPGN	12.05	5.95E-11	9.35E-09	chr4:75174190-75181024 (+)	4q13.3	epithelial mitogen homolog (mouse)
S100A7	10.52	2.33E-10	2.39E-08	chr1:153430220-153433177 (-)	1q21	S100 calcium binding protein A7
CENPE	9.56	5.95E-13	3.65E-10	chr4:104026963-104119566 (-)	4q24-q25	centromere protein E, 312kDa
GJB2	9.32	2.82E-14	4.33E-11	chr13:20761604-20767114 (-)	13q11-q12	gap junction protein, beta 2, 26kDa
S100A8	9.05	1.19E-13	1.14E-10	chr1:153362508-153363664 (-)	1q21	S100 calcium binding protein A8
RAB31	8.67	1.18E-12	5.57E-10	chr18:9708228-9862553 (+)	18p11.3	RAB31, member RAS oncogene family
KIF20B	8.56	3.47E-11	6.28E-09	chr10:91461367-91534700 (+)	10q23.31	kinesin family member 20B
SAMD9	8.39	7.95E-12	2.12E-09	chr7:92728826-92747336 (-)	7q21.2	sterile alpha motif domain containing 9
MKI67	8.27	1.08E-14	2.31E-11	chr10:129894923-129924649 (-)	10q26.2	marker of proliferation Ki-67
EIF5B	8.21	1.32E-09	8.98E-08	chr2:99953816-100016728 (+)	2q11.2	eukaryotic translation initiation factor 5B
CENPF	7.71	2.20E-14	3.74E-11	chr1:214776532-214837931 (+)	1q41	centromere protein F, 350 400kDa
ASPM	7.63	4.94E-12	1.52E-09	chr1:197053257-197115824 (-)	1q31	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
SPRR2F	7.56	1.19E-06	1.45E-05	chr1:153084590-153085991 (-)	1q21-q22	small proline-rich protein 2F
FABP5	7.52	1.28E-15	5.91E-12	chr8:82192598-82197012 (+)	8q21.13	fatty acid binding protein 5 (psoriasis-associated)
HERC6	7.49	3.02E-09	1.65E-07	chr4:89299891-89364263 (+)	4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
KRT16	7.36	3.55E-15	1.19E-11	chr17:39766030-39769079 (-)	17q21.2	keratin 16
AASS	7.34	1.06E-16	9.36E-13	chr7:121713598-121784344 (-)	7q31.3	aminoadipate-semialdehyde synthase
AKR1B15	7.05	9.03E-14	1.01E-10	chr7:134233849-134264592 (+)	7q33	aldo-keto reductase family 1, member B15
CLEC7A	6.93	5.25E-16	2.85E-12	chr12:10269376-10282868 (-)	12p13.2	C-type lectin domain family 7, member A
CYP4Z2P	6.90	1.98E-08	7.01E-07	chr1:47308767-47366147 (-)	1p33	cytochrome P450, family 4, subfamily Z, polypeptide 2, pseudogene
CD36	6.86	3.90E-12	1.28E-09	chr7:79998891-80308593 (+)	7q11.2	CD36 molecule (thrombospondin receptor)
FAM111B	6.74	6.37E-13	3.79E-10	chr11:58874658-58894888 (+)	11q12.1	family with sequence similarity 111, member B
IRAK3	6.70	7.72E-13	4.16E-10	chr12:66582659-66648402 (+)	12q14.3	interleukin-1 receptor-associated kinase 3
CTSC	6.62	5.55E-17	5.59E-13	chr11:88026760-88070955 (-)	11q14.2	cathepsin C
IL36G	6.62	6.54E-10	5.23E-08	chr2:113730780-113743227 (+)	2q12-q21	interleukin 36, gamma
DSC2	6.49	2.39E-14	3.92E-11	chr18:28645940-28682388 (-)	18q12.1	desmocollin 2
RHCG	6.35	1.16E-11	2.72E-09	chr15:89998680-90039844 (-)	15q25	Rh family, C glycoprotein
SLC7A11	6.35	7.78E-13	4.16E-10	chr4:139085248-139163503 (-)	4q28-q32	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
STEAP4	6.19	7.69E-11	1.11E-08	chr7:87900207-87936228 (-)	7q21.12	STEAP family member 4
EEA1	5.95	8.65E-08	2.12E-06	chr12:93164413-93323107 (-)	12q22	early endosome antigen 1
PARP14	5.91	7.50E-13	4.16E-10	chr3:122399465-122449687 (+)	3q21.1	poly (ADP-ribose) polymerase family, member 14
DLGAP5	5.87	1.73E-13	1.49E-10	chr14:55614830-55658396 (-)	14q22.3	discs, large (Drosophila) homolog-associated protein 5
XAF1	5.85	8.76E-10	6.54E-08	chr17:6658794-6678964 (+)	17p13.1	XIAP associated factor 1
RAD50	5.48	5.23E-07	7.91E-06	chr5:131891711-131980313 (+)	5q31	RAD50 homolog (S. cerevisiae)
TOP2A	5.47	3.20E-10	3.07E-08	chr17:38544768-38574408 (-)	17q21-q22	topoisomerase (DNA) II alpha 170kDa
PPIG	5.43	1.94E-09	1.20E-07	chr2:170440850-170504696 (+)	2q31.1	peptidylprolyl isomerase G (cyclophilin G)
SMC4	5.27	2.71E-10	2.71E-08	chr3:160117062-160152750 (+)	3q26.1	structural maintenance of chromosomes 4
TPR	5.24	5.93E-08	1.59E-06	chr1:186280786-186344864 (-)	1q25	translocated promoter region, nuclear basket protein
GBP6	5.21	1.14E-09	8.04E-08	chr1:89829436-89853719 (+)	1p22.2	guanylate binding protein family, member 6
NETO2	5.20	6.14E-14	7.73E-11	chr16:47115431-47177936 (-)	16q11	neuropilin (NRP) and tolloid (TLL)-like 2
SERPINB13	5.04	7.45E-12	2.06E-09	chr18:61254223-61271873 (+)	18q21.33	serpin peptidase inhibitor, clade B (ovalbumin), member 13
S100A12	5.00	7.39E-12	2.05E-09	chr1:153346181-153348125 (-)	1q21	S100 calcium binding protein A12
TNIP3	4.99	2.30E-08	7.86E-07	chr4:122052563-122148621 (-)	4q27	TNFAIP3 interacting protein 3
AKAP9	4.92	7.86E-07	1.07E-05	chr7:91570181-91739987 (+)	7q21-q22	A kinase (PRKA) anchor protein 9
DOCK11	4.84	3.16E-11	5.87E-09	chrX:117629861-117820126 (+)	Xq24	dedicator of cytokinesis 11
KTN1	4.71	6.51E-06	5.24E-05	chr14:56046925-56151302 (+)	14q22.1	kinectin 1 (kinesin receptor)
OR56B1	4.70	4.60E-10	4.00E-08	chr11:5710817-5821759 (+)	11p15.4	olfactory receptor, family 56, subfamily B, member 1
SMC2	4.70	2.09E-10	2.22E-08	chr9:106856541-106903700 (+)	9q31.1	structural maintenance of chromosomes 2
SLC23A2	4.63	1.78E-10	2.00E-08	chr20:4833002-4990939 (-)	20p13	solute carrier family 23 (ascorbic acid transporter), member 2
BRCA2	4.61	2.45E-14	3.93E-11	chr13:32889611-32973809 (+)	13q12.3	breast cancer 2, early onset
KRT6C	4.57	5.81E-08	1.57E-06	chr12:52862300-52867569 (-)	12q13.13	keratin 6C
PLSCR1	4.55	1.06E-12	5.22E-10	chr3:146232967-146262651 (-)	3q23	phospholipid scramblase 1
KIF14	4.45	6.81E-12	1.93E-09	chr1:200520625-200589862 (-)	1q32.1	kinesin family member 14
ESF1	4.41	3.32E-06	3.15E-05	chr20:13694969-13765565 (-)	20p12.1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
NDC80	4.38	1.80E-12	7.47E-10	chr18:2571510-2616634 (+)	18p11.32	NDC80 kinetochore complex component
KRT6A	4.36	3.19E-07	5.52E-06	chr12:52880958-52887181 (-)	12q13.13	keratin 6A
GOLGA4	4.35	4.29E-07	6.82E-06	chr3:37284668-37408370 (+)	3p22-p21.3	golgin A4
GDA	4.33	1.36E-09	9.17E-08	chr9:74729511-74872109 (+)	9q21.13	guanine deaminase
TRIP11	4.30	9.52E-08	2.27E-06	chr14:92432335-92506403 (-)	14q31-q32	thyroid hormone receptor interactor 11
ROCK1	4.28	1.06E-06	1.34E-05	chr18:18529701-18691812 (-)	18p11.1	Rho-associated, coiled-coil containing protein kinase 1
NCAPG	4.25	1.89E-13	1.55E-10	chr4:17812525-17846487 (+)	4p15.33	non-SMC condensin I complex, subunit G
IFI16	4.25	4.32E-12	1.38E-09	chr1:158969758-159024945 (+)	1q22	interferon, gamma-inducible protein 16
DDX60	4.22	9.21E-07	1.21E-05	chr4:169137442-169239958 (-)	4q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
DDX60L	4.20	4.28E-09	2.15E-07	chr4:169277886-169458937 (-)	4q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like
PARP9	4.19	4.38E-11	7.47E-09	chr3:122246760-122283523 (-)	3q21	poly (ADP-ribose) polymerase family, member 9
EPSTI1	4.09	1.75E-09	1.12E-07	chr13:43460524-43566385 (-)	13q13.3	epithelial stromal interaction 1 (breast)
CD274	4.07	3.23E-09	1.73E-07	chr9:5450503-5470567 (+)	9p24	CD274 molecule
TICRR	4.00	9.59E-12	2.41E-09	chr15:90118713-90171253 (+)	15q26.1	TOPBP1-interacting checkpoint and replication regulator
SPRR2B	4.00	1.88E-04	7.43E-04	chr1:153042704-153044111 (-)	1q21-q22	small proline-rich protein 2B
KIF11	3.99	2.27E-10	2.35E-08	chr10:94352825-94415152 (+)	10q24.1	kinesin family member 11
A2ML1	3.99	1.11E-08	4.49E-07	chr12:8975068-9039597 (+)	12p13.31	alpha-2-macroglobulin-like 1
HORMAD1	3.98	3.50E-03	8.52E-03	chr1:150670535-150693364 (-)	1q21.3	HORMA domain containing 1
SLC6A14	3.97	2.17E-05	1.32E-04	chrX:115567747-115592625 (+)	Xq23	solute carrier family 6 (amino acid transporter), member 14
CCNA2	3.94	1.75E-12	7.29E-10	chr4:122737599-122745088 (-)	4q27	cyclin A2
CASC5	3.92	4.32E-13	2.87E-10	chr15:40886218-40956540 (+)	15q14	cancer susceptibility candidate 5
OAS3	3.88	3.36E-10	3.19E-08	chr12:113376157-113411054 (+)	12q24.2	2-5-oligoadenylate synthetase 3, 100kDa
LYN	3.88	1.56E-09	1.02E-07	chr8:56792372-56925006 (+)	8q13	LYN proto-oncogene, Src family tyrosine kinase
KIF18A	3.84	1.25E-12	5.73E-10	chr11:28042163-28129746 (-)	11p14.1	kinesin family member 18A
FMNL2	3.84	1.84E-13	1.54E-10	chr2:153191751-153506348 (+)	2q23.3	formin-like 2
ANKRD12	3.82	5.57E-06	4.66E-05	chr18:9136751-9285983 (+)	18p11.22	ankyrin repeat domain 12
MX1	3.82	2.03E-08	7.14E-07	chr21:42792231-42831141 (+)	21q22.3	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
IFIH1	3.80	2.09E-09	1.27E-07	chr2:163123589-163175213 (-)	2q24	interferon induced with helicase C domain 1
MPHOSPH6	3.79	6.82E-14	8.15E-11	chr16:82181767-82203831 (-)	16q23.3	M-phase phosphoprotein 6
ROCK2	3.76	3.47E-07	5.84E-06	chr2:11319887-11488456 (-)	2p24	Rho-associated, coiled-coil containing protein kinase 2
BOD1L1	3.73	6.38E-08	1.69E-06	chr4:13570362-13629347 (-)	4p16.1	biorientation of chromosomes in cell division 1-like 1
SULT1E1	3.72	3.69E-08	1.13E-06	chr4:70676498-70725870 (-)	4q13.1	sulfotransferase family 1E, estrogen-preferring, member 1
CCNB1	3.71	1.05E-11	2.54E-09	chr5:68462837-68474072 (+)	5q12	cyclin B1
GK	3.70	2.73E-14	4.28E-11	chrX:30671476-30749577 (+)	Xp21.3	glycerol kinase
STAT1	3.69	1.99E-10	2.15E-08	chr2:191829084-191885686 (-)	2q32.2	signal transducer and activator of transcription 1, 91kDa
SPRR2D	3.66	5.64E-05	2.82E-04	chr1:153012201-153014407 (-)	1q21-q22	small proline-rich protein 2D
KIF23	3.66	3.94E-11	6.90E-09	chr15:59706585-59740764 (+)	15q23	kinesin family member 23
INA	3.65	2.85E-08	9.25E-07	chr10:105036920-105050108 (+)	10q24.33	internexin neuronal intermediate filament protein, alpha
CEP55	3.64	2.59E-12	9.61E-10	chr10:95256369-95288849 (+)	10q23.33	centrosomal protein 55kDa
LTF	3.63	4.54E-07	7.11E-06	chr3:46477136-46526724 (-)	3p21.31	lactotransferrin
ATAD5	3.62	5.18E-09	2.49E-07	chr17:29158988-29222295 (+)	17q11.2	ATPase family, AAA domain containing 5
MPZL2	3.61	1.81E-16	1.23E-12	chr11:118124118-118135251 (-)	11q24	myelin protein zero-like 2
SERPINB1	3.61	4.02E-10	3.61E-08	chr6:2832566-2842240 (-)	6p25	serpin peptidase inhibitor, clade B (ovalbumin), member 1
UPF3B	3.58	1.93E-09	1.20E-07	chrX:118987985-118986991 (-)	Xq25-q26	UPF3 regulator of nonsense transcripts homolog B (yeast)
GJB6	3.55	1.21E-10	1.52E-08	chr13:20796101-20806534 (+)	13q12	gap junction protein, beta 6, 30kDa
DSG3	3.53	2.02E-12	8.20E-10	chr18:29027732-29058665 (+)	18q12.1	desmoglein 3
OAS1	3.50	2.92E-10	2.87E-08	chr12:113344582-113369991 (+)	12q24.2	2-5-oligoadenylate synthetase 1, 40 46kDa
KPNA2	3.49	4.11E-11	7.13E-09	chr17:66031848-66042970 (+)	17q24.2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
HMGN5	3.48	7.31E-11	1.07E-08	chrX:80369200-80457441 (-)	Xq13.3	high mobility group nucleosome binding domain 5
SLC7A5	3.45	2.59E-07	4.77E-06	chr16:87863622-87903125 (-)	16q24.3	solute carrier family 7 (amino acid transporter light chain, L system), member 5
PRR11	3.44	8.93E-09	3.79E-07	chr17:57232860-57284070 (+)	17q22	proline rich 11
SLC4A7	3.42	7.98E-11	1.14E-08	chr3:27414214-27525911 (-)	3p22	solute carrier family 4, sodium bicarbonate cotransporter, member 7
PYGL	3.41	1.17E-10	1.48E-08	chr14:51324609-51411454 (-)	14q21-q22	phosphorylase, glycogen, liver
EHF	3.41	1.27E-13	1.18E-10	chr11:34642588-34684834 (+)	11p12	ets homologous factor
SPRR2C	3.39	5.98E-08	1.60E-06	chr1:153112594-153113969 (-)	1q21-q22	small proline-rich protein 2C (pseudogene)
MLKL	3.39	6.57E-18	9.27E-14	chr16:74705753-74734789 (-)	16q23.1	mixed lineage kinase domain-like
CDK1	3.39	1.33E-11	3.06E-09	chr10:62538089-62554610 (+)	10q21.1	cyclin-dependent kinase 1
CEP152	3.39	9.65E-12	2.41E-09	chr15:49030132-49103343 (-)	15q21.1	centrosomal protein 152kDa
SAMD9L	3.38	2.22E-05	1.34E-04	chr7:92759368-92777682 (-)	7q21.2	sterile alpha motif domain containing 9-like
ATRX	3.36	2.17E-06	2.27E-05	chrX:76760356-77041719 (-)	Xq21.1	alpha thalassemia mental retardation syndrome X-linked
SMC6	3.36	4.22E-07	6.75E-06	chr2:17845079-17981509 (-)	2p24.2	structural maintenance of chromosomes 6
GEN1	3.35	4.25E-10	3.76E-08	chr2:17935125-17966632 (+)	2p24.2	GEN1 Holliday junction 5 flap endonuclease
MIS18BP1	3.35	2.67E-07	4.87E-06	chr14:45672393-45722743 (-)	14q21.2	MIS18 binding protein 1
RSAD2	3.30	5.53E-05	2.78E-04	chr2:7005937-7038370 (+)	2p25.2	radical S-adenosyl methionine domain containing 2
SASS6	3.29	6.46E-10	5.19E-08	chr1:100549102-100598511 (-)	1p21.2	spindle assembly 6 homolog (C. elegans)
CCDC186	3.28	8.07E-05	3.75E-04	chr10:115880621-115934364 (-)	10q25.3	coiled-coil domain containing 186
GBP1	3.27	6.98E-10	5.51E-08	chr1:89517987-89531043 (-)	1p22.2	guanylate binding protein 1, interferon-inducible
TNFSF10	3.26	1.44E-12	6.32E-10	chr3:172223298-172241297 (-)	3q26	tumor necrosis factor (ligand) superfamily, member 10
IFIT1	3.26	2.67E-06	2.67E-05	chr10:91152303-91163745 (+)	10q23.31	interferon-induced protein with tetratricopeptide repeats 1
DDX58	3.25	7.90E-09	3.44E-07	chr9:32455300-32526322 (-)	9p12	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
IFIT3	3.24	2.43E-08	8.21E-07	chr10:91087602-91100728 (+)	10q24	interferon-induced protein with tetratricopeptide repeats 3
MELK	3.22	9.47E-13	4.83E-10	chr9:36572859-36677679 (+)	9p13.2	maternal embryonic leucine zipper kinase
PLAT	3.22	1.51E-08	5.67E-07	chr8:42032236-42065242 (-)	8p12	plasminogen activator, tissue
SMC3	3.21	3.02E-05	1.72E-04	chr10:112327449-112364394 (+)	10q25	structural maintenance of chromosomes 3
ARNTL2	3.20	4.87E-13	3.09E-10	chr12:27485787-27578746 (+)	12p12.2-p11.2	aryl hydrocarbon receptor nuclear translocator-like 2
KIAA1524	3.20	3.58E-12	1.19E-09	chr3:108268718-108308491 (-)	3q13.13	KIAA1524
CKAP2L	3.18	7.62E-11	1.10E-08	chr2:113493930-113522254 (-)	2q13	cytoskeleton associated protein 2-like
LOX	3.17	3.18E-10	3.07E-08	chr5:121398890-121414206 (-)	5q23.2	lysyl oxidase
CCNB2	3.16	4.48E-10	3.93E-08	chr15:59397277-59417244 (+)	15q22.2	cyclin B2
CATSPERB	3.16	4.31E-11	7.40E-09	chr14:92047118-92198430 (-)	14q32.12	catsper channel auxiliary subunit beta
KIF20A	3.15	4.90E-10	4.19E-08	chr5:137514408-137523404 (+)	5q31	kinesin family member 20A
ANLN	3.15	1.14E-08	4.58E-07	chr7:36429415-36493400 (+)	7p15-p14	anillin, actin binding protein
KRT6B	3.14	9.97E-06	7.24E-05	chr12:52840435-52845971 (-)	12q13.13	keratin 6B
CARD6	3.13	6.40E-13	3.79E-10	chr5:40841286-40860275 (+)	5p13.1	caspase recruitment domain family, member 6

DTX3L	3.13	6.06E-10	4.95E-08	chr3:122283085-122294050 (+)	3q21.1	deltex 3 like, E3 ubiquitin ligase
ATP10B	3.13	2.14E-10	2.26E-08	chr5:159990127-160279221 (-)	5q34	ATPase, class V, type 10B
RRM2	3.13	7.00E-15	1.90E-11	chr2:10262455-10271546 (+)	2p25-p24	ribonucleotide reductase M2
BUB1	3.13	8.32E-12	2.18E-09	chr2:111395275-111435691 (-)	2q14	BUB1 mitotic checkpoint serine threonine kinase
GBP3	3.13	7.22E-09	3.20E-07	chr1:89472360-89488549 (-)	1p22.2	guanylate binding protein 3
PRKCQ	3.12	5.84E-09	2.73E-07	chr10:6469105-6622263 (-)	10p15	protein kinase C, theta
IFITM1	3.12	5.02E-10	4.27E-08	chr11:313506-315272 (+)	11p15.5	interferon induced transmembrane protein 1
MAN1A1	3.11	5.55E-10	4.62E-08	chr6:119498374-119670926 (-)	6q22	mannosidase, alpha, class 1A, member 1
STIL	3.09	1.95E-12	7.96E-10	chr1:47715811-47779819 (-)	1p32	SCL TAL1 interrupting locus
TPX2	3.09	6.21E-10	5.02E-08	chr20:30326904-30389608 (+)	20q11.2	TPX2, microtubule-associated
HMMR	3.09	4.08E-11	7.11E-09	chr5:162887175-162918953 (+)	5q34	hyaluronan-mediated motility receptor (RHAMM)
ESCO2	3.08	2.65E-12	9.79E-10	chr8:27629466-27670157 (+)	8p21.1	establishment of sister chromatid cohesion N-acetyltransferase 2
TTK	3.08	3.81E-11	6.74E-09	chr6:80713604-80752244 (+)	6q14.1	TTK protein kinase
IL13RA1	3.05	1.75E-11	3.73E-09	chrX:117861535-117928502 (+)	Xq24	interleukin 13 receptor, alpha 1
NUF2	3.03	4.90E-12	1.52E-09	chr1:163291690-163325554 (+)	1q23.3	NUF2, NDC80 kinetochore complex component
IL20	3.02	7.67E-07	1.05E-05	chr1:207038699-207042568 (+)	1q32	interleukin 20
CA5BP1	3.01	4.42E-11	7.51E-09	chrX:15719057-15721483 (+)	Xp22.2	carbonic anhydrase VB pseudogene 1
ANKRD26	3.00	6.02E-08	1.61E-06	chr10:27280843-27389427 (-)	10p12.1	ankyrin repeat domain 26
CCDC18	2.99	7.03E-11	1.04E-08	chr1:93645476-93744287 (+)	1p22.1	coiled-coil domain containing 18
ECT2	2.99	4.52E-12	1.43E-09	chr3:172468472-172539264 (+)	3q26.1-q26.2	epithelial cell transforming 2
DPP4	2.99	7.07E-06	5.58E-05	chr2:162848751-162931052 (-)	2q24.3	dipeptidyl-peptidase 4
ALOX15B	2.99	8.61E-07	1.15E-05	chr17:7942358-7952452 (+)	17p13.1	arachidonate 15-lipoxygenase, type B
PRPF38B	2.97	3.89E-08	1.17E-06	chr1:109234932-109244425 (+)	1p13.3	pre-mRNA processing factor 38B
ZWILCH	2.97	2.19E-12	8.80E-10	chr15:66797431-66841823 (+)	15q22.31	zwilch kinetochore protein
MYO1B	2.97	5.26E-11	8.56E-09	chr2:192109911-192290115 (+)	2q12-q34	myosin IB
IL33	2.97	4.20E-05	2.23E-04	chr9:6215786-6257983 (+)	9p24.1	interleukin 33
BAZ1A	2.95	1.11E-06	1.38E-05	chr14:35221937-35344853 (-)	14q13.2	bromodomain adjacent to zinc finger domain, 1A
HSPH1	2.95	1.37E-10	1.65E-08	chr13:31710762-31736525 (-)	13q12.3	heat shock 105kDa 110kDa protein 1
NAMPT	2.95	1.78E-08	6.46E-07	chr7:105888731-105926772 (-)	7q22.3	nicotinamide phosphoribosyltransferase
LUZP2	2.94	3.66E-09	1.89E-07	chr11:24518516-25104186 (+)	11p14.3	leucine zipper protein 2
ARHGAP11B	2.94	2.63E-10	2.65E-08	chr15:30916697-30931023 (+)	15q13.2	Rho GTPase activating protein 11B
SP100	2.93	7.65E-09	3.36E-07	chr2:231280657-231410317 (+)	2q37.1	SP100 nuclear antigen
PLBD1	2.93	1.00E-14	2.20E-11	chr12:14656595-14721283 (-)	12p13.1	phospholipase B domain containing 1
ZFC3H1	2.92	2.95E-06	2.87E-05	chr12:72003252-72057749 (-)	12q21.1	zinc finger, C3H1-type containing
GOLGB1	2.92	1.66E-08	6.14E-07	chr3:121382046-121468602 (-)	3q13	golgin B1
SGOL1	2.92	1.13E-11	2.68E-09	chr3:20202085-20227784 (-)	3p24.3	shugoshin-like 1 (S. pombe)
CEP290	2.92	2.71E-08	8.91E-07	chr12:88442790-88535993 (-)	12q21.32	centrosomal protein 290kDa
TOP1	2.91	2.95E-09	1.62E-07	chr20:39657458-39753127 (+)	20q12-q13.1	topoisomerase (DNA) I
GSDMC	2.91	2.73E-12	9.93E-10	chr8:130760442-130799134 (-)	8q24.21	gasdermin C
LARP7	2.90	5.02E-08	1.42E-06	chr4:113558120-113578748 (+)	4q25	La ribonucleoprotein domain family, member 7
NAMPTL	2.90	1.80E-10	2.00E-08	chr10:36810649-36813162 (-)	10p11.21	nicotinamide phosphoribosyltransferase-like
PLA2G4E	2.90	5.75E-11	9.17E-09	chr15:42273780-42343388 (-)	15q15.1	phospholipase A2, group IVE
DDX21	2.89	9.92E-08	2.35E-06	chr10:70715884-70744829 (+)	10q21	DEAD (Asp-Glu-Ala-Asp) box helicase 21
MNS1	2.89	4.29E-12	1.38E-09	chr15:56720929-56757335 (-)	15q21.3	meiosis-specific nuclear structural 1
S100A2	2.88	3.58E-11	6.41E-09	chr1:153533584-153540366 (-)	1q21	S100 calcium binding protein A2
BDP1	2.87	3.84E-06	3.51E-05	chr5:70751442-70863649 (+)	5q13	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB
POLQ	2.85	8.40E-12	2.18E-09	chr3:121150273-121265488 (-)	3q13.33	polymerase (DNA directed), theta
NEMF	2.85	1.53E-05	1.00E-04	chr14:50033027-50319921 (-)	14q22	nuclear export mediator factor
KIF15	2.84	2.58E-12	9.61E-10	chr3:44803209-44914868 (+)	3p21.31	kinesin family member 15
LTB4R	2.83	5.64E-15	1.66E-11	chr14:24780705-24787242 (+)	14q11.2-q12	leukotriene B4 receptor
ARHGAP11A	2.83	5.77E-10	4.77E-08	chr15:32907345-32932150 (+)	15q13.2	Rho GTPase activating protein 11A
C12orf5	2.83	1.57E-10	1.82E-08	chr12:4430359-4469190 (+)	12p13.3	chromosome 12 open reading frame 5
CYP4Z1	2.83	1.70E-07	3.51E-06	chr1:47533160-47583992 (+)	1p33	cytochrome P450, family 4, subfamily Z, polypeptide 1
FANCI	2.81	2.83E-12	1.01E-09	chr15:89787180-89860492 (+)	15q26.1	Fanconi anemia, complementation group I
ADAM23	2.80	1.10E-09	7.81E-08	chr2:207308263-207485851 (+)	2q33	ADAM metallopeptidase domain 23
CCDC144B	2.80	7.62E-06	5.91E-05	chr17:18441115-18528930 (-)	17p11.2	coiled-coil domain containing 144B (pseudogene)
RBM41	2.79	6.91E-09	3.10E-07	chrX:106305118-106362057 (-)	Xq22.3	RNA binding motif protein 41
CCL20	2.78	7.03E-06	5.56E-05	chr2:228678558-228682280 (+)	2q36.3	chemokine (C-C motif) ligand 20
SLTM	2.77	1.48E-06	1.71E-05	chr15:59171244-59225886 (-)	15q22.1	SAFB-like, transcription modulator
ESCO1	2.77	9.20E-06	6.83E-05	chr18:19109242-19180845 (-)	18q11.2	establishment of sister chromatid cohesion N-acetyltransferase 1
KIAA1731	2.77	4.31E-08	1.27E-06	chr11:93394805-93463522 (+)	11q21	KIAA1731
C9orf84	2.77	3.04E-12	1.08E-09	chr9:114449453-114557288 (-)	9q31.3	chromosome 9 open reading frame 84
SOD2	2.77	1.35E-09	9.15E-08	chr6:160100099-160114360 (-)	6q25.3	superoxide dismutase 2, mitochondrial
CARD17	2.76	1.53E-06	1.76E-05	chr11:104963196-104972158 (-)	11q22.3	caspase recruitment domain family, member 17
MPHOSPH10	2.75	3.35E-07	5.70E-06	chr2:71357444-71377232 (+)	2p13.3	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
LRRCC1	2.75	7.33E-07	1.02E-05	chr8:86019323-86058315 (+)	8q21.2	leucine rich repeat and coiled-coil centrosomal protein 1
PRC1	2.75	3.63E-10	3.34E-08	chr15:91509268-91538859 (-)	15q26.1	protein regulator of cytokinesis 1
DPYD	2.75	7.29E-12	2.03E-09	chr1:97543299-98386615 (-)	1p22	dihydropyrimidine dehydrogenase
TNFRSF21	2.75	4.03E-10	3.61E-08	chr6:47199288-47277680 (-)	6p21.1	tumor necrosis factor receptor superfamily, member 21
NOP58	2.74	1.39E-06	1.63E-05	chr2:203130439-203168389 (+)	2q33.1	NOP58 ribonucleoprotein
PLK1	2.74	2.30E-08	7.86E-07	chr16:23690143-23701688 (+)	16p12.2	polo-like kinase 1
POLR3G	2.73	6.65E-12	1.90E-09	chr5:89767565-89810370 (+)	5q14.3	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
SCD	2.72	9.42E-05	4.25E-04	chr10:102106772-102124591 (+)	10q24.31	stearoyl-CoA desaturase (delta-9-desaturase)
CARHSP1	2.72	3.37E-14	4.85E-11	chr16:8946799-8962866 (-)	16p13.2	calcium regulated heat stable protein 1, 24kDa
C12orf75	2.71	1.27E-08	4.98E-07	chr12:105720744-105789875 (+)	12q23.3	chromosome 12 open reading frame 75
KIAA0020	2.71	2.30E-08	7.85E-07	chr9:2720469-2844241 (-)	9p24.2	KIAA0020
DIAPH3	2.71	4.17E-13	2.83E-10	chr13:60239717-60738119 (-)	13q21.2	diaphanous-related formin 3
TMEM165	2.71	7.22E-10	5.62E-08	chr4:56262090-56292342 (+)	4q12	transmembrane protein 165
SLK	2.71	7.55E-05	3.56E-04	chr10:105726959-105788991 (+)	10q24.33	STE20-like kinase
ZC3H12A	2.70	1.38E-09	9.25E-08	chr1:37940119-37949978 (+)	1p34.3	zinc finger CCCH-type containing 12A
RBM25	2.69	2.85E-06	2.80E-05	chr14:73525144-73588122 (+)	14q24.3	RNA binding motif protein 25
TRANK1	2.67	3.84E-08	1.16E-06	chr3:36868308-36986548 (-)	3p22.2	tetratricopeptide repeat and ankyrin repeat containing 1
ARSF	2.67	2.79E-09	1.56E-07	chrX:2958275-3030770 (+)	Xp22.3	arylsulfatase F
CCDC109B	2.67	1.13E-13	1.11E-10	chr4:110481355-110609874 (+)	4q25	coiled-coil domain containing 109B
BRIP1	2.67	1.94E-08	6.91E-07	chr17:59756547-59940920 (-)	17q22.2	BRCA1 interacting protein C-terminal helicase 1
TGM1	2.67	1.51E-06	1.74E-05	chr14:24718320-24732416 (-)	14q11.2	transglutaminase 1
SREK1	2.66	8.12E-07	1.10E-05	chr5:65435799-65479443 (+)	5q12.3	splicing regulatory glutamine lysine-rich protein 1
CCDC88A	2.66	8.03E-10	6.12E-08	chr2:55514978-55647057 (-)	2p16.1	coiled-coil domain containing 88A
PLA2G4D	2.65	7.37E-09	3.26E-07	chr15:42359881-42386752 (-)	15q15.1	phospholipase A2, group IVD (cytosolic)
SLC7A1	2.65	1.55E-10	1.80E-08	chr13:30083547-30169825 (-)	13q12.3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
CLSPN	2.64	8.98E-15	2.16E-11	chr1:36185819-36235568 (-)	1p34.2	claspin
HRH2	2.64	8.90E-09	3.78E-07	chr5:175085033-175113245 (+)	5q35.2	histamine receptor H2
CD47	2.64	2.20E-12	8.80E-10	chr3:107761941-107809935 (-)	3q13.1-q13.2	CD47 molecule
PRPF4B	2.64	3.97E-06	3.61E-05	chr6:4021501-4065217 (+)	6p25.2	pre-mRNA processing factor 4B
CACNB4	2.63	1.42E-10	1.69E-08	chr2:152689286-152955593 (-)	2q22-q23	calcium channel, voltage-dependent, beta 4 subunit
SLC36A4	2.63	1.52E-08	5.68E-07	chr11:92877341-92879656 (-)	11q21	solute carrier family 36 (proton amino acid symporter), member 4
IFITM3	2.62	1.40E-08	5.36E-07	chr11:319669-321340 (-)	11p15.5	interferon induced transmembrane protein 3
TXNDC5	2.62	8.00E-11	1.14E-08	chr6:7881483-7911047 (-)	6p24.3	thioredoxin domain containing 5 (endoplasmic reticulum)
NAA15	2.62	1.94E-07	3.89E-06	chr4:140222609-140341187 (+)	4q31.1	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
PBK	2.62	2.32E-11	4.66E-09	chr8:27667137-27695612 (-)	8p21.2	PDZ binding kinase
SLC39A6	2.61	7.77E-13	4.16E-10	chr18:33688494-33709357 (-)	18q12.2	solute carrier family 39 (zinc transporter), member 6
KIAA1551	2.61	9.51E-07	1.23E-05	chr12:32112353-32146043 (+)	12p11.21	KIAA1551
SKA3	2.61	9.28E-12	2.37E-09	chr13:21727734-21750741 (-)	13q12.11	spindle and kinetochore associated complex subunit 3
NOL8	2.61	1.01E-08	4.17E-07	chr9:95059640-95087876 (-)	9q22.31	nucleolar protein 8
SPTSSA	2.61	7.16E-11	1.05E-08	chr14:34901995-34931562 (-)	14q13.1	serine palmitoyltransferase, small subunit A
LMNB1	2.61	1.05E-13	1.07E-10	chr5:126112315-126172712 (+)	5q23.2	lamin B1
NMI	2.60	1.59E-14	3.02E-11	chr2:152126979-152146571 (-)	2q23	N-myc (and STAT) interactor
CCAR1	2.60	1.27E-08	4.99E-07	chr10:70480971-70552134 (+)	10q21.3	cell division cycle and apoptosis regulator 1
CDC6	2.59	7.44E-13	4.16E-10	chr17:38443885-38459413 (+)	17q21.3	cell division cycle 6
CDKN3	2.58	1.33E-10	1.62E-08	chr14:54863673-54886936 (+)	14q22	cyclin-dependent kinase inhibitor 3
ZC3H13	2.58	1.61E-07	3.38E-06	chr13:46528600-46626894 (-)	13q14.13	zinc finger CCCH-type containing 13
IL4R	2.58	1.91E-12	7.87E-10	chr16:27325247-27376099 (+)	16p12.1-p11.2	interleukin 4 receptor
NUSAP1	2.57	3.52E-08	1.09E-06	chr15:41624892-41673248 (+)	15q15.1	nucleolar and spindle associated protein 1
PRRC2C	2.57	6.70E-09	3.03E-07	chr1:171454651-171562650 (+)	1q23.3	proline-rich coiled-coil 2C
FGFBP1	2.57	7.50E-07	1.03E-05	chr4:15937192-15940363 (-)	4p15.32	fibroblast growth factor binding protein 1
USP18	2.57	2.05E-06	2.18E-05	chr22:18632666-18672923 (+)	22q11.21	ubiquitin specific peptidase 18
SHCBP1	2.57	5.26E-11	8.56E-09	chr16:46614466-46655538 (-)	16q11.2	SHC SH2-domain binding protein 1
FUT2	2.57	8.81E-07	1.17E-05	chr19:49199228-49209207 (+)	19q13.3	fucosyltransferase 2 (secretor status included)
PDSS1	2.56	1.84E-13	1.54E-10	chr10:26986588-27035727 (+)	10p12.1	prenyl (decaprenyl) diphosphate synthase, subunit 1
PITPNC1	2.56	2.70E-10	2.71E-08	chr17:65373720-65689647 (+)	17q24.2	phosphatidylinositol transfer protein, cytoplasmic 1
HELLS	2.55	2.92E-10	2.87E-08	chr10:96305543-96373662 (+)	10q24.2	helicase, lymphoid-specific
EIF2AK2	2.54	1.18E-05	8.20E-05	chr2:37326353-37384208 (-)	2p22-p21	eukaryotic translation initiation factor 2-alpha kinase 2
CTSL	2.54	1.31E-13	1.20E-10	chr9:90340434-90346384 (+)	9q21.33	cathepsin L
VSNL1	2.53	1.26E-12	5.59E-10	chr2:177203393-178338285 (+)	2p24.3	visinin-like 1
ASCC3	2.53	5.83E-11	9.26E-09	chr6:100956070-101329248 (-)	6q16	activating signal cointegrator 1 complex subunit 3
UBA6	2.53	1.51E-09	9.91E-08	chr4:68481479-68566897 (-)	4q13.2	ubiquitin-like modifier activating enzyme 6
KIF4A	2.52	4.96E-11	8.25E-09	chrX:69509879-69640774 (+)	Xq13.1	kinesin family member 4A
GOT2	2.52	4.01E-12	1.31E-09	chr16:58741035-58768246 (-)	16q21	glutamic-oxaloacetic transaminase 2, mitochondrial
GCNT4	2.52	7.15E-10	5.59E-08	chr5:74321171-74326724 (-)	5q12	glucosaminyl (N-acetyl) transferase 4, core 2
KLK13	2.51	1.72E-06	1.91E-05	chr19:51559463-51568367 (-)	19q13.33	kallikrein-related peptidase 13
THOC2	2.50	3.19E-05	1.79E-04	chrX:122734412-122866906 (-)	Xq25-q26.3	THO complex 2
PUS10	2.50	2.40E-12	9.15E-10	chr2:61167548-61245389 (-)	2p16.1	pseudouridylate synthase 10
ERP27	2.49	8.80E-06	6.61E-05	chr12:15066969-15092016 (-)	12p12.3	endoplasmic reticulum protein 27
FASTKD1	2.49	9.48E-15	2.16E-11	chr2:170386259-170430424 (-)	2q31	FAST kinase domains 1
MCM10	2.49	8.69E-15	2.16E-11	chr10:13203554-13253104 (+)	10p13	minichromosome maintenance complex component 10
SP110	2.49	2.57E-10	2.60E-08	chr2:231032009-231090444 (-)	2q37.1	SP110 nuclear body protein
WNT5A	2.48	5.86E-09	2.73E-07	chr3:55499743-55523973 (-)	3p21-p14	wingless-type MMTV integration site family, member 5A
MPHOSPH9	2.48	6.54E-12	1.88E-09	chr12:123638867-123717785 (-)	12q24.31	M-phase phosphoprotein 9
CYP24A1	2.48	4.68E-04	1.57E-03	chr20:52769988-52790516 (-)	20q13	cytochrome P450, family 24, subfamily A, polypeptide 1
USP8	2.47	2.81E-05	1.62E-04	chr15:50716579-50793280 (+)	15q21.2	ubiquitin specific peptidase 8
CDCA2	2.47	2.99E-10	2.92E-08	chr8:25316513-25365436 (+)	8p21.2	cell division cycle associated 2
GCC2	2.47	1.58E-06	1.79E-05	chr2:109065017-109125871 (+)	2q12.3	GRIP and coiled-coil domain containing 2
HSP90B1	2.46	1.24E-07	2.79E-06	chr12:104324112-104341704 (+)	12q24.2-q24.3	heat shock protein 90kDa beta (Grp94), member 1
SPTLC2	2.46	8.36E-11	1.18E-08	chr14:77972340-78083116 (-)	14q24.3	serine palmitoyltransferase, long chain base subunit 2
RBBP6	2.46	2.85E-09	1.58E-07	chr16:24549014-24584184 (+)	16p12.2	retinoblastoma binding protein 6
ADAP2	2.46	3.49E-10	3.26E-08	chr17:29248698-29286340 (+)	17q11.2	ArfGAP with dual PH domains 2
SLC18B1	2.44	2.72E-13	2.02E-10	chr6:133090507-133119747 (-)	6q22.3-q23.3	solute carrier family 18, subfamily B, member 1
DEPDC1B	2.44	7.75E-12	2.10E-09	chr5:59892739-59996017 (-)	5q12.1	DEP domain containing 1B
CLEC3A	2.44	8.41E-03	1.80E-02	chr16:78056412-78066003 (+)	16q23	C-type lectin domain family 3, member A
DNMT1	2.43	1.42E-14	2.78E-11	chr19:10244022-10305755 (-)	19p13.2	DNA (cytosine-5-)-methyltransferase 1
PSMA3	2.43	1.07E-10	1.37E-08	chr14:58711523-58738730 (+)	14q23	proteasome (prosome, macropain) subunit, alpha type, 3
NPR3	2.43	2.48E-07	4.63E-06	chr5:32689176-32791830 (+)	5p13.3	natriuretic peptide receptor 3
APOL1	2.43	5.84E-08	1.58E-06	chr22:36649056-36663577 (+)	22q13.1	apolipoprotein L, 1
DNAJC2	2.43	7.72E-10	5.93E-08	chr7:102952921-102985320 (-)	7q22	DnaJ (Hsp40) homotog, subfamily C, member 2
KIAA0101	2.42	1.14E-11	2.70E-09	chr15:64657193-64679886 (-)	15q22.31	KIAA0101
SLFN5	2.42	7.67E-07	1.05E-05	chr17:33570086-33594761 (+)	17q12	schlafen family member 5
SAMHD1	2.42	8.80E-04	2.67E-03	chr20:35518632-35580246 (-)	20pter-q12	SAM domain and HD domain 1
STAT2	2.42	7.77E-08	1.96E-06	chr12:56735381-56754037 (-)	12q13.3	signal transducer and activator of transcription 2, 113kDa
MAB21L3	2.42	1.37E-07	3.00E-06	chr1:116654376-116677861 (+)	1p13.1	mab-21-like 3 (C. elegans)
CEP83	2.42	3.27E-08	1.03E-06	chr12:94702056-94853764 (-)	12q22	centrosomal protein 83kDa

C1R	2.42	1.01E-10	1.32E-08	chr12:7187513-7245203 (-)	12p13	complement component 1, r subcomponent
ROCK1P1	2.42	3.62E-08	1.11E-06	chr18:109065-122222 (+)	18p11.32	Rho-associated, coiled-coil containing protein kinase 1 pseudogene 1
CKMT1A	2.41	4.73E-10	4.10E-08	chr15:43985084-43991420 (+)	15q15	creatine kinase, mitochondrial 1A
UACA	2.41	2.52E-07	4.67E-06	chr15:70946893-71055932 (-)	15q22-q24	uveal autoantigen with coiled-coil domains and ankyrin repeats
PRPF40A	2.41	3.08E-05	1.74E-04	chr2:153508107-153574511 (-)	2q23.3	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
DGKH	2.40	5.82E-07	8.59E-06	chr13:42813346-42817026 (+)	13q14.11	diacylglycerol kinase, eta
CHD1	2.40	3.24E-05	1.82E-04	chr5:98190908-98262240 (-)	5q15-q21	chromodomain helicase DNA binding protein 1
SCAPER	2.40	1.14E-06	1.41E-05	chr15:76640527-77197744 (-)	15q24	S-phase cyclin A-associated protein in the ER
CENPN	2.40	3.32E-12	1.14E-09	chr16:81040103-81066719 (+)	16q23.2	centromere protein N
CLCA2	2.40	3.45E-12	1.16E-09	chr1:86889769-86922241 (+)	1p22.3	chloride channel accessory 2
ANKRD29	2.40	1.14E-12	5.45E-10	chr18:21178890-21242849 (-)	18q11.2	ankyrin repeat domain 29
HSPA4L	2.39	2.98E-07	5.27E-06	chr4:128702976-128755226 (+)	4q28	heat shock 70kDa protein 4-like
TARS	2.39	2.42E-12	9.18E-10	chr5:33440802-33469644 (+)	5p13.2	threonyl-tRNA synthetase
SLIRP	2.39	1.54E-08	5.76E-07	chr14:78174414-78187450 (+)	14q24.3	SRA stem-loop interacting RNA binding protein
PGM2	2.39	2.80E-12	1.00E-09	chr4:37828255-37864559 (+)	4p14	phosphoglucomutase 2
FAM110C	2.39	5.49E-12	1.66E-09	chr2:38814-46870 (-)	2p25.3	family with sequence similarity 110, member C
WDHD1	2.38	3.10E-10	3.02E-08	chr14:55405656-55493823 (-)	14q22.2	WD repeat and HMG-box DNA binding protein 1
FBXO9	2.38	6.98E-13	4.04E-10	chr6:52916789-52965671 (+)	6p12.3-p11.2	F-box protein 9
UPF2	2.37	7.13E-07	9.97E-06	chr10:11962021-12085169 (-)	10p14-p13	UPF2 regulator of nonsense transcripts homolog (yeast)
HIF1A	2.37	1.16E-07	2.65E-06	chr14:62162119-62214977 (+)	14q23.2	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
XRCC2	2.37	4.85E-10	4.15E-08	chr7:152341864-152373250 (-)	7q36.1	X-ray repair complementing defective repair in Chinese hamster cells 2
KNTC1	2.37	6.78E-09	3.06E-07	chr12:123011795-123110947 (+)	12q24.31	kinetochore associated 1
MYO5A	2.37	1.97E-08	7.00E-07	chr15:52599480-52821247 (-)	15q21	myosin VA (heavy chain 12, myoxin)
NCAPH	2.36	2.16E-10	2.27E-08	chr2:97001484-97041274 (+)	2q11.2	non-SMC condensin I complex, subunit H
CD24	2.36	2.97E-07	5.26E-06	chrY:21152526-21154705 (-)	6q21	CD24 molecule
CENPK	2.35	5.46E-11	8.82E-09	chr5:64813593-64858998 (-)	5q12.3	centromere protein K
PSME2	2.35	6.54E-14	7.95E-11	chr14:24612571-24616430 (-)	14q11.2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
GPX3	2.35	1.69E-05	1.08E-04	chr5:150399999-150408554 (+)	5q23	glutathione peroxidase 3 (plasma)
GOT1	2.35	1.69E-10	1.92E-08	chr10:101156627-101190530 (-)	10q24.1-q25.1	glutamic-oxaloacetic transaminase 1, soluble
CWC22	2.35	4.59E-05	2.39E-04	chr2:180809603-180871840 (-)	2q31.3	CWC22 spliceosome-associated protein homolog (S. cerevisiae)
HIST1H2AB	2.35	2.80E-07	5.05E-06	chr6:26033320-26033796 (-)	6p22.1	histone cluster 1, H2ab
EXO1	2.34	3.43E-12	1.16E-09	chr1:242011269-242058450 (+)	1q42-q43	exonuclease 1
DDIAS	2.34	4.40E-13	2.90E-10	chr11:82612737-82669319 (+)	11q14.1	DNA damage-induced apoptosis suppressor
IFIT5	2.34	3.85E-07	6.31E-06	chr10:91174325-91180759 (+)	10q23.31	interferon-induced protein with tetratricopeptide repeats 5
LDLR	2.33	7.07E-08	1.82E-06	chr19:11200038-11244505 (+)	19p13.2	low density lipoprotein receptor
BRCC3	2.33	1.29E-07	2.87E-06	chrX:154299695-154351349 (+)	Xq28	BRCA1 BRCA2-containing complex, subunit 3
KIF5B	2.33	9.76E-05	4.37E-04	chr10:32297938-32345371 (-)	10p11.22	kinesin family member 5B
KIF2C	2.33	3.84E-09	1.97E-07	chr1:45205490-45233439 (+)	1p34.1	kinesin family member 2C
SMC5	2.33	2.13E-04	8.24E-04	chr9:72873878-72969804 (+)	9q21.12	structural maintenance of chromosomes 5
POLB	2.32	5.84E-11	9.26E-09	chr8:42195972-42229331 (+)	8p11.2	polymerase (DNA directed), beta
CEP162	2.32	9.19E-08	2.22E-06	chr6:84833960-84937353 (-)	6q14.3	centrosomal protein 162kDa
FANCD2	2.32	7.59E-11	1.10E-08	chr3:10068098-10143614 (+)	3p26	Fanconi anemia, complementation group D2
APOL6	2.32	6.13E-09	2.83E-07	chr22:36044424-36064456 (+)	22q12.3	apolipoprotein L, 6
IFNGR1	2.31	1.36E-09	9.17E-08	chr6:137518621-137540586 (-)	6q23.3	interferon gamma receptor 1
RAD51AP1	2.31	3.03E-11	5.67E-09	chr12:4647950-4669214 (+)	12p13.2-p13.1	RAD51 associated protein 1
PON2	2.31	7.06E-12	1.98E-09	chr7:95034174-95064510 (-)	7q21.3	paraoxonase 2
CKAP2	2.31	4.33E-07	6.87E-06	chr13:53029495-53050763 (+)	13q14	cytoskeleton associated protein 2
REV3L	2.30	4.79E-07	7.42E-06	chr6:111620234-111804918 (-)	6q21	REV3-like, polymerase (DNA directed), zeta, catalytic subunit
CROT	2.29	1.05E-09	7.53E-08	chr7:86974951-87029112 (+)	7q21.1	carnitine O-octanoyltransferase
PDE8A	2.29	2.40E-10	2.46E-08	chr15:85523671-85682376 (+)	15q25.3	phosphodiesterase 8A
ATAD2	2.29	2.29E-08	7.84E-07	chr8:124332090-124428590 (-)	8q24.13	ATPase family, AAA domain containing 2
ABCC1	2.29	7.51E-12	2.07E-09	chr16:16043434-16236931 (+)	16p13.1	ATP-binding cassette, sub-family C (CFTR MRP), member 1
ALDH7A1	2.29	4.39E-10	3.86E-08	chr5:125877533-125931110 (-)	5q31	aldehyde dehydrogenase 7 family, member A1
STARD4	2.29	8.10E-07	1.10E-05	chr5:110831731-110848288 (-)	5q22.1	StAR-related lipid transfer (START) domain containing 4
CKMT1B	2.29	3.40E-10	3.21E-08	chr15:43885252-43897089 (+)	15q15	creatine kinase, mitochondrial 1B
USP16	2.29	7.04E-05	3.36E-04	chr21:30396938-30426809 (+)	21q22.11	ubiquitin specific peptidase 16
DDX10	2.27	3.23E-09	1.73E-07	chr11:108535752-108811657 (+)	11q22-q23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
PAK1IP1	2.27	1.46E-07	3.14E-06	chr6:10694928-10710015 (+)	6p24.2	PAK1 interacting protein 1
GNL2	2.27	7.01E-08	1.81E-06	chr1:38032413-38061586 (-)	1p34.3	guanine nucleotide binding protein-like 2 (nucleolar)
CENPI	2.26	2.32E-11	4.66E-09	chrX:100353178-100418670 (+)	Xq22.1	centromere protein I
SPRR2E	2.25	1.28E-02	2.58E-02	chr1:153065611-153078660 (-)	1q21-q22	small proline-rich protein 2E
CDH3	2.25	3.19E-07	5.52E-06	chr16:68678151-68732971 (+)	16q22.1	cadherin 3, type 1, P-cadherin (placental)
IDH3A	2.24	9.68E-11	1.31E-08	chr15:78441663-78464291 (+)	15q25.1-q25.2	isocitrate dehydrogenase 3 (NAD+) alpha
CCDC144CP	2.24	1.22E-05	8.41E-05	chr17:20224477-20305504 (+)	17p11.2	coiled-coil domain containing 144C, pseudogene
RASGRP1	2.24	4.60E-08	1.33E-06	chr15:38780302-38857776 (-)	15q14	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
NIPBL	2.24	2.22E-04	8.51E-04	chr5:36876861-37066515 (+)	5p13.2	Nipped-B homolog (Drosophila)
FOXM1	2.24	1.55E-09	1.01E-07	chr12:2966847-2986321 (-)	12p13	forkhead box M1
LGALS3BP	2.24	1.02E-08	4.20E-07	chr17:76967335-76976061 (-)	17q25	lectin, galactoside-binding, soluble, 3 binding protein
SLC22A3	2.23	2.36E-08	8.04E-07	chr6:160769300-160876014 (+)	6q25.3	solute carrier family 22 (organic cation transporter), member 3
NOLC1	2.23	3.50E-10	3.26E-08	chr10:103911933-103923627 (+)	10q24.32	nucleolar and coiled-body phosphoprotein 1
CTPS1	2.22	2.06E-10	2.20E-08	chr1:41445007-41478235 (+)	1p34.1	CTP synthase 1
ASUN	2.22	2.73E-09	1.54E-07	chr12:27058112-27091254 (-)	12p11.23	asunder spermatogenesis regulator
NOC3L	2.22	8.31E-08	2.06E-06	chr10:96075004-96122716 (-)	10q23.33	nucleolar complex associated 3 homolog (S. cerevisiae)
PARPBP	2.22	8.87E-12	2.28E-09	chr12:102513956-102591298 (+)	12q23.2	PARP1 binding protein
ODF2L	2.22	4.39E-08	1.29E-06	chr1:86786611-86862025 (-)	1p22.3	outer dense fiber of sperm tails 2-like
OSMR	2.22	5.08E-09	2.47E-07	chr5:38845960-38945698 (+)	5p13.1	oncostatin M receptor
CYCS	2.21	4.34E-10	3.82E-08	chr7:25158270-25164980 (-)	7p15.3	cytochrome c, somatic
TC2N	2.21	8.45E-13	4.48E-10	chr14:92246095-92333880 (-)	14q32.12	tandem C2 domains, nuclear
TXNDC17	2.21	9.18E-11	1.27E-08	chr17:6544078-6547920 (+)	17p13.1	thioredoxin domain containing 17
CASP8AP2	2.20	3.31E-07	5.67E-06	chr6:90539619-90584155 (+)	6q15	caspase 8 associated protein 2
DEPDC1	2.20	1.97E-07	3.93E-06	chr1:68939835-68962904 (-)	1p31.2	DEP domain containing 1
C20orf24	2.20	6.57E-12	1.88E-09	chr20:35234137-35240960 (+)	20q11.23	chromosome 20 open reading frame 24
CXCL10	2.20	4.51E-05	2.36E-04	chr4:76942269-76944689 (-)	4q21	chemokine (C-X-C motif) ligand 10
C12orf4	2.19	2.81E-11	5.38E-09	chr12:4596894-4647674 (-)	12p13.3	chromosome 12 open reading frame 4
C12orf56	2.19	4.27E-13	2.87E-10	chr12:64660763-64784471 (-)	12q14.2	chromosome 12 open reading frame 56
GART	2.19	1.33E-14	2.68E-11	chr21:34870940-34915797 (-)	21q22.11	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
VNN1	2.19	2.16E-11	4.40E-09	chr6:133001997-133035194 (-)	6q23-q24	vanin 1
LUC7L3	2.19	2.14E-04	8.26E-04	chr17:48796905-48834076 (+)	17q21.33	LUC7-like 3 (S. cerevisiae)
MAPK6	2.19	4.38E-09	2.20E-07	chr15:52311398-52358462 (+)	15q21	mitogen-activated protein kinase 6
MFHAS1	2.18	2.29E-12	8.92E-10	chr8:8640864-8751155 (-)	8p23.1	malignant fibrous histiocytoma amplified sequence 1
TMEM45B	2.18	1.18E-08	4.69E-07	chr11:129685714-129729898 (+)	11q24.3	transmembrane protein 45B
EIF2S2	2.18	3.29E-09	1.73E-07	chr20:32676104-32700138 (-)	20q11.2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
CXCR4	2.17	2.89E-07	5.18E-06	chr2:136871919-136875735 (-)	2q21	chemokine (C-X-C motif) receptor 4
TGFBR1	2.16	1.75E-09	1.12E-07	chr9:101867371-101916585 (+)	9q22	transforming growth factor, beta receptor 1
HK2	2.16	8.00E-08	2.00E-06	chr2:75059782-75120486 (+)	2p13	hexokinase 2
MTIF2	2.15	2.71E-10	2.71E-08	chr2:55463731-55496483 (-)	2p16.1	mitochondrial translational initiation factor 2
ALOX12B	2.15	2.98E-04	1.09E-03	chr17:7975954-7991022 (-)	17p13.1	arachidonate 12-lipoxygenase, 12R type
IL12RB2	2.15	1.73E-10	1.95E-08	chr1:67773047-67862583 (+)	1p31.3-p31.2	interleukin 12 receptor, beta 2
IVL	2.15	1.35E-04	5.69E-04	chr1:152881021-152884362 (+)	1q21	involucrin
HPSE	2.15	3.46E-07	5.83E-06	chr4:84213614-84256306 (-)	4q21.3	heparanase
BRCA1	2.15	1.30E-12	5.84E-10	chr17:41196312-41322420 (-)	17q21	breast cancer 1, early onset
EPB41L4A	2.15	2.24E-12	8.80E-10	chr5:111478138-111755013 (-)	5q21.3	erythrocyte membrane protein band 4.1 like 4A
HSPA4	2.14	5.62E-09	2.65E-07	chr5:132387654-132442141 (+)	5q31.1	heat shock 70kDa protein 4
BLM	2.14	3.13E-12	1.09E-09	chr15:91260558-91358692 (+)	15q26.1	Bloom syndrome, RecQ helicase-like
GALNT6	2.14	5.59E-08	1.54E-06	chr12:51745682-51785436 (-)	12q13	polypeptide N-acetylgalactosaminyltransferase 6
SRFBP1	2.14	2.08E-06	2.20E-05	chr5:121297656-121411265 (+)	5q23.1	serum response factor binding protein 1
MCM6	2.13	2.99E-09	1.63E-07	chr2:136597196-136634011 (-)	2q21	minichromosome maintenance complex component 6
AGPAT5	2.13	2.81E-10	2.79E-08	chr8:65658078-66190021 (+)	8p23.1	1-acylglycerol-3-phosphate O-acyltransferase 5
CFB	2.13	1.60E-07	3.36E-06	chr6:31913486-31919861 (+)	6p21.3	complement factor B
PMM2	2.13	1.06E-10	1.37E-08	chr16:8891670-8943194 (+)	16p13	phosphomannomutase 2
MRPS25	2.13	6.82E-10	5.42E-08	chr3:15083967-15106842 (-)	3p25	mitochondrial ribosomal protein S25
PPP4R1	2.13	3.74E-10	3.42E-08	chr18:9546789-9614600 (-)	18p11.22	protein phosphatase 4, regulatory subunit 1
EPRS	2.12	2.12E-08	7.38E-07	chr1:220141942-220220000 (-)	1q41	glutamyl-prolyl-tRNA synthetase
CTAGE5	2.12	1.90E-08	6.78E-07	chr14:39734476-39856156 (+)	14q13.3	CTAGE family, member 5
FAT1	2.12	3.17E-07	5.50E-06	chr4:187508937-187647876 (-)	4q35	FAT atypical cadherin 1
PNPT1	2.12	2.20E-08	7.62E-07	chr2:55861198-55921045 (-)	2p15	polyribonucleotide nucleotidyltransferase 1
RB1	2.12	3.17E-10	3.07E-08	chr13:48877883-49056122 (+)	13q14.2	retinoblastoma 1
SPRR1B	2.12	6.87E-04	2.17E-03	chr1:153003678-153005376 (+)	1q21-q22	small proline-rich protein 1B
ID1	2.12	2.69E-06	2.69E-05	chr20:30193086-30194318 (+)	20q11	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
CEP78	2.12	8.52E-14	9.69E-11	chr9:80850978-80894606 (+)	9q21.2	centrosomal protein 78kDa
AURKA	2.12	1.88E-10	2.07E-08	chr20:54944445-54967393 (-)	20q13	aurora kinase A
CEBPZ	2.11	9.07E-06	6.76E-05	chr2:37428755-37458856 (-)	EBP), zeta	CCAAT enhancer binding protein (C
THOC1	2.11	1.77E-06	1.95E-05	chr18:2145220-2680591 (-)	18p11.32	THO complex 1
ME1	2.11	2.97E-06	2.89E-05	chr6:83920108-84140938 (-)	6q12	malic enzyme 1, NADP(+)-dependent, cytosolic
PANX1	2.11	5.67E-07	8.39E-06	chr11:93862094-93915138 (+)	11q21	pannexin 1
FERMT1	2.11	8.33E-08	2.06E-06	chr20:6055492-6104191 (-)	20p12.3	fermitin family member 1
CDC25B	2.11	2.70E-10	2.71E-08	chr20:3767578-3786762 (+)	20p13	cell division cycle 25B
KCNJ15	2.11	2.11E-10	2.24E-08	chr21:39628663-39673748 (+)	21q22.2	potassium inwardly-rectifying channel, subfamily J, member 15
E2F8	2.10	1.63E-07	3.42E-06	chr11:19245610-19263389 (-)	11p15.1	E2F transcription factor 8
HEATR5A	2.10	1.15E-12	5.46E-10	chr14:31760994-31889788 (-)	14q12	HEAT repeat containing 5A
SCAF11	2.10	4.50E-05	2.36E-04	chr12:46312914-46385903 (-)	12q12	SR-related CTD-associated factor 11
ATR	2.10	5.70E-09	2.68E-07	chr3:142168077-142297668 (-)	3q23	ATR serine threonine kinase
SKA1	2.09	7.72E-09	3.38E-07	chr18:47901365-47920543 (+)	18q21.1	spindle and kinetochore associated complex subunit 1
RIF1	2.09	1.49E-04	6.16E-04	chr2:152266397-152364527 (+)	2q23.3	replication timing regulatory factor 1
YARS	2.09	8.15E-11	1.15E-08	chr1:33240840-33283754 (-)	1p35.1	tyrosyl-tRNA synthetase
GOLIM4	2.08	3.05E-06	2.94E-05	chr3:167726465-167813763 (-)	3q26.2	golgi integral membrane protein 4
DICER1	2.08	2.56E-09	1.47E-07	chr14:95552565-95624347 (-)	14q32.13	dicer 1, ribonuclease type III
LEO1	2.08	1.22E-05	8.41E-05	chr15:52230222-52264003 (-)	15q21.2	Leo1, Paf1 RNA polymerase II complex component, homolog (S. cerevisiae)
GTF3C6	2.08	4.76E-13	3.08E-10	chr6:111279763-111289093 (+)	6q21	general transcription factor IIIC, polypeptide 6, alpha 35kDa
PUS7L	2.08	4.27E-07	6.80E-06	chr12:44122410-44152620 (-)	12q12	pseudouridylate synthase 7 homolog (S. cerevisiae)-like
USP28	2.08	3.16E-09	1.71E-07	chr11:113668596-113746292 (-)	11q23	ubiquitin specific peptidase 28
HIBCH	2.08	6.89E-08	1.78E-06	chr2:191054461-191208919 (-)	2q32.2	3-hydroxyisobutyryl-CoA hydrolase
C1S	2.08	4.74E-12	1.49E-09	chr12:7096260-7178336 (+)	12p13	complement component 1, s subcomponent
PRMT3	2.07	2.12E-10	2.25E-08	chr11:20409076-20530879 (+)	11p15.1	protein arginine methyltransferase 3
KRT16P2	2.07	2.95E-11	5.58E-09	chr17:16733797-16736147 (-)	17p11.2	keratin 16 pseudogene 2
CDC20	2.07	1.43E-08	5.45E-07	chr1:43824599-43828874 (+)	1p34.1	cell division cycle 20
BAZ2B	2.07	1.61E-04	6.53E-04	chr2:160175490-160473203 (-)	2q24.2	bromodomain adjacent to zinc finger domain, 2B
TIMELESS	2.07	5.54E-12	1.67E-09	chr12:56810157-56843200 (-)	12q13.3	timeless circadian clock
MASTL	2.07	3.51E-09	1.83E-07	chr10:27443753-27475848 (+)	10p12.1	microtubule associated serine threonine kinase-like
RAB27A	2.06	1.67E-14	3.04E-11	chr15:55495164-55582013 (-)	15q15-q21.1	RAB27A, member RAS oncogene family
FRK	2.06	2.13E-09	1.28E-07	chr6:116262693-116381921 (-)	6q21-q22.3	fyn-related Src family tyrosine kinase
PRRG4	2.06	7.75E-13	4.16E-10	chr11:32851481-32879669 (+)	11p13	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
THBD	2.06	9.51E-08	2.27E-06	chr20:23026270-23030378 (-)	20p11.2	thrombomodulin
SYK	2.06	1.38E-11	3.11E-09	chr9:93564012-93660842 (+)	9q22	spleen tyrosine kinase
PLOD2	2.06	9.61E-09	3.99E-07	chr3:145787227-145881440 (-)	3q24	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
PTTG1	2.05	7.61E-11	1.10E-08	chr5:159848829-159855748 (+)	5q35.1	pituitary tumor-transforming 1
DBF4	2.05	1.40E-09	9.37E-08	chr7:87505531-87538856 (+)	7q21.3	DBF4 zinc finger
KLK10	2.05	6.38E-04	2.04E-03	chr19:51516000-51523431 (-)	19q13	kallikrein-related peptidase 10
CASP10	2.05	2.07E-09	1.27E-07	chr2:202047604-202094129 (+)	2q33-q34	caspase 10, apoptosis-related cysteine peptidase
CYB5R4	2.05	7.06E-11	1.04E-08	chr6:84569362-84670146 (+)	6pter-q22.33	cytochrome b5 reductase 4

