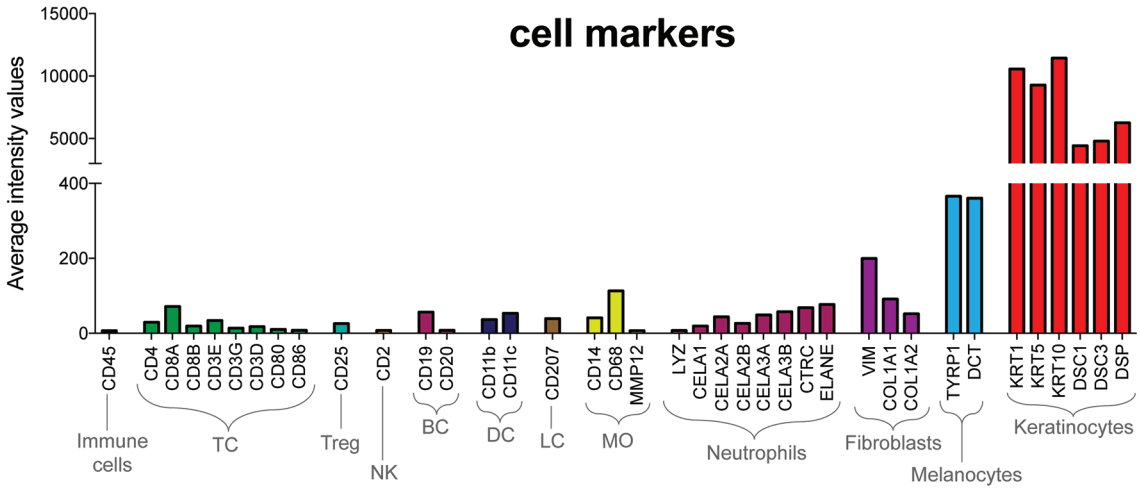

Fig. S1. Expression (intensity values) of marker genes for different cell types in the sorted CD45^{neg} cell population.
TC: T-cell; Treg: Regulatory T cell; NK: Natural Killer cell; BC: B-cell; DC: Dendritic cell; LC: Langerhans cell; MO: Macrophage.

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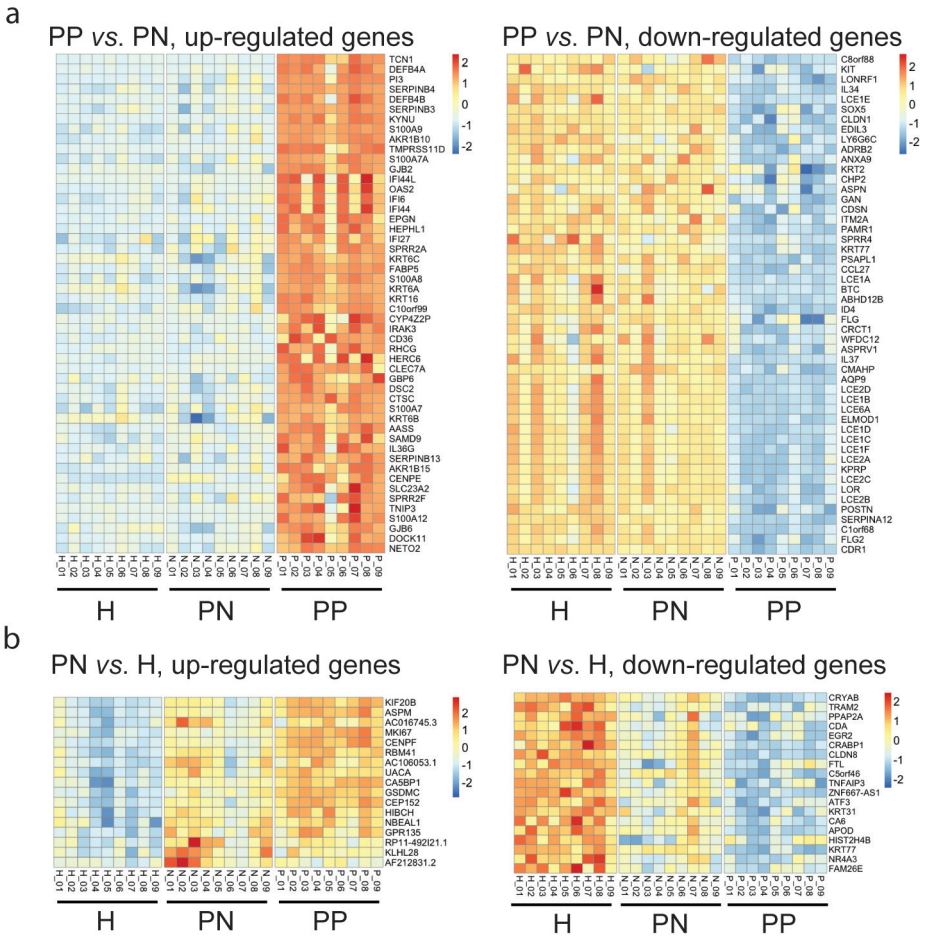

Fig. S2. Heatmap showing differentially expressed genes (DEGs) **in keratinocytes from psoriasis skin lesions compared with those from non-lesional skin** (PP vs. PN)**, and in keratinocytes from non-lesional psoriasis skin compared with those from healthy skin** (PN vs. H).