AGPS	2.05	2.83E-10	2.81E-08	chr2:178257372-178408564 (+)	2q31.2	alkylglycerone phosphate synthase
PSMD1	2.05	1.17E-09	8.18E-08	chr2:231921578-232037541 (+)	2q37.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
PHF14	2.04	2.27E-06	2.35E-05	chr7:11013499-11209250 (+)	7p21.3	PHD finger protein 14
RIOK1	2.04	5.89E-08	1.59E-06	chr6:7389729-7418270 (+)	6p24.3	RIO kinase 1
KIAA1217	2.04	4.17E-11	7.21E-09	chr10:23983675-24836772 (+)	10p12.31	KIAA1217
KRT16P1	2.04	1.03E-11	2.51E-09	chr17:18343222-18344919 (+)	17p11.2	keratin 16 pseudogene 1
SMARCA5	2.04	3.81E-08	1.15E-06	chr4:144434616-144478642 (+)	4q31.1-q31.2	SWI SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
ENTPD7	2.03	7.77E-10	5.97E-08	chr10:101419263-101471002 (+)	10q24.2	ectonucleoside triphosphate diphosphohydrolase 7
NEDD4	2.03	4.28E-10	3.78E-08	chr15:56119120-56285835 (-)	15q	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase
RBL1	2.03	2.59E-09	1.48E-07	chr20:35624752-35724410 (-)	20q11.2	retinoblastoma-like 1
KITLG	2.03	4.42E-07	6.97E-06	chr12:88885885-88974628 (-)	12q22	KIT ligand
PNN	2.03	7.19E-06	5.65E-05	chr14:39644387-39652422 (+)	14q21.1	pinin, desmosome associated protein
ZDHHC21	2.03	9.61E-09	3.99E-07	chr9:14555481-14693480 (-)	9p22.3	zinc finger, DHHC-type containing 21
PSME4	2.03	1.43E-09	9.51E-08	chr2:54091204-54197977 (-)	2p16.2	proteasome (prosome, macropain) activator subunit 4
ARHGDIB	2.03	4.79E-09	2.35E-07	chr12:15094949-15114603 (-)	12p12.3	Rho GDP dissociation inhibitor (GDI) beta
POP1	2.03	4.83E-13	3.09E-10	chr8:99129521-99172069 (+)	8q22.1	processing of precursor 1, ribonuclease P MRP subunit (S. cerevisiae)
CCDC58	2.03	4.56E-10	3.96E-08	chr3:122078436-122102078 (-)	3q21.1	coiled-coil domain containing 58
PDZK1IP1	2.02	2.53E-08	8.46E-07	chr1:47649261-47656716 (-)	1p33	PDZK1 interacting protein 1
SPIN4	2.02	6.00E-11	9.39E-09	chrX:62567107-62571223 (-)	Xq11.1	spindlin family, member 4
CTR9	2.02	1.66E-07	3.45E-06	chr11:10772534-10801290 (+)	11p15.3	CTR9, Paf1 RNA polymerase II complex component
FAAH2	2.02	4.60E-08	1.33E-06	chrX:57313110-57515629 (+)	Xp11.21	fatty acid amide hydrolase 2
COX7B	2.02	2.10E-09	1.27E-07	chrX:77154935-77162870 (+)	Xq21.1	cytochrome c oxidase subunit VIIb
SSB	2.02	4.00E-06	3.63E-05	chr2:170648443-170668575 (+)	2q31.1	Sjogren syndrome antigen B (autoantigen La)
LAMP3	2.02	1.02E-04	4.55E-04	chr3:182840001-182881627 (-)	3q26.3-q27	lysosomal-associated membrane protein 3
GPR110	2.02	2.43E-09	1.42E-07	chr6:46963107-47010099 (-)	6p12.3	G protein-coupled receptor 110
DHFR	2.02	1.66E-11	3.60E-09	chr5:79922045-79950802 (-)	5q11.2-q13.2	dihydrofolate reductase
CDC7	2.02	1.30E-09	8.87E-08	chr1:91966404-91991321 (+)	1p22	cell division cycle 7
PSMA4	2.02	8.00E-09	3.47E-07	chr15:78832747-78841604 (+)	15q25.1	proteasome (prosome, macropain) subunit, alpha type, 4
CCDC34	2.01	1.64E-08	6.07E-07	chr11:27352374-27385415 (-)	11p14.1	coiled-coil domain containing 34
UTP20	2.01	2.28E-07	4.34E-06	chr12:101673887-101780397 (+)	12q23	UTP20, small subunit (SSU) processome component, homolog (yeast)
DDX46	2.01	1.52E-09	1.02E-07	chr1:95995528-96042833 (+)	1p36.22	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
ITSN2	2.01	8.13E-07	1.10E-05	chr2:24425733-24583583 (-)	2p23.3	intersectin 2
SLMAP	2.01	1.36E-06	1.60E-05	chr3:57741177-57914895 (+)	3p21.2-p14.3	sarcolemma associated protein
CYP4X1	2.01	5.08E-07	7.75E-06	chr1:47427036-47516423 (+)	1p33|1	cytochrome P450, family 4, subfamily X, polypeptide 1
RAB38	2.01	5.02E-10	4.27E-08	chr11:87846415-87908635 (-)	11q14	RAB38, member RAS oncogene family
ENAH	2.01	1.28E-08	5.00E-07	chr1:225674534-225840845 (-)	1q42.12	enabled homolog (Drosophila)
MTFR2	2.01	5.29E-10	4.46E-08	chr6:136552162-136571462 (-)	6q23.3	mitochondrial fission regulator 2
MTAP	2.01	1.75E-11	3.73E-09	chr9:21802635-21867077 (+)	9p21	methylthioadenosine phosphorylase
BZW1	2.01	4.29E-10	3.78E-08	chr2:201675317-201688569 (+)	2q33	basic leucine zipper and W2 domains 1
SLC25A33	2.01	1.57E-09	1.02E-07	chr1:95995528-96042833 (+)	1p36.22	solute carrier family 25 (pyrimidine nucleotide carrier), member 33
NCAPG2	2.01	2.45E-11	4.85E-09	chr7:158424003-158497520 (-)	7q36.3	non-SMC condensin II complex, subunit G2
IGFL1	2.01	2.21E-07	4.27E-06	chr19:46733009-46734500 (+)	19q13.32	IGF-like family member 1
KIAA1033	2.01	7.26E-07	1.01E-05	chr12:105501492-105562912 (+)	12q24.11	KIAA1033
SLFN13	2.01	5.44E-10	4.55E-08	chr17:33762115-33775856 (-)	17q12	schlafen family member 13
FAM98A	2.01	6.53E-12	1.88E-09	chr2:33808725-33824449 (-)	2p22.3	family with sequence similarity 98, member A
DNTTIP2	2.01	8.28E-07	1.12E-05	chr1:94331839-94345474 (-)	1p22.1	deoxynucleotidyltransferase, terminal, interacting protein 2
TLDC1	2.00	8.53E-11	1.20E-08	chr16:84509966-84538296 (-)	16q24.1	TBC LysM-associated domain containing 1
XPR1	2.00	7.29E-10	5.65E-08	chr1:180601140-180859415 (+)	1q25.1	xenotropic and polytropic retrovirus receptor 1
DIMT1	2.00	2.44E-11	4.84E-09	chr5:61683081-61699766 (-)	5q12.1	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae)
DNM1L	2.00	3.16E-08	1.00E-06	chr12:32832134-32905700 (+)	12p11.21	dynamin 1-like
GBP1P1	1.99	7.61E-11	1.10E-08	chr1:89873238-89890493 (+)	1p22.2	guanylate binding protein 1, interferon-inducible pseudogene 1
APOO	1.99	1.34E-08	5.18E-07	chrX:23851465-23926057 (-)	Xp22.11	apolipoprotein O
HEATR3	1.99	2.75E-11	5.31E-09	chr16:50099881-50140298 (+)	16q12.1	HEAT repeat containing 3
AFAP1L2	1.99	1.72E-09	1.10E-07	chr10:116054583-116164515 (-)	10q26.3	actin filament associated protein 1-like 2
SACS	1.99	6.71E-11	1.02E-08	chr13:23902965-24007841 (-)	13q12	sacsin molecular chaperone
MPZL1	1.99	6.29E-13	3.79E-10	chr1:167690429-167761156 (+)	1q24.2	myelin protein zero-like 1
HIST1H1A	1.99	7.04E-06	5.56E-05	chr6:26017248-26018040 (-)	6p21.3	histone cluster 1, H1a
AC016745.3	1.99	2.36E-04	8.96E-04	chr2:114182072-114182901 (+)	---	novel transcript
ARID4B	1.99	7.36E-05	3.48E-04	chr1:235330210-235491534 (-)	1q42.1-q43	AT rich interactive domain 4B (RBP1-like)
DEK	1.99	2.52E-05	1.48E-04	chr6:18224099-18265054 (-)	6p22.3	DEK proto-oncogene
GPR1	1.99	2.03E-09	1.24E-07	chr2:207040040-207082771 (-)	2q33.3	G protein-coupled receptor 1
EML6	1.98	6.92E-11	1.04E-08	chr2:54950636-55199157 (+)	2p16.1	echinoderm microtubule associated protein like 6
GARS	1.98	7.66E-10	5.90E-08	chr7:30634181-30673649 (+)	7p15	glycyl-tRNA synthetase
GBP2	1.98	8.30E-08	2.06E-06	chr1:89573310-89591799 (-)	1p22.2	guanylate binding protein 2, interferon-inducible
LOC284581	1.98	4.57E-03	1.07E-02	chr1:205831207-205865215 (+)	1q32.1	uncharacterized LOC284581
RPF2	1.98	9.31E-07	1.21E-05	chr6:111303218-111347303 (+)	6q21	ribosome production factor 2 homolog (S. cerevisiae)
GGH	1.98	4.14E-10	3.69E-08	chr8:63927638-63951730 (-)	8q12.3	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
PRIM1	1.98	1.47E-08	5.57E-07	chr12:57125364-57146146 (-)	12q13	primase, DNA, polypeptide 1 (49kDa)
CHRNA5	1.98	4.38E-08	1.29E-06	chr15:78857862-78887611 (+)	15q24	cholinergic receptor, nicotinic, alpha 5 (neuronal)
NOD2	1.98	4.46E-13	2.91E-10	chr16:50727514-50766987 (+)	16q21	nucleotide-binding oligomerization domain containing 2
SP140L	1.98	1.07E-09	7.65E-08	chr2:231191894-231268447 (+)	2q37.1	SP140 nuclear body protein-like
HYOU1	1.98	3.35E-10	3.19E-08	chr11:118914896-118927925 (-)	11q23.1-q23.3	hypoxia up-regulated 1
HOMER1	1.98	2.44E-09	1.42E-07	chr5:78668459-78810040 (-)	5q14.2	homer homolog 1 (Drosophila)
VNN3	1.97	3.80E-09	1.95E-07	chr6:133043923-133055904 (-)	6q23.2	vanin 3
AKR1C2	1.97	7.05E-07	9.88E-06	chr10:5029967-5060225 (-)	10p15-p14	aldo-keto reductase family 1, member C2
PLK4	1.97	1.08E-07	2.51E-06	chr4:128802016-128820377 (+)	4q28	polo-like kinase 4
GSPT1	1.97	1.09E-10	1.39E-08	chr16:119619985-120105119 (-)	16p13.1	G1 to S phase transition 1
PPIL1	1.97	3.19E-11	5.90E-09	chr6:36822603-36842800 (-)	6p21.1	peptidylprolyl isomerase (cyclophilin)-like 1
HNRNPU-AS1	1.97	3.54E-03	8.61E-03	chr1:245003940-245010243 (-)	1q44	HNRNPU antisense RNA 1
DNA2	1.97	2.56E-09	1.47E-07	chr10:70173821-70231879 (-)	10q21.3-q22.1	DNA replication helicasenuclease 2
NUS1	1.97	1.09E-09	7.77E-08	chr6:117996617-118031886 (+)	6q22.1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)
PIBF1	1.97	1.51E-03	4.20E-03	chr13:73356197-73590592 (+)	13q22.1	progesterone immunomodulatory binding factor 1
ZGRF1	1.96	2.67E-09	1.51E-07	chr4:113460489-113558151 (-)	4q25	zinc finger, GRF-type containing 1
GLRX3	1.96	2.05E-10	2.19E-08	chr10:131934639-131982785 (+)	10q26	glutaredoxin 3
ABCA12	1.96	2.02E-05	1.25E-04	chr2:215796266-216003151 (-)	2q34	ATP-binding cassette, sub-family A (ABC1), member 12
SCLT1	1.96	1.03E-10	1.34E-08	chr4:129786076-130014764 (-)	4q28.2	sodium channel and clathrin linker 1
CKAP5	1.96	9.53E-09	3.97E-07	chr11:46764598-46867859 (-)	11p11.2	cytoskeleton associated protein 5
LOC100288814	1.96	4.24E-08	1.25E-06	chrX:9935392-9936134 (+)	Xp22.2	uncharacterized LOC100288814
GBP4	1.96	5.03E-05	2.58E-04	chr1:89646831-89664633 (-)	1p22.2	guanylate binding protein 4
LRRC59	1.96	3.51E-09	1.84E-07	chr17:48458594-48474914 (-)	17q21.33	leucine rich repeat containing 59
SAT1	1.96	1.62E-03	4.45E-03	chrX:23801275-23804343 (+)	Xp22.1	spermidinespermine N1-acetyltransferase 1
IL19	1.96	4.69E-05	2.43E-04	chr1:206972215-207016326 (+)	1q32.2	interleukin 19
ATP12A	1.96	2.62E-03	6.68E-03	chr13:25254549-25285923 (+)	13q12.12|13q12.1-q12.3	ATPase, H+K+ transporting, nongastric, alpha polypeptide
BORA	1.95	4.54E-10	3.96E-08	chr13:73302042-73330328 (+)	13q22.1	bora, aurora kinase A activator
PNISR	1.95	1.48E-04	6.12E-04	chr6:99845927-99873207 (-)	6q16.3	PNN-interacting serinearginine-rich protein
CCND2	1.95	1.14E-05	8.04E-05	chr12:4382902-4414522 (+)	12p13	cyclin D2
PHIP	1.95	2.42E-04	9.13E-04	chr6:79644136-79788011 (-)	6q14	pleckstrin homology domain interacting protein
EDEM3	1.95	1.94E-09	1.20E-07	chr1:184659625-184724047 (-)	1q25	ER degradation enhancer, mannosidase alpha-like 3
HOOK1	1.94	5.08E-05	2.59E-04	chr1:60280458-60342050 (+)	1p32.1	hook microtubule-tethering protein 1
TXLNG	1.94	1.08E-09	7.73E-08	chrX:168040550-168062642 (+)	Xp22.2	taxilin gamma
DTL	1.94	3.99E-07	6.43E-06	chr1:212208919-212280742 (+)	1q32	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
LOC100132287	1.94	3.41E-07	5.78E-06	chr5:180743354-180755196 (+)	1p36.33	uncharacterized LOC100132287
HYAL4	1.94	1.37E-10	1.65E-08	chr7:123469037-123517532 (+)	7q31.3	hyaluronoglucosaminidase 4
NSRP1	1.94	3.20E-06	3.05E-05	chr17:28443799-28513493 (+)	17q11.2	nuclear speckle splicing regulatory protein 1
ADAT2	1.94	2.33E-07	4.41E-06	chr6:143743969-143771841 (-)	6q24.2	adenosine deaminase, tRNA-specific 2
CASP4	1.94	6.07E-10	4.95E-08	chr11:104813593-104840163 (-)	11q22.2-q22.3	caspase 4, apoptosis-related cysteine peptidase
TMSB10	1.94	3.09E-07	5.42E-06	chr2:85132749-85133799 (+)	2p11.2	thymosin beta 10
EDNRA	1.94	7.01E-06	5.55E-05	chr4:148402069-148466106 (+)	4q31.22	endothelin receptor type A
EIF2B2	1.94	1.62E-09	1.05E-07	chr14:75469612-75476294 (+)	14q24.3	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
TRIM14	1.94	1.30E-10	1.60E-08	chr9:100831557-100881494 (-)	9q22.33	tripartite motif containing 14
RP11-318K15.2	1.94	1.30E-06	1.55E-05	chr8:56806154-56808276 (+)	---	putative novel transcript
U2SURP	1.94	7.86E-05	3.67E-04	chr3:142720010-142779567 (+)	3q23	U2 snRNP-associated SURP domain containing
DOCK10	1.93	2.08E-06	2.20E-05	chr2:225629807-225907330 (-)	2q36.2	dedicator of cytokinesis 10
TMEM117	1.93	3.30E-10	3.16E-08	chr12:44229886-44783543 (+)	12q12	transmembrane protein 117
FAM208B	1.93	3.21E-07	5.54E-06	chr10:5726801-5805703 (+)	10p15.1	family with sequence similarity 208, member B
CACHD1	1.93	1.93E-08	6.89E-07	chr1:64936428-65158741 (+)	1p31.3	cache domain containing 1
TUBGCP4	1.93	2.42E-09	1.41E-07	chr15:43663313-43698240 (+)	15q15	tubulin, gamma complex associated protein 4
RP11-419K12.1	1.93	9.35E-05	4.22E-04	chr8:130691381-130695925 (-)	---	putative novel transcript
ACACA	1.93	6.82E-11	1.03E-08	chr17:35441923-35766902 (-)	17q21	acetyl-CoA carboxylase alpha
TPBG	1.93	5.06E-11	8.38E-09	chr6:83072923-83080545 (+)	6q14-q15	trophoblast glycoprotein
SLC1A1	1.93	2.01E-04	7.86E-04	chr9:4490427-4587469 (+)	9p24	solute carrier family 1 (neuronalepithelial high affinity glutamate transporter, system Xag), member 1
DMXL2	1.93	6.46E-12	1.87E-09	chr15:51739908-51915030 (-)	15q21.2	Dmx-like 2
LOC101929819	1.93	4.70E-07	7.30E-06	chr16:90224863-90233897 (+)	---	putative uncharacterized protein encoded by LINC00174-like
FOLH1	1.93	2.95E-09	1.62E-07	chr11:49168187-49230222 (-)	11p11.2	folate hydrolase (prostate-specific membrane antigen) 1
CHD7	1.93	1.12E-08	4.50E-07	chr8:61591324-61780586 (+)	8q12.2	chromodomain helicase DNA binding protein 7
DIS3	1.92	5.52E-07	8.23E-06	chr13:73329540-73356344 (-)	13q22.1	DIS3 exosome endoribonuclease and 3-5 exoribonuclease
CENPJ	1.92	1.13E-11	2.68E-09	chr13:25456412-25497085 (-)	13q12.12	centromere protein J
CEP350	1.92	2.51E-04	9.43E-04	chr1:179923873-180093886 (+)	1q25.2	centrosomal protein 350kDa
SLC1A5	1.92	6.44E-09	2.94E-07	chr19:47278140-47291851 (-)	19q13.3	solute carrier family 1 (neutral amino acid transporter), member 5
KIF2A	1.92	2.93E-08	9.44E-07	chr5:61601989-61683011 (+)	5q12-q13	kinesin heavy chain member 2A
MTHFD1	1.92	5.14E-11	8.50E-09	chr14:64854749-64926725 (+)	14q24	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
RP11-504P24.4	1.92	1.72E-04	6.90E-04	chr1:224183659-224197818 (+)	---	novel transcript
FOLH1B	1.92	2.83E-09	1.58E-07	chr11:89372398-89431886 (+)	11q14.3	folate hydrolase 1B
SPDL1	1.92	2.15E-10	2.26E-08	chr5:169010638-169031782 (+)	5q35.1	spindle apparatus coiled-coil protein 1
RNF213	1.92	1.21E-06	1.47E-05	chr17:78234660-78372581 (+)	17q25.3	ring finger protein 213
CIR1	1.92	1.17E-03	3.38E-03	chr2:175212749-175260443 (-)	2q31.1	corepressor interacting with RBPJ, 1
CFB	1.92	6.47E-07	9.31E-06	chr6_mann_hap4:3256541-3261361 (+	6p21.3	complement factor B
LTV1	1.92	7.09E-05	3.38E-04	chr6:144164481-144184949 (+)	6q24.2	LTV1 ribosome biogenesis factor
DCUN1D5	1.92	1.91E-08	6.81E-07	chr11:102921413-102962944 (-)	11q22.3	DCN1, defective in cullin neddylation 1, domain containing 5
MCM8	1.92	7.14E-08	1.83E-06	chr20:5931298-5975852 (+)	20p12.3	minichromosome maintenance complex component 8
OIP5	1.92	8.65E-10	6.46E-08	chr15:41601466-41624819 (-)	15q15.1	Opa interacting protein 5
TIMM17A	1.92	3.91E-10	3.54E-08	chr1:201924619-201939789 (+)	1q32.1	translocase of inner mitochondrial membrane 17 homolog A (yeast)
SNRPD1	1.91	7.14E-08	1.83E-06	chr18:19192260-19210208 (+)	18q11.2	small nuclear ribonucleoprotein D1 polypeptide 16kDa
RNU6-705P	1.91	1.95E-04	7.68E-04	chr5:180728968-180729071 (+)	---	RNA, U6 small nuclear 705, pseudogene
CYP7B1	1.91	1.10E-08	4.46E-07	chr8:65500320-65711348 (-)	8q21.3	cytochrome P450, family 7, subfamily B, polypeptide 1
KLF7	1.91	9.97E-07	1.28E-05	chr2:207938861-208031991 (-)	2q32	Kruppel-like factor 7 (ubiquitous)
TMPO	1.91	4.85E-10	4.15E-08	chr12:98909290-98944157 (+)	12q22	thymopoietin
LOC101927023	1.91	2.33E-07	4.42E-06	chr5:111563980-111593006 (+)	5q22.2	uncharacterized LOC101927023
NARS	1.91	8.22E-10	6.20E-08	chr18:55267888-55289177 (-)	18q21.31	asparaginyl-tRNA synthetase
IFITM2	1.91	1.48E-04	6.12E-04	chr11:307631-309410 (+)	11p15.5	interferon induced transmembrane protein 2
TRIB2	1.91	1.12E-08	4.51E-07	chr2:12856998-12882860 (+)	2p24.3	tribbles pseudokinase 2
KNSTRN	1.91	1.78E-07	3.64E-06	chr15:40674922-40686489 (+)	15q15.1	kinetochore-localized astrinSPAG5 binding protein
USP41	1.91	2.55E-07	4.72E-06	chr22:20704868-20745048 (-)	22q11.21	ubiquitin specific peptidase 41
TMPRSS4	1.91	5.56E-09	2.63E-07	chr11:117947727-117996323 (+)	11q23.3	transmembrane protease, serine 4
GABRA4	1.91	4.14E-04	1.42E-03	chr4:46920917-46996424 (-)	4p12	gamma-aminobutyric acid (GABA) A receptor, alpha 4
CHI3L2	1.91	2.86E-06	2.81E-05	chr1:111743393-111786062 (+)	1p13.3	chitinase 3-like 2
RB1CC1	1.91	1.82E-03	4.89E-03	chr8:53535016-53658403 (-)	8q11	RB1-inducible coiled-coil 1
MAP4K4	1.90	8.56E-11	1.20E-08	chr2:102123002-102511152 (+)	2q11.2-q12	mitogen-activated protein kinase kinase kinase kinase 4
GNA15	1.90	1.82E-09	1.14E-07	chr19:3136191-3163766 (+)	19p13.3	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
CNTLN	1.90	7.72E-09	3.38E-07	chr9:17134980-17503921 (+)	9p22.2	centlein, centrosomal protein

SLPI	1.90	1.00E-03	2.97E-03	chr20:43880879-43883206 (-)	20q12	secretory leukocyte peptidase inhibitor
PTGR1	1.90	1.76E-09	1.12E-07	chr9:114312002-114362135 (-)	9q31.3	prostaglandin reductase 1
C1QBP	1.90	1.26E-09	8.70E-08	chr17:5336097-5342471 (-)	17p13.3	complement component 1, q subcomponent binding protein
LYAR	1.90	7.26E-10	5.64E-08	chr4:4269428-4291896 (-)	4p16.3	Ly1 antibody reactive
C9orf41	1.90	9.86E-11	1.31E-08	chr9:77595936-77643339 (-)	9q21.13	chromosome 9 open reading frame 41
VPS13A	1.90	9.07E-05	4.12E-04	chr9:79792269-80036457 (+)	9q21	vacuolar protein sorting 13 homolog A (S. cerevisiae)
UTP14A	1.89	3.43E-10	3.22E-08	chrX:129040097-129063738 (+)	Xq26.1	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
FOXN2	1.89	3.95E-10	3.56E-08	chr2:48541776-48606434 (+)	2p22-p16	forkhead box N2
TMF1	1.89	6.26E-04	2.00E-03	chr3:69068978-69101484 (-)	3p21-p12	TATA element modulatory factor 1
FAM157A	1.89	2.91E-07	5.19E-06	chr3:197879237-197955678 (+)	3q29	family with sequence similarity 157, member A
PAK6	1.89	7.07E-10	5.54E-08	chr15:40453210-40569688 (+)	15q14	p21 protein (Cdc42Rac)-activated kinase 6
TUBG1	1.89	4.40E-09	2.20E-07	chr17:40761358-40767256 (+)	17q21	tubulin, gamma 1
ZCCHC6	1.89	2.01E-06	2.14E-05	chr9:88902648-88969402 (-)	9q21	zinc finger, CCHC domain containing 6
PYROXD1	1.89	4.38E-05	2.30E-04	chr12:21590538-21624182 (+)	12p12.1	pyridine nucleotide-disulphide oxidoreductase domain 1
PGD	1.88	4.77E-08	1.37E-06	chr1:10458649-10480233 (+)	1p36.22	phosphogluconate dehydrogenase
GNL3	1.88	1.02E-06	1.30E-05	chr3:52715172-52728510 (+)	3p21.1	guanine nucleotide binding protein-like 3 (nucleolar)
LRRC8B	1.88	4.13E-09	2.08E-07	chr1:89990395-90063423 (+)	1p22.2	leucine rich repeat containing 8 family, member B
RP11-164P12.3	1.88	1.57E-06	1.79E-05	chr4:152595635-152599045 (+)	---	novel transcript, antisense to PET112L
PHACTR2	1.88	3.16E-10	3.07E-08	chr6:143857982-144152322 (+)	6q24.2	phosphatase and actin regulator 2
ACER3	1.88	2.67E-07	4.87E-06	chr11:76571917-76737841 (+)	11q13.5	alkaline ceramidase 3
RABEP1	1.88	5.29E-06	4.49E-05	chr17:5185558-5289132 (+)	17p13.2	rabaptin, RAB GTPase binding effector protein 1
PRKDC	1.88	3.20E-11	5.91E-09	chr8:48685669-48872743 (-)	8q11	protein kinase, DNA-activated, catalytic polypeptide
EIF3A	1.88	1.77E-06	1.95E-05	chr10:120794356-120840396 (-)	10q26	eukaryotic translation initiation factor 3, subunit A
AC106053.1	1.88	4.72E-05	2.45E-04	chr2:18966073-18969018 (+)	---	novel transcript
RP11-49O14.2	1.88	1.06E-04	4.69E-04	chr9:97662711-97667036 (+)	---	novel transcript
DCAF13	1.88	3.65E-08	1.12E-06	chr8:104426942-104455681 (+)	8q22.3	DDB1 and CUL4 associated factor 13
DARS2	1.87	6.54E-11	9.99E-09	chr1:173793641-173827684 (+)	1q25.1	aspartyl-tRNA synthetase 2, mitochondrial
RDX	1.87	2.36E-05	1.41E-04	chr11:110045605-110167447 (-)	11q23	radixin
USMG5	1.87	6.26E-10	5.05E-08	chr10:105148798-105156270 (-)	10q24.33	up-regulated during skeletal muscle growth 5 homolog (mouse)
DGKH	1.87	3.47E-08	1.08E-06	chr13:42614172-42830716 (+)	13q14.11	diacylglycerol kinase, eta
RNU6-162P	1.87	2.99E-06	2.91E-05	chr7:143271839-143271941 (+)	---	RNA, U6 small nuclear 162, pseudogene
PNP	1.86	5.34E-06	4.52E-05	chr14:20937538-20946165 (+)	14q13.1	purine nucleoside phosphorylase
MOXD1	1.86	6.40E-05	3.12E-04	chr6:132617194-132722684 (-)	6q23.2	monooxygenase, DBH-like 1
CWF19L2	1.86	2.12E-04	8.21E-04	chr11:107197071-107328572 (-)	11q22.3	CWF19-like 2, cell cycle control (S. pombe)
RNU6-267P	1.86	3.01E-06	2.91E-05	chr7:143451721-143451823 (-)	---	RNA, U6 small nuclear 267, pseudogene
ANAPC7	1.86	9.51E-13	4.83E-10	chr12:110810705-110841535 (-)	12q24.11	anaphase promoting complex subunit 7
VRK1	1.86	3.41E-06	3.21E-05	chr14:97263641-97347951 (+)	14q32	vaccinia related kinase 1
RP11-242C19.2	1.86	2.90E-08	9.37E-07	chrX:30716324-30740049 (+)	---	novel transcript, sense intronic to GK
MTO1	1.86	1.46E-12	6.33E-10	chr6:74171301-74218959 (+)	6q13	mitochondrial tRNA translation optimization 1
PCNA	1.86	1.47E-09	9.68E-08	chr20:5095599-5107272 (-)	20pter-p12	proliferating cell nuclear antigen
PSMA5	1.86	6.20E-11	9.57E-09	chr1:109941653-109969108 (-)	1p13	proteasome (prosome, macropain) subunit, alpha type, 5
ERI2	1.86	6.94E-11	1.04E-08	chr16:20791515-20817795 (-)	16p12.3	ERI1 exoribonuclease family member 2
HERC5	1.86	4.72E-06	4.11E-05	chr4:89378268-89427314 (+)	4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase 5
EZH2	1.86	3.37E-11	6.15E-09	chr7:148504464-148581441 (-)	7q35-q36	enhancer of zeste 2 polycomb repressive complex 2 subunit
TCERG1	1.85	6.74E-06	5.38E-05	chr5:145826873-145891524 (+)	5q31	transcription elongation regulator 1
WDR3	1.85	8.21E-08	2.04E-06	chr1:118472343-118503049 (+)	1p12	WD repeat domain 3
ZSWIM6	1.85	7.72E-10	5.93E-08	chr5:60628100-60841999 (+)	5q12.1	zinc finger, SWIM-type containing 6
SRSF11	1.85	2.04E-04	7.96E-04	chr1:70671365-70718735 (+)	1p31	serinearginine-rich splicing factor 11
WDR77	1.85	3.29E-12	1.13E-09	chr1:111981260-111991998 (-)	1p13.2	WD repeat domain 77
CRABP2	1.85	1.32E-09	8.98E-08	chr1:156669398-156675608 (-)	1q21.3	cellular retinoic acid binding protein 2
MREG	1.85	8.35E-10	6.28E-08	chr2:216807314-216898819 (-)	2q35	melanoregulin
TRPM6	1.85	4.46E-10	3.91E-08	chr9:77337411-77503010 (-)	9q21.13	transient receptor potential cation channel, subfamily M, member 6
PUS7	1.84	1.92E-08	6.85E-07	chr7:105080108-105162714 (-)	7q22.3	pseudouridylate synthase 7 (putative)
KIAA0586	1.84	1.13E-06	1.40E-05	chr14:58894103-59015549 (+)	14q23.1	KIAA0586
GTPBP4	1.84	7.09E-09	3.17E-07	chr10:1034338-1065876 (+)	10p15-p14	GTP binding protein 4
LRPPRC	1.84	1.30E-07	2.87E-06	chr2:44113363-44223144 (-)	2p21	leucine-rich pentatricopeptide repeat containing
CWC27	1.84	7.23E-06	5.67E-05	chr5:64064755-64314590 (+)	5q12.3	CWC27 spliceosome-associated protein homolog (S. cerevisiae)
ZNF326	1.84	5.84E-06	4.83E-05	chr1:90457722-90494097 (+)	1p22.2	zinc finger protein 326
TRMT6	1.84	3.44E-10	3.22E-08	chr20:5917881-5931182 (-)	20p12.3	tRNA methyltransferase 6 homolog (S. cerevisiae)
NUP107	1.84	9.07E-10	6.70E-08	chr12:69080514-69136785 (+)	12q15	nucleoporin 107kDa
CCT5	1.84	2.81E-10	2.79E-08	chr5:10250033-10266524 (+)	5p15.2	chaperonin containing TCP1, subunit 5 (epsilon)
ZWINT	1.84	1.04E-10	1.34E-08	chr10:58116989-58121036 (-)	10q21-q22	ZW10 interacting kinetochore protein
PARP4	1.84	5.25E-07	7.93E-06	chr13:24995064-25086948 (-)	13q11	poly (ADP-ribose) polymerase family, member 4
CHORDC1	1.84	9.25E-07	1.21E-05	chr11:89933597-89956532 (-)	11q14.3	cysteine and histidine-rich domain (CHORD) containing 1
ANGPTL4	1.84	1.12E-07	2.58E-06	chr19:8429011-8439257 (+)	19p13.3	angiopoietin-like 4
FANCL	1.84	3.11E-07	5.44E-06	chr2:58386378-58468515 (-)	2p16.1	Fanconi anemia, complementation group L
ARID4A	1.83	4.87E-04	1.63E-03	chr14:58765103-58840605 (+)	14q23.1	AT rich interactive domain 4A (RBP1-like)
SYNE2	1.83	6.73E-04	2.13E-03	chr14:64319683-64693167 (+)	14q23.2	spectrin repeat containing, nuclear envelope 2
RACGAP1	1.83	1.20E-08	4.77E-07	chr12:50370706-50419307 (-)	12q13.12	Rac GTPase activating protein 1
NDUFAF2	1.83	1.01E-10	1.31E-08	chr5:60240956-60448864 (+)	5q12.1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2
MTRR	1.83	1.05E-09	7.54E-08	chr5:7851299-7906138 (+)	5p15.31	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
LOC100288069	1.83	1.51E-06	1.74E-05	chr1:694412-714068 (-)	1p36.33	uncharacterized LOC100288069
ZNF518A	1.83	3.13E-05	1.77E-04	chr10:97889472-97923517 (+)	10q24.1	zinc finger protein 518A
RNU6-701P	1.83	1.38E-04	5.79E-04	chr5:118474554-118474660 (+)	---	RNA, U6 small nuclear 701, pseudogene
BPTF	1.83	3.83E-05	2.07E-04	chr17:65821637-65980494 (+)	17q24.3	bromodomain PHD finger transcription factor
CNDP2	1.83	1.07E-09	7.64E-08	chr18:72163443-72190689 (+)	18q22.3	CNDP dipeptidase 2 (metallopeptidase M20 family)
UGT1A1	1.83	8.97E-05	4.08E-04	chr2:234526291-234681956 (+)	2q37	UDP glucuronosyltransferase 1 family, polypeptide A1
DDX52	1.83	1.11E-09	7.84E-08	chr17:35969826-36003493 (-)	17q21.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
COBLL1	1.83	1.54E-06	1.76E-05	chr2:165510134-165700189 (-)	2q24.3	cordon-bleu WH2 repeat protein-like 1
COL12A1	1.83	1.08E-05	7.70E-05	chr6:75794042-75915767 (-)	6q12-q13	collagen, type XII, alpha 1
C18orf54	1.83	1.25E-08	4.93E-07	chr18:51884955-51908404 (+)	18q21.2	chromosome 18 open reading frame 54
DCAF13P3	1.83	5.29E-07	7.99E-06	chr15:51236326-51238762 (+)	15q21.2	DDB1 and CUL4 associated factor 13 pseudogene 3
LOC101928670	1.83	1.47E-06	1.70E-05	chr1:164405-173864 (-)	---	uncharacterized LOC101928670
CNTRL	1.83	3.33E-08	1.04E-06	chr9:123837141-123939888 (+)	9q33.2	centriolin
STON2	1.83	7.04E-10	5.53E-08	chr14:81726994-81893748 (-)	14q31.1	stonin 2
RABGGTB	1.83	3.66E-08	1.12E-06	chr1:76251879-76261100 (+)	1p31	Rab geranylgeranyltransferase, beta subunit
CTC-428G20.3	1.82	4.49E-07	7.05E-06	chr5:114539713-114541943 (-)	---	novel transcript
NOL10	1.82	5.18E-07	7.85E-06	chr2:10710892-10830112 (-)	2p25.1	nucleolar protein 10
UTP6	1.82	1.12E-10	1.42E-08	chr17:30187923-30228731 (-)	17q11.2	UTP6, small subunit (SSU) processome component, homolog (yeast)
MFN1	1.82	1.02E-07	2.41E-06	chr3:179065480-179112719 (+)	3q26.33	mitofusin 1
APC	1.82	1.65E-04	6.68E-04	chr5:112043195-112181936 (+)	5q21-q22	adenomatous polyposis coli
GCH1	1.82	4.79E-11	8.04E-09	chr14:55308724-55369570 (-)	14q22.1-q22.2	GTP cyclohydrolase 1
SMC1A	1.82	1.44E-06	1.68E-05	chrX:53401070-53449677 (-)	Xp11.22-p11.21	structural maintenance of chromosomes 1A
UCHL3	1.82	6.95E-09	3.11E-07	chr13:76123619-76180085 (+)	13q22.2	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
NFKB1	1.82	1.09E-12	5.26E-10	chr4:103422486-103538459 (+)	4q24	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
TMEM14A	1.82	2.23E-06	2.32E-05	chr6:52535884-52551386 (+)	6p12.2	transmembrane protein 14A
PGAM1	1.82	9.67E-10	7.02E-08	chr10:99185917-99193198 (+)	10q25.3	phosphoglycerate mutase 1 (brain)
RDH11	1.82	2.21E-07	4.27E-06	chr14:68143518-68162531 (-)	11-cis)	retinol dehydrogenase 11 (all-trans9-cis
CKS2	1.82	9.78E-07	1.26E-05	chr9:91926113-91931618 (+)	9q22	CDC28 protein kinase regulatory subunit 2
NUP62CL	1.82	8.67E-12	2.24E-09	chrX:106366657-106449670 (-)	Xq22.3	nucleoporin 62kDa C-terminal like
NKTR	1.82	4.78E-04	1.61E-03	chr3:42642106-42690233 (+)	3p22.1	natural killer cell triggering receptor
RP11-259O2.3	1.82	4.16E-05	2.21E-04	chr5:1968208-1969127 (+)	---	putative novel transcript
NFXL1	1.82	2.46E-08	8.29E-07	chr4:47849257-47916680 (-)	4p12	nuclear transcription factor, X-box binding-like 1
TTF2	1.82	1.39E-10	1.66E-08	chr1:117602925-117645492 (+)	1p22	transcription termination factor, RNA polymerase II
MRPS7	1.82	2.34E-09	1.38E-07	chr17:73257749-73262457 (+)	17q25	mitochondrial ribosomal protein S7
DUOXA1	1.82	3.50E-10	3.26E-08	chr15:45409569-45422078 (-)	15q21.1	dual oxidase maturation factor 1
MAD2L1	1.82	2.26E-09	1.34E-07	chr4:120980577-120988229 (-)	4q27	MAD2 mitotic arrest deficient-like 1 (yeast)
HSPA8	1.82	2.90E-08	9.37E-07	chr11:122928197-122933188 (-)	11q24.1	heat shock 70kDa protein 8
IARS	1.81	1.67E-09	1.07E-07	chr9:94972489-95056038 (-)	9q21	isoleucyl-tRNA synthetase
SLC16A6P1	1.81	4.74E-09	2.33E-07	chr17:62950242-62952716 (+)	---	SLC16A6 pseudogene 1
CASP7	1.81	2.90E-09	1.60E-07	chr10:115438935-115490664 (+)	10q25	caspase 7, apoptosis-related cysteine peptidase
GOLGA8A	1.81	2.26E-05	1.36E-04	chr15:34671265-34729667 (-)	15q11.2	golgin A8 family, member A
UQCRHL	1.81	2.05E-09	1.25E-07	chr1:16133657-16134194 (-)	1p36.21	ubiquinol-cytochrome c reductase hinge protein-like
NASP	1.81	1.53E-08	5.74E-07	chr1:46049518-46084578 (+)	1p34.1	nuclear autoantigenic sperm protein (histone-binding)
SLC16A1	1.81	2.84E-06	2.80E-05	chr1:113454469-113499635 (-)	1p12	solute carrier family 16 (monocarboxylate transporter), member 1
RPS15AP10	1.81	7.94E-04	2.45E-03	chr1:46111452-46112357 (-)	1p34.1	ribosomal protein S15a pseudogene 10
GPATCH4	1.81	9.86E-11	1.31E-08	chr1:156564100-156571302 (-)	1q22	G patch domain containing 4
UGGT2	1.81	4.50E-07	7.06E-06	chr13:96453834-96705736 (-)	13q32.1	UDP-glucose glycoprotein glucosyltransferase 2
LOC730378	1.81	8.90E-06	6.67E-05	chr19:205025-205055 (-)	---	uncharacterized LOC730378
PSMB6	1.81	2.81E-08	9.18E-07	chr17:4699439-4701798 (+)	17p13	proteasome (prosome, macropain) subunit, beta type, 6
CIT	1.81	6.65E-08	1.74E-06	chr12:120123595-120315095 (-)	12q24	citron rho-interacting serinethreonine kinase
LOC100132062	1.81	1.13E-06	1.40E-05	chr7:45847217-45847251 (+)	5q35.3	uncharacterized LOC100132062
XPOT	1.81	9.06E-09	3.83E-07	chr12:64798130-64844907 (+)	12q14.2	exportin, tRNA
PLEKHG7	1.81	1.04E-07	2.43E-06	chr12:93115281-93166231 (+)	12q22	pleckstrin homology domain containing, family G (with RhoGef domain) member 7
ZDBF2	1.81	4.88E-09	2.38E-07	chr2:207139387-207179148 (+)	2q33.3	zinc finger, DBF-type containing 2
IWS1	1.80	2.38E-09	1.40E-07	chr2:128193783-128284462 (-)	2q14.3	IWS1 homolog (S. cerevisiae)
NCAPD2	1.80	1.02E-05	7.39E-05	chr12:6602545-6641132 (+)	12p13.3	non-SMC condensin I complex, subunit D2
NCBP1	1.80	3.87E-11	6.80E-09	chr9:100395705-100436030 (+)	9q34.1	nuclear cap binding protein subunit 1, 80kDa
ZNF638	1.80	1.98E-04	7.76E-04	chr2:71503691-71662199 (+)	2p13.1	zinc finger protein 638
CSTA	1.80	7.62E-07	1.04E-05	chr3:122044011-122060819 (+)	3q21	cystatin A (stefin A)
CSNK1A1	1.80	3.74E-11	6.64E-09	chr5:148871760-148931007 (-)	5q32	casein kinase 1, alpha 1
NAV1	1.80	2.70E-09	1.53E-07	chr1:201592411-201796102 (+)	1q32.3	neuron navigator 1
COA7	1.80	7.88E-10	6.02E-08	chr1:53152014-53164038 (-)	1p32.3	cytochrome c oxidase assembly factor 7 (putative)
ATP13A3	1.80	2.22E-05	1.34E-04	chr3:194123401-194219093 (-)	3q29	ATPase type 13A3
ZFYVE16	1.80	1.38E-06	1.62E-05	chr5:79703832-79775498 (+)	5q14	zinc finger, FYVE domain containing 16
GOLGA8B	1.80	2.10E-05	1.28E-04	chr15:34817408-34875771 (-)	15q14	golgin A8 family, member B
POLE2	1.80	2.68E-11	5.23E-09	chr14:50110270-50155140 (-)	14q21-q22	polymerase (DNA directed), epsilon 2, accessory subunit
PIGW	1.80	2.90E-08	9.38E-07	chr17:34890847-34895150 (+)	17q12	phosphatidylinositol glycan anchor biosynthesis, class W
LARS	1.80	6.91E-10	5.47E-08	chr5:145492589-145562294 (-)	5q32	leucyl-tRNA synthetase
SRD5A3	1.80	3.64E-08	1.12E-06	chr4:56212276-56239266 (+)	4q12	steroid 5 alpha-reductase 3
ENOSF1	1.80	9.36E-08	2.25E-06	chr18:670324-712676 (-)	18p11.32	enolase superfamily member 1
TYMS	1.80	3.46E-09	1.82E-07	chr18:657604-673578 (+)	18p11.32	thymidylate synthetase
CCT2	1.80	4.31E-08	1.27E-06	chr12:69979114-69995357 (+)	12q15	chaperonin containing TCP1, subunit 2 (beta)
RAB11B-AS1	1.80	4.00E-08	1.20E-06	chr19:8439260-8455575 (-)	---	RAB11B antisense RNA 1
SLC16A6	1.80	1.05E-08	4.28E-07	chr17:66263167-66287405 (-)	17q24.2	solute carrier family 16, member 6
SEL1L3	1.80	4.19E-07	6.72E-06	chr4:25749049-25865382 (-)	4p15.2	sel-1 suppressor of lin-12-like 3 (C. elegans)
ARHGAP21	1.80	1.46E-06	1.69E-05	chr10:24872538-25012597 (-)	10p12.1|10p12.3	Rho GTPase activating protein 21
CDCA7	1.80	3.59E-08	1.11E-06	chr2:174219548-174233725 (+)	2q31	cell division cycle associated 7
BLZF1	1.80	2.34E-07	4.43E-06	chr1:169337194-169365780 (+)	1q24	basic leucine zipper nuclear factor 1
AC104088.1	1.80	6.91E-06	5.49E-05	chr2:173180015-173188465 (+)	---	novel transcript
PCCA	1.80	5.45E-09	2.59E-07	chr13:100741269-101182691 (+)	13q32	propionyl CoA carboxylase, alpha polypeptide
MAOB	1.80	4.43E-05	2.33E-04	chrX:43625857-43741721 (-)	Xp11.23	monoamine oxidase B
FOXE1	1.79	1.76E-08	6.40E-07	chr9:100615536-100618997 (+)	9q22	forkhead box E1 (thyroid transcription factor 2)
DCLRE1C	1.79	1.96E-10	2.14E-08	chr10:14939358-15063862 (-)	10p13	DNA cross-link repair 1C
PPP1R12A	1.79	3.37E-03	8.26E-03	chr12:80167343-80329240 (-)	12q15-q21	protein phosphatase 1, regulatory subunit 12A
BAZ1B	1.79	2.84E-08	9.24E-07	chr7:72854728-72936615 (-)	7q11.23	bromodomain adjacent to zinc finger domain, 1B
RNU7-96P	1.79	5.70E-04	1.85E-03	chr2:98529517-98529580 (-)	---	RNA, U7 small nuclear 96 pseudogene
LRP8	1.79	2.98E-08	9.58E-07	chr1:53708041-53793821 (-)	1p34	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
SLC35B4	1.79	1.30E-10	1.60E-08	chr7:133974084-134001827 (-)	7q33	solute carrier family 35 (UDP-xyloseUDP-N-acetylglucosamine transporter), member B4
UTP11L	1.79	1.15E-11	2.71E-09	chr1:38474930-38490497 (+)	1p34.3	UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)

FH	1.79	2.00E-08	7.07E-07	chr1:241660857-241683085 (-)	1q42.1	fumarate hydratase
TMEM171	1.79	6.95E-05	3.33E-04	chr5:72416119-72427644 (+)	5q13.2	transmembrane protein 171
CWH43	1.79	5.11E-08	1.44E-06	chr4:48988264-49064098 (+)	4p11	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
NEK1	1.79	2.11E-09	1.28E-07	chr4:170314421-170533780 (-)	4q33	NIMA-related kinase 1
PARP12	1.79	6.77E-07	9.61E-06	chr7:139723544-139763521 (-)	7q34	poly (ADP-ribose) polymerase family, member 12
PPIC	1.79	1.11E-10	1.41E-08	chr5:122358945-122372436 (-)	5q23.2	peptidylprolyl isomerase C (cyclophilin C)
TAP2	1.79	2.27E-10	2.35E-08	chr6:32789610-32806557 (-)	6p21.3	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
TMX3	1.79	5.83E-08	1.58E-06	chr18:66340925-66382362 (-)	18q22	thioredoxin-related transmembrane protein 3
LTBP1	1.79	4.84E-03	1.12E-02	chr2:33172039-33624576 (+)	2q22-q21	latent transforming growth factor beta binding protein 1
IL36RN	1.79	3.60E-03	8.74E-03	chr2:113816215-113822959 (+)	2q14	interleukin 36 receptor antagonist
AGPAT4	1.78	5.93E-05	2.94E-04	chr6:161551011-161695107 (-)	6q26	1-acylglycerol-3-phosphate O-acyltransferase 4
UBE2F	1.78	2.52E-12	9.51E-10	chr2:238875469-238951423 (+)	2q37.3	ubiquitin-conjugating enzyme E2F (putative)
CCNE2	1.78	5.07E-08	1.43E-06	chr8:95891998-95908906 (-)	8q22.1	cyclin E2
CHD9	1.78	1.49E-03	4.15E-03	chr16:53088945-53361414 (+)	16q12.2	chromodomain helicase DNA binding protein 9
PPIF	1.78	5.22E-06	4.44E-05	chr10:81107220-81115093 (+)	10q22-q23	peptidylprolyl isomerase F
SOX7	1.78	3.06E-08	9.75E-07	chr8:10581278-10588022 (-)	8p23.1	SRY (sex determining region Y)-box 7
FANCM	1.78	1.02E-05	7.37E-05	chr14:45605136-45670093 (+)	14q21.2	Fanconi anemia, complementation group M
TAF1D	1.78	2.90E-07	5.18E-06	chr11:93463438-93475111 (-)	11q21	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa
RNU7-124P	1.78	2.55E-05	1.50E-04	chr9:37936704-37936765 (-)	---	RNA, U7 small nuclear 124 pseudogene
CEP135	1.78	1.41E-06	1.65E-05	chr4:56815037-56899527 (+)	4q12	centrosomal protein 135kDa
CTAGE15	1.78	6.76E-04	2.14E-03	chr7:143268819-143271480 (+)	7q35	CTAGE family, member 15
ENO1	1.78	5.39E-11	8.76E-09	chr1:8921059-9288096 (-)	1p36.2	enolase 1, (alpha)
SLC16A10	1.78	4.48E-07	7.04E-06	chr6:111408706-111545145 (+)	6q21-q22	solute carrier family 16 (aromatic amino acid transporter), member 10
TWF1	1.78	1.26E-08	4.94E-07	chr12:44187526-44200178 (-)	12q12	twinfilin actin-binding protein 1
TUBG2	1.78	6.94E-11	1.04E-08	chr17:40811266-40819024 (+)	17q21	tubulin, gamma 2
CAPN2	1.78	5.93E-06	4.89E-05	chr1:223889295-223963720 (+)	1q41-q42	calpain 2, (mll) large subunit
FAM133B	1.78	1.67E-06	1.87E-05	chr7:92190072-92219708 (-)	7q21.2	family with sequence similarity 133, member B
E2F3-IT1	1.78	4.45E-08	1.30E-06	chr6:20438052-20440409 (+)	---	E2F3 intronic transcript 1 (non-protein coding)
WDR12	1.78	2.25E-09	1.33E-07	chr2:203744993-203879521 (-)	2q33.2	WD repeat domain 12
SUB1	1.78	1.16E-08	4.64E-07	chr5:32531739-32604185 (+)	5p13.3	SUB1 homolog (S. cerevisiae)
HNRNPA2B1	1.77	5.16E-10	4.36E-08	chr7:26229547-26241149 (-)	7p15	heterogeneous nuclear ribonucleoprotein A2/B1
RPAP3	1.77	4.46E-04	1.51E-03	chr12:48055715-48099844 (-)	12q13.11	RNA polymerase II associated protein 3
PTPN2	1.77	1.32E-09	8.96E-08	chr18:12785477-12884337 (-)	18p11.3-p11.2	protein tyrosine phosphatase, non-receptor type 2
MRS2	1.77	1.66E-08	6.13E-07	chr6:24403153-24425816 (+)	6p22.3-p22.1	MRS2 magnesium transporter
ATP1A1	1.77	1.30E-06	1.55E-05	chr1:116915004-116952883 (+)	1p21	ATPase, Na+/K+ transporting, alpha 1 polypeptide
PDCD5	1.77	3.43E-09	1.80E-07	chr19:33072094-33078358 (+)	19q13.11	programmed cell death 5
CASK	1.77	6.48E-07	9.32E-06	chrX:41374187-41782716 (-)	Xp11.4	calciumcalmodulin-dependent serine protein kinase (MAGUK family)
BMS1P15	1.77	5.18E-07	7.86E-06	chr15:20362688-20364420 (+)	15q11.1	BMS1 pseudogene 15
DNAJC7	1.77	5.43E-09	2.58E-07	chr17:40128439-40169715 (-)	17q11.2	DnaJ (Hsp40) homolog, subfamily C, member 7
CCDC14	1.77	4.52E-05	2.36E-04	chr3:123616152-123680564 (-)	3q21.1	coiled-coil domain containing 14
MID1	1.77	4.51E-09	2.24E-07	chrX:10413350-10851809 (-)	Xp22	midline 1
ABCE1	1.77	1.28E-06	1.53E-05	chr4:146019084-146050676 (+)	4q31	ATP-binding cassette, sub-family E (OABP), member 1
MARS	1.77	1.72E-08	6.30E-07	chr12:57881077-57911334 (+)	12q13.3	methionyl-tRNA synthetase
TRIM38	1.77	3.70E-07	6.12E-06	chr6:25963030-25985352 (+)	6p21.3	tripartite motif containing 38
NEIL3	1.76	1.51E-05	9.90E-05	chr4:178230990-178284097 (+)	4q34.3	nei endonuclease VIII-like 3 (E. coli)
IFNE	1.76	2.51E-04	9.43E-04	chr9:21480838-21482312 (-)	9p21.3	interferon, epsilon
SLC25A5	1.76	2.29E-10	2.36E-08	chrX:118602363-118605359 (+)	Xq24	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
AHCTF1	1.76	3.06E-05	1.73E-04	chr1:247002400-247095280 (-)	1q44	AT hook containing transcription factor 1
MPHOSPH8	1.76	1.68E-06	1.87E-05	chr13:20207788-20247599 (+)	13q12.11	M-phase phosphoprotein 8
MYD88	1.76	2.41E-08	8.16E-07	chr3:38179969-38184513 (+)	3p22	myeloid differentiation primary response 88
HSPA9	1.76	1.17E-08	4.67E-07	chr5:137890571-137911318 (-)	5q31.1	heat shock 70kDa protein 9 (mortalin)
C10orf113	1.76	1.20E-05	8.31E-05	chr10:21414692-21435488 (-)	10p12.31	chromosome 10 open reading frame 113
PEX3	1.76	3.10E-07	5.42E-06	chr6:143771918-143811753 (+)	6q24.2	peroxisomal biogenesis factor 3
CXCR2	1.76	1.13E-06	1.40E-05	chr2:218990012-219001976 (+)	2q35	chemokine (C-X-C motif) receptor 2
NEAT1	1.76	6.81E-05	3.28E-04	chr11:65190269-65213011 (+)	11q13.1	nuclear paraspeckle assembly transcript 1 (non-protein coding)
CCDC138	1.76	4.71E-07	7.33E-06	chr2:109403213-109493034 (+)	2q12.3	coiled-coil domain containing 138
GSTA4	1.76	1.16E-08	4.61E-07	chr6:52842746-52860178 (-)	6p12.1	glutathione S-transferase alpha 4
MED8	1.76	5.55E-07	8.27E-06	chr1:43849588-43855483 (-)	1p34.2	mediator complex subunit 8
PRSS12	1.76	1.37E-06	1.61E-05	chr4:119201193-119274158 (-)	4q28.1	protease, serine, 12 (neurotrypsin, motopsin)
GGCT	1.76	2.53E-06	2.55E-05	chr7:30536237-30544460 (-)	7p15-p14	gamma-glutamylcyclotransferase
DENND1B	1.75	3.15E-11	5.87E-09	chr1:197473878-197744826 (-)	1q31.3	DENNMADD domain containing 1B
COX5A	1.75	5.32E-09	2.54E-07	chr15:75212132-75230509 (-)	15q24.1	cytochrome c oxidase subunit Va
FAM126A	1.75	2.80E-05	1.62E-04	chr7:22980878-23053770 (-)	7p15.3	family with sequence similarity 126, member A
HSP90AA1	1.75	1.17E-05	8.17E-05	chr14:102547075-102606086 (-)	14q32.33	heat shock protein 90kDa alpha (cytosolic), class A member 1
AHI1	1.75	1.11E-05	7.85E-05	chr6:135604670-135830219 (-)	6q23.3	Abelson helper integration site 1
LIPG	1.75	1.19E-04	5.13E-04	chr18:47088427-47119278 (+)	18q21.1	lipase, endothelial
NEK2	1.75	3.77E-08	1.14E-06	chr1:211831599-211848972 (-)	1q32.3	NIMA-related kinase 2
TTC13	1.75	8.85E-08	2.16E-06	chr1:231041987-231114621 (-)	1q42.2	tetratricopeptide repeat domain 13
FLJ25917	1.75	7.77E-05	3.63E-04	chrX:45707327-45710920 (-)	Xp11.3	uncharacterized LOC401585
BDH1	1.75	1.98E-10	2.15E-08	chr3:197236654-197300194 (-)	3q29	3-hydroxybutyrate dehydrogenase, type 1
TSEN15	1.75	1.71E-10	1.93E-08	chr1:184020811-184043346 (+)	1q25	TSEN15 tRNA splicing endonuclease subunit
ECHDC1	1.75	4.09E-08	1.22E-06	chr6:127609855-127664754 (-)	6q22.33	enoyl CoA hydratase domain containing 1
FAM129A	1.75	6.66E-08	1.74E-06	chr1:184759858-184943682 (-)	1q25	family with sequence similarity 129, member A
MRPL32	1.75	1.26E-09	8.70E-08	chr7:42971799-42988557 (+)	7p14	mitochondrial ribosomal protein L32
SUCO	1.75	2.59E-06	2.61E-05	chr1:172501489-172580973 (+)	1q24	SUN domain containing ossification factor
MCM3	1.75	1.37E-08	5.28E-07	chr6:52128807-52149582 (-)	6p12	minichromosome maintenance complex component 3
SESTD1	1.75	1.04E-07	2.44E-06	chr2:179966419-180129517 (-)	2q31.2	SEC14 and spectrin domains 1
ORC1	1.75	5.26E-11	8.56E-09	chr1:52838501-52870143 (-)	1p32	origin recognition complex, subunit 1
MCTP2	1.74	1.27E-10	1.57E-08	chr15:94774767-95027181 (+)	15q26.2	multiple C2 domains, transmembrane 2
CSRP2	1.74	2.01E-06	2.14E-05	chr12:77252495-77272840 (-)	12q21.1	cysteine and glycine-rich protein 2
KPNB1	1.74	2.92E-10	2.87E-08	chr17:45726842-45761004 (+)	17q21.32	karyopherin (importin) beta 1
GPR135	1.74	1.09E-05	7.72E-05	chr14:59927483-59932060 (-)	14q23.1	G protein-coupled receptor 135
ROBO1	1.74	2.95E-08	9.50E-07	chr3:78646388-79817059 (-)	3p12	roundabout, axon guidance receptor, homolog 1 (Drosophila)
PNPO	1.74	1.89E-10	2.07E-08	chr17:46018889-46026674 (+)	17q21.32	pyridoxamine 5-phosphate oxidase
TAS2R30	1.74	1.20E-02	2.43E-02	chr12:11285557-11287243 (-)	12p13.2	taste receptor, type 2, member 30
ADAM10	1.74	2.14E-09	1.29E-07	chr15:58887403-59042177 (-)	15q22	ADAM metallopeptidase domain 10
CERS3	1.74	2.21E-07	4.27E-06	chr15:100940600-101084925 (-)	15q26.3	ceramide synthase 3
CTSB	1.74	6.65E-08	1.74E-06	chr8:11700033-11725738 (-)	8p22	cathepsin B
ATP1B1	1.74	3.03E-05	1.72E-04	chr1:169074935-169101960 (+)	1q24	ATPase, Na+/K+ transporting, beta 1 polypeptide
SKP2	1.74	2.56E-09	1.47E-07	chr5:36152091-36184421 (+)	5p13	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase
RNF168	1.74	5.86E-09	2.73E-07	chr3:196195654-196230639 (-)	3q29	ring finger protein 168, E3 ubiquitin protein ligase
STAG3L4	1.74	6.61E-07	9.45E-06	chr7:66767608-66786513 (+)	7p11.2-q11.2	stromal antigen 3-like 4 (pseudogene)
PLA2G3	1.74	6.42E-07	9.25E-06	chr22:31530793-31536593 (-)	22q12.2	phospholipase A2, group III
CEACAM5	1.74	1.26E-03	3.59E-03	chr19:42212504-42234437 (+)	19q13.1-q13.2	carcinoembryonic antigen-related cell adhesion molecule 5
CCDC144A	1.74	6.46E-05	3.14E-04	chr17:16592851-16681195 (+)	17p11.2	coiled-coil domain containing 144A
USP47	1.74	4.84E-05	2.50E-04	chr11:11862970-11980872 (+)	11p15.3	ubiquitin specific peptidase 47
PSMA6	1.74	3.20E-08	1.01E-06	chr14:35747839-35786699 (+)	14q13	proteasome (prosome, macropain) subunit, alpha type, 6
GINS2	1.74	3.30E-09	1.75E-07	chr16:85709804-85722605 (-)	16q24.1	GINS complex subunit 2 (Psf2 homolog)
ACTR3C	1.74	1.61E-09	1.04E-07	chr7:149941005-150020814 (-)	7q36.1	ARP3 actin-related protein 3 homolog C (yeast)
MSH3	1.74	7.95E-07	1.08E-05	chr5:79950294-80172634 (+)	5q11-q12	mutS homolog 3
CHEK1	1.73	1.67E-10	1.90E-08	chr11:125495031-125546150 (+)	11q24.2	checkpoint kinase 1
USP14	1.73	1.23E-07	2.78E-06	chr18:158483-213739 (+)	18p11.32	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
SQRDL	1.73	2.19E-08	7.58E-07	chr15:45923346-45983492 (+)	15q15	sulfide quinone reductase-like (yeast)
ZNF252P	1.73	3.91E-08	1.18E-06	chr8:146198975-146228285 (-)	8q24.3	zinc finger protein 252, pseudogene
FBXO22	1.73	4.32E-08	1.27E-06	chr15:76196200-76227609 (+)	15q24.2	F-box protein 22
GLMN	1.73	5.56E-07	8.27E-06	chr1:92711955-92764566 (-)	1p22.1	glomulin, FKBP associated protein
FLOT2	1.73	1.59E-07	3.35E-06	chr17:27206353-27224715 (-)	17q11-q12	flotillin 2
UGGT1	1.73	1.11E-10	1.41E-08	chr2:128848754-128953251 (+)	2q14.3	UDP-glucose glycoprotein glucosyltransferase 1
NUP88	1.73	1.46E-09	9.63E-08	chr17:5289346-5323059 (-)	17p13.2	nucleoporin 88kDa
DONSON	1.73	3.26E-12	1.13E-09	chr21:34931848-34961267 (-)	21q22.1	downstream neighbor of SON
SUCLG1	1.73	2.83E-09	1.58E-07	chr2:84650647-84687169 (-)	2p11.2	succinate-CoA ligase, alpha subunit
ACLY	1.73	1.05E-06	1.33E-05	chr17:40023161-40075272 (-)	17q21.2	ATP citrate lyase
PRKY	1.73	8.45E-03	1.81E-02	chrY:7142013-7249589 (+)	Yp11.2	protein kinase, Y-linked, pseudogene
PGAM4	1.73	4.88E-09	2.38E-07	chrX:77223458-77225135 (-)	Xq13	phosphoglycerate mutase family member 4
RP11-107M16.2	1.73	1.16E-04	5.03E-04	chr1:152178334-152179533 (+)	---	novel transcript
GRHL3	1.73	4.17E-05	2.22E-04	chr1:24645812-24690972 (+)	1p36.11	grainyhead-like 3 (Drosophila)
FAM178A	1.73	3.80E-06	3.49E-05	chr10:102672326-102724893 (+)	10q24.31	family with sequence similarity 178, member A
PDHA1	1.73	1.24E-10	1.55E-08	chrX:19362011-19379825 (+)	Xp22.1	pyruvate dehydrogenase (lipoamide) alpha 1
HSP90AA4P	1.73	9.04E-06	6.74E-05	chr4:190394299-190396344 (+)	4q35.2	heat shock protein 90kDa alpha (cytosolic), class A member 4, pseudogene
RBM28	1.73	4.05E-09	2.05E-07	chr7:127950436-127983962 (-)	7q32.1	RNA binding motif protein 28
GALNT3	1.72	4.81E-10	4.13E-08	chr2:166604101-166651192 (-)	2q24-q31	polypeptide N-acetylgalactosaminyltransferase 3
PLSCR4	1.72	1.37E-07	2.99E-06	chr3:145910124-145968966 (-)	3q24	phospholipid scramblase 4
ATP1B3	1.72	6.71E-11	1.02E-08	chr3:141594966-141645382 (+)	3q23	ATPase, Na+/K+ transporting, beta 3 polypeptide
AGL	1.72	6.73E-08	1.75E-06	chr1:100315640-100389579 (+)	1p21	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase
EIF5	1.72	3.99E-09	2.03E-07	chr14:103800339-103811362 (+)	14q32.32	eukaryotic translation initiation factor 5
TTC3	1.72	1.43E-03	4.00E-03	chr21:38445526-38575413 (+)	21q22.2	tetratricopeptide repeat domain 3
RRM1	1.72	7.89E-10	6.02E-08	chr11:4115924-4223885 (+)	11p15.5	ribonucleotide reductase M1
RP13-348B13.2	1.72	2.35E-02	4.34E-02	chrX:88678737-88701982 (+)	---	novel transcript
RNASSP385	1.72	5.16E-04	1.71E-03	chr14:52159470-52159579 (+)	---	RNA, 5S ribosomal pseudogene 385
HIST1H3F	1.72	8.75E-05	4.00E-04	chr6:26250369-26250835 (-)	6p22.2	histone cluster 1, H3f
NDUFAF4	1.72	1.18E-08	4.69E-07	chr6:97337187-97345767 (-)	6q16.1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4
ADAM9	1.72	1.45E-07	3.13E-06	chr8:38854388-38962779 (+)	8p11.22	ADAM metallopeptidase domain 9
SPC25	1.72	7.29E-10	5.65E-08	chr2:169690645-169769881 (-)	2q31.1	SPC25, NDC80 kinetochore complex component
ACAP2-IT1	1.72	1.63E-03	4.47E-03	chr3:195001452-195003470 (-)	---	ACAP2 intronic transcript 1 (non-protein coding)
KCNK10	1.72	9.95E-09	4.11E-07	chr14:88646452-88793256 (-)	14q31.3	potassium channel, subfamily K, member 10
UBXN8	1.72	5.26E-10	4.43E-08	chr8:30589764-30624522 (+)	8p12-p11.2	UBX domain protein 8
FGFR1OP	1.72	1.37E-10	1.65E-08	chr6:167412670-167455906 (+)	6q27	FGFR1 oncogene partner
MARK3	1.72	2.10E-08	7.34E-07	chr14:103851701-103970168 (+)	14q32.32	MAP/microtubule affinity-regulating kinase 3
IFITM4P	1.71	3.60E-06	3.34E-05	chr6_cox_hap2:1234756-1235098 (-)	6p22.1	interferon induced transmembrane protein 4 pseudogene
SKA2	1.71	3.78E-06	3.47E-05	chr17:57187308-57232800 (-)	17q22	spindle and kinetochore associated complex subunit 2
CDC5L	1.71	3.02E-05	1.71E-04	chr6:44355251-44418163 (+)	6p21	cell division cycle 5-like
TGS1	1.71	6.13E-06	5.01E-05	chr8:56685701-56738007 (+)	8q11	trimethylguanosine synthase 1
ACADM	1.71	1.11E-08	4.48E-07	chr1:76190036-76229364 (+)	1p31	acyl-CoA dehydrogenase, C-4 to C-12 straight chain
CASP1	1.71	6.48E-07	9.31E-06	chr11:104896235-104972158 (-)	11q23	caspase 1, apoptosis-related cysteine peptidase
SMCHD1	1.71	3.41E-05	1.89E-04	chr18:2655886-2805015 (+)	18p11.32	structural maintenance of chromosomes flexible hinge domain containing 1
EIF4A1P2	1.71	2.53E-07	4.69E-06	chrY:5205788-5206981 (-)	---	eukaryotic translation initiation factor 4A1 pseudogene 2
MRPL47	1.71	3.34E-07	5.70E-06	chr3:179306073-179322442 (-)	3q26.33	mitochondrial ribosomal protein L47
LOC100506100	1.71	4.85E-07	7.49E-06	chr9:131486724-131495473 (+)	---	uncharacterized LOC100506100
HMGCS1	1.71	2.28E-04	8.70E-04	chr5:43289493-43313614 (-)	5p14-p13	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)
PCM1	1.71	1.80E-03	4.85E-03	chr8:17780349-17887457 (+)	8p22-p21.3	pericentriolar material 1
CASP8	1.71	1.61E-09	1.04E-07	chr2:202098166-202152434 (+)	2q33-q34	caspase 8, apoptosis-related cysteine peptidase
ZNF215	1.71	2.49E-04	9.36E-04	chr11:69476635-70058863 (+)	11p15.4	zinc finger protein 215
GYS1	1.71	4.04E-09	2.05E-07	chr19:49471382-49496610 (-)	19q13.3	glycogen synthase 1 (muscle)
GAS2L3	1.71	2.77E-06	2.75E-05	chr12:100967461-101018697 (+)	12q23.1	growth arrest-specific 2 like 3
UBE2T	1.71	9.08E-11	1.26E-08	chr1:202300785-202311108 (-)	1q32.1	ubiquitin-conjugating enzyme E2T (putative)
AP5M1	1.71	5.99E-10	4.91E-08	chr14:57735606-57756797 (+)	14q22.3	adaptor-related protein complex 5, mu 1 subunit
FAM83D	1.71	1.61E-06	1.82E-05	chr20:37554955-37581703 (+)	20q11.23	family with sequence similarity 83, member D
TOP2B	1.71	7.05E-04	2.21E-03	chr3:25639475-25706430 (-)	3p24	topoisomerase (DNA) II beta 180kDa
SFXN1	1.71	6.57E-13	3.86E-10	chr5:174904065-174956745 (+)	5q35.3	sideroflexin 1
WBP5	1.71	9.38E-06	6.93E-05	chrX:102611373-102613397 (+)	Xq22.2	WW domain binding protein 5