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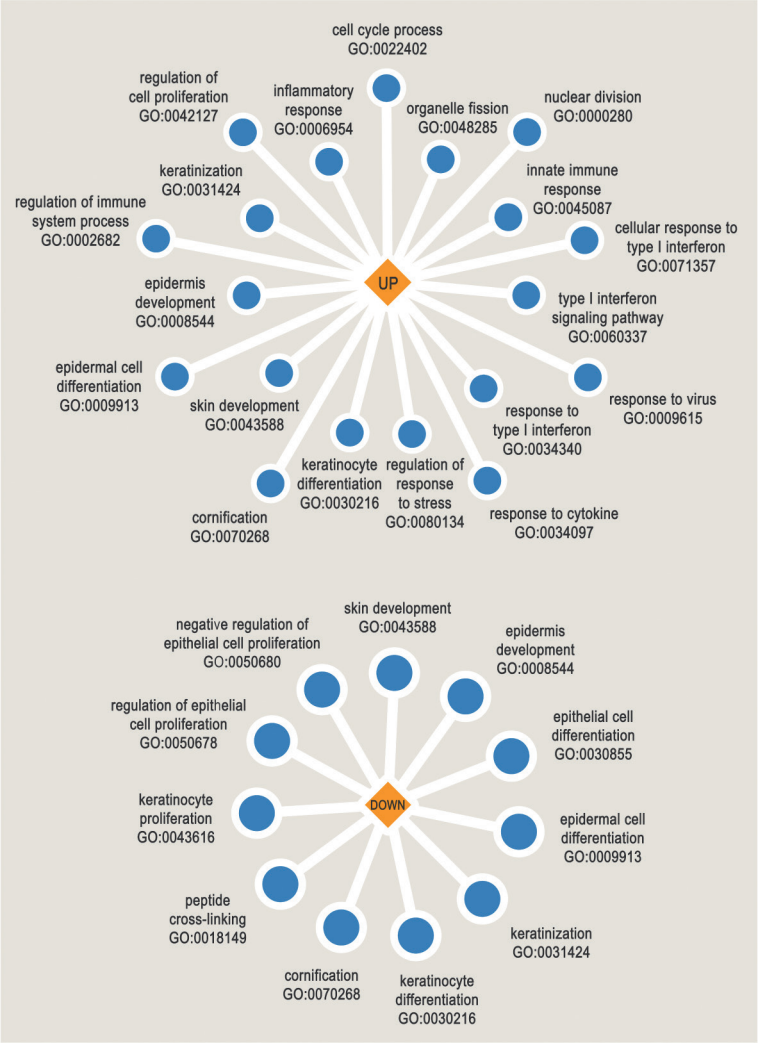

Fig. S3. Cytoscape-BINGO functional enrichment analysis.

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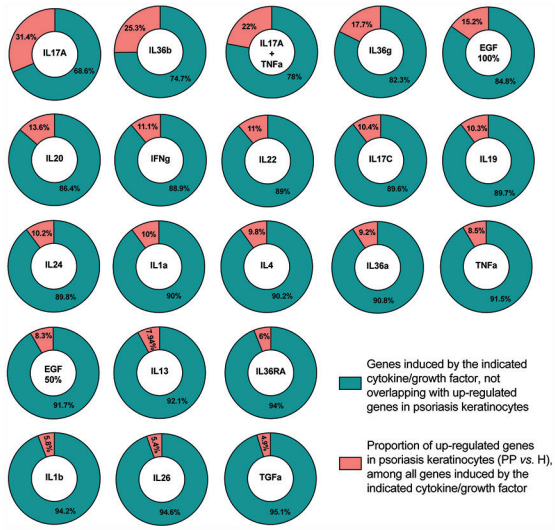

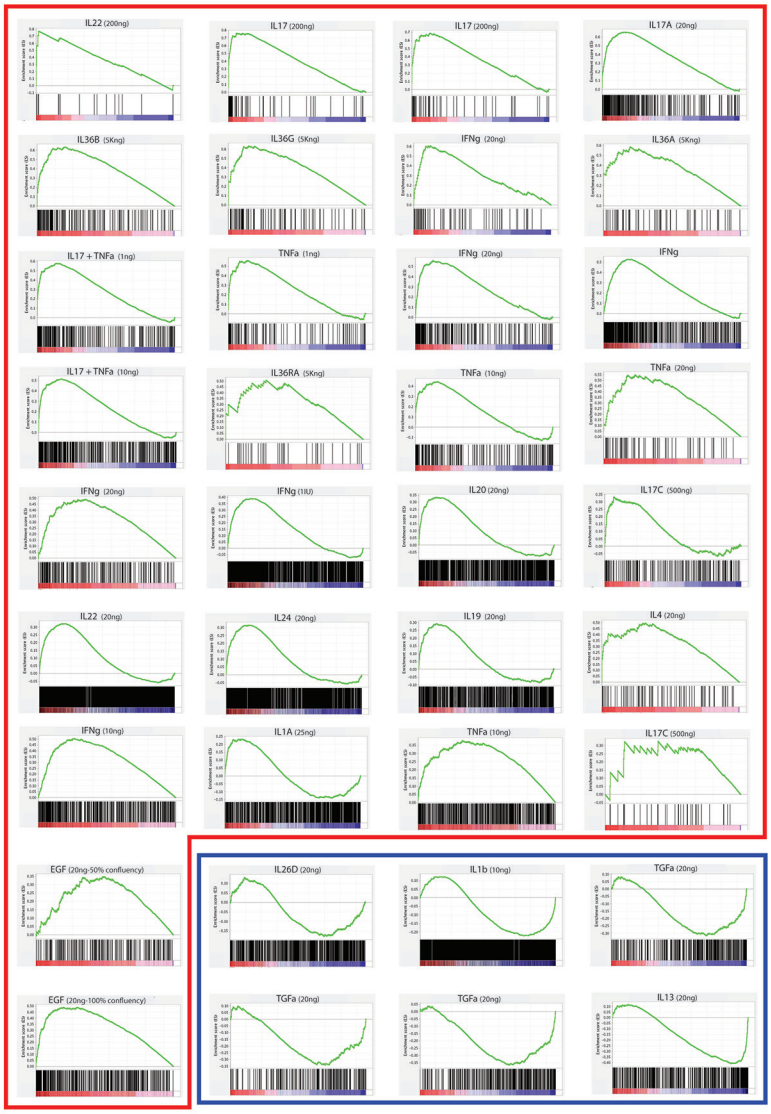

Fig. S4. Cytokine signatures and enrichment score.