RFC4	1.70	1.69E-11	3.65E-09	chr3:186507669-186524847 (-)	3q27	replication factor C (activator 1) 4, 37kDa
HIST1H4K	1.70	4.88E-08	1.39E-06	chr6:27798952-27799306 (-)	6p22.1	histone cluster 1, H4k
REV1	1.70	1.89E-09	1.17E-07	chr2:100016938-100106497 (-)	2q11.1-q11.2	REV1, polymerase (DNA directed)
IMMT	1.70	1.37E-10	1.65E-08	chr2:86371055-86422893 (-)	2p11.2|2	inner membrane protein, mitochondrial
MAP7D3	1.70	1.31E-09	8.95E-08	chrX:135295379-135338641 (-)	Xq26.3	MAP7 domain containing 3
LOC728554	1.70	1.83E-05	1.15E-04	chr5:177302262-177311273 (+)	5q35.3	THO complex 3 pseudogene
ITGA6	1.70	6.31E-05	3.08E-04	chr2:173292082-173371181 (+)	2q31.1	integrin, alpha 6
BCLAF1	1.70	1.24E-03	3.55E-03	chr6:136578001-136610989 (-)	6q22-q23	BCL2-associated transcription factor 1
PGLYRP4	1.70	4.28E-06	3.82E-05	chr1:153302596-153321316 (-)	1q21	peptidoglycan recognition protein 4
GPCPD1	1.70	7.48E-06	5.83E-05	chr20:5525080-5591672 (-)	20p12.3	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)
RANBP2	1.70	4.98E-05	2.56E-04	chr2:109335902-109402267 (+)	2q12.3	RAN binding protein 2
NCL	1.70	1.45E-06	1.68E-05	chr2:232318242-232348352 (-)	2q37.1	nucleolin
ABCC5	1.70	1.59E-07	3.35E-06	chr3:183637722-183735803 (-)	3q27	ATP-binding cassette, sub-family C (CFTRMRP), member 5
FANCB	1.70	2.23E-09	1.33E-07	chrX:14861529-14891191 (-)	Xp22.2	Fanconi anemia, complementation group B
TAF15	1.70	4.61E-11	7.77E-09	chr17:34136486-34174238 (+)	17q11.1-q11.2	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
SRPRB	1.70	4.91E-07	7.54E-06	chr3:133502877-133544416 (+)	3q22.1	signal recognition particle receptor, B subunit
PLRG1	1.70	1.15E-09	8.06E-08	chr4:155456149-155471587 (-)	4q31.2-q32.1	pleiotropic regulator 1
AZI2	1.70	1.99E-07	3.95E-06	chr3:28356494-28390618 (-)	3p24.1	5-azacytidine induced 2
ACOT13	1.70	4.93E-08	1.40E-06	chr6:24667263-24705295 (+)	6p22.3	acyl-CoA thioesterase 13
RFC5	1.70	7.57E-10	5.84E-08	chr12:118454506-118470935 (+)	12q24.23	replication factor C (activator 1) 5, 36.5kDa
DNAJC21	1.70	1.99E-05	1.23E-04	chr5:34929698-34959069 (+)	5p13.2	DnaJ (Hsp40) homolog, subfamily C, member 21
POLA1	1.70	1.40E-07	3.04E-06	chrX:24712036-25015103 (+)	Xp22.1-p21.3	polymerase (DNA directed), alpha 1, catalytic subunit
AKR1C1	1.70	1.01E-06	1.29E-05	chr10:4934796-5022159 (+)	10p15-p14	aldo-keto reductase family 1, member C1
AP3B1	1.70	5.91E-06	4.88E-05	chr5:77296349-77590579 (-)	5q14.1	adaptor-related protein complex 3, beta 1 subunit
RAD18	1.70	6.92E-09	3.11E-07	chr3:8817088-9005457 (-)	3p25-p24	RAD18 homolog (S. cerevisiae)
SEC63	1.70	1.03E-04	4.58E-04	chr6:108188960-108279482 (-)	6q21	SEC63 homolog (S. cerevisiae)
RECQL	1.70	1.77E-05	1.12E-04	chr12:21621844-21654603 (-)	12p12	RecQ helicase-like
UAP1	1.70	6.21E-07	9.02E-06	chr1:162531296-162569633 (+)	1q23.3	UDP-N-acteylglucosamine pyrophosphorylase 1
CLIP1	1.70	4.57E-04	1.54E-03	chr12:122755981-122907179 (-)	12q24.3	CAP-GLY domain containing linker protein 1
THUMPD2	1.70	2.03E-05	1.25E-04	chr2:39963200-40006416 (-)	2p22.1|2p22-p21	THUMP domain containing 2
KLHL2	1.69	2.87E-08	9.29E-07	chr4:166128770-166244308 (+)	4q21.2	kelch-like family member 2
SMYD2	1.69	3.74E-08	1.14E-06	chr1:214454444-214510477 (+)	1q32.3	SET and MYND domain containing 2
ZNF770	1.69	2.12E-08	7.38E-07	chr15:35270542-35280497 (-)	15q14	zinc finger protein 770
TYW3	1.69	1.07E-07	2.50E-06	chr1:75198836-75232362 (+)	1p31.1	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)
PHF3	1.69	8.70E-03	1.86E-02	chr6:64345725-64489229 (+)	6q12	PHD finger protein 3
S100A14	1.69	3.81E-06	3.49E-05	chr1:153586731-153589462 (-)	1q21.3	S100 calcium binding protein A14
SGK494	1.69	2.73E-12	9.93E-10	chr17:26782770-26941211 (-)	17q11.2	uncharacterized serinethreonine-protein kinase SgK494
CIRH1A	1.69	1.73E-08	6.32E-07	chr16:69166418-69202937 (+)	16q22.1	cirrhosis, autosomal recessive 1A (cirhin)
TJP1	1.69	9.92E-09	4.09E-07	chr15:29991571-30248497 (-)	15q13	tight junction protein 1
FAM157B	1.69	1.31E-06	1.56E-05	chr9:141106537-141149300 (+)	9q34.3	family with sequence similarity 157, member B
RNU6-912P	1.69	3.76E-04	1.32E-03	chr7:65279659-65279762 (+)	---	RNA, U6 small nuclear 912, pseudogene
MTHFD2	1.69	5.88E-07	8.66E-06	chr2:74425689-74444692 (+)	2p13.1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
IFT74	1.69	8.03E-04	2.47E-03	chr9:26947037-27062931 (+)	9p21.2	intraflagellar transport 74 homolog (Chlamydomonas)
BLNK	1.69	7.11E-06	5.61E-05	chr10:97951455-98031333 (-)	10q23.2-q23.33	B-cell linker
MBD4	1.69	1.78E-07	3.64E-06	chr3:129149787-129158878 (-)	3q21.3	methyl-CpG binding domain protein 4
XBP1	1.69	6.11E-07	8.92E-06	chr22:29190543-29196585 (-)	22q12.1|22q12	X-box binding protein 1
OFD1	1.69	5.89E-05	2.93E-04	chrX:13752832-13787480 (+)	Xp22	oral-facial-digital syndrome 1
MINA	1.69	9.13E-09	3.85E-07	chr3:97660661-97691301 (-)	3q11.2	MYC induced nuclear antigen
STC1	1.69	8.71E-04	2.65E-03	chr8:23699428-23712320 (-)	8p21-p11.2	stanniocalcin 1
STRN3	1.68	1.97E-07	3.92E-06	chr14:31363005-31495607 (-)	14q13-q21	striatin, calmodulin binding protein 3
NLRP2	1.68	5.53E-03	1.26E-02	chr19:55476620-55512510 (+)	19q13.42	NLR family, pyrin domain containing 2
NRP2	1.68	1.26E-06	1.51E-05	chr2:206546562-206662857 (+)	2q33.3	neuropilin 2
RNU6-957P	1.68	4.07E-04	1.40E-03	chr6:111043453-111043551 (-)	---	RNA, U6 small nuclear 957, pseudogene
PAPSS2	1.68	1.62E-08	6.00E-07	chr10:89419370-89507462 (+)	10q24	3-phosphoadenosine 5-phosphosulfate synthase 2
MLIP-IT1	1.68	1.52E-03	4.21E-03	chr6:53863688-53871950 (+)	---	MLIP intronic transcript 1 (non-protein coding)
MOCOS	1.68	3.00E-05	1.70E-04	chr18:33767480-33852120 (+)	18q12	molybdenum cofactor sulfurase
ATP13A4	1.68	7.05E-04	2.21E-03	chr3:193119866-193310900 (-)	3q29	ATPase type 13A4
SETX	1.68	6.85E-05	3.29E-04	chr9:135136743-135230372 (-)	9q34.13	senataxin
TNFRSF10A	1.68	9.48E-09	3.95E-07	chr8:23047965-23082680 (-)	8p21	tumor necrosis factor receptor superfamily, member 10a
CENPU	1.68	1.72E-03	4.66E-03	chr4:185615219-185655287 (-)	4q35.1	centromere protein U
ANKEF1	1.68	1.22E-08	4.83E-07	chr20:10015689-10037410 (+)	20p12.2	ankyrin repeat and EF-hand domain containing 1
FAM106CP	1.68	3.45E-05	1.90E-04	chr17:16692057-16693815 (+)	17p11.2	family with sequence similarity 106, member C pseudogene
INVS	1.68	4.82E-10	4.13E-08	chr9:102861511-103063426 (+)	9q31	inversin
RPP40	1.68	5.33E-09	2.54E-07	chr6:4994966-5004297 (-)	6p25.1	ribonuclease PMRP 40kDa subunit
PSMG1	1.68	1.95E-11	4.08E-09	chr21:40546695-40555777 (-)	21q22.3	proteasome (prosome, macropain) assembly chaperone 1
ATP5B	1.68	7.23E-09	3.21E-07	chr12:57031959-57039852 (-)	12q13.13	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
IPO7	1.68	1.16E-07	2.65E-06	chr11:9406169-9469674 (+)	11p15.4	importin 7
FEN1	1.68	1.82E-10	2.02E-08	chr11:61560109-61564716 (+)	11q12	flap structure-specific endonuclease 1
GPX2	1.68	1.15E-05	8.09E-05	chr14:65405870-65409531 (-)	14q24.1	glutathione peroxidase 2 (gastrointestinal)
METAP1	1.68	5.49E-11	8.84E-09	chr4:99916771-99983964 (+)	4q23	methionyl aminopeptidase 1
FASTKD2	1.68	4.03E-08	1.20E-06	chr2:207630081-207660911 (+)	2q33.3	FAST kinase domains 2
TRIP13	1.68	2.44E-08	8.25E-07	chr5:892758-919472 (+)	5p15.33	thyroid hormone receptor interactor 13
YES1	1.68	1.06E-06	1.34E-05	chr18:721588-812542 (-)	18p11.31-p11.21	YES proto-oncogene 1, Src family tyrosine kinase
FAR1	1.68	2.33E-06	2.40E-05	chr11:13690206-13753893 (+)	11p15.2	fatty acyl CoA reductase 1
METTL8	1.67	6.33E-07	9.17E-06	chr2:172173913-172291312 (-)	2q31.1	methyltransferase like 8
NUDCD1	1.67	3.60E-09	1.87E-07	chr8:110253148-110346614 (-)	8q23	NudC domain containing 1
DHX29	1.67	1.83E-04	7.26E-04	chr5:54552073-54603550 (-)	5q11.2	DEAH (Asp-Glu-Ala-His) box polypeptide 29
PDCD11	1.67	3.21E-09	1.72E-07	chr10:105156405-105206049 (+)	10q24.33	programmed cell death 11
HIST1H2BB	1.67	2.18E-04	8.37E-04	chr6:26043455-26043885 (-)	6p21.3	histone cluster 1, H2bb
CDCA8	1.67	1.58E-07	3.32E-06	chr1:38158090-38175391 (+)	1p34.3	cell division cycle associated 8
TENM2	1.67	1.04E-04	4.62E-04	chr5:166711804-167691162 (+)	5q34	teneurin transmembrane protein 2
CEP57	1.67	8.16E-05	3.78E-04	chr11:95523129-95565857 (+)	11q21	centrosomal protein 57kDa
AARS	1.67	3.32E-08	1.04E-06	chr16:70286288-70323412 (-)	16q22	alanyl-tRNA synthetase
PLS1	1.67	2.51E-09	1.45E-07	chr3:142315229-142432506 (+)	3q23	plastin 1
ATP8B1	1.67	5.74E-08	1.56E-06	chr18:55313658-55470327 (-)	18q21.31	ATPase, aminophospholipid transporter, class I, type 8B, member 1
SIPA1L2	1.67	1.79E-05	1.13E-04	chr1:232533711-232697304 (-)	1q42.2	signal-induced proliferation-associated 1 like 2
CCDC25	1.67	4.64E-08	1.34E-06	chr8:27590833-27630170 (-)	8p21.1	coiled-coil domain containing 25
RP11-20B7.1	1.67	1.68E-11	3.62E-09	chr3:73857752-73952017 (+)	---	novel transcript
CMC2	1.67	1.50E-09	9.88E-08	chr16:81009699-81040719 (-)	16q23.2	C-x(9)-C motif containing 2
PSMA2	1.67	5.27E-07	7.96E-06	chr7:42956460-42971822 (-)	7p13	proteasome (prosome, macropain) subunit, alpha type, 2
MTBP	1.67	1.03E-08	4.21E-07	chr8:121457640-121554373 (+)	8q24.12	MDM2 binding protein
NBN	1.67	3.04E-06	2.94E-05	chr8:90945564-91015456 (-)	8q21	nibrin
DPY19L3	1.67	6.52E-10	5.22E-08	chr19:32896655-32976799 (+)	19q13.11	dpy-19-like 3 (C. elegans)
POLD3	1.67	1.27E-09	8.74E-08	chr11:74303575-74354102 (+)	11q14	polymerase (DNA-directed), delta 3, accessory subunit
HNRNPM	1.67	2.13E-10	2.25E-08	chr19:8509651-8554002 (+)	19p13.2	heterogeneous nuclear ribonucleoprotein M
RTP4	1.67	9.90E-06	7.20E-05	chr3:187086120-187089864 (+)	3q27.3	receptor (chemosensory) transporter protein 4
DHTKD1	1.67	3.10E-09	1.68E-07	chr10:12110934-12165224 (+)	10p14	dehydrogenase E1 and transketolase domain containing 1
NIN	1.67	2.27E-05	1.37E-04	chr14:51186481-51297848 (-)	14q22.1	ninein (GSK3B interacting protein)
NBEAL1	1.67	2.65E-05	1.54E-04	chr2:203879602-204091101 (+)	2q33.2	neurobeachin-like 1
UQCRH	1.67	4.34E-12	1.38E-09	chr1:46769303-46782448 (+)	1p34.1	ubiquinol-cytochrome c reductase hinge protein
NDUFAB1	1.66	5.10E-09	2.47E-07	chr16:23592323-23607677 (-)	16p12.2	NADH dehydrogenase (ubiquinone) 1, alphabeta subcomplex, 1, 8kDa
GLYATL2	1.66	5.83E-08	1.58E-06	chr11:58601540-58671688 (-)	11q12.1	glycine-N-acyltransferase-like 2
CENPQ	1.66	1.16E-07	2.65E-06	chr6:49431096-49460820 (+)	6p12.3	centromere protein Q
PSIP1	1.66	5.13E-04	1.70E-03	chr9:15464064-15511017 (-)	9p22.3	PC4 and SFRS1 interacting protein 1
MTDH	1.66	8.07E-06	6.18E-05	chr8:98656407-98742488 (+)	8q22.1	metadherin
RCOR1	1.66	8.42E-10	6.32E-08	chr14:103058996-103196913 (+)	14q32.31	REST corepressor 1
CPSF2	1.66	9.25E-07	1.21E-05	chr14:92588281-92630755 (+)	14q31.1	cleavage and polyadenylation specific factor 2, 100kDa
NPM1	1.66	6.39E-07	9.23E-06	chr5:170814120-170838141 (+)	5q35.1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
ALDH3B2	1.66	3.33E-06	3.15E-05	chr11:67429633-67448685 (-)	11q13	aldehyde dehydrogenase 3 family, member B2
NIFK	1.66	1.90E-07	3.82E-06	chr2:122484521-122494503 (-)	2q14.3	nucleolar protein interacting with the FHA domain of MKI67
ZC3H15	1.66	1.13E-04	4.92E-04	chr2:187350883-187374090 (+)	2q32.1	zinc finger CCCH-type containing 15
EHD4	1.66	8.34E-07	1.12E-05	chr15:42190570-42264776 (-)	15q11.1	EH-domain containing 4
CNOT6	1.66	1.54E-11	3.39E-09	chr5:179921412-180005405 (+)	5q35.3	CCR4-NOT transcription complex, subunit 6
CTTNBP2NL	1.66	1.08E-03	3.18E-03	chr1:112957339-112958909 (+)	1p13.2	CTTNBP2 N-terminal like
INTS7	1.66	2.54E-09	1.46E-07	chr1:212113741-212209002 (-)	1q32.3	integrator complex subunit 7
SRP72	1.66	1.21E-05	8.40E-05	chr4:57333081-57369847 (+)	4q11	signal recognition particle 72kDa
ENOX2	1.66	2.15E-10	2.26E-08	chrX:129751713-130037208 (-)	Xq25	ecto-NOX disulfide-thiol exchanger 2
RNF149	1.66	1.64E-07	3.42E-06	chr2:101887681-101925178 (-)	2q11.2	ring finger protein 149
C1orf27	1.66	2.54E-04	9.52E-04	chr1:186344890-186390507 (+)	1q25	chromosome 1 open reading frame 27
PGK1	1.66	1.28E-08	5.02E-07	chrX:77320685-77384793 (+)	Xq13.3	phosphoglycerate kinase 1
NPL	1.66	1.18E-07	2.69E-06	chr1:182758428-182799519 (+)	1q25	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)
AHCTF1P1	1.66	3.22E-06	3.07E-05	chr2:162362408-162364216 (-)	2q24.2	AT hook containing transcription factor 1 pseudogene 1
HSPD1	1.66	9.79E-09	4.05E-07	chr2:198351305-198381461 (-)	2q33.1	heat shock 60kDa protein 1 (chaperonin)
CDC42BPA	1.66	3.46E-05	1.91E-04	chr1:227177566-227506175 (-)	1q42.11	CDC42 binding protein kinase alpha (DMPK-like)
OASL	1.66	1.47E-04	6.09E-04	chr12:121458095-121477045 (-)	12q24.2	2-5-oligoadenylate synthetase-like
TIMM21	1.66	8.55E-11	1.20E-08	chr18:71815746-71826204 (+)	18q22.3	translocase of inner mitochondrial membrane 21 homolog (yeast)
TTL	1.66	1.85E-07	3.74E-06	chr2:113239731-113290227 (+)	2q13	tubulin tyrosine ligase
FMO1	1.66	1.39E-02	2.77E-02	chr1:171217633-171255117 (+)	1q24.3	flavin containing monooxygenase 1
TRMT13	1.66	1.32E-05	8.92E-05	chr1:100598706-100616054 (+)	1p21.2	tRNA methyltransferase 13 homolog (S. cerevisiae)
SLC25A13	1.66	7.46E-10	5.77E-08	chr7:95749532-95951459 (-)	7q21.3	solute carrier family 25 (aspartate|glutamate carrier), member 13
MMS22L	1.66	4.15E-08	1.23E-06	chr6:97590037-97731093 (-)	6q16.1	MMS22-like, DNA repair protein
STAT3	1.65	4.33E-07	6.87E-06	chr17:40465342-40540513 (-)	17q21.31	signal transducer and activator of transcription 3 (acute-phase response factor)
ZNF562	1.65	4.09E-07	6.60E-06	chr19:9759338-9785776 (-)	19p13.2	zinc finger protein 562
AVEN	1.65	2.32E-09	1.37E-07	chr15:34158427-34331377 (-)	15q13.1	apoptosis, caspase activation inhibitor
RP1-45C12.1	1.65	1.83E-04	7.29E-04	chr1:171137243-171220933 (-)	---	novel transcript, antisense to FMO1
SPATA5L1	1.65	1.64E-09	1.06E-07	chr15:45694519-45713617 (+)	15q21.1	spermatogenesis associated 5-like 1
BCCIP	1.65	1.32E-07	2.93E-06	chr10:127512104-127542264 (+)	10q26.1	BRCA2 and CDKN1A interacting protein
ARPC3	1.65	3.27E-09	1.74E-07	chr12:110872630-110888212 (-)	12q24.11	actin related protein 23 complex, subunit 3, 21kDa
HNRNPAB	1.65	2.08E-09	1.27E-07	chr5:177631508-177638184 (+)	5q35.3	heterogeneous nuclear ribonucleoprotein AB
SRSF1	1.65	1.96E-11	4.09E-09	chr17:56078280-56084707 (-)	17q22	serinearginine-rich splicing factor 1
PCAT1	1.65	4.12E-06	3.71E-05	chr8:128025399-128033259 (+)	8q24.21	prostate cancer associated transcript 1 (non-protein coding)
PTBP2	1.65	1.10E-06	1.37E-05	chr1:97187175-97280605 (+)	1p21.3	polypyrimidine tract binding protein 2
TIMM23	1.65	7.89E-08	1.98E-06	chr10:51371390-51741805 (+)	10q11.23	translocase of inner mitochondrial membrane 23 homolog (yeast)
KRR1	1.65	6.13E-04	1.97E-03	chr12:75890684-75905418 (-)	12q21.2	KRR1, small subunit (SSU) processome component, homolog (yeast)
SFXN4	1.65	4.25E-08	1.26E-06	chr10:120900279-120925204 (-)	10q26.11	sideroflexin 4
SNX5	1.65	2.23E-09	1.33E-07	chr20:17922241-17949623 (-)	20p11	sorting nexin 5
ADH7	1.65	1.14E-05	8.00E-05	chr4:100333418-100356894 (-)	4q23-q24	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
COX6A1	1.65	1.87E-06	2.03E-05	chr12:120875893-120878545 (+)	12q24.2|12q24.2	cytochrome c oxidase subunit VIa polypeptide 1
DNAJB11	1.65	9.63E-09	3.99E-07	chr3:186285192-186314892 (+)	3q27.3	DnaJ (Hsp40) homolog, subfamily B, member 11
E2F7	1.65	2.23E-08	7.68E-07	chr12:77415026-77459360 (-)	12q21.2	E2F transcription factor 7
HJURP	1.65	3.04E-07	5.35E-06	chr2:234742062-234763212 (-)	2q37.1	Holliday junction recognition protein
METTL4	1.65	4.00E-09	2.03E-07	chr18:2537524-2571508 (-)	18p11.32	methyltransferase like 4
LOC729218	1.65	1.79E-06	1.96E-05	chr4:119512928-119554881 (+)	4q26	uncharacterized LOC729218
LIMA1	1.65	1.70E-07	3.20E-06	chr12:50569563-50677353 (-)	12q13	LIM domain and actin binding 1
RP11-34P13.9	1.64	7.90E-06	6.08E-05	chr1:160446-161525 (+)	---	putative novel transcript
NOP16	1.64	5.07E-08	1.43E-06	chr5:175810942-175815976 (-)	5q35.2	NOP16 nucleolar protein
PLA2R1	1.64	1.52E-05	1.00E-04	chr2:160788519-160919126 (-)	2q23-q24	phospholipase A2 receptor 1, 180kDa
NOP14	1.64	3.54E-09	1.85E-07	chr4:2939660-2965118 (-)	4p16.3	NOP14 nucleolar protein
SRM	1.64	1.83E-06	2.00E-05	chr1:11114641-11120091 (-)	1p36-p22	spermidine synthase
RNASEH2A	1.64	8.43E-08	2.08E-06	chr19:12917428-12924462 (+)	19p13.2	ribonuclease H2, subunit A

TUSC3	1.64	3.02E-04	1.10E-03	chr8:15274724-15624158 (+)	8p22	tumor suppressor candidate 3
RALGAPA2	1.64	1.75E-05	1.11E-04	chr20:20370196-20693266 (-)	20p11.22	Ral GTPase activating protein, alpha subunit 2 (catalytic)
CSE1L	1.64	2.76E-09	1.55E-07	chr20:47662783-47713497 (+)	20q13	CSE1 chromosome segregation 1-like (yeast)
RNFT1	1.64	3.03E-08	9.67E-07	chr17:58029601-58042122 (-)	17q23.1	ring finger protein, transmembrane 1
YEATS4	1.64	7.55E-06	5.87E-05	chr12:69753483-69784576 (+)	12q13-q15	YEATS domain containing 4
TIMMDC1	1.64	1.67E-08	6.18E-07	chr3:119217368-119243937 (+)	3q13.33	translocase of inner mitochondrial membrane domain containing 1
C6orf62	1.64	7.20E-09	3.20E-07	chr6:24705089-24721064 (-)	6p22.3	chromosome 6 open reading frame 62
SUGP2	1.64	1.59E-12	6.76E-10	chr19:19101697-19144832 (-)	19p12	SURP and G patch domain containing 2
HEATR1	1.64	6.06E-07	8.87E-06	chr1:236712305-236767841 (-)	1q43	HEAT repeat containing 1
MRPS15	1.64	6.28E-08	1.67E-06	chr1:36921319-36930040 (-)	1p34.3	mitochondrial ribosomal protein S15
RCC1	1.64	2.51E-11	4.94E-09	chr1:28832455-28865708 (+)	1p36.1	regulator of chromosome condensation 1
ERVK-7	1.64	5.14E-05	2.62E-04	chr1:155596546-155618335 (-)	1q22	endogenous retrovirus group K, member 7
CCP110	1.64	8.27E-05	3.82E-04	chr16:19535179-19564730 (+)	16p12.3	centriolar coiled coil protein 110kDa
SLC24A3	1.64	7.13E-08	1.83E-06	chr20:19193290-19703545 (+)	20q13.33	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
E2F4	1.64	5.12E-09	2.48E-07	chr16:67226068-67232821 (+)	16q22.1	E2F transcription factor 4, p107/p130-binding
FUCA2	1.64	8.58E-10	6.43E-08	chr6:143815949-143833020 (-)	6q24	fucosidase, alpha-L- 2, plasma
LMAN1	1.64	1.03E-07	2.42E-06	chr18:56995055-57026508 (-)	18q21.3-q22	lectin, mannose-binding, 1
TMEM87B	1.64	6.08E-11	9.45E-09	chr2:112812800-112876895 (+)	2q13	transmembrane protein 87B
RPAP2	1.63	1.75E-05	1.11E-04	chr1:92764522-92853732 (+)	1p22.1	RNA polymerase II associated protein 2
COPB2	1.63	7.27E-10	5.64E-08	chr3:139074442-139108574 (-)	3q23	coatomer protein complex, subunit beta 2 (beta prime)
RFC1	1.63	7.44E-04	2.31E-03	chr4:39289069-39368001 (-)	4p14-p13	replication factor C (activator 1) 1, 145kDa
NDUFB3	1.63	4.49E-09	2.23E-07	chr2:201936156-201950473 (+)	2q31.3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
ICE1	1.63	8.84E-05	4.03E-04	chr5:5420777-5490347 (+)	5p15.32	interactor of little elongator complex ELL subunit 1
BMS1	1.63	6.78E-08	1.76E-06	chr10:43277954-43330385 (+)	10q11.21	BMS1 ribosome biogenesis factor
TIMM8B	1.63	6.87E-08	1.78E-06	chr11:111955524-111957522 (-)	11q23.1-q23.2	translocase of inner mitochondrial membrane 8 homolog B (yeast)
TMPRSS11A	1.63	6.12E-06	5.00E-05	chr4:68775103-68829858 (-)	4q13.2	transmembrane protease, serine 11A
ALDH2	1.63	1.63E-05	1.05E-04	chr12:112204691-112247789 (+)	12q24.2	aldehyde dehydrogenase 2 family (mitochondrial)
HSPA5	1.63	1.28E-05	8.72E-05	chr9:127997127-128003666 (-)	9q33.3	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
SLAMF7	1.63	1.91E-07	3.84E-06	chr1:160709037-160724611 (+)	1q23.1-q24.1	SLAM family member 7
ITGB6	1.63	5.20E-07	7.88E-06	chr2:160956177-161128399 (-)	2q24.2	integrin, beta 6
MED21	1.63	3.92E-08	1.18E-06	chr12:27175479-27183689 (+)	12p11.23	mediator complex subunit 21
RNU6-82P	1.63	7.68E-03	1.67E-02	chr13:28806638-28806744 (+)	---	RNA, U6 small nuclear 82, pseudogene
NAA50	1.63	7.01E-09	3.14E-07	chr3:113435307-113465147 (-)	3q13.2	N(alpha)-acetyltransferase 50, NatE catalytic subunit
IGSF3	1.63	1.48E-10	1.74E-08	chr1:117117031-117210377 (-)	1p13	immunoglobulin superfamily, member 3
UHRF1BP1L	1.63	1.48E-05	9.78E-05	chr12:100430854-100536642 (-)	12q23.1	UHRF1 binding protein 1-like
LOC100506123	1.63	1.02E-04	4.54E-04	chr2:97948229-97957632 (+)	2q11	uncharacterized LOC100506123
EPHB2	1.63	3.98E-08	1.19E-06	chr1:23037331-23241823 (+)	1p36.1-p35	EPH receptor B2
RFC3	1.63	2.41E-08	8.16E-07	chr13:34392186-34540695 (+)	13q13.2	replication factor C (activator 1) 3, 38kDa
IBTK	1.63	1.31E-05	8.88E-05	chr6:82879700-82957471 (-)	6q14.1	inhibitor of Bruton agammaglobulinemia tyrosine kinase
AKAP6	1.63	1.09E-09	7.77E-08	chr14:32798479-33302268 (+)	14q12	A kinase (PRKA) anchor protein 6
MIS18A	1.63	1.38E-11	3.11E-09	chr21:33640530-33651380 (-)	21q22.11	MIS18 kinetochore protein A
ERV3-1	1.63	4.30E-04	1.47E-03	chr7:64434830-64467124 (-)	7q11.2	endogenous retrovirus group 3, member 1
LOC100507516	1.63	2.51E-05	1.48E-04	chr8:54427731-54436491 (-)	---	uncharacterized LOC100507516
LOC101928706	1.63	2.16E-03	5.67E-03	chr1:334140-342806 (+)	---	uncharacterized LOC101928706
FNBP4	1.63	5.67E-05	2.83E-04	chr11:47738069-47788993 (-)	11p11.2	formin binding protein 4
QRSL1	1.63	6.60E-08	1.73E-06	chr6:107077441-107116292 (+)	6q21	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
XRN2	1.63	9.02E-07	1.19E-05	chr20:21283942-21370463 (+)	20p11.2-p11.1	5-3 exoribonuclease 2
RN7SKP35	1.63	4.07E-04	1.40E-03	chr4:152497918-152498068 (+)	---	RNA, 7SK small nuclear pseudogene 35
TPI1	1.63	9.92E-08	2.35E-06	chr12:6976283-6980112 (+)	12p13	triosephosphate isomerase 1
TOMM70A	1.62	1.66E-07	3.46E-06	chr3:100082275-100120283 (-)	3q12.2	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
PSMD12	1.62	3.98E-07	6.47E-06	chr17:65334032-65362743 (-)	17q24.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
ZNF587	1.62	5.89E-07	8.66E-06	chr19:58379177-58380140 (+)	19q13.43	zinc finger protein 587
ISG20L2	1.62	3.68E-08	1.12E-06	chr1:156691683-156698591 (-)	1q23.1	interferon stimulated exonuclease gene 20kDa-like 2
MRPS5	1.62	5.78E-12	1.72E-09	chr2:95752952-95787754 (-)	2p11.2-q11.2	mitochondrial ribosomal protein S5
NMU	1.62	1.40E-05	9.36E-05	chr4:56461395-56502865 (-)	4q12	neuromedin U
ETHE1	1.62	2.49E-06	2.53E-05	chr19:44010871-44031396 (-)	19q13.31	ethylmalonic encephalopathy 1
CENPW	1.62	5.40E-08	1.50E-06	chr6:126661253-126670021 (+)	6q22.32	centromere protein W
RNU6-522P	1.62	2.40E-03	6.19E-03	chr6:15315151-15315257 (+)	---	RNA, U6 small nuclear 522, pseudogene
PSMB5	1.62	4.49E-06	3.96E-05	chr14:23495060-23504439 (-)	14q11.2	proteasome (prosome, macropain) subunit, beta type, 5
LOC100506497	1.62	3.40E-10	3.21E-08	chr7:29019583-29052985 (+)	---	uncharacterized LOC100506497
RP11-86D1.2	1.62	4.87E-05	2.51E-04	chr6:128752086-128753913 (-)	---	novel transcript
CBFB	1.62	2.97E-11	5.60E-09	chr16:67063050-67134961 (+)	16q22.1	core-binding factor, beta subunit
RNU6-360P	1.62	1.36E-07	2.98E-06	chr2:208884362-208884465 (-)	---	RNA, U6 small nuclear 360, pseudogene
MGA	1.62	1.43E-05	9.52E-05	chr15:41913764-42062141 (+)	15q14	MGA, MAX dimerization protein
RBM26	1.62	2.53E-04	9.49E-04	chr13:79888876-79980612 (-)	13q31.1	RNA binding motif protein 26
LTB4R2	1.62	9.57E-12	2.41E-09	chr14:24778161-24781259 (+)	14q12	leukotriene B4 receptor 2
GPSM2	1.62	1.62E-06	1.83E-05	chr1:109417972-109476957 (+)	1p13.3	G-protein signaling modulator 2
FAM72D	1.62	2.33E-04	8.85E-04	chr1:143896452-143913143 (-)	1q21.1	family with sequence similarity 72, member D
NUDT5	1.62	2.86E-08	9.27E-07	chr10:12207324-12238143 (-)	10p14	nudix (nucleoside diphosphate linked moiety X)-type motif 5
TMEM38B	1.62	4.05E-07	6.56E-06	chr9:108456825-108538893 (+)	9q31.2	transmembrane protein 38B
SKIV2L2	1.62	2.49E-06	2.52E-05	chr5:54603576-54721409 (+)	5q11.2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
NRIP1	1.62	5.58E-06	4.67E-05	chr21:16333556-16437321 (-)	21q11.2	nuclear receptor interacting protein 1
TOMM40	1.62	4.33E-09	2.17E-07	chr19:45394477-45406946 (+)	19q13	translocase of outer mitochondrial membrane 40 homolog (yeast)
SRBD1	1.61	3.65E-09	1.89E-07	chr2:45615819-45839304 (-)	2p21	S1 RNA binding domain 1
RP11-798M19.3	1.61	5.50E-07	8.22E-06	chr4:174243357-174250845 (-)	---	novel transcript
DIAPH2	1.61	6.78E-03	1.50E-02	chrX:95939662-96859996 (+)	Xq21.33	diaphanous-related formin 2
STOML2	1.61	1.05E-06	1.33E-05	chr9:35099888-35103154 (-)	9p13.1	stomatin (EPB72)-like 2
EFTUD1P1	1.61	1.27E-06	1.52E-05	chr15:84748920-84795353 (+)	15q25.2	elongation factor Tu GTP binding domain containing 1 pseudogene 1
RAP1GDS1	1.61	9.27E-08	2.24E-06	chr4:99182527-99365012 (+)	4q23-q25	RAP1, GTP-GDP dissociation stimulator 1
HDAC1	1.61	3.18E-10	3.07E-08	chr1:32757687-32799236 (+)	1p34	histone deacetylase 1
MRPL35	1.61	3.38E-11	6.15E-09	chr2:86426556-86440917 (+)	2p11.2	mitochondrial ribosomal protein L35
SH2D4A	1.61	7.68E-09	3.37E-07	chr8:19171081-19253729 (+)	8p21.2	SH2 domain containing 4A
EEF1E1	1.61	3.38E-10	3.20E-08	chr6:8073593-8102828 (-)	6p24.3	eukaryotic translation elongation factor 1 epsilon 1
OTUD6B	1.61	5.90E-06	4.87E-05	chr8:92082424-92099323 (+)	8q21.3	OTU domain containing 6B
ATP6V1D	1.61	6.00E-08	1.61E-06	chr14:67804581-67826966 (-)	14q23-q24.2	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
AGGF1	1.61	2.48E-05	1.46E-04	chr5:76325076-76361059 (+)	5q13.3	angiogenic factor with G patch and FHA domains 1
CSPP1	1.61	4.05E-06	3.66E-05	chr8:67974661-68108849 (+)	8q13.2	centrosome and spindle pole associated protein 1
CXCL8	1.61	1.81E-03	4.88E-03	chr4:74606223-74609433 (+)	4q13-q21	chemokine (C-X-C motif) ligand 8
KCNJ2	1.61	6.54E-05	3.17E-04	chr17:68164814-68176183 (+)	17q24.3	potassium inwardly-rectifying channel, subfamily J, member 2
MAK16	1.61	4.80E-07	7.43E-06	chr8:33342268-33358778 (+)	8p12	MAK16 homolog (S. cerevisiae)
FCF1	1.61	3.53E-11	6.35E-09	chr14:75179847-75203498 (+)	14q24.3	FCF1 rRNA-processing protein
TXNDC9	1.61	1.65E-07	3.45E-06	chr2:99923088-99957165 (-)	2q11.2	thioredoxin domain containing 9
UBXN4	1.61	5.27E-05	2.67E-04	chr2:136499189-136542633 (+)	2q21.3	UBX domain protein 4
LARP4	1.61	5.60E-07	8.31E-06	chr12:50794592-50873788 (+)	12q13.12	La ribonucleoprotein domain family, member 4
FIGNL1	1.61	3.88E-09	1.98E-07	chr7:50511831-50518088 (-)	7p12.1	fidgetin-like 1
EIF2S1	1.61	2.31E-06	2.38E-05	chr14:67826714-67853233 (+)	14q23.3	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
PDS5A	1.61	2.04E-06	2.17E-05	chr4:39824483-39979576 (-)	4p14	PDS5, regulator of cohesin maintenance, homolog A (S. cerevisiae)
LOC100506974	1.61	9.36E-06	6.92E-05	chr17:13932609-13972775 (-)	---	uncharacterized LOC100506974
ERCC8	1.61	1.27E-08	4.99E-07	chr5:60169658-60240905 (-)	5q12.1	excision repair cross-complementation group 8
WDR36	1.61	5.98E-07	8.75E-06	chr5:110427414-110469906 (+)	5q22.1	WD repeat domain 36
HIGD1A	1.61	5.23E-07	7.91E-06	chr3:42824400-42846027 (-)	3p22.1	HIG1 hypoxia inducible domain family, member 1A
CCT3	1.61	1.49E-08	5.60E-07	chr1:156278752-156337664 (-)	1q23	chaperonin containing TCP1, subunit 3 (gamma)
SKA2P1	1.61	5.77E-06	4.79E-05	chr9:125524123-125524948 (+)	---	spindle and kinetochore associated complex subunit 2 pseudogene 1
PRDX3	1.61	2.80E-08	9.14E-07	chr10:120927211-120938345 (-)	10q25-q26	peroxiredoxin 3
PAPOLA	1.61	2.98E-06	2.90E-05	chr14:96968710-97033453 (+)	14q32.31	poly(A) polymerase alpha
AC093382.1	1.61	1.52E-07	3.23E-06	chr2:216804031-216806442 (-)	---	putative novel transcript
TMEM65	1.61	1.42E-09	9.46E-08	chr8:125323159-125384940 (-)	8q24.13	transmembrane protein 65
TTC7B	1.61	5.01E-09	2.44E-07	chr14:91006932-91282761 (-)	14q32.11	tetratricopeptide repeat domain 7B
DDX18	1.60	1.46E-05	9.69E-05	chr2:118572226-118589955 (+)	2q14.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
NSUN2	1.60	3.20E-09	1.72E-07	chr5:6599352-6633473 (-)	5p15.31	NOP2Sun RNA methyltransferase family, member 2
HRSP12	1.60	8.50E-07	1.14E-05	chr8:99114567-99129469 (-)	8q22	heat-responsive protein 12
TRUB2	1.60	1.65E-08	6.10E-07	chr9:131071382-131085021 (-)	9q34.11	TruB pseudouridine (psi) synthase family member 2
WASF1	1.60	2.19E-09	1.31E-07	chr6:110421022-110501207 (-)	6q21	WAS protein family, member 1
DHRS7	1.60	1.59E-06	1.81E-05	chr14:60610838-60636574 (-)	14q23.1	dehydrogenase/reductase (SDR family) member 7
NT5C2	1.60	1.87E-09	1.16E-07	chr10:104845940-104953063 (-)	10q24.32	5-nucleotidase, cytosolic II
LOC440434	1.60	8.38E-07	1.12E-05	chr17:36351796-36421858 (-)	17q12	aminopeptidase puromycin sensitive pseudogene
PSTPIP2	1.60	2.74E-08	8.99E-07	chr18:43563502-43652250 (-)	18q12	proline-serine-threonine phosphatase interacting protein 2
STK39	1.60	1.59E-04	6.47E-04	chr2:168810530-169104651 (-)	2q24.3	serine threonine kinase 39
NGLY1	1.60	5.40E-10	4.52E-08	chr3:25760435-25831530 (-)	3p24.2	N-glycanase 1
DSN1	1.60	2.92E-09	1.61E-07	chr20:35380194-35402230 (-)	20q11.23	DSN1, MIS12 kinetochore complex component
BRMS1L	1.60	2.18E-09	1.30E-07	chr14:36295524-36341169 (+)	14q13.2	breast cancer metastasis-suppressor 1-like
CLOCK	1.60	8.31E-06	6.32E-05	chr4:56298643-56413305 (-)	4q12	clock circadian regulator
UBLCP1	1.60	4.91E-06	4.24E-05	chr5:158690089-158713048 (+)	5q33.3	ubiquitin-like domain containing CTD phosphatase 1
REXO2	1.60	1.36E-07	2.98E-06	chr11:114310108-114321001 (+)	11q23.2	RNA exonuclease 2
RSF1	1.60	2.29E-03	5.94E-03	chr11:77371041-77532063 (-)	11q14.1	remodeling and spacing factor 1
CHCHD1	1.60	5.43E-07	8.16E-06	chr10:75541805-75543410 (+)	10q22.2	coiled-coil-helix-coiled-coil-helix domain containing 1
APOL2	1.60	2.28E-07	4.35E-06	chr22:36622255-36636000 (-)	22q12	apolipoprotein L, 2
HDDC2	1.60	1.07E-08	4.34E-07	chr6:125596496-125623282 (-)	6q13-q24.3	HD domain containing 2
ATP11B	1.60	4.07E-07	6.58E-06	chr3:182511288-182639423 (+)	3q27	ATPase, class VI, type 11B
EMC3-AS1	1.60	2.29E-06	2.36E-05	chr3:10028595-10046928 (+)	3p25.3	EMC3 antisense RNA 1
HLTF	1.60	1.38E-04	5.78E-04	chr3:148747904-148804341 (-)	3q25.1-q26.1	helicase-like transcription factor
SLC4A1AP	1.60	7.84E-06	6.04E-05	chr2:27886338-27917847 (+)	2p23.3	solute carrier family 4 (anion exchanger), member 1, adaptor protein
CD44	1.60	1.48E-02	2.91E-02	chr11:35218709-35220102 (+)	11p13	CD44 molecule (Indian blood group)
NDC1	1.60	5.40E-09	2.57E-07	chr1:54231133-54304533 (-)	1p32.3	NDC1 transmembrane nucleoporin
XDH	1.60	2.93E-05	1.67E-04	chr2:31178437-31637611 (-)	2p23.1	xanthine dehydrogenase
SPATA6L	1.60	1.13E-06	1.40E-05	chr9:4553386-4666674 (-)	9p24.2	spermatogenesis associated 6-like
ADAM17	1.60	7.22E-07	1.01E-05	chr2:9628615-9695921 (-)	2p25	ADAM metallopeptidase domain 17
NUP160	1.60	2.00E-10	2.16E-08	chr11:47799639-47870107 (-)	11p11.2	nucleoporin 160kDa
PLD2	1.59	2.12E-07	4.15E-06	chr17:4710391-4726727 (+)	17p13.1	phospholipase D2
ZC3HAV1	1.59	1.76E-08	6.39E-07	chr7:138728266-138794465 (-)	7q34	zinc finger CCCH-type, antiviral 1
GLTP	1.59	2.60E-06	2.61E-05	chr12:110288748-110318293 (-)	12q24.11	glycolipid transfer protein
EIF3J	1.59	1.01E-05	7.33E-05	chr15:44829255-44855001 (+)	15q21.1	eukaryotic translation initiation factor 3, subunit J
CCT8	1.59	1.06E-06	1.34E-05	chr21:30428126-30446118 (-)	21q22.11	chaperonin containing TCP1, subunit 8 (theta)
PPRC1	1.59	6.87E-08	1.78E-06	chr10:103892787-103910090 (+)	10q24.32	peroxisome proliferator-activated receptor gamma, coactivator-related 1
NSA2	1.59	3.76E-05	2.04E-04	chr5:74062817-74072737 (+)	5q13.3	NSA2 ribosome biogenesis homolog (S. cerevisiae)
SGOL2	1.59	3.00E-10	2.93E-08	chr2:201374731-201448818 (+)	2q33.1	shugoshin-like 2 (S. pombe)
MTFMT	1.59	4.87E-08	1.39E-06	chr15:65293850-65321977 (-)	15q22.31	mitochondrial methionyl-tRNA formyltransferase
ADH5	1.59	8.46E-07	1.13E-05	chr4:99992130-100009952 (-)	4q23	alcohol dehydrogenase 5 (class III), chi polypeptide
EFTUD1	1.59	2.62E-06	2.63E-05	chr15:82422561-82555104 (-)	15q25.2	elongation factor Tu GTP binding domain containing 1
TEFM	1.59	1.35E-06	1.59E-05	chr17:29226001-29233286 (-)	---	transcription elongation factor, mitochondrial
VRK2	1.59	1.21E-08	4.80E-07	chr2:58134786-58387055 (+)	2p16.1	vaccinia related kinase 2
MRPL16	1.59	6.79E-10	5.40E-08	chr11:59573608-59578345 (-)	11q12.1	mitochondrial ribosomal protein L16
SLC38A9	1.59	2.44E-09	1.42E-07	chr5:54921673-55069022 (-)	5q11.2	solute carrier family 38, member 9
P2RY1	1.59	3.74E-08	1.14E-06	chr3:152552482-152555843 (+)	3q25.2	purinergic receptor P2Y, G-protein coupled, 1
PHKA1	1.59	9.43E-11	1.29E-08	chrX:71798664-71934167 (-)	Xq12-q13	phosphorylase kinase, alpha 1 (muscle)
EXOSC8	1.59	1.27E-07	2.83E-06	chr13:37572953-37583751 (+)	13q13.1	exosome component 8
MYCBP2	1.59	1.37E-04	5.74E-04	chr13:77618792-77901185 (-)	13q22	MYC binding protein 2, E3 ubiquitin protein ligase
POLA2	1.59	1.47E-10	1.73E-08	chr11:65029233-65066156 (+)	11q13.1	polymerase (DNA directed), alpha 2, accessory subunit
ATP5C1	1.59	5.24E-06	4.45E-05	chr10:7830092-7849778 (+)	10p15.1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
SMAD1	1.59	9.39E-05	4.24E-04	chr4:146459754-146461633 (+)	4q31	SMAD family member 1

FANCA	1.59	1.97E-10	2.15E-08	chr16:89803959-89883065 (-)	16q24.3	Fanconi anemia, complementation group A
RNU6-322P	1.59	1.83E-04	7.27E-04	chr15:101092025-101092127 (-)	---	RNA, U6 small nuclear 322, pseudogene
PSMD14	1.59	1.62E-07	3.40E-06	chr2:162164549-162268228 (+)	2q24.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
CHML	1.59	1.36E-03	3.85E-03	chr1:241792155-241799232 (-)	1q43	choroideremia-like (Rab escort protein 2)
PIK3C2A	1.59	3.92E-04	1.36E-03	chr11:17099277-17229530 (-)	11p15.5-p14	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha
RABGGTA	1.59	3.00E-08	9.62E-07	chr14:24734744-24740945 (-)	14q11.2	Rab geranylgeranyltransferase, alpha subunit
AGAP6	1.59	2.74E-04	1.01E-03	chr10:51748078-51770259 (+)	10q11.23	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6
THSD4	1.59	3.40E-07	5.77E-06	chr15:71389291-72075722 (+)	15q23	thrombospondin, type I, domain containing 4
PALLD	1.59	2.04E-05	1.26E-04	chr4:169418217-169849608 (+)	4q32.3	palladin, cytoskeletal associated protein
IQGAP2	1.59	3.07E-04	1.11E-03	chr5:75699074-76003957 (+)	5q13.3	IQ motif containing GTPase activating protein 2
TDG	1.59	3.97E-07	6.46E-06	chr12:104359582-104382656 (+)	12q24.1	thymine-DNA glycosylase
USP15	1.58	2.75E-04	1.02E-03	chr12:62654119-62803501 (+)	12q14	ubiquitin specific peptidase 15
RBBP8	1.58	1.50E-03	4.17E-03	chr18:20513290-20606449 (+)	18q11.2	retinoblastoma binding protein 8
ZNF655	1.58	3.17E-06	3.04E-05	chr7:99156029-99174076 (+)	7q22.1	zinc finger protein 655
TPRXL	1.58	2.76E-11	5.31E-09	chr3:13978807-14124311 (+)	3p25.1	tetra-peptide repeat homeobox-like
SLC27A4	1.58	4.83E-06	4.18E-05	chr9:131102839-131123749 (+)	9q34.11	solute carrier family 27 (fatty acid transporter), member 4
NOP56	1.58	9.07E-09	3.84E-07	chr20:2632791-2639039 (+)	20p13	NOP56 ribonucleoprotein
WDR43	1.58	1.26E-05	8.65E-05	chr2:29117509-29171088 (+)	2p23.2	WD repeat domain 43
RP11-346D19.1	1.58	1.37E-05	9.23E-05	chr6:113852320-113864995 (+)	---	putative novel transcript
PTPN22	1.58	5.03E-04	1.67E-03	chr1:114356433-114414381 (-)	1p13.2	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
FER	1.58	9.35E-04	2.81E-03	chr5:108083523-108532542 (+)	5q21	fer (fps/fes related) tyrosine kinase
MTF1	1.58	1.42E-08	5.42E-07	chr1:38275239-38325292 (-)	1p33	metal-regulatory transcription factor 1
TTC14	1.58	6.01E-04	1.94E-03	chr3:180319918-180335616 (+)	3q26.33	tetratricopeptide repeat domain 14
LOC101928231	1.58	2.10E-10	2.24E-08	chr6:134749378-134841723 (-)	---	uncharacterized LOC101928231
TMEM185B	1.58	4.56E-07	7.13E-06	chr2:120975047-120980984 (-)	2q14.2	transmembrane protein 185B
C8orf59	1.58	2.17E-05	1.32E-04	chr8:86126288-86132650 (-)	8q21.2	chromosome 8 open reading frame 59
SAP30L	1.58	9.84E-06	7.18E-05	chr5:153829528-153831927 (+)	5q33.2	SAP30-like
BACH1-IT3	1.58	1.50E-07	3.20E-06	chr21:30868367-30872706 (+)	---	BACH1 intronic transcript 3 (non-protein coding)
SGK1	1.58	1.12E-05	7.94E-05	chr6:134490384-134639196 (-)	6q23	serumglucocorticoid regulated kinase 1
TTC1	1.58	1.23E-06	1.49E-05	chr5:159436120-159492550 (+)	5q33.3	tetratricopeptide repeat domain 1
LOC101060578	1.58	9.04E-04	2.73E-03	chr9:42668608-42714962 (+)	---	COBW domain-containing protein 5-like
C14orf2	1.58	2.24E-07	4.31E-06	chr14:104378625-104394606 (-)	14q32.33	chromosome 14 open reading frame 2
YWHAQ	1.58	8.06E-09	3.49E-07	chr2:9724101-9771143 (-)	2p25.1	tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta
TNPO1	1.58	2.85E-08	9.25E-07	chr5:72112139-72212560 (+)	5q13.2	transportin 1
TLE3	1.58	6.38E-09	2.92E-07	chr15:70340129-70390515 (-)	15q22	transducin-like enhancer of split 3
SF3A3	1.58	1.46E-09	9.67E-08	chr1:38422647-38456593 (-)	1p34.3	splicing factor 3a, subunit 3, 60kDa
COX10	1.58	9.10E-11	1.26E-08	chr17:13972719-14111996 (+)	17p12	cytochrome c oxidase assembly homolog 10 (yeast)
DNAJC13	1.58	2.90E-05	1.66E-04	chr3:132136370-132257876 (+)	3q22.1	DnaJ (Hsp40) homolog, subfamily C, member 13
OXCT1	1.58	1.27E-06	1.53E-05	chr5:41730167-41870791 (-)	5p13.1	3-oxoacid CoA transferase 1
SYNCRIP	1.58	4.99E-08	1.41E-06	chr6:86317502-86353510 (-)	6q14-q15	synaptotagmin binding, cytoplasmic RNA interacting protein
COX6A1P2	1.57	1.63E-06	1.83E-05	chr6:37012607-37013177 (+)	---	cytochrome c oxidase subunit VIa polypeptide 1 pseudogene 2
NAPG	1.57	3.06E-08	9.74E-07	chr18:10525873-10552766 (+)	18p11.22	N-ethylmaleimide-sensitive factor attachment protein, gamma
TMX2	1.57	6.95E-07	9.79E-06	chr11:57479995-57508445 (+)	11cen-q22.3	thioredoxin-related transmembrane protein 2
DNAAF2	1.57	2.88E-07	5.16E-06	chr14:50091892-50101948 (-)	14q21.3	dynein, axonemal, assembly factor 2
SCFD1	1.57	1.86E-05	1.17E-04	chr14:31091318-31205018 (+)	14q12	sec1 family domain containing 1
NOP10	1.57	3.75E-05	2.04E-04	chr15:34633914-34635378 (-)	15q14-q15	NOP10 ribonucleoprotein
PKM	1.57	1.34E-08	5.20E-07	chr15:72491370-72524163 (-)	15q22	pyruvate kinase, muscle
ALAS1	1.57	6.70E-07	9.53E-06	chr3:52232099-52248343 (+)	3p21.1	aminolevulinate, delta-, synthase 1
SDAD1	1.57	3.32E-04	1.19E-03	chr4:76871059-76912115 (-)	4q21.1	SDA1 domain containing 1
CUL1	1.57	1.61E-07	3.39E-06	chr7:148395006-148498202 (+)	7q36.1	cullin 1
COQ3	1.57	4.34E-09	2.17E-07	chr6:99817276-99842082 (-)	6q16.2	coenzyme Q3 methyltransferase
RNU2-42P	1.57	1.75E-03	4.75E-03	chr10:127579135-127579247 (-)	---	RNA, U2 small nuclear 42, pseudogene
DPP3	1.57	9.67E-09	4.01E-07	chr11:66247484-66277130 (+)	11q12-q13.1	dipeptidyl-peptidase 3
PPA1	1.57	2.22E-07	4.28E-06	chr10:71962586-71993667 (-)	10q11.1-q24	pyrophosphatase (inorganic) 1
NOP2	1.57	1.04E-07	2.43E-06	chr12:6666029-6677857 (-)	12p13	NOP2 nucleolar protein
RP11-49O14.3	1.57	3.53E-04	1.25E-03	chr9:97586554-97587055 (+)	---	novel transcript
GOLGA6L9	1.57	2.71E-04	1.01E-03	chr15:82710856-82731586 (+)	15q25.2	golgin A6 family-like 9
CDC37	1.57	2.60E-10	2.63E-08	chr19:10501809-10514271 (-)	19p13.2	cell division cycle 37
LACE1	1.57	7.86E-12	2.12E-09	chr6:108616098-108847999 (+)	6q22.1	lactation elevated 1
RNU6-301P	1.57	4.70E-05	2.44E-04	chr14:52190821-52190927 (+)	---	RNA, U6 small nuclear 301, pseudogene
BBS7	1.57	1.74E-07	3.58E-06	chr4:122745484-122791652 (-)	4q27	Bardet-Biedl syndrome 7
H2AFY	1.57	2.47E-13	1.85E-10	chr5:134669590-134735604 (-)	5q31.1	H2A histone family, member Y
TDRD7	1.57	2.27E-08	7.64E-07	chr9:100174232-100228407 (+)	9q22.33	tudor domain containing 7
RPN2	1.57	6.30E-08	1.67E-06	chr20:35806813-35870025 (+)	20q12-q13.1	ribophorin II
IKBKAP	1.57	3.45E-07	5.82E-06	chr9:111629797-111696608 (-)	9q31	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein
NCOA7	1.57	7.02E-10	5.52E-08	chr6:126102307-126253176 (+)	6q22.32	nuclear receptor coactivator 7
METAP2	1.57	1.11E-05	7.88E-05	chr12:95867727-95909615 (+)	12q22	methionyl aminopeptidase 2
TRPM7	1.57	4.66E-04	1.57E-03	chr15:50849352-50979012 (-)	15q21	transient receptor potential cation channel, subfamily M, member 7
RP11-464F9.9	1.57	3.32E-04	1.19E-03	chr10:75432880-75435692 (-)	---	----
GM2A	1.57	1.04E-07	2.44E-06	chr5:150591711-150650001 (+)	5q33.1	GM2 ganglioside activator
SPATA5	1.57	6.44E-08	1.70E-06	chr4:123844225-124240604 (+)	4q28.1	spermatogenesis associated 5
NIPA2	1.57	5.42E-09	2.58E-07	chr15:23004684-23034427 (-)	15q11.2	non imprinted in Prader-WilliAngelman syndrome 2
PRKCI	1.57	3.82E-07	6.28E-06	chr3:169940153-170023770 (+)	3q26.3	protein kinase C, iota
ACAT2	1.57	5.24E-05	2.66E-04	chr6:160181360-160200144 (+)	6q25.3	acetyl-CoA acetyltransferase 2
AIFM1	1.57	4.92E-12	1.52E-09	chrX:129263337-129299861 (-)	Xq26.1	apoptosis-inducing factor, mitochondrion-associated, 1
C14orf119	1.57	1.98E-07	3.95E-06	chr14:23563974-23569671 (+)	14q11.2	chromosome 14 open reading frame 119
OXNAD1	1.57	1.95E-09	1.20E-07	chr3:16306667-16378868 (+)	3p25-p24	oxidoreductase NAD-binding domain containing 1
NSDHL	1.57	1.93E-07	3.87E-06	chrX:151999511-152038273 (+)	Xq28	NAD(P) dependent steroid dehydrogenase-like
TRAP1	1.57	6.82E-07	9.65E-06	chr16:3708038-3767598 (-)	16p13.3	TNF receptor-associated protein 1
ICT1	1.57	3.82E-06	3.50E-05	chr17:73008776-73017356 (+)	17q25.1	immature colon carcinoma transcript 1
RARS	1.57	2.18E-08	7.55E-07	chr5:167913450-167946309 (+)	5q35.1	arginyl-tRNA synthetase
ATP5G3	1.56	1.46E-10	1.72E-08	chr2:176040986-176049335 (-)	2q31.1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
MTX2	1.56	3.50E-10	3.26E-08	chr2:177134123-177202753 (+)	2q31.1	metaxin 2
RNGTT	1.56	2.23E-09	1.33E-07	chr6:89319985-89673348 (-)	6q16	RNA guanylyltransferase and 5-phosphatase
KNOP1	1.56	8.14E-10	6.16E-08	chr16:19717674-19729492 (-)	16p12.3	lysine-rich nucleolar protein 1
ILF2	1.56	7.06E-07	9.89E-06	chr1:153634512-153643524 (-)	1q21.3	interleukin enhancer binding factor 2
ARFGEF1	1.56	1.48E-04	6.11E-04	chr8:68085747-68255912 (-)	8q13	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)
CCDC47	1.56	8.37E-07	1.12E-05	chr17:61822610-61851088 (-)	17q23.3	coiled-coil domain containing 47
TCP1	1.56	9.29E-08	2.24E-06	chr6:160199530-160210781 (-)	6q25.3-q26	t-complex 1
NIP7	1.56	1.89E-06	2.05E-05	chr16:69373343-69377014 (+)	16q22.1	NIP7, nucleolar pre-rRNA processing protein
RP11-150O12.1	1.56	7.24E-11	1.06E-08	chr8:37278859-37411701 (-)	---	novel transcript
MKKS	1.56	5.09E-09	2.47E-07	chr20:10385832-10414870 (-)	20p12	McKusick-Kaufman syndrome
TTC39A	1.56	3.57E-07	5.97E-06	chr1:51752930-51810788 (-)	1p32.3	tetratricopeptide repeat domain 39A
PPIB	1.56	3.33E-08	1.04E-06	chr15:64448011-64455404 (-)	15q21-q22	peptidylprolyl isomerase B (cyclophilin B)
CALR	1.56	1.09E-07	2.53E-06	chr19:13049414-13055304 (+)	19p13.3-p13.2	calreticulin
ITGA2	1.56	2.15E-03	5.65E-03	chr5:52285156-52390609 (+)	5q11.2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
YTHDC2	1.56	6.51E-05	3.16E-04	chr5:112849380-112930984 (+)	5q22.2	YTH domain containing 2
VCP	1.56	1.28E-07	2.84E-06	chr9:35056061-35073246 (-)	9p13.3	valosin containing protein
C6orf47	1.56	8.03E-06	6.15E-05	chr6_dbb_hap3:2911654-2914128 (-)	6p21.3	chromosome 6 open reading frame 47
FAM72C	1.56	2.79E-05	1.61E-04	chr1:149438750-149459549 (-)	1q21.2	family with sequence similarity 72, member C
PHF20L1	1.56	6.39E-05	3.12E-04	chr8:133787604-133861052 (+)	8q24.22	PHD finger protein 20-like 1
MRPL13	1.56	1.34E-09	9.06E-08	chr8:121393000-121457647 (-)	8q22.1-q22.3	mitochondrial ribosomal protein L13
RNU4-72P	1.56	1.78E-04	7.11E-04	chr6:86461299-86461471 (+)	---	RNA, U4 small nuclear 72, pseudogene
CCT6P1	1.56	6.69E-08	1.74E-06	chr7:65216092-65228662 (+)	7q11.21	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1
PA2G4	1.56	9.38E-08	2.25E-06	chr12:56498103-56509935 (+)	12q13.2	proliferation-associated 2G4, 38kDa
GDAP1	1.56	7.17E-09	3.19E-07	chr8:75233365-75401107 (+)	8q21.11	ganglioside induced differentiation associated protein 1
EIF4E	1.56	2.52E-09	1.46E-07	chr4:99792835-99851788 (-)	4q21-q25	eukaryotic translation initiation factor 4E
ATIC	1.56	3.13E-08	9.91E-07	chr2:216176540-216214496 (+)	2q35	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferaseIMP cyclohydrolase
ERGIC2	1.56	1.40E-04	5.84E-04	chr12:29490285-29534143 (-)	12p11.22	ERGIC and golgi 2
CRYBG3	1.56	5.30E-03	1.21E-02	chr3:97595819-97663810 (+)	3q11.2	beta-gamma crystallin domain containing 3
HAUS6	1.56	7.22E-05	3.43E-04	chr9:19053141-19103117 (-)	9p22.1	HAUS augmin-like complex, subunit 6
TIPIN	1.56	2.28E-07	4.35E-06	chr15:66628722-66649054 (-)	15q22.31	TIMELESS interacting protein
RNASSP108	1.56	2.36E-07	4.44E-06	chr2:162266065-162266181 (+)	---	RNA, 5S ribosomal pseudogene 108
AK2	1.56	9.69E-12	2.41E-09	chr1:33473541-33502593 (-)	1p34	adenylate kinase 2
PINX1	1.56	1.19E-10	1.50E-08	chr8:10622473-10697394 (-)	8p23	PIN2/TERF1 interacting, telomerase inhibitor 1
PPAT	1.56	1.09E-06	1.36E-05	chr4:57259528-57301802 (-)	4q12	phosphoribosyl pyrophosphate amidotransferase
RP11-1D12.1	1.55	7.83E-05	3.66E-04	chr8:65616331-65647016 (-)	---	novel transcript
C6orf211	1.55	1.27E-07	2.84E-06	chr6:151773422-151791236 (+)	6q25.1	chromosome 6 open reading frame 211
SNRNP48	1.55	4.03E-07	6.54E-06	chr6:7590432-7612200 (+)	6p24.3	small nuclear ribonucleoprotein 48kDa (U11/U12)
BZW2	1.55	2.54E-09	1.46E-07	chr7:16685756-16746148 (+)	7p21.1	basic leucine zipper and W2 domains 2
MORC3	1.55	1.24E-05	8.55E-05	chr21:37692487-37748944 (+)	21q22.13	MORC family CW-type zinc finger 3
DCBLD1	1.55	1.63E-06	1.84E-05	chr6:117803820-117891021 (+)	6q22.1	discoidin, CUB and LCCL domain containing 1
SEC23B	1.55	7.32E-08	1.87E-06	chr20:18488137-18542059 (+)	20p11.23	Sec23 homolog B (S. cerevisiae)
CENPC	1.55	8.20E-03	1.76E-02	chr4:68337521-68411324 (-)	4q13.2	centromere protein C
AP1B1	1.55	6.48E-08	1.71E-06	chr22:29723669-29819168 (-)	22q12.2	adaptor-related protein complex 1, beta 1 subunit
EXT1	1.55	3.29E-08	1.03E-06	chr8:118806729-119124092 (-)	8q24.11	exostosin glycosyltransferase 1
SLC25A28	1.55	1.64E-09	1.06E-07	chr10:101370275-101418994 (-)	10q24.2	solute carrier family 25 (mitochondrial iron transporter), member 28
EIF4G3	1.55	2.52E-06	2.55E-05	chr1:21132785-21503381 (-)	1p36.12	eukaryotic translation initiation factor 4 gamma, 3
NDUFA9	1.55	2.12E-08	7.38E-07	chr12:4758264-4798454 (+)	12p13.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa
MCM5	1.55	3.93E-07	6.42E-06	chr22:35796056-35820495 (+)	22q13.1	minichromosome maintenance complex component 5
SQLE	1.55	1.36E-04	5.71E-04	chr8:126010720-126034525 (+)	8q24.1	squalene epoxidase
MTERF3	1.55	2.25E-08	7.74E-07	chr8:97251626-97273838 (-)	8q22.1	mitochondrial transcription termination factor 3
CSTF3	1.55	1.76E-05	1.12E-04	chr11:33106130-33183077 (-)	11p13	cleavage stimulation factor, 3 pre-RNA, subunit 3, 77kDa
TMEM69	1.55	3.53E-07	5.92E-06	chr1:46152886-46160115 (+)	1p34.1	transmembrane protein 69
LGALS9C	1.55	6.14E-09	2.83E-07	chr17:18380098-18398259 (+)	17p11.2	lectin, galactoside-binding, soluble, 9C
RALGPS2	1.55	7.17E-05	3.41E-04	chr1:178694300-179065553 (+)	1q25.2	Ral GEF with PH domain and SH3 binding motif 2
CDC25C	1.55	4.09E-06	3.69E-05	chr5:137620954-137674044 (-)	5q31	cell division cycle 25C
ZDHHC16	1.55	4.39E-09	2.20E-07	chr10:99205927-99217127 (+)	10q24.1	zinc finger, DHHC-type containing 16
SRSF10	1.55	1.41E-06	1.64E-05	chr1_gl000191_random:36273-50281 (	1p36.11	serinearginine-rich splicing factor 10
GTF2H3	1.55	1.46E-06	1.70E-05	chr12:124118376-124146479 (+)	12q24.31	general transcription factor IIH, polypeptide 3, 34kDa
MRPL1	1.55	2.48E-08	8.32E-07	chr4:78783674-78882347 (+)	4q21.1	mitochondrial ribosomal protein L1
SLC30A7	1.55	4.61E-08	1.33E-06	chr1:101361632-101447311 (+)	1p21.2	solute carrier family 30 (zinc transporter), member 7
ABCF2	1.55	8.52E-07	1.14E-05	chr7:150904923-150924317 (-)	7q36	ATP-binding cassette, sub-family F (GCN20), member 2
RP11-159F24.6	1.55	2.38E-05	1.42E-04	chr5:43511160-43521913 (+)	---	putative novel transcript
ZSCAN31	1.55	9.80E-07	1.26E-05	chr6:28292470-28324048 (-)	6p21.31|6p22.3-p22.1	zinc finger and SCAN domain containing 31
LAP3	1.55	8.56E-07	1.14E-05	chr4:17578815-17609595 (+)	4p15.32	leucine aminopeptidase 3
TMEM126B	1.55	1.23E-06	1.49E-05	chr11:85339622-85347583 (+)	11q14.1	transmembrane protein 126B
OR5P3	1.55	9.53E-03	2.01E-02	chr11:7846584-7847519 (-)	11p15.4	olfactory receptor, family 5, subfamily P, member 3
MTOR	1.55	2.31E-09	1.36E-07	chr1:11166588-11322608 (-)	1p36.2	mechanistic target of rapamycin (serinethreonine kinase)
TTC39B	1.55	4.21E-06	3.77E-05	chr9:15170842-15307358 (-)	9p22.3	tetratricopeptide repeat domain 39B
ABHD17C	1.55	6.96E-07	9.79E-06	chr15:80972025-81047962 (+)	15q25.1	abhydrolase domain containing 17C
ELOVL7	1.55	5.60E-05	2.80E-04	chr5:60047616-60140216 (-)	5q12.1	ELOVL fatty acid elongase 7
ZNF780B	1.55	1.96E-07	3.91E-06	chr19:40534167-40562116 (-)	19q13.2	zinc finger protein 780B
RNU6-1052P	1.55	4.93E-04	1.64E-03	chr7:56469763-56469866 (-)	---	RNA, U6 small nuclear 1052, pseudogene
ANAPC1	1.54	3.08E-09	1.68E-07	chr2:112523848-112642267 (-)	2q12.1	anaphase promoting complex subunit 1
AKIRIN2	1.54	6.31E-07	9.15E-06	chr6:88384578-88411985 (-)	6q15	akirin 2
HIPK2	1.54	3.41E-10	3.21E-08	chr7:139246316-139477693 (-)	7q32-q34	homeodomain interacting protein kinase 2
AQR	1.54	3.49E-08	1.08E-06	chr15:35147732-35262040 (-)	15q14	aquarius intron-binding spliceosomal factor
BOLA2	1.54	4.90E-08	1.39E-06	chr16:30204256-30205627 (-)	16p11.2	bolA family member 2
TKT	1.54	2.41E-07	4.52E-06	chr3:53258723-53290130 (-)	3p14.3	transketolase