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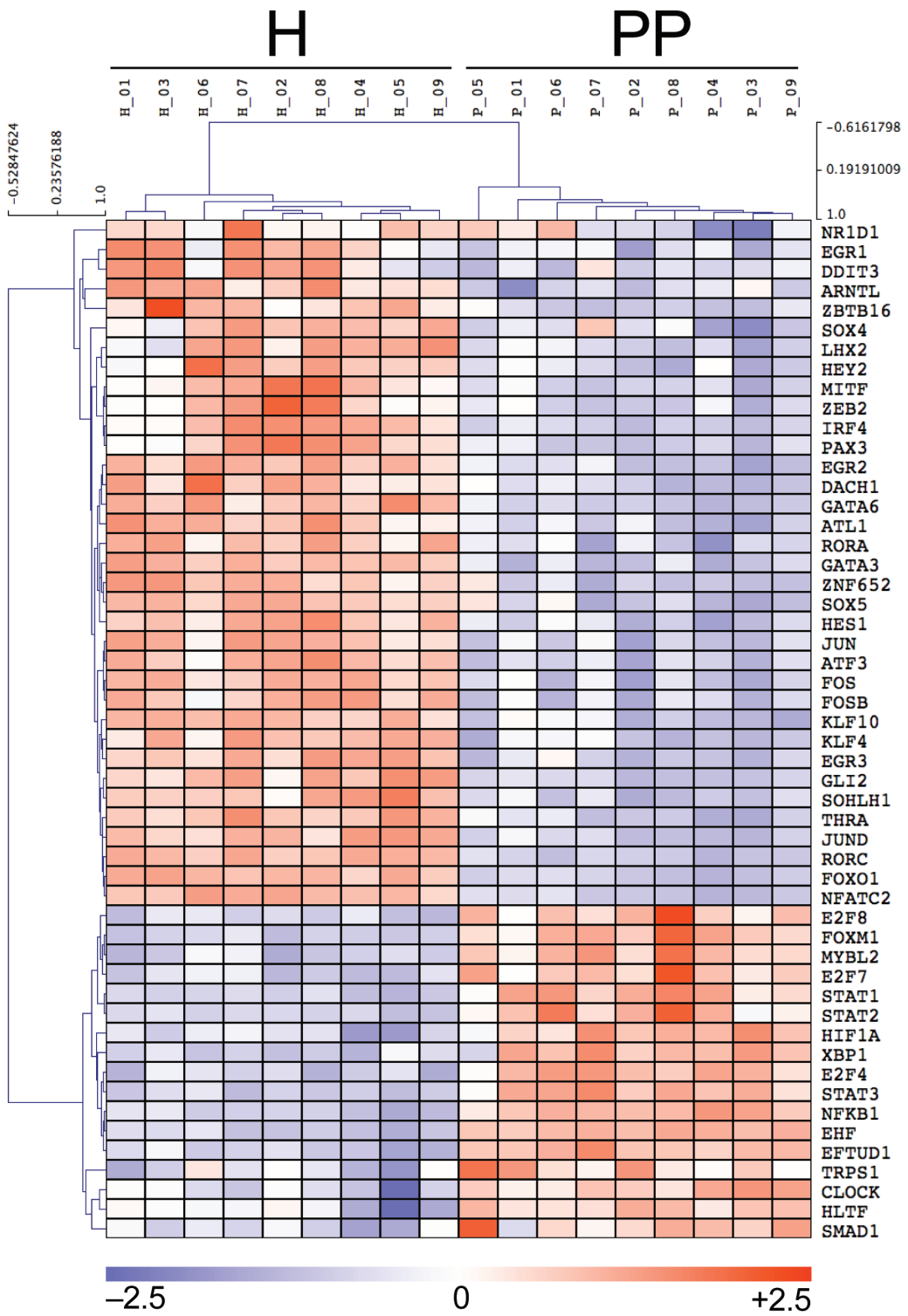

Fig. S5. Transcription factors with enriched binding site motifs in psoriatic keratinocytes (lesional (PP) **vs. non-lesional** (PN)**), which also show differential expression in psoriatic keratinocytes.**

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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

The format and content has not been edited by ActaDV.

Supplementary Table S2 - Genes involved in the significantly enriched gene ontology biological processes (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways among differentially expressed genes in keratinocytes from psoriasis lesions compared to those from healthy skin (PP vs. H comparison).

GO-BP up-regulated

Term	Overlap	P-value	Adjusted P-value	Z-score	Genes
DNA-dependent DNA replication (GO:0006261)	40/118	1.56E-15	1.21E-11	-3.19	BLM;FEN1;RNASEH2A;MCM8;MCM10;BRCA1;POLB;BRIP1;CDC45;ORC1;EXO1;CHEK1;RBBP8;REV3L;CLSPN;RFC5;TIPIN;RFC3;RFC4;RFC1;REV1;CDC7;BAZ1A;CDC6;CDC25C;TICRR;POLA1;POLA2;RAD50;DBF4;NASP;POLE2;CDK1;MCM3;TIMELESS;MCM5;DNA2;MCM6;TOP1;ATR
DNA replication (GO:0006260)	37/125	2.01E-12	3.90E-09	-3.16	BLM;FEN1;RNASEH2A;MCM8;MCM10;BRCA1;BRIP1;CDC45;ORC1;EXO1;CHEK1;RBBP8;CLSPN;KPNA2;RFC5;TIPIN;RFC3;RFC4;REV1;CDC7;CDC6;CDC25C;TICRR;POLA1;POLA2;RAD50;DBF4;NASP;POLE2;CDK1;MCM3;TIMELESS;MCM5;DNA2;MCM6;TOP1;ATR
Double-strand break repair (GO:0006302)	42/164	1.32E-11	2.04E-08	-3.26	BLM;VCP;FEN1;PRKDC;BRCC3;BRCA1;PDS5A;BRCA2;RAD51AP1;POLB;BRIP1;EXO1;CHEK1;RBBP8;RFC5;MBD4;NPM1;PARP4;XRCC4;DTX3L;FANCL;XRCC2;RECQL;FANCA;BAZ1B;SMC1A;GTF2H3;PARP9;TICRR;RNF168;SETX;RAD50;RAD51C;MSH3;FANCD2;POLE2;UBE2T;PSME4;CDK1;TRIP13;RAD18;ATR
G2/M transition of mitotic cell cycle (GO:0000086)	35/130	1.49E-10	1.44E-07	-3.13	CEP57;CUL1;CCP110;HMMR;FOXM1;AURKA;CCNB2;CCNB1;CEP70;CNTRL;NEK2;CEP290;CEP78;PLK4;OFD1;HSP90AA1;BORA;PPP1R12A;CEP135;CEP152;PLK1;HAUS6;CDC25C;TUBG1;MASTL;CKAP5;CDC25B;HAUS1;CCNA2;TPX2;MELK;CENPJ;AKAP9;CDK1;FGFR1OP
Viral DNA repair (GO:0046787)	38/160	1.28E-09	8.27E-07	-3.31	BLM;VCP;FEN1;NUP107;PDS5A;NUP160;RAD51AP1;POLB;EXO1;CHEK1;TPR;RBBP8;RCC1;NUP88;RFC5;NDC1;RANBP2;MBD4;NPM1;PARP4;FANCL;XRCC2;RECQL;FANCA;SMC1A;GTF2H3;TICRR;RAD50;RAD51C;MSH3;FANCD2;POLE2;UBE2T;PSME4;CDK1;RAD18;ATR;NUP37
DNA repair (GO:0006281)	54/279	1.70E-09	1.01E-06	-3.99	TOP2A;FEN1;MCM8;SMC5;MCM10;SMC6;BRCA1;POLB;NIPBL;EXO1;CHEK1;ZC3H12A;KPNA2;RFC5;USP47;PARP4;DTX3L;RECQL;BAZ1B;MASTL;SMC1A;RNF168;RAD51C;MSH3;FANCD2;PSME4;TIMELESS;DTL;BLM;VCP;USP16;BOD1L1;PDS5A;RAD51AP1;RBBP8;RBBP6;LYN;MBD4;NPM1;FANCL;XRCC2;FANCA;GTF2H3;USP28;TICRR;SETX;RAD50;APC;POLE2;UBE2T;CDK1;ERCC8;RAD18;ATR
Keratinocyte development (GO:0003334)	16/59	1.29E-05	8.56E-04	-2.32	SPRR2E;CERS3;SPRR2F;MBD4;CSTA;WNT5A;TGM1;KRT16;ADAM9;SPRR2A;SPRR2B;SPRR1B;IVL;S100A7;EPHA2;SPRR2D
Keratinocyte differentiation (GO:0030216)	19/80	1.68E-05	1.03E-03	-2.56	SPRR2E;CERS3;SPRR2F;MBD4;CSTA;HDAC2;HDAC1;WNT5A;TGM1;KRT16;ADAM9;ITGA6;SPRR2A;SPRR2B;SPRR1B;IVL;S100A7;EPHA2;SPRR2D
NIK/NF-kappaB signaling (GO:0038061)	16/64	3.90E-05	2.19E-03	-2.28	PSMD12;PSMD14;CHUK;CUL1;NFKB1;PSMA5;PSMB6;PSMA6;PSMA3;PSMA4;PSMB5;PSMC4;PSMA2;PSME4;PSMD1;PSME2
Type I interferon signaling pathway (GO:0060337)	27/148	5.68E-05	3.00E-03	-2.95	IFITM3;IFITM1;SP100;IFITM2;IFI6;ADAR;IFIT1;SAMHD1;LRP8;IFIT3;OASL;GBP2;RSAD2;STAT1;STAT2;MX1;STAT3;IL36G;IRAK3;FER;IFI27;OAS1;OAS2;IFNE;OAS3;XAF1;MYD88

GO-BP down-regulated

Term	Overlap	P-value	Adjusted P-value	Z-score	Genes
Limb spinous cell differentiation (GO:0060890)	18/59	1.88E-12	6.87E-10	-2.66	SPRR4;FLG;CDSN;LCE1E;LCE1F;LCE1C;LOR;LCE2D;LCE1D;LCE1A;LCE2B;SCEL;LCE1B;LCE2C;ACER1;LCE2A;LCE5A;TXNIP
Limb granular cell differentiation (GO:0060891)	18/59	1.88E-12	6.87E-10	-2.65	SPRR4;FLG;CDSN;LCE1E;LCE1F;LCE1C;LOR;LCE2D;LCE1D;LCE1A;LCE2B;SCEL;LCE1B;LCE2C;ACER1;LCE2A;LCE5A;TXNIP
Keratinocyte development (GO:0003334)	18/59	1.88E-12	6.87E-10	-2.63	SPRR4;FLG;CDSN;LCE1E;LCE1F;LCE1C;LOR;LCE2D;LCE1D;LCE1A;LCE2B;SCEL;LCE1B;LCE2C;ACER1;LCE2A;LCE5A;TXNIP
Keratinocyte differentiation (GO:0030216)	20/80	6.78E-12	1.20E-09	-2.80	SPRR4;FLG;CDSN;PDGFA;LCE1E;LCE1F;ASPRV1;LCE1C;LOR;LCE2D;LCE1D;LCE1A;LCE2B;SCEL;LCE1B;LCE2C;ACER1;LCE2A;LCE5A;TXNIP
Skin epidermis development (GO:0098773)	18/94	7.82E-09	1.18E-06	-2.84	FLG;CDSN;KRT2;KLK5;PDGFA;LAMC2;KRT31;ASPRV1;LOR;ALDH3A2;LCE2B;SCEL;CASP14;ACER1;DCT;KRT15;GJB5;TGM5
Epidermis development (GO:0008544)	14/68	1.39E-07	2.05E-05	-2.49	CDSN;KRT2;KLK5;LAMC2;KRT31;ALDH3A2;LCE2B;SCEL;CASP14;ACER1;DCT;KRT15;GJB5;TGM5
Epidermis morphogenesis (GO:0048730)	14/75	5.00E-07	7.18E-05	-2.54	CDSN;KRT2;KLK5;LAMC2;KRT31;ALDH3A2;LCE2B;SCEL;CASP14;ACER1;DCT;KRT15;GJB5;TGM5
Epidermal cell differentiation (GO:0009913)	17/124	2.91E-06	4.08E-04	-2.98	CDSN;KRT2;KLK5;LAMC2;KRT31;ALDH3A2;LCE2B;SCEL;ACER1;LGALS3;CASP14;UPK1A;DCT;KRT15;GJB5;ALDOC;TGM5
Peptide cross-linking (GO:0018149)	17/128	4.52E-06	6.19E-04	-3.22	SPRR4;FLG;KRT2;FN1;LCE1E;LCE1F;LCE1C;LOR;LCE2D;LCE1D;LCE1A;LCE2B;LCE1B;LCE2C;LCE2A;LCE5A;TGM5
Fat cell differentiation (GO:0045444)	9/44	2.57E-05	3.36E-03	-2.64	NR4A2;TFAP2B;NR4A1;EGR2;NR4A3;INHBB;KLF4;ALOXE3;FOXO1