RP11-195E2.4	1.54	2.38E-02	4.38E-02	chr5:70328995-70330227 (-)	---	novel transcript
PRMT5	1.54	1.68E-07	3.48E-06	chr14:23389720-23398794 (-)	14q11.2	protein arginine methyltransferase 5
ALG2	1.54	7.82E-08	1.97E-06	chr9:101978707-101984246 (-)	9q22.33	ALG2, alpha-1,31,6-mannosyltransferase
ZRANB2	1.54	1.94E-04	7.62E-04	chr1:71528974-71546980 (-)	1p31	zinc finger, RAN-binding domain containing 2
PURB	1.54	1.32E-06	1.57E-05	chr7:44915892-44924966 (-)	7p13	purine-rich element binding protein B
MALT1	1.54	4.22E-06	3.77E-05	chr18:56338618-56421130 (+)	18q21	mucosa associated lymphoid tissue lymphoma translocation gene 1
MARK1	1.54	1.97E-07	3.92E-06	chr1:220701568-220837803 (+)	1q41	MAPmicrotubule affinity-regulating kinase 1
RP11-278J6.3	1.54	1.97E-03	5.24E-03	chr5:142755193-142755448 (-)	---	---
MCCC2	1.54	1.05E-09	7.55E-08	chr5:70883115-70954531 (+)	5q12-q13	methylcrotonoyl-CoA carboxylase 2 (beta)
MRPL3	1.54	6.37E-07	9.21E-06	chr3:131181045-131221860 (-)	3q21-q23	mitochondrial ribosomal protein L3
HCG18	1.54	4.42E-08	1.29E-06	chr6:30255174-30294927 (-)	6p21.3	HLA complex group 18 (non-protein coding)
MAP3K5	1.54	3.79E-05	2.05E-04	chr6:136878185-137113657 (-)	6q22.33	mitogen-activated protein kinase kinase kinase 5
RRBP1	1.54	5.89E-11	9.29E-09	chr20:17594323-17662940 (-)	20p12	ribosome binding protein 1
TRMT1L	1.54	2.72E-07	4.94E-06	chr1:185087218-185126230 (-)	1q25.2	tRNA methyltransferase 1 homolog (S. cerevisiae)-like
USO1	1.54	1.33E-04	5.60E-04	chr4:76648697-76735382 (+)	4q21.1	USO1 vesicle transport factor
KLF7-IT1	1.54	2.06E-05	1.27E-04	chr2:207985608-207986768 (-)	---	KLF7 intronic transcript 1 (non-protein coding)
RSRC2	1.54	5.58E-04	1.82E-03	chr12:122989190-123011560 (-)	12q24.31	arginine/serine-rich coiled-coil 2
APEH	1.54	1.63E-06	1.84E-05	chr3:49711435-49721396 (+)	3p21.31	acylaminoacyl-peptide hydrolase
SENP6	1.54	2.41E-03	6.22E-03	chr6:76311225-76427997 (+)	6q13-q14.3	SUMO1sentrin specific peptidase 6
RPGRIP1L	1.54	9.21E-07	1.21E-05	chr16:53633818-53737771 (-)	16q12.2	RPGRIP1-like
ATP5E	1.54	1.51E-06	1.74E-05	chr20:57600522-57607437 (-)	20q13.32	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
MRPL46	1.54	5.73E-08	1.56E-06	chr15:89002707-89054752 (-)	15q25.3	mitochondrial ribosomal protein L46
HMGB3	1.54	3.94E-07	6.43E-06	chrX:150148982-150159248 (+)	Xq28	high mobility group box 3
DYNLT1	1.54	1.22E-08	4.80E-07	chr6:159057506-159065804 (-)	6q25.2-q25.3	dynein, light chain, Tctex-type 1
NSFP1	1.54	2.81E-03	7.08E-03	chr17:44450179-44500463 (+)	17q21.31	N-ethylmaleimide-sensitive factor pseudogene 1
ZNF37A	1.54	3.74E-06	3.44E-05	chr10:38383264-38412278 (+)	10p11.2	zinc finger protein 37A
CCT6A	1.54	1.12E-08	4.50E-07	chr7:56119323-56131682 (+)	7p11.2	chaperonin containing TCP1, subunit 6A (zeta 1)
DNAJC10	1.54	3.48E-05	1.92E-04	chr2:183580999-183653542 (+)	2q32.1	DnaJ (Hsp40) homolog, subfamily C, member 10
CMSS1	1.54	1.07E-06	1.35E-05	chr3:99536678-99897476 (+)	3q12.1	cms1 ribosomal small subunit homolog (yeast)
NUP37	1.53	6.50E-08	1.71E-06	chr12:102467967-102513902 (-)	12q23.2	nucleoporin 37kDa
DDX55	1.53	1.30E-08	5.06E-07	chr12:124086646-124105482 (+)	12q24.31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
AMD1	1.53	8.30E-07	1.12E-05	chr6:111135824-111216916 (+)	6q21	adenosylmethionine decarboxylase 1
ZNF33A	1.53	1.99E-03	5.28E-03	chr10:38299578-38356282 (+)	10p11.2	zinc finger protein 33A
ANKRD32	1.53	2.69E-07	4.90E-06	chr5:93954052-94075141 (+)	5q15	ankyrin repeat domain 32
ACYP1	1.53	4.71E-07	7.32E-06	chr14:75519924-75536186 (-)	14q24.3	acylphosphatase 1, erythrocyte (common) type
PRELID1	1.53	9.41E-07	1.22E-05	chr5:176730775-176733960 (+)	5q35.3	PRELI domain containing 1
TBK1	1.53	6.01E-06	4.93E-05	chr12:64845660-64895899 (+)	12q14.1	TANK-binding kinase 1
SDHB	1.53	3.41E-09	1.80E-07	chr1:17345217-17380665 (-)	1p36.1-p35	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
NDUFA1	1.53	1.69E-06	1.88E-05	chrX:119005450-119010629 (+)	Xq24	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
RAD51C	1.53	4.14E-06	3.72E-05	chr17:56769934-56811703 (+)	17q22	RAD51 paralog C
CTSS	1.53	1.73E-08	6.33E-07	chr1:150702551-150738433 (-)	1q21	cathepsin S
FAM162A	1.53	1.55E-07	3.27E-06	chr3:122103023-122131181 (+)	3q21.1	family with sequence similarity 162, member A
RBM47	1.53	9.46E-12	2.40E-09	chr4:40425272-40632892 (-)	4p14	RNA binding motif protein 47
LAD1	1.53	5.42E-07	8.14E-06	chr1:201349966-201368736 (-)	1q25.1-q32.3	ladinin 1
TUBGCP5	1.53	5.76E-06	4.78E-05	chr15:22833395-22873892 (+)	15q11.2	tubulin, gamma complex associated protein 5
PANK2	1.53	1.75E-04	7.02E-04	chr20:3898237-3899061 (+)	20p13	pantothenate kinase 2
RNU6-1045P	1.53	1.66E-05	1.07E-04	chr2:192235664-192235770 (+)	---	RNA, U6 small nuclear 1045, pseudogene
HNRNPA3	1.53	2.43E-10	2.48E-08	chr2:178077291-178088685 (+)	2q31.2	heterogeneous nuclear ribonucleoprotein A3
HIST1H2BF	1.53	1.25E-03	3.58E-03	chr6:26199748-26200942 (+)	6p22.1	histone cluster 1, H2bf
DNAJC8	1.53	1.14E-06	1.40E-05	chr1:28526790-28559542 (-)	1p35.3	DnaJ (Hsp40) homolog, subfamily C, member 8
HDAC2	1.53	9.75E-08	2.32E-06	chr6:114254192-114332472 (-)	6q21	histone deacetylase 2
TRIM21	1.53	1.24E-04	5.30E-04	chr11:4406127-4414926 (-)	11p15.5	tripartite motif containing 21
HIVEP2	1.53	7.61E-05	3.58E-04	chr6:143072604-143266338 (-)	6q23-q24	human immunodeficiency virus type I enhancer binding protein 2
TNFAIP2	1.53	8.22E-07	1.11E-05	chr14:103589779-103603776 (+)	14q32	tumor necrosis factor, alpha-induced protein 2
IRAK2	1.53	9.03E-06	6.74E-05	chr3:10206549-10285427 (+)	3p25.3	interleukin-1 receptor-associated kinase 2
TMEM135	1.53	1.12E-06	1.39E-05	chr11:86748886-87039876 (+)	11q14.2	transmembrane protein 135
SUPT16H	1.53	3.51E-05	1.93E-04	chr14:21819631-21852425 (-)	14q11.2	suppressor of Ty 16 homolog (S. cerevisiae)
TYW1B	1.53	7.09E-13	4.07E-10	chr7:72023729-72298813 (-)	7q11.23	tRNA-yW synthesizing protein 1 homolog B (S. cerevisiae)
MYBL2	1.53	2.34E-07	4.42E-06	chr20:42295709-42345136 (+)	20q13.1	v-myb avian myeloblastosis viral oncogene homolog-like 2
PSMC4	1.53	2.11E-05	1.29E-04	chr19:40477073-40487353 (+)	19q13.11-q13.13	proteasome (prosome, macropain) 26S subunit, ATPase, 4
GUF1	1.53	5.41E-05	2.73E-04	chr4:44680433-44702943 (+)	4p12	GUF1 GTPase homolog (S. cerevisiae)
HAUS1	1.53	6.10E-10	4.97E-08	chr18:43684298-43708299 (+)	18q21.1	HAUS augmin-like complex, subunit 1
ELL2	1.53	5.11E-05	2.61E-04	chr5:95220802-95297775 (-)	5q15	elongation factor, RNA polymerase II, 2
UQCR10	1.53	8.20E-06	6.25E-05	chr22:30163352-30166402 (+)	22q12.2	ubiquinol-cytochrome c reductase, complex III subunit X
TMTC2	1.53	4.42E-09	2.21E-07	chr12:83080659-83528649 (+)	12q21.31	transmembrane and tetratricopeptide repeat containing 2
DLAT	1.53	1.56E-07	3.29E-06	chr11:111895538-111935114 (+)	11q23.1	dihydrolipoamide S-acetyltransferase
SREK1IP1	1.53	3.78E-03	9.11E-03	chr5:64013978-64064512 (-)	5q12.3	SREK1-interacting protein 1
CCDC82	1.53	1.54E-03	4.26E-03	chr11:96085929-96123083 (-)	11q21	coiled-coil domain containing 82
FOCAD	1.53	5.93E-07	8.72E-06	chr9:20658308-20995954 (+)	9p21	focadhesin
KRT17P2	1.53	5.95E-05	2.95E-04	chr17:18330175-18335162 (+)	---	keratin 17 pseudogene 2
ADAL	1.53	8.96E-08	2.18E-06	chr15:43622872-43646096 (+)	15q15.3	adenosine deaminase-like
HERC2P2	1.53	5.64E-05	2.82E-04	chr15:28878269-28887567 (+)	15q11.2	hect domain and RLD 2 pseudogene 2
PTCD3	1.53	6.04E-08	1.61E-06	chr2:86333305-86369280 (+)	2p11.2	pentatricopeptide repeat domain 3
DMTF1	1.53	6.31E-04	2.02E-03	chr7:86781677-86825648 (+)	7q21	cyclin D binding myb-like transcription factor 1
SNRPG	1.53	8.39E-08	2.07E-06	chr2:70508494-70520903 (-)	2p13.3	small nuclear ribonucleoprotein polypeptide G
MYH9	1.53	3.24E-08	1.02E-06	chr22:36677323-36784063 (-)	22q13.1	myosin, heavy chain 9, non-muscle
EPHA2	1.52	7.02E-07	9.86E-06	chr1:16450832-16482582 (-)	1p36	EPH receptor A2
TXN	1.52	2.11E-05	1.29E-04	chr9:113006091-113018920 (-)	9q31	thioredoxin
CLEC2B	1.52	1.52E-02	2.99E-02	chr12:10004968-10022735 (-)	12p13-p12	C-type lectin domain family 2, member B
UBE3C	1.52	7.08E-10	5.54E-08	chr7:156931607-157062066 (+)	7q36.3	ubiquitin protein ligase E3C
EIF4A1	1.52	3.60E-07	6.01E-06	chr17:7475602-7482324 (+)	17p13	eukaryotic translation initiation factor 4A1
RUVBL1	1.52	1.21E-08	4.78E-07	chr3:127783625-127872757 (-)	3q21	RuvB-like AAA ATPase 1
R3HDM1	1.52	6.03E-08	1.61E-06	chr2:136289025-136482840 (+)	2q21.3	R3H domain containing 1
BTG3	1.52	9.57E-07	1.24E-05	chr21:18965968-18985268 (-)	21q21.1	BTG family, member 3
TAS2R19	1.52	6.59E-04	2.09E-03	chr12:11174218-11175219 (-)	12p13.2	taste receptor, type 2, member 19
IDH1	1.52	6.48E-08	1.71E-06	chr2:209100951-209130798 (-)	2q33.3	isocitrate dehydrogenase 1 (NADP+), soluble
IQGAP3	1.52	4.49E-06	3.96E-05	chr1:156495197-156542396 (-)	1q21.3	IQ motif containing GTPase activating protein 3
BCAS2	1.52	8.29E-05	3.83E-04	chr1:115110178-115124265 (-)	1p13.2	breast carcinoma amplified sequence 2
MTRF1	1.52	1.53E-07	3.24E-06	chr13:41790516-41837742 (-)	13q14.1-q14.3	mitochondrial translational release factor 1
OPA1	1.52	5.97E-04	1.93E-03	chr3:193310933-193415612 (+)	3q29	optic atrophy 1 (autosomal dominant)
AIMP1	1.52	9.23E-04	2.78E-03	chr4:107236701-107270383 (+)	4q24	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1
RNY4P19	1.52	2.23E-05	1.35E-04	chr2:230922945-230923040 (-)	---	RNA, Ro-associated Y4 pseudogene 19
CD68	1.52	4.12E-06	3.71E-05	chr17:7482805-7485431 (+)	17p13	CD68 molecule
RCN1P2	1.52	2.21E-06	2.30E-05	chr13:45964486-45964983 (-)	---	reticulocalbin 1, EF-hand calcium binding domain pseudogene 2
HERC2P9	1.52	1.13E-05	7.96E-05	chr15:28896567-28930410 (+)	15q13.1	hect domain and RLD 2 pseudogene 9
LRRC1	1.52	2.44E-08	8.24E-07	chr6:53783772-53785586 (+)	---	---
ACSL3	1.52	5.09E-06	4.35E-05	chr2:223725652-223809357 (+)	2q34-q35	acyl-CoA synthetase long-chain family member 3
XPO6	1.52	8.93E-08	2.18E-06	chr16:28109316-28223190 (-)	16p11.2	exportin 6
PPP2R3C	1.52	2.41E-09	1.41E-07	chr14:35554673-35591679 (-)	14q13.2	protein phosphatase 2, regulatory subunit B, gamma
SLC10A7	1.52	1.70E-09	1.09E-07	chr4:147175127-147443123 (-)	4q31.22	solute carrier family 10, member 7
FLVCR1	1.52	9.20E-07	1.20E-05	chr1:213031597-213072705 (+)	1q32.3	feline leukemia virus subgroup C cellular receptor 1
CHUK	1.52	7.61E-07	1.04E-05	chr10:101948055-101989376 (-)	10q24-q25	conserved helix-loop-helix ubiquitous kinase
LARP1B	1.52	1.22E-05	8.42E-05	chr4:128982423-129144086 (+)	4q28.2	La ribonucleoprotein domain family, member 1B
SERBP1	1.52	1.28E-08	5.00E-07	chr1:67873493-67896123 (-)	1p31	SERPINE1 mRNA binding protein 1
TAS2R14	1.52	6.45E-04	2.06E-03	chr12:11090005-11091862 (-)	12p13	taste receptor, type 2, member 14
SUV39H2	1.52	2.02E-10	2.18E-08	chr10:14920782-14946314 (+)	10p13	suppressor of variegation 3-9 homolog 2 (Drosophila)
ZNF33B	1.52	3.01E-04	1.10E-03	chr10:43069631-43134018 (-)	10q11.2	zinc finger protein 33B
MDH1	1.52	5.23E-09	2.51E-07	chr2:63815743-63834331 (+)	2p13.3	malate dehydrogenase 1, NAD (soluble)
DKC1	1.52	3.18E-07	5.52E-06	chrX:153991031-154005964 (+)	Xq28	dyskeratosis congenita 1, dyskerin
XRCC4	1.52	3.66E-08	1.12E-06	chr5:82373317-82652548 (+)	5q14.2	X-ray repair complementing defective repair in Chinese hamster cells 4
PIGF	1.52	2.39E-08	8.10E-07	chr2:46808076-46844258 (-)	2p21-p16	phosphatidylinositol glycan anchor biosynthesis, class F
POLR1B	1.52	1.24E-07	2.78E-06	chr2:113299492-113334727 (+)	2q13	polymerase (RNA) I polypeptide B, 128kDa
GOLGA6L5P	1.52	6.70E-04	2.12E-03	chr15:85047738-85070180 (-)	15q25.2	golgin A6 family-like 5, pseudogene
EDRF1	1.52	9.45E-06	6.97E-05	chr10:127408084-127452712 (+)	10q26.13	erythroid differentiation regulatory factor 1
ARAP2	1.52	1.30E-03	3.69E-03	chr4:36067620-36246131 (-)	4p14	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
CAMSAP2	1.52	1.34E-03	3.80E-03	chr1:200708686-200829832 (+)	1q32.1	calmodulin regulated spectrin-associated protein family, member 2
CDC45	1.52	1.56E-12	6.67E-10	chr22:19466982-19508135 (+)	22q11.21	cell division cycle 45
VPS45	1.52	1.55E-07	3.27E-06	chr1:150039342-150117505 (+)	1q21.2	vacuolar protein sorting 45 homolog (S. cerevisiae)
GINS1	1.52	9.10E-10	6.71E-08	chr20:25388321-25433264 (+)	20p11.21	GINS complex subunit 1 (Psf1 homolog)
CEP70	1.52	9.54E-07	1.24E-05	chr3:138213186-138313380 (-)	3q22.3	centrosomal protein 70kDa
ATP10D	1.52	3.42E-06	3.22E-05	chr4:47487305-47595503 (+)	4p12	ATPase, class V, type 10D
PITPNB	1.51	3.59E-08	1.10E-06	chr22:28202413-28316122 (-)	22q12.1	phosphatidylinositol transfer protein, beta
DST	1.51	4.83E-03	1.12E-02	chr6:56322785-56819426 (-)	6p12.1	dystonin
SCML1	1.51	3.63E-05	1.98E-04	chrX:17755588-17773105 (+)	Xq22	sex comb on midleg-like 1 (Drosophila)
RNU6-212P	1.51	7.14E-06	5.62E-05	chr15:59633513-59633616 (-)	---	RNA, U6 small nuclear 212, pseudogene
RIN2	1.51	1.98E-06	2.12E-05	chr20:19867165-19983103 (+)	20p11.22	Ras and Rab interactor 2
RAB1A	1.51	1.32E-06	1.57E-05	chr2:65297835-65357435 (-)	2p14	RAB1A, member RAS oncogene family
NAA25	1.51	3.11E-05	1.76E-04	chr12:112464493-112546826 (-)	12q24.13	N(alpha)-acetyltransferase 25, NatB auxiliary subunit
LPCAT3	1.51	2.07E-04	8.03E-04	chr12:7085347-7125842 (-)	12p13	lysophosphatidylcholine acyltransferase 3
MGC24103	1.51	1.42E-02	2.81E-02	chr9:16525993-16527731 (-)	9p22.3	uncharacterized MGC24103
ANKRD17	1.51	3.43E-05	1.89E-04	chr4:73939093-74124515 (-)	4q13.3	ankyrin repeat domain 17
TARBP1	1.51	9.37E-05	4.23E-04	chr1:234527059-234614849 (-)	1q42.3	TAR (HIV-1) RNA binding protein 1
RNASSP129	1.51	2.65E-03	6.74E-03	chr3:37383140-37383257 (+)	---	RNA, 5S ribosomal pseudogene 129
ARHGAP5	1.51	7.34E-04	2.29E-03	chr14:32546173-32628934 (+)	14q12	Rho GTPase activating protein 5
PDE12	1.51	5.73E-05	2.86E-04	chr3:57541981-57547768 (+)	3p14.3	phosphodiesterase 12
TRIM27	1.51	1.51E-07	3.22E-06	chr6:28870779-28891768 (-)	6p22	tripartite motif containing 27
LACTB	1.51	1.55E-06	1.77E-05	chr15:63413999-63434260 (+)	15q22.1	lactamase, beta
HSBP1	1.51	6.65E-08	1.74E-06	chr16:83841593-83846594 (+)	16q23.3	heat shock factor binding protein 1
NDUFB9	1.51	1.95E-08	6.88E-07	chr8:125551343-125580751 (+)	8q13.3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
LINS	1.51	1.38E-07	3.01E-06	chr15:101107119-101142445 (-)	15q26.3	lines homolog (Drosophila)
TRIM25	1.51	3.57E-05	1.96E-04	chr17:54965270-54991409 (-)	17q23.2	tripartite motif containing 25
APOL3	1.51	6.86E-07	9.69E-06	chr22:36536371-36562225 (-)	22q13.1	apolipoprotein L, 3
NDUFA4	1.51	6.66E-07	9.50E-06	chr7:10971578-10979883 (-)	7p21.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
RNU5A-8P	1.51	4.12E-04	1.42E-03	chr1:210547498-210547611 (-)	---	RNA, U5A small nuclear 8, pseudogene
ZNF518B	1.51	7.03E-11	1.04E-08	chr4:10441498-10459034 (-)	4p16.1	zinc finger protein 518B
CTAGE4	1.51	2.06E-02	3.88E-02	chr7:143880548-143883173 (+)	7q35	CTAGE family, member 4
KPNA3	1.51	8.33E-06	6.33E-05	chr13:50273443-50367057 (+)	13q14.3	karyopherin alpha 3 (importin alpha 4)
UBE2Q2P2	1.51	1.47E-04	6.08E-04	chr15:82647286-82708204 (+)	15q25	ubiquitin-conjugating enzyme E2Q family member 2 pseudogene 2
ZNF146	1.51	2.51E-04	9.43E-04	chr19:36705504-36729675 (+)	19q13.1	zinc finger protein 146
SNAPC3	1.51	9.87E-06	7.19E-05	chr9:15422702-15465951 (+)	9p22.3	small nuclear RNA activating complex, polypeptide 3, 50kDa
ILF3	1.51	1.24E-11	2.89E-09	chr19:10764937-10803095 (+)	19p13.2	interleukin enhancer binding factor 3, 90kDa
WDR76	1.51	4.10E-07	6.61E-06	chr15:44119112-44160617 (+)	15q15.3	WD repeat domain 76
DNAJC9	1.51	9.76E-11	1.31E-08	chr10:75002582-75012451 (-)	10q22.2	DnaJ (Hsp40) homolog, subfamily C, member 9
PFKFB2	1.51	3.59E-06	3.33E-05	chr1:207207761-207254369 (+)	1q31	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
MTCH2	1.51	5.44E-07	8.16E-06	chr11:47638858-47664206 (-)	11p11.2	mitochondrial carrier 2
WDR75	1.51	7.15E-05	3.40E-04	chr2:190306159-190340291 (+)	2q32.2	WD repeat domain 75
NAE1	1.51	1.07E-04	4.73E-04	chr16:66836778-66864900 (-)	16q22	NEDD8 activating enzyme E1 subunit 1
RPS6KC1	1.51	9.07E-10	6.70E-08	chr1:213224588-213448116 (+)	1q41	ribosomal protein S6 kinase, 52kDa, polypeptide 1
AURKB	1.51	1.40E-05	9.38E-05	chr17:8108049-8113936 (-)	17p13.1	aurora kinase B
KRT17P1	1.51	2.63E-05	1.53E-04	chr17:16744057-16749197 (-)	---	keratin 17 pseudogene 1

VMP1	1.51	9.33E-07	1.22E-05	chr17:57784863-57917952 (+)	17q23.1	vacuole membrane protein 1
HSPE1	1.51	1.34E-08	5.20E-07	chr2:198364718-198368187 (+)	2q33.1	heat shock 10kDa protein 1
HSPA14	1.51	9.59E-10	6.98E-08	chr10:14880163-14913740 (+)	10p13	heat shock 70kDa protein 14
TANGO6	1.51	6.14E-12	1.79E-09	chr16:68877509-69119085 (+)	16q22.1	transport and golgi organization 6 homolog (Drosophila)
EIF4A3	1.51	1.02E-05	7.38E-05	chr17:78109013-78120982 (-)	17q25.3	eukaryotic translation initiation factor 4A3
YWHAB	1.51	8.19E-09	3.53E-07	chr20:43514317-43537173 (+)	20q13.1	tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, beta
ALG8	1.51	6.53E-10	5.22E-08	chr11:77811988-77850706 (-)	11q14.1	ALG8, alpha-1,3-glucosyltransferase
SUCLA2	1.50	9.70E-07	1.25E-05	chr13:48510622-48612125 (-)	13q12.2-q13.3	succinate-CoA ligase, ADP-forming, beta subunit
GMCL1	1.50	3.40E-07	5.76E-06	chr2:70056774-70108528 (+)	2p13.3	germ cell-less, spermatogenesis associated 1
SCO1	1.50	3.03E-09	1.65E-07	chr17:10583649-10600885 (-)	17p13.1	SCO1 cytochrome c oxidase assembly protein
RNU6-1222P	1.50	7.51E-07	1.03E-05	chr6:148599808-148599914 (+)	---	RNA, U6 small nuclear 1222, pseudogene
RSL1D1	1.50	3.84E-04	1.34E-03	chr16:11928055-11945442 (-)	16p13.13	ribosomal L1 domain containing 1
TRPS1	1.50	3.04E-03	7.57E-03	chr8:116420724-116821899 (-)	8q24.12	trichorhinophalangeal syndrome I
RPS6KB2	1.50	9.12E-06	6.78E-05	chr11:67195935-67202879 (+)	11q13.2	ribosomal protein S6 kinase, 70kDa, polypeptide 2
COMMD8	1.50	2.40E-06	2.45E-05	chr4:47452811-47465736 (-)	4p12	COMM domain containing 8
APAE1	1.50	3.63E-05	1.98E-04	chr15:51200869-51298097 (+)	15q21.2	adaptor-related protein complex 4, epsilon 1 subunit
RRS1	1.50	3.50E-05	1.93E-04	chr8:67341263-67342968 (+)	8q13.1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
ADAR	1.50	9.27E-06	6.87E-05	chr1:154554534-154600475 (-)	1q21.3	adenosine deaminase, RNA-specific
ELAC2	1.50	2.44E-08	8.25E-07	chr17:12894929-12921381 (-)	17p11.2	elaC ribonuclease Z 2
CCRN4L	1.50	1.92E-08	6.86E-07	chr4:139936943-139967095 (+)	4q31.1	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
DPYD-IT1	1.50	2.36E-04	8.94E-04	chr1:97859710-97885697 (-)	---	DPYD intronic transcript 1 (non-protein coding)
H2AFZ	1.50	5.62E-07	8.34E-06	chr4:100869243-100871547 (-)	4q24	H2A histone family, member Z
HAT1	1.50	1.61E-06	1.82E-05	chr2:172778935-172848600 (+)	2q31.2-q33.1	histone acetyltransferase 1
RNU6-719P	1.50	2.93E-04	1.07E-03	chr7:39807940-39808043 (+)	---	RNA, U6 small nuclear 719, pseudogene
SMIM15	1.50	9.98E-10	7.21E-08	chr5:60453536-60458302 (-)	5q12.1	small integral membrane protein 15
OSTC	1.50	9.83E-09	4.07E-07	chr4:109571740-109588980 (+)	4q25	oligosaccharyltransferase complex subunit (non-catalytic)
UQCRC2	1.50	2.88E-07	5.17E-06	chr16:21963981-21994981 (+)	16p12	ubiquinol-cytochrome c reductase core protein II
TLR2	1.50	2.54E-07	4.70E-06	chr4:154605441-154627242 (+)	4q32	toll-like receptor 2
LOC100132686	1.50	1.37E-02	2.73E-02	chr11:112130988-112132119 (+)	11q23.1	uncharacterized LOC100132686
MEMO1P1	1.50	4.52E-08	1.32E-06	chr21:37502669-37504208 (+)	---	mediator of cell motility 1 pseudogene 1
HNRNPU	1.50	1.89E-06	2.05E-05	chr1:245013602-245027844 (-)	1q44	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
PTP4A1	1.50	1.54E-04	6.31E-04	chr6:64231651-64293492 (+)	6q12	protein tyrosine phosphatase type IVA, member 1
DUX4L4	0.67	2.21E-07	4.27E-06	chr4:191001979-191003583 (+)	4q35.2	double homeobox 4 like 4
NUPR1L	0.67	4.82E-07	7.45E-06	chr7:56182374-56184093 (-)	7p11.2	nuclear protein, transcriptional regulator, 1-like
ZFP36L1	0.67	1.34E-08	5.21E-07	chr14:69254372-69262960 (-)	14q22-q24	ZFP36 ring finger protein-like 1
RFTN2	0.67	8.42E-07	1.13E-05	chr2:198435524-198540769 (-)	2q33.1	raftlin family member 2
SMURF2	0.67	1.41E-05	9.40E-05	chr17:62540735-62658386 (-)	17q22-q23	SMAD specific E3 ubiquitin protein ligase 2
RP11-288G11.3	0.67	3.97E-09	2.02E-07	chr10:134596683-134598269 (-)	---	novel transcript
IFRD1	0.67	1.85E-05	1.16E-04	chr7:112063023-112117258 (+)	7q31.1	interferon-related developmental regulator 1
N4BP2L1	0.67	2.21E-07	4.27E-06	chr13:32974860-33002315 (-)	13q13.1	NEDD4 binding protein 2-like 1
EPHB1	0.67	8.95E-10	6.65E-08	chr3:134316643-134979309 (+)	3q21-q23	EPH receptor B1
RP11-108M9.2	0.67	2.20E-07	4.26E-06	chr1:17181902-17185779 (+)	---	putative novel transcript
XCR1	0.67	1.81E-07	3.68E-06	chr3:46058516-46069234 (-)	3p21.3	chemokine (C motif) receptor 1
DUSP10	0.67	3.51E-06	3.29E-05	chr1:221874764-221915518 (-)	1q41	dual specificity phosphatase 10
CTD-2330K9.2	0.67	5.35E-09	2.55E-07	chr3:49936735-49941190 (+)	---	novel transcript
ZNF358	0.67	1.51E-08	5.68E-07	chr19:7581004-7585912 (+)	19p13.2	zinc finger protein 358
NFIB	0.67	8.13E-05	3.77E-04	chr9:14081842-14398982 (-)	9p24.1	nuclear factor IB
NPBWR1	0.67	3.45E-08	1.07E-06	chr8:53850991-53853677 (+)	8p22-q21.13	neuropeptides BW receptor 1
EFCAB1	0.67	1.33E-06	1.57E-05	chr8:49623348-49647870 (-)	8q11.21	EF-hand calcium binding domain 1
MYO3A	0.67	6.38E-07	9.22E-06	chr10:26223002-26501465 (+)	10p11.1	myosin IIIA
TERC	0.67	1.68E-05	1.08E-04	chr3:169482398-169482848 (-)	3q26	telomerase RNA component
PGAM2	0.67	9.88E-06	7.19E-05	chr7:44102326-44105186 (-)	7p13-p12	phosphoglycerate mutase 2 (muscle)
RP1-213J1P__B.:	0.67	7.86E-07	1.07E-05	chr22:28103578-28105929 (+)	---	putative novel transcript
DLGAP4	0.67	3.58E-09	1.86E-07	chr20:34894258-35157040 (+)	20q11.23	discs, large (Drosophila) homolog-associated protein 4
FMOD	0.67	2.82E-07	5.07E-06	chr1:203309752-203320617 (-)	1q32	fibromodulin
TRAJ25	0.67	3.06E-07	5.38E-06	chr14:22987790-22987849 (+)	---	T cell receptor alpha joining 25 (non-functional)
RP5-827C21.2	0.67	3.84E-08	1.16E-06	chr1:234492752-234501574 (+)	---	putative novel transcript
ACADL	0.67	6.78E-06	5.40E-05	chr2:211052663-211090215 (-)	2q34	acyl-CoA dehydrogenase, long chain
LOC101928399	0.67	3.01E-09	1.64E-07	chr21:44778027-44782229 (-)	---	uncharacterized LOC101928399
RNA5-8SP5	0.67	9.03E-06	6.74E-05	chr2:133010727-133010878 (-)	---	RNA, 5.8S ribosomal pseudogene 5
PCDHGB2	0.67	1.30E-04	5.50E-04	chr5:140739640-140742196 (+)	5q31	protocadherin gamma subfamily B, 2
ETNK2	0.66	9.00E-11	1.25E-08	chr1:204100190-204121307 (-)	1q32.1	ethanolamine kinase 2
OLFML2A	0.66	6.60E-08	1.73E-06	chr9:127539437-127577164 (+)	9q33.3	olfactomedin-like 2A
RNASSP116	0.66	2.06E-07	4.06E-06	chr2:208918885-208918982 (-)	---	RNA, 5S ribosomal pseudogene 116
CKB	0.66	4.91E-05	2.53E-04	chr14:103985995-103989448 (-)	14q32	creatine kinase, brain
SORL1	0.66	1.95E-05	1.21E-04	chr11:121322912-121504471 (+)	11q23.2-q24.2	sortilin-related receptor, L(DLR class) A repeats containing
C1orf229	0.66	4.03E-10	3.61E-08	chr1:247273462-247275719 (-)	1q44	chromosome 1 open reading frame 229
SPTAN1	0.66	3.55E-08	1.09E-06	chr9:131314837-131395944 (+)	9q34.11	spectrin, alpha, non-erythrocytic 1
RNU6-667P	0.66	2.72E-04	1.01E-03	chr15:80109991-80109792 (-)	---	RNA, U6 small nuclear 667, pseudogene
SPINK1	0.66	1.99E-07	3.95E-06	chr5:147204131-147211349 (-)	5q32	serine peptidase inhibitor, Kazal type 1
ARL4A	0.66	5.38E-06	4.54E-05	chr7:12726452-12730559 (+)	7p21.3	ADP-ribosylation factor-like 4A
CYBRD1	0.66	2.21E-04	8.48E-04	chr2:172378757-172414643 (+)	2q31.1	cytochrome b reductase 1
PCDHB4	0.66	1.74E-03	4.71E-03	chr5:140501422-140505205 (+)	5q31	protocadherin beta 4
UCP2	0.66	3.90E-06	3.55E-05	chr11:73685712-73694352 (-)	11q13	uncoupling protein 2 (mitochondrial, proton carrier)
LOC100507373	0.66	3.12E-06	3.00E-05	chr19:14247964-14282075 (+)	---	uncharacterized LOC100507373
YOD1	0.66	5.08E-04	1.69E-03	chr1:207217194-207226325 (-)	1q32.2	YOD1 deubiquitinase
VWA2	0.66	6.94E-11	1.04E-08	chr10:115999018-116051737 (+)	10q25.3	von Willebrand factor A domain containing 2
C3orf52	0.66	5.63E-04	1.84E-03	chr3:111805182-111849851 (+)	3q13.2	chromosome 3 open reading frame 52
SERPINA9	0.66	2.29E-07	4.37E-06	chr14:94929054-94946026 (-)	14q32.13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9
SOD3	0.66	7.80E-09	3.40E-07	chr4:24797085-24802467 (+)	4p15.2	superoxide dismutase 3, extracellular
SELM	0.66	1.51E-07	3.22E-06	chr22:31500758-31516055 (-)	22q12.2	selenoprotein M
CD207	0.66	2.86E-06	2.81E-05	chr2:71057343-71062953 (-)	2p13	CD207 molecule, langerin
CORO2B	0.66	1.95E-10	2.13E-08	chr15:68871308-69020145 (+)	15q23	coronin, actin binding protein, 2B
ANO1	0.66	7.08E-04	2.22E-03	chr11:69924408-70035652 (+)	11q13.3	anoctamin 1, calcium activated chloride channel
LKAAEAR1	0.66	3.08E-08	9.79E-07	chr20:62714733-62715712 (-)	20q13.33	LKAAEAR motif containing 1
SEMA5A	0.66	1.01E-04	4.50E-04	chr5:9035138-9546233 (-)	5p15.2	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
SIDT2	0.66	1.92E-06	2.07E-05	chr11:117049449-117068161 (+)	11q23.3	SID1 transmembrane family, member 2
AC008440.10	0.66	7.05E-08	1.82E-06	chr19:54368017-54369394 (+)	---	putative novel transcript
PLEKHG1	0.66	3.65E-06	3.38E-05	chr6:150920999-151164799 (+)	6q25.1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1
DDIT3	0.66	1.84E-03	4.94E-03	chr12:57910371-57914300 (-)	12q13.1-q13.2	DNA-damage-inducible transcript 3
SOWAHB	0.66	3.23E-09	1.73E-07	chr4:77816081-77819300 (-)	4q21.1	sosondowah ankyrin repeat domain family member B
PDK2	0.66	8.93E-08	2.18E-06	chr17:48172101-48189516 (+)	17q21.33	pyruvate dehydrogenase kinase, isozyme 2
FA2H	0.66	2.64E-07	4.84E-06	chr16:74746853-74808730 (-)	16q23	fatty acid 2 hydroxylase
CRISPLD1	0.66	6.17E-08	1.65E-06	chr8:75896708-75946793 (+)	8q21.11	cysteine-rich secretory protein LCCL domain containing 1
ID2B	0.66	3.17E-04	1.14E-03	chr3:62109159-62110392 (-)	3p14.2	inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)
PPP1R14C	0.66	7.64E-07	1.05E-05	chr6:150464188-150571528 (+)	6q24.3-q25.3	protein phosphatase 1, regulatory (inhibitor) subunit 14C
NPAS2	0.66	6.15E-04	1.98E-03	chr2:101436613-101613291 (+)	2q11.2	neuronal PAS domain protein 2
NUAK1	0.66	2.15E-03	5.63E-03	chr12:106457118-106533811 (-)	12q23.3	NUAK family, SNF1-like kinase, 1
CTF1	0.66	4.80E-09	2.35E-07	chr16:30907928-30914881 (+)	16p11.2	cardiotrophin 1
DUX4L3	0.66	6.62E-08	1.73E-06	chrUn_gl000228:105687-114676 (+)	4q35.2	double homeobox 4 like 3
MCOLN3	0.66	2.08E-03	5.48E-03	chr1:85483765-85514223 (-)	1p22.3	mucolipin 3
TGFBR3	0.66	4.40E-06	3.90E-05	chr1:92145900-92371892 (-)	1p33-p32	transforming growth factor, beta receptor III
LIPN	0.66	2.64E-02	4.78E-02	chr10:90519952-90537999 (+)	10q23.31	lipase, family member N
AC018685.2	0.66	3.22E-08	1.01E-06	chr2:2733680-2734729 (-)	---	novel transcript
CTC-338M12.9	0.66	1.19E-06	1.45E-05	chr5:180708376-180710653 (+)	---	novel transcript
AC118754.4	0.66	2.11E-06	2.23E-05	chr17:4400689-4402969 (-)	---	novel transcript
FGF14-AS2	0.66	7.89E-08	1.98E-06	chr13:103046928-103048055 (+)	13q33.1	FGF14 antisense RNA 2
POM121L12	0.66	1.09E-07	2.53E-06	chr7:53103335-53104618 (+)	7p12.1	POM121 transmembrane nucleoporin-like 12
CTNNBIP1	0.66	9.08E-10	6.70E-08	chr1:9827077-9970394 (-)	1p36.22	catenin, beta interacting protein 1
AP001891.1	0.66	2.14E-07	4.17E-06	chr11:116367616-116371347 (-)	---	putative novel transcript
PTGS2	0.66	1.16E-03	3.36E-03	chr1:186640923-186649559 (-)	1q25.2-q25.3	prostaglandin-endoperoxide synthase 2 (prostaglandin GH synthase and cyclooxygenase)
ANKH	0.66	2.59E-07	4.77E-06	chr5:14704909-14871887 (-)	5p15.1	ANKH inorganic pyrophosphate transport regulator
RNASSP113	0.66	3.38E-05	1.87E-04	chr2:182913549-182913632 (+)	---	RNA, 5S ribosomal pseudogene 113
RP11-363D14.1	0.66	9.10E-08	2.21E-06	chr2:97193677-97198043 (-)	---	novel transcript
S1PR4	0.66	4.29E-08	1.27E-06	chr19:3178736-3180330 (+)	19p13.3	sphingosine-1-phosphate receptor 4
ZDHHC9	0.66	6.54E-06	5.26E-05	chrX:128937264-128978124 (-)	Xq26.1	zinc finger, DHHC-type containing 9
TRAJ59	0.66	7.32E-07	1.01E-05	chr14:22945543-22945596 (+)	---	T cell receptor alpha joining 59 (non-functional)
RNASSP283	0.66	2.30E-07	4.37E-06	chr9:66458144-66458262 (-)	---	RNA, 5S ribosomal pseudogene 283
ABHD16B	0.66	3.90E-07	6.38E-06	chr20:62492566-62494659 (+)	20q13.33	abhydrolase domain containing 16B
HOXB2	0.66	2.79E-06	2.76E-05	chr17:46618256-46623441 (-)	17q21.32	homeobox B2
WNK2	0.66	5.15E-12	1.57E-09	chr9:95947198-96082854 (+)	9q22.3	WNK lysine deficient protein kinase 2
CA13	0.66	4.40E-07	6.95E-06	chr8:86132816-86196302 (+)	8q21.2	carbonic anhydrase XIII
LOC100996246	0.66	2.26E-07	4.32E-06	chr12:132671287-132674240 (-)	---	uncharacterized LOC100996246
SCARNA11	0.66	2.46E-06	2.50E-05	chr12:6690639-6690775 (-)	12p13.31	small Cajal body-specific RNA 11
CABLES1	0.66	1.52E-06	1.75E-05	chr18:20714528-20840434 (+)	18q11.2	Cdk5 and Abl enzyme substrate 1
LGALSL	0.66	3.01E-04	1.09E-03	chr2:64681103-64688517 (+)	2p14	lectin, galactoside-binding-like
ZEB2	0.66	6.79E-06	5.41E-05	chr2:145121063-145282147 (-)	2q22.3	zinc finger E-box binding homeobox 2
PLXNA4	0.66	6.23E-11	9.59E-09	chr7:131808091-132333447 (-)	7q32.3	plexin A4
COX4I2	0.66	4.18E-07	6.70E-06	chr20:30225691-30232809 (+)	20q11.21	cytochrome c oxidase subunit IV isoform 2 (lung)
WNT2	0.66	3.20E-08	1.01E-06	chr7:116916685-116963343 (-)	7q31.2	wingless-type MMTV integration site family member 2
ITPKB	0.66	9.52E-10	6.95E-08	chr1:226819391-226927024 (-)	1q42.13	inositol-trisphosphate 3-kinase B
RP4-781K5.2	0.66	7.30E-07	1.01E-05	chr1:234742754-234745229 (+)	---	novel transcript
FAM218A	0.66	4.51E-08	1.31E-06	chr4:165878100-165880274 (+)	4q32.3	family with sequence similarity 218, member A
CELF2	0.66	2.79E-07	5.04E-06	chr10:11047259-11378672 (+)	10p13	CUGBP, Elav-like family member 2
FXYD6	0.66	2.63E-10	2.65E-08	chr11:117690785-117748201 (-)	11q23.3	FXYD domain containing ion transport regulator 6
AZGP1P1	0.66	1.11E-07	2.56E-06	chr7:99578385-99591588 (+)	7q22.1	alpha-2-glycoprotein 1, zinc-binding pseudogene 1
PCDHB16	0.65	5.88E-06	4.86E-05	chr5:140560980-140565974 (+)	5q31	protocadherin beta 16
C1QL2	0.65	1.22E-06	1.47E-05	chr2:119913819-119916471 (-)	2q14.2	complement component 1, q subcomponent-like 2
RP11-379F12.4	0.65	6.46E-06	5.21E-05	chr10:80935504-80950047 (+)	---	putative novel transcript
ZFP36	0.65	3.26E-03	8.02E-03	chr19:39897487-39900047 (+)	19q13.1	ZFP36 ring finger protein
ZSCAN18	0.65	2.64E-11	5.18E-09	chr19:58595206-58629793 (-)	19q13.43	zinc finger and SCAN domain containing 18
COL6A2	0.65	1.71E-09	1.09E-07	chr21:47518011-47552763 (+)	21q22.3	collagen, type VI, alpha 2
GLCCI1	0.65	5.87E-06	4.85E-05	chr7:8008423-8133902 (+)	7p21.3	glucocorticoid induced transcript 1
SLC29A1	0.65	1.35E-08	5.21E-07	chr6:44187242-44201888 (+)	6p21.1	solute carrier family 29 (equilibrative nucleoside transporter), member 1
ADAMTS15	0.65	1.90E-07	3.82E-06	chr11:130318869-130346539 (+)	11q25	ADAM metallopeptidase with thrombospondin type 1 motif, 15
AKAP12	0.65	1.58E-09	1.03E-07	chr6:151561134-151679694 (+)	6q24-q25	A kinase (PRKA) anchor protein 12
AGBL5-AS1	0.65	2.78E-07	5.03E-06	chr2:27272551-27273132 (-)	2p23.3	AGBL5 antisense RNA 1
MYL9	0.65	2.29E-08	7.85E-07	chr20:35169887-35178228 (+)	20q11.23	myosin, light chain 9, regulatory
NFIX	0.65	8.33E-08	2.06E-06	chr19:13106584-13209610 (+)	19p13.3	nuclear factor IX (CCAAT-binding transcription factor)
RNASSP488	0.65	9.00E-09	3.81E-07	chr21:15443192-15443307 (+)	---	RNA, 5S ribosomal pseudogene 488
ZNF727P	0.65	4.19E-05	2.23E-04	chr7:63505821-63538927 (+)	7q11.21	zinc finger protein 727, pseudogene
ZDHHC11	0.65	4.70E-08	1.35E-06	chr5:795720-851101 (-)	5p15.33	zinc finger, DHHC-type containing 11
INHBB	0.65	1.13E-04	4.91E-04	chr2:121103719-121109384 (+)	2cen-q13	inhibin, beta B
NR3C2	0.65	2.34E-12	9.02E-10	chr4:148999913-149365850 (-)	4q31.1	nuclear receptor subfamily 3, group C, member 2
FAM47C	0.65	6.58E-06	5.28E-05	chrX:37026432-37029739 (+)	Xp21.1	family with sequence similarity 47, member C
LOC101930415	0.65	1.69E-08	6.22E-07	chr6:158703295-158733390 (+)	---	uncharacterized LOC101930415
SLC37A2	0.65	8.31E-04	2.54E-03	chr11:124932963-124960412 (+)	11q24.2	solute carrier family 37 (glucose-6-phosphate transporter), member 2
AC079154.1	0.65	1.65E-06	1.85E-05	chr2:124774435-124782750 (-)	---	putative novel transcript
IRX1	0.65	1.55E-07	3.28E-06	chr5:3596168-3601517 (+)	5p15.3	iroquois homeobox 1
AGFG2	0.65	7.81E-08	1.97E-06	chr7:100136834-100165843 (+)	7q22.1	ArfGAP with FG repeats 2

DEGS2	0.65	1.18E-08	4.69E-07	chr14:100612753-100626500 (-)	14q32.2	delta(4)-desaturase, sphingolipid 2
SYT8	0.65	9.37E-10	6.85E-08	chr11:1484439-1858751 (+)	11p15.5	synaptotagmin VIII
FOXI3	0.65	3.43E-06	3.23E-05	chr2:88747726-88752053 (-)	2p11.2	forkhead box I3
ALDH3A2	0.65	1.20E-06	1.46E-05	chr17:19551459-19580909 (+)	17p11.2	aldehyde dehydrogenase 3 family, member A2
ABCC3	0.65	7.42E-09	3.27E-07	chr17:48712138-48769063 (+)	17q22	ATP-binding cassette, sub-family C (CFTRMRP), member 3
FAM58BP	0.65	3.51E-07	5.90E-06	chr1:200182656-200183643 (+)	1q32.1	family with sequence similarity 58, member B, pseudogene
OR2T10	0.65	8.60E-03	1.84E-02	chr1:248756052-248757100 (-)	1q44	olfactory receptor, family 2, subfamily T, member 10
VRTN	0.65	5.47E-07	8.19E-06	chr14:74815116-74826711 (+)	14q24.3	vertebrae development associated
SYT17	0.65	1.77E-06	1.95E-05	chr16:19179571-19279652 (+)	16p12.3	synaptotagmin XVII
GPM6B	0.65	7.74E-06	5.98E-05	chrX:13789062-13956831 (-)	Xp22.2	glycoprotein M6B
AGO4	0.65	3.01E-06	2.91E-05	chr1:36273773-36323491 (+)	1p34	argonaute RISC catalytic component 4
PTPN21	0.65	5.25E-08	1.47E-06	chr14:88932122-89021123 (-)	14q31.3	protein tyrosine phosphatase, non-receptor type 21
LOC101929476	0.65	4.30E-03	1.02E-02	chr1:209541007-209553035 (+)	---	uncharacterized LOC101929476
XG	0.65	8.26E-04	2.53E-03	chrX:2670091-2734541 (+)	Xp22.33	Xg blood group
PYY2	0.65	2.03E-09	1.24E-07	chr17:26553589-26555091 (+)	17q11	peptide YY, 2 (pseudogene)
EPPK1	0.64	1.41E-02	2.81E-02	chr8:144939497-144952632 (-)	8q24.3	epiplakin 1
GRAMD3	0.65	1.17E-06	1.43E-05	chr5:125695788-125832186 (+)	5q23.2	GRAM domain containing 3
EEF1A2	0.65	1.66E-09	1.06E-07	chr20:62119366-62130637 (-)	20q13.3	eukaryotic translation elongation factor 1 alpha 2
HEY2	0.65	8.09E-05	3.76E-04	chr6:126068780-126082415 (+)	6q21	hes-related family bHLH transcription factor with YRPW motif 2
CAB39L	0.65	1.14E-09	8.03E-08	chr13:49882786-50020554 (-)	13q14.2	calcium binding protein 39-like
HOXC-AS1	0.65	1.37E-05	9.21E-05	chr12:54392806-54393794 (-)	12q13.13	HOXC cluster antisense RNA 1
SOX4	0.65	9.34E-05	4.22E-04	chr6:21593000-21598850 (+)	6p22.3	SRY (sex determining region Y)-box 4
AC091729.7	0.65	2.05E-08	7.20E-07	chr7:1114086-1117672 (+)	---	novel transcript
GSTO2	0.65	2.47E-06	2.51E-05	chr10:106061962-106064704 (+)	10q25.1	glutathione S-transferase omega 2
IGH	0.65	9.66E-08	2.31E-06	chr14:106173457-106175002 (-)	14q32.33	immunoglobulin heavy locus
MAGEH1	0.65	8.98E-10	6.67E-08	chrX:55478538-55479999 (+)	Xp11.21	melanoma antigen family H, 1
FLJ13224	0.65	2.17E-08	7.54E-07	chr12:31477250-31478879 (+)	12p11.21	uncharacterized LOC79857
PNMA6D	0.65	5.43E-09	2.58E-07	chrX:152243996-152246070 (-)	Xq28	paraneoplastic Ma antigen family member 6D
ZNF608	0.65	8.86E-10	6.60E-08	chr5:123972608-124084500 (-)	5q23.2	zinc finger protein 608
RP11-485M7.3	0.65	7.93E-06	6.09E-05	chr5:132446747-132450167 (-)	---	novel transcript
MYO5B	0.65	2.17E-04	8.36E-04	chr18:47349156-47721451 (-)	18q21	myosin VB
ZNF677	0.64	4.50E-10	3.93E-08	chr19:53727087-53758126 (-)	19q13.42	zinc finger protein 677
ZFP28	0.64	1.42E-07	3.08E-06	chr19:57050317-57068170 (+)	---	ZFP28 zinc finger protein
AC002117.1	0.64	5.12E-03	1.18E-02	chr17:43227985-43236822 (-)	---	novel transcript, antisense to HEXIM1 and HEXIM2
SEMA7A	0.64	1.35E-07	2.97E-06	chr15:74701630-74726300 (-)	15q22.3-q23	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
FZD10	0.64	5.15E-05	2.63E-04	chr12:130647004-130650285 (+)	12q24.33	frizzled class receptor 10
GAS1	0.64	2.57E-09	1.47E-07	chr9:89559277-89562104 (-)	9q21.3-q22	growth arrest-specific 1
FCHO1	0.64	1.60E-10	1.84E-08	chr19:17858527-17899377 (+)	19p13.11	FCH domain only 1
EPS8L1	0.64	4.66E-09	2.30E-07	chr19:55583388-55599291 (+)	19q13.42	EPS8-like 1
TRPV6	0.64	2.31E-07	4.39E-06	chr7:142568956-142583507 (-)	7q34	transient receptor potential cation channel, subfamily V, member 6
TULP3	0.64	9.88E-06	7.19E-05	chr12:3000033-3050306 (+)	12p13.3	tubby like protein 3
GJB5	0.64	9.72E-06	7.11E-05	chr1:35220648-35224113 (+)	1p35.1	gap junction protein, beta 5, 31.1kDa
SLC43A1	0.64	1.32E-03	3.76E-03	chr11:57252004-57283259 (-)	11q12.1	solute carrier family 43 (amino acid system L transporter), member 1
AC011247.3	0.64	1.45E-05	9.63E-05	chr2:38828740-38829320 (+)	---	putative novel transcript
CMTM8	0.64	1.24E-07	2.79E-06	chr3:32280171-32411817 (+)	3p22.3	CKLF-like MARVEL transmembrane domain containing 8
DBX2	0.64	4.27E-09	2.15E-07	chr12:45408455-45444882 (-)	12q12	developing brain homeobox 2
SLC46A3	0.64	2.62E-04	9.77E-04	chr13:29274201-29293150 (-)	13q12.3	solute carrier family 46, member 3
CYP4F8	0.64	1.58E-04	6.45E-04	chr19:15726029-15740448 (+)	19p13.1	cytochrome P450, family 4, subfamily F, polypeptide 8
LIPH	0.64	1.52E-03	4.20E-03	chr3:185224050-185270401 (-)	3q27	lipase, member H
LOC100128703	0.64	6.44E-09	2.94E-07	chr11:528907-529659 (+)	11p15.5	uncharacterized LOC100128703
SLITRK2	0.64	4.12E-09	2.08E-07	chrX:144899347-144907360 (+)	Xq27.3	SLIT and NTRK-like family, member 2
ANKRD37	0.64	3.19E-06	3.05E-05	chr4:186317175-186321782 (+)	4q35.1	ankyrin repeat domain 37
RNU5E-9P	0.64	9.78E-08	2.33E-06	chr2:179007275-179007378 (+)	---	RNA, U5E small nuclear 9, pseudogene
ALOXE3	0.64	6.84E-03	1.51E-02	chr17:7999218-8022234 (-)	17p13.1	arachidonate lipoxygenase 3
P2RX7	0.64	1.98E-06	2.12E-05	chr12:121570622-121624354 (+)	12q24	purinergic receptor P2X, ligand-gated ion channel, 7
ABHD6	0.64	3.62E-07	6.02E-06	chr3:58223233-58281420 (+)	3p14.3	abhydrolase domain containing 6
HCFC1-AS1	0.64	3.02E-08	9.65E-07	chrX:153234776-153235538 (+)	---	HCFC1 antisense RNA 1
VAMP2	0.64	3.21E-10	3.08E-08	chr17:8062465-8066864 (-)	17p13.1	vesicle-associated membrane protein 2 (synaptobrevin 2)
SOHLH1	0.64	2.36E-08	8.04E-07	chr9:138585383-138585490 (+)	9q34.3	spermatogenesis and oogenesis specific basic helix-loop-helix 1
LOC100289511	0.64	7.75E-08	1.96E-06	chr14:70233000-70234430 (-)	14q24.2	uncharacterized LOC100289511
SSFA2	0.64	7.04E-06	5.57E-05	chr2:182756472-182795465 (+)	2q31.3	sperm specific antigen 2
PDGFA	0.64	4.72E-10	4.10E-08	chr7:536895-559933 (-)	7p22	platelet-derived growth factor alpha polypeptide
PCDHB11	0.64	7.09E-05	3.38E-04	chr5:140579183-140582618 (+)	5q31	protocadherin beta 11
RNASSP441	0.64	6.54E-07	9.38E-06	chr17:38530341-38530428 (+)	---	RNA, 5S ribosomal pseudogene 441
RNASSP417	0.64	2.66E-09	1.51E-07	chr16:34986199-34986306 (+)	---	RNA, 5S ribosomal pseudogene 417
C15orf48	0.64	8.89E-05	4.06E-04	chr15:45722727-45725647 (+)	15q21.1	chromosome 15 open reading frame 48
KRT15	0.64	1.23E-03	3.54E-03	chr17:39669995-39678781 (-)	17q21.2	keratin 15
CASP14	0.64	4.14E-03	9.82E-03	chr19:15160291-15169103 (+)	19p13.1	caspase 14, apoptosis-related cysteine peptidase
FGF22	0.64	2.91E-09	1.61E-07	chr19:639895-643703 (+)	19p13.3	fibroblast growth factor 22
RNVU1-14	0.64	1.47E-04	6.07E-04	chr1:148241465-148241628 (+)	1q21.2	RNA, variant U1 small nuclear 14
TRAPPC6A	0.64	2.30E-12	8.92E-10	chr19:45666186-45681495 (-)	19q13.32	trafficking protein particle complex 6A
MGP	0.64	4.23E-04	1.45E-03	chr12:15034115-15038860 (-)	12p12.3	matrix Gla protein
RNVU1-8	0.64	2.11E-07	4.14E-06	chr1:146551295-146551419 (+)	---	RNA, variant U1 small nuclear 8
FAM95B1	0.64	1.42E-07	3.08E-06	chr9:66368738-66368772 (-)	9p12	family with sequence similarity 95, member B1
SORBS1	0.64	4.94E-11	8.24E-09	chr10:97071528-97321171 (-)	10q23.33	sorbin and SH3 domain containing 1
LOC286189	0.64	8.94E-07	1.18E-05	chr8:69214472-69243727 (-)	8q13.1	uncharacterized LOC286189
AS3MT	0.64	5.02E-05	2.57E-04	chr10:104629210-104661656 (+)	10q24.32	arsenite methyltransferase
FGL2	0.64	6.23E-03	1.39E-02	chr7:76822688-76829150 (-)	7q11.23	fibrinogen-like 2
P2RY4	0.64	9.31E-10	6.83E-08	chrX:69478016-69479654 (-)	Xq13	pyrimidinergic receptor P2Y, G-protein coupled, 4
CCSAP	0.64	6.44E-09	2.94E-07	chr1:229456752-229479041 (-)	1q42.13	centriole, cilia and spindle-associated protein
ECM1	0.64	1.00E-07	2.37E-06	chr1:150480487-150486265 (+)	1q21	extracellular matrix protein 1
LCP1	0.64	5.85E-07	8.62E-06	chr13:46700058-46786006 (-)	13q14.3	lymphocyte cytosolic protein 1 (L-plastin)
KCNJ13	0.64	5.13E-07	7.80E-06	chr2:233630512-233641278 (-)	2q37	potassium inwardly-rectifying channel, subfamily J, member 13
PAX3	0.64	2.86E-07	5.13E-06	chr2:223064606-223163715 (-)	2q35	paired box 3
DMD	0.64	6.85E-08	1.78E-06	chrX:31132808-33357726 (-)	Xp21.2	dystrophin
IL17RE	0.64	2.53E-09	1.46E-07	chr3:9944296-9958086 (+)	3p25.3	interleukin 17 receptor E
FAM107B	0.63	5.81E-09	2.71E-07	chr10:14560556-14816896 (-)	10p13	family with sequence similarity 107, member B
AC084082.3	0.63	3.27E-10	3.13E-08	chr8:67024902-67027414 (+)	---	novel transcript
CSNK2A2	0.63	8.70E-06	6.55E-05	chr16:58191811-58231782 (-)	16q21	casein kinase 2, alpha prime polypeptide
LOC643355	0.63	2.48E-08	8.33E-07	chr1:112532392-112533795 (+)	1p13.2	uncharacterized LOC643355
RP11-98L5.5	0.63	1.51E-08	5.67E-07	chr9:138506142-138507354 (+)	---	novel transcript
TNFAIP8L3	0.63	1.94E-09	1.20E-07	chr15:51348795-51397473 (-)	15q21.2	tumor necrosis factor, alpha-induced protein 8-like 3
EFEMP2	0.63	1.43E-07	3.10E-06	chr11:65633912-65640405 (-)	11q13.1	EGF containing fibulin-like extracellular matrix protein 2
UST	0.63	2.41E-06	2.46E-05	chr6:149068271-149398126 (+)	6q25.1	uronyl-2-sulfotransferase
RNU2-36P	0.63	4.78E-06	4.15E-05	chr9:89037853-89038043 (-)	---	RNA, U2 small nuclear 36, pseudogene
KLF10	0.63	3.23E-08	1.02E-06	chr8:103661005-103668130 (-)	8q22.2	Kruppel-like factor 10
SNAR-H	0.63	2.07E-07	4.08E-06	chr2:78182033-78182152 (-)	2p12	small ILF3NF90-associated RNA H
RNASSP432	0.63	2.83E-06	2.79E-05	chr16:84073523-84073638 (-)	---	RNA, 5S ribosomal pseudogene 432
RNY4P4	0.63	1.88E-06	2.04E-05	chr3:136307051-136307153 (+)	---	RNA, Ro-associated Y4 pseudogene 4
HLA-DRB5	0.63	1.30E-05	8.86E-05	chr6:32485120-32498064 (-)	6p21.3	major histocompatibility complex, class II, DR beta 5
LNX1	0.63	3.44E-09	1.81E-07	chr4:54325468-54567572 (-)	4q12	ligand of numb-protein X 1, E3 ubiquitin protein ligase
MT1X	0.63	6.12E-05	3.01E-04	chr16:56716336-56718108 (+)	16q13	metallothionein 1X
OCLN	0.63	1.83E-06	2.00E-05	chr5:68788119-68853931 (+)	5q13.1	occludin
OTUD1	0.63	8.59E-11	1.20E-08	chr10:23728198-23731319 (+)	10p12.2	OTU deubiquitinase 1
LYPD5	0.63	1.47E-02	2.91E-02	chr19:44300079-44324808 (-)	19q13.31	LY6PLAUR domain containing 5
FAM27E3	0.63	1.05E-09	7.54E-08	chr9:46385691-46387031 (-)	9q13	family with sequence similarity 27, member E3
LYPD6B	0.63	2.49E-05	1.47E-04	chr2:149894621-150071776 (+)	2q23.2	LY6PLAUR domain containing 6B
NLRP10	0.63	8.05E-03	1.74E-02	chr11:7980971-7985204 (-)	11p15.4	NLR family, pyrin domain containing 10
FRMPD1	0.63	4.49E-07	7.05E-06	chr9:37650997-37746901 (+)	9p13.2	FERM and PDZ domain containing 1
RNASSP203	0.63	1.73E-07	3.57E-06	chr6:10753024-10753159 (-)	---	RNA, 5S ribosomal pseudogene 203
SYNPO2	0.63	1.24E-03	3.56E-03	chr4:119809996-119982402 (+)	4q26	synaptopodin 2
SCARNA4	0.63	1.13E-04	4.93E-04	chr1:155895749-155895877 (-)	1q22	small Cajal body-specific RNA 4
RNASSP69	0.63	9.83E-08	2.34E-06	chr1:178530048-178530164 (+)	---	RNA, 5S ribosomal pseudogene 69
KLF4	0.63	1.35E-08	5.22E-07	chr9:110247133-110252763 (-)	9q31	Kruppel-like factor 4 (gut)
RNY1P8	0.63	7.21E-07	1.01E-05	chr13:73801284-73801397 (+)	---	RNA, Ro-associated Y1 pseudogene 8
BLMH	0.63	3.95E-04	1.37E-03	chr17:28575213-28619184 (-)	17q11.2	bleomycin hydrolase
SDC2	0.63	8.01E-09	3.47E-07	chr8:97505579-97624037 (+)	8q22-q23	syndecan 2
RP11-758P17.2	0.63	1.00E-07	2.37E-06	chr7:100032880-100034133 (+)	---	novel transcript
CAT	0.63	2.94E-05	1.68E-04	chr11:34460472-34493609 (+)	11p13	catalase
COL6A1	0.63	1.25E-10	1.56E-08	chr21:47401651-47424964 (+)	21q22.3	collagen, type VI, alpha 1
ZNF14	0.63	3.22E-08	1.01E-06	chr19:19821281-19843921 (-)	19p13.11	zinc finger protein 14
ZNF528	0.63	1.96E-07	3.91E-06	chr19:52901102-52921657 (+)	19q13	zinc finger protein 528
ARHGEF28	0.62	7.44E-08	1.89E-06	chr5:72921983-73237818 (+)	5q13.2	Rho guanine nucleotide exchange factor (GEF) 28
SCARNA3	0.62	5.57E-08	1.53E-06	chr1:175937533-175937676 (-)	1q25.1	small Cajal body-specific RNA 3
LOC643923	0.62	2.94E-07	5.22E-06	chr11:107462471-107463949 (+)	11q22.3	uncharacterized LOC643923
CA9	0.62	1.82E-09	1.14E-07	chr9:35673710-35681156 (+)	9p13.3	carbonic anhydrase IX
GLI2	0.62	5.08E-10	4.31E-08	chr2:121493199-121750229 (+)	2q14	GLI family zinc finger 2
TMEM150C	0.62	8.99E-06	6.72E-05	chr4:83405604-83483510 (-)	4q21.22	transmembrane protein 150C
LDOC1	0.62	3.81E-07	6.27E-06	chrX:140269930-140271310 (-)	Xq27	leucine zipper, down-regulated in cancer 1
BTBD16	0.62	7.00E-08	1.81E-06	chr10:124030821-124097677 (+)	10q26.13	BTB (POZ) domain containing 16
FYN	0.62	1.46E-11	3.27E-09	chr6:111981535-112194655 (-)	6q21	FYN proto-oncogene, Src family tyrosine kinase
WNT7B	0.62	1.39E-10	1.66E-08	chr22:46316242-46373009 (-)	22q13	wingless-type MMTV integration site family, member 7B
PIFO	0.62	5.21E-11	8.56E-09	chr1:111888910-111895639 (+)	1p13.2	primary cilia formation
LSP1	0.62	4.26E-11	7.33E-09	chr11:1874200-1913497 (+)	11p15.5	lymphocyte-specific protein 1
RNU5B-1	0.62	9.02E-06	6.73E-05	chr15:65597015-65597130 (+)	15q22.31	RNA, U5B small nuclear 1
NRARP	0.62	1.47E-05	9.74E-05	chr9:140194083-140196703 (-)	9q34.3	NOTCH-regulated ankyrin repeat protein
SH3KBP1	0.62	2.50E-09	1.45E-07	chrX:19552083-19905744 (-)	Xp22.1-p21.3	SH3-domain kinase binding protein 1
SRPX	0.62	3.09E-06	2.98E-05	chrX:38008588-38080696 (-)	Xq21.1	sushi-repeat containing protein, X-linked
ABCC9	0.62	9.18E-07	1.20E-05	chr12:21950324-22094336 (-)	12p12.1	ATP-binding cassette, sub-family C (CFTRMRP), member 9
LMBRD1	0.62	1.66E-10	1.90E-08	chr6:70385641-70507049 (-)	6q13	LMBR1 domain containing 1
AHNAK2	0.62	2.78E-07	5.03E-06	chr14:105403590-105444694 (-)	14q32.33	AHNAK nucleoprotein 2
SCNN1G	0.62	1.10E-06	1.38E-05	chr16:23194036-23228204 (+)	16p12	sodium channel, non-voltage-gated 1, gamma subunit
IDS	0.62	1.07E-08	4.36E-07	chrX:148558521-148586884 (-)	Xq28	iduronate 2-sulfatase
PDLIM4	0.62	1.19E-09	8.29E-08	chr5:131593337-131609147 (+)	5q31.1	PDZ and LIM domain 4
EGR3	0.62	4.51E-08	1.31E-06	chr8:22545172-22550815 (-)	8p23-p21	early growth response 3
HCP5	0.62	2.08E-04	8.06E-04	chr6_mcf_hap5:2811904-2813367 (+)	6p21.3	HLA complex P5 (non-protein coding)
CAMSAP3	0.62	2.34E-07	4.43E-06	chr19:7660788-7683196 (+)	19p13.2	calmodulin regulated spectrin-associated protein family, member 3
SCD5	0.62	9.65E-11	1.31E-08	chr4:83550690-83720010 (-)	4q21.22	stearoyl-CoA desaturase 5
CACNA1H	0.62	1.05E-08	4.28E-07	chr16:1203241-1271772 (+)	16p13.3	calcium channel, voltage-dependent, T type, alpha 1H subunit
GSDMA	0.62	1.11E-02	2.29E-02	chr17:38119226-38134019 (+)	17q21.1	gasdermin A
MAPRE2	0.62	2.84E-06	2.80E-05	chr18:32556892-32725381 (+)	18q12.1	microtubule-associated protein, RPEB family, member 2
MFAP3L	0.62	1.82E-07	3.69E-06	chr4:170907748-170954182 (-)	4q32.3	microfibrillar-associated protein 3-like
RNF24	0.62	3.42E-10	3.22E-08	chr20:3912068-3996229 (-)	20p13	ring finger protein 24
RNASSP288	0.62	4.92E-09	2.40E-07	chr9:97904731-97904823 (-)	---	RNA, 5S ribosomal pseudogene 288
GMPR	0.62	3.79E-05	2.05E-04	chr6:16238807-16295780 (+)	6p23	guanosine monophosphate reductase
INPP5A	0.62	3.19E-10	3.07E-08	chr10:134351324-134596984 (+)	10q26.3	inositol polyphosphate-5-phosphatase, 40kDa
RP11-407H12.8	0.62	3.21E-05	1.80E-04	chr1:248647546-248648785 (-)	---	novel transcript
ZBTB16	0.62	6.69E-06	5.36E-05	chr11:113930315-114121398 (+)	11q23.1	zinc finger and BTB domain containing 16
THRA	0.62	6.49E-10	5.21E-08	chr17:38218163-38250120 (+)	17q11.2	thyroid hormone receptor, alpha
RNU1-120P	0.62	5.04E-03	1.16E-02	chr1:147735751-147735907 (+)	---	RNA, U1 small nuclear 120, pseudogene