KEGG up-regulated

Term	Overlap	P-value	Adjusted P-value	Z-score	Genes
Cell cycle_Homo sapiens_hsa04110	39/124	5.75E-14	1.57E-11	-1.73	RB1;HDAC2;PCNA;PRKDC;YWHAB;HDAC1;CUL1;TTK;SMC3;CDC20;CCNB2;CCNB1;CCND2;CDC45;PTTG1;ORC1;YWHAQ;CHEK1;E2F4;SKP2;BUB1;ANAPC7;PLK1;CDC7;CDC6;CDC25C;SMC1A;CDC25B;CCNA2;RBL1;DBF4;CCNE2;CDK1;MCM3;MCM5;MCM6;ANAPC1;MAD2L1;ATR
Ribosome biogenesis in eukaryotes_Homo sapiens_hsa03008	26/89	5.15E-09	4.72E-07	-1.96	RBM28;POP1;WDR3;HEATR1;FCF1;SPATA5;WDR43;EFTUD1;BMS1;RIOK1;UTP14A;NOP56;WDR36;NOP58;UTP6;RPP40;WDR75;REXO2;GNL2;GTPBP4;GNL3;CIRH1A;DKC1;XRN2;MPHOSPH10;NOP10
DNA replication_Homo sapiens_hsa03030	16/36	5.20E-09	4.72E-07	-1.87	RFC5;RFC3;FEN1;RFC4;RNASEH2A;PCNA;RFC1;PRIM1;POLD3;POLA1;POLA2;POLE2;MCM3;MCM5;MCM6;DNA2
Metabolic pathways_Homo sapiens_hsa01100	143/1239	1.01E-05	5.48E-04	-1.91	PANK2;GDA;TUSC3;ATP5C1;ENO1;COX6A1;EPRS;SAT1;CNDP2;NSDHL;PNP;PPAT;LIPG;NAMPT;CKMT1B;MCCC2;ALG8;ALG2;ACSL3;PGD;SDHB;ACLY;MTAP;FOLH1;MTHFD1;MTHFD2;SUCLG1;UQCRC2;LAP3;ALDH7A1;DGKH;DNMT1;RPN2;MAOB;AK2;PLA2G3;UAP1;FUT2;ADH7;ACAT2;UQCRH;ACACA;ADH5;PLD2;ATP5B;ALDH3B2;RDH11;ATP5E;PGK1;PNPO;ATP6V1D;COX10;PDHA1;GOT1;IDH1;PMM2;GOT2;ALOX15B;DHFR;EXT1;POLA1;SQLE;COQ3;POLA2;AKR1B10;CYCS;HPSE;COX7B;ALAS1;AMD1;PYGL;ATP5G3;PIGW;PIK3C2A;HK2;ATIC;SPTLC2;ALDH2;KYNU;ME1;HYAL4;REV3L;PGM2;MAN1A1;ACADM;DLAT;AASS;HIBCH;IDH3A;CERS3;TPI1;PLA2G4D;HMGCS1;UGT1A1;PLA2G4E;PGAM1;CTPS1;QRSL1;PKM;BDH1;PCCA;POLR1B;DPYD;AGPS;PGAM4;TKT;PIGF;GART;AGPAT5;NDUFB9;FH;PON2;PRIM1;NDUFB3;ALOX12B;UQCR10;NT5C2;TYMS;COX5A;PAPSS2;SRM;AGPAT4;POLD3;GCNT4;XDH;NDUFA9;GALNT6;RRM1;RRM2;MDH1;GK;GCH1;GALNT3;NDUFA4;CKMT1A;AGL;NDUFA1;UQCRHL;SUCLA2;CYP24A1;POLE2;NDUFAB1;POLR3G
Fanconi anemia pathway_Homo sapiens_hsa03460	15/53	1.37E-05	6.19E-04	-1.58	FANCI;BLM;FANCM;FANCL;REV1;FANCA;BRCA1;FANCB;BRCA2;BRIP1;RAD51C;FANCD2;UBE2T;REV3L;ATR
RNA transport_Homo sapiens_hsa03013	31/172	2.13E-05	8.28E-04	-1.72	EIF4A1;NUP107;POP1;EIF4A3;NUP160;PNN;TGS1;TPR;NUP88;EIF4E;UPF2;NDC1;RANBP2;EIF5B;PRMT5;EIF2B2;NCBP1;ELAC2;RPP40;THOC1;UPF3B;THOC2;EIF2S2;EIF2S1;EIF5;XPOT;EIF3J;EIF4G3;EIF3A;KPNB1;NUP37
Proteasome_Homo sapiens_hsa03050	13/44	3.08E-05	1.05E-03	-1.38	PSMD12;PSMD14;PSMA5;PSMB6;PSMA6;PSMA3;PSMA4;PSMB5;PSMA2;PSMC4;PSME4;PSME2;PSMD1
Influenza A_Homo sapiens_hsa05164	27/175	9.36E-04	1.40E-02	-1.53	CXCL8;TMPRSS4;ADAR;IFIH1;TBK1;TNFSF10;CASP1;TRIM25;KPNA2;HSPA8;IL33;RSAD2;DDX58;STAT1;IFNGR1;STAT2;MX1;EIF2AK2;TNFRSF10A;EIF2S1;NFKB1;CXCL10;OAS1;OAS2;OAS3;CYCS;MYD88
Oxidative phosphorylation_Homo sapiens_hsa00190	22/133	1.06E-03	1.45E-02	-1.34	NDUFA9;NDUFB9;COX7B;NDUFA4;NDUFB3;NDUFA1;ATP5C1;UQCR10;ATP5G3;COX6A1;ATP12A;SDHB;COX5A;UQCRH;UQCRHL;ATP5B;PPA1;ATP5E;NDUFAB1;UQCRC2;ATP6V1D;COX10
TGF-beta signaling pathway_Homo sapiens_hsa04350	7/84	3.46E-02	3.30E-01	-1.18	BMP2;SMURF2;FST;ID4;INHBB;DCN;TGFBR2

KEGG down-regulated

Term	Overlap	P-value	Adjusted P-value	Z-score	Genes
Circadian rhythm_Homo sapiens_hsa04710	8/30	9.05E-06	2.17E-03	-1.97	CRY2;BHLHE41;CRY1;RORC;RORA;NR1D1;NPAS2;ARNTL
Melanogenesis_Homo sapiens_hsa04916	12/100	2.98E-04	3.58E-02	-1.91	DCT;PRKCB;FZD7;WNT7B;KIT;TYRP1;FZD8;MITF;ADCY2;FZD10;TYR;WNT2
Basal cell carcinoma_Homo sapiens_hsa05217	7/55	3.82E-03	1.53E-01	-1.70	BMP2;FZD7;WNT7B;FZD8;FZD10;WNT2;GLI2
MAPK signaling pathway_Homo sapiens_hsa04010	18/255	6.34E-03	2.14E-01	-1.85	DUSP5;NTRK2;JUN;JUND;GADD45B;PRKCB;DUSP1;CACNA2D1;PDGFA;FOS;HSPA2;CACNA1H;TGFBR2;NR4A1;DUSP10;DDIT3;FGF22;HSPA1A
AGE-RAGE signaling pathway in diabetic complications_Homo sapiens_hsa04933	9/101	1.19E-02	2.51E-01	-1.78	EGR1;JUN;CCND1;PRKCB;FN1;BCL2;F3;FOXO1;TGFBR2
HTLV-I infection_Homo sapiens_hsa05166	17/258	1.48E-02	2.51E-01	-1.67	EGR1;EGR2;HLA-DRB5;JUN;FZD7;WNT7B;FZD8;PDGFA;NFATC2;ADCY2;FZD10;FOS;TGFBR2;ZFP36;CCND1;WNT2;ATF3
Wnt signaling pathway_Homo sapiens_hsa04310	11/142	1.57E-02	2.51E-01	-1.52	JUN;CCND1;PRKCB;FZD7;WNT7B;CTNNBIP1;CSNK2A2;FZD8;NFATC2;FZD10;WNT2
Apoptosis_Homo sapiens_hsa04210	10/140	3.37E-02	3.30E-01	-1.40	JUN;GADD45B;DDIT3;BCL2;PMAIP1;CTSH;CTSV;CTSF;FOS;SPTAN1
Tight junction_Homo sapiens_hsa04530	10/139	3.23E-02	3.30E-01	-1.22	RAB3B;OCLN;PRKCB;CLDN8;CSNK2A2;CLDN23;MYH14;MYL9;CLDN1;SPTAN1
TGF-beta signaling pathway_Homo sapiens_hsa04350	7/84	3.46E-02	3.30E-01	-1.18	BMP2;SMURF2;FST;ID4;INHBB;DCN;TGFBR2ù

Table SIII. List of 36 datasets with differentially expressed genes (DEGs) in cytokine-treated cultured keratinocytes, obtained from the Gene Expression Omnibus (GEO) database

Experiment	Cell type	Array platform	References
IL1a (25 ng|48 h|GSE9120)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Yano et al. 2008 (J Cell Physiol 214:1-13)
IL1b (10 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL4 (20 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
IL13 (20 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
IL17A (200 ng|24 h|GSE12109)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Nograles et al. 2008 (Br J Dermatol 159:1092-102)
IL17A (200 ng|24 h|GSE24767)	Primary keratinocytes	Illumina HumanHT-12 V3.0 expression beadchip (GPL6947)	Chiricozzi et al. 2011 (J Invest Dermatol 131:677-87)
IL17A (20 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
IL17C (500 ng|3 h|GSE32620)	Primary keratinocytes	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (GPL6480)	Ramirez-Carrozzi et al. 2011 (Nat Immunol 12:1159-66)
IL17C (500 ng|24 h|GSE32620)	Primary keratinocytes	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (GPL6480)	Ramirez-Carrozzi et al. 2011 (Nat Immunol 12:1159-66)
IL19 (20 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL20 (20 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL22 (20 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL22 (200 ng|24 h|GSE12109)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Nograles et al. 2008 (Br J Dermatol 159:1092-102)
IL24 (20 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL26d (20 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IL36RA (5 µg|24 h|GSE25400)	Reconsituted epidermis	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Johnston et al. 2011 (J Immunol 186:2613-22)
IL36a (5 µg|24 h|GSE25400)	Reconsituted epidermis	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Johnston et al. 2011 (J Immunol 186:2613-22)
IL36b (5 µg|24 h|GSE25400)	Reconsituted epidermis	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Johnston et al. 2011 (J Immunol 186:2613-22)
IL36g (5 µg|24 h|GSE25400)	Reconsituted epidermis	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Johnston et al. 2011 (J Immunol 186:2613-22)
IFNa (20 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
IFNg (1 IU|24 h|GSE1132)	Primary keratinocytes	Affymetrix Human Genome U133A/U133B Array (GPL96/GPL97)	Mansourian et al. 2004 (Bioinformatics 20:2726-37)
IFNg (48 h|GSE440)	Primary keratinocytes	Affymetrix Human Genome U95 Version 2 Array (GPL8300)	Banno et al. 2003 (Antivir Ther 8:541-54)
IFNg (10 ng|4 d|GSE7216)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Sa et al. 2007 (J Immunol 178:2229-40)
IFNg (20 ng|24 h|GSE12109)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Nograles et al. 2008 (Br J Dermatol 159:1092-102)
IFNg (20 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
TGFa (20 ng|30 min|GSE8531)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Cheng et al. 2008 (J Invest Dermatol 128:1981-90)
TGFa (20 ng|1 h|GSE8531)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Cheng et al. 2008 (J Invest Dermatol 128:1981-90)
TGFa (20 ng|2 h|GSE8531)	Primary keratinocytes	Affymetrix Human Genome U133A 2.0 Array (GPL571)	Cheng et al. 2008 (J Invest Dermatol 128:1981-90)
TNFa (1 ng|24 h|GSE24767)	Primary keratinocytes	Illumina HumanHT-12 V3.0 expression beadchip (GPL6947)	Chiricozzi et al. 2011 (J Invest Dermatol 131:677-87)
TNFa (10 ng|24 h|GSE24767)	Primary keratinocytes	Illumina HumanHT-12 V3.0 expression beadchip (GPL6947)	Chiricozzi et al. 2011 (J Invest Dermatol 131:677-87)
TNFa (10 ng|24 h|GSE36287)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
TNFa (20 ng|20 h|GSE36387)	Primary keratinocytes	Affymetrix Human Genome U133 Plus 2.0 Array (GPL570)	Swindell et al. 2012 (PLoS ONE 7:e34594)
IL17A+TNF (1 ng|24 h|GSE24767)	Primary keratinocytes	Illumina HumanHT-12 V3.0 expression beadchip (GPL6947)	Chiricozzi et al. 2011 (J Invest Dermatol 131:677-87)
IL17A+TNF (10 ng|24 h|GSE24767)	Primary keratinocytes	Illumina HumanHT-12 V3.0 expression beadchip (GPL6947)	Chiricozzi et al. 2011 (J Invest Dermatol 131:677-87)
EGF (10 ng|48 h|50%|GSE32217)	Primary keratinocytes	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Tran et al. 2012 (Physiol Genomics 44(8):455-69)
EGF (10 ng|48 h|100%|GSE32217)	Primary keratinocytes	Affymetrix Human Gene 1.0 ST Array (GPL6244)	Tran et al. 2012 (Physiol Genomics 44(8):455-69)

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

Supplementary Table S4. List of differentially expressed genes in psoriasis keratinocytes (PP vs . H) in proximity to psoriasis-associated SNPs (overlapping with a region +/- 250 kbp from the SNP).