F2R	0.62	2.54E-08	8.47E-07	chr5:76011868-76031606 (+)	5q13	coagulation factor II (thrombin) receptor
ABCG1	0.62	1.06E-04	4.66E-04	chr21:43719104-43720919 (+)	21q22.3	ATP-binding cassette, sub-family G (WHITE), member 1
FTLP3	0.62	5.43E-05	2.74E-04	chr20:4004552-4004814 (+)	---	ferritin, light polypeptide pseudogene 3
ZNF134	0.61	1.77E-08	6.42E-07	chr19:58125619-58134723 (+)	19q13.4	zinc finger protein 134
RNY1P5	0.61	2.23E-08	7.67E-07	chr13:74863237-74863351 (-)	---	RNA, Ro-associated Y1 pseudogene 5
PDGFC	0.61	2.48E-06	2.52E-05	chr4:157681606-157892546 (-)	4q32	platelet derived growth factor C
SCARNA7	0.61	5.35E-06	4.52E-05	chr3:160232695-160233024 (-)	3q25.22	small Cajal body-specific RNA 7
C1orf116	0.61	1.17E-05	8.17E-05	chr1:207191866-207206101 (-)	1q32.1	chromosome 1 open reading frame 116
WFS1	0.61	2.53E-07	4.69E-06	chr4:6271576-6304992 (+)	4p16.1	Wolfram syndrome 1 (wolframin)
SPRY1	0.61	3.70E-07	6.13E-06	chr4:124317950-124324910 (+)	4q28.1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)
PPP1R15A	0.61	2.08E-05	1.28E-04	chr19:49375649-49379319 (+)	19q13.2	protein phosphatase 1, regulatory subunit 15A
SMPD3	0.61	1.21E-07	2.73E-06	chr16:68392230-68482591 (-)	16q22.1	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
RASGEF1B	0.61	2.30E-08	7.86E-07	chr4:82347547-82393082 (-)	4q21.21	RasGEF domain family, member 1B
MSMB	0.61	2.32E-04	8.85E-04	chr10:51549498-51562518 (+)	10q11.2	microseminoprotein, beta-
PLP1	0.61	3.24E-07	5.58E-06	chrX:103028647-103047548 (+)	Xq22	proteolipid protein 1
TGFBR2	0.61	1.66E-04	6.71E-04	chr3:30647994-30735634 (+)	3p22	transforming growth factor, beta receptor II (7080kDa)
RNASSP304	0.61	6.99E-08	1.80E-06	chr10:23286184-23286287 (+)	---	RNA, 5S ribosomal pseudogene 304
CREBRF	0.61	1.01E-06	1.29E-05	chr5:172483355-172566291 (+)	5q35.1	CREB3 regulatory factor
DYNLRB1	0.61	3.32E-08	1.04E-06	chr20:33104204-33128762 (+)	20q11.21	dynein, light chain, roadblock-type 1
LIFR	0.61	1.75E-05	1.11E-04	chr5:38475065-38608456 (-)	5p13-p12	leukemia inhibitory factor receptor alpha
SPRY2	0.61	3.51E-10	3.26E-08	chr13:80910111-80915086 (-)	13q31.1	sprouty homolog 2 (Drosophila)
SYNE1	0.61	3.31E-05	1.84E-04	chr6:152442819-152958534 (-)	6q25	spectrin repeat containing, nuclear envelope 1
ITGA9	0.61	3.17E-11	5.88E-09	chr3:37493606-37865005 (+)	3p21.3	integrin, alpha 9
RNASSP348	0.61	1.68E-05	1.08E-04	chr11:104123307-104123343 (+)	---	RNA, 5S ribosomal pseudogene 348
CYGB	0.61	1.39E-08	5.33E-07	chr17:74523438-74533782 (-)	17q25	cytoglobin
CLU	0.61	7.16E-09	3.19E-07	chr8:27454434-27472548 (-)	8p21-p12	clusterin
PTPN14	0.61	2.03E-07	4.01E-06	chr1:214517515-214725792 (-)	1q32.2	protein tyrosine phosphatase, non-receptor type 14
ENPP1	0.61	4.36E-04	1.49E-03	chr6:132129156-132216295 (+)	6q22-q23	ectonucleotide pyrophosphatasephosphodiesterase 1
CBX6	0.61	1.02E-10	1.32E-08	chr22:39257455-39268319 (-)	22q13.1	chromobox homolog 6
GPC6	0.60	3.61E-05	1.97E-04	chr13:93879078-95060273 (+)	13q32	glypican 6
SLC24A5	0.60	7.91E-03	1.71E-02	chr15:48413169-48434869 (+)	calcium exchanger), member 5	solute carrier family 24 (sodiumpotassium
CTSF	0.60	3.20E-08	1.01E-06	chr11:66330934-66336067 (-)	11q13	cathepsin F
FAM13C	0.60	6.04E-09	2.79E-07	chr10:61005889-61122939 (-)	10q21.1	family with sequence similarity 13, member C
UPK1A-AS1	0.60	2.07E-02	3.89E-02	chr19:36158850-36164193 (-)	19q13.12	UPK1A antisense RNA 1
EMBP1	0.60	7.87E-05	3.67E-04	chr1:121260910-121313686 (+)	1p11.2	embigin pseudogene 1
LSAMP	0.60	2.20E-06	2.29E-05	chr3:115521210-117716439 (-)	3q13.2-q21	limbic system-associated membrane protein
PARK2	0.60	6.20E-11	9.57E-09	chr6:161768452-163148834 (-)	6q25.2-q27	parkin RBR E3 ubiquitin protein ligase
USP54	0.60	8.39E-12	2.18E-09	chr10:75257296-75385711 (-)	10q22.2	ubiquitin specific peptidase 54
RNY3P3	0.60	1.62E-07	3.40E-06	chr13:78929362-78929463 (-)	---	RNA, Ro-associated Y3 pseudogene 3
EPHB6	0.60	2.52E-07	4.67E-06	chr7:142552792-142568847 (+)	7q33-q35	EPH receptor B6
MT1G	0.60	1.82E-05	1.15E-04	chr16:56700647-56701977 (-)	16q13	metallothionein 1G
EFHC2	0.60	2.72E-06	2.71E-05	chrX:44007128-44202923 (-)	Xp11.3	EF-hand domain (C-terminal) containing 2
DLX3	0.60	5.69E-07	8.42E-06	chr17:48067369-48072588 (-)	17q21	distal-less homeobox 3
BICC1	0.60	3.67E-08	1.12E-06	chr10:60272897-60591195 (+)	10q21.1	BicC family RNA binding protein 1
KLK1	0.60	1.96E-08	6.97E-07	chr19:51322404-51327043 (-)	19q13.3	kallikrein 1
RASA3	0.60	5.64E-13	3.52E-10	chr13:114747194-114898095 (-)	13q34	RAS p21 protein activator 3
NYNRIN	0.60	2.08E-06	2.20E-05	chr14:24867992-24886494 (+)	14q12	NYN domain and retroviral integrase containing
PRSS8	0.60	5.54E-05	2.78E-04	chr16:31142754-31147151 (-)	16p11.2	protease, serine, 8
ALX1	0.60	2.56E-09	1.47E-07	chr12:85673885-85695562 (+)	12q21.31	ALX homeobox 1
LRRC8C	0.60	6.14E-13	3.73E-10	chr1:90098631-90235462 (+)	1p22.2	leucine rich repeat containing 8 family, member C
CHPT1	0.60	1.15E-07	2.64E-06	chr12:102090725-102123424 (+)	12q	choline phosphotransferase 1
LGALS1	0.60	6.72E-08	1.75E-06	chr22:38071613-38075813 (+)	22q13.1	lectin, galactoside-binding, soluble, 1
EFNA4	0.60	2.19E-07	4.25E-06	chr1:155036207-155042029 (+)	1q21-q22	ephrin-A4
ZNF415	0.60	4.78E-10	4.12E-08	chr19:53611132-53636173 (-)	19q13.42	zinc finger protein 415
DNAJB4	0.59	2.12E-09	1.28E-07	chr1:78444859-78483648 (+)	1p31.1	DnaJ (Hsp40) homolog, subfamily B, member 4
DAPK1	0.59	9.75E-08	2.32E-06	chr9:90112143-90323549 (+)	9q21.33	death-associated protein kinase 1
MMP28	0.59	3.19E-08	1.01E-06	chr17:34083269-34122640 (-)	17q21.1	matrix metallopeptidase 28
CTD-3135A9.3	0.59	1.45E-08	5.50E-07	chr8:143328948-143329227 (-)	---	Eukaryotic type signal recognition particle RNA (SRP_euk_arch)
KCTD4	0.59	2.84E-05	1.63E-04	chr13:45766988-45775175 (-)	13q14.12	potassium channel tetramerization domain containing 4
RGMB	0.59	1.07E-11	2.57E-09	chr5:98104354-98134347 (+)	5q15	repulsive guidance molecule family member b
APBA1	0.59	1.24E-12	5.73E-10	chr9:72042449-72287275 (-)	9q13-q21.1	amyloid beta (A4) precursor protein-binding, family A, member 1
KRT33B	0.59	1.59E-10	1.83E-08	chr17:39519746-39528052 (-)	17q21.2	keratin 33B
HIST2H4B	0.59	1.45E-04	6.02E-04	chr1:149825607-149832725 (-)	1q21	histone cluster 2, H4b
SLCO3A1	0.59	1.70E-08	6.23E-07	chr15:92396925-92715665 (+)	15q26	solute carrier organic anion transporter family, member 3A1
RNASSP162	0.59	9.72E-07	1.26E-05	chr4:57197343-57197383 (-)	---	RNA, 5S ribosomal pseudogene 162
PSORS1C2	0.59	1.71E-06	1.90E-05	chr6:31105311-31107127 (-)	6p21.3	psoriasis susceptibility 1 candidate 2
BOC	0.59	3.61E-09	1.87E-07	chr3:112929850-113006305 (+)	3q13.2	BOC cell adhesion associated, oncogene regulated
TFAP2B	0.59	1.73E-05	1.10E-04	chr6:50786436-50815326 (+)	6p12	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
BCAN	0.59	1.40E-08	5.34E-07	chr1:156611182-156629324 (+)	1q31	brevican
BTG2	0.59	1.68E-07	3.49E-06	chr1:203274619-203278730 (+)	1q32	BTG family, member 2
APOC1	0.59	8.97E-07	1.18E-05	chr19:45417577-45422606 (+)	19q13.2	apolipoprotein C-I
ATP6V1C2	0.59	5.41E-04	1.78E-03	chr2:10861775-10925236 (+)	---	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2
KIAA1549L	0.59	1.59E-07	3.34E-06	chr11:33563821-33695648 (+)	11p13	KIAA1549-like
LOC100506834	0.59	6.11E-06	5.00E-05	chr9:89563613-89616948 (+)	---	uncharacterized LOC100506834
CD200	0.59	5.23E-07	7.91E-06	chr3:112051915-112081659 (+)	3q13.2	CD200 molecule
SLC27A2	0.59	3.86E-06	3.53E-05	chr15:50474393-50528592 (+)	15q21.2	solute carrier family 27 (fatty acid transporter), member 2
ZNF844	0.59	1.27E-05	8.69E-05	chr19:12175514-12192380 (+)	19p13.2	zinc finger protein 844
ANKRD33B	0.59	1.86E-10	2.05E-08	chr5:10564435-10657928 (+)	5p15.2	ankyrin repeat domain 33B
EPCAM	0.59	3.12E-09	1.69E-07	chr2:47572297-47614740 (+)	2p21	epithelial cell adhesion molecule
IGFBP7	0.59	5.38E-03	1.23E-02	chr4:57896939-57976551 (-)	4q12	insulin-like growth factor binding protein 7
C14orf132	0.58	1.40E-08	5.37E-07	chr14:96505661-96560417 (+)	14q32.2	chromosome 14 open reading frame 132
USP2	0.58	5.56E-04	1.81E-03	chr11:119225925-119252436 (-)	11q23.3	ubiquitin specific peptidase 2
DGAT2	0.58	1.94E-05	1.21E-04	chr11:75479777-75512581 (+)	11q13.5	diacylglycerol O-acyltransferase 2
HBP1	0.58	2.56E-08	8.54E-07	chr7:106809406-106842974 (+)	7q22-q31	HMG-box transcription factor 1
APCDD1	0.58	2.13E-09	1.29E-07	chr18:10454543-10488698 (+)	18p11.22	adenomatosis polyposis coli down-regulated 1
IGHD3-16	0.58	4.73E-04	1.59E-03	chr14:106361492-106361528 (-)	---	immunoglobulin heavy diversity 3-16
ROR1	0.58	1.91E-05	1.19E-04	chr1:64239690-64647181 (+)	1p32-p31	receptor tyrosine kinase-like orphan receptor 1
ACSBG1	0.58	2.84E-05	1.63E-04	chr15:78459810-78538030 (-)	15q23-q24	acyl-CoA synthetase bubblegum family member 1
BNIP3L	0.58	5.55E-10	4.62E-08	chr8:26240414-26363152 (+)	8p21	BCL2adenovirus E1B 19kDa interacting protein 3-like
RP11-353N4.1	0.58	3.58E-06	3.33E-05	chr1:149590752-149591762 (-)	---	putative novel transcript
FTL	0.58	1.81E-05	1.14E-04	chr19:49468506-49470136 (+)	19q13.33	ferritin, light polypeptide
UBL3	0.58	1.42E-08	5.41E-07	chr13:30338508-30424821 (-)	13q12-q13	ubiquitin-like 3
BHLHE41	0.58	3.21E-05	1.80E-04	chr12:26272078-26278060 (-)	12p12.1	basic helix-loop-helix family, member e41
TSPYL2	0.58	3.99E-07	6.48E-06	chrX:53111542-53117728 (+)	Xp11.2	TSPY-like 2
BCAR3	0.58	2.40E-16	1.41E-12	chr1:94027347-94312706 (-)	1p22.1	breast cancer anti-estrogen resistance 3
AK7	0.58	3.63E-06	3.37E-05	chr14:96858448-96955764 (+)	14q32.2	adenylate kinase 7
CHRM4	0.58	1.01E-06	1.29E-05	chr11:46406640-46408158 (-)	11p12-p11.2	cholinergic receptor, muscarinic 4
SEMA3D	0.58	1.31E-06	1.56E-05	chr7:84624869-84816171 (-)	7q21.11	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
C11orf49	0.58	1.03E-13	1.07E-10	chr11:46958248-47185936 (+)	11p11.2	chromosome 11 open reading frame 49
LIF	0.58	3.15E-09	1.70E-07	chr22:30636436-30642840 (-)	22q12.2	leukemia inhibitory factor
AWAT2	0.58	2.05E-02	3.85E-02	chrX:69260392-69269788 (-)	Xq13.1	acyl-CoA wax alcohol acyltransferase 2
FMN1	0.58	1.89E-05	1.18E-04	chr15:33057747-33486897 (-)	15q13.3	formin 1
RAP2C-AS1	0.58	2.63E-08	8.68E-07	chrX:131351175-131566890 (+)	Xq26.2	RAP2C antisense RNA 1
ANO1-AS1	0.58	1.43E-08	5.45E-07	chr11:70033894-70034615 (-)	---	ANO1 antisense RNA 1
CDA	0.57	1.57E-06	1.79E-05	chr1:20915441-20945401 (+)	1p36.2-p35	cytidine deaminase
AC096649.2	0.57	3.53E-09	1.84E-07	chr2:176032632-176033250 (+)	---	putative novel transcript
LHX2	0.57	3.51E-05	1.93E-04	chr9:126773889-126795580 (+)	9q33.3	LIM homeobox 2
WFDC5	0.57	1.44E-03	4.03E-03	chr20:43738093-43743813 (-)	20q13.12	WAP four-disulfide core domain 5
NINJ1	0.57	6.30E-08	1.67E-06	chr9:95883771-95896570 (-)	9q22	ninjurin 1
GAB2	0.57	7.97E-11	1.14E-08	chr11:77926336-78128868 (-)	11q14.1	GRB2-associated binding protein 2
PPP1R3B	0.57	4.84E-11	8.08E-09	chr8:8993764-9009152 (-)	8p23.1	protein phosphatase 1, regulatory subunit 3B
RCAN2	0.57	4.19E-10	3.72E-08	chr6:46188467-46459804 (-)	6p12.3	regulator of calcineurin 2
FZD8	0.57	5.00E-09	2.44E-07	chr10:35927177-35930362 (-)	10p11.21	frizzled class receptor 8
EMB	0.57	6.79E-05	3.27E-04	chr5:49692026-49739082 (-)	5q11.1	embigin
RNY1	0.57	2.74E-11	5.31E-09	chr7:148684228-148684340 (-)	7q36	RNA, Ro-associated Y1
MXRA7	0.57	7.29E-08	1.86E-06	chr17:74671809-74707087 (-)	17q25.1	matrix-remodelling associated 7
DUSP5	0.57	1.03E-07	2.42E-06	chr10:112257596-112271302 (+)	10q25	dual specificity phosphatase 5
DPYSL3	0.57	2.17E-07	4.22E-06	chr5:146770371-146889619 (-)	5q32	dihydropyrimidinase-like 3
ARHGEF26	0.57	1.75E-08	6.37E-07	chr3:153838792-153975616 (+)	3q25.2	Rho guanine nucleotide exchange factor (GEF) 26
PHYHD1	0.57	8.58E-13	4.52E-10	chr9:131683174-131704320 (+)	9q34.11	phytanoyl-CoA dioxygenase domain containing 1
LGALS3	0.57	1.34E-10	1.63E-08	chr14:55595762-55612148 (+)	14q22.3	lectin, galactoside-binding, soluble, 3
CYR61	0.57	1.56E-06	1.78E-05	chr1:86046444-86049648 (+)	1p22.3	cysteine-rich, angiogenic inducer, 61
SPNS2	0.57	7.67E-08	1.94E-06	chr17:44021229-44443228 (+)	17p13.2	spinster homolog 2 (Drosophila)
CRY1	0.57	4.01E-04	1.39E-03	chr12:107385142-107487607 (-)	12q23-q24.1	cryptochrome circadian clock 1
NDUFA4L2	0.57	4.96E-07	7.61E-06	chr12:57628686-57634498 (-)	12q13.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2
NR1D1	0.57	1.32E-02	2.66E-02	chr17:38249037-38256978 (-)	17q11.2	nuclear receptor subfamily 1, group D, member 1
CERS6	0.57	9.48E-09	3.95E-07	chr2:169312372-169631644 (+)	2q24.3	ceramide synthase 6
ATP6V0A4	0.57	3.24E-07	5.58E-06	chr7:138391039-138484305 (-)	7q34	ATPase, H+ transporting, lysosomal V0 subunit a4
CAMK2N1	0.57	6.01E-10	4.91E-08	chr1:20808884-20812728 (-)	1p36.12	calciumcalmodulin-dependent protein kinase II inhibitor 1
ZNF135	0.57	2.51E-09	1.45E-07	chr19:58570607-58597677 (+)	19q13.4	zinc finger protein 135
RP11-386B13.4	0.57	1.23E-06	1.49E-05	chr4:185910151-185926340 (+)	---	novel transcript
FADS2	0.57	7.03E-08	1.81E-06	chr11:61583728-61634826 (+)	11q12.2	fatty acid desaturase 2
CLEC12B	0.56	3.45E-06	3.24E-05	chr12:10163231-10171399 (+)	12p13.2	C-type lectin domain family 12, member B
EFNA3	0.56	1.04E-08	4.24E-07	chr1:155051348-155060014 (+)	1q21-q22	ephrin-A3
SLC8A1	0.56	7.34E-09	3.25E-07	chr2:40339286-40838193 (-)	2p22.1	solute carrier family 8 (sodiumcalcium exchanger), member 1
GLTSCR2	0.56	3.92E-13	2.71E-10	chr19:48248793-48274141 (+)	19q13.3	glioma tumor suppressor candidate region gene 2
SPARC	0.56	1.58E-07	3.33E-06	chr5:151040657-151066726 (-)	5q31.3-q32	secreted protein, acidic, cysteine-rich (osteonectin)
NPR2	0.56	7.42E-08	1.89E-06	chr9:35792151-35809729 (+)	9p21-p12	natriuretic peptide receptor 2
SNCA	0.56	6.40E-11	9.82E-09	chr4:90645250-90759466 (-)	4q21	synuclein, alpha (non A4 component of amyloid precursor)
FREM2	0.56	1.14E-03	3.33E-03	chr13:39261173-39461267 (+)	13q13.3	FRAS1 related extracellular matrix protein 2
SCARNA9	0.56	7.56E-10	5.83E-08	chr11:93454679-93455032 (+)	11q21	small Cajal body-specific RNA 9
FST	0.56	4.34E-05	2.29E-04	chr5:52776239-52782964 (+)	5q11.2	follistatin
AL353791.1	0.56	2.34E-02	4.31E-02	chr9:40028620-40032417 (+)	---	novel protein similar to contactin associated protein-like 3 (CNTNAP3)
YPEL2	0.56	2.32E-07	4.40E-06	chr17:57409053-57479095 (+)	17q22	yippee-like 2 (Drosophila)
VGLL3	0.56	3.14E-09	1.70E-07	chr3:86987119-87040269 (-)	3p12.1	vestigial-like family member 3
EPB41L4B	0.56	1.04E-11	2.51E-09	chr9:111934254-112083244 (-)	9q31-q32	erythrocyte membrane protein band 4.1 like 4B
SCARNA5	0.56	7.42E-09	3.27E-07	chr2:234184372-234184649 (+)	2q37.1	small Cajal body-specific RNA 5
PARM1	0.56	2.44E-03	6.28E-03	chr4:75858285-75975325 (+)	4q13.3-q21.3	prostate androgen-regulated mucin-like protein 1
VAT1	0.56	1.98E-09	1.22E-07	chr17:41166622-41174459 (-)	17q21	vesicle amine transport 1
SRGAP2	0.56	1.06E-06	1.34E-05	chr1:121107152-121131151 (+)	1q32.1	SLIT-ROBO Rho GTPase activating protein 2
RELL1	0.56	3.66E-10	3.36E-08	chr4:37592422-37687999 (-)	4p14	RELT-like 1
HBA2	0.56	1.54E-06	1.77E-05	chr16:222846-223709 (+)	16p13.3	hemoglobin, alpha 2
ATL1	0.56	6.56E-08	1.72E-06	chr14:50999227-51099786 (+)	14q22.1	atlastin GTPase 1
SHISA2	0.56	1.10E-05	7.81E-05	chr13:26618735-26625198 (-)	13q12.13	shisa family member 2
TRIM2	0.55	1.57E-05	1.02E-04	chr4:154073494-154260474 (+)	4q31.3	tripartite motif containing 2
EPS8	0.55	2.25E-07	4.31E-06	chr12:15773075-15942510 (-)	12p12.3	epidermal growth factor receptor pathway substrate 8
IRS2	0.55	6.31E-08	1.67E-06	chr13:110406184-110438915 (-)	13q34	insulin receptor substrate 2
RP11-84A14.5	0.55	4.08E-13	2.80E-10	chr1:9908376-9910212 (+)	---	novel transcript
CYSLTR1	0.55	1.37E-06	1.61E-05	chrX:77526961-77583087 (-)	Xq13.2-q21.1	cysteinyl leukotriene receptor 1
SLCO2A1	0.55	7.98E-06	6.12E-05	chr3:133651540-133771028 (-)	3q21	solute carrier organic anion transporter family, member 2A1

PCDHGB5	0.55	2.58E-07	4.75E-06	chr5:140777604-140780223 (+)	5q31	protocadherin gamma subfamily B, 5
LAMB2P1	0.55	1.20E-08	4.75E-07	chr3:49190292-49191834 (-)	3p21.3-p21.2	laminin, beta 2 pseudogene 1
FARP1	0.55	1.29E-06	1.54E-05	chr13:98794816-99102023 (+)	13q32.2	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)
LOC645553	0.55	4.07E-07	6.58E-06	chr19:46692286-46706319 (-)	19q13.32	uncharacterized LOC645553
ZIK1	0.55	7.22E-10	5.62E-08	chr19:58095508-58105253 (+)	19q13.43	zinc finger protein interacting with K protein 1
PPAP2A	0.55	1.70E-06	1.89E-05	chr5:54720682-54830878 (-)	5q11	phosphatidic acid phosphatase type 2A
TRAM2	0.55	7.16E-09	3.19E-07	chr6:52362200-52441862 (-)	6p21.1-p12	translocation associated membrane protein 2
KIAA1467	0.55	1.32E-07	2.92E-06	chr12:13197218-13236383 (+)	12p13.1	KIAA1467
OCA2	0.55	2.65E-07	4.85E-06	chr15:28000021-28344504 (-)	15q	oculocutaneous albinism II
HS3ST6	0.55	9.36E-15	2.16E-11	chr16:1961464-1968441 (-)	16p13.3	heparan sulfate (glucosamine) 3-O-sulfotransferase 6
CRY2	0.55	5.00E-10	4.27E-08	chr11:45834606-45904799 (+)	11p11.2	cryptochrome circadian clock 2
PRLR	0.55	1.74E-06	1.92E-05	chr5:35048861-35230823 (-)	5p13.2	prolactin receptor
IGLJ4	0.55	2.75E-07	4.99E-06	chr22:23252744-23252776 (+)	---	immunoglobulin lambda joining 4 (non-functional)
POF1B	0.55	1.89E-05	1.18E-04	chrX:84532395-84634748 (-)	Xq21.2	premature ovarian failure, 1B
RNA5SP186	0.55	1.57E-08	5.84E-07	chr5:75387533-75387626 (-)	---	RNA, 5S ribosomal pseudogene 186
SAMD5	0.55	1.06E-05	7.61E-05	chr6:147829828-147891157 (+)	6q24.3	sterile alpha motif domain containing 5
LAMC2	0.54	6.67E-07	9.50E-06	chr1:183155174-183214262 (+)	1q25-q31	laminin, gamma 2
ZBTB10	0.54	1.75E-08	6.36E-07	chr8:81397854-81438500 (+)	8q13-q21.1	zinc finger and BTB domain containing 10
LOC340357	0.54	1.45E-04	6.02E-04	chr8:12623358-12668987 (-)	8p23.1	uncharacterized LOC340357
GFRA1	0.54	2.63E-06	2.64E-05	chr10:117816442-118033126 (-)	10q26.11	GDNF family receptor alpha 1
GATM	0.54	3.03E-05	1.72E-04	chr15:45653322-45670991 (-)	15q21.1	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
ACSS3	0.54	3.29E-05	1.84E-04	chr12:81470990-81650533 (+)	12q21.31	acyl-CoA synthetase short-chain family member 3
LOC100653515	0.54	1.00E-12	5.04E-10	chr17:76849059-76921472 (-)	17q25	differential display clone 8
LPPR4	0.54	3.59E-06	3.34E-05	chr1:99729509-99775146 (+)	1p21.2	lipid phosphate phosphatase-related protein type 4
ALDOC	0.54	7.11E-10	5.56E-08	chr17:26900133-26903952 (-)	17cen-q12	aldolase C, fructose-bisphosphate
LOC284023	0.54	3.53E-10	3.27E-08	chr17:7816640-7819589 (-)	17p13.1	uncharacterized LOC284023
JUND	0.54	1.09E-10	1.39E-08	chr19:18390563-18392432 (-)	19p13.2	jun D proto-oncogene
CHL1	0.54	2.55E-03	6.51E-03	chr3:238279-451097 (+)	3p26.1	cell adhesion molecule L1-like
NPY1R	0.54	3.80E-05	2.06E-04	chr4:164245062-164265984 (-)	4q31.3-q32	neuropeptide Y receptor Y1
HSPA2	0.54	7.11E-07	9.94E-06	chr14:65002623-65009955 (+)	14q24.1	heat shock 70kDa protein 2
DCN	0.54	3.45E-04	1.22E-03	chr12:91538025-91576900 (-)	12q21.33	decorin
GJC3	0.54	3.28E-07	5.64E-06	chr7:99520892-99527243 (-)	7q22.1	gap junction protein, gamma 3, 30.2kDa
ZNF652	0.54	3.20E-08	1.01E-06	chr17:47366568-47439835 (-)	17q21.32	zinc finger protein 652
NAV2	0.53	8.66E-07	1.15E-05	chr12:77718421-77966055 (+)	11p15.1	neuron navigator 2
CLDN23	0.53	2.34E-10	2.40E-08	chr8:8559448-8561617 (+)	8p23.1	claudin 23
HBA1	0.53	4.91E-06	4.23E-05	chr16:226679-227521 (+)	16p13.3	hemoglobin, alpha 1
RTN4RL1	0.53	7.73E-09	3.38E-07	chr17:1837971-1928178 (-)	17p13.3	reticulon 4 receptor-like 1
RAI14	0.53	2.14E-08	7.43E-07	chr5:34656342-34832732 (+)	5p13.3-p13.2	retinoic acid induced 14
IRF4	0.53	4.55E-09	2.26E-07	chr6:391739-411447 (+)	6p25-p23	interferon regulatory factor 4
BCL2	0.53	9.49E-08	2.27E-06	chr18:60790579-60987361 (-)	18q21.3	B-cell CLL/lymphoma 2
CDHR1	0.53	4.08E-07	6.58E-06	chr10:85954410-85979377 (+)	10q23.1	cadherin-related family member 1
PMEL	0.53	1.50E-03	4.17E-03	chr12:56347889-56360520 (-)	12q13-q14	premelanosome protein
GPC3	0.53	1.67E-10	1.90E-08	chrX:132669773-133119922 (-)	Xq26.1	glypican 3
ASAP2	0.53	2.67E-09	1.51E-07	chr2:9346894-9545812 (+)	2p25|2p24	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2
ZDHHC11B	0.53	3.62E-06	3.35E-05	chr5:710472-767323 (-)	5p15.33	zinc finger, DHHC-type containing 11B
OLFM2	0.53	1.13E-08	4.55E-07	chr19:9964394-10047070 (-)	19p13.2	olfactomedin 2
ODF3L1	0.53	1.09E-08	4.43E-07	chr15:76016318-76020029 (+)	15q24.2	outer dense fiber of sperm tails 3-like 1
TPPP	0.52	1.84E-10	2.03E-08	chr5:659977-693510 (-)	5p15.3	tubulin polymerization promoting protein
LRP4	0.52	3.90E-07	6.38E-06	chr11:46878268-46940173 (-)	11p11.2	low density lipoprotein receptor-related protein 4
PMAIP1	0.52	1.15E-04	4.98E-04	chr18:57567180-57571538 (+)	18q21.32	phorbol-12-myristate-13-acetate-induced protein 1
THRSP	0.52	2.04E-02	3.84E-02	chr11:77774907-77779403 (+)	11q14.1	thyroid hormone responsive
FHL1	0.52	2.23E-14	3.74E-11	chrX:135228861-135293518 (+)	Xq26	four and a half LIM domains 1
CDR2	0.52	1.86E-10	2.05E-08	chr16:22357257-22385938 (-)	16p12.3	cerebellar degeneration-related protein 2, 62kDa
COLEC12	0.52	4.06E-07	6.57E-06	chr18:319355-500729 (-)	18p11.32	collectin sub-family member 12
SGPP1	0.52	2.04E-03	5.39E-03	chr14:64150932-64194773 (-)	14q23.2	sphingosine-1-phosphate phosphatase 1
ISM1	0.52	9.51E-05	4.28E-04	chr20:13202418-13281298 (+)	20p12.1	isthmin 1, angiogenesis inhibitor
LRRN1	0.52	1.73E-10	1.95E-08	chr3:3841121-3889387 (+)	3p26.2	leucine rich repeat neuronal 1
CLEC2A	0.52	1.76E-03	4.76E-03	chr12:10051272-10084980 (-)	12p13.31	C-type lectin domain family 2, member A
RNA5SP496	0.52	7.46E-04	2.32E-03	chr22:31701390-31701498 (+)	---	RNA, 5S ribosomal pseudogene 496
TMEM255A	0.52	1.17E-09	8.19E-08	chrX:119392505-119445411 (-)	Xq24	transmembrane protein 255A
CDH11	0.52	1.54E-08	5.75E-07	chr16:64977656-65156101 (-)	16q21	cadherin 11, type 2, OB-cadherin (osteoblast)
CRIP2	0.51	3.76E-11	6.67E-09	chr14:105939299-105946507 (+)	14q32.3	cysteine-rich protein 2
NTRK2	0.51	2.52E-06	2.55E-05	chr9:87283466-87638505 (+)	9q22.1	neurotrophic tyrosine kinase, receptor, type 2
LAMB4	0.51	5.88E-05	2.92E-04	chr7:107663993-107770801 (-)	7q31	laminin, beta 4
FBXO32	0.51	5.64E-07	8.37E-06	chr8:124510127-124553493 (-)	8q24.13	F-box protein 32
NR4A2	0.51	1.94E-05	1.20E-04	chr2:157180944-157198860 (-)	2q22-q23	nuclear receptor subfamily 4, group A, member 2
RP11-124N14.3	0.51	2.62E-07	4.81E-06	chr10:17275324-17276832 (-)	---	novel transcript
P4HA1	0.51	9.33E-08	2.25E-06	chr10:74766975-74856732 (-)	10q21.3-q23.1	prolyl 4-hydroxylase, alpha polypeptide I
KLK5	0.51	5.26E-07	7.95E-06	chr19:51446559-51456344 (-)	19q13.33	kallikrein-related peptidase 5
GAS7	0.51	2.96E-10	2.91E-08	chr17:9813926-10101868 (-)	17p13.1	growth arrest-specific 7
ASPA	0.51	2.79E-08	9.11E-07	chr17:3377404-3406713 (+)	17p13.3	aspartoacylase
CNTNAP3B	0.51	1.22E-03	3.51E-03	chr9:43684885-43924049 (+)	9p11.2	contactin associated protein-like 3B
BMP2	0.51	2.46E-11	4.85E-09	chr20:6748311-6760910 (+)	20p12	bone morphogenetic protein 2
TGM5	0.51	1.29E-04	5.46E-04	chr15:43524793-43559055 (-)	15q15.2	transglutaminase 5
TMEM116	0.51	5.85E-08	1.58E-06	chr12:112369087-112451023 (-)	12q24.13	transmembrane protein 116
SCARNA10	0.51	3.66E-09	1.89E-07	chr12:6619388-6619717 (+)	12p13.31	small Cajal body-specific RNA 10
EGR1	0.51	3.90E-04	1.35E-03	chr5:137801169-137805004 (+)	5q31.1	early growth response 1
RNU12-2P	0.51	5.20E-05	2.64E-04	chrX:46992070-46992225 (+)	---	RNA, U12 small nuclear 2, pseudogene
COBL	0.51	3.12E-12	1.09E-09	chr7:51083909-51384515 (-)	7p12.1	cordon-bleu WH2 repeat protein
SIK1	0.51	8.75E-08	2.15E-06	chr21:44834395-44847008 (-)	21q22.3	salt-inducible kinase 1
SCARNA1	0.51	1.15E-10	1.46E-08	chr1:28160912-28161077 (+)	1p35.3	small Cajal body-specific RNA 1
TPPP3	0.50	4.03E-04	1.39E-03	chr16:67423712-67427438 (-)	16q22.1	tubulin polymerization-promoting protein family member 3
FOXO1	0.50	2.13E-15	8.35E-12	chr13:41129801-41240734 (-)	13q14.1	forkhead box O1
CITED2	0.50	2.21E-10	2.30E-08	chr6:139693393-139695785 (-)	6p22.1	Cbpp300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
IGFBP5	0.50	3.90E-07	6.38E-06	chr2:217536828-217560272 (-)	2q33-q36	insulin-like growth factor binding protein 5
RP11-275I14.4	0.50	2.56E-07	4.73E-06	chr1:226335704-226342772 (+)	---	novel transcript
HSPA1A	0.50	2.64E-07	4.84E-06	chr6_dbb_hap3:3068907-3071309 (-)	6p21.3	heat shock 70kDa protein 1A
HES1	0.50	1.74E-07	3.59E-06	chr3:193853931-193856521 (+)	3q28-q29	hes family bHLH transcription factor 1
ARNTL	0.50	4.64E-05	2.42E-04	chr11:13299325-13408813 (+)	11p15	aryl hydrocarbon receptor nuclear translocator-like
EFEMP1	0.50	8.96E-06	6.70E-05	chr2:56093097-56151298 (-)	2p16	EGF containing fibulin-like extracellular matrix protein 1
TYRP1	0.50	3.98E-03	9.52E-03	chr9:12685439-12710274 (+)	9p23	tyrosinase-related protein 1
KIAA1683	0.50	2.68E-09	1.52E-07	chr19:18367906-18385319 (-)	19p13.1	KIAA1683
MARCH3	0.50	9.88E-11	1.31E-08	chr5:126203406-126366500 (-)	5q23.2	membrane-associated ring finger (C3HC4) 3, E3 ubiquitin protein ligase
TOB1	0.50	4.83E-09	2.37E-07	chr17:48939584-48945339 (-)	17q21	transducer of ERBB2, 1
CYP27A1	0.50	3.51E-09	1.84E-07	chr2:219646472-219680016 (+)	2q35	cytochrome P450, family 27, subfamily A, polypeptide 1
KRT79	0.50	9.19E-04	2.77E-03	chr12:53215231-53228079 (-)	12q13.13	keratin 79
CNTNAP3	0.50	5.44E-04	1.78E-03	chr9:39072764-39288456 (-)	9p13.1	contactin associated protein-like 3
FOXC1	0.50	6.67E-07	9.50E-06	chr6:1610207-1614132 (+)	6p25	forkhead box C1
LGI3	0.50	3.53E-11	6.35E-09	chr8:22004338-22014597 (-)	8p21.3	leucine-rich repeat LGI family, member 3
HSPA1A	0.50	1.76E-07	3.61E-06	chr6:31783320-31785722 (-)	6p21.3	heat shock 70kDa protein 1A
CYP1B1	0.50	3.23E-06	3.10E-05	chr2:38294652-38337044 (-)	2p22.2	cytochrome P450, family 1, subfamily B, polypeptide 1
APOE	0.49	1.32E-12	5.91E-10	chr19:45408956-45412650 (+)	19q13.2	apolipoprotein E
NR4A1	0.49	1.17E-09	8.16E-08	chr12:52416616-52453291 (+)	12q13	nuclear receptor subfamily 4, group A, member 1
TSPAN2	0.49	8.87E-09	3.77E-07	chr1:115590632-115632121 (-)	1p13.2	tetraspanin 2
TYR	0.49	1.33E-04	5.62E-04	chr11:88910620-89028927 (+)	11q14.3	tyrosinase
ADAMTSL3	0.49	8.94E-11	1.25E-08	chr15:84322838-84708594 (+)	15q25.2	ADAMTS-like 3
ENPP2	0.49	2.34E-04	8.90E-04	chr8:120569317-120685693 (-)	8q24.1	ectonucleotide pyrophosphatase phosphodiesterase 2
PPARGC1A	0.49	1.49E-10	1.75E-08	chr4:23756664-23905712 (-)	4p15.1	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
RORA	0.49	1.84E-08	6.62E-07	chr15:60780483-61521518 (-)	15q22.2	RAR-related orphan receptor A
MLANA	0.48	2.19E-05	1.33E-04	chr9:5890802-5910606 (+)	9p24.1	melan-A
RORC	0.48	1.92E-16	1.23E-12	chr1:151778547-151804348 (-)	1q21	RAR-related orphan receptor C
GDPD2	0.48	7.73E-07	1.06E-05	chrX:69642881-69653241 (+)	Xq13.1	glycerophosphodiester phosphodiesterase domain containing 2
TNFAIP3	0.48	1.39E-07	3.03E-06	chr6:138188351-138204449 (+)	6q23	tumor necrosis factor, alpha-induced protein 3
TCP11L2	0.48	3.11E-10	3.02E-08	chr12:106696581-106740793 (+)	12q23.3	t-complex 11, testis-specific-like 2
FOXQ1	0.48	8.23E-12	2.18E-09	chr6:1312675-1314993 (+)	6p25	forkhead box Q1
PDK4	0.48	2.94E-05	1.68E-04	chr7:95212809-95225925 (-)	7q21.3	pyruvate dehydrogenase kinase, isozyme 4
HOPX	0.48	5.49E-10	4.59E-08	chr4:57514154-57548065 (-)	4q12	HOP homeobox
KCNMB4	0.48	1.70E-08	6.25E-07	chr12:70760056-70828072 (+)	12q	potassium large conductance calcium-activated channel, subfamily M, beta member 4
SUSD2	0.48	7.48E-10	5.78E-08	chr22:24577227-24585078 (+)	22q11-q12	sushi domain containing 2
CGNL1	0.48	8.35E-09	3.59E-07	chr15:57668703-57842925 (+)	15q21.3	cingulin-like 1
GATA6	0.48	2.17E-09	1.30E-07	chr18:19749404-19782491 (+)	18q11.1-q11.2	GATA binding protein 6
MYH14	0.47	4.02E-11	7.02E-09	chr19:50706885-50813802 (+)	19q13.33	myosin, heavy chain 14, non-muscle
TIMP3	0.47	4.83E-08	1.38E-06	chr22:33196802-33259030 (+)	22q12.3	TIMP metallopeptidase inhibitor 3
H19	0.47	1.84E-10	2.03E-08	chr11:2016406-2022700 (-)	11p15.5	H19, imprinted maternally expressed transcript (non-protein coding)
CYP2J2	0.47	8.06E-08	2.01E-06	chr1:60358980-60392462 (-)	1p31.3-p31.2	cytochrome P450, family 2, subfamily J, polypeptide 2
TRPC6	0.47	2.12E-07	4.15E-06	chr11:101322295-101743293 (-)	11q22.1	transient receptor potential cation channel, subfamily C, member 6
EEF2K	0.47	3.04E-08	9.70E-07	chr16:22217592-22300066 (+)	16p12.2	eukaryotic elongation factor-2 kinase
ASPN	0.47	1.78E-03	4.80E-03	chr9:95218487-95244844 (-)	9q22	asporin
CCND1	0.47	3.42E-10	3.22E-08	chr11:69455855-69469242 (+)	11q13	cyclin D1
EGR2	0.47	1.95E-09	1.20E-07	chr10:64571756-64679660 (-)	10q21.1	early growth response 2
PTN	0.47	2.60E-06	2.61E-05	chr7:136912088-137028611 (-)	7q33	pleiotrophin
GADD45B	0.47	2.32E-05	1.39E-04	chr19:2476123-2478257 (+)	19p13.3	growth arrest and DNA-damage-inducible, beta
LPHN3	0.47	1.77E-03	4.77E-03	chr4:62941884-62944051 (+)	4q13.1	latrophilin 3
FN1	0.46	2.81E-07	5.07E-06	chr2:216225163-216300895 (-)	2q34	fibronectin 1
RNF39	0.46	7.33E-08	1.87E-06	chr6_cox_hap2:1550143-1555764 (-)	6p21.3	ring finger protein 39
ARHGAP29	0.46	3.97E-04	1.37E-03	chr1:94615403-94740624 (-)	1p22.1	Rho GTPase activating protein 29
SLITRK6	0.46	4.91E-07	7.55E-06	chr13:86366922-86373623 (-)	13q31.1	SLIT and NTRK-like family, member 6
JUN	0.46	8.32E-07	1.12E-05	chr1:59246460-59249999 (-)	1p32-p31	jun proto-oncogene
CST6	0.46	1.97E-13	1.59E-10	chr11:65778955-65780976 (+)	11q13	cystatin E M
MYADM	0.46	1.71E-09	1.10E-07	chr19:54369477-54379691 (+)	19q13.42	myeloid-associated differentiation marker
RAB3B	0.46	1.67E-10	1.90E-08	chr1:52373628-52456436 (-)	1p32-p31	RAB3B, member RAS oncogene family
KRT80	0.46	2.01E-07	3.97E-06	chr12:52562780-52585784 (-)	12q13.13	keratin 80
PCSK2	0.46	3.72E-05	2.02E-04	chr20:17206752-17465223 (+)	20p11.2	proprotein convertase subtilisin kexin type 2
PNRC1	0.46	1.08E-12	5.24E-10	chr6:89790429-89794879 (+)	6q15	proline-rich nuclear receptor coactivator 1
FAM134B	0.45	2.88E-10	2.85E-08	chr5:16473147-16617167 (-)	5p15.1	family with sequence similarity 134, member B
STXBP6	0.45	5.79E-12	1.72E-09	chr14:25278862-25519503 (-)	14q12	syntaxin binding protein 6 (amisyn)
RNASE7	0.45	1.75E-05	1.11E-04	chr14:21510385-21512393 (+)	14q11.2	ribonuclease, RNase A family, 7
PELI2	0.45	5.05E-09	2.46E-07	chr14:56585093-56768244 (+)	14q21	pellino E3 ubiquitin protein ligase family member 2
CPA4	0.45	1.35E-08	5.21E-07	chr7:129932974-129964020 (+)	7q32	carboxypeptidase A4
CNTNAP3P2	0.45	2.85E-04	1.05E-03	chr9:40498481-40633261 (-)	9q12	contactin associated protein-like 3 pseudogene 2
CYP1A2	0.45	1.46E-04	6.06E-04	chr15:75041184-75048941 (+)	15q24.1	cytochrome P450, family 1, subfamily A, polypeptide 2
SNTB1	0.44	1.22E-13	1.14E-10	chr8:121547985-121825513 (-)	8q23-q24	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
CRIP1	0.44	7.93E-15	2.07E-11	chr14:105952654-105955284 (+)	14q32.33	cysteine-rich protein 1 (intestinal)
SCCPDH	0.44	5.46E-08	1.51E-06	chr1:246887349-246931440 (+)	1q44	saccharopine dehydrogenase (putative)
PLXNC1	0.44	1.24E-05	8.52E-05	chr12:94542499-94701451 (+)	12q23.3	plexin C1
F3	0.44	8.37E-14	9.68E-11	chr1:94994732-95007413 (-)	1p22-p21	coagulation factor III (thromboplastin, tissue factor)
RHOB	0.44	2.03E-08	7.14E-07	chr2:20646835-20649206 (+)	2p24	ras homolog family member B
CYP1A1	0.44	4.32E-04	1.48E-03	chr15:75011883-75017951 (-)	15q24.1	cytochrome P450, family 1, subfamily A, polypeptide 1
FZD7	0.44	2.03E-07	4.00E-06	chr2:202899310-202903168 (+)	2q33	frizzled class receptor 7
PHYHIP	0.43	3.16E-08	1.00E-06	chr8:22077216-22089854 (-)	8p21.3	phytanoyl-CoA 2-hydroxylase interacting protein

C14orf64	0.43	1.79E-09	1.13E-07	chr14:98391947-98444461 (-)	14q32.2	chromosome 14 open reading frame 64
TMPRSS11E	0.43	1.79E-06	1.96E-05	chr4:69313167-69363322 (+)	4q13.2	transmembrane protease, serine 11E
PRKCB	0.43	1.34E-15	5.91E-12	chr16:23847300-24231932 (+)	16p11.2	protein kinase C, beta
TUFT1	0.43	1.98E-13	1.59E-10	chr1:151512781-151556059 (+)	1q21	tuftelin 1
CNTNAP3B	0.43	1.28E-03	3.66E-03	chr9:65647281-65664071 (+)	9p11.2	contactin associated protein-like 3B
THEM5	0.43	5.70E-05	2.85E-04	chr1:151818220-151826173 (-)	1q21.3	thioesterase superfamily member 5
MITF	0.43	1.55E-06	1.78E-05	chr3:69788586-70017488 (+)	3p14.2-p14.1	microphthalmia-associated transcription factor
KRT23	0.43	6.25E-09	2.87E-07	chr17:39078948-39093836 (-)	17q21.2	keratin 23 (histone deacetylase inducible)
UPK1A	0.42	2.39E-02	4.38E-02	chr19:36157715-36169367 (+)	19q13.13	uroplakin 1A
SCIN	0.42	5.69E-12	1.71E-09	chr7:12596187-12693228 (+)	7p21.3	scinderin
MAML2	0.42	9.77E-06	7.14E-05	chr11:95709762-96076382 (-)	11q21	mastermind-like 2 (Drosophila)
ARRDC4	0.42	1.09E-11	2.61E-09	chr15:98462784-98517068 (+)	15q26.3	arrestin domain containing 4
GSTA3	0.42	1.24E-07	2.79E-06	chr6:52761437-52774496 (-)	6p12.1	glutathione S-transferase alpha 3
DACH1	0.42	3.66E-06	3.38E-05	chr13:72012098-72441330 (-)	13q22	dachshund family transcription factor 1
NFATC2	0.42	3.62E-13	2.53E-10	chr20:50003494-50179339 (-)	20q13.2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
KRT25	0.42	3.70E-03	8.94E-03	chr17:38904272-38911584 (-)	17q21.2	keratin 25
SH3BGRL2	0.42	4.22E-07	6.75E-06	chr6:80341000-80413373 (+)	6q14.1	SH3 domain binding glutamate-rich protein like 2
CRABP1	0.42	1.23E-09	8.53E-08	chr15:78632666-78640573 (+)	15q24	cellular retinoic acid binding protein 1
PTPRM	0.41	2.83E-07	5.09E-06	chr18:7566780-8406859 (+)	18p11.2	protein tyrosine phosphatase, receptor type, M
SDC4	0.41	9.59E-12	2.41E-09	chr20:43953928-43977064 (-)	20q12	syndecan 4
ARHGAP31	0.41	2.85E-11	5.43E-09	chr3:119013220-119139561 (+)	3q13.33	Rho GTPase activating protein 31
LGR5	0.41	1.38E-02	2.75E-02	chr12:71833550-71980090 (+)	12q22-q23	leucine-rich repeat containing G protein-coupled receptor 5
TMEM47	0.41	1.04E-07	2.44E-06	chrX:34645181-34675405 (-)	Xp11.4	transmembrane protein 47
TSPYL5	0.41	5.75E-06	4.78E-05	chr8:98285702-98290192 (-)	8q22.1	TSPY-like 5
ATF3	0.41	5.75E-08	1.57E-06	chr1:212738676-212794119 (+)	1q32.3	activating transcription factor 3
CA6	0.40	5.31E-08	1.48E-06	chr1:9005922-9035151 (+)	1p36.2	carbonic anhydrase VI
HSD11B1	0.40	7.19E-10	5.61E-08	chr1:209859510-209908295 (+)	1q32-q41	hydroxysteroid (11-beta) dehydrogenase 1
CDON	0.40	3.10E-07	5.42E-06	chr11:125825691-125933187 (-)	11q24.2	cell adhesion associated, oncogene regulated
SCEL	0.40	1.10E-05	7.78E-05	chr13:78049967-78219398 (+)	13q22	sciellin
ANG	0.40	2.11E-13	1.66E-10	chr14:21152259-21168761 (+)	14q11.1-q11.2	angiogenin, ribonuclease, RNase A family, 5
LONRF1	0.40	4.20E-12	1.36E-09	chr8:12579403-12613582 (-)	8p23.1	LON peptidase N-terminal domain and ring finger 1
GATA3	0.40	1.45E-12	6.32E-10	chr10:8095567-8117164 (+)	10p15	GATA binding protein 3
AADACL2	0.40	4.06E-06	3.67E-05	chr3:151451704-151479127 (+)	3q25.1	arylacetamide deacetylase-like 2
EFNB2	0.40	3.38E-11	6.15E-09	chr13:107142079-107187462 (-)	13q33	ephrin-B2
FAM171B	0.40	2.27E-07	4.34E-06	chr2:187558698-187630685 (+)	2q32.1	family with sequence similarity 171, member B
FOS	0.40	4.22E-07	6.75E-06	chr14:75745477-75748937 (+)	14q24.3	FBJ murine osteosarcoma viral oncogene homolog
C8orf88	0.39	2.38E-09	1.40E-07	chr8:91968167-91997485 (-)	8q21.3	chromosome 8 open reading frame 88
CTSH	0.39	7.66E-07	1.05E-05	chr15:79213400-79237433 (-)	15q25.1	cathepsin H
HPGD	0.39	1.09E-08	4.41E-07	chr4:175411328-175444305 (-)	4q34-q35	hydroxyprostaglandin dehydrogenase 15-(NAD)
PRELP	0.39	8.40E-10	6.32E-08	chr1:203444883-203460480 (+)	1q32	proline arginine-rich end leucine-rich repeat protein
SOX5	0.39	3.68E-09	1.89E-07	chr12:23682440-24715524 (-)	12p12.1	SRY (sex determining region Y)-box 5
SLURP1	0.39	8.63E-06	6.50E-05	chr8:143822362-143823829 (-)	8q24.3	secreted LY6 PLAUR domain containing 1
CTSV	0.38	1.56E-08	5.84E-07	chr9:99791959-99822167 (-)	9q22.2	cathepsin V
RHOBTB3	0.38	5.17E-13	3.26E-10	chr5:95049226-95160087 (+)	5q15	Rho-related BTB domain containing 3
ANKFN1	0.38	8.01E-14	9.41E-11	chr17:54230836-54560007 (+)	17q22	ankyrin-repeat and fibronectin type III domain containing 1
SLC46A2	0.38	2.06E-09	1.26E-07	chr9:115641200-115653193 (-)	9q32	solute carrier family 46, member 2
HMGCS2	0.38	4.69E-07	7.30E-06	chr1:120290619-120311555 (-)	1p13-p12	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)
CRYAB	0.38	1.44E-13	1.28E-10	chr11:111779289-111794446 (-)	11q22.3-q23.1	crystallin, alpha B
SLCO4C1	0.38	1.11E-03	3.25E-03	chr5:101569690-101632253 (-)	5q21.2	solute carrier organic anion transporter family, member 4C1
AZGP1	0.38	3.20E-08	1.01E-06	chr7:99564343-99573780 (-)	7q22.1	alpha-2-glycoprotein 1, zinc-binding
SVIP	0.37	3.33E-10	3.17E-08	chr11:22840475-22851411 (-)	11p14.2	small VCP p97-interacting protein
KRT31	0.37	2.68E-09	1.52E-07	chr17:39549976-39553844 (-)	17q21.2	keratin 31
VIM	0.37	3.76E-07	6.20E-06	chr10:17270258-17279592 (+)	10p13	vimentin
ADCY2	0.37	1.95E-12	7.96E-10	chr5:7396321-7830194 (+)	5p15.3	adenylate cyclase 2 (brain)
WFDC12	0.37	4.80E-04	1.61E-03	chr20:43752066-43753106 (-)	20q13.12	WAP four-disulfide core domain 12
FAM26E	0.37	2.08E-07	4.08E-06	chr6:116832808-116845955 (+)	6q22.1	family with sequence similarity 26, member E
SCNN1B	0.37	2.77E-08	9.07E-07	chr16:23313591-23392620 (+)	16p12.2-p12.1	sodium channel, non-voltage-gated 1, beta subunit
TGFBI	0.37	5.88E-11	9.29E-09	chr5:135364584-135399507 (+)	5q31	transforming growth factor, beta-induced, 68kDa
EGLN3	0.37	3.84E-08	1.16E-06	chr14:34393421-34638972 (-)	14q13.1	egl-9 family hypoxia-inducible factor 3
IGFL2	0.36	1.24E-08	4.88E-07	chr19:46651039-46664561 (+)	19q13.32	IGF-like family member 2
ACER1	0.36	1.25E-06	1.51E-05	chr19:6306510-6333640 (-)	19p13.3	alkaline ceramidase 1
FAM189A2	0.36	5.54E-14	7.10E-11	chr9:71939488-72007371 (+)	9q21.11	family with sequence similarity 189, member A2
GJB4	0.35	2.12E-13	1.66E-10	chr1:35225342-35229325 (+)	1p34.3	gap junction protein, beta 4, 30.3kDa
ANXA9	0.35	6.39E-06	5.17E-05	chr1:150954493-150968114 (+)	1q21	annexin A9
FRZB	0.35	4.66E-04	1.57E-03	chr2:183698002-183731890 (-)	2q32.1	frizzled-related protein
PLLP	0.35	2.13E-11	4.36E-09	chr16:57290009-57318599 (-)	16q13	plasmolipin
BGN	0.35	4.35E-07	6.88E-06	chrX:152760347-152775012 (+)	Xq28	biglycan
LCE5A	0.35	2.02E-08	7.13E-07	chr1:152483320-152484653 (+)	1q21.3	late cornified envelope 5A
CHP2	0.33	8.11E-08	2.02E-06	chr16:23765948-23770272 (+)	16p12.2	calcineurin-like EF-hand protein 2
CACNA2D1	0.33	6.22E-08	1.65E-06	chr7:81575760-82073114 (-)	7q21-q22	calcium channel, voltage-dependent, alpha 2 delta subunit 1
UGT3A2	0.33	5.46E-08	1.51E-06	chr5:36035119-36071460 (-)	5p13.2	UDP glycosyltransferase 3 family, polypeptide A2
NR4A3	0.33	3.95E-07	6.43E-06	chr9:102584137-102629173 (+)	9q22	nuclear receptor subfamily 4, group A, member 3
EMP3	0.33	1.45E-07	3.13E-06	chr19:48828629-48833810 (+)	19q13.3	epithelial membrane protein 3
FOSB	0.33	3.35E-07	5.70E-06	chr19:45971253-45978437 (+)	19q13.32	FBJ murine osteosarcoma viral oncogene homolog B
TXNIP	0.32	1.36E-08	5.24E-07	chr1:145438462-145442635 (+)	1q21.1	thioredoxin interacting protein
CLDN1	0.32	2.72E-12	9.93E-10	chr3:190023490-190040264 (-)	3q28-q29	claudin 1
DCT	0.32	2.66E-05	1.55E-04	chr13:95090830-95131936 (-)	13q32	dopachrome tautomerase
IGFL3	0.32	2.91E-07	5.19E-06	chr19:46623328-46627931 (-)	19q13.32	IGF-like family member 3
IL34	0.32	8.01E-12	2.13E-09	chr16:70613798-70694585 (+)	16q22.1	interleukin 34
CLDN8	0.32	1.22E-13	1.14E-10	chr21:31586324-31588469 (-)	21q22.11	claudin 8
DUSP1	0.32	2.75E-10	2.74E-08	chr5:172195093-172198203 (-)	5q34	dual specificity phosphatase 1
PMP22	0.31	3.51E-08	1.09E-06	chr17:15133095-15168644 (-)	17p12	peripheral myelin protein 22
KRT2	0.31	2.04E-04	7.96E-04	chr12:53038342-53045959 (-)	12q13.13	keratin 2
PSAPL1	0.30	4.15E-11	7.19E-09	chr4:7432021-7436700 (-)	4p16.1	prosaposin-like 1 (gene pseudogene)
FLG	0.30	3.18E-05	1.79E-04	chr1:152274651-152297679 (-)	1q21.3	filaggrin
ADRB2	0.30	3.51E-12	1.17E-09	chr5:148204808-148208250 (+)	5q31-q32	adrenoceptor beta 2, surface
SERPINB7	0.30	1.36E-07	2.97E-06	chr18:61420169-61472604 (+)	18q21.33	serpin peptidase inhibitor, clade B (ovalbumin), member 7
PAMR1	0.29	4.92E-14	6.54E-11	chr11:35453370-35551848 (-)	11p13	peptidase domain containing associated with muscle regeneration 1
CMAHP	0.29	1.19E-10	1.50E-08	chr6:25081295-25218698 (-)	6p21.32	cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene
LCE1E	0.29	7.50E-09	3.30E-07	chr1:152758690-152760902 (+)	1q21.3	late cornified envelope 1E
GAN	0.28	3.51E-12	1.17E-09	chr16:81348571-81413940 (+)	16q24.1	gigaxonin
EDIL3	0.28	5.03E-11	8.35E-09	chr5:83236373-83680611 (-)	5q14	EGF-like repeats and discoidin I-like domains 3
CDSN	0.28	2.17E-06	2.27E-05	chr6_qbl_hap6:2378683-2384073 (-)	6p21.3	corneodesmosin
C5orf46	0.28	4.21E-12	1.36E-09	chr5:147260289-147286101 (-)	5q32	chromosome 5 open reading frame 46
ABI3BP	0.27	6.61E-08	1.73E-06	chr3:100468000-100712359 (-)	3q12	ABI family, member 3 (NESH) binding protein
ABHD12B	0.27	1.35E-07	2.96E-06	chr14:51338878-51371688 (+)	14q22.1	abhydrolase domain containing 12B
APOD	0.27	1.01E-11	2.49E-09	chr3:195295573-195311076 (-)	3q29	apolipoprotein D
CCL27	0.24	4.94E-12	1.52E-09	chr9:34661877-34664045 (-)	9p13	chemokine (C-C motif) ligand 27
ASPRV1	0.24	1.39E-07	3.02E-06	chr2:70187221-70189397 (-)	2p13.3	aspartic peptidase, retroviral-like 1
LCE1A	0.23	7.75E-09	3.38E-07	chr1:152798523-152800665 (+)	1q21.3	late cornified envelope 1A
ITM2A	0.23	2.04E-10	2.19E-08	chrX:78615881-78623164 (-)	Xq13.3-Xq21.2	integral membrane protein 2A
BTC	0.22	6.50E-07	9.32E-06	chr4:75669969-75719896 (-)	4q13.3	betacellulin
ID4	0.21	5.38E-15	1.65E-11	chr6:19837601-19842431 (+)	6p22.3	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
LY6G6C	0.21	4.16E-09	2.10E-07	chr6_qbl_hap6:2980058-2983255 (-)	6p21.33	lymphocyte antigen 6 complex, locus G6C
KIT	0.20	1.25E-07	2.80E-06	chr4:55524085-55606881 (+)	4q12	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
HSD17B13	0.19	2.99E-06	2.90E-05	chr4:88224941-88244058 (-)	4q22.1	hydroxysteroid (17-beta) dehydrogenase 13
CRCT1	0.19	1.25E-07	2.80E-06	chr1:152486978-152488486 (+)	1q21	cysteine-rich C-terminal 1
IL37	0.16	2.79E-09	1.56E-07	chr2:113670548-113676459 (+)	2q12-q14.1	interleukin 37
KRT77	0.15	9.39E-14	1.04E-10	chr12:53083410-53097247 (-)	12q13.13	keratin 77
AQP9	0.15	1.05E-11	2.53E-09	chr15:58430368-58478110 (+)	15q	aquaporin 9
LCE2D	0.15	2.07E-09	1.27E-07	chr1:152635872-152637135 (+)	1q21.3	late cornified envelope 2D
ELMOD1	0.14	2.00E-10	2.16E-08	chr11:107461817-107537505 (+)	11q22.3	ELMO CED-12 domain containing 1
LCE1B	0.13	3.31E-11	6.07E-09	chr1:152784447-152785585 (+)	1q21.3	late cornified envelope 1B
SPRR4	0.12	1.10E-07	2.55E-06	chr1:152943128-152945069 (+)	1q21.3	small proline-rich protein 4
LOR	0.12	9.05E-09	3.83E-07	chr1:153232176-153234600 (+)	1q21	loricrin
LCE1C	0.11	1.78E-11	3.76E-09	chr1:152777311-152779107 (-)	1q21.3	late cornified envelope 1C
LCE6A	0.11	9.26E-11	1.28E-08	chr1:152815330-152816459 (+)	1q21.3	late cornified envelope 6A
LCE1F	0.11	1.34E-10	1.63E-08	chr1:152748848-152749445 (+)	1q21.3	late cornified envelope 1F
LCE1D	0.10	9.77E-11	1.31E-08	chr1:152769217-152771396 (+)	1q21.3	late cornified envelope 1D
LCE2A	0.09	1.28E-09	8.78E-08	chr1:152670840-152671918 (+)	1q21.3	late cornified envelope 2A
KPRP	0.08	3.45E-13	2.46E-10	chr1:152730506-152734529 (+)	1q21.3	keratinocyte proline-rich protein
LCE2B	0.08	1.10E-11	2.61E-09	chr1:152658599-152659877 (+)	1q21	late cornified envelope 2B
LCE2C	0.08	7.74E-11	1.11E-08	chr1:152647771-152649050 (+)	1q21.3	late cornified envelope 2C
FLG2	0.07	8.53E-10	6.40E-08	chr1:152321213-152332482 (-)	1q21.3	filaggrin family member 2
SERPINA12	0.05	3.48E-19	8.19E-15	chr14:94953611-94984181 (-)	14q32.13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12
C1orf68	0.05	3.04E-14	4.47E-11	chr1:152691082-152692946 (+)	1q21.3	chromosome 1 open reading frame 68
POSTN	0.05	1.76E-10	1.98E-08	chr13:38136719-38183563 (-)	13q13.3	periostin, osteoblast specific factor
CDR1	0.03	5.94E-19	1.05E-14	chrX:139864570-139867036 (-)	Xq27.1	cerebellar degeneration-related protein 1, 34kDa

Supplementary Table S1b - Differentially expressed genes (DEGs) between keratinocytes from psoriasis lesional skin (PP) and keratinocytes from psoriasis non-lesional skin (PN).

GeneName	lin FCH	P-value	FDR	Molecular location	Cytogenic location	Official Full Name
TCN1	45.43	2.83E-20	2.00E-15	chr11:59620273-59634048 (-)	11q11-q12	transcobalamin I (vitamin B12 binding protein, R binder family)
DEFB4A	42.46	1.30E-10	4.20E-08	chr8:7752151-7754237 (+)	8p23.1	defensin, beta 4A
PI3	40.20	9.06E-11	3.18E-08	chr20:43803517-43805185 (+)	20q13.12	peptidase inhibitor 3, skin-derived
SERPINB4	38.22	7.25E-13	1.07E-09	chr18:61304493-61311532 (-)	18q21.3	serpin peptidase inhibitor, clade B (ovalbumin), member 4
DEFB4B	32.82	1.83E-10	5.17E-08	chr8:7272382-7274385 (-)	8p23.1	defensin, beta 4B
SERPINB3	21.12	2.89E-13	5.98E-10	chr18:61322431-61329197 (-)	18q21.3	serpin peptidase inhibitor, clade B (ovalbumin), member 3
KYNU	20.43	1.48E-19	5.23E-15	chr2:143635067-143799890 (+)	2q22.2	kynureninase
S100A9	15.75	1.20E-11	8.35E-09	chr1:153330330-153333503 (+)	1q21	S100 calcium binding protein A9
AKR1B10	13.88	1.44E-14	6.78E-11	chr7:134212344-134226166 (+)	7q33	aldo-keto reductase family 1, member B10 (aldose reductase)
TMPRSS11D	13.42	2.98E-13	5.98E-10	chr4:68686594-68749750 (-)	4q13.2	transmembrane protease, serine 11D
S100A7A	13.05	1.85E-11	1.09E-08	chr1:153388945-153395701 (+)	1q21.3	S100 calcium binding protein A7A
GJB2	12.73	1.11E-15	8.45E-12	chr13:20761604-20767114 (-)	13q11-q12	gap junction protein, beta 2, 26kDa
IFI44L	12.40	1.31E-06	3.37E-05	chr1:79085607-79111830 (+)	1p31.1	interferon-induced protein 44-like
OAS2	11.68	6.77E-11	2.54E-08	chr12:113416200-113449528 (+)	12q24.2	2-5-oligoadenylate synthetase 2, 69 71kDa
IFI6	11.32	3.09E-07	1.08E-05	chr1:27992572-27998729 (-)	1p35	interferon, alpha-inducible protein 6
IFI44	10.42	4.01E-09	4.40E-07	chr1:79115477-79129763 (+)	1p31.1	interferon-induced protein 44
EPGN	9.99	3.24E-10	7.55E-08	chr4:75174190-75181024 (+)	4q13.3	epithelial mitogen homolog (mouse)
HEPHL1	9.72	1.61E-10	4.78E-08	chr11:93754378-93847374 (+)	11q21	hephaestin-like 1
IFI27	9.55	1.08E-06	2.92E-05	chr14:94577079-94583033 (+)	14q32	interferon, alpha-inducible protein 27
SPRR2A	9.36	2.50E-07	9.18E-06	chr1:153028589-153030013 (-)	1q21-q22	small proline-rich protein 2A
KRT6C	7.77	1.36E-10	4.25E-08	chr12:52862300-52867569 (-)	12q13.13	keratin 6C
FABP5	7.69	9.85E-16	8.45E-12	chr8:82192598-82197012 (+)	8q21.13	fatty acid binding protein 5 (psoriasis-associated)
S100A8	7.44	1.07E-12	1.35E-09	chr1:153362508-153363664 (-)	1q21	S100 calcium binding protein A8
KRT6A	7.41	8.51E-10	1.48E-07	chr12:52880958-52887181 (-)	12q13.13	keratin 6A
KRT16	7.40	3.28E-15	1.69E-11	chr17:39766030-39769079 (-)	17q21.2	keratin 16
C10orf99	7.39	3.36E-10	7.73E-08	chr10:85933494-85945050 (+)	10q23.1	chromosome 10 open reading frame 99
CYP4Z2P	6.85	2.13E-08	1.41E-06	chr1:47308767-47366147 (-)	1p33	cytochrome P450, family 4, subfamily Z, polypeptide 2, pseudogene
IRAK3	6.70	7.69E-13	1.08E-09	chr12:66582659-66648402 (+)	12q14.3	interleukin-1 receptor-associated kinase 3
CD36	6.57	6.56E-12	5.47E-09	chr7:79998891-80308593 (+)	7q11.2	CD36 molecule (thrombospondin receptor)
RHCG	6.55	7.92E-12	6.28E-09	chr15:89998680-90039844 (-)	15q25	Rh family, C glycoprotein
HERC6	6.54	1.21E-08	9.45E-07	chr4:89299891-89364263 (+)	4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
CLEC7A	6.51	1.20E-15	8.45E-12	chr12:10269376-10282868 (-)	12p13.2	C-type lectin domain family 7, member A
GBP6	6.22	1.33E-10	4.24E-08	chr1:89829436-89853719 (+)	1p22.2	guanylate binding protein family, member 6
DSC2	6.19	4.45E-14	1.57E-10	chr18:28645940-28682388 (-)	18q12.1	desmocollin 2
CTSC	6.19	1.40E-16	1.65E-12	chr11:88026760-88070955 (-)	11q14.2	cathepsin C
S100A7	6.17	4.16E-08	2.36E-06	chr1:153430220-153433177 (-)	1q21	S100 calcium binding protein A7
KRT6B	6.06	3.61E-09	4.02E-07	chr12:52840435-52845971 (-)	12q13.13	keratin 6B
AASS	5.94	1.81E-15	1.16E-11	chr7:121713598-121784344 (-)	7q31.3	aminoadipate-semialdehyde synthase
SAMD9	5.72	6.21E-10	1.19E-07	chr7:92728826-92747336 (-)	7q21.2	sterile alpha motif domain containing 9
IL36G	5.61	4.33E-09	4.63E-07	chr2:113730780-113743227 (+)	2q12-q21	interleukin 36, gamma
SERPINB13	5.38	3.00E-12	3.09E-09	chr18:61254223-61271873 (+)	18q21.33	serpin peptidase inhibitor, clade B (ovalbumin), member 13
AKR1B15	5.24	4.36E-12	3.94E-09	chr7:134233849-134264592 (+)	7q33	aldo-keto reductase family 1, member B15
CENPE	5.10	8.72E-10	1.50E-07	chr4:104026963-104119566 (-)	4q24-q25	centromere protein E, 312kDa
SLC23A2	5.06	5.10E-11	2.09E-08	chr20:4833002-4990939 (-)	20p13	solute carrier family 23 (ascorbic acid transporter), member 2
SPRR2F	5.06	3.21E-05	3.79E-04	chr1:153084590-153085991 (-)	1q21-q22	small proline-rich protein 2F
TNIP3	5.05	1.99E-08	1.35E-06	chr4:122052563-122148621 (-)	4q27	TNFAIP3 interacting protein 3
S100A12	4.88	1.06E-11	7.53E-09	chr1:153346181-153348125 (-)	1q21	S100 calcium binding protein A12
GJB6	4.83	8.67E-13	1.16E-09	chr13:20796101-20806534 (-)	13q12	gap junction protein, beta 6, 30kDa
DOCK11	4.74	4.27E-11	1.89E-08	chrX:117629861-117820126 (+)	Xq24	dedicator of cytokinesis 11
NETO2	4.71	2.73E-13	5.98E-10	chr16:47115431-47177936 (-)	16q11	neuropilin (NRP) and tolloid (TLL)-like 2
STEAP4	4.62	3.08E-09	3.55E-07	chr7:87900207-87936228 (-)	7q21.12	STEAP family member 4
RAB31	4.44	3.98E-09	4.38E-07	chr18:9708228-9862553 (+)	18p11.3	RAB31, member RAS oncogene family
MKI67	4.31	6.04E-11	2.31E-08	chr10:129894923-129924649 (-)	10q26.2	marker of proliferation Ki-67
SLC7A11	4.24	2.05E-10	5.66E-08	chr4:139085248-139163503 (-)	4q28-q32	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
CD274	4.17	2.29E-09	2.86E-07	chr9:5450503-5470567 (+)	9p24	CD274 molecule
XAF1	4.10	7.26E-08	3.53E-06	chr17:6658794-6678964 (+)	17p13.1	XIAP associated factor 1
CENPF	4.08	1.29E-10	4.18E-08	chr1:214776532-214837931 (+)	1q41	centromere protein F, 350 400kDa
OR56B1	3.99	4.58E-09	4.78E-07	chr11:5710817-5821759 (+)	11p15.4	olfactory receptor, family 56, subfamily B, member 1
PARP14	3.91	2.89E-10	6.94E-08	chr3:122399465-122449687 (+)	3q21.1	poly (ADP-ribose) polymerase family, member 14
SLC6A14	3.89	2.70E-05	3.33E-04	chrX:115567747-115592625 (+)	Xq23	solute carrier family 6 (amino acid transporter), member 14
FAM111B	3.87	1.30E-09	1.93E-07	chr11:58874658-58894888 (+)	11q12.1	family with sequence similarity 111, member B
SERPINB1	3.82	1.63E-10	4.78E-08	chr6:2832566-2842240 (-)	6p25	serpin peptidase inhibitor, clade B (ovalbumin), member 1
DLGAP5	3.78	1.20E-10	3.94E-08	chr14:55614830-55658396 (-)	14q22.3	discs, large (Drosophila) homolog-associated protein 5
LTF	3.77	2.76E-07	9.93E-06	chr3:46477136-46526724 (-)	3p21.31	lactotransferrin
EPSTI1	3.75	6.33E-09	6.00E-07	chr13:43460524-43566385 (-)	13q13.3	epithelial stromal interaction 1 (breast)
CCL2	3.68	2.42E-05	3.06E-04	chr17:32582296-32584222 (+)	17q11.2-q12	chemokine (C-C motif) ligand 2
IFITM1	3.64	3.11E-11	1.52E-08	chr11:313506-315272 (+)	11p15.5	interferon induced transmembrane protein 1
PLSCR1	3.61	4.65E-11	1.98E-08	chr3:146232967-146262651 (-)	3q23	phospholipid scramblase 1
PLAT	3.61	2.38E-09	2.94E-07	chr8:42032236-42065242 (-)	8p12	plasminogen activator, tissue
MX1	3.49	7.28E-08	3.53E-06	chr21:42792231-42831141 (+)	21q22.3	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
CARD17	3.48	4.09E-08	2.34E-06	chr11:104963196-104972158 (-)	11q22.3	caspase recruitment domain family, member 17
IL33	3.47	6.21E-06	1.09E-04	chr9:6215786-6257983 (+)	9p24.1	interleukin 33
LYN	3.47	8.99E-09	7.68E-07	chr8:56792372-56925006 (+)	8q13	LYN proto-oncogene, Src family tyrosine kinase
TICRR	3.39	1.63E-10	4.78E-08	chr15:90118713-90171253 (+)	15q26.1	TOPBP1-interacting checkpoint and replication regulator
DDX60L	3.31	1.34E-07	5.70E-06	chr4:169277886-169458937 (-)	4q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like
RSAD2	3.30	5.64E-05	5.82E-04	chr2:7005937-7038370 (+)	2p25.2	radical S-adenosyl methionine domain containing 2
PRKCQ	3.28	2.47E-09	3.03E-07	chr10:6469105-6622263 (-)	10p15	protein kinase C, theta
KIF20B	3.24	3.47E-06	7.06E-05	chr10:91461367-91534700 (+)	10q23.31	kinesin family member 20B
ASPM	3.24	3.46E-07	1.19E-05	chr1:197053257-197115824 (-)	1q31	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
NDC80	3.22	3.40E-10	7.79E-08	chr18:2571510-2616634 (+)	18p11.32	NDC80 kinetochore complex component
IFITM3	3.21	2.89E-10	6.94E-08	chr11:319669-321340 (-)	11p15.5	interferon induced transmembrane protein 3
IFIT1	3.21	3.38E-06	6.94E-05	chr10:91152303-91163745 (+)	10q23.31	interferon-induced protein with tetratricopeptide repeats 1
LOX	3.19	2.84E-10	6.86E-08	chr5:121398890-121414206 (-)	5q23.2	lysyl oxidase
OAS3	3.18	8.58E-09	7.46E-07	chr12:113376157-113411054 (+)	12q24.2	2-5-oligoadenylate synthetase 3, 100kDa
KIF14	3.18	1.71E-09	2.31E-07	chr1:200520625-200589862 (-)	1q32.1	kinesin family member 14
INA	3.18	2.24E-07	8.42E-06	chr10:105036920-105050108 (+)	10q24.33	internexin neuronal intermediate filament protein, alpha
SLC7A5	3.18	8.39E-07	2.40E-05	chr16:87863622-87903125 (-)	16q24.3	solute carrier family 7 (amino acid transporter light chain, L system), member 5
EHF	3.15	6.36E-13	9.97E-10	chr11:34642588-34684834 (+)	11p12	ets homologous factor
MPZL2	3.14	3.35E-15	1.69E-11	chr11:118124118-118135251 (-)	11q24	myelin protein zero-like 2
CCNB1	3.10	2.80E-10	6.82E-08	chr5:68462837-68474072 (+)	5q12	cyclin B1
BRCA2	3.09	2.96E-11	1.51E-08	chr13:32889611-32973809 (+)	13q12.3	breast cancer 2, early onset
IFI16	3.08	1.04E-09	1.69E-07	chr1:158969758-159024945 (+)	1q22	interferon, gamma-inducible protein 16
TOP2A	3.08	8.53E-07	2.43E-05	chr17:38544768-38574408 (-)	17q21-q22	topoisomerase (DNA) II alpha 170kDa
FMNL2	3.07	1.26E-11	8.52E-09	chr2:153191751-153506348 (+)	2q23.3	formin-like 2
NAMPT	3.06	9.48E-09	7.96E-07	chr7:105888731-105926772 (-)	7q22.3	nicotinamide phosphoribosyltransferase
IL20	3.06	6.60E-07	1.99E-05	chr1:207038699-207042568 (+)	1q32	interleukin 20
SCD	3.05	2.36E-05	3.00E-04	chr10:102106772-102124591 (+)	10q24.31	stearoyl-CoA desaturase (delta-9-desaturase)
CDH3	3.02	8.30E-10	1.47E-07	chr16:68678151-68732971 (+)	16q22.1	cadherin 3, type 1, P-cadherin (placental)
SLPI	3.01	8.60E-07	2.44E-05	chr20:43880879-43883206 (-)	20q12	secretory leukocyte peptidase inhibitor
ZC3H12A	3.01	1.53E-10	4.63E-08	chr1:37940119-37949978 (+)	1p34.3	zinc finger CCCH-type containing 12A
MYO1B	3.00	4.37E-11	1.93E-08	chr2:192109911-192290115 (+)	2q12-q34	myosin IB
IFIT3	2.98	9.53E-08	4.40E-06	chr10:91087602-91100728 (+)	10q24	interferon-induced protein with tetratricopeptide repeats 3
DDX60	2.98	5.43E-05	5.67E-04	chr4:169137442-169239958 (-)	4q32.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
EIF5B	2.98	7.97E-05	7.54E-04	chr2:99953816-100016728 (+)	2q11.2	eukaryotic translation initiation factor 5B
ID1	2.98	3.14E-09	3.60E-07	chr20:30193086-30194318 (+)	20q11	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
A2ML1	2.98	8.07E-07	2.33E-05	chr12:8975068-9039597 (+)	12p13.31	alpha-2-macroglobulin-like 1
NCAPG	2.97	1.28E-10	4.18E-08	chr4:17812525-17846487 (+)	4p15.33	non-SMC condensin I complex, subunit G
PARP9	2.97	1.38E-08	1.04E-06	chr3:122246760-122283523 (-)	3q21	poly (ADP-ribose) polymerase family, member 9
CCL20	2.95	3.01E-06	6.36E-05	chr2:228678558-228682280 (+)	2q36.3	chemokine (C-C motif) ligand 20
STAT1	2.94	1.00E-08	8.25E-07	chr2:191829084-191885686 (-)	2q32.2	signal transducer and activator of transcription 1, 91kDa
CATSPERB	2.93	1.82E-10	5.17E-08	chr14:92047118-92198430 (-)	14q32.12	catsper channel auxiliary subunit beta
NAMPTL	2.93	1.47E-10	4.48E-08	chr10:36810649-36813162 (-)	10p11.21	nicotinamide phosphoribosyltransferase-like
MLKL	2.93	1.73E-16	1.75E-12	chr16:74705753-74734789 (-)	16q23.1	mixed lineage kinase domain-like
HRH2	2.91	1.33E-09	1.95E-07	chr5:175085033-175113245 (+)	5q35.2	histamine receptor H2
KPNA2	2.90	1.29E-09	1.92E-07	chr17:66031848-66042970 (+)	17q24.2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
TGM1	2.89	4.03E-07	1.34E-05	chr14:24718320-24732416 (-)	14q11.2	transglutaminase 1
ALOX15B	2.89	1.44E-06	3.61E-05	chr17:7942358-7952452 (+)	17p13.1	arachidonate 15-lipoxygenase, type B
CARD6	2.87	4.06E-12	3.72E-09	chr5:40841286-40860275 (+)	5p13.1	caspase recruitment domain family, member 6
ATP10B	2.87	1.12E-09	1.72E-07	chr5:159990127-160279221 (-)	5q34	ATPase, class V, type 10B
SLC4A7	2.86	2.24E-09	2.82E-07	chr3:27414214-27525911 (-)	3p22	solute carrier family 4, sodium bicarbonate cotransporter, member 7
SOD2	2.85	7.27E-10	1.34E-07	chr6:160100096-160114360 (-)	6q25.3	superoxide dismutase 2, mitochondrial
LUZP2	2.85	6.74E-09	6.31E-07	chr11:24518516-25104186 (+)	11p14.3	leucine zipper protein 2
CEP55	2.83	3.17E-10	7.45E-08	chr10:95256369-95288849 (+)	10q23.33	centrosomal protein 55kDa
CCNA2	2.83	8.09E-10	1.45E-07	chr4:122737599-122745088 (-)	4q27	cyclin A2
ATP12A	2.83	2.08E-05	2.74E-04	chr13:25254549-25285923 (+)	13q12.12|13q12.1-q12.3	ATPase, H+ K+ transporting, nongastric, alpha polypeptide
CARHSP1	2.81	1.59E-14	7.01E-11	chr16:8946799-8962866 (-)	16p13.2	calcium regulated heat stable protein 1, 24kDa
TXNDC5	2.81	1.72E-11	1.05E-08	chr6:7881483-7911047 (-)	6p24.3	thioredoxin domain containing 5 (endoplasmic reticulum)
KLK13	2.80	2.52E-07	9.22E-06	chr19:51559463-51568367 (-)	19q13.33	kallikrein-related peptidase 13
CASC5	2.79	2.84E-10	6.86E-08	chr15:40886218-40956540 (+)	15q14	cancer susceptibility candidate 5
OAS1	2.78	1.79E-08	1.25E-06	chr12:113344582-113369991 (+)	12q24.2	2-5-oligoadenylate synthetase 1, 40 46kDa
ADAM23	2.78	1.29E-09	1.92E-07	chr2:207308263-207485851 (+)	2q33	ADAM metallopeptidase domain 23
TNFSF10	2.78	4.14E-11	1.86E-08	chr3:172223298-172241297 (-)	3q26	tumor necrosis factor (ligand) superfamily, member 10
GDA	2.77	1.20E-06	3.16E-05	chr9:74729511-74872109 (+)	9q21.13	guanine deaminase
CYP4Z1	2.75	2.71E-07	9.77E-06	chr1:47533160-47583992 (+)	1p33	cytochrome P450, family 4, subfamily Z, polypeptide 1
MPHOSPH6	2.74	4.50E-11	1.95E-08	chr16:82181767-82203831 (-)	16q23.3	M-phase phosphoprotein 6
GBP1	2.72	2.11E-08	1.40E-06	chr1:89517987-89531043 (-)	1p22.2	guanylate binding protein 1, interferon-inducible
KIF23	2.71	9.51E-09	7.98E-07	chr15:69706585-69740764 (+)	15q23	kinesin family member 23
GK	2.70	1.75E-11	1.06E-08	chrX:30671476-30749577 (+)	Xp21.3	glycerol kinase
MAN1A1	2.69	8.94E-09	7.66E-07	chr6:119498374-119670926 (-)	6q22	mannosidase, alpha, class 1A, member 1
SAMD9L	2.69	2.96E-04	2.00E-03	chr7:92759368-92777682 (-)	7q21.2	sterile alpha motif domain containing 9-like
SLC7A1	2.69	1.18E-10	3.92E-08	chr13:30083547-30169825 (-)	13q12.3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
SMC4	2.68	4.36E-06	8.41E-05	chr3:160117062-160152750 (+)	3q26.1	structural maintenance of chromosomes 4

CDK1	2.67	1.47E-09	2.12E-07	chr10:62538089-62554610 (+)	10q21.1	cyclin-dependent kinase 1
C1R	2.67	9.67E-12	7.03E-09	chr12:7187513-7245203 (-)	12p13	complement component 1, r subcomponent
SMC2	2.66	1.31E-06	3.37E-05	chr9:106856541-106903700 (+)	9q31.1	structural maintenance of chromosomes 2
KIF18A	2.64	1.68E-09	2.28E-07	chr11:28042163-28129746 (-)	11p14.1	kinesin family member 18A
KIF20A	2.64	1.48E-08	1.10E-06	chr5:137514408-137523404 (+)	5q31	kinesin family member 20A
HK2	2.63	9.69E-10	1.62E-07	chr2:75059782-75120486 (+)	2p13	hexokinase 2
IFIH1	2.62	8.85E-07	2.50E-05	chr2:163123589-163175213 (-)	2q24	interferon induced with helicase C domain 1
GOT1	2.62	1.26E-11	8.52E-09	chr10:101156627-101190530 (-)	10q24.1-q25.1	glutamic-oxaloacetic transaminase 1, soluble
S100A2	2.61	3.10E-10	7.30E-08	chr1:153533584-153540366 (-)	1q21	S100 calcium binding protein A2
PLBD1	2.60	1.75E-13	4.57E-10	chr12:14656595-14721283 (-)	12p13.1	phospholipase B domain containing 1
SLIRP	2.60	2.49E-09	3.05E-07	chr14:78174414-78187450 (+)	14q24.3	SRA stem-loop interacting RNA binding protein
KIF11	2.59	3.28E-07	1.14E-05	chr10:94352825-94415152 (+)	10q24.1	kinesin family member 11
CACNB4	2.59	2.12E-10	5.70E-08	chr2:152689286-152955593 (-)	2q22-q23	calcium channel, voltage-dependent, beta 4 subunit
TNFRSF21	2.58	1.52E-09	2.17E-07	chr6:47199268-47277680 (-)	6p21.1	tumor necrosis factor receptor superfamily, member 21
HIF1A	2.58	2.10E-08	1.40E-06	chr14:62162119-62214977 (+)	14q23.2	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
SPRR2C	2.58	4.49E-06	8.58E-05	chr1:153112594-153113969 (-)	1q21-q22	small proline-rich protein 2C (pseudogene)
PYGL	2.57	2.48E-08	1.60E-06	chr14:51324609-51411454 (-)	14q21-q22	phosphorylase, glycogen, liver
LTBP1	2.57	2.96E-05	3.57E-04	chr2:33172039-33624576 (+)	2p22-p21	latent transforming growth factor beta binding protein 1
PITPNC1	2.56	2.56E-10	6.30E-08	chr17:65373720-65689647 (+)	17q24.2	phosphatidylinositol transfer protein, cytoplasmic 1
GPX3	2.56	4.11E-06	8.03E-05	chr5:150399999-150408554 (+)	5q23	glutathione peroxidase 3 (plasma)
C12orf75	2.56	3.87E-08	2.24E-06	chr12:105720744-105789875 (+)	12q23.3	chromosome 12 open reading frame 75
PLA2G4D	2.55	1.63E-08	1.18E-06	chr15:42359881-42386752 (-)	15q15.1	phospholipase A2, group IVD (cytosolic)
DSG3	2.55	1.45E-09	2.10E-07	chr18:29027732-29058665 (+)	18q12.1	desmoglein 3
PRR11	2.54	1.41E-06	3.56E-05	chr17:57232860-57284070 (+)	17q22	proline rich 11
ARSF	2.54	8.04E-09	7.16E-07	chrX:2958275-3030770 (+)	Xp22.3	arylsulfatase F
TMSB10	2.53	4.55E-10	9.48E-08	chr2:85132749-85133799 (+)	2p11.2	thymosin beta 10
STIL	2.52	1.77E-10	5.09E-08	chr1:47715811-47779819 (-)	1p32	SCL TAL1 interrupting locus
USP18	2.52	2.84E-06	6.08E-05	chr22:18632666-18672923 (+)	22q11.21	ubiquitin specific peptidase 18
WNT5A	2.51	4.42E-09	4.68E-07	chr3:55499743-55523973 (-)	3p21-p14	wingless-type MMTV integration site family, member 5A
IL13RA1	2.51	1.11E-09	1.72E-07	chrX:117861535-117928502 (+)	Xq24	interleukin 13 receptor, alpha 1
ARNTL2	2.50	1.12E-10	3.77E-08	chr12:27485787-27578746 (+)	12p12.2-p11.2	aryl hydrocarbon receptor nuclear translocator-like 2
RRM2	2.50	1.32E-12	1.63E-09	chr2:10262455-10271546 (+)	2p25-p24	ribonucleotide reductase M2
CKMT1A	2.50	2.09E-10	5.66E-08	chr15:43985084-43991420 (+)	15q15	creatine kinase, mitochondrial 1A
MELK	2.50	2.41E-10	6.06E-08	chr9:36572859-36677679 (+)	9p13.2	maternal embryonic leucine zipper kinase
PPIG	2.49	6.17E-05	6.24E-04	chr2:170440850-170504696 (+)	2q31.1	peptidylprolyl isomerase G (cyclophilin G)
SAT1	2.47	6.45E-05	6.45E-04	chrX:23801275-23804343 (+)	Xp22.1	spermidine spermine N1-acetyltransferase 1
HMMR	2.46	4.78E-09	4.94E-07	chr5:162887175-162918953 (+)	5q34	hyaluronan-mediated motility receptor (RHAMM)
IFITM2	2.46	1.46E-06	3.65E-05	chr11:307631-309410 (+)	11p15.5	interferon induced transmembrane protein 2
FAM110C	2.44	3.09E-12	3.12E-09	chr2:38814-46870 (-)	2p25.3	family with sequence similarity 110, member C
PLK1	2.44	2.20E-07	8.30E-06	chr16:23690143-23701688 (+)	16p12.2	polo-like kinase 1
GBP3	2.44	6.71E-07	2.01E-05	chr1:89472360-89488549 (-)	1p22.2	guanylate binding protein 3
CCNB2	2.44	7.31E-08	3.54E-06	chr15:59397277-59417244 (+)	15q22.2	cyclin B2
CD24	2.43	1.65E-07	6.64E-06	chrY:21152526-21154705 (-)	6q21	CD24 molecule
MNS1	2.42	2.41E-10	6.06E-08	chr15:56720929-56757335 (-)	15q21.3	meiosis-specific nuclear structural 1
BUB1	2.42	2.07E-09	2.66E-07	chr2:111395275-111435691 (-)	2q14	BUB1 mitotic checkpoint serine threonine kinase
SULT1E1	2.42	2.50E-05	3.15E-04	chr4:70676498-70725870 (-)	4q13.1	sulfotransferase family 1E, estrogen-preferring, member 1
GCNT4	2.41	1.87E-09	2.49E-07	chr5:74321171-74326724 (-)	5q12	glucosaminyl (N-acetyl) transferase 4, core 2
SPTSSA	2.41	4.53E-10	9.48E-08	chr14:34901995-34931562 (-)	14q13.1	serine palmitoyltransferase, small subunit A
ME1	2.41	1.87E-07	7.37E-06	chr6:83920108-84140938 (-)	6q12	malic enzyme 1, NADP(+)-dependent, cytosolic
NUF2	2.41	8.12E-10	1.45E-07	chr1:163291690-163325554 (+)	1q23.3	NUF2, NDC80 kinetochore complex component
CTSL	2.41	5.29E-13	9.21E-10	chr9:90340434-90346384 (+)	9q21.33	cathepsin L
FUT2	2.39	3.19E-06	6.63E-05	chr19:49199228-49209207 (+)	19q13.3	fucosyltransferase 2 (secretor status included)
APOL1	2.37	9.75E-08	4.48E-06	chr22:36649056-36663577 (+)	22q13.1	apolipoprotein L, 1
VNN1	2.37	2.56E-12	2.78E-09	chr6:133001997-133035194 (-)	6q23-q24	vanin 1
TTK	2.37	1.02E-08	8.32E-07	chr6:80713604-80752244 (+)	6q14.1	TTK protein kinase
CKAP2L	2.37	3.28E-08	1.96E-06	chr2:113493930-113522254 (-)	2q13	cytoskeleton associated protein 2-like
DTX3L	2.37	1.48E-07	6.17E-06	chr3:122283085-122294050 (+)	3q21.1	deltex 3 like, E3 ubiquitin ligase
ESCO2	2.36	9.85E-10	1.63E-07	chr8:27629466-27670157 (+)	8p21.1	establishment of sister chromatid cohesion N-acetyltransferase 2
CKMT1B	2.36	1.47E-10	4.48E-08	chr15:43885252-43897099 (+)	15q15	creatine kinase, mitochondrial 1B
CLEC3A	2.36	1.07E-02	3.04E-02	chr16:78056412-78066003 (+)	16q23	C-type lectin domain family 3, member A
TPX2	2.36	1.36E-07	5.75E-06	chr20:30326904-30389608 (+)	20q11.2	TPX2, microtubule-associated
VSNL1	2.36	7.90E-12	6.28E-09	chr2:17720393-17838285 (+)	2p24.3	visinin-like 1
KLK10	2.35	8.62E-05	7.99E-04	chr19:51516000-51523431 (-)	19q13	kallikrein-related peptidase 10
LIPG	2.35	2.19E-07	8.28E-06	chr18:47088427-47119278 (+)	18q21.1	lipase, endothelial
PDSS1	2.35	1.86E-12	2.16E-09	chr10:26986588-27035727 (+)	10p12.1	prenyl (decaprenyl) diphosphate synthase, subunit 1
CXCR4	2.34	5.61E-08	2.91E-06	chr2:136871919-136875735 (-)	2q21	chemokine (C-X-C motif) receptor 4
SLC39A6	2.32	1.69E-11	1.05E-08	chr18:33688494-33709357 (-)	18q12.2	solute carrier family 39 (zinc transporter), member 6
ARHGDIB	2.32	1.34E-10	4.25E-08	chr12:15094949-15114603 (-)	12p12.3	Rho GDP dissociation inhibitor (GDI) beta
SPRR1B	2.31	2.13E-04	1.56E-03	chr1:153003678-153005376 (+)	1q21-q22	small proline-rich protein 1B
CDC6	2.31	1.41E-11	9.03E-09	chr17:38443885-38459413 (+)	17q21.3	cell division cycle 6
GOT2	2.30	4.45E-11	1.94E-08	chr16:58741035-58768246 (-)	16q21	glutamic-oxaloacetic transaminase 2, mitochondrial
SAMHD1	2.29	1.60E-03	7.05E-03	chr20:35518632-35580246 (-)	20pter-q12	SAM domain and HD domain 1
HIST1H2AB	2.29	4.63E-07	1.50E-05	chr6:26033320-26033796 (-)	6p22.1	histone cluster 1, H2ab
IDH3A	2.29	5.49E-11	2.20E-08	chr15:78441663-78464291 (+)	15q25.1-q25.2	isocitrate dehydrogenase 3 (NAD+) alpha
PSME2	2.28	1.55E-13	4.21E-10	chr14:24612571-24616430 (-)	14q11.2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
EEA1	2.28	2.48E-03	9.87E-03	chr12:93164413-93323107 (-)	12q22	early endosome antigen 1
DDX21	2.28	6.58E-06	1.14E-04	chr10:70715884-70744829 (+)	10q21	DEAD (Asp-Glu-Ala-Asp) box helicase 21
KIAA0101	2.28	5.86E-11	2.27E-08	chr15:64657193-64679886 (-)	15q22.31	KIAA0101
ZWILCH	2.28	1.05E-09	1.69E-07	chr15:66797431-66841823 (+)	15q22.31	zwilch kinetochore protein
SGOL1	2.27	3.37E-09	3.82E-07	chr3:20202085-20227784 (-)	3p24.3	shugoshin-like 1 (S. pombe)
RASGRP1	2.27	3.39E-08	2.01E-06	chr15:38780302-38857776 (-)	15q14	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
IL4R	2.26	5.32E-11	2.14E-08	chr16:27325247-27376099 (+)	16p12.1-p11.2	interleukin 4 receptor
FANCI	2.26	5.10E-10	1.02E-07	chr15:89787180-89860492 (+)	15q26.1	Fanconi anemia, complementation group I
KIAA1524	2.26	7.85E-09	7.03E-07	chr3:108268718-108308491 (-)	3q13.13	KIAA1524
KIF15	2.26	6.63E-10	1.26E-07	chr3:44803209-44914868 (+)	3p21.31	kinesin family member 15
PDZK1IP1	2.26	1.47E-09	2.12E-07	chr1:47649261-47656716 (-)	1p33	PDZK1 interacting protein 1
DDX58	2.26	5.24E-06	9.62E-05	chr9:32455300-32526322 (-)	9p12	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
CLSPN	2.25	7.12E-13	1.07E-09	chr1:36185819-36235568 (-)	1p34.2	claspin
SPTLC2	2.25	8.18E-10	1.46E-07	chr14:77972340-78083116 (-)	14q24.3	serine palmitoyltransferase, long chain base subunit 2
TRANK1	2.24	1.20E-06	3.16E-05	chr3:36868308-36986548 (-)	3p22.2	tetratricopeptide repeat and ankyrin repeat containing 1
PLA2G4E	2.24	1.70E-08	1.21E-06	chr15:42273780-42343388 (-)	15q15.1	phospholipase A2, group IVE
SASS6	2.24	1.02E-06	2.79E-05	chr1:100549102-100598511 (-)	1p21.2	spindle assembly 6 homolog (C. elegans)
C9orf84	2.24	5.29E-10	1.05E-07	chr9:114448453-114557288 (-)	9q31.3	chromosome 9 open reading frame 84
RAD51AP1	2.24	7.16E-11	2.60E-08	chr12:4647950-4669214 (+)	12p13.2-p13.1	RAD51 associated protein 1
SKA3	2.22	5.14E-10	1.03E-07	chr13:21727734-21750741 (-)	13q12.11	spindle and kinetochore associated complex subunit 3
LDHB	2.22	2.80E-08	1.75E-06	chr12:21788275-21910765 (-)	12p12.2-p12.1	lactate dehydrogenase B
ABCC1	2.22	1.79E-11	1.07E-08	chr16:16043434-16236931 (+)	16p13.1	ATP-binding cassette, sub-family C (CFTR MRP), member 1
IVL	2.22	8.31E-05	7.79E-04	chr1:152881021-152884362 (+)	1q21	involucrin
ANKRD29	2.22	9.27E-12	6.95E-09	chr18:21178890-21242849 (-)	18q11.2	ankyrin repeat domain 29
PRC1	2.22	4.26E-08	2.40E-06	chr15:91509268-91538859 (-)	15q26.1	protein regulator of cytokinesis 1
LGALS3BP	2.22	1.23E-08	9.54E-07	chr17:76967335-76976061 (-)	17q25	lectin, galactoside-binding, soluble, 3 binding protein
MCM10	2.22	2.39E-13	5.82E-10	chr10:13203554-13253104 (+)	10p13	minichromosome maintenance complex component 10
NCAPH	2.21	1.10E-09	1.72E-07	chr2:97001484-97041274 (+)	2q11.2	non-SMC condensin I complex, subunit H
TXNDC17	2.21	8.92E-11	3.15E-08	chr17:6544078-6547920 (+)	17p13.1	thioredoxin domain containing 17
FGFBP1	2.21	1.13E-05	1.74E-04	chr4:15937192-15940363 (-)	4p15.32	fibroblast growth factor binding protein 1
GABRA4	2.21	3.53E-05	4.07E-04	chr4:46920917-46996424 (-)	4p12	gamma-aminobutyric acid (GABA) A receptor, alpha 4
KCNJ15	2.21	5.61E-11	2.22E-08	chr21:39628663-39673748 (+)	21q22.2	potassium inwardly-rectifying channel, subfamily J, member 15
POLR3G	2.20	1.31E-09	1.93E-07	chr5:89767565-89810370 (+)	5q14.3	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
ATAD5	2.19	2.28E-05	2.93E-04	chr17:29158988-29222295 (+)	17q11.2	ATPase family, AAA domain containing 5
CD47	2.19	2.51E-10	6.25E-08	chr3:107761941-107809935 (-)	3q13.1-q13.2	CD47 molecule
SPRR2D	2.19	7.87E-03	2.39E-02	chr1:153012201-153014407 (-)	1q21-q22	small proline-rich protein 2D
KIF4A	2.18	1.92E-09	2.53E-07	chrX:69509879-69640774 (+)	Xq13.1	kinesin family member 4A
SOX7	2.17	7.10E-11	2.60E-08	chr8:10581278-10588022 (-)	8p23.1	SRY (sex determining region Y)-box 7
CCDC18	2.17	7.67E-08	3.68E-06	chr1:93645476-93744287 (+)	1p22.1	coiled-coil domain containing 18
CLCA2	2.17	5.07E-11	2.09E-08	chr1:86889769-86922241 (+)	1p22.3	chloride channel accessory 2
SLC18B1	2.17	7.51E-12	6.09E-09	chr6:133090507-133119747 (-)	6q22.3-q23.3	solute carrier family 18, subfamily B, member 1
POLQ	2.17	5.70E-09	5.55E-07	chr3:121150273-121265488 (-)	3q13.33	polymerase (DNA directed), theta
ROCK1	2.17	2.60E-03	1.02E-02	chr18:18529701-18691812 (-)	18q11.1	Rho-associated, coiled-coil containing protein kinase 1
SP100	2.16	2.93E-06	6.22E-05	chr2:231280657-231410317 (+)	2q37.1	SP100 nuclear antigen
NMI	2.16	2.77E-12	2.92E-09	chr2:152126979-152146571 (-)	2q23	N-myc (and STAT) interactor
EIF2AK2	2.16	1.49E-04	1.20E-03	chr2:37326353-37384208 (-)	2p22-p21	eukaryotic translation initiation factor 2-alpha kinase 2
LMNB1	2.16	1.86E-11	1.09E-08	chr5:126112315-126172712 (+)	5q23.2	lamin B1
TOP1	2.15	1.27E-06	3.28E-05	chr20:39657458-39753127 (+)	20q12-q13.1	topoisomerase (DNA) I
HMGN5	2.15	9.22E-07	2.58E-05	chrX:80369200-80457441 (-)	Xq13.3	high mobility group nucleosome binding domain 5
PNP	2.15	1.77E-07	7.03E-06	chr14:20937538-20946165 (+)	14q13.1	purine nucleoside phosphorylase
CYCS	2.15	9.73E-10	1.62E-07	chr7:25158270-25164980 (-)	7p15.3	cytochrome c, somatic
C12orf5	2.14	7.79E-08	3.72E-06	chr12:44303059-4469190 (+)	12p13.3	chromosome 12 open reading frame 5
KIF2C	2.14	2.99E-08	1.84E-06	chr1:45205490-45233439 (+)	1p34.1	kinesin family member 2C
PBK	2.14	3.47E-09	3.93E-07	chr8:27667137-27695612 (-)	8p21.2	PDZ binding kinase
CRABP2	2.14	1.24E-11	8.52E-09	chr1:156669398-156675608 (-)	1q21.3	cellular retinoic acid binding protein 2
HSPH1	2.13	1.62E-07	6.55E-06	chr13:31710762-31736525 (-)	13q12.3	heat shock 105kDa 110kDa protein 1
NUSAP1	2.13	1.68E-06	4.08E-05	chr15:41624892-41673248 (+)	15q15.1	nucleolar and spindle associated protein 1
ALDH7A1	2.13	2.80E-09	3.32E-07	chr5:125877533-125931110 (-)	5q31	aldehyde dehydrogenase 7 family, member A1
PGD	2.13	1.53E-09	2.17E-07	chr1:10458649-10480233 (+)	1p36.22	phosphogluconate dehydrogenase
SPRR1A	2.13	7.57E-03	2.32E-02	chr1:152956557-152958290 (+)	1q21-q22	small proline-rich protein 1A
MYO5A	2.13	2.31E-07	8.62E-06	chr15:52599480-52821247 (-)	15q21	myosin VA (heavy chain 12, myoxin)
PSMA3	2.12	3.67E-09	4.08E-07	chr14:58711523-58738730 (+)	14q23	proteasome (prosome, macropain) subunit, alpha type, 3
RAD50	2.12	7.85E-03	2.39E-02	chr5:131891711-131980313 (+)	5q31	RAD50 homolog (S. cerevisiae)
IFNGR1	2.12	1.27E-08	9.76E-07	chr6:137518621-137540586 (-)	6q23.3	interferon gamma receptor 1
TPR	2.11	2.55E-03	1.01E-02	chr1:186280786-186344864 (-)	1q25	translocated promoter region, nuclear basket protein
CCDC109B	2.11	6.16E-11	2.33E-08	chr4:110481355-110609874 (+)	4q25	coiled-coil domain containing 109B
IFIT5	2.11	3.11E-06	6.50E-05	chr10:91174325-91180759 (+)	10q23.31	interferon-induced protein with tetratricopeptide repeats 5
BRIP1	2.10	2.51E-06	5.54E-05	chr17:59756547-59940920 (-)	17q22.2	BRCA1 interacting protein C-terminal helicase 1
XRCC2	2.10	1.01E-08	8.28E-07	chr7:152341864-152373250 (-)	7q36.1	X-ray repair complementing defective repair in Chinese hamster cells 2
HPSE	2.10	5.85E-07	1.81E-05	chr4:84213614-84256306 (-)	4q21.3	heparanase

C20orf24	2.10	2.55E-11	1.35E-08	chr20:35234137-35240960 (+)	20q11.23	chromosome 20 open reading frame 24
EXO1	2.10	7.85E-11	2.80E-08	chr1:242011269-242058450 (+)	1q42-q43	exonuclease 1
SHCBP1	2.10	8.15E-09	7.23E-07	chr16:46614466-46655538 (-)	16q11.2	SHC SH2-domain binding protein 1
STAT2	2.10	1.64E-06	4.01E-05	chr12:56735381-56754037 (-)	12q13.3	signal transducer and activator of transcription 2, 113kDa
IGFL1	2.10	7.61E-08	3.66E-06	chr19:46733009-46734500 (+)	19q13.32	IGF-like family member 1
PON2	2.10	1.06E-10	3.60E-08	chr7:95034174-95064510 (-)	7q21.3	paraoxonase 2
CDKN3	2.09	2.16E-08	1.43E-06	chr14:54863673-54886936 (+)	14q22	cyclin-dependent kinase inhibitor 3
COL12A1	2.09	4.33E-07	1.42E-05	chr6:75794042-75915767 (-)	6q12-q13	collagen, type XII, alpha 1
CTSB	2.09	2.08E-10	5.66E-08	chr8:11700033-11725738 (-)	8p22	cathepsin B
CXCL10	2.09	1.01E-04	9.00E-04	chr4:76942269-76944689 (-)	4q21	chemokine (C-X-C motif) ligand 10
ADAP2	2.09	1.99E-08	1.35E-06	chr17:29248698-29286340 (+)	17q11.2	ArfGAP with dual PH domains 2
APOO	2.09	3.67E-09	4.08E-07	chrX:23851465-23926057 (-)	Xp22.11	apolipoprotein O
APOL6	2.08	9.10E-08	4.23E-06	chr22:36044424-36064456 (+)	22q12.3	apolipoprotein L, 6
ANGPTL4	2.08	3.34E-09	3.80E-07	chr19:8429011-8439257 (+)	19p13.3	angiopoietin-like 4
NOLC1	2.07	2.64E-09	3.19E-07	chr10:103911933-103923627 (+)	10q24.32	nucleolar and coiled-body phosphoprotein 1
SP110	2.07	2.59E-08	1.65E-06	chr2:231032009-231090444 (-)	2q37.1	SP110 nuclear body protein
COX7B	2.07	1.06E-09	1.71E-07	chrX:77154935-77162870 (+)	Xq21.1	cytochrome c oxidase subunit VIIb
HIST1H1A	2.07	2.97E-06	6.29E-05	chr6:26017248-26018040 (-)	6p21.3	histone cluster 1, H1a
BLNK	2.07	2.67E-08	1.68E-06	chr10:97951455-98031333 (-)	10q23.2-q23.33	B-cell linker
DPYD	2.06	8.71E-09	7.54E-07	chr1:97543299-98386615 (-)	1p22	dihydropyrimidine dehydrogenase
FERMT1	2.06	1.41E-07	5.93E-06	chr20:6055492-6104191 (-)	20p12.3	fermitin family member 1
C1S	2.06	6.03E-12	5.19E-09	chr12:7096260-7178336 (+)	12p13	complement component 1, s subcomponent
SLFN5	2.06	1.77E-05	2.45E-04	chr17:33570086-33594761 (+)	17q12	schlafen family member 5
ECT2	2.06	3.06E-08	1.87E-06	chr3:172468472-172539264 (+)	3q26.1-q26.2	epithelial cell transforming 2
ENTPD7	2.06	5.56E-10	1.09E-07	chr10:101419263-101471002 (+)	10q24.2	ectonucleoside triphosphate diphosphohydrolase 7
LTB4R	2.06	3.34E-11	1.59E-08	chr14:24780705-24787242 (+)	14q11.2-q12	leukotriene B4 receptor
CYP4X1	2.05	3.08E-07	1.08E-05	chr1:47427036-47516423 (+)	1p33|1	cytochrome P450, family 4, subfamily X, polypeptide 1
SLC25A33	2.05	8.37E-10	1.47E-07	chr1:9599528-9642833 (+)	1p36.22	solute carrier family 25 (pyrimidine nucleotide carrier), member 33
VNN3	2.05	1.21E-09	1.83E-07	chr6:133043923-133055904 (-)	6q23.2	vanin 3
EDNRA	2.05	1.98E-06	4.62E-05	chr4:148402069-148466106 (+)	4q31.22	endothelin receptor type A
CFB	2.05	7.44E-07	2.18E-05	chr6_cox_hap2:3423477-3429617	6p21.3	complement factor B
DNMT1	2.05	2.31E-12	2.58E-09	chr19:10244022-10305755 (-)	19p13.2	DNA (cytosine-5-)-methyltransferase 1
PDE8A	2.04	5.39E-09	5.36E-07	chr15:85523671-85682376 (+)	15q25.3	phosphodiesterase 8A
MCM6	2.04	9.76E-09	8.12E-07	chr2:136597196-136634011 (-)	2q21	minichromosome maintenance complex component 6
CKS2	2.04	4.39E-08	2.45E-06	chr9:91926113-91931618 (+)	9q22	CDC28 protein kinase regulatory subunit 2
FRK	2.04	2.86E-09	3.37E-07	chr6:116262693-116381921 (-)	6q21-q22.3	fyn-related Src family tyrosine kinase
CEP152	2.04	4.76E-07	1.53E-05	chr15:49030132-49103343 (-)	15q21.1	centrosomal protein 152kDa
DEPDC1B	2.04	1.03E-09	1.68E-07	chr5:59892739-59996017 (-)	5q12.1	DEP domain containing 1B
STARD4	2.04	8.50E-06	1.39E-04	chr5:110831731-110848288 (-)	5q22.1	StAR-related lipid transfer (START) domain containing 4
AURKA	2.04	5.79E-10	1.13E-07	chr20:54944445-54967393 (-)	20q13	aurora kinase A
ALOX12B	2.03	6.81E-04	3.70E-03	chr17:7975954-7991022 (-)	17p13.1	arachidonate 12-lipoxygenase, 12R type
HSP90B1	2.03	6.61E-06	1.15E-04	chr12:104324112-104341704 (+)	12q24.2-q24.3	heat shock protein 90kDa beta (Grp94), member 1
FOXM1	2.03	2.06E-08	1.38E-06	chr12:2966847-2986321 (-)	12p13	forkhead box M1
DDIAS	2.03	3.01E-11	1.51E-08	chr11:82612737-82669319 (+)	11q14.1	DNA damage-induced apoptosis suppressor
PPIF	2.03	1.92E-07	7.55E-06	chr10:81107220-81115093 (+)	10q22-q23	peptidylprolyl isomerase F
KRT16P2	2.03	5.81E-11	2.27E-08	chr17:16733797-16736147 (-)	17p11.2	keratin 16 pseudogene 2
CDCA2	2.03	4.34E-08	2.44E-06	chr8:25316513-25365436 (+)	8p21.2	cell division cycle associated 2
CENPN	2.03	3.81E-10	8.33E-08	chr16:81040103-81066719 (+)	16q23.2	centromere protein N
DIAPH3	2.03	9.35E-10	1.59E-07	chr13:60239717-60738119 (-)	13q21.2	diaphanous-related formin 3
RAB38	2.02	4.21E-10	8.99E-08	chr11:87846415-87908635 (-)	11q14	RAB38, member RAS oncogene family
SLC1A5	2.02	1.41E-09	2.06E-07	chr19:47227814O-47291851 (-)	19q13.3	solute carrier family 1 (neutral amino acid transporter), member 5
CASK	2.02	1.50E-08	1.11E-06	chrX:41374187-41782716 (-)	Xp11.4	calcium calmodulin-dependent serine protein kinase (MAGUK family)
TARS	2.02	2.96E-10	7.06E-08	chr5:33440802-33469644 (+)	5p13.2	threonyl-tRNA synthetase
TENM2	2.02	1.21E-06	3.18E-05	chr5:166711804-167691162 (+)	5q34	teneurin transmembrane protein 2
GBP4	2.02	2.97E-05	3.58E-04	chr1:89646831-89664633 (-)	1p22.2	guanylate binding protein 4
PGLYRP4	2.01	3.78E-08	2.20E-06	chr1:153302596-153321316 (-)	1q21	peptidoglycan recognition protein 4
PPIL1	2.01	1.60E-11	1.01E-08	chr6:36822603-36842800 (-)	6p21.1	peptidylprolyl isomerase (cyclophilin)-like 1
ATP1B1	2.01	9.02E-07	2.54E-05	chr1:169074935-169101960 (+)	1q24	ATPase, Na+ K+ transporting, beta 1 polypeptide
FMO1	2.01	1.13E-03	5.43E-03	chr1:171217633-171255117 (+)	1q24.3	flavin containing monooxygenase 1
GPR110	2.01	2.67E-09	3.22E-07	chr6:46963107-47010099 (-)	6p12.3	G protein-coupled receptor 110
CCDC88A	2.01	5.12E-07	1.62E-05	chr2:55514978-55647057 (-)	2p16.1	coiled-coil domain containing 88A
TC2N	2.01	1.61E-11	1.01E-08	chr14:92246095-92333880 (-)	14q32.12	tandem C2 domains, nuclear
GEN1	2.01	9.33E-06	1.49E-04	chr2:17935125-17966632 (+)	2p24.2	GEN1 Holliday junction 5 flap endonuclease
SGK1	2.00	8.38E-09	7.32E-07	chr6:134490384-134639196 (-)	6q23	serum glucocorticoid regulated kinase 1
OSMR	2.00	7.25E-08	3.52E-06	chr5:38845960-38945698 (+)	5p13.1	oncostatin M receptor
KRT16P1	2.00	1.92E-11	1.09E-08	chr17:18343222-18344919 (+)	17p11.2	keratin 16 pseudogene 1
CNDP2	2.00	5.77E-11	2.27E-08	chr18:72163443-72190689 (+)	18q22.3	CNDP dipeptidase 2 (metallopeptidase M20 family)
MAST4-IT1	2.00	1.01E-05	1.58E-04	chr5:65958159-65958816 (+)	---	MAST4 intronic transcript 1 (non-protein coding)
PGAM1	2.00	4.46E-11	1.94E-08	chr10:99185917-99193198 (+)	10q25.3	phosphoglycerate mutase 1 (brain)
COX6A1	1.99	5.83E-09	5.64E-07	chr12:120875893-120878545 (+)	12q24.2|12q24.2	cytochrome c oxidase subunit VIa polypeptide 1
ATP1A1	1.99	5.02E-08	2.69E-06	chr1:116915004-116952883 (+)	1p21	ATPase, Na+K+ transporting, alpha 1 polypeptide
CCND2	1.99	7.14E-06	1.21E-04	chr12:4382902-4414522 (+)	12p13	cyclin D2
MPHOSPH9	1.99	2.68E-09	3.23E-07	chr12:123636867-123717785 (-)	12q24.31	M-phase phosphoprotein 9
SLC22A3	1.99	3.97E-07	1.32E-05	chr6:160769300-160876014 (+)	6q25.3	solute carrier family 22 (organic cation transporter), member 3
ACAA2	1.99	8.96E-04	4.56E-03	chr18:47309869-47340273 (-)	18q21.1	acetyl-CoA acyltransferase 2
FOXE1	1.99	7.10E-10	1.32E-07	chr9:100615536-100618997 (+)	9q22	forkhead box E1 (thyroid transcription factor 2)
PRRC2C	1.99	2.11E-06	4.83E-05	chr1:171454651-171562650 (+)	1q23.3	proline-rich coiled-coil 2C
NOP58	1.98	2.86E-04	1.95E-03	chr2:203130439-203168388 (+)	2q33.1	NOP58 ribonucleoprotein
LOC101929988	1.98	5.25E-06	9.64E-05	chr15:34147101-34149010 (-)	---	uncharacterized LOC101929988
AGPAT4	1.98	6.17E-06	1.09E-04	chr6:161551011-161695107 (-)	6q26	1-acylglycerol-3-phosphate O-acyltransferase 4
SIPA1L2	1.98	1.89E-07	7.42E-06	chr1:232533711-232697304 (-)	1q42.2	signal-induced proliferation-associated 1 like 2
HELLS	1.98	1.58E-07	6.44E-06	chr10:96305543-96373662 (+)	10q24.2	helicase, lymphoid-specific
BLM	1.98	3.98E-11	1.81E-08	chr15:91260558-91358692 (+)	15q26.1	Bloom syndrome, RecQ helicase-like
BZW1	1.98	7.31E-10	1.34E-07	chr2:201675317-201688569 (+)	2q33	basic leucine zipper and W2 domains 1
SLC16A6	1.97	5.06E-10	1.02E-07	chr17:66263167-66287405 (-)	17q24.2	solute carrier family 16, member 6
ARHGAP11A	1.97	1.67E-06	4.06E-05	chr15:32907345-32932150 (+)	15q13.2	Rho GTPase activating protein 11A
TGFBR1	1.97	2.17E-08	1.43E-06	chr9:101867371-101916585 (+)	9q22	transforming growth factor, beta receptor 1
PRICKLE2	1.97	1.54E-07	6.32E-06	chr3:64079526-64253655 (-)	3p14.1	prickle homolog 2 (Drosophila)
IL19	1.97	4.14E-05	4.61E-04	chr1:206972215-207016326 (+)	1q32.2	interleukin 19
MPZL1	1.97	8.73E-13	1.16E-09	chr1:167690429-167761156 (+)	1q24.2	myelin protein zero-like 1
HBEGF	1.97	9.99E-05	8.93E-04	chr5:139712428-139726216 (-)	5q23	heparin-binding EGF-like growth factor
ARHGAP11B	1.97	1.73E-06	4.16E-05	chr15:30916697-30931023 (+)	15q13.2	Rho GTPase activating protein 11B
CSTA	1.97	6.64E-08	3.30E-06	chr3:122044011-122060819 (+)	3q21	cystatin A (stefin A)
CACHD1	1.96	1.16E-08	9.17E-07	chr1:64936428-65158741 (+)	1p31.3	cache domain containing 1
HSPA5	1.96	6.91E-08	3.39E-06	chr9:127997127-128003666 (-)	9q33.3	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
HERC5	1.96	1.26E-06	3.28E-05	chr4:89378268-89427314 (+)	4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase 5
FBXO9	1.96	2.21E-10	5.89E-08	chr6:52916789-52965671 (+)	6p12.3-p11.2	F-box protein 9
UPF3B	1.96	8.24E-05	7.74E-04	chrX:118967985-118986991 (-)	Xq25-q26	UPF3 regulator of nonsense transcripts homolog B (yeast)
AFAP1L2	1.96	2.84E-09	3.36E-07	chr10:116054583-116164515 (-)	10q25.3	actin filament associated protein 1-like 2
LAMP3	1.96	1.76E-04	1.35E-03	chr3:182840001-182881627 (-)	3q26.3-q27	lysosomal-associated membrane protein 3
ESF1	1.96	1.40E-02	3.73E-02	chr20:13694969-13765565 (-)	20p12.1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
ROCK2	1.96	2.26E-03	9.20E-03	chr2:11319887-11488456 (-)	2p24	Rho-associated, coiled-coil containing protein kinase 2
TIMELESS	1.95	3.58E-11	1.67E-08	chr12:56810157-56843200 (-)	12q13.3	timeless circadian clock
ERP27	1.95	4.51E-04	2.74E-03	chr12:15066969-15092016 (-)	12p12.3	endoplasmic reticulum protein 27
GTF3C6	1.95	3.89E-12	3.61E-09	chr6:111279763-111289093 (+)	6q21	general transcription factor IIIC, polypeptide 6, alpha 35kDa
TMEM171	1.95	1.06E-05	1.65E-04	chr5:72416119-72427644 (+)	5q13.2	transmembrane protein 171
TRIB2	1.95	5.94E-09	5.73E-07	chr2:12856998-12882860 (+)	2p24.3	tribbles pseudokinase 2
PANX1	1.95	3.53E-06	7.15E-05	chr11:93862094-93915138 (+)	11q21	pannexin 1
LRRC59	1.94	4.55E-09	4.76E-07	chr17:48458594-48474914 (-)	17q21.33	leucine rich repeat containing 59
TLDC1	1.94	2.56E-10	6.30E-08	chr16:84509966-84538296 (-)	16q24.1	TBCLysM-associated domain containing 1
HIST1H2BB	1.93	8.44E-06	1.38E-04	chr6:26043455-26043885 (-)	6p21.3	histone cluster 1, H2bb
COX6A1P2	1.93	1.76E-09	2.37E-07	chr6:37012607-37013177 (+)	---	cytochrome c oxidase subunit VIa polypeptide 1 pseudogene 2
USMG5	1.93	2.23E-10	5.92E-08	chr10:105148798-105156270 (-)	10q24.33	up-regulated during skeletal muscle growth 5 homolog (mouse)
SKA2	1.93	1.40E-07	5.91E-06	chr17:57187308-57232800 (-)	17q22	spindle and kinetochore associated complex subunit 2
CENPK	1.93	1.42E-08	1.06E-06	chr5:64813593-64858998 (-)	5q12.3	centromere protein K
SLC1A1	1.92	2.07E-04	1.53E-03	chr9:4490427-4587469 (+)	9p24	solute carrier family 1 (neuronalepithelial high affinity glutamate transporter, system Xag), member 1
HIGD1A	1.92	1.21E-09	1.83E-07	chr3:42824400-42846027 (-)	3p22.1	HIG1 hypoxia inducible domain family, member 1A
CHI3L1	1.92	6.26E-07	1.90E-05	chr1:203148059-203155922 (-)	1q32.1	chitinase 3-like 1 (cartilage glycoprotein-39)
CDC20	1.92	1.08E-07	4.85E-06	chr1:43824599-43828874 (+)	1p34.1	cell division cycle 20
GNL2	1.92	3.20E-06	6.63E-05	chr1:38032413-38061586 (-)	1p34.3	guanine nucleotide binding protein-like 2 (nucleolar)
TIMM17A	1.92	3.60E-10	8.10E-08	chr1:201924619-201939789 (+)	1q32.1	translocase of inner mitochondrial membrane 17 homolog A (yeast)
LOC101928670	1.92	1.59E-04	1.26E-03	chr1:141474-149707 (-)	---	uncharacterized LOC101928670
TUBG1	1.92	2.99E-09	3.47E-07	chr17:40761358-40767256 (+)	17q21	tubulin, gamma 1
TMPRSS4	1.91	4.90E-09	5.03E-07	chr11:117947727-117996323 (+)	11q23.3	transmembrane protease, serine 4
SNRPD1	1.91	7.27E-08	3.53E-06	chr18:19192260-19210208 (+)	18q11.2	small nuclear ribonucleoprotein D1 polypeptide 16kDa
PON3	1.91	1.09E-06	2.94E-05	chr7:94989184-95025687 (-)	7q21.3	paraoxonase 3
KRT17P2	1.91	7.51E-08	3.62E-06	chr17:18330175-18335162 (+)	---	keratin 17 pseudogene 2
FANCD2	1.91	1.89E-08	1.30E-06	chr3:10068098-10143614 (+)	3p26	Fanconi anemia, complementation group D2
BOD1L1	1.91	1.28E-03	5.97E-03	chr4:13570362-13629347 (-)	4p16.1	biorientation of chromosomes in cell division 1-like 1
PSMA4	1.90	4.09E-08	2.34E-06	chr15:78832747-78841604 (+)	15q25.1	proteasome (prosome, macropain) subunit, alpha type, 4
EIF2B2	1.90	2.85E-09	3.36E-07	chr14:75469612-75476294 (+)	14q24.3	eukarycotic translation initiation factor 2B, subunit 2 beta, 39kDa
PGM2	1.90	2.16E-09	2.73E-07	chr4:37828255-37864559 (+)	4p14	phosphoglucomutase 2
KCNJ2	1.90	8.52E-07	2.43E-05	chr17:68164814-68176183 (+)	17q24.3	potassium inwardly-rectifying channel, subfamily J, member 2
FASTKD1	1.89	4.19E-11	1.87E-08	chr2:170386259-170430424 (-)	2q31	FAST kinase domains 1
TUBG2	1.89	6.93E-12	5.69E-09	chr17:40811266-40819024 (+)	17q21	tubulin, gamma 2
LARP7	1.89	1.34E-04	1.11E-03	chr4:113558120-113578748 (+)	4q25	La ribonucleoprotein domain family, member 7
UBA6	1.89	1.64E-06	4.00E-05	chr4:68481479-68566897 (-)	4q13.2	ubiquitin-like modifier activating enzyme 6
CTPS1	1.89	2.21E-08	1.45E-06	chr1:41445007-41478235 (+)	1p34.1	CTP synthase 1
PTTG1	1.89	1.07E-09	1.71E-07	chr5:159848829-159855748 (+)	5q35.1	pituitary tumor-transforming 1
SQRDL	1.89	1.25E-09	1.88E-07	chr15:45923346-45983492 (+)	15q15	sulfide quinone reductase-like (yeast)
SMC3	1.89	1.15E-02	3.20E-02	chr10:112327449-112364394 (+)	10q25	structural maintenance of chromosomes 3
CEACAM5	1.89	3.07E-04	2.05E-03	chr19:42212504-42234437 (+)	19q13.1-q13.2	carcinoembryonic antigen-related cell adhesion molecule 5
COX5A	1.88	4.54E-10	9.48E-08	chr15:75212132-75230509 (-)	15q24.1	cytochrome c oxidase subunit Va
HYAL4	1.88	3.75E-10	8.29E-08	chr7:123469037-123517532 (+)	7q31.3	hyaluronoglucosaminidase 4
TMEM165	1.88	3.04E-06	6.41E-05	chr4:56262090-56292342 (+)	4q12	transmembrane protein 165

KIAA0020	1.88	3.87E-05	4.38E-04	chr9:2720469-2844241 (-)	9p24.2	KIAA0020
CROT	1.88	2.09E-07	7.97E-06	chr7:86974951-87029112 (+)	7q21.1	carnitine O-octanoyltransferase
TMEM45B	1.88	5.83E-07	1.81E-05	chr11:129685714-129729898 (+)	11q24.3	transmembrane protein 45B
CXCR2	1.88	1.65E-07	6.65E-06	chr2:218990012-219001976 (+)	2q35	chemokine (C-X-C motif) receptor 2
MPHOSPH10	1.88	2.88E-04	1.96E-03	chr2:71357444-71377232 (+)	2p13.3	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
SLC16A6P1	1.88	1.53E-09	2.17E-07	chr17:62950242-62952716 (+)	---	SLC16A6 pseudogene 1
USP41	1.87	4.31E-07	1.41E-05	chr22:20704868-20745048 (-)	22q11.21	ubiquitin specific peptidase 41
UQCR10	1.87	9.36E-09	7.89E-07	chr22:30163352-30166402 (+)	22q12.2	ubiquinol-cytochrome c reductase, complex III subunit X
TPBG	1.87	1.39E-10	4.34E-08	chr6:83072923-83080545 (+)	6q14-q15	trophoblast glycoprotein
EIF2S2	1.87	1.97E-07	7.66E-06	chr20:32676104-32700138 (-)	20q11.2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
DEPDC1	1.87	8.66E-06	1.41E-04	chr1:68939835-68962904 (-)	1p31.2	DEP domain containing 1
SP140L	1.87	6.26E-09	5.96E-07	chr2:231191894-231268447 (+)	2q37.1	SP140 nuclear body protein-like
RAB27A	1.87	5.98E-13	9.59E-10	chr15:55495164-55582013 (-)	15q15-q21.1	RAB27A, member RAS oncogene family
PLOD2	1.86	1.49E-07	6.17E-06	chr3:145787227-145881440 (-)	3q24	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2
ANLN	1.86	1.71E-04	1.33E-03	chr7:36429415-36493400 (+)	7p15-p14	anillin, actin binding protein
C1QBP	1.86	2.46E-09	3.02E-07	chr17:5336097-5342471 (-)	17p13.3	complement component 1, q subcomponent binding protein
CASP1	1.86	4.67E-08	2.56E-06	chr11:104896235-104972158 (-)	11q23	caspase 1, apoptosis-related cysteine peptidase
ETHE1	1.86	3.32E-08	1.98E-06	chr19:44010871-44031396 (-)	19q13.31	ethylmalonic encephalopathy 1
TRIP11	1.86	5.02E-03	1.69E-02	chr14:92432335-92506403 (-)	14q31-q32	thyroid hormone receptor interactor 11
PLEKHG7	1.86	4.42E-08	2.46E-06	chr12:93115281-93166231 (+)	12q22	pleckstrin homology domain containing, family G (with RhoGef domain) member 7
TMEM14A	1.86	1.34E-06	3.44E-05	chr6:52535884-52551386 (+)	6p12.2	transmembrane protein 14A
RNU6-1319P	1.86	1.73E-03	7.51E-03	chr1:224163848-224163951 (-)	---	RNA, U6 small nuclear 1319, pseudogene
RNU6-747P	1.86	1.73E-03	7.51E-03	chr1:243244458-243244561 (-)	---	RNA, U6 small nuclear 747, pseudogene
RNU6-241P	1.86	1.73E-03	7.51E-03	chr7:45829184-45829287 (+)	---	RNA, U6 small nuclear 241, pseudogene
TRPM6	1.85	3.84E-10	8.35E-08	chr9:77337411-77503010 (-)	9q21.13	transient receptor potential cation channel, subfamily M, member 6
PCNA	1.85	1.62E-09	2.22E-07	chr20:5095599-5107272 (-)	20pter-p12	proliferating cell nuclear antigen
STOML2	1.85	1.09E-08	8.68E-07	chr9:35099888-35103154 (-)	9p13.1	stomatin (EPB72)-like 2
PTGR1	1.85	4.38E-09	4.67E-07	chr9:114312002-114362135 (-)	9q31.3	prostaglandin reductase 1
PAPSS2	1.85	5.84E-10	1.13E-07	chr10:89419370-89507462 (+)	10q24	3-phosphoadenosine 5-phosphosulfate synthase 2
MGC24103	1.85	5.85E-04	3.31E-03	chr9:16525993-16527731 (-)	9p22.3	uncharacterized MGC24103
KITLG	1.85	4.54E-06	8.65E-05	chr12:88885885-88974628 (-)	12q22	KIT ligand
CAPN2	1.85	2.20E-06	5.01E-05	chr1:223889295-223963720 (+)	1q41-q42	calpain 2, (mII) large subunit
CXCL8	1.85	1.34E-04	1.11E-03	chr4:74606223-74609433 (+)	4q13-q21	chemokine (C-X-C motif) ligand 8
GARS	1.85	6.95E-09	6.41E-07	chr7:30634181-30673649 (+)	7p15	glycyl-tRNA synthetase
ACTN1	1.85	1.72E-05	2.39E-04	chr14:69340840-69446157 (-)	14q24|14q22-q24	actinin, alpha 1
KRT17	1.85	8.82E-08	4.13E-06	chr17:39775689-39781094 (-)	17q21.2	keratin 17
TYMS	1.85	1.43E-09	2.08E-07	chr18:657604-673578 (+)	18p11.32	thymidylate synthetase
HYOU1	1.84	3.07E-09	3.55E-07	chr11:118914896-118927925 (-)	11q23.1-q23.3	hypoxia up-regulated 1
GOLGA4	1.84	1.07E-02	3.04E-02	chr3:37284668-37408370 (+)	3p22-p21.3	golgin A4
NAA15	1.84	1.60E-04	1.26E-03	chr4:140222609-140341187 (+)	4q31.1	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
PAK1IP1	1.84	1.63E-05	2.29E-04	chr6:10694928-10710015 (+)	6p24.2	PAK1 interacting protein 1
CYP24A1	1.84	1.25E-02	3.42E-02	chr20:52769988-52790516 (-)	20q13	cytochrome P450, family 24, subfamily A, polypeptide 1
HSPA4L	1.84	6.58E-05	6.54E-04	chr4:128702976-128755226 (+)	4q28	heat shock 70kDa protein 4-like
UCHL3	1.84	4.94E-09	5.05E-07	chr13:76123619-76180085 (+)	13q22.2	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)
POLB	1.84	4.44E-08	2.46E-06	chr8:42195972-42229331 (+)	8p11.2	polymerase (DNA directed), beta
PRRG4	1.84	3.80E-11	1.75E-08	chr11:32851481-32879669 (+)	11p13	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
HOMER1	1.84	2.20E-08	1.45E-06	chr5:78668459-78810040 (-)	5q14.2	homer homolog 1 (Drosophila)
MED8	1.84	1.42E-07	5.94E-06	chr1:43849588-43855483 (-)	1p34.2	mediator complex subunit 8
GBP1P1	1.84	1.10E-09	1.72E-07	chr1:89873238-89890493 (+)	1p22.2	guanylate binding protein 1, interferon-inducible pseudogene 1
ATP5B	1.84	2.66E-10	6.52E-08	chr12:57031959-57039852 (-)	12q13.13	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
HSPA4	1.84	3.86E-07	1.29E-05	chr5:132387654-132442141 (+)	5q31.1	heat shock 70kDa protein 4
SUB1P1	1.84	1.43E-08	1.07E-06	chr8:11647514-11647897 (+)	---	SUB1 homolog (S. cerevisiae) pseudogene 1
CDC25B	1.84	1.70E-08	1.21E-06	chr20:3767578-3786762 (+)	20p13	cell division cycle 25B
MTFR2	1.84	9.27E-09	7.84E-07	chr6:136552162-136571462 (-)	6q23.3	mitochondrial fission regulator 2
MYD88	1.84	6.08E-09	5.82E-07	chr3:38179969-38184513 (+)	3p22	myeloid differentiation primary response 88
SUB1	1.83	4.10E-09	4.45E-07	chr5:32531739-32604185 (+)	5p13.3	SUB1 homolog (S. cerevisiae)
CHRNA5	1.83	3.90E-07	1.30E-05	chr15:78857862-78887611 (+)	15q24	cholinergic receptor, nicotinic, alpha 5 (neuronal)
WDHD1	1.83	3.61E-07	1.22E-05	chr14:55405656-55493823 (-)	14q22.2	WD repeat and HMG-box DNA binding protein 1
MRPS7	1.83	1.93E-09	2.53E-07	chr17:73257749-73262457 (+)	17q25	mitochondrial ribosomal protein S7
DTL	1.83	1.97E-06	4.59E-05	chr1:212208919-212280742 (+)	1q32	denticleless E3 ubiquitin protein ligase homolog (Drosophila)
UAP1	1.83	6.01E-08	3.07E-06	chr1:162531296-162569633 (+)	1q23.3	UDP-N-acteylglucosamine pyrophosphorylase 1
PARPBP	1.83	3.78E-09	4.19E-07	chr12:102513956-102591298 (+)	12q23.2	PARP1 binding protein
PHACTR2	1.83	8.76E-10	1.51E-07	chr6:143857982-144152322 (+)	6q24.2	phosphatase and actin regulator 2
SKA1	1.83	3.50E-07	1.20E-05	chr18:47901365-47920543 (+)	18q21.1	spindle and kinetochore associated complex subunit 1
LRP8	1.82	1.67E-08	1.20E-06	chr1:53708041-53793821 (-)	1p34	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
SLC28A3	1.82	3.41E-08	2.01E-06	chr9:86890372-86983413 (-)	9q22.2	solute carrier family 28 (concentrative nucleoside transporter), member 3
CENPI	1.82	1.50E-08	1.11E-06	chrX:100353178-100418670 (+)	Xq22.1	centromere protein I
ATAD2	1.82	5.94E-06	1.06E-04	chr8:124332090-124428590 (-)	8q24.13	ATPase family, AAA domain containing 2
KRT17P1	1.82	5.61E-08	2.91E-06	chr17:16744057-16749197 (-)	---	keratin 17 pseudogene 1
GALNT6	1.82	3.50E-06	7.11E-05	chr12:51745682-51785436 (-)	12q13	polypeptide N-acetylgalactosaminyltransferase 6
CHI3L2	1.82	9.07E-06	1.46E-04	chr1:111743393-111786062 (+)	1p13.3	chitinase 3-like 2
PNPT1	1.81	1.37E-06	3.49E-05	chr2:55861198-55921045 (-)	2p15	polyribonucleotide nucleotidyltransferase 1
MAD2L1	1.81	2.45E-09	3.02E-07	chr4:120980577-120988229 (-)	4q27	MAD2 mitotic arrest deficient-like 1 (yeast)
PMM2	1.81	1.55E-08	1.14E-06	chr16:8891670-8943194 (+)	16p13	phosphomannomutase 2
SERTAD4	1.81	2.84E-06	6.08E-05	chr1:210406144-210419976 (+)	1q32.1-q41	SERTA domain containing 4
PPP4R1	1.81	4.77E-08	2.60E-06	chr18:9546789-9614600 (-)	18p11.22	protein phosphatase 4, regulatory subunit 1
KLF7	1.81	4.24E-06	8.24E-05	chr2:207938861-208031991 (-)	2q32	Kruppel-like factor 7 (ubiquitous)
RNU6-1118P	1.81	3.23E-03	1.21E-02	chr10:38712553-38712656 (+)	---	RNA, U6 small nuclear 1118, pseudogene
LOC100288814	1.81	4.34E-07	1.42E-05	chrX:9935392-9936134 (+)	Xp22.2	uncharacterized LOC100288814
SMC6	1.81	3.30E-03	1.22E-02	chr2:17845079-17981509 (-)	2p24.2	structural maintenance of chromosomes 6
PGK1	1.81	5.63E-10	1.10E-07	chrX:77320685-77384793 (+)	Xq13.3	phosphoglycerate kinase 1
PRDX3	1.80	3.29E-10	7.61E-08	chr10:120927211-120938345 (-)	10q25-q26	peroxiredoxin 3
FLOT2	1.80	4.19E-08	2.37E-06	chr17:27206353-27224715 (-)	17q11-q12	flotillin 2
LOC101927023	1.80	1.18E-06	3.13E-05	chr5:111563980-111593006 (+)	5q22.2	uncharacterized LOC101927023
ADH5	1.80	1.16E-08	9.17E-07	chr4:99992130-100009952 (-)	4q23	alcohol dehydrogenase 5 (class III), chi polypeptide
FH	1.80	1.64E-08	1.18E-06	chr1:241660857-241683085 (-)	1q42.1	fumarate hydratase
CASP4	1.80	6.93E-09	6.41E-07	chr11:104813593-104840163 (-)	11q22.2-q22.3	caspase 4, apoptosis-related cysteine peptidase
TRIM14	1.80	1.56E-09	2.17E-07	chr9:100831557-100881494 (-)	9q22.33	tripartite motif containing 14
RP4-714D9.2	1.80	2.30E-07	8.60E-06	chr1:100523546-100550027 (-)	---	novel transcript
MAP4K4	1.80	6.44E-10	1.23E-07	chr2:102123002-102511152 (+)	2q11.2-q12	mitogen-activated protein kinase kinase kinase kinase 4
BAZ1A	1.80	2.30E-03	9.32E-03	chr14:35221937-35344853 (-)	14q13.2	bromodomain adjacent to zinc finger domain, 1A
MTIF2	1.80	6.04E-08	3.08E-06	chr2:55463731-55496483 (-)	2p16.1	mitochondrial translational initiation factor 2
KIAA1217	1.79	2.93E-09	3.42E-07	chr10:23983675-24836772 (+)	10p12.31	KIAA1217
PARP12	1.79	6.18E-07	1.89E-05	chr7:139723544-139763521 (-)	7q34	poly (ADP-ribose) polymerase family, member 12
KNSTRN	1.79	1.03E-06	2.81E-05	chr15:40674922-40686489 (+)	15q15.1	kinetochore-localized astrinSPAG5 binding protein
RDH11	1.79	3.49E-07	1.19E-05	chr14:68143518-68162531 (-)	11-cis)	retinol dehydrogenase 11 (all-trans9-cis
C14orf2	1.79	2.05E-09	2.63E-07	chr14:104378625-104394606 (-)	14q32.33	chromosome 14 open reading frame 2
TIMM8B	1.79	2.41E-09	2.98E-07	chr11:111955524-111957522 (-)	11q23.1-q23.2	translocase of inner mitochondrial membrane 8 homolog B (yeast)
LDLR	1.79	2.96E-05	3.58E-04	chr19:11200038-11244505 (+)	19p13.2	low density lipoprotein receptor
CCT2	1.79	5.15E-08	2.73E-06	chr12:69979114-69995357 (+)	12q15	chaperonin containing TCP1, subunit 2 (beta)
PSMA2	1.79	5.60E-08	2.91E-06	chr7:42956460-42971822 (-)	7p13	proteasome (prosome, macropain) subunit, alpha type, 2
RNU6-447P	1.79	3.63E-03	1.32E-02	chr11:152999-153102 (-)	---	RNA, U6 small nuclear 447, pseudogene
BRCA1	1.78	6.25E-10	1.19E-07	chr17:41196312-41322420 (-)	17q21	breast cancer 1, early onset
MAOB	1.78	5.10E-05	5.41E-04	chrX:43625857-43741721 (-)	Xp11.23	monoamine oxidase B
CCAR1	1.78	4.76E-05	5.13E-04	chr10:70480971-70552134 (+)	10q21.3	cell division cycle and apoptosis regulator 1
LPCAT3	1.78	2.17E-06	4.96E-05	chr12:7085347-7125842 (-)	12p13	lysophosphatidylcholine acyltransferase 3
COX8A	1.78	1.44E-06	3.61E-05	chr11:63742079-63744015 (+)	11q12-q13	cytochrome c oxidase subunit VIIIA (ubiquitous)
DIMT1	1.78	1.26E-09	1.89E-07	chr5:61683081-61699766 (-)	5q12.1	DIM1 dimethyladenosine transferase 1 homolog (S. cerevisiae)
NOP10	1.78	1.03E-06	2.81E-05	chr15:34633914-34635378 (-)	15q14-q15	NOP10 ribonucleoprotein
MFHAS1	1.78	1.88E-09	2.50E-07	chr8:8640864-8751155 (-)	8p23.1	malignant fibrous histiocytoma amplified sequence 1
BORA	1.78	1.02E-08	8.34E-07	chr13:73302042-73330328 (+)	13q22.1	bora, aurora kinase A activator
EPB41L4A	1.78	1.17E-09	1.79E-07	chr5:111478138-111755013 (-)	5q21.3	erythrocyte membrane protein band 4.1 like 4A
NARS	1.78	9.47E-09	7.96E-07	chr18:55267888-55289177 (-)	18q21.31	asparaginyl-tRNA synthetase
YARS	1.77	1.39E-08	1.04E-06	chr1:33240840-33283754 (-)	1p35.1	tyrosyl-tRNA synthetase
ZWINT	1.77	3.81E-10	8.33E-08	chr10:58116989-58121036 (-)	10q21-q22	ZW10 interacting kinetochore protein
SLC24A3	1.77	3.97E-09	4.37E-07	chr20:19193290-19703545 (+)	20q13.33	solute carrier family 24 (sodiumpotassium/calcium exchanger), member 3
UQCRH	1.77	2.84E-13	5.98E-10	chr1:46769303-46782448 (+)	1p34.1	ubiquinol-cytochrome c reductase hinge protein
ASCC3	1.77	7.50E-07	2.19E-05	chr6:100956070-101329248 (-)	6q16	activating signal cointegrator 1 complex subunit 3
AGPAT5	1.77	7.50E-08	3.62E-06	chr8:6565878-6619021 (+)	8p23.1	1-acylglycerol-3-phosphate O-acyltransferase 5
RNU6-1100P	1.77	3.81E-03	1.37E-02	chr1:157784-157887 (-)	---	RNA, U6 small nuclear 1100, pseudogene
RNU6-791P	1.77	3.81E-03	1.37E-02	chr1:222676974-222677077 (-)	---	RNA, U6 small nuclear 791, pseudogene
RNU6-1217P	1.77	3.81E-03	1.37E-02	chr4:120355160-120355263 (-)	---	RNA, U6 small nuclear 1217, pseudogene
RNU6-785P	1.77	3.81E-03	1.37E-02	chr9:141150045-141150148 (+)	---	RNA, U6 small nuclear 785, pseudogene
RNU6-355P	1.77	3.81E-03	1.37E-02	chr16:90211000-90211103 (+)	---	RNA, U6 small nuclear 355, pseudogene
RNU6-1076P	1.77	3.81E-03	1.37E-02	chr19:223158-223261 (-)	---	RNA, U6 small nuclear 1076, pseudogene
PSMA6	1.77	1.67E-08	1.20E-06	chr14:35747839-35786699 (+)	14q13	proteasome (prosome, macropain) subunit, alpha type, 6
HNRNPA3P3	1.77	3.40E-10	7.79E-08	chrX:139115445-139115665 (+)	---	heterogeneous nuclear ribonucleoprotein A3 pseudogene 3
PSMA5	1.77	3.79E-10	8.33E-08	chr1:109941653-109969108 (-)	1p13	proteasome (prosome, macropain) subunit, alpha type, 5
NUS1	1.77	3.40E-08	2.01E-06	chr6:117996617-118031886 (+)	6q22.1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)
IFNE	1.77	2.44E-04	1.73E-03	chr9:21480838-21482312 (-)	9p21.3	interferon, epsilon
VRK1	1.76	1.28E-05	1.90E-04	chr14:97263641-97347951 (+)	14q32	vaccinia related kinase 1
PGAM4	1.76	2.28E-09	2.85E-07	chrX:77223458-77225135 (-)	Xq13	phosphoglycerate mutase family member 4
EPHB2	1.76	2.02E-09	2.62E-07	chr1:23037331-23241823 (+)	1p36.1-p35	EPH receptor B2
POP1	1.76	7.11E-11	2.60E-08	chr8:99129521-99172069 (+)	8q22.1	processing of precursor 1, ribonuclease PMRP subunit (S. cerevisiae)
LOC100506100	1.76	1.81E-07	7.18E-06	chr9:131486724-131495473 (+)	---	uncharacterized LOC100506100
SLC25A5	1.76	2.30E-10	5.92E-08	chrX:118602363-118605359 (+)	Xq24	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
PLK4	1.76	2.40E-06	5.37E-05	chr4:128802016-128820377 (+)	4q28	polo-like kinase 4
NRP2	1.76	3.15E-07	1.10E-05	chr2:206546562-206662857 (+)	2q33.3	neuropilin 2
LMAN1	1.76	7.60E-09	6.88E-07	chr18:56995055-57026508 (-)	18q21.3-q22	lectin, mannose-binding, 1
PRPF38B	1.76	5.67E-04	3.24E-03	chr1:109234932-109244425 (+)	1p13.3	pre-mRNA processing factor 38B
MTHFD1	1.76	1.15E-09	1.76E-07	chr14:64854749-64926725 (+)	14q24	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
FOLH1B	1.76	4.76E-08	2.59E-06	chr11:89372398-89431886 (+)	11q14.3	folate hydrolase 1B
OASL	1.76	3.71E-05	4.23E-04	chr12:121458095-121477045 (-)	12q24.2	2-5-oligoadenylate synthetase-like
C12orf56	1.76	7.12E-10	1.32E-07	chr12:64660763-64784471 (-)	12q14.2	chromosome 12 open reading frame 56
ZSWIM6	1.76	4.53E-09	4.75E-07	chr5:60628100-60841999 (+)	5q12.1	zinc finger, SWIM-type containing 6