Gene Name	SNP(s)
GJB2	rs3751385
RAD50	rs1295685, rs20541
IFI16	rs2276405
IFIH1	rs17716942, rs17715343, rs13431841
GJB6	rs3751385
DDX58	rs11795343
SCD	rs61871342
FUT2	rs492602
PUS10	rs4672409, rs702873, rs62149416
DNMT1	rs280519, rs12720356, rs34536443
STAT2	rs2066808, rs201230143, rs2066819
GPX3	rs17728338, rs999556, rs146571698, rs3762999, rs2233278, rs10036748
REV3L	rs240993, rs458017
GART	rs9808753, rs3174808
IVL	rs41268474, rs76337351
IL12RB2	rs2201841, rs113935720, rs9988642
ID1	rs6088273
TIMELESS	rs2066808, rs201230143, rs2066819
PTTG1	rs2431697
CCDC58	rs1042636
DHFR	rs249038
RNF213	rs11652075
TUBG1	rs963986
RDX	rs4561177, rs7126662
SYNE2	rs2781377
C18orf54	rs545979
NFKB1	rs1020760
NCAPD2	rs2243750, rs758739
CSTA	rs1042636
ZFYVE16	rs249038
PPIF	rs1250546, rs1250544
E2F3-IT1	rs4712528
PTPN2	rs559406
DENND1B	rs2477077
SUCO	rs12118303
PSMA6	rs12884468, rs12586317, rs8016947
DONSON	rs9808753, rs3174808
GRHL3	rs4090311, rs7552167, rs4649203
CLIP1	rs11059675
IPO7	rs10743108
STAT3	rs963986, rs3869549
ALDH2	rs11065979
UBLCP1	rs12188300, rs918520, rs6887695, rs1473247, rs10076782, rs953861, rs7709212, rs2546890, rs3213094, rs2288831, rs3212227, rs2082412
CHCHD1	rs2675669, rs2675662
NOP2	rs2243750, rs758739
CDC37	rs34536443, rs12720356, rs280519
RP11-464F9.9	rs2675669, rs2675662
GM2A	rs10036748, rs2233278, rs3762999, rs146571698, rs999556, rs17728338
PRKCI	rs6444895
PA2G4	rs201230143, rs2066808
FAM162A	rs1042636
PPP2R3C	rs12586317
CHUK	rs61871342
SERBP1	rs2201841, rs113935720, rs9988642
ILF3	rs873016, rs892085
EIF4A3	rs11652075
CTF1	rs12445568, rs10782001, rs34033855, rs12924903
SCARNA11	rs2243750, rs758739
COX4I2	rs6088273
EFEMP2	rs610037, rs118086960
GSDMA	rs12936231, rs10852936
THRA	rs12936231, rs10852936
PPP1R15A	rs492602
PRSS8	rs12924903, rs10782001, rs12445568
ZNF415	rs9304742
DNAJB4	rs34517439
PSORS1C2	rs10484554, rs4406273, rs12191877, rs12189871, rs1265181
NR1D1	rs12936231, rs10852936
IRF4	rs9504361

SCARNA10	rs2243750, rs758739
TNFAIP3	rs610604, rs582757
CST6	rs610037, rs118086960
LCE5A	rs41268474, rs10888503, rs4845454, rs1886734, rs6677595, rs4112788, rs4085613, rs10888501
SERPINB7	rs514315
LCE1E	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE1A	rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
CRCT1	rs76337351, rs41268474, rs10888503, rs4845454, rs1886734, rs6677595, rs4112788, rs4085613, rs10888501
LCE2D	rs10888501, rs76337351, rs4085613, rs4112788, rs41268474, rs6677595, rs1886734, rs4845454, rs10888503
LCE1B	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
SPRR4	rs76337351
LCE1C	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE6A	rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE1F	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE1D	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE2A	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs76337351, rs41268474
KPRP	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE2B	rs10888501, rs4085613, rs4112788, rs76337351, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474
LCE2C	rs10888501, rs4085613, rs4112788, rs76337351, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474
FLG2	rs4112788, rs4085613, rs10888501
C1orf68	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs76337351, rs41268474
PARP9	rs1042636
ATP10B	rs2431697
DPP4	rs17715343, rs13431841
REV3L	rs9481169, rs13210247, rs33980500
IL12RB2	rs72933970
SLC16A10	rs458017, rs240993
TUBG2	rs963986
MSH3	rs249038
PA2G4	rs2066819
PPP2R3C	rs8016947
FYN	rs33980500, rs13210247, rs9481169
USP54	rs2675662
EGR2	rs2944542
C14orf64	rs142903734
LCE5A	rs76337351
FLG	rs10888501
LCE1A	rs4085613

Supplementary Table S4. List of differentially expressed genes in psoriasis keratinocytes (PP vs . PN) in proximity to psoriasis-associated SNPs (overlapping with a region +/- 250 kbp from the SNP).

Gene Name	SNP(s)
GJB2	rs3751385
GJB6	rs3751385
IFI16	rs2276405
SCD	rs61871342
ID1	rs6088273
IFIH1	rs17716942, rs17715343, rs13431841
GPX3	rs17728338, rs999556, rs146571698, rs3762999, rs2233278, rs10036748
FUT2	rs492602
DDX58	rs11795343
IVL	rs41268474, rs76337351
SPRR1A	rs76337351
RAD50	rs1295685, rs20541
STAT2	rs2066808, rs201230143, rs2066819
DNMT1	rs280519, rs12720356, rs34536443
PPIF	rs1250546, rs1250544
CSTA	rs1042636
TIMELESS	rs2066808, rs201230143, rs2066819
TUBG1	rs963986
PTTG1	rs2431697
PSMA6	rs12884468, rs12586317, rs8016947
GART	rs9808753, rs3174808
DHFR	rs249038
PUS10	rs4672409, rs702873, rs62149416
EIF4A3	rs11652075
CHCHD1	rs2675669, rs2675662
STAT3	rs963986, rs3869549
IL12RB2	rs2201841, rs113935720, rs9988642
CCDC58	rs1042636
GRHL3	rs4090311, rs7552167, rs4649203
RNF213	rs11652075
NFKB1	rs1020760
E2F3-IT1	rs4712528
RNU7-40P	rs2066808, rs201230143, rs2066819