SLTM	1.76	2.22E-03	9.07E-03	chr15:59171244-59225886 (-)	15q22.1	SAFB-like, transcription modulator
TPI1	1.76	5.75E-09	5.59E-07	chr12:6976283-6980112 (+)	12p13	triosephosphate isomerase 1
MOCOS	1.76	9.97E-06	1.57E-04	chr18:33767480-33852120 (+)	18q12	molybdenum cofactor sulfurase
GART	1.76	3.29E-11	1.58E-08	chr21:34870940-34915797 (-)	21q22.11	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
SUCLG1	1.75	1.66E-09	2.27E-07	chr2:84650647-84687169 (-)	2p11.2	succinate-CoA ligase, alpha subunit
MCM3	1.75	1.21E-08	9.44E-07	chr6:52128807-52149582 (-)	6p12	minichromosome maintenance complex component 3
CA5BP1	1.75	1.18E-05	1.79E-04	chrX:15719057-15721483 (+)	Xp22.2	carbonic anhydrase VB pseudogene 1
ABCA12	1.75	2.07E-04	1.52E-03	chr2:215796266-216003151 (-)	2q34	ATP-binding cassette, sub-family A (ABC1), member 12
DNAJC2	1.75	3.43E-06	7.01E-05	chr7:102952921-102985320 (-)	7q22	DnaJ (Hsp40) homolog, subfamily C, member 2
GGH	1.75	2.21E-08	1.45E-06	chr8:63927638-63951730 (-)	8q12.3	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
NOD2	1.75	4.04E-11	1.83E-08	chr16:50727514-50766987 (+)	16q21	nucleotide-binding oligomerization domain containing 2
CDC20P1	1.75	3.01E-06	6.36E-05	chr9:89626696-89628066 (+)	---	cell division cycle 20 pseudogene 1
DHFR	1.75	2.21E-09	2.79E-07	chr5:79922045-79950802 (-)	5q11.2-q13.2	dihydrofolate reductase
RPF2	1.75	1.98E-05	2.65E-04	chr6:111303218-111347303 (+)	6q21	ribosome production factor 2 homolog (S. cerevisiae)
PSMB3	1.75	2.06E-07	7.89E-06	chr17:36909002-36920483 (+)	17q12	proteasome (prosome, macropain) subunit, beta type, 3
XPR1	1.75	5.28E-08	2.79E-06	chr1:180601140-180859415 (+)	1q25.1	xenotropic and polytropic retrovirus receptor 1
FOLH1	1.75	6.62E-08	3.30E-06	chr11:49168187-49230222 (-)	11p11.2	folate hydrolase (prostate-specific membrane antigen) 1
HMGCS1	1.75	1.41E-04	1.15E-03	chr5:43289493-43313614 (-)	5p14-p13	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)
GPR1	1.75	1.10E-07	4.91E-06	chr2:207040040-207082771 (-)	2q33.3	G protein-coupled receptor 1
PUS10	1.75	7.99E-08	3.80E-06	chr2:61167548-61245389 (-)	2p16.1	pseudouridylate synthase 10
MASTL	1.74	4.99E-07	1.59E-05	chr10:27443753-27475848 (+)	10p12.1	microtubule associated serinethreonine kinase-like
HSPA9	1.74	1.62E-08	1.18E-06	chr5:137890571-137911318 (-)	5q31.1	heat shock 70kDa protein 9 (mortalin)
SEL1L3	1.74	1.04E-06	2.84E-05	chr4:25749049-25865382 (-)	4p15.2	sel-1 suppressor of lin-12-like 3 (C. elegans)
ATP13A4	1.74	3.58E-04	2.30E-03	chr3:193119866-193310900 (-)	3q29	ATPase type 13A4
CCNE2	1.74	1.09E-07	4.86E-06	chr8:95891998-95908906 (-)	8q22.1	cyclin E2
PRMT3	1.74	5.16E-08	2.73E-06	chr11:20409076-20530879 (+)	11p15.1	protein arginine methyltransferase 3
AKAP6	1.74	7.02E-11	2.59E-08	chr14:32798479-33302268 (+)	14q12	A kinase (PRKA) anchor protein 6
GTPBP4	1.74	4.75E-08	2.59E-06	chr10:1034338-1065876 (+)	10p15-p14	GTP binding protein 4
SFXN1	1.74	2.82E-13	5.98E-10	chr5:174904065-174956745 (+)	5q35.3	sideroflexin 1
RBM25	1.74	2.86E-03	1.10E-02	chr14:73525144-73588122 (+)	14q24.3	RNA binding motif protein 25
NCAPG2	1.74	3.57E-09	3.99E-07	chr7:158424003-158497520 (-)	7q36.3	non-SMC condensin II complex, subunit G2
MOXD1	1.74	2.65E-04	1.84E-03	chr6:132617194-132722684 (-)	6q23.2	monooxygenase, DBH-like 1
FAM83D	1.74	9.22E-07	2.58E-05	chr20:37554955-37581703 (+)	20q11.23	family with sequence similarity 83, member D
HSPA8	1.74	1.25E-07	5.43E-06	chr11:122928197-122933186 (-)	11q24.1	heat shock 70kDa protein 8
SYK	1.73	4.52E-09	4.75E-07	chr9:93564012-93660842 (+)	9q22	spleen tyrosine kinase
SLK	1.73	1.59E-02	4.11E-02	chr10:105726959-105788991 (+)	10q24.33	STE20-like kinase
PLRG1	1.73	5.56E-10	1.09E-07	chr4:155456149-155471587 (-)	4q31.2-q32.1	pleiotropic regulator 1
ANKEF1	1.73	4.08E-09	4.45E-07	chr20:10015689-10037410 (+)	20p12.2	ankyrin repeat and EF-hand domain containing 1
KIF2A	1.73	6.88E-07	2.04E-05	chr5:61601989-61683011 (+)	5q12-q13	kinesin heavy chain member 2A
PRPF40A	1.73	4.43E-03	1.54E-02	chr2:153508107-153574511 (-)	2q23.3	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
EIF4A3	1.73	8.66E-08	4.06E-06	chr17:78109013-78120982 (-)	17q25.3	eukaryotic translation initiation factor 4A3
CKAP2	1.73	1.93E-04	1.45E-03	chr13:53029495-53050763 (+)	13q14	cytoskeleton associated protein 2
ATP1B3	1.73	5.94E-11	2.29E-08	chr3:141594966-141645382 (+)	3q23	ATPase, Na+K+ transporting, beta 3 polypeptide
LOC101927841	1.73	1.66E-02	4.25E-02	chr7:22895705-22900458 (+)	---	uncharacterized LOC101927841
TRUB2	1.73	9.11E-10	1.55E-07	chr9:131071382-131085021 (-)	9q34.11	TruB pseudouridine (psi) synthase family member 2
ENO1	1.73	1.77E-10	5.09E-08	chr1:8921059-9288096 (-)	1p36.2	enolase 1, (alpha)
LOC729737	1.73	1.11E-05	1.70E-04	chr1:134773-140566 (-)	1p36.33	uncharacterized LOC729737
PSMD1	1.73	2.18E-07	8.22E-06	chr2:231921578-232037541 (+)	2q37.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1
CHCHD1	1.73	3.85E-08	2.23E-06	chr10:75541805-75543410 (+)	10q22.2	coiled-coil-helix-coiled-coil-helix domain containing 1
MRPS15	1.73	9.56E-09	8.00E-07	chr1:36921319-36930040 (-)	1p34.3	mitochondrial ribosomal protein S15
ACAT2	1.72	3.33E-06	6.84E-05	chr6:160181360-160200144 (+)	6q25.3	acetyl-CoA acetyltransferase 2
HIST1H2BG	1.72	1.07E-04	9.35E-04	chr6:26216428-26216872 (-)	6p21.3	histone cluster 1, H2bg
PSMB5	1.72	6.57E-07	1.98E-05	chr14:23495060-23504439 (-)	14q11.2	proteasome (prosome, macropain) subunit, beta type, 5
NDUFA9	1.72	2.70E-10	6.58E-08	chr12:4758264-4798454 (+)	12p13.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa
PDHA1	1.72	1.34E-10	4.25E-08	chrX:19362011-19379825 (+)	Xp22.1	pyruvate dehydrogenase (lipoamide) alpha 1
HDAC1	1.72	1.90E-11	1.09E-08	chr1:32757687-32799236 (+)	1p34	histone deacetylase 1
RNA5SP217	1.72	1.25E-03	5.87E-03	chr6:127639028-127639118 (-)	---	RNA, 5S ribosomal pseudogene 217
SKA2P1	1.72	6.54E-07	1.97E-05	chr9:125524123-125524948 (+)	---	spindle and kinetochore associated complex subunit 2 pseudogene 1
HNRNPA3P5	1.72	4.10E-09	4.45E-07	chr13:66362064-66362255 (-)	---	heterogeneous nuclear ribonucleoprotein A3 pseudogene 5
GCLM	1.72	6.58E-07	1.98E-05	chr1:94350761-94375012 (-)	1p22.1	glutamate-cysteine ligase, modifier subunit
GSDMC	1.72	1.92E-06	4.50E-05	chr8:130760442-130799134 (-)	8q24.21	gasdermin C
MID1	1.72	1.16E-08	9.17E-07	chrX:10413350-10851809 (-)	Xp22	midline 1
HEATR5A	1.72	1.17E-09	1.79E-07	chr14:31760994-31889788 (-)	14q12	HEAT repeat containing 5A
OIP5	1.72	3.21E-08	1.93E-06	chr15:41601466-41624819 (-)	15q15.1	Opa interacting protein 5
ACLY	1.72	1.26E-06	3.28E-05	chr17:40023161-40075272 (-)	17q21.2	ATP citrate lyase
AKR1C2	1.72	2.33E-05	2.98E-04	chr10:5029967-5060225 (-)	10p15-p14	aldo-keto reductase family 1, member C2
PPIB	1.72	6.92E-10	1.29E-07	chr15:64448011-64455404 (-)	15q21-q22	peptidylprolyl isomerase B (cyclophilin B)
CASP7	1.72	1.95E-08	1.33E-06	chr10:115438935-115490664 (+)	10q25	caspase 7, apoptosis-related cysteine peptidase
CASP10	1.72	4.31E-07	1.41E-05	chr2:202047604-202094129 (+)	2q33-q34	caspase 10, apoptosis-related cysteine peptidase
STAT3	1.72	1.28E-07	5.51E-06	chr17:40465342-40540513 (-)	17q21.31	signal transducer and activator of transcription 3 (acute-phase response factor)
PAK6	1.72	2.07E-08	1.39E-06	chr15:40453210-40569688 (+)	15q14	p21 protein (Cdc42Rac)-activated kinase 6
BRCC3	1.71	1.17E-04	1.00E-03	chrX:154299695-154351349 (+)	Xq28	BRCA1BRCA2-containing complex, subunit 3
MAPK6	1.71	3.46E-06	7.05E-05	chr15:52311398-52358462 (+)	15q21	mitogen-activated protein kinase 6
GPX2	1.71	6.46E-06	1.13E-04	chr14:65405870-65409531 (-)	14q24.1	glutathione peroxidase 2 (gastrointestinal)
HIST1H2BF	1.71	9.95E-05	8.90E-04	chr6:26199748-26200942 (+)	6p22.1	histone cluster 1, H2bf
EPRS	1.71	6.71E-06	1.16E-04	chr1:220141942-220220000 (-)	1q41	glutamyl-prolyl-tRNA synthetase
SMAGP	1.71	4.73E-08	2.59E-06	chr12:51639133-51664202 (-)	12q13.13	small cell adhesion glycoprotein
PPIC	1.71	6.10E-10	1.18E-07	chr5:122358945-122372436 (-)	5q23.2	peptidylprolyl isomerase C (cyclophilin C)
KIAA1731	1.71	5.12E-04	3.00E-03	chr11:93394805-93463522 (+)	11q21	KIAA1731
NDUFAF2	1.71	1.40E-09	2.05E-07	chr5:60240956-60448864 (+)	5q12.1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2
YWHAQ	1.71	2.98E-10	7.08E-08	chr2:9724101-9771143 (-)	2p25.1	tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta
HIPK2	1.71	3.30E-12	3.23E-09	chr7:139246316-139477693 (-)	7q32-q34	homeodomain interacting protein kinase 2
PSMC4	1.71	5.93E-07	1.83E-05	chr19:40477073-40487353 (+)	19q13.11-q13.13	proteasome (prosome, macropain) 26S subunit, ATPase, 4
UPF2	1.71	4.92E-04	2.92E-03	chr10:11962021-12085169 (-)	10p14-p13	UPF2 regulator of nonsense transcripts homolog (yeast)
GCH1	1.71	5.88E-10	1.14E-07	chr14:55308724-55369570 (-)	14q22.1-q22.2	GTP cyclohydrolase 1
ALAS1	1.71	3.41E-08	2.02E-06	chr3:52232099-52248343 (+)	3p21.1	aminolevulinate, delta-, synthase 1
CHD7	1.71	4.71E-07	1.51E-05	chr8:61591324-61780586 (+)	8q12.2	chromodomain helicase DNA binding protein 7
PRKDC	1.71	1.13E-09	1.74E-07	chr8:48685669-48872743 (-)	8q11	protein kinase, DNA-activated, catalytic polypeptide
RP11-318K15.2	1.71	3.13E-05	3.72E-04	chr8:56806154-56808276 (+)	---	putative novel transcript
LOC100506497	1.71	3.73E-11	1.73E-08	chr7:29019583-29052985 (+)	---	uncharacterized LOC100506497
PSMB6	1.70	1.99E-07	7.74E-06	chr17:4699439-4701798 (+)	17p13	proteasome (prosome, macropain) subunit, beta type, 6
KCNK10	1.70	1.29E-08	9.83E-07	chr14:88646452-88793256 (-)	14q31.3	potassium channel, subfamily K, member 10
ORC1	1.70	1.41E-10	4.34E-08	chr1:52838501-52870143 (-)	1p32	origin recognition complex, subunit 1
SPIN4	1.70	1.95E-08	1.33E-06	chrX:62567107-62571223 (-)	Xq11.1	spindlin family, member 4
DCAF13	1.70	7.27E-07	2.14E-05	chr8:104426942-104455681 (+)	8q22.3	DDB1 and CUL4 associated factor 13
SLFN13	1.70	1.14E-07	5.06E-06	chr17:33762115-33775856 (-)	17q12	schlafen family member 13
CYB5R4	1.70	3.27E-08	1.96E-06	chr6:84569362-84670146 (+)	6pter-q22.33	cytochrome b5 reductase 4
COBLL1	1.70	1.10E-05	1.69E-04	chr2:165510134-165700189 (-)	2q24.3	cordon-bleu WH2 repeat protein-like 1
CALR	1.70	3.80E-09	4.20E-07	chr19:13049414-13055304 (+)	19p13.3-p13.2	calreticulin
PLSCR4	1.70	2.16E-07	8.18E-06	chr3:145910124-145968966 (-)	3q24	phospholipid scramblase 4
GNL3	1.70	1.59E-05	2.25E-04	chr3:52715172-52728510 (+)	3p21.1	guanine nucleotide binding protein-like 3 (nucleolar)
ANXA1	1.70	2.67E-03	1.05E-02	chr9:75766673-75785309 (+)	9q21.13	annexin A1
MARS	1.70	6.62E-08	3.30E-06	chr12:57881077-57911334 (+)	12q13.3	methionyl-tRNA synthetase
ICT1	1.70	2.44E-07	9.02E-06	chr17:73008776-73017356 (+)	17q25.1	immature colon carcinoma transcript 1
MAB21L3	1.70	2.49E-04	1.75E-03	chr1:116654376-116677861 (+)	1p13.1	mab-21-like 3 (C. elegans)
MREG	1.70	1.62E-08	1.17E-06	chr2:216807314-216898819 (-)	2q35	melanoregulin
STON2	1.70	9.79E-09	8.12E-07	chr14:81726994-81893748 (-)	14q31.1	stonin 2
GBP2	1.70	6.04E-06	1.07E-04	chr1:89573310-89591799 (-)	1p22.2	guanylate binding protein 2, interferon-inducible
RRM1	1.70	1.34E-09	1.97E-07	chr11:4115924-4223885 (+)	11p15.5	ribonucleotide reductase M1
CCDC34	1.70	2.37E-06	5.31E-05	chr11:27352374-27385415 (-)	11p14.1	coiled-coil domain containing 34
DNA2	1.70	2.90E-07	1.03E-05	chr10:70173821-70231879 (-)	10q21.3-q22.1	DNA replication helicasenuclease 2
TRIL	1.70	4.95E-10	1.00E-07	chr7:28992974-28998029 (-)	7p14.3	TLR4 interactor with leucine-rich repeats
ANKRD26	1.69	1.52E-03	6.81E-03	chr10:27280843-27389427 (-)	10p12.1	ankyrin repeat domain 26
ROCK1P1	1.69	1.10E-04	9.56E-04	chr18:109065-122222 (+)	18p11.32	Rho-associated, coiled-coil containing protein kinase 1 pseudogene 1
DHRS7	1.69	2.54E-07	9.30E-06	chr14:60610838-60636574 (-)	14q23.1	dehydrogenasereductase (SDR family) member 7
VCP	1.69	5.11E-09	5.17E-07	chr9:35056061-35073246 (-)	9p13.3	valosin containing protein
RIOK1	1.69	9.64E-06	1.53E-04	chr6:7389729-7418270 (+)	6p24.3	RIO kinase 1
DCUN1D5	1.69	8.82E-07	2.49E-05	chr11:102921413-102962944 (-)	11q22.3	DCN1, defective in cullin neddylation 1, domain containing 5
NASP	1.69	1.57E-07	6.42E-06	chr1:46049518-46084578 (+)	1p34.1	nuclear autoantigenic sperm protein (histone-binding)
CIRH1A	1.69	1.81E-08	1.26E-06	chr16:69166418-69202937 (+)	16q22.1	cirrhosis, autosomal recessive 1A (cirhin)
COA7	1.69	8.16E-09	7.23E-07	chr1:53152014-53164038 (-)	1p32.3	cytochrome c oxidase assembly factor 7 (putative)
CEP290	1.69	8.34E-04	4.32E-03	chr12:88442790-88535993 (-)	12q21.32	centrosomal protein 290kDa
SQLE	1.69	1.33E-05	1.96E-04	chr8:126010720-126034525 (+)	8q24.1	squalene epoxidase
NLRP2	1.69	5.39E-03	1.78E-02	chr19:55476620-55512510 (+)	19q13.42	NLR family, pyrin domain containing 2
PRIM1	1.69	1.66E-06	4.04E-05	chr12:57125364-57146146 (-)	12q13	primase, DNA, polypeptide 1 (49kDa)
KPNB1	1.69	1.05E-09	1.69E-07	chr17:45726842-45761004 (+)	17q21.32	karyopherin (importin) beta 1
CCT5	1.68	6.97E-09	6.41E-07	chr5:10250033-10266524 (+)	5p15.2	chaperonin containing TCP1, subunit 5 (epsilon)
FAT1	1.68	7.80E-05	7.42E-04	chr4:187508937-187647876 (-)	4q35	FAT atypical cadherin 1
RBBP6	1.68	3.08E-05	3.68E-04	chr16:24549014-24584184 (+)	16p12.2	retinoblastoma binding protein 6
SACS	1.68	2.07E-08	1.39E-06	chr13:23902965-24007841 (-)	13q12	sacsin molecular chaperone
LOC90784	1.68	8.52E-09	7.41E-07	chr2:86247339-86250991 (-)	2p11.2	uncharacterized LOC90784
TM4SF1	1.68	5.66E-03	1.85E-02	chr3:149086805-149095652 (-)	3q21-q25	transmembrane 4 L six family member 1
IL12RB2	1.68	3.44E-07	1.18E-05	chr1:67773047-67862583 (+)	1p31.3-p31.2	interleukin 12 receptor, beta 2
KNTC1	1.68	3.29E-05	3.86E-04	chr12:123011795-123110947 (+)	12q24.31	kinetochore associated 1
LOC100134822	1.68	3.56E-05	4.09E-04	chr11:141453-180341 (-)	---	uncharacterized LOC100134822
LOC100132287	1.68	4.78E-05	5.15E-04	chr1:317811-328581 (+)	1p36.33	uncharacterized LOC100132287
USP16	1.68	6.77E-03	2.13E-02	chr21:30396938-30426809 (+)	21q22.11	ubiquitin specific peptidase 16
MRPL46	1.68	1.49E-09	2.15E-07	chr15:89002707-89054752 (-)	15q25.3	mitochondrial ribosomal protein L46
CHD1	1.68	6.69E-03	2.11E-02	chr5:98190908-98262240 (-)	5q15-q21	chromodomain helicase DNA binding protein 1
TRMT6	1.68	1.01E-08	8.29E-07	chr20:5917881-5931182 (-)	20p12.3	tRNA methyltransferase 6 homolog (S. cerevisiae)
DBF4	1.68	6.80E-07	2.03E-05	chr7:87505531-87538856 (+)	7q21.3	DBF4 zinc finger
WDR3	1.68	1.70E-06	4.11E-05	chr1:118472343-118503049 (+)	1p12	WD repeat domain 3
CCDC58	1.68	2.00E-07	7.75E-06	chr3:122078436-122102078 (-)	3q21.1	coiled-coil domain containing 58
POLE2	1.68	4.58E-10	9.48E-08	chr14:50110270-50155140 (-)	14q21-q22	polymerase (DNA directed), epsilon 2, accessory subunit
ASUN	1.67	6.52E-06	1.13E-04	chr12:27058112-27091254 (-)	12p11.23	asunder spermatogenesis regulator

RB1	1.67	4.71E-07	1.52E-05	chr13:48877883-49056122 (+)	13q14.2	retinoblastoma 1
DICER1	1.67	1.66E-06	4.04E-05	chr14:95552565-95624347 (-)	14q32.13	dicer 1, ribonuclease type III
HIST1H3F	1.67	1.61E-04	1.27E-03	chr6:26250369-26250835 (-)	6p22.2	histone cluster 1, H3f
RP1-45C12.1	1.67	1.43E-04	1.16E-03	chr1:171137243-171220933 (-)	---	novel transcript, antisense to FMO1
TNFAIP2	1.67	2.79E-08	1.74E-06	chr14:103589779-103603776 (+)	14q32	tumor necrosis factor, alpha-induced protein 2
EHD4	1.67	7.05E-07	2.08E-05	chr15:42190570-42264776 (-)	15q11.1	EH-domain containing 4
MRPS25	1.67	9.78E-07	2.69E-05	chr3:15083967-15106842 (-)	3p25	mitochondrial ribosomal protein S25
NRIP1	1.67	1.92E-06	4.50E-05	chr21:16333556-16437321 (-)	21q11.2	nuclear receptor interacting protein 1
CTR9	1.67	2.43E-05	3.08E-04	chr11:10772534-10801290 (+)	11p15.3	CTR9, Paf1RNA polymerase II complex component
PSME4	1.67	6.08E-07	1.87E-05	chr2:54091204-54197977 (-)	2p16.2	proteasome (prosome, macropain) activator subunit 4
ILF2	1.67	6.04E-08	3.08E-06	chr1:153634512-153643524 (-)	1q21.3	interleukin enhancer binding factor 2
ATP2A2	1.67	2.86E-09	3.36E-07	chr12:110718561-110788897 (+)	12q24.11	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
GRHL3	1.67	9.35E-05	8.48E-04	chr1:24645812-24690972 (+)	1p36.11	grainyhead-like 3 (Drosophila)
TUSC3	1.67	2.12E-04	1.55E-03	chr8:15274724-15624158 (+)	8p22	tumor suppressor candidate 3
AGPS	1.67	2.05E-07	7.89E-06	chr2:178257372-178408564 (+)	2q31.2	alkylglycerone phosphate synthase
USP8	1.67	8.45E-03	2.53E-02	chr15:50716579-50793280 (+)	15q21.2	ubiquitin specific peptidase 8
LGMN	1.67	4.40E-07	1.43E-05	chr14:93170152-93215047 (-)	14q32.1	legumain
HIST1H2BO	1.67	1.01E-04	8.99E-04	chr6:27861203-27861669 (+)	6p22.1	histone cluster 1, H2bo
SH2D4A	1.67	1.93E-09	2.54E-07	chr8:19171081-19253729 (+)	8p21.2	SH2 domain containing 4A
MRPL32	1.67	7.66E-09	6.91E-07	chr7:42971799-42988557 (+)	7p14	mitochondrial ribosomal protein L32
LPHN2	1.67	4.17E-06	8.13E-05	chr1:81771845-82458107 (+)	1p31.1	latrophilin 2
SRFBP1	1.67	4.15E-04	2.57E-03	chr5:121297656-121411265 (+)	5q23.1	serum response factor binding protein 1
TMX2	1.67	8.91E-08	4.16E-06	chr11:57479995-57508445 (+)	11cen-q22.3	thioredoxin-related transmembrane protein 2
DUOXA1	1.67	8.82E-09	7.59E-07	chr15:45409569-45422078 (-)	15q21.1	dual oxidase maturation factor 1
RNF213	1.66	4.55E-05	4.96E-04	chr17:78234660-78372581 (+)	17q25.3	ring finger protein 213
RNU6-1291P	1.66	1.03E-02	2.95E-02	chr14:51989582-51989685 (+)	---	RNA, U6 small nuclear 1291, pseudogene
UQCRC2	1.66	4.13E-09	4.46E-07	chr16:21963981-21994981 (+)	16p12	ubiquinol-cytochrome c reductase core protein II
STC1	1.66	1.11E-03	5.36E-03	chr8:23699428-23712320 (-)	8p21-p11.2	stanniocalcin 1
MIS18BP1	1.66	8.29E-03	2.49E-02	chr14:45672393-45722743 (-)	14q21.2	MIS18 binding protein 1
RABGGTA	1.66	4.51E-09	4.74E-07	chr14:24734744-24740945 (-)	14q11.2	Rab geranylgeranyltransferase, alpha subunit
XBP1	1.66	9.59E-07	2.66E-05	chr22:29190543-29196585 (-)	22q12.1|22q12	X-box binding protein 1
WBP5	1.66	1.90E-05	2.57E-04	chrX:102611373-102613397 (+)	Xq22.2	WW domain binding protein 5
NFKB1	1.66	4.79E-11	2.01E-08	chr4:103422486-103538459 (+)	4q24	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
MTO1	1.66	1.33E-10	4.24E-08	chr6:74171301-74218959 (+)	6q13	mitochondrial tRNA translation optimization 1
SLC26A9	1.66	6.06E-06	1.08E-04	chr1:205882176-205912588 (-)	1q32.1	solute carrier family 26 (anion exchanger), member 9
LOC100507516	1.66	1.42E-05	2.07E-04	chr8:54427731-54436491 (-)	---	uncharacterized LOC100507516
RNU6-202P	1.66	2.25E-04	1.62E-03	chrX:41778507-41778602 (-)	---	RNA, U6 small nuclear 202, pseudogene
GSPT1	1.66	4.24E-08	2.40E-06	chr16:11961985-12010519 (-)	16p13.1	G1 to S phase transition 1
NDUFAB1	1.66	5.90E-09	5.71E-07	chr16:23592323-23607677 (-)	16p12.2	NADH dehydrogenase (ubiquinone) 1, alphabeta subcomplex, 1, 8kDa
RNU6-1199P	1.66	5.10E-03	1.71E-02	chr1:693613-693716 (-)	---	RNA, U6 small nuclear 1199, pseudogene
LRRC8B	1.66	2.78E-07	9.97E-06	chr1:89990395-90063423 (+)	1p22.2	leucine rich repeat containing 8 family, member B
NOL8	1.66	2.24E-04	1.62E-03	chr9:95059640-95087876 (-)	9q22.31	nucleolar protein 8
ZNF562	1.66	3.80E-07	1.28E-05	chr19:9759338-9785776 (-)	19p13.2	zinc finger protein 562
RTP4	1.66	1.17E-05	1.78E-04	chr3:187086120-187089864 (+)	3q27.3	receptor (chemosensory) transporter protein 4
SRPRB	1.66	1.11E-06	2.99E-05	chr3:133502877-133544616 (+)	3q22.1	signal recognition particle receptor, B subunit
PVT1	1.66	1.67E-09	2.28E-07	chr8:128806779-129113499 (+)	8q24	Pvt1 oncogene (non-protein coding)
VMP1	1.66	2.21E-08	1.45E-06	chr17:57784863-57917952 (+)	17q23.1	vacuole membrane protein 1
WDR12	1.66	2.86E-08	1.77E-06	chr2:203744993-203879521 (-)	2q33.2	WD repeat domain 12
FEN1	1.65	3.28E-10	7.61E-08	chr11:61560109-61564716 (+)	11q12	flap structure-specific endonuclease 1
IMMT	1.65	4.58E-10	9.48E-08	chr2:86371055-86422893 (-)	2p11.2|2	inner membrane protein, mitochondrial
CD68	1.65	2.09E-07	7.97E-06	chr17:7482805-7485431 (+)	17p13	CD68 molecule
STOM	1.65	5.63E-06	1.02E-04	chr9:124101353-124132545 (-)	9q34.1	stomatin
LOC101928231	1.65	2.73E-11	1.43E-08	chr6:134749378-134841723 (-)	---	uncharacterized LOC101928231
MTCH2	1.65	1.33E-08	1.01E-06	chr11:47638858-47664206 (-)	11p11.2	mitochondrial carrier 2
ACER3	1.65	1.04E-05	1.62E-04	chr11:76571917-76737841 (+)	11q13.5	alkaline ceramidase 3
C12orf4	1.65	2.33E-07	8.70E-06	chr12:4596894-4647674 (-)	12p13.3	chromosome 12 open reading frame 4
TALDO1	1.65	3.32E-07	1.15E-05	chr11:747329-765024 (+)	11p15.5-p15.4	transaldolase 1
GHITM	1.65	5.15E-09	5.20E-07	chr10:85899185-85913311 (+)	10q23.1	growth hormone inducible transmembrane protein
UBE2T	1.65	3.65E-10	8.12E-08	chr1:202300785-202311108 (-)	1q32.1	ubiquitin-conjugating enzyme E2T (putative)
SLC16A1	1.65	3.43E-05	3.98E-04	chr1:113454469-113499635 (-)	1p12	solute carrier family 16 (monocarboxylate transporter), member 1
RFC5	1.65	2.49E-09	3.05E-07	chr12:118454506-118470935 (+)	12q24.23	replication factor C (activator 1) 5, 36.5kDa
PRELID1	1.65	5.99E-08	3.07E-06	chr5:176730775-176733960 (+)	5q35.3	PRELI domain containing 1
FAM98A	1.65	7.90E-09	7.06E-07	chr2:33808725-33824449 (-)	2p22.3	family with sequence similarity 98, member A
ACADM	1.65	4.35E-08	2.44E-06	chr1:76190036-76229364 (+)	1p31	acyl-CoA dehydrogenase, C-4 to C-12 straight chain
MTRR	1.65	4.91E-08	2.66E-06	chr5:7851299-7906138 (+)	5p15.31	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
RPN2	1.65	9.00E-09	7.68E-07	chr20:35806813-35870025 (+)	20q12-q13.1	ribophorin II
ATP5C1	1.65	1.66E-06	4.05E-05	chr10:7830092-7849778 (+)	10p15.1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
GOLGB1	1.65	1.07E-03	5.21E-03	chr3:121382046-121468602 (-)	3q13	golgin B1
HLA-DRA	1.65	1.88E-02	4.67E-02	chr6:32407619-32412826 (+)	6p21.3	major histocompatibility complex, class II, DR alpha
RNU6-1054P	1.65	3.78E-03	1.36E-02	chr4:119527605-119527708 (+)	---	RNA, U6 small nuclear 1054, pseudogene
SPDL1	1.65	5.02E-08	2.69E-06	chr5:169010638-169031782 (+)	5q35.1	spindle apparatus coiled-coil protein 1
LAP3	1.64	8.65E-08	4.06E-06	chr4:17578815-17609595 (+)	4p15.32	leucine aminopeptidase 3
CKAP5	1.64	2.12E-06	4.86E-05	chr11:46764598-46867859 (-)	11p11.2	cytoskeleton associated protein 5
LRRC55	1.64	6.29E-08	3.18E-06	chr11:56949221-56959191 (+)	11q12.1	leucine rich repeat containing 55
PRINS	1.64	5.35E-06	9.78E-05	chr10:24536051-24544975 (+)	10p12.1	psoriasis associated RNA induced by stress (non-protein coding)
H2AFZ	1.64	1.49E-08	1.10E-06	chr4:100869243-100871547 (-)	4q24	H2A histone family, member Z
NDUFB9	1.64	4.76E-10	9.73E-08	chr8:125551343-125580751 (+)	8q13.3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
IQGAP2	1.64	1.30E-04	1.09E-03	chr5:75699074-76003957 (+)	5q13.3	IQ motif containing GTPase activating protein 2
RP11-242C19.2	1.64	1.48E-06	3.70E-05	chrX:30716324-30740049 (+)	---	novel transcript, sense intronic to GK
SLC36A4	1.64	2.31E-06	5.20E-05	chr11:92880307-92931129 (-)	11q21	solute carrier family 36 (protonamino acid symporter), member 4
CEP78	1.64	1.00E-09	1.65E-07	chr9:80850978-80894606 (+)	9q21.2	centrosomal protein 78kDa
PARP4	1.64	1.30E-05	1.93E-04	chr13:24995064-25086948 (-)	13q11	poly (ADP-ribose) polymerase family, member 4
LYAR	1.64	1.09E-07	4.88E-06	chr4:4269428-4291896 (-)	4p16.3	Ly1 antibody reactive
GPI	1.64	2.22E-07	8.35E-06	chr19:34855645-34893318 (+)	19q13.1	glucose-6-phosphate isomerase
CSTB	1.64	1.06E-07	4.75E-06	chr21:45192393-45196326 (-)	21q22.3	cystatin B (stefin B)
FAM129A	1.64	5.73E-07	1.78E-05	chr1:184759858-184943682 (-)	1q25	family with sequence similarity 129, member A
ODF2L	1.64	7.97E-05	7.54E-04	chr1:86786611-86862025 (-)	1p22.3	outer dense fiber of sperm tails 2-like
ESCO1	1.64	1.39E-02	3.72E-02	chr18:19109242-19180845 (-)	18q11.2	establishment of sister chromatid cohesion N-acetyltransferase 1
ATP5E	1.64	1.42E-07	5.96E-06	chr20:57600522-57607437 (-)	20q13.32	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
EIF4A1P2	1.64	1.04E-06	2.83E-05	chrY:5205788-5206981 (-)	---	eukaryotic translation initiation factor 4A1 pseudogene 2
ELF5	1.64	2.30E-03	9.33E-03	chr11:34500340-34535352 (-)	11p13-p12	E74-like factor 5 (ets domain transcription factor)
GDAP1	1.64	8.47E-10	1.48E-07	chr8:75233365-75401107 (+)	8q21.11	ganglioside induced differentiation associated protein 1
WDR77	1.64	4.45E-10	9.39E-08	chr1:111981260-111991998 (-)	1p13.2	WD repeat domain 77
LOC100133331	1.63	6.98E-05	6.84E-04	chr1:661139-685396 (-)	1p36.33	uncharacterized LOC100133331
UTP20	1.63	5.29E-05	5.55E-04	chr12:101673887-101780397 (+)	12q23	UTP20, small subunit (SSU) processome component, homolog (yeast)
COX7C	1.63	2.00E-09	2.60E-07	chr5:85913721-85916779 (+)	5q14	cytochrome c oxidase subunit VIIc
DUSP6	1.63	3.74E-04	2.37E-03	chr12:89741050-89747048 (-)	12q22-q23	dual specificity phosphatase 6
ENAH	1.63	5.96E-06	1.06E-04	chr1:225674534-225840845 (-)	1q42.12	enabled homolog (Drosophila)
PRPF4B	1.63	7.27E-03	2.25E-02	chr6:4021501-4065217 (+)	6p25.2	pre-mRNA processing factor 4B
TMEM69	1.63	4.85E-08	2.63E-06	chr1:46152886-46160115 (+)	1p34.1	transmembrane protein 69
PSMD7	1.63	3.92E-06	7.74E-05	chr16:74330673-74344205 (+)	16q22.3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
SERPING1	1.63	1.56E-04	1.24E-03	chr11:57364860-57382326 (+)	11q12.1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
DIS3	1.63	4.52E-05	4.94E-04	chr13:73329540-73356344 (-)	13q22.1	DIS3 exosome endoribonuclease and 3-5 exoribonuclease
RP11-20B7.1	1.63	4.82E-11	2.01E-08	chr3:73857752-73952017 (+)	---	novel transcript
NAV1	1.63	9.89E-08	4.52E-06	chr1:201592411-201796102 (+)	1q32.3	neuron navigator 1
TIMM21	1.63	2.08E-10	5.66E-08	chr18:71815746-71826204 (+)	18q22.3	translocase of inner mitochondrial membrane 21 homolog (yeast)
TRIP13	1.62	7.88E-08	3.75E-06	chr5:892758-919472 (+)	5p15.33	thyroid hormone receptor interactor 13
SNRPA	1.62	8.21E-07	2.37E-05	chr19:41256759-41271297 (+)	19q13.1	small nuclear ribonucleoprotein polypeptide A
GLTP	1.62	1.41E-06	3.56E-05	chr12:110288748-110318293 (-)	12q24.11	glycolipid transfer protein
DHTKD1	1.62	8.93E-09	7.66E-07	chr10:12110934-12165224 (+)	10p14	dehydrogenase E1 and transketolase domain containing 1
SSB	1.62	4.87E-04	2.90E-03	chr2:170648443-170668575 (+)	2q31.1	Sjogren syndrome antigen B (autoantigen La)
USP28	1.62	4.95E-06	9.22E-05	chr11:113668596-113746292 (-)	11q23	ubiquitin specific peptidase 28
ADH7	1.62	1.91E-05	2.59E-04	chr4:100333418-100356894 (-)	4q23-q24	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
NDUFA1	1.62	2.13E-07	8.09E-06	chrX:119005450-119010629 (+)	Xq24	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
NDUFB3	1.62	6.39E-09	6.04E-07	chr2:201936156-201950473 (+)	2q31.3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
TXLNG	1.62	4.84E-07	1.55E-05	chrX:16804550-16862642 (+)	Xp22.2	taxilin gamma
PTPN22	1.62	2.94E-04	1.99E-03	chr1:114356433-114414381 (-)	1p13.2	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
ABCF2	1.62	1.57E-07	6.43E-06	chr7:150904923-150924317 (-)	7q36	ATP-binding cassette, sub-family F (GCN20), member 2
MTAP	1.62	3.97E-08	2.28E-06	chr9:21802635-21867077 (+)	9p21	methylthioadenosine phosphorylase
UBE2F	1.62	1.60E-10	4.78E-08	chr2:238875469-238951423 (+)	2q37.3	ubiquitin-conjugating enzyme E2F (putative)
CMC2	1.62	5.32E-09	5.35E-07	chr16:81009699-81040719 (-)	16q23.2	C-x(9)-C motif containing 2
HNRNPM	1.62	7.81E-10	1.41E-07	chr19:8509651-8554002 (+)	19p13.2	heterogeneous nuclear ribonucleoprotein M
GYS1	1.62	3.26E-08	1.96E-06	chr19:49471382-49496610 (-)	19q13.3	glycogen synthase 1 (muscle)
DARS2	1.62	1.64E-08	1.18E-06	chr1:173793641-173827684 (+)	1q25.1	aspartyl-tRNA synthetase 2, mitochondrial
COX6B1	1.62	2.03E-06	4.70E-05	chr19:36139125-36149686 (+)	19q13.1	cytochrome c oxidase subunit VIb polypeptide 1 (ubiquitous)
LOC730378	1.62	1.50E-04	1.20E-03	chr19:205025-205055 (-)	---	uncharacterized LOC730378
UTP14A	1.62	1.02E-07	4.63E-06	chrX:129040097-129063738 (+)	Xq26.1	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
SEC61B	1.62	1.17E-08	9.19E-07	chr9:101984346-101992901 (+)	9q22.32-q31.3	Sec61 beta subunit
E2F3-IT1	1.61	1.08E-06	2.92E-05	chr6:20438052-20440409 (+)	---	E2F3 intronic transcript 1 (non-protein coding)
ZGRF1	1.61	1.44E-06	3.62E-05	chr4:113460489-113558151 (-)	4q25	zinc finger, GRF-type containing 1
ZDHHC21	1.61	8.29E-06	1.36E-04	chr9:14555481-14693480 (-)	9p22.3	zinc finger, DHHC-type containing 21
TWF1	1.61	3.81E-07	1.28E-05	chr12:44187526-44200178 (-)	12q12	twinfilin actin-binding protein 1
MCM5	1.61	8.51E-08	4.01E-06	chr22:35796056-35820495 (+)	22q13.1	minichromosome maintenance complex component 5
MRPL16	1.61	3.62E-10	8.10E-08	chr11:59573608-59578345 (-)	11q12.1	mitochondrial ribosomal protein L16
DNTTIP2	1.61	1.70E-04	1.32E-03	chr1:94331839-94345474 (-)	1p22.1	deoxynucleotidyltransferase, terminal, interacting protein 2
CNTLN	1.61	1.63E-06	4.00E-05	chr9:17134980-17503921 (+)	9p22.2	centlein, centrosomal protein
APOL2	1.61	1.70E-07	6.83E-06	chr22:36622255-36636000 (-)	22q12	apolipoprotein L, 2
BNC2	1.61	7.32E-06	1.23E-04	chr9:16409501-16870841 (-)	9p22.2	basonuclin 2
LRG1	1.61	8.82E-06	1.43E-04	chr19:4537227-4540092 (-)	19p13.3	leucine-rich alpha-2-glycoprotein 1
ECHDC1	1.61	6.93E-07	2.05E-05	chr6:127609855-127664754 (-)	6q22.33	enoyl CoA hydratase domain containing 1
PGBD5	1.61	1.95E-08	1.33E-06	chr1:230457392-230561475 (-)	1q42.13	piggyBac transposable element derived 5
ZC3H13	1.61	1.61E-03	7.08E-03	chr13:46528600-46626894 (-)	13q14.13	zinc finger CCCH-type containing 13
TMPRSS11A	1.61	9.49E-06	1.51E-04	chr4:68775103-68829858 (-)	4q13.2	transmembrane protease, serine 11A
EML6	1.61	1.06E-07	4.76E-06	chr2:54950636-55199157 (+)	2p16.1	echinoderm microtubule associated protein like 6
ROBO1	1.61	4.87E-07	1.55E-05	chr3:78646388-79817059 (-)	3p12	roundabout, axon guidance receptor, homolog 1 (Drosophila)

THSD4	1.61	2.06E-07	7.89E-06	chr15:71389291-72075722 (+)	15q23	thrombospondin, type I, domain containing 4
TMPO	1.61	2.13E-07	8.09E-06	chr12:98909290-98944157 (+)	12q22	thymopoietin
TOMM40	1.61	5.32E-09	5.35E-07	chr19:45394477-45406946 (+)	19q13	translocase of outer mitochondrial membrane 40 homolog (yeast)
CHEK1	1.61	3.73E-09	4.14E-07	chr11:125495031-125546150 (+)	11q24.2	checkpoint kinase 1
RNASEH2A	1.61	1.98E-07	7.70E-06	chr19:12917428-12924462 (+)	19p13.2	ribonuclease H2, subunit A
MRPL47	1.61	2.59E-06	5.66E-05	chr3:179306073-179322442 (-)	3q26.33	mitochondrial ribosomal protein L47
NPM1	1.61	2.08E-06	4.79E-05	chr5:170814120-170838141 (+)	5q35.1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
EIF4A1	1.61	4.28E-08	2.41E-06	chr17:7475602-7482324 (+)	17p13	eukaryotic translation initiation factor 4A1
GNA15	1.60	5.96E-07	1.84E-05	chr19:3136191-3163766 (+)	19p13.3	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
CCT3	1.60	1.59E-08	1.16E-06	chr1:156278752-156337664 (-)	1q23	chaperonin containing TCP1, subunit 3 (gamma)
SMC1A	1.60	4.79E-05	5.15E-04	chrX:53401070-53449677 (-)	Xp11.22-p11.21	structural maintenance of chromosomes 1A
PRDX1	1.60	3.01E-07	1.07E-05	chr1:45976707-45988719 (-)	1p34.1	peroxiredoxin 1
NUDT5	1.60	3.89E-08	2.25E-06	chr10:12207324-12238143 (-)	10p14	nudix (nucleoside diphosphate linked moiety X)-type motif 5
CYP7B1	1.60	3.02E-06	6.38E-05	chr8:65500320-65711348 (-)	8q21.3	cytochrome P450, family 7, subfamily B, polypeptide 1
CERS3	1.60	3.20E-06	6.64E-05	chr15:100940600-101084925 (-)	15q26.3	ceramide synthase 3
IGSF3	1.60	3.21E-10	7.49E-08	chr1:117117031-117210377 (-)	1p13	immunoglobulin superfamily, member 3
E2F8	1.60	1.47E-04	1.19E-03	chr11:19245610-19263389 (-)	11p15.1	E2F transcription factor 8
BOLA2	1.60	1.03E-08	8.38E-07	chr16:30204256-30205627 (-)	16p11.2	bolA family member 2
SCAPER	1.60	2.41E-03	9.67E-03	chr15:76640527-77197744 (-)	15q24	S-phase cyclin A-associated protein in the ER
E2F4	1.60	1.27E-08	9.76E-07	chr16:67226068-67232821 (+)	16q22.1	E2F transcription factor 4, p107p130-binding
XDH	1.60	2.70E-05	3.33E-04	chr2:31178437-31637611 (-)	2p23.1	xanthine dehydrogenase
NEK2	1.60	8.35E-07	2.39E-05	chr1:211831599-211848972 (-)	1q32.3	NIMA-related kinase 2
CTAGE5	1.60	4.06E-05	4.55E-04	chr14:39734476-39856156 (+)	14q13.3	CTAGE family, member 5
FAM157A	1.60	3.30E-05	3.87E-04	chr3:197879237-197955678 (+)	3q29	family with sequence similarity 157, member A
DNAJB11	1.60	3.13E-08	1.90E-06	chr3:186285192-186314892 (+)	3q27.3	DnaJ (Hsp40) homolog, subfamily B, member 11
CIT	1.60	3.44E-06	7.01E-05	chr12:120123595-120315095 (-)	12q24	citron rho-interacting serinethreonine kinase
CAPNS1	1.60	8.36E-05	7.82E-04	chr19:36630918-36641255 (+)	19q13.12	calpain, small subunit 1
NOL10	1.60	2.38E-05	3.03E-04	chr2:10710892-10830112 (-)	2p25.1	nucleolar protein 10
DNAJC7	1.60	2.17E-07	8.21E-06	chr17:40128439-40169715 (-)	17q11.2	DnaJ (Hsp40) homolog, subfamily C, member 7
GRN	1.60	2.74E-06	5.91E-05	chr17:42422491-42430470 (+)	17q21.32	granulin
RNU7-40P	1.60	2.02E-03	8.43E-03	chr12:56746171-56746234 (-)	---	RNA, U7 small nuclear 40 pseudogene
SREK1	1.60	5.31E-03	1.76E-02	chr5:65435799-65479443 (+)	5q12.3	splicing regulatory glutaminelysine-rich protein 1
ISG20L2	1.60	7.00E-08	3.42E-06	chr1:156691683-156698591 (-)	1q23.1	interferon stimulated exonuclease gene 20kDa-like 2
ADAR	1.60	1.06E-06	2.89E-05	chr1:154554534-154600475 (-)	1q21.3	adenosine deaminase, RNA-specific
HIST1H2BI	1.60	7.86E-05	7.46E-04	chr6:26273144-26273640 (+)	6p22.1	histone cluster 1, H2bi
P4HB	1.60	1.96E-07	7.64E-06	chr17:79801034-79818545 (-)	17q25	prolyl 4-hydroxylase, beta polypeptide
FAM72D	1.60	3.12E-04	2.07E-03	chr1:143896452-143913143 (-)	1q21.1	family with sequence similarity 72, member D
DPM1	1.60	3.31E-07	1.15E-05	chr20:49551404-49575092 (-)	20q13.13	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
HEATR3	1.59	7.84E-08	3.74E-06	chr16:50099881-50140298 (+)	16q12.1	HEAT repeat containing 3
MYBL2	1.59	4.14E-08	2.36E-06	chr20:42295709-42345136 (+)	20q13.1	v-myb avian myeloblastosis viral oncogene homolog-like 2
ARPC3	1.59	1.40E-08	1.05E-06	chr12:110872630-110888212 (-)	12q24.11	actin related protein 23 complex, subunit 3, 21kDa
TDG	1.59	3.22E-07	1.12E-05	chr12:104359582-104382656 (+)	12q24.1	thymine-DNA glycosylase
SMARCA5	1.59	3.56E-05	4.10E-04	chr4:144434616-144478642 (+)	4q31.1-q31.2	SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
LOC728554	1.59	1.05E-04	9.23E-04	chr5:177302262-177311273 (+)	5q35.3	THO complex 3 pseudogene
FOXN2	1.59	1.96E-07	7.64E-06	chr2:48541776-48606434 (+)	2p22-p16	forkhead box N2
RNU7-124P	1.59	3.65E-04	2.33E-03	chr9:37936704-37936765 (-)	---	RNA, U7 small nuclear 124 pseudogene
NOP16	1.59	1.76E-07	7.01E-06	chr5:175810942-175815976 (-)	5q35.2	NOP16 nucleolar protein
PRMT5	1.59	4.73E-08	2.59E-06	chr14:23389720-23398794 (-)	14q11.2	protein arginine methyltransferase 5
SDR9C7	1.59	5.01E-03	1.68E-02	chr12:57316938-57328189 (-)	12q13.3	short chain dehydrogenasereductase family 9C, member 7
RFC4	1.59	3.64E-10	8.12E-08	chr3:186507669-186524847 (-)	3q27	replication factor C (activator 1) 4, 37kDa
FAM162A	1.59	3.38E-08	2.01E-06	chr3:122103023-122131181 (+)	3q21.1	family with sequence similarity 162, member A
NDUFA4	1.59	8.68E-08	4.07E-06	chr7:10971578-10979883 (-)	7p21.3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
LOC101929819	1.59	8.22E-05	7.72E-04	chr16:90224863-90233897 (+)	---	putative uncharacterized protein encoded by LINC00174-like
PTPRE	1.59	1.84E-12	2.16E-09	chr10:129705325-129884164 (+)	10q26	protein tyrosine phosphatase, receptor type, E
UTP11L	1.59	1.68E-09	2.28E-07	chr1:38474930-38490497 (+)	1p34.3	UTP11-like, U3 small nucleolar ribonucleoprotein (yeast)
DDX39A	1.59	2.57E-07	9.39E-06	chr19:14519610-14530195 (-)	19p13.12	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A
VPS25	1.59	1.41E-06	3.55E-05	chr17:40925454-40931617 (+)	17q21.31	vacuolar protein sorting 25 homolog (S. cerevisiae)
PSME1	1.59	2.67E-06	5.81E-05	chr14:24605367-24608176 (+)	14q11.2	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
DLAT	1.59	3.12E-08	1.89E-06	chr11:111895538-111935114 (+)	11q23.1	dihydrolipoamide S-acetyltransferase
RNF152	1.59	3.09E-04	2.06E-03	chr18:59475296-59560992 (-)	18q21.33	ring finger protein 152
CDCA8	1.59	1.02E-06	2.80E-05	chr1:38158090-38175391 (+)	1p34.3	cell division cycle associated 8
CDC7	1.59	2.78E-06	5.97E-05	chr1:91966404-91991321 (+)	1p22	cell division cycle 7
IL36RN	1.59	1.74E-02	4.41E-02	chr2:113816215-113822959 (+)	2q14	interleukin 36 receptor antagonist
SLC35B4	1.59	1.60E-08	1.16E-06	chr7:133974084-134001827 (-)	7q33	solute carrier family 35 (UDP-xyloseUDP-N-acetylglucosamine transporter), member B4
GPATCH4	1.59	1.81E-08	1.26E-06	chr1:156564100-156571302 (-)	1q22	G patch domain containing 4
ZNF215	1.59	1.17E-03	5.58E-03	chr11:6947635-7005863 (+)	11p15.4	zinc finger protein 215
HMGB3	1.58	1.16E-07	5.11E-06	chrX:150148982-150159248 (+)	Xq28	high mobility group box 3
LOC100288069	1.58	7.90E-05	7.49E-04	chr1:694412-714068 (-)	1p36.33	uncharacterized LOC100288069
E2F7	1.58	1.03E-07	4.66E-06	chr12:77415026-77459360 (-)	12q21.2	E2F transcription factor 7
RPP40	1.58	5.37E-08	2.82E-06	chr6:4994966-5004297 (-)	6p25.1	ribonuclease PMRP 40kDa subunit
SLC43A3	1.58	1.58E-03	7.00E-03	chr11:57174427-57195053 (-)	11q11	solute carrier family 43, member 3
C14orf119	1.58	1.30E-07	5.59E-06	chr14:23563974-23569671 (+)	14q11.2	chromosome 14 open reading frame 119
IRAK2	1.58	2.77E-06	5.96E-05	chr3:10206549-10285427 (+)	3p25.3	interleukin-1 receptor-associated kinase 2
METAP1	1.58	6.91E-10	1.29E-07	chr4:99916771-99983964 (+)	4q23	methionyl aminopeptidase 1
EPB41L1	1.58	6.66E-07	2.00E-05	chr20:34679426-34820721 (+)	20q11.2-q12	erythrocyte membrane protein band 4.1-like 1
ABCA1	1.58	3.25E-05	3.83E-04	chr9:107543283-107690527 (-)	9q31.1	ATP-binding cassette, sub-family A (ABC1), member 1
RNU5A-8P	1.58	1.24E-04	1.05E-03	chr1:210547498-210547611 (-)	---	RNA, U5A small nuclear 8, pseudogene
PLA2G3	1.58	1.20E-05	1.81E-04	chr22:31530793-31536593 (-)	22q12.2	phospholipase A2, group III
NUP62CL	1.58	2.87E-09	3.37E-07	chrX:106366657-106449670 (-)	Xq22.3	nucleoporin 62kDa C-terminal like
RAB1A	1.58	2.45E-07	9.05E-06	chr2:65297835-65357435 (-)	2p14	RAB1A, member RAS oncogene family
PNPO	1.58	1.00E-08	8.27E-07	chr17:46018889-46026674 (+)	17q21.32	pyridoxamine 5-phosphate oxidase
PKM	1.58	1.09E-08	8.69E-07	chr15:72491370-72524163 (-)	15q22	pyruvate kinase, muscle
ACACA	1.58	1.03E-07	4.66E-06	chr17:35441923-35766902 (-)	17q21	acetyl-CoA carboxylase alpha
FAM157B	1.58	1.09E-05	1.68E-04	chr9:141106637-141149300 (+)	9q34.3	family with sequence similarity 157, member B
ERH	1.58	3.57E-07	1.21E-05	chr14:69846840-69865344 (-)	14q24.1	enhancer of rudimentary homolog (Drosophila)
ITGB6	1.58	1.64E-06	4.01E-05	chr2:160956177-161128399 (-)	2q24.2	integrin, beta 6
HJURP	1.58	1.37E-06	3.49E-05	chr2:234742062-234763212 (-)	2q37.1	Holliday junction recognition protein
EIF5	1.58	1.11E-07	4.95E-06	chr14:103800339-103811362 (+)	14q32.32	eukaryotic translation initiation factor 5
CYP4F22	1.58	9.79E-04	4.88E-03	chr19:15619336-15663128 (+)	19p13.12	cytochrome P450, family 4, subfamily F, polypeptide 22
DDX52	1.58	2.46E-07	9.07E-06	chr17:35969826-36003493 (-)	17q21.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52
ARHGAP21	1.58	5.72E-05	5.88E-04	chr10:24872538-25012597 (-)	10p12.1|10p12.3	Rho GTPase activating protein 21
SRM	1.58	7.22E-06	1.22E-04	chr1:11114641-11120091 (-)	1p36-p22	spermidine synthase
CSRP2	1.58	3.78E-05	4.29E-04	chr12:77252495-77272840 (-)	12q21.1	cysteine and glycine-rich protein 2
SKP2	1.58	1.13E-07	5.00E-06	chr5:36152091-36184421 (+)	5p13	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase
DEK	1.57	2.41E-03	9.67E-03	chr6:18224099-18265054 (-)	6p22.3	DEK proto-oncogene
SLC5A1	1.57	3.10E-03	1.17E-02	chr22:32439019-32509016 (+)	22q12.3	solute carrier family 5 (sodiumglucose cotransporter), member 1
LGALS9C	1.57	5.46E-09	5.40E-07	chr17:20352708-20372296 (-)	17p11.2	lectin, galactoside-binding, soluble, 9C
EIF2S1	1.57	4.97E-06	9.26E-05	chr14:67826714-67853233 (+)	14q23.3	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
CEP83	1.57	5.75E-04	3.27E-03	chr12:94702056-94853764 (-)	12q22	centrosomal protein 83kDa
MCTP2	1.57	9.04E-09	7.70E-07	chr15:94774767-95027181 (+)	15q26.2	multiple C2 domains, transmembrane 2
AKIRIN2	1.57	3.10E-07	1.09E-05	chr6:88384578-88411985 (-)	6q15	akirin 2
STIP1	1.57	1.70E-06	4.11E-05	chr11:63952744-63970220 (+)	11q13	stress-induced phosphoprotein 1
SNX5	1.57	1.74E-08	1.23E-06	chr20:17922241-17949623 (-)	20p11	sorting nexin 5
AP1B1	1.57	3.99E-08	2.29E-06	chr22:29723669-29819168 (-)	22q12.2	adaptor-related protein complex 1, beta 1 subunit
PALLD	1.57	2.75E-05	3.38E-04	chr4:169418217-169849608 (+)	4q32.3	palladin, cytoskeletal associated protein
TMEM117	1.57	5.00E-07	1.59E-05	chr12:44229886-44783543 (+)	12q12	transmembrane protein 117
SLAMF7	1.57	7.90E-07	2.29E-05	chr1:160709037-160724611 (+)	1q23.1-q24.1	SLAM family member 7
LTV1	1.57	3.19E-03	1.19E-02	chr6:144164481-144184949 (+)	6q24.2	LTV1 ribosome biogenesis factor
SFN	1.57	1.20E-06	3.16E-05	chr1:27189629-27190948 (+)	1p36.11	stratifin
ALDH3B2	1.57	2.01E-05	2.67E-04	chr11:67429633-67448685 (-)	11q13	aldehyde dehydrogenase 3 family, member B2
NAV3	1.57	1.46E-04	1.18E-03	chr12:78225069-78606790 (+)	12q14.3	neuron navigator 3
WIPI1	1.57	8.93E-06	1.44E-04	chr17:66417422-66453653 (-)	17q24.2	WD repeat domain, phosphoinositide interacting 1
SEC23B	1.57	4.92E-08	2.66E-06	chr20:18488137-18542059 (+)	20p11.23	Sec23 homolog B (S. cerevisiae)
ACO2	1.57	6.47E-08	3.24E-06	chr22:41865117-41924993 (+)	22q13.2	aconitase 2, mitochondrial
NOP2	1.57	1.14E-07	5.04E-06	chr12:6666029-6677857 (-)	12p13	NOP2 nucleolar protein
RP11-164P12.3	1.57	1.81E-04	1.38E-03	chr4:152595635-152599045 (+)	---	novel transcript, antisense to PET112L
CCDC25	1.57	4.85E-07	1.55E-05	chr8:27590833-27630170 (-)	8p21.1	coiled-coil domain containing 25
ATIC	1.57	2.50E-08	1.61E-06	chr2:216176540-216214496 (+)	2q35	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferaseIMP cyclohydrolase
IARS	1.57	3.70E-07	1.25E-05	chr9:94972489-95056038 (-)	9q21	isoleucyl-tRNA synthetase
DNM1L	1.57	3.61E-05	4.14E-04	chr12:32832134-32905700 (+)	12p11.21	dynamin 1-like
PRSS12	1.57	4.00E-05	4.49E-04	chr4:119201193-119274158 (-)	4q28.1	protease, serine, 12 (neurotrypsin, motopsin)
PLS1	1.56	3.55E-08	2.08E-06	chr3:142315229-142432506 (+)	3q23	plastin 1
NCAPD2	1.56	3.39E-04	2.21E-03	chr12:6602545-6641132 (+)	12p13.3	non-SMC condensin I complex, subunit D2
RACGAP1	1.56	2.58E-06	5.66E-05	chr12:50370706-50419307 (-)	12q13.12	Rac GTPase activating protein 1
DGKH	1.56	9.36E-06	1.49E-04	chr13:42614172-42830716 (+)	13q14.11	diacylglycerol kinase, eta
PA2G4	1.56	8.40E-08	3.97E-06	chr12:56498103-56509935 (+)	12q13.2	proliferation-associated 2G4, 38kDa
KLHL2	1.56	5.81E-07	1.80E-05	chr4:166128770-166244308 (+)	4q21.2	kelch-like family member 2
MRPS11	1.56	5.42E-09	5.38E-07	chr15:89010684-89022222 (+)	15q25	mitochondrial ribosomal protein S11
GM2A	1.56	1.24E-07	5.42E-06	chr5:150591711-150650001 (+)	5q33.1	GM2 ganglioside activator
RRP36	1.56	1.30E-06	3.36E-05	chr6:42989383-42997337 (+)	6p21.1	ribosomal RNA processing 36 homolog (S. cerevisiae)
PEX3	1.56	1.37E-05	2.00E-04	chr6:143771918-143811753 (+)	6q24.2	peroxisomal biogenesis factor 3
CUL1	1.56	2.19E-07	8.25E-06	chr7:148395006-148498202 (+)	7q36.1	cullin 1
NIPA2	1.56	6.78E-09	6.33E-07	chr15:23004684-23034427 (-)	15q11.2	non imprinted in Prader-WilliAngelman syndrome 2
ATR	1.56	3.04E-05	3.64E-04	chr3:142168077-142297668 (-)	3q23	ATR serinethreonine kinase
SDHB	1.56	1.56E-09	2.17E-07	chr1:17345217-17380665 (-)	1p36.1-p35	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
POLD3	1.56	2.11E-08	1.41E-06	chr11:74303575-74354102 (+)	11q14	polymerase (DNA-directed), delta 3, accessory subunit
LRPPRC	1.56	2.13E-05	2.78E-04	chr2:44113363-44223144 (-)	2p21	leucine-rich pentatricopeptide repeat containing
SUCO	1.56	6.83E-05	6.72E-04	chr1:172501489-172580973 (+)	1q24	SUN domain containing ossification factor
COX10	1.56	1.59E-10	4.78E-08	chr17:13972719-14111996 (+)	17p12	cytochrome c oxidase assembly homolog 10 (yeast)
MTFMT	1.56	1.18E-07	5.19E-06	chr15:65293850-65321977 (-)	15q22.31	mitochondrial methionyl-tRNA formyltransferase
HIST1H3I	1.56	8.27E-04	4.29E-03	chr6:27839623-27840099 (-)	6p22.1	histone cluster 1, H3i
PYROXD1	1.56	2.17E-03	8.93E-03	chr12:21590538-21624182 (+)	12p12.1	pyridine nucleotide-disulphide oxidoreductase domain 1
GINS2	1.56	2.17E-07	8.20E-06	chr16:85709804-85722605 (-)	16q24.1	GINS complex subunit 2 (Psf2 homolog)
CEBPZ	1.56	3.39E-03	1.25E-02	chr2:37428755-37458856 (-)	EBP), zeta	CCAATenhancer binding protein (C
ABCE1	1.56	5.18E-05	5.47E-04	chr4:146019084-146050676 (+)	4q31	ATP-binding cassette, sub-family E (OABP), member 1

DPP3	1.56	1.50E-08	1.11E-06	chr11:66247484-66277130 (+)	11q12-q13.1	dipeptidyl-peptidase 3
TLE3	1.55	1.19E-08	9.35E-07	chr15:70340129-70390515 (-)	15q22	transducin-like enhancer of split 3
HRNR	1.55	2.25E-06	5.10E-05	chr1:152184558-152196669 (-)	1q21.3	hornerin
RAB11B-AS1	1.55	5.15E-06	9.49E-05	chr19:8439260-8455575 (-)	---	RAB11B antisense RNA 1
COX7A2	1.55	3.20E-08	1.93E-06	chr6:75947391-75960039 (-)	6q12	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
XPOT	1.55	1.79E-06	4.28E-05	chr12:64798130-64844907 (+)	12q14.2	exportin, tRNA
TIMM13	1.55	5.37E-07	1.68E-05	chr19:2425622-2427875 (-)	19p13.3	translocase of inner mitochondrial membrane 13 homolog (yeast)
UBXN8	1.55	3.15E-08	1.91E-06	chr8:30589764-30624522 (+)	8p12-p11.2	UBX domain protein 8
TFRC	1.55	1.16E-04	9.97E-04	chr3:195754054-195809060 (-)	3q29	transferrin receptor
ATP5H	1.55	2.74E-08	1.72E-06	chr17:73032145-73043080 (-)	17q25	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d
RP11-419K12.1	1.55	4.90E-03	1.66E-02	chr8:130691381-130695925 (-)	---	putative novel transcript
PSMD14	1.55	4.13E-07	1.36E-05	chr2:162164549-162268228 (+)	2q24.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
TCERG1	1.55	5.14E-04	3.02E-03	chr5:145826873-145891524 (+)	5q31	transcription elongation regulator 1
HSBP1	1.55	2.27E-08	1.47E-06	chr16:83841593-83846594 (+)	16q23.3	heat shock factor binding protein 1
WARS	1.55	3.59E-07	1.22E-05	chr14:100800125-100843142 (-)	14q32.31	tryptophanyl-tRNA synthetase
NQO1	1.55	9.68E-06	1.53E-04	chr16:69743304-69760707 (-)	16q22.1	NAD(P)H dehydrogenase, quinone 1
CRYL1	1.55	1.00E-07	4.56E-06	chr13:20977806-21100012 (-)	13q12.11	crystallin, lambda 1
CENPJ	1.55	5.12E-08	2.72E-06	chr13:25456412-25497085 (-)	13q12.12	centromere protein J
C18orf54	1.55	3.64E-06	7.32E-05	chr18:51884955-51908404 (+)	18q21.2	chromosome 18 open reading frame 54
OGFOD1	1.55	1.91E-05	2.58E-04	chr16:56485407-56511407 (+)	16q12.2	2-oxoglutarate and iron-dependent oxygenase domain containing 1
PLK2	1.55	4.33E-04	2.65E-03	chr5:57749809-57756087 (-)	5q12.1-q13.2	polo-like kinase 2
SSRP1	1.55	4.36E-08	2.44E-06	chr11:57093459-57103351 (-)	11q12	structure specific recognition protein 1
GLRX3	1.55	9.12E-07	2.56E-05	chr10:131934639-131982785 (+)	10q26	glutaredoxin 3
TIMM50	1.55	7.65E-08	3.68E-06	chr19:39971052-39981528 (+)	19q13.2	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)
RBM41	1.55	1.67E-03	7.30E-03	chrX:106305118-106362057 (-)	Xq22.3	RNA binding motif protein 41
CCT8	1.55	3.19E-06	6.62E-05	chr21:30428126-30446118 (-)	21q22.11	chaperonin containing TCP1, subunit 8 (theta)
TPD52L1	1.55	3.18E-11	1.55E-08	chr6:125474795-125585553 (+)	6q22-q23	tumor protein D52-like 1
ADAM10	1.54	2.21E-07	8.31E-06	chr15:58887403-59042177 (-)	15q22	ADAM metallopeptidase domain 10
TIMMDC1	1.54	1.88E-07	7.39E-06	chr3:119217368-119243937 (+)	3q13.33	translocase of inner mitochondrial membrane domain containing 1
BCCIP	1.54	1.58E-06	3.89E-05	chr10:127512104-127542264 (+)	10q26.1	BRCA2 and CDKN1A interacting protein
SHC1	1.54	3.32E-09	3.79E-07	chr1:154934774-154946959 (-)	1q21	SHC (Src homology 2 domain containing) transforming protein 1
NT5C2	1.54	9.88E-09	8.18E-07	chr10:104845940-104953063 (-)	10q24.32	5-nucleotidase, cytosolic II
HIST1H4H	1.54	1.08E-04	9.47E-04	chr6:26281283-26285762 (-)	6p22.1	histone cluster 1, H4h
SHC3	1.54	2.97E-04	2.00E-03	chr9:91620686-91793682 (-)	9q22.1	SHC (Src homology 2 domain containing) transforming protein 3
ELAC2	1.54	7.08E-09	6.47E-07	chr17:12894929-12921381 (-)	17p11.2	elaC ribonuclease Z 2
ATP5L	1.54	4.60E-10	9.49E-08	chr11:118271869-118302211 (+)	11q23.3	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G
NDUFA6	1.54	7.60E-08	3.66E-06	chr22:42481529-42486959 (-)	22q13.2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
ATP5EP2	1.54	3.92E-06	7.74E-05	chr13:28519343-28519727 (+)	13q12	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2
MRPL21	1.54	3.05E-06	6.41E-05	chr11:68658744-68671303 (-)	11q13.3	mitochondrial ribosomal protein L21
PIGW	1.54	5.54E-06	1.00E-04	chr17:34890847-34895150 (+)	17q12	phosphatidylinositol glycan anchor biosynthesis, class W
LEO1	1.54	4.05E-03	1.43E-02	chr15:52230222-52264003 (-)	15q21.2	Leo1, Paf1RNA polymerase II complex component, homolog (S. cerevisiae)
ECH1	1.54	6.24E-04	3.49E-03	chr19:39306062-39322497 (-)	19q13.1	enoyl CoA hydratase 1, peroxisomal
NCL	1.54	3.19E-05	3.78E-04	chr2:232318242-232348352 (-)	2q37.1	nucleolin
NOP56	1.54	3.08E-08	1.88E-06	chr20:2632791-2639039 (+)	20p13	NOP56 ribonucleoprotein
DDX10	1.54	1.19E-04	1.02E-03	chr11:108535752-108811657 (+)	11q22-q23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10
HRSP12	1.54	3.86E-06	7.67E-05	chr8:99114567-99129469 (-)	8q22	heat-responsive protein 12
ATP5G3	1.54	3.45E-10	7.85E-08	chr2:176040986-176049335 (-)	2q31.1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
RFC3	1.54	2.37E-07	8.80E-06	chr13:34392186-34540695 (+)	13q13.2	replication factor C (activator 1) 3, 38kDa
NIP7	1.54	3.39E-06	6.95E-05	chr16:69373343-69377014 (+)	16q22.1	NIP7, nucleolar pre-rRNA processing protein
SOAT1	1.54	9.99E-04	4.95E-03	chr1:179262849-179327815 (+)	1q25	sterol O-acyltransferase 1
CENPQ	1.54	2.15E-06	4.92E-05	chr6:49431096-49460820 (+)	6p12.3	centromere protein Q
TRAP1	1.54	1.40E-06	3.54E-05	chr16:3708038-3767598 (-)	16p13.3	TNF receptor-associated protein 1
TUBGCP4	1.54	5.01E-06	9.30E-05	chr15:43663313-43698240 (+)	15q15	tubulin, gamma complex associated protein 4
IDH1	1.54	4.51E-08	2.50E-06	chr2:209100951-209130798 (-)	2q33.3	isocitrate dehydrogenase 1 (NADP+), soluble
TAP2	1.53	9.92E-08	4.52E-06	chr6:32789610-32806557 (-)	6p21.3	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
NOC3L	1.53	6.14E-04	3.44E-03	chr10:96075004-96122716 (-)	10q23.33	nucleolar complex associated 3 homolog (S. cerevisiae)
ENOX2	1.53	7.57E-09	6.87E-07	chrX:129751713-130037208 (-)	Xq25	ecto-NOX disulfide-thiol exchanger 2
CDCA7	1.53	7.28E-06	1.23E-04	chr2:174219548-174233725 (+)	2q31	cell division cycle associated 7
DNAJC11	1.53	3.40E-08	2.01E-06	chr1:6694228-6761984 (-)	1p36.31	DnaJ (Hsp40) homolog, subfamily C, member 11
MTF1	1.53	5.30E-08	2.79E-06	chr1:38275239-38325292 (-)	1p33	metal-regulatory transcription factor 1
NEDD4	1.53	4.79E-06	9.02E-05	chr15:56119120-56285835 (-)	15q	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase
MRPL35	1.53	3.97E-10	8.62E-08	chr2:86426556-86440917 (+)	2p11.2	mitochondrial ribosomal protein L35
SGPP2	1.53	1.10E-04	9.61E-04	chr2:223289236-223425667 (+)	2q36.1	sphingosine-1-phosphate phosphatase 2
PSMA7	1.53	2.28E-09	2.85E-07	chr20:60711785-60718496 (-)	20q13.33	proteasome (prosome, macropain) subunit, alpha type, 7
STK39	1.53	4.87E-04	2.90E-03	chr2:168810530-169104651 (-)	2q24.3	serine threonine kinase 39
EXOSC8	1.53	5.58E-07	1.74E-05	chr13:37572953-37583751 (+)	13q13.1	exosome component 8
PPARGC1B	1.53	1.58E-08	1.15E-06	chr5:149109815-149234585 (+)	5q32	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
GGCT	1.53	1.22E-04	1.04E-03	chr7:30536237-30544460 (-)	7p15-p14	gamma-glutamylcyclotransferase
DLD	1.53	2.44E-06	5.45E-05	chr7:107531415-107572175 (+)	7q31-q32	dihydrolipoamide dehydrogenase
NDUFB6	1.53	1.36E-06	3.48E-05	chr9:32552997-32573182 (-)	9p21.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
HNRNPA2B1	1.53	1.77E-07	7.06E-06	chr7:26229547-26241149 (-)	7p15	heterogeneous nuclear ribonucleoprotein A2B1
UBE2M	1.53	2.18E-05	2.83E-04	chr19:59067079-59070343 (-)	19q13.43	ubiquitin-conjugating enzyme E2M
FAM20A	1.53	4.66E-04	2.80E-03	chr17:66531257-66597095 (-)	17q24.2	family with sequence similarity 20, member A
NSDHL	1.53	5.03E-07	1.60E-05	chrX:151999511-152038273 (+)	Xq28	NAD(P) dependent steroid dehydrogenase-like
DYNLT1	1.53	1.50E-08	1.11E-06	chr6:159057506-159065804 (-)	6q25.2-q25.3	dynein, light chain, Tctex-type 1
NES	1.53	8.50E-06	1.39E-04	chr1:156638555-156647189 (-)	1q23.1	nestin
OAZ1	1.53	1.61E-07	6.51E-06	chr19:2269520-2273487 (+)	19p13.3	ornithine decarboxylase antizyme 1
NIFK	1.53	3.88E-06	7.70E-05	chr2:122484521-122494503 (-)	2q14.3	nucleolar protein interacting with the FHA domain of MKI67
RNU6-177P	1.53	5.32E-03	1.77E-02	chr7:128267226-128267329 (+)	---	RNA, U6 small nuclear 177, pseudogene
TOMM70A	1.53	1.69E-06	4.09E-05	chr3:100082275-100120283 (-)	3q12.2	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
EPHA2	1.53	6.56E-07	1.98E-05	chr1:16450832-16482582 (-)	1p36	EPH receptor A2
PFN1	1.53	1.30E-06	3.35E-05	chr17:4848947-4852309 (-)	17p13.3	profilin 1
CWC27	1.53	7.01E-04	3.79E-03	chr5:64064755-64314590 (+)	5q12.3	CWC27 spliceosome-associated protein homolog (S. cerevisiae)
ZC3HAV1	1.53	1.12E-07	4.99E-06	chr7:138728266-138794465 (-)	7q34	zinc finger CCCH-type, antiviral 1
SNRPEP4	1.53	3.45E-07	1.19E-05	chr19:5576671-5576949 (-)	---	small nuclear ribonucleoprotein polypeptide E pseudogene 4
KIAA1551	1.53	1.02E-02	2.92E-02	chr12:32112353-32146043 (+)	12p11.21	KIAA1551
CMPK2	1.53	2.15E-05	2.81E-04	chr2:6980503-7006766 (-)	2p25.2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
SLC27A4	1.53	1.65E-05	2.31E-04	chr9:131102839-131123749 (+)	9q34.11	solute carrier family 27 (fatty acid transporter), member 4
ATP6V0B	1.53	2.89E-06	6.16E-05	chr1:44440320-44443972 (+)	1p32.3	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b
PNN	1.52	2.78E-03	1.08E-02	chr14:39644387-39652422 (+)	14q21.1	pinin, desmosome associated protein
NDC1	1.52	4.14E-08	2.35E-06	chr1:54231133-54304533 (-)	1p32.3	NDC1 transmembrane nucleoporin
ABHD17C	1.52	1.20E-06	3.15E-05	chr15:80972025-81047962 (+)	15q25.1	abhydrolase domain containing 17C
CBFB	1.52	5.34E-10	1.06E-07	chr16:67063050-67134961 (+)	16q22.1	core-binding factor, beta subunit
CNN2	1.52	4.25E-05	4.71E-04	chr19:1026298-1039064 (+)	19p13.3	calponin 2
PSMD12	1.52	3.98E-06	7.84E-05	chr17:65334032-65362743 (-)	17q24.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
EIF3K	1.52	7.11E-07	2.10E-05	chr19:39109722-39127595 (+)	19q13.2	eukaryotic translation initiation factor 3, subunit K
CDC25C	1.52	7.41E-06	1.25E-04	chr5:137620954-137674044 (-)	5q31	cell division cycle 25C
PDPN	1.52	1.34E-03	6.18E-03	chr1:13909960-13944452 (+)	1p36.21	podoplanin
TMEM185B	1.52	1.86E-06	4.40E-05	chr2:120975047-120980984 (-)	2q14.2	transmembrane protein 185B
TIMM23	1.52	2.31E-07	8.62E-06	chr10:51592080-51623386 (-)	10q11.23	translocase of inner mitochondrial membrane 23 homolog (yeast)
NPL	1.52	2.81E-06	6.02E-05	chr1:182758428-182799519 (+)	1q25	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)
ADAM9	1.52	8.88E-06	1.43E-04	chr8:38854388-38962779 (+)	8p11.22	ADAM metallopeptidase domain 9
BZW2	1.52	6.76E-09	6.32E-07	chr7:16685756-16746148 (+)	7p21.1	basic leucine zipper and W2 domains 2
CENPW	1.52	6.52E-07	1.97E-05	chr6:126661253-126670021 (+)	6q22.32	centromere protein W
AZI2	1.52	8.68E-06	1.41E-04	chr3:28356494-28390618 (-)	3p24.1	5-azacytidine induced 2
ALDH1A1	1.52	3.84E-03	1.38E-02	chr9:75515578-75695358 (-)	9q21.13	aldehyde dehydrogenase 1 family, member A1
PTPN2	1.52	4.86E-07	1.55E-05	chr18:12785477-12884337 (-)	18p11.3-p11.2	protein tyrosine phosphatase, non-receptor type 2
ANAPC7	1.52	5.06E-09	5.13E-07	chr12:110810705-110841535 (-)	12q24.11	anaphase promoting complex subunit 7
HIST1H3C	1.52	2.72E-04	1.88E-03	chr6:26045639-26046097 (+)	6p22.1	histone cluster 1, H3c
TKT	1.52	4.44E-07	1.44E-05	chr3:53258723-53290130 (-)	3p14.3	transketolase
TJP1	1.52	6.23E-07	1.90E-05	chr15:29991571-30248497 (-)	15q13	tight junction protein 1
COQ3	1.52	1.98E-08	1.35E-06	chr6:99817276-99842082 (-)	6q16.2	coenzyme Q3 methyltransferase
U2AF2	1.52	1.23E-06	3.21E-05	chr19:56165416-56186082 (+)	19q13.42	U2 small nuclear RNA auxiliary factor 2
CNOT6	1.52	1.07E-09	1.71E-07	chr5:179921412-180005405 (+)	5q35.3	CCR4-NOT transcription complex, subunit 6
KAL1	1.52	4.77E-03	1.62E-02	chrX:8496915-8700227 (-)	Xp22.32	Kallmann syndrome 1 sequence
ZNF326	1.52	6.78E-04	3.69E-03	chr1:90457722-90494097 (+)	1p22.2	zinc finger protein 326
DMXL2	1.52	7.83E-08	3.74E-06	chr15:51739908-51915030 (-)	15q21.2	Dmx-like 2
HSD17B2	1.52	3.37E-05	3.94E-04	chr16:82068858-82132139 (+)	16q24.1-q24.2	hydroxysteroid (17-beta) dehydrogenase 2
REV3L	1.52	2.87E-03	1.10E-02	chr6:111620234-111804918 (-)	6q21	REV3-like, polymerase (DNA directed), zeta, catalytic subunit
EFTUD2	1.52	2.70E-07	9.75E-06	chr17:42927655-42976993 (-)	17q21.31	elongation factor Tu GTP binding domain containing 2
IL1A	1.52	1.03E-05	1.61E-04	chr2:113531492-113542971 (-)	2q14	interleukin 1, alpha
AP5M1	1.52	8.40E-08	3.97E-06	chr14:57735606-57756797 (+)	14q22.3	adaptor-related protein complex 5, mu 1 subunit
PSMD11	1.52	5.68E-08	2.94E-06	chr17:30771502-30809398 (+)	17q11.2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
RABEP1	1.52	9.31E-04	4.70E-03	chr17:5185558-5289132 (+)	17p13.2	rabaptin, RAB GTPase binding effector protein 1
FAM208B	1.52	2.37E-04	1.69E-03	chr10:5726801-5805703 (+)	10p15.1	family with sequence similarity 208, member B
NDUFAF4	1.51	1.38E-06	3.51E-05	chr6:97337187-97345767 (-)	6q16.1	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4
SPATA5L1	1.51	7.00E-08	3.42E-06	chr15:45694519-45713617 (+)	15q21.1	spermatogenesis associated 5-like 1
ATP5J	1.51	1.71E-10	4.97E-08	chr21:27088815-27107984 (-)	21q21.1	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
GLYATL2	1.51	2.08E-06	4.79E-05	chr11:58601540-58671688 (-)	11q12.1	glycine-N-acyltransferase-like 2
TOMM34	1.51	3.28E-05	3.86E-04	chr20:43570771-43589127 (-)	---	translocase of outer mitochondrial membrane 34
CCDC47	1.51	2.82E-06	6.03E-05	chr17:61822610-61851088 (-)	17q23.3	coiled-coil domain containing 47
TTC9	1.51	2.70E-04	1.86E-03	chr14:71108504-71142077 (+)	14q24.2	tetratricopeptide repeat domain 9
PTPRD	1.51	3.87E-04	2.44E-03	chr9:8314246-10612723 (-)	9p23-p24.3	protein tyrosine phosphatase, receptor type, D
HIST1H2AE	1.51	4.68E-04	2.81E-03	chr6:26217148-26217711 (+)	6p22.1	histone cluster 1, H2ae
ALDH5A1	1.51	8.70E-10	1.50E-07	chr6:24495080-24537435 (+)	6p22	aldehyde dehydrogenase 5 family, member A1
TUFM	1.51	9.90E-07	2.72E-05	chr16:28853732-28857729 (-)	16p11.2	Tu translation elongation factor, mitochondrial
HIST1H2BM	1.51	1.26E-03	5.90E-03	chr6:27782822-27783267 (+)	6p22.1	histone cluster 1, H2bm
MRPS35	1.51	1.53E-06	3.79E-05	chr12:27863706-27909237 (+)	12p11	mitochondrial ribosomal protein S35
SLC30A7	1.51	1.30E-07	5.59E-06	chr1:101361632-101447311 (+)	1p21.2	solute carrier family 30 (zinc transporter), member 7
MAP3K5	1.51	6.69E-05	6.63E-04	chr6:136878185-137113657 (-)	6q22.33	mitogen-activated protein kinase kinase kinase 5
SFXN4	1.51	1.28E-06	3.31E-05	chr10:120900279-120925204 (-)	10q26.11	sideroflexin 4
PLD2	1.51	1.69E-06	4.10E-05	chr17:4710391-4726727 (+)	17p13.1	phospholipase D2
AKR1C1	1.51	4.09E-05	4.57E-04	chr10:4934796-5022159 (+)	10p15-p14	aldo-keto reductase family 1, member C1
DKC1	1.51	4.10E-07	1.35E-05	chrX:153991031-154005964 (+)	Xq28	dyskeratosis congenita 1, dyskerin
ADAM17	1.51	5.51E-06	9.99E-05	chr2:9628615-9695921 (-)	2p25	ADAM metallopeptidase domain 17