FAM162A	rs1042636
STIP1	rs645078, rs694739, rs887314
NOP2	rs2243750, rs758739
NCAPD2	rs2243750, rs758739
PA2G4	rs201230143, rs2066808
GM2A	rs10036748, rs2233278, rs3762999, rs146571698, rs999556, rs17728338
SUCO	rs12118303
C18orf54	rs545979
NDUFB6	rs11795343
PTPN2	rs559406
REV3L	rs240993, rs458017
DNAJB4	rs34517439
GIPC2	rs34517439
CST6	rs610037, rs118086960
SCARNA11	rs2243750, rs758739
SCARNA10	rs2243750, rs758739
WEE1	rs10743108
NR1D1	rs12936231, rs10852936
LCE5A	rs41268474, rs10888503, rs4845454, rs1886734, rs6677595, rs4112788, rs4085613, rs10888501
SERPINB7	rs514315
LCE1E	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
SPRR4	rs76337351
LCE1A	rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
CRCT1	rs76337351, rs41268474, rs10888503, rs4845454, rs1886734, rs6677595, rs4112788, rs4085613, rs10888501
LCE1B	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE2D	rs10888501, rs76337351, rs4085613, rs4112788, rs41268474, rs6677595, rs1886734, rs4845454, rs10888503
LCE1C	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE1D	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE6A	rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE1F	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE2A	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs76337351, rs41268474
KPRP	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474, rs76337351
LCE2B	rs10888501, rs4085613, rs4112788, rs76337351, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474
LCE2C	rs10888501, rs4085613, rs4112788, rs76337351, rs6677595, rs1886734, rs4845454, rs10888503, rs41268474
C1orf68	rs10888501, rs4085613, rs4112788, rs6677595, rs1886734, rs4845454, rs10888503, rs76337351, rs41268474
FLG2	rs4112788, rs4085613, rs10888501
PARP9	rs1042636
ATP10B	rs2431697
TUBG2	rs963986
IL12RB2	rs72933970
PA2G4	rs2066819
CRYL1	rs3751385
REV3L	rs9481169, rs13210247, rs33980500
LCE5A	rs76337351
C14orf64	rs142903734
LCE1A	rs4085613
FLG	rs10888501

Supplementary Table S4. List of differentially expressed genes in psoriasis keratinocytes (PN vs . H) in proximity to psoriasis-associated SNPs (overlapping with a region +/- 250 kbp from the SNP).

Gene Name	SNP(s)
TNFAIP3	rs610604, rs582757
EGR2	rs2944542

The format and content has not been edited by ActaDV.

Supplementary Table S5. Transcription factors with overrepresented binding site motifs among genes differentially expressed in psoriatic keratinocytes (PP vs. H) genes differentially expressed in psoriatic keratinocytes (PP vs. H).

Transcription Factor	TF gene name	N. of target genes	p-value	z-score
E2F4	E2F transcription factor 4	121	2.14E-59	22.72
FOXM1	Forkhead box M1	62	9.53E-37	18.52
HIF1A	Hypoxia inducible factor 1 alpha subunit	151	2.51E-40	16.50
c-Jun	Jun proto-oncogene, AP-1 transcription factor subunit	160	1.97E-38	15.83
IRF4	Interferon regulatory factor 4	100	1.86E-31	14.87
STAT3	Signal transducer and activator of transcription 3	133	2.66E-30	13.86
b-Myb	MYB proto-oncogene like 2	38	2.86E-20	13.06
STAT1	Signal transducer and activator of transcription 1	82	9.35E-25	12.98
NF-kB1 (p50)	Nuclear factor kappa B subunit 1	91	5.06E-23	12.14
KLF4	Kruppel like factor 4	69	5.04E-19	11.07
E2F8	E2F transcription factor 8	16	3.34E-12	10.71
EGR1	Early growth response 1	82	2.42E-18	10.53
FKHR	Forkhead box O1	62	4.85E-17	10.40
E2F7	E2F transcription factor 7	19	2.79E-11	9.54
STAT2	Signal transducer and activator of transcription 2	24	5.35E-12	9.50
MITF	Melanogenesis associated transcription factor	35	6.17E-13	9.33
GATA-3	GATA binding protein 3	94	4.63E-15	9.06
C/EBP zeta	DNA damage inducible transcript 3	25	4.61E-10	8.15
BMAL1	Aryl hydrocarbon receptor nuclear translocator like	28	3.28E-10	8.07
NF-kB p50/p50	Nuclear receptor subfamily 1 group D member 1	20	2.93E-09	7.97
XBP1	X-box binding protein 1	32	1.54E-09	7.48
JunD	JunD proto-oncogene, AP-1 transcription factor subunit	36	5.31E-09	7.03
ATF-3	Activating transcription factor 3	32	8.53E-09	7.02
c-Fos	Fos proto-oncogene, AP-1 transcription factor subunit	53	2.68E-09	6.88
CLOCK	Clock circadian regulator	20	2.39E-07	6.56
REV-ERBalpha	Nuclear receptor subfamily 1 group D member 1	14	2.47E-06	6.18
GLI-2	GLI family zinc finger 2	14	4.94E-06	5.91
ZNF652	Zinc finger protein 652	5	1.50E-04	5.86
ZNF145	Zinc finger and BTB domain containing 16	12	1.92E-05	5.55
NF-kB1 (p105)	Nuclear receptor subfamily 1 group D member 1	16	9.16E-06	5.54
TRPS1	Transcriptional repressor GATA binding 1	7	1.07E-04	5.47
ROR-alpha	RAR related orphan receptor A	19	7.92E-06	5.44
EGR2 (Krox20)	Early growth response 2	21	7.70E-06	5.37
ESE3	ETS homologous factor	8	9.68E-05	5.33
SOX4	SRY-box 4	19	4.12E-05	4.85
LHX2	LIM homeobox 2	45	1.46E-05	4.75
SMARCA3	Helicase like transcription factor	3	3.75E-03	4.54
TR-alpha	Thyroid hormone receptor, alpha	19	1.49E-04	4.39
HEY2	Hes related family bHLH transcription factor with YRPW motif 2	7	1.65E-03	4.00
SIP1 (ZFHX1B)	Zinc finger E-box binding homeobox 2	7	1.65E-03	4.00
DACH1	Dachshund family transcription factor 1	4	4.31E-03	3.99
ELF1	Elongation Factor Like GTPase 1 (EFL1)	14	6.44E-04	3.97
ROR-gamma	RAR related orphan receptor C	8	1.59E-03	3.91
GATA-6	GATA binding protein 6	17	6.12E-04	3.90
SOHLH1	Spermatogenesis and oogenesis specific basic helix-loop-helix 1	2	1.99E-02	3.71
PAX3	Paired box 3	8	2.65E-03	3.65
CTIP2	Atlastin GTPase 1	7	4.94E-03	3.40
SOX5	SRY-box 5	6	7.87E-03	3.23
TIEG1	Kruppel like factor 10	6	9.27E-03	3.14
EGR3	Early growth response 3	6	1.09E-02	3.04
HES1	Hes family bHLH transcription factor 1	11	7.33E-03	2.97
FosB	FosB proto-oncogene, AP-1 transcription factor subunit	9	1.24E-02	2.78
NF-AT1(NFATC2)	Nuclear factor of activated T cells 2	14	1.11E-02	2.69
SMAD1	SMAD family member 1	15	1.65E-02	2.48

54 transcription factors whose binding site motifs showed the highest enrichment are shown (TF = transcription factor; N. of target genes = number of target genes in PP vs H comparison; p-value = for the given predicted N. of target genes; z-score = Actual N. of target genes – Expected N. of target genes) / sqrt(variance)).