ATP5A1	1.51	4.05E-09	4.43E-07	chr18:43664110-43684300 (-)	18q21	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
CYB5R2	1.51	9.28E-06	1.48E-04	chr11:7686326-7695439 (-)	11p15.4	cytochrome b5 reductase 2
THOC1	1.51	2.51E-03	9.96E-03	chr18:214520-268059 (-)	18p11.32	THO complex 1
CTSD	1.51	6.12E-06	1.08E-04	chr11:1773982-1785222 (-)	11p15.5	cathepsin D
GTF2H3	1.51	3.90E-06	7.73E-05	chr12:124118376-124146479 (+)	12q24.31	general transcription factor IIH, polypeptide 3, 34kDa
ATP5F1	1.51	2.14E-07	8.14E-06	chr1:111991462-112005395 (+)	1p13.2	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
KLF7-IT1	1.51	3.91E-05	4.41E-04	chr2:207985608-207986768 (-)	---	KLF7 intronic transcript 1 (non-protein coding)
ANAPC1	1.51	9.34E-08	4.32E-06	chr2:87407211-87423980 (+)	2q12.1	anaphase promoting complex subunit 1
MTX2	1.51	2.15E-09	2.73E-07	chr2:177134123-177202753 (+)	2q31.1	metaxin 2
LOC100132062	1.51	9.21E-06	1.47E-04	chr1:222646723-222646767 (-)	5q35.3	uncharacterized LOC100132062
GABRE	1.51	5.24E-05	5.51E-04	chrX:151121596-151143152 (-)	Xq28	gamma-aminobutyric acid (GABA) A receptor, epsilon
CETN2	1.51	3.67E-07	1.24E-05	chrX:151995517-151999321 (-)	Xq28	centrin, EF-hand protein, 2
CWH43	1.51	1.63E-05	2.29E-04	chr4:48988264-49064098 (+)	4p11	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
QRSL1	1.51	1.30E-06	3.36E-05	chr6:107077441-107116292 (+)	6q21	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
MTHFD2	1.51	2.52E-05	3.16E-04	chr2:74425689-74444692 (+)	2p13.1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
PCP4L1	1.51	3.84E-07	1.29E-05	chr1:161228517-161255240 (+)	1q23.3	Purkinje cell protein 4 like 1
DCBLD1	1.51	5.31E-06	9.71E-05	chr6:117803820-117891021 (+)	6q22.1	discoidin, CUB and LCCL domain containing 1
MDH1	1.50	8.20E-09	7.25E-07	chr2:63815743-63834331 (+)	2p13.3	malate dehydrogenase 1, NAD (soluble)
SLC1A3	1.50	1.36E-06	3.47E-05	chr5:36606457-36688436 (+)	5p13	solute carrier family 1 (glial high affinity glutamate transporter), member 3
SDHD	1.50	1.03E-09	1.68E-07	chr11:111957497-111990353 (+)	11q23	succinate dehydrogenase complex, subunit D, integral membrane protein
SAE1	1.50	1.31E-09	1.93E-07	chr19:47634080-47713893 (+)	19q13.32	SUMO1 activating enzyme subunit 1
NAA50	1.50	2.16E-07	8.18E-06	chr3:113435307-113465147 (-)	3q13.2	N(alpha)-acetyltransferase 50, NatE catalytic subunit
RABGGTB	1.50	2.20E-05	2.86E-04	chr1:76251879-76261100 (+)	1p31	Rab geranylgeranyltransferase, beta subunit
CDC45	1.50	2.67E-12	2.85E-09	chr22:19466982-19508135 (+)	22q11.21	cell division cycle 45
LCN2	1.50	2.12E-04	1.55E-03	chr9:130911350-130915734 (+)	9q34	lipocalin 2
TMEM126A	1.50	4.86E-07	1.55E-05	chr11:85358963-85367597 (+)	11q14.1	transmembrane protein 126A
RBL1	1.50	3.39E-05	3.95E-04	chr20:35624752-35724410 (-)	20q11.2	retinoblastoma-like 1
PTPRG	1.50	3.10E-08	1.89E-06	chr3:61547243-62283288 (+)	3p21-p14	protein tyrosine phosphatase, receptor type, G
PTBP1	1.50	2.85E-06	6.09E-05	chr19:797392-812327 (+)	19p13.3	polypyrimidine tract binding protein 1
FASTKD2	1.50	2.63E-06	5.74E-05	chr2:207630081-207660911 (+)	2q33.3	FAST kinase domains 2
MRS2	1.50	6.35E-06	1.11E-04	chr6:24403153-24425816 (+)	6p22.3-p22.1	MRS2 magnesium transporter
RNU4-42P	0.67	3.18E-03	1.19E-02	chr1:160362558-160362699 (-)	---	RNA, U4 small nuclear 42, pseudogene
AMY2A	0.67	5.42E-04	3.13E-03	chr1:104257375-104262492 (+)	1p21	amylase, alpha 2A (pancreatic)
CAB39L	0.67	4.99E-09	5.10E-07	chr13:49882786-50020554 (-)	13q14.2	calcium binding protein 39-like
LOC101930415	0.67	4.53E-08	2.50E-06	chr6:158703295-158733390 (+)	---	uncharacterized LOC101930415
AC093110.3	0.67	5.79E-05	5.93E-04	chr2:54888148-54889929 (-)	---	novel transcript, antisense to SPTBN1
RNA5SP441	0.67	3.18E-06	6.61E-05	chr17:38530341-38530428 (+)	---	RNA, 5S ribosomal pseudogene 441
CTD-3135A9.3	0.67	1.19E-06	3.14E-05	chr8:143328948-143329227 (-)	---	Eukaryotic type signal recognition particle RNA (SRP_euk_arch)
OR7C1	0.66	9.01E-06	1.45E-04	chr19:14909958-14911023 (-)	19p13.1	olfactory receptor, family 7, subfamily C, member 1
C11orf63	0.66	2.43E-07	8.99E-06	chr11:122753391-122830506 (+)	11q24.1	chromosome 11 open reading frame 63
CBX6	0.66	7.04E-09	6.44E-07	chr22:39257455-39268319 (-)	22q13.1	chromobox homolog 6
IMMP2L-IT1	0.66	9.57E-04	4.79E-03	chr7:110364215-110365881 (-)	---	novel transcript
N4BP2L1	0.66	1.66E-07	6.70E-06	chr13:32974860-33002315 (-)	13q13.1	NEDD4 binding protein 2-like 1
TRAM1L1	0.66	1.37E-04	1.13E-03	chr4:118004710-118006736 (-)	4q26	translocation associated membrane protein 1-like 1
CREBRF	0.66	1.78E-05	2.45E-04	chr5:172483355-172566291 (+)	5q35.1	CREB3 regulatory factor
ZNF528	0.66	1.81E-06	4.30E-05	chr19:52901102-52921657 (+)	19q13	zinc finger protein 528
IFFO2	0.66	1.69E-03	7.35E-03	chr1:19230774-19283180 (-)	1p36.13	intermediate filament family orphan 2
KLRF2	0.66	2.22E-06	5.04E-05	chr12:10034088-10048432 (+)	12p13	killer cell lectin-like receptor subfamily F, member 2
LOC643923	0.66	2.68E-06	5.81E-05	chr11:107462471-107463949 (+)	11q22.3	uncharacterized LOC643923
SGK3	0.66	9.99E-08	4.55E-06	chr8:67624653-67774257 (+)	8q12	serumglucocorticoid regulated kinase family, member 3
VAT1	0.66	1.16E-06	3.09E-05	chr17:41166622-41174459 (-)	17q21	vesicle amine transport 1
ANKRD50	0.66	1.16E-04	1.00E-03	chr4:125585204-125633887 (-)	4q28.1	ankyrin repeat domain 50
EFNA3	0.66	3.11E-06	6.51E-05	chr1:155051348-155060014 (+)	1q21-q22	ephrin-A3
DZIP1L	0.66	9.49E-08	4.38E-06	chr3:137780827-137834660 (-)	3q22.3	DAZ interacting zinc finger protein 1-like
UBL3	0.66	1.67E-06	4.07E-05	chr13:30338508-30424821 (-)	13q12-q13	ubiquitin-like 3
PHYHD1	0.66	6.90E-10	1.29E-07	chr9:131683174-131704320 (+)	9q34.11	phytanoyl-CoA dioxygenase domain containing 1
RASA3	0.66	6.86E-11	2.55E-08	chr13:114747194-114898095 (-)	13q34	RAS p21 protein activator 3
TMEM255A	0.66	4.45E-06	8.51E-05	chrX:119392505-119445411 (-)	Xq24	transmembrane protein 255A
MFAP3L	0.66	2.02E-06	4.69E-05	chr4:170907748-170954182 (-)	4q32.3	microfibrillar-associated protein 3-like
DPYSL3	0.66	2.32E-05	2.97E-04	chr5:146770371-146889619 (-)	5q32	dihydropyrimidinase-like 3
RNU4-62P	0.66	7.93E-04	4.17E-03	chr3:121374322-121374451 (-)	---	RNA, U4 small nuclear 62, pseudogene
NAB1	0.66	6.81E-07	2.03E-05	chr2:191511472-191557492 (+)	2q32.3-q33	NGFI-A binding protein 1 (EGR1 binding protein 1)
FMO5	0.66	3.95E-08	2.28E-06	chr1:146655884-146697230 (-)	1q21.1	flavin containing monooxygenase 5
PAIP2B	0.66	1.38E-03	6.32E-03	chr2:71409868-71454233 (-)	2p13.3	poly(A) binding protein interacting protein 2B
CCSAP	0.66	2.92E-08	1.81E-06	chr1:229456752-229479041 (-)	1q42.13	centriole, cilia and spindle-associated protein
PDZD2	0.66	1.08E-04	9.43E-04	chr5:31639517-32111038 (+)	5p13.3	PDZ domain containing 2
CRABP1	0.66	2.03E-04	1.50E-03	chr15:78632666-78640573 (+)	15q24	cellular retinoic acid binding protein 1
RP11-312O7.2	0.66	8.29E-08	3.93E-06	chr1:206135293-206137828 (-)	---	novel transcript
OCA2	0.66	6.29E-05	6.32E-04	chr15:28000021-28344504 (-)	15q	oculocutaneous albinism II
RNU5B-1	0.66	4.98E-05	5.32E-04	chr15:65597015-65597130 (+)	15q22.31	RNA, U5B small nuclear 1
LIFR	0.66	1.50E-04	1.20E-03	chr5:38475065-38608456 (-)	5p13-p12	leukemia inhibitory factor receptor alpha
ALCAM	0.66	1.63E-04	1.28E-03	chr3:105085557-105295757 (+)	3q13.1	activated leukocyte cell adhesion molecule
RP11-407H12.8	0.66	1.80E-04	1.37E-03	chr1:248647546-248648785 (-)	---	novel transcript
ABCA8	0.66	1.02E-08	8.32E-07	chr17:66863431-66951533 (-)	17q24	ATP-binding cassette, sub-family A (ABC1), member 8
RP11-124N14.3	0.66	2.10E-04	1.54E-03	chr10:17275324-17276832 (-)	---	novel transcript
RNA5SP29	0.66	2.82E-06	6.03E-05	chr13:51601883-51601988 (-)	---	RNA, 5S ribosomal pseudogene 29
EPB41L4B	0.65	8.17E-09	7.23E-07	chr9:111934254-112083244 (-)	9q31-q32	erythrocyte membrane protein band 4.1 like 4B
PARK2	0.65	2.55E-09	3.10E-07	chr6:161768452-163148834 (-)	6q25.2-q27	parkin RBR E3 ubiquitin protein ligase
SSFA2	0.65	1.39E-05	2.03E-04	chr2:182756472-182795465 (+)	2q31.3	sperm specific antigen 2
RNA5SP69	0.65	4.09E-07	1.35E-05	chr1:178530048-178530164 (+)	---	RNA, 5S ribosomal pseudogene 69
F3	0.65	1.04E-07	4.70E-06	chr1:94994732-95007413 (-)	1p22-p21	coagulation factor III (thromboplastin, tissue factor)
RNY1	0.65	7.69E-09	6.92E-07	chr7:148684228-148684340 (-)	7q36	RNA, Ro-associated Y1
IL31RA	0.65	2.07E-03	8.60E-03	chr5:55147207-55218682 (+)	5q11.2	interleukin 31 receptor A
KIAA0895	0.65	2.09E-07	7.99E-06	chr7:36363759-36429734 (-)	7p14.2	KIAA0895
TSPAN2	0.65	3.62E-05	4.14E-04	chr1:115590632-115632121 (-)	1p13.2	tetraspanin 2
HSPA2	0.65	1.39E-04	1.14E-03	chr14:65002623-65009955 (+)	14q24.1	heat shock 70kDa protein 2
RNA5SP186	0.65	5.71E-06	1.03E-04	chr5:75387533-75387626 (-)	---	RNA, 5S ribosomal pseudogene 186
LRRC37A4P	0.65	7.80E-03	2.37E-02	chr17:43590734-43593064 (-)	17q21.31	leucine rich repeat containing 37, member A4, pseudogene
ARNTL	0.65	5.70E-03	1.86E-02	chr11:13299325-13408813 (+)	11p15	aryl hydrocarbon receptor nuclear translocator-like
FOS	0.65	5.01E-03	1.68E-02	chr14:75745477-75748937 (+)	14q24.3	FBJ murine osteosarcoma viral oncogene homolog
ARHGEF28	0.65	3.56E-07	1.21E-05	chr5:72921983-73237818 (+)	5q13.2	Rho guanine nucleotide exchange factor (GEF) 28
LOC100653515	0.65	2.32E-09	2.89E-07	chr17:76849059-76921472 (-)	17q25	differential display clone 8
CLDN16	0.65	5.32E-09	5.35E-07	chr3:190040330-190129932 (+)	3q28	claudin 16
RP11-84A14.5	0.65	4.85E-10	9.86E-08	chr1:9908376-9910212 (+)	---	novel transcript
RNU1-123P	0.65	1.14E-06	3.05E-05	chr16:67424594-67424753 (-)	---	RNA, U1 small nuclear 123, pseudogene
LRRC8C	0.65	3.23E-11	1.56E-08	chr1:90098631-90235462 (+)	1p22.2	leucine rich repeat containing 8 family, member C
WNT7B	0.65	9.03E-10	1.54E-07	chr22:46316242-46373009 (-)	22q13	wingless-type MMTV integration site family, member 7B
AZGP1P1	0.65	6.65E-08	3.31E-06	chr7:99578385-99591588 (+)	7q22.1	alpha-2-glycoprotein 1, zinc-binding pseudogene 1
ZNF135	0.65	4.11E-07	1.36E-05	chr19:58570607-58597677 (+)	19q13.4	zinc finger protein 135
DNAJB4	0.65	6.41E-08	3.22E-06	chr1:78444859-78483648 (+)	1p31.1	DnaJ (Hsp40) homolog, subfamily B, member 4
FOXQ1	0.65	3.39E-07	1.17E-05	chr6:1312675-1314993 (+)	6p25	forkhead box Q1
ISM1	0.65	5.01E-03	1.69E-02	chr20:13202418-13281298 (+)	20p12.1	isthmin 1, angiogenesis inhibitor
RGMB	0.65	5.34E-10	1.06E-07	chr5:98104354-98134347 (+)	5q15	repulsive guidance molecule family member b
BHLHE41	0.65	4.34E-04	2.66E-03	chr12:26272078-26278060 (-)	12p12.1	basic helix-loop-helix family, member e41
LOC101928784	0.65	3.32E-05	3.89E-04	chr15:60771377-60922836 (+)	15q22.2	uncharacterized LOC101928784
LOC100506990	0.64	4.96E-05	5.30E-04	chr8:7010239-7044422 (+)	8p23.1	uncharacterized LOC100506990
KRT31	0.64	6.15E-04	3.44E-03	chr17:39549976-39553844 (-)	17q21.2	keratin 31
SPNS2	0.64	4.76E-06	8.97E-05	chr17:4402129-4443228 (+)	17p13.2	spinster homolog 2 (Drosophila)
CLDN23	0.64	2.20E-07	8.30E-06	chr8:8559448-8561617 (+)	8p23.1	claudin 23
HCG26	0.64	6.17E-06	1.09E-04	chr6_qbl_hap6:2732712-2733891 (	6p21.3	HLA complex group 26 (non-protein coding)
OR2T3	0.64	1.32E-06	3.38E-05	chr1:248636627-248637634 (+)	1q44	olfactory receptor, family 2, subfamily T, member 3
OR2T35	0.64	9.80E-06	1.55E-04	chr1:248801588-248802562 (-)	1q44	olfactory receptor, family 2, subfamily T, member 35
MMP28	0.64	5.14E-07	1.62E-05	chr17:34083269-34122640 (-)	17q21.1	matrix metallopeptidase 28
SLC37A2	0.64	5.50E-04	3.16E-03	chr11:124932963-124960412 (+)	11q24.2	solute carrier family 37 (glucose-6-phosphate transporter), member 2
FN1	0.64	5.31E-04	3.09E-03	chr2:216225163-216300895 (-)	2q34	fibronectin 1
IGHD2-21	0.64	9.40E-04	4.73E-03	chr14:106354409-106354436 (-)	---	immunoglobulin heavy diversity 2-21
GATM	0.64	1.16E-03	5.56E-03	chr15:45653322-45670991 (-)	15q21.1	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
CAMSAP3	0.64	8.12E-07	2.34E-05	chr19:7660788-7683196 (+)	19p13.2	calmodulin regulated spectrin-associated protein family, member 3
SCARNA3	0.64	1.50E-07	6.20E-06	chr1:175937533-175937676 (-)	1q25.1	small Cajal body-specific RNA 3
NPR2	0.64	5.46E-06	9.95E-05	chr9:35792151-35809729 (+)	9p21-p12	natriuretic peptide receptor 2
RP11-438F14.3	0.64	2.49E-03	9.91E-03	chr1:248712057-248727140 (+)	---	novel transcript
CYBRD1	0.64	7.57E-05	7.26E-04	chr2:172378757-172414643 (+)	2q31.1	cytochrome b reductase 1
USP12	0.64	6.45E-07	1.95E-05	chr13:27640287-27746033 (-)	13q12.13	ubiquitin specific peptidase 12
KLK5	0.64	1.60E-04	1.26E-03	chr19:51446559-51456344 (-)	19q13.33	kallikrein-related peptidase 5
FAM13C	0.64	5.18E-08	2.74E-06	chr10:61005889-61122939 (-)	10q21.1	family with sequence similarity 13, member C
ACSS3	0.64	1.12E-03	5.40E-03	chr12:81470990-81650533 (+)	12q21.31	acyl-CoA synthetase short-chain family member 3
FZD7	0.64	8.83E-04	4.51E-03	chr2:202899310-202903168 (+)	2q33	frizzled class receptor 7
KIAA1467	0.64	1.37E-05	2.00E-04	chr12:13197218-13236383 (+)	12p13.1	KIAA1467
ZNF667-AS1	0.64	3.42E-06	6.99E-05	chr19:56989243-57006805 (+)	19q13.43	ZNF667 antisense RNA 1 (head to head)
PCSK2	0.64	8.66E-03	2.57E-02	chr20:17206752-17465223 (+)	20p11.2	proprotein convertase subtilisinkexin type 2
KCNJ13	0.64	5.26E-07	1.66E-05	chr2:233630512-233641278 (-)	2q37	potassium inwardly-rectifying channel, subfamily J, member 13
UST	0.64	2.91E-06	6.19E-05	chr6:149068271-149398126 (+)	6q25.1	uronyl-2-sulfotransferase
EFEMP1	0.63	1.35E-03	6.22E-03	chr2:56093097-56151298 (-)	2p16	EGF containing fibulin-like extracellular matrix protein 1
DGAT2	0.63	1.69E-04	1.31E-03	chr11:75479777-75512581 (+)	11q13.5	diacylglycerol O-acyltransferase 2
SCARNA21	0.63	5.80E-06	1.04E-04	chr17:7809440-7809578 (+)	17p13.1	small Cajal body-specific RNA 21
F2R	0.63	7.35E-08	3.56E-06	chr5:76011868-76031606 (+)	5q13	coagulation factor II (thrombin) receptor
OCLN	0.63	2.62E-04	1.82E-03	chr5:70370030-70388897 (-)	5q13.1	occludin
SCARNA9	0.63	6.47E-08	3.24E-06	chr11:93454679-93455032 (+)	11q21	small Cajal body-specific RNA 9
LSP1	0.63	7.58E-11	2.74E-08	chr11:1874200-1913497 (+)	11p15.5	lymphocyte-specific protein 1
AC092635.1	0.63	1.79E-08	1.25E-06	chr2:13677798-13749293 (+)	---	novel transcript
GATA6	0.63	9.19E-06	1.47E-04	chr18:19749404-19782491 (+)	18q11.1-q11.2	GATA binding protein 6
LOC101929476	0.63	2.47E-03	9.84E-03	chr1:209541007-209553035 (+)	---	uncharacterized LOC101929476
EMBP1	0.63	2.13E-04	1.55E-03	chr1:121260910-121313686 (+)	1p11.2	embigin pseudogene 1
SMURF2	0.63	1.52E-06	3.78E-05	chr17:62540735-62658386 (-)	17q22-q23	SMAD specific E3 ubiquitin protein ligase 2
CYP2J2	0.63	1.15E-04	9.94E-04	chr1:60358980-60392462 (-)	1p31.3-p31.2	cytochrome P450, family 2, subfamily J, polypeptide 2

RNA5SP162	0.63	6.17E-06	1.09E-04	chr4:57197343-57197383 (-)	---	RNA, 5S ribosomal pseudogene 162
P4HA1	0.63	2.70E-05	3.33E-04	chr10:74766975-74856732 (-)	10q21.3-q23.1	prolyl 4-hydroxylase, alpha polypeptide I
GAB2	0.63	2.98E-09	3.47E-07	chr11:77926336-78128868 (-)	11q14.1	GRB2-associated binding protein 2
PLXNC1	0.63	4.99E-03	1.68E-02	chr12:94542499-94701451 (+)	12q23.3	plexin C1
SGPP1	0.62	2.04E-02	4.98E-02	chr14:64150932-64194773 (-)	14q23.2	sphingosine-1-phosphate phosphatase 1
ANKRD33B	0.62	2.49E-09	3.05E-07	chr5:10564435-10657928 (+)	5p15.2	ankyrin repeat domain 33B
FOXO1	0.62	1.46E-11	9.29E-09	chr13:41129801-41240734 (-)	13q14.1	forkhead box O1
PIK3C2G	0.62	3.73E-03	1.35E-02	chr12:18400548-18801352 (+)	12p12	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma
CITED2	0.62	3.03E-07	1.07E-05	chr6:139693393-139695785 (-)	6p22.1	Cbpp300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2
LYPD5	0.62	1.24E-02	3.39E-02	chr19:44300079-44324808 (-)	19q13.31	LY6PLAUR domain containing 5
AHNAK2	0.62	3.06E-07	1.08E-05	chr14:105403590-105444694 (-)	14q32.33	AHNAK nucleoprotein 2
ANO1	0.62	1.49E-04	1.20E-03	chr11:69924408-70035652 (+)	11q13.3	anoctamin 1, calcium activated chloride channel
LOC284023	0.62	6.02E-08	3.08E-06	chr17:7816640-7819589 (-)	17p13.1	uncharacterized LOC284023
GDPD2	0.62	2.73E-04	1.88E-03	chrX:69642881-69653241 (+)	Xq13.1	glycerophosphodiester phosphodiesterase domain containing 2
HS3ST6	0.62	2.37E-12	2.61E-09	chr16:1961464-1968441 (-)	16p13.3	heparan sulfate (glucosamine) 3-O-sulfotransferase 6
GLTSCR2	0.62	2.44E-11	1.31E-08	chr19:48248793-48274141 (+)	19q13.3	glioma tumor suppressor candidate region gene 2
CRY2	0.62	4.41E-08	2.46E-06	chr11:45834606-45904799 (+)	11p11.2	cryptochrome circadian clock 2
DACH1	0.62	3.43E-03	1.26E-02	chr13:72012098-72441330 (-)	13q22	dachshund family transcription factor 1
SYT17	0.62	2.67E-07	9.68E-06	chr16:19179571-19279652 (+)	16p12.3	synaptotagmin XVII
SLC27A2	0.62	1.49E-05	2.14E-04	chr15:50474393-50528592 (+)	15q21.2	solute carrier family 27 (fatty acid transporter), member 2
ODF3L1	0.62	1.62E-06	3.98E-05	chr15:76016318-76020029 (+)	15q24.2	outer dense fiber of sperm tails 3-like 1
TIMP3	0.62	4.66E-05	5.04E-04	chr22:33196802-33259030 (+)	22q12.3	TIMP metallopeptidase inhibitor 3
LOC400590	0.61	1.79E-04	1.37E-03	chr17:29351203-29359585 (+)	17q11.2	uncharacterized LOC400590
SUSD2	0.61	1.95E-06	4.55E-05	chr22:24577227-24585078 (+)	22q11-q12	sushi domain containing 2
P2RX7	0.61	4.43E-07	1.44E-05	chr12:121570622-121624354 (+)	12q24	purinergic receptor P2X, ligand-gated ion channel, 7
GJC3	0.61	1.55E-05	2.20E-04	chr7:99520892-99527243 (-)	7q22.1	gap junction protein, gamma 3, 30.2kDa
RP11-353N4.1	0.61	1.56E-05	2.21E-04	chr1:149590752-149591762 (-)	---	putative novel transcript
OR2T11	0.61	8.29E-06	1.36E-04	chr1:248789420-248790491 (-)	1q44	olfactory receptor, family 2, subfamily T, member 11
CYP1B1	0.61	3.44E-04	2.23E-03	chr2:38294652-38337044 (-)	2p22.2	cytochrome P450, family 1, subfamily B, polypeptide 1
ACADL	0.61	2.85E-07	1.02E-05	chr2:211052663-211090215 (-)	2q34	acyl-CoA dehydrogenase, long chain
LGALS3	0.61	1.92E-09	2.53E-07	chr14:55595762-55612148 (+)	14q22.3	lectin, galactoside-binding, soluble, 3
FMN1	0.61	7.33E-05	7.09E-04	chr15:33057747-33486897 (-)	15q13.3	formin 1
BBS2	0.61	1.66E-06	4.05E-05	chr16:56518259-56554008 (-)	16q21	Bardet-Biedl syndrome 2
ATP6V1C2	0.61	9.90E-04	4.92E-03	chr2:10861775-10925236 (+)	---	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2
BLMH	0.61	1.76E-04	1.35E-03	chr17:28575213-28619184 (-)	17q11.2	bleomycin hydrolase
LGI3	0.61	3.39E-08	2.01E-06	chr8:22004338-22014597 (-)	8p21.3	leucine-rich repeat LGI family, member 3
RFESD	0.60	2.09E-07	7.97E-06	chr5:94982458-94993786 (+)	5q15	Rieske (Fe-S) domain containing
GIPC2	0.60	5.25E-04	3.06E-03	chr1:78511586-78604133 (+)	1p31.1	GIPC PDZ domain containing family, member 2
ZNF844	0.60	2.70E-05	3.33E-04	chr19:12175514-12192380 (+)	19p13.2	zinc finger protein 844
APOE	0.60	2.08E-09	2.66E-07	chr19:45408956-45412650 (+)	19q13.2	apolipoprotein E
AADAC	0.60	2.53E-03	1.00E-02	chr3:151531825-151546276 (+)	3q25.1	arylacetamide deacetylase
LOC100506674	0.60	1.39E-05	2.03E-04	chr5:44745002-44808879 (-)	5p12	uncharacterized LOC100506674
ATL1	0.60	7.88E-07	2.28E-05	chr14:50999227-51099786 (+)	14q22.1	atlastin GTPase 1
BCL2	0.60	3.39E-06	6.94E-05	chr18:60790579-60987361 (-)	18q21.3	B-cell CLLlymphoma 2
SLC26A5	0.60	1.16E-07	5.11E-06	chr7:102993177-103086624 (-)	7q22.1	solute carrier family 26 (anion exchanger), member 5
CERS6	0.60	6.97E-08	3.42E-06	chr2:169312372-169631644 (+)	2q24.3	ceramide synthase 6
CGNL1	0.60	5.86E-06	1.05E-04	chr15:57668703-57842925 (+)	15q21.3	cingulin-like 1
RP11-218C14.5	0.60	1.16E-06	3.08E-05	chr20:23635862-23637027 (-)	---	putative novel transcript
LAMB2P1	0.60	2.12E-07	8.05E-06	chr3:49190292-49191834 (-)	3p21.3-p21.2	laminin, beta 2 pseudogene 1
RORC	0.60	9.78E-13	1.25E-09	chr1:151778547-151804348 (-)	1q21	RAR-related orphan receptor C
PTPRM	0.60	5.44E-04	3.14E-03	chr18:7566780-8406859 (+)	18p11.2	protein tyrosine phosphatase, receptor type, M
KCTD4	0.60	3.17E-05	3.76E-04	chr13:45766988-45775175 (-)	13q14.12	potassium channel tetramerization domain containing 4
ZC3H6	0.60	4.27E-03	1.49E-02	chr2:113033171-113097640 (+)	2q13	zinc finger CCCH-type containing 6
NFATC2	0.60	2.77E-08	1.74E-06	chr20:50003494-50179339 (-)	20q13.2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
GLCCI1	0.60	2.23E-07	8.36E-06	chr7:8008423-8133902 (+)	7p21.3	glucocorticoid induced transcript 1
AC004231.2	0.59	1.36E-07	5.77E-06	chr17:39077682-39132178 (+)	---	novel transcript
RNY3P7	0.59	6.34E-04	3.53E-03	chr13:78197507-78197607 (+)	---	RNA, Ro-associated Y3 pseudogene 7
GAS7	0.59	3.65E-08	2.13E-06	chr17:9813926-10101868 (-)	17p13.1	growth arrest-specific 7
PELI2	0.59	6.36E-06	1.11E-04	chr14:56585093-56768244 (+)	14q21	pellino E3 ubiquitin protein ligase family member 2
LAMC2	0.59	5.96E-06	1.06E-04	chr1:183155174-183214262 (+)	1q25-q31	laminin, gamma 2
RELL1	0.59	2.78E-09	3.31E-07	chr4:37592422-37687999 (-)	4p14	RELT-like 1
EMB	0.59	1.30E-04	1.08E-03	chr5:49692026-49739082 (-)	5q11.1	embigin
CST6	0.59	1.12E-09	1.72E-07	chr11:65778955-65780976 (+)	11q13	cystatin EM
RNY4P18	0.59	1.15E-05	1.75E-04	chr9:113859605-113859693 (-)	---	RNA, Ro-associated Y4 pseudogene 18
ASPA	0.59	1.72E-06	4.15E-05	chr17:3377404-3406713 (+)	17p13.3	aspartoacylase
CRIP2	0.59	4.06E-09	4.43E-07	chr14:105939299-105946507 (+)	14q32.3	cysteine-rich protein 2
H19	0.59	1.63E-07	6.59E-06	chr11:2016406-2022700 (-)	11p15.5	H19, imprinted maternally expressed transcript (non-protein coding)
SCARNA5	0.59	3.79E-08	2.20E-06	chr2:234184372-234184649 (+)	2q37.1	small Cajal body-specific RNA 5
TGM5	0.59	1.49E-03	6.68E-03	chr15:43524793-43559055 (-)	15q15.2	transglutaminase 5
SCARNA8	0.59	1.83E-06	4.35E-05	chr9:19063654-19063784 (-)	9p22.1	small Cajal body-specific RNA 8
CRYAB	0.58	5.16E-08	2.73E-06	chr11:111779289-111794446 (-)	11q22.3-q23.1	crystallin, alpha B
RP4-760C5.3	0.58	5.00E-03	1.68E-02	chr20:25989427-25991167 (-)	---	putative novel transcript
OLFM2	0.58	2.79E-07	9.99E-06	chr19:9964394-10047070 (-)	19p13.2	olfactomedin 2
SLCO3A1	0.58	9.62E-09	8.04E-07	chr15:92396925-92715665 (+)	15q26	solute carrier organic anion transporter family, member 3A1
MITF	0.58	5.98E-04	3.37E-03	chr3:69788586-70017488 (+)	3p14.2-p14.1	microphthalmia-associated transcription factor
SCARNA11	0.58	2.85E-08	1.77E-06	chr12:6690639-6690775 (-)	12p13.31	small Cajal body-specific RNA 11
TPPP	0.58	6.33E-09	6.00E-07	chr5:659977-693510 (-)	5p15.3	tubulin polymerization promoting protein
CDR2	0.58	7.56E-09	6.86E-07	chr16:22357257-22385938 (-)	16p12.3	cerebellar degeneration-related protein 2, 62kDa
SCARNA10	0.58	1.88E-07	7.40E-06	chr12:6619388-6619717 (+)	12p13.31	small Cajal body-specific RNA 10
TSPYL5	0.58	1.82E-03	7.80E-03	chr8:98285702-98290192 (-)	8q22.1	TSPY-like 5
TMEM47	0.57	1.31E-04	1.09E-03	chrX:34645181-34675405 (-)	Xp11.4	transmembrane protein 47
PRLR	0.57	6.38E-06	1.12E-04	chr5:35048861-35230823 (-)	5p13.2	prolactin receptor
IGFL3	0.57	2.88E-03	1.11E-02	chr19:46623328-46627931 (-)	19q13.32	IGF-like family member 3
ARHGEF26	0.57	1.83E-08	1.27E-06	chr3:153838792-153975616 (+)	3q25.2	Rho guanine nucleotide exchange factor (GEF) 26
PNRC1	0.57	1.77E-09	2.38E-07	chr6:89790429-89794879 (+)	6q15	proline-rich nuclear receptor coactivator 1
YPEL2	0.57	3.97E-07	1.32E-05	chr17:57409053-57479095 (+)	17q22	yippee-like 2 (Drosophila)
RNU6ATAC12P	0.57	3.21E-04	2.12E-03	chr11:131255144-131255258 (+)	---	RNA, U6atac small nuclear 12, pseudogene
SLC43A1	0.57	9.74E-05	8.76E-04	chr11:57252004-57283259 (-)	11q12.1	solute carrier family 43 (amino acid system L transporter), member 1
SLC8A1	0.57	1.02E-08	8.34E-07	chr2:40339286-40838193 (-)	2p22.1	solute carrier family 8 (sodiumcalcium exchanger), member 1
PHYHIP	0.57	1.91E-05	2.59E-04	chr8:22077216-22089854 (-)	8p21.3	phytanoyl-CoA 2-hydroxylase interacting protein
NLRP10	0.57	1.55E-03	6.90E-03	chr11:7980971-7985204 (-)	11p15.4	NLR family, pyrin domain containing 10
GPC3	0.57	1.64E-09	2.25E-07	chrX:132669773-133119922 (-)	Xq26.1	glypican 3
AC016730.1	0.57	3.66E-07	1.24E-05	chr2:13863173-13898277 (+)	---	novel transcript
IRS2	0.57	1.27E-07	5.49E-06	chr13:110406184-110438915 (-)	13q34	insulin receptor substrate 2
RNA5SP348	0.57	2.36E-06	5.29E-05	chr11:104123307-104123343 (+)	---	RNA, 5S ribosomal pseudogene 348
SRGAP2	0.56	1.47E-06	3.68E-05	chr1:121107152-121131151 (+)	1q32.1	SLIT-ROBO Rho GTPase activating protein 2
IGFL2	0.56	1.01E-04	8.97E-04	chr19:46651039-46664561 (+)	19q13.32	IGF-like family member 2
ANO1-AS1	0.56	5.94E-09	5.73E-07	chr11:70033894-70034615 (-)	---	ANO1 antisense RNA 1
ANKRD20A4	0.56	4.69E-03	1.60E-02	chr9:69381812-69425560 (+)	9q21.11	ankyrin repeat domain 20 family, member A4
RAI14	0.56	1.04E-07	4.70E-06	chr5:34656342-34832732 (+)	5p13.3-p13.2	retinoic acid induced 14
HSPA1A	0.56	4.23E-06	8.21E-05	chr6:31783320-31785722 (-)	6p21.3	heat shock 70kDa protein 1A
COLEC12	0.56	2.90E-06	6.17E-05	chr18:3193355-500729 (-)	18p11.32	collectin sub-family member 12
SP8	0.56	1.44E-07	6.00E-06	chr7:20821894-20826508 (-)	7p21.2	Sp8 transcription factor
BMP2	0.56	6.87E-10	1.29E-07	chr20:6748311-6760910 (+)	20p12	bone morphogenetic protein 2
MYADM	0.56	4.93E-07	1.57E-05	chr19:54369477-54379691 (+)	19q13.42	myeloid-associated differentiation marker
HOPX	0.56	5.32E-08	2.80E-06	chr4:57514154-57548065 (-)	4q12	HOP homeobox
C14orf132	0.56	2.37E-09	2.94E-07	chr14:96505661-96560417 (+)	14q32.2	chromosome 14 open reading frame 132
CYP39A1	0.56	1.06E-04	9.32E-04	chr6:46517445-46620523 (-)	6p21.1-p11.2	cytochrome P450, family 39, subfamily A, polypeptide 1
WEE1	0.55	9.28E-05	8.43E-04	chr11:9595228-9615004 (+)	11p15.4	WEE1 G2 checkpoint kinase
FAM134B	0.55	9.01E-08	4.19E-06	chr5:16473147-16617167 (-)	5p15.1	family with sequence similarity 134, member B
KRT80	0.55	1.61E-05	2.27E-04	chr12:52562780-52585784 (-)	12q13.13	keratin 80
AK7	0.55	9.26E-07	2.59E-05	chr14:96858448-96955764 (+)	14q32.2	adenylate kinase 7
TGFBR2	0.55	1.36E-05	2.00E-04	chr3:30647994-30735634 (+)	3p22	transforming growth factor, beta receptor II (7080kDa)
EFHC2	0.55	1.94E-07	7.58E-06	chrX:44007128-44202923 (-)	Xp11.3	EF-hand domain (C-terminal) containing 2
RAB3B	0.55	3.87E-08	2.24E-06	chr1:52373628-52456436 (-)	1p32-p31	RAB3B, member RAS oncogene family
RP11-222A11.1	0.55	8.96E-05	8.21E-04	chr10:67345446-67441220 (+)	---	novel transcript
ASAP2	0.55	7.56E-09	6.86E-07	chr2:9346894-9545812 (+)	2p25|2p24	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2
HSD11B1	0.55	1.46E-06	3.65E-05	chr1:209859510-209908295 (+)	1q32-q41	hydroxysteroid (11-beta) dehydrogenase 1
BTBD16	0.55	5.80E-10	1.13E-07	chr10:124030821-124097677 (+)	10q26.13	BTB (POZ) domain containing 16
SNTB1	0.55	1.05E-10	3.60E-08	chr8:121547985-121825513 (-)	8q23-q24	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
EPPK1	0.55	1.08E-03	5.28E-03	chr8:144939497-144952632 (-)	8q24.3	epiplakin 1
VIM	0.55	3.69E-04	2.35E-03	chr10:17270258-17279592 (+)	10p13	vimentin
AC002117.1	0.54	2.48E-04	1.75E-03	chr17:43227985-43236822 (-)	---	novel transcript, antisense to HEXIM1 and HEXIM2
ANKFN1	0.54	1.73E-09	2.34E-07	chr17:54230836-54560007 (+)	17q22	ankyrin-repeat and fibronectin type III domain containing 1
RTN4RL1	0.54	1.18E-08	9.25E-07	chr17:1837971-1928178 (-)	17p13.3	reticulon 4 receptor-like 1
mar-03	0.54	1.29E-09	1.92E-07	chr5:126203406-126366500 (-)	5q23.2	membrane-associated ring finger (C3HC4) 3, E3 ubiquitin protein ligase
SH3BGRL2	0.54	7.57E-05	7.25E-04	chr6:80341000-80413373 (+)	6q14.1	SH3 domain binding glutamate-rich protein like 2
ZBTB16	0.54	1.15E-07	5.10E-06	chr11:113930315-114121398 (+)	11q23.1	zinc finger and BTB domain containing 16
RHOB	0.54	3.03E-06	6.40E-05	chr2:20646835-20649206 (+)	2p24	ras homolog family member B
C3orf52	0.54	2.55E-06	5.60E-05	chr3:111805182-111849851 (+)	3q13.2	chromosome 3 open reading frame 52
NR1D1	0.54	7.19E-03	2.23E-02	chr17:38249037-38256978 (-)	17q11.2	nuclear receptor subfamily 1, group D, member 1
PRELP	0.54	2.07E-06	4.77E-05	chr1:203444883-203460480 (+)	1q32	prolinearginine-rich end leucine-rich repeat protein
UGT3A2	0.54	3.00E-04	2.02E-03	chr5:36035119-36071460 (-)	5p13.2	UDP glycosyltransferase 3 family, polypeptide A2
LCE5A	0.53	8.34E-05	7.81E-04	chr1:152483320-152484653 (+)	1q21.3	late cornified envelope 5A
TCP11L2	0.53	8.47E-09	7.39E-07	chr12:106696581-106740793 (+)	12q23.3	t-complex 11, testis-specific-like 2
ZNF652	0.53	2.47E-08	1.59E-06	chr17:47366568-47439835 (-)	17q21.32	zinc finger protein 652
TLL1	0.53	4.59E-09	4.78E-07	chr4:166794410-167025609 (+)	4q32-q33	tolloid-like 1
LYPD6B	0.53	1.61E-07	6.51E-06	chr2:149894621-150071776 (+)	2q23.2	LY6PLAUR domain containing 6B
RNF39	0.53	3.20E-06	6.63E-05	chr6:30038043-30043664 (-)	6p21.3	ring finger protein 39
POF1B	0.53	8.03E-06	1.33E-04	chrX:84532395-84634748 (-)	Xq21.2	premature ovarian failure, 1B
ADAMTSL3	0.53	8.91E-10	1.53E-07	chr15:84322838-84708594 (+)	15q25.2	ADAMTS-like 3
FAM171B	0.52	5.83E-05	5.97E-04	chr2:187558698-187630685 (+)	2q32.1	family with sequence similarity 171, member B
LPHN3	0.52	1.28E-02	3.48E-02	chr4:62066974-62938184 (+)	4q13.1	latrophilin 3
SVIP	0.52	7.98E-07	2.31E-05	chr11:22840475-22851411 (-)	11p14.2	small VCPp97-interacting protein
DUSP1	0.52	8.50E-06	1.39E-04	chr5:172195093-172198203 (-)	5q34	dual specificity phosphatase 1

EMP3	0.52	3.41E-04	2.22E-03	chr19:48828629-48833810 (+)	19q13.3	epithelial membrane protein 3
EFNB2	0.52	4.23E-08	2.39E-06	chr13:107142079-107187462 (-)	13q33	ephrin-B2
MYH14	0.52	6.80E-10	1.28E-07	chr19:50706885-50813802 (+)	19q13.33	myosin, heavy chain 14, non-muscle
ZDHHC11B	0.52	2.25E-06	5.10E-05	chr5:710472-767323 (-)	5p15.33	zinc finger, DHHC-type containing 11B
LRP4	0.52	2.92E-07	1.04E-05	chr11:46878268-46940173 (-)	11p11.2	low density lipoprotein receptor-related protein 4
SYNE1	0.52	4.66E-07	1.50E-05	chr6:152442819-152958534 (-)	6q25	spectrin repeat containing, nuclear envelope 1
RNY5	0.52	7.66E-09	6.91E-07	chr7:148638580-148638658 (+)	7q36	RNA, Ro-associated Y5
FGL2	0.52	1.71E-04	1.33E-03	chr7:76822688-76829150 (-)	7q11.23	fibrinogen-like 2
TUFT1	0.51	4.58E-11	1.97E-08	chr1:151512781-151556059 (+)	1q21	tuftelin 1
CRIP1	0.51	9.54E-13	1.25E-09	chr14:105952654-105955284 (+)	14q32.33	cysteine-rich protein 1 (intestinal)
ACER1	0.51	3.89E-04	2.45E-03	chr19:6306510-6333640 (-)	19p13.3	alkaline ceramidase 1
MAML2	0.51	2.19E-04	1.59E-03	chr11:95709762-96076382 (-)	11q21	mastermind-like 2 (Drosophila)
SERPINB7	0.51	5.84E-04	3.31E-03	chr18:61420169-61472604 (+)	18q21.33	serpin peptidase inhibitor, clade B (ovalbumin), member 7
CLDN8	0.51	1.31E-08	9.94E-07	chr21:31586324-31588469 (-)	21q22.11	claudin 8
LOC100506834	0.51	1.00E-07	4.55E-06	chr9:89563613-89616948 (+)	---	uncharacterized LOC100506834
ANKRD20A3	0.50	5.88E-04	3.33E-03	chr9:43064953-43091857 (-)	9p12	ankyrin repeat domain 20 family, member A3
TGFBI	0.50	1.11E-07	4.92E-06	chr5:135364584-135399507 (+)	5q31	transforming growth factor, beta-induced, 68kDa
EGLN3	0.50	1.82E-05	2.49E-04	chr14:34393421-34638972 (-)	14q13.1	egl-9 family hypoxia-inducible factor 3
CHL1	0.50	9.23E-04	4.66E-03	chr3:238279-451097 (+)	3p26.1	cell adhesion molecule L1-like
ANG	0.50	1.16E-10	3.89E-08	chr14:21152259-21168761 (+)	14q11.1-q11.2	angiogenin, ribonuclease, RNase A family, 5
COBL	0.50	1.66E-12	1.98E-09	chr7:51083909-51384515 (-)	7p12.1	cordon-bleu WH2 repeat protein
SCIN	0.50	5.07E-10	1.02E-07	chr7:12596187-12693228 (+)	7p21.3	scinderin
STXBP6	0.49	6.87E-11	2.55E-08	chr14:25278862-25519503 (-)	14q12	syntaxin binding protein 6 (amisyn)
PRKCB	0.49	1.06E-13	3.34E-10	chr16:23847300-24231932 (+)	16p11.2	protein kinase C, beta
CCND1	0.49	1.32E-09	1.95E-07	chr11:69455855-69469242 (+)	11q13	cyclin D1
SCCPDH	0.49	6.16E-07	1.89E-05	chr1:246887349-246931440 (+)	1q44	saccharopine dehydrogenase (putative)
TSHZ2	0.49	5.82E-07	1.80E-05	chr20:51588946-52111869 (+)	20q13.2	teashirt zinc finger homeobox 2
GJB4	0.49	8.47E-10	1.48E-07	chr1:35225342-35229325 (+)	1p34.3	gap junction protein, beta 4, 30.3kDa
KRT23	0.48	1.37E-07	5.81E-06	chr17:39078948-39093836 (-)	17q21.2	keratin 23 (histone deacetylase inducible)
LAMB4	0.48	1.76E-05	2.43E-04	chr7:107663993-107770801 (-)	7q31	laminin, beta 4
OR2T10	0.48	5.25E-05	5.52E-04	chr1:248756052-248757100 (-)	1q44	olfactory receptor, family 2, subfamily T, member 10
ADCY2	0.48	1.53E-09	2.17E-07	chr5:7396321-7830194 (+)	5p15.3	adenylate cyclase 2 (brain)
APOD	0.48	1.18E-06	3.13E-05	chr3:195295573-195311076 (-)	3q29	apolipoprotein D
ANKRD18A	0.48	6.62E-05	6.57E-04	chr9:38540566-38620657 (-)	9p13.1	ankyrin repeat domain 18A
RNASE7	0.48	4.76E-05	5.13E-04	chr14:21510385-21512393 (+)	14q11.2	ribonuclease, RNase A family, 7
ARHGAP29	0.48	6.99E-04	3.78E-03	chr1:94615403-94740624 (-)	1p22.1	Rho GTPase activating protein 29
SDC4	0.48	4.74E-10	9.71E-08	chr20:43953928-43977064 (-)	20q12	syndecan 4
RORA	0.48	1.06E-08	8.48E-07	chr15:60780483-61521518 (-)	15q22.2	RAR-related orphan receptor A
CTSV	0.48	1.39E-06	3.52E-05	chr9:99791959-99822167 (-)	9q22.2	cathepsin V
CTSH	0.47	2.52E-05	3.16E-04	chr15:79213400-79237433 (-)	15q25.1	cathepsin H
TMEM116	0.47	8.04E-09	7.16E-07	chr12:112369087-112451023 (-)	12q24.13	transmembrane protein 116
KCNMB4	0.47	1.39E-08	1.04E-06	chr12:70760056-70828072 (+)	12q	potassium large conductance calcium-activated channel, subfamily M, beta member 4
SLURP1	0.47	2.05E-04	1.51E-03	chr8:143822362-143823829 (-)	8q24.3	secreted LY6 PLAUR domain containing 1
TXNIP	0.47	1.39E-05	2.03E-04	chr1:145438462-145442635 (+)	1q21.1	thioredoxin interacting protein
CPA4	0.47	4.17E-08	2.37E-06	chr7:129932974-129964020 (+)	7q32	carboxypeptidase A4
NPY1R	0.47	2.08E-06	4.79E-05	chr4:164245062-164265984 (-)	4q31.3-q32	neuropeptide Y receptor Y1
PMP22	0.47	4.37E-05	4.80E-04	chr17:15133095-15168644 (-)	17p12	peripheral myelin protein 22
ARRDC4	0.47	2.07E-10	5.66E-08	chr15:98462784-98517068 (+)	15q26.3	arrestin domain containing 4
HSD17B13	0.46	1.13E-02	3.16E-02	chr4:88224941-88244058 (-)	4q22.1	hydroxysteroid (17-beta) dehydrogenase 13
CNTNAP3	0.46	1.76E-04	1.35E-03	chr9:39072764-39288456 (-)	9p13.1	contactin associated protein-like 3
CNTNAP3B	0.46	2.84E-04	1.93E-03	chr9:43684885-43924049 (+)	9p11.2	contactin associated protein-like 3B
EEF2K	0.45	1.25E-08	9.64E-07	chr16:22217592-22300066 (+)	16p12.2	eukaryotic elongation factor-2 kinase
TPPP3	0.45	7.52E-05	7.22E-04	chr16:67423712-67427438 (-)	16q22.1	tubulin polymerization-promoting protein family member 3
C14orf64	0.45	5.47E-09	5.40E-07	chr14:98391947-98444461 (-)	14q32.2	chromosome 14 open reading frame 64
FAM189A2	0.45	1.90E-11	1.09E-08	chr9:71939488-72007371 (+)	9q21.11	family with sequence similarity 189, member A2
GATA3	0.45	2.98E-11	1.51E-08	chr10:8095567-8117164 (+)	10p15	GATA binding protein 3
C5orf46	0.45	7.69E-08	3.68E-06	chr5:147260289-147286101 (-)	5q32	chromosome 5 open reading frame 46
ARHGAP31	0.44	2.08E-10	5.66E-08	chr3:119013220-119139561 (+)	3q13.33	Rho GTPase activating protein 31
BGN	0.44	2.35E-05	3.00E-04	chrX:152760347-152775012 (+)	Xq28	biglycan
PDK4	0.44	7.70E-06	1.29E-04	chr7:95212809-95225925 (-)	7q21.3	pyruvate dehydrogenase kinase, isozyme 4
DCT	0.44	1.30E-03	6.03E-03	chr13:95090830-95131936 (-)	13q32	dopachrome tautomerase
TRPC6	0.44	5.16E-08	2.73E-06	chr11:101322295-101743293 (-)	11q22.1	transient receptor potential cation channel, subfamily C, member 6
PLLP	0.44	4.14E-09	4.46E-07	chr16:57290009-57318599 (-)	16q13	plasmolipin
SCNN1B	0.44	8.12E-07	2.34E-05	chr16:23313591-23392620 (+)	16p12.2-p12.1	sodium channel, non-voltage-gated 1, beta subunit
SIK1	0.44	1.80E-09	2.42E-07	chr21:44834395-44847008 (-)	21q22.3	salt-inducible kinase 1
CDHR1	0.43	2.09E-09	2.66E-07	chr10:85954410-85979377 (+)	10q23.1	cadherin-related family member 1
SCEL	0.43	3.53E-05	4.07E-04	chr13:78049967-78219398 (+)	13q22	sciellin
SLC46A2	0.43	2.90E-08	1.80E-06	chr9:115641200-115653193 (-)	9q32	solute carrier family 46, member 2
CDON	0.43	1.17E-06	3.11E-05	chr11:125825691-125933187 (-)	11q24.2	cell adhesion associated, oncogene regulated
RHOBTB3	0.43	8.71E-12	6.75E-09	chr5:95049226-95160087 (+)	5q15	Rho-related BTB domain containing 3
ABI3BP	0.43	4.95E-05	5.29E-04	chr3:100468000-100712359 (-)	3q12	ABI family, member 3 (NESH) binding protein
CNTNAP3P2	0.42	1.26E-04	1.06E-03	chr9:40498481-40633261 (-)	9q12	contactin associated protein-like 3 pseudogene 2
CLEC2A	0.42	1.03E-04	9.11E-04	chr12:10051272-10084980 (-)	12p13.31	C-type lectin domain family 2, member A
AADACL2	0.42	8.71E-06	1.41E-04	chr3:151451704-151479127 (+)	3q25.1	arylacetamide deacetylase-like 2
CACNA2D1	0.41	3.21E-06	6.65E-05	chr7:81575760-82073114 (-)	7q21-q22	calcium channel, voltage-dependent, alpha 2 delta subunit 1
GSTA3	0.41	8.38E-08	3.97E-06	chr6:52761437-52774496 (-)	6p12.1	glutathione S-transferase alpha 3
AZGP1	0.40	1.16E-07	5.12E-06	chr7:99564343-99573780 (-)	7q22.1	alpha-2-glycoprotein 1, zinc-binding
SLITRK6	0.40	2.69E-08	1.70E-06	chr13:86366922-86373623 (-)	13q31.1	SLIT and NTRK-like family, member 6
HPGD	0.40	1.47E-08	1.09E-06	chr4:175411328-175444305 (-)	4q34-q35	hydroxyprostaglandin dehydrogenase 15-(NAD)
C8orf88	0.39	1.72E-09	2.33E-07	chr8:91968167-91997485 (-)	8q21.3	chromosome 8 open reading frame 88
KIT	0.38	2.04E-04	1.51E-03	chr4:55524085-55606881 (+)	4q12	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
LONRF1	0.37	7.98E-13	1.10E-09	chr8:12579403-12613582 (-)	8p23.1	LON peptidase N-terminal domain and ring finger 1
IL34	0.37	2.12E-10	5.70E-08	chr16:70613798-70694585 (+)	16q22.1	interleukin 34
LCE1E	0.37	5.38E-07	1.69E-05	chr1:152758690-152760902 (+)	1q21.3	late cornified envelope 1E
SOX5	0.37	1.57E-09	2.17E-07	chr12:23682440-24715524 (-)	12p12.1	SRY (sex determining region Y)-box 5
CLDN1	0.37	4.69E-11	1.98E-08	chr3:190023490-190040264 (-)	3q28-q29	claudin 1
EDIL3	0.37	5.49E-09	5.41E-07	chr5:83236373-83680611 (-)	5q14	EGF-like repeats and discoidin I-like domains 3
LY6G6C	0.36	1.05E-05	1.64E-04	chr6_qbl_hap6:2980058-2983255 (	6p21.33	lymphocyte antigen 6 complex, locus G6C
ADRB2	0.35	1.03E-10	3.54E-08	chr5:148204808-148208250 (+)	5q31-q32	adrenoceptor beta 2, surface
ANXA9	0.34	4.01E-06	7.88E-05	chr1:150954493-150968114 (+)	1q21	annexin A9
KRT2	0.32	3.39E-04	2.21E-03	chr12:53038342-53045959 (-)	12q13.13	keratin 2
CHP2	0.32	4.02E-08	2.30E-06	chr16:23765948-23770272 (+)	16p12.2	calcineurin-like EF-hand protein 2
ASPN	0.32	1.60E-05	2.26E-04	chr9:95218487-95244844 (-)	9q22	asporin
GAN	0.32	3.51E-11	1.65E-08	chr16:81348571-81413940 (+)	16q24.1	gigaxonin
CDSN	0.31	1.91E-06	4.50E-05	chr6_cox_hap2:2597569-2602957 (	6p21.3	corneodesmosin
ITM2A	0.31	1.78E-08	1.25E-06	chrX:78615881-78623164 (-)	Xq13.3-Xq21.2	integral membrane protein 2A
PAMR1	0.31	1.09E-13	3.34E-10	chr11:35453370-35551848 (-)	11p13	peptidase domain containing associated with muscle regeneration 1
SPRR4	0.30	4.26E-04	2.62E-03	chr1:152943128-152945069 (+)	1q21.3	small proline-rich protein 4
KRT77	0.30	1.95E-09	2.55E-07	chr12:53083410-53097247 (-)	12q13.13	keratin 77
PSAPL1	0.30	3.09E-11	1.52E-08	chr4:7432021-7436700 (-)	4p16.1	prosaposin-like 1 (gene pseudogene)
CCL27	0.30	1.58E-10	4.77E-08	chr9:34661877-34664045 (-)	9p13	chemokine (C-C motif) ligand 27
LCE1A	0.29	1.93E-07	7.56E-06	chr1:152798523-152800665 (+)	1q21.3	late cornified envelope 1A
BTC	0.29	1.60E-05	2.26E-04	chr4:75669969-75719896 (-)	4q13.3	betacellulin
ABHD12B	0.26	9.89E-08	4.52E-06	chr14:51338878-51371688 (+)	14q22.1	abhydrolase domain containing 12B
ID4	0.26	3.05E-13	5.98E-10	chr6:19837601-19842431 (+)	6p22.3	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
FLG	0.25	3.41E-06	6.97E-05	chr1:152274651-152297679 (-)	1q21.3	filaggrin
CRCT1	0.24	1.86E-06	4.41E-05	chr1:152486978-152488486 (+)	1q21	cysteine-rich C-terminal 1
WFDC12	0.24	3.94E-06	7.77E-05	chr20:43752066-43753106 (-)	20q13.12	WAP four-disulfide core domain 12
ASPRV1	0.23	8.51E-08	4.01E-06	chr2:70187221-70189397 (-)	2p13.3	aspartic peptidase, retroviral-like 1
IL37	0.23	1.80E-07	7.15E-06	chr2:113670548-113676459 (+)	2q12-q14.1	interleukin 37
CMAHP	0.21	5.64E-13	9.48E-10	chr6:25081295-25218698 (-)	6p21.32	cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene
AQP9	0.19	2.62E-10	6.45E-08	chr15:58430368-58478110 (+)	15q	aquaporin 9
LCE2D	0.16	7.20E-09	6.57E-07	chr1:152635872-152637135 (+)	1q21.3	late cornified envelope 2D
LCE1B	0.16	4.68E-10	9.61E-08	chr1:152784447-152785585 (+)	1q21.3	late cornified envelope 1B
LCE6A	0.15	2.60E-09	3.16E-07	chr1:152815330-152816459 (+)	1q21.3	late cornified envelope 6A
ELMOD1	0.15	7.11E-10	1.32E-07	chr11:107461817-107537505 (+)	11q22.3	ELMO CED-12 domain containing 1
LCE1D	0.15	4.06E-09	4.43E-07	chr1:152769217-152771396 (+)	1q21.3	late cornified envelope 1D
LCE1C	0.15	3.62E-10	8.10E-08	chr1:152777311-152779107 (-)	1q21.3	late cornified envelope 1C
LCE1F	0.13	1.11E-09	1.72E-07	chr1:152748848-152749445 (+)	1q21.3	late cornified envelope 1F
LCE2A	0.11	8.07E-09	7.17E-07	chr1:152670840-152671918 (+)	1q21.3	late cornified envelope 2A
KPRP	0.10	5.96E-12	5.19E-09	chr1:152730506-152734529 (+)	1q21.3	keratinocyte proline-rich protein
LCE2C	0.09	4.20E-10	8.99E-08	chr1:152647771-152649050 (+)	1q21.3	late cornified envelope 2C
LOR	0.09	1.06E-09	1.71E-07	chr1:153232176-153234600 (+)	1q21	loricrin
LCE2B	0.09	5.86E-11	2.27E-08	chr1:152658599-152659877 (+)	1q21	late cornified envelope 2B
POSTN	0.09	1.36E-08	1.03E-06	chr13:38136719-38183563 (-)	13q13.3	periostin, osteoblast specific factor
SERPINA12	0.09	3.26E-17	6.15E-13	chr14:94953611-94984181 (-)	14q32.13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 12
C1orf68	0.08	1.62E-12	1.98E-09	chr1:152691082-152692946 (+)	1q21.3	chromosome 1 open reading frame 68
FLG2	0.06	2.39E-10	6.06E-08	chr1:152321213-152332482 (-)	1q21.3	filaggrin family member 2
CDR1	0.05	3.49E-17	6.15E-13	chrX:139864570-139867036 (-)	Xq27.1	cerebellar degeneration-related protein 1, 34kDa

Supplementary Table S1c - Differentially expressed genes (DEGs) between keratinocytes from psoriasis non-lesional skin (PN) and keratinocytes from healthy skin (H).

GeneName	lin FCH	P-value	FDR	Molecular location	Cytogenic location	Official Full Name
KIF20B	2.64	5.33E-05	3.73E-02	chr10:91461367-91534700 (+)	10q23.31	kinesin family member 20B
ASPM	2.35	4.31E-05	3.58E-02	chr1:197053257-197115824 (-)	1q31	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
AC016745.3	2.13	7.27E-05	3.94E-02	chr2:114182072-114182901 (+)	---	novel transcript
MKI67	1.92	8.88E-05	4.06E-02	chr10:129894923-129924649 (-)	10q26.2	marker of proliferation Ki-67
CENPF	1.89	1.09E-04	4.27E-02	chr1:214776532-214837931 (+)	1q41	centromere protein F, 350/400kDa
RBM41	1.81	5.99E-05	3.73E-02	chrX:106305118-106362057 (-)	Xq22.3	RNA binding motif protein 41
AC106053.1	1.78	1.40E-04	4.54E-02	chr2:18966073-18969018 (+)	---	novel transcript
UACA	1.78	1.32E-04	4.49E-02	chr15:70946893-71055932 (-)	15q22-q24	uveal autoantigen with coiled-coil domains and ankyrin repeats
CA5BP1	1.72	2.12E-05	3.28E-02	chrX:15719057-15721483 (+)	Xp22.2	carbonic anhydrase VB pseudogene 1
GSDMC	1.69	3.31E-06	1.80E-02	chr8:130760442-130799134 (-)	8q24.21	gasdermin C
CEP152	1.66	7.62E-05	3.94E-02	chr15:49030132-49103343 (-)	15q21.1	centrosomal protein 152kDa
HIBCH	1.61	5.70E-05	3.73E-02	chr2:191054461-191208919 (-)	2q32.2	3-hydroxyisobutyryl-CoA hydrolase
NBEAL1	1.58	1.01E-04	4.18E-02	chr2:203879602-204091101 (+)	2q33.2	neurobeachin-like 1
GPR135	1.58	1.33E-04	4.49E-02	chr14:59927483-59932060 (-)	14q23.1	G protein-coupled receptor 135
RP11-492I21.1	1.57	8.32E-05	4.06E-02	chr1:175986413-175987896 (-)	---	putative novel transcript
KLHL28	1.54	2.82E-05	3.30E-02	chr14:45412933-45415138 (-)	14q21.2	kelch-like family member 28
AF212831.2	1.54	1.55E-04	4.69E-02	chr21:18235195-18246011 (-)	---	novel gene
CRYAB	0.65	2.06E-06	1.61E-02	chr11:111779289-111794446 (-)	11q22.3-q23.1	crystallin, alpha B
TRAM2	0.65	2.40E-06	1.70E-02	chr6:52362200-52441862 (-)	6p21.1-p12	translocation associated membrane protein 2
PPAP2A	0.65	1.47E-04	4.60E-02	chr5:54720682-54830878 (-)	5q11	phosphatidic acid phosphatase type 2A
CDA	0.64	4.61E-05	3.58E-02	chr1:20915441-20945401 (+)	1p36.2-p35	cytidine deaminase
EGR2	0.64	2.00E-05	3.28E-02	chr10:64571756-64679660 (-)	10q21.1	early growth response 2
CRABP1	0.63	7.16E-05	3.94E-02	chr15:78632666-78640573 (+)	15q24	cellular retinoic acid binding protein 1
CLDN8	0.63	7.09E-06	2.16E-02	chr21:31586324-31588469 (-)	21q22.11	claudin 8
FTL	0.62	1.07E-04	4.27E-02	chr19:49468566-49470136 (+)	19q13.33	ferritin, light polypeptide
C5orf46	0.62	1.69E-04	4.87E-02	chr5:147260289-147286101 (-)	5q32	chromosome 5 open reading frame 46
TNFAIP3	0.61	5.92E-05	3.73E-02	chr6:138188351-138204449 (+)	6q23	tumor necrosis factor, alpha-induced protein 3
ZNF667-AS1	0.61	6.44E-07	9.09E-03	chr19:56989243-57006805 (+)	19q13.43	ZNF667 antisense RNA 1 (head to head)
ATF3	0.58	1.42E-04	4.54E-02	chr1:212738676-212794119 (+)	1q32.3	activating transcription factor 3
KRT31	0.58	5.74E-05	3.73E-02	chr17:39549976-39553844 (-)	17q21.2	keratin 31
CA6	0.58	1.14E-04	4.27E-02	chr1:9005922-9035151 (+)	1p36.2	carbonic anhydrase VI
APOD	0.56	3.19E-05	3.36E-02	chr3:195295573-195311076 (-)	3q29	apolipoprotein D
HIST2H4B	0.53	1.17E-05	2.76E-02	chr1:149804221-149811339 (+)	1q21	histone cluster 2, H4b
KRT77	0.51	4.09E-05	3.58E-02	chr12:53083410-53097247 (-)	12q13.13	keratin 77
NR4A3	0.44	4.87E-05	3.58E-02	chr9:102584137-102629173 (+)	9q22	nuclear receptor subfamily 4, group A, member 3
FAM26E	0.44	5.23E-06	2.05E-02	chr6:116832808-116845955 (+)	6q22.1	family with sequence similarity 26, member E