

Supplemental Figures

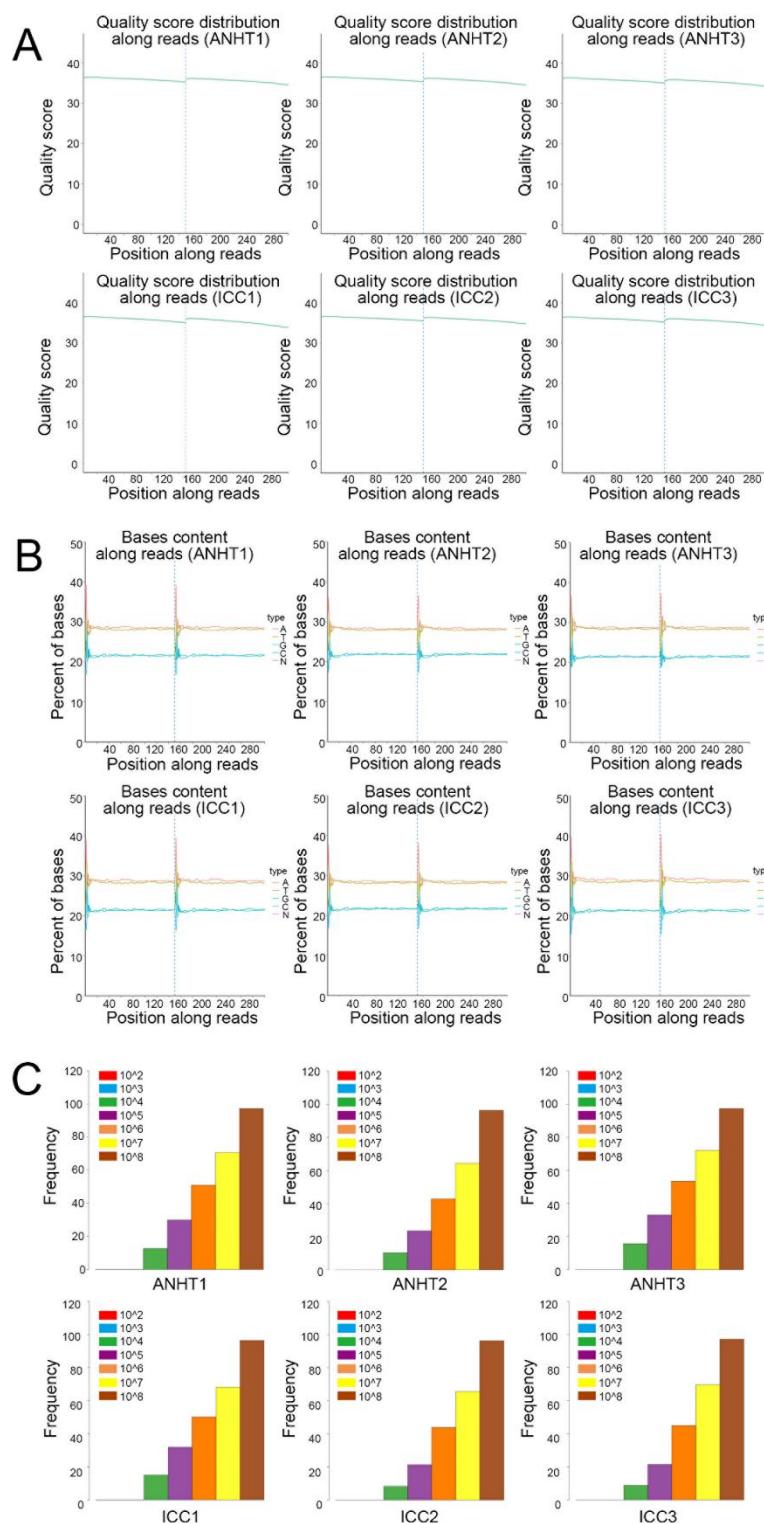


Figure S1

Figure S1. Sequencing data quality assessment. (A) Sequencing quality distribution check. The sequencing error rate of each base is obtained by the sequencing Phred score (Qphred), which is transformed by the formula ($Q_{phred} = -10\log_{10}(e)$), and the Phred value is calculated through a probability model in the base calling process, which can accurately predict the error rate of base

discrimination. The correspondence between incorrect base recognition rate and Qphred are as follows: Q10-10%; Q20-20%; Q30-30%; Q40-40%. (B) GC content distribution. GC content distribution check is used to detect whether AT and GC separation occurs. **c** Insert fragment statistics. According to the comparison results, the length of inserted fragments of all sample are counted. Generally, the cumulative frequency of the fragments with insert sizes of 100bp, 1000bp, 10,000bp, 100,000bp, 1,000,000bp, 10,000,000bp and 100,000,000bp is counted. The cumulative frequency of large inserts was higher, which indicated that the library captures more long-distance interactions.

Figure S2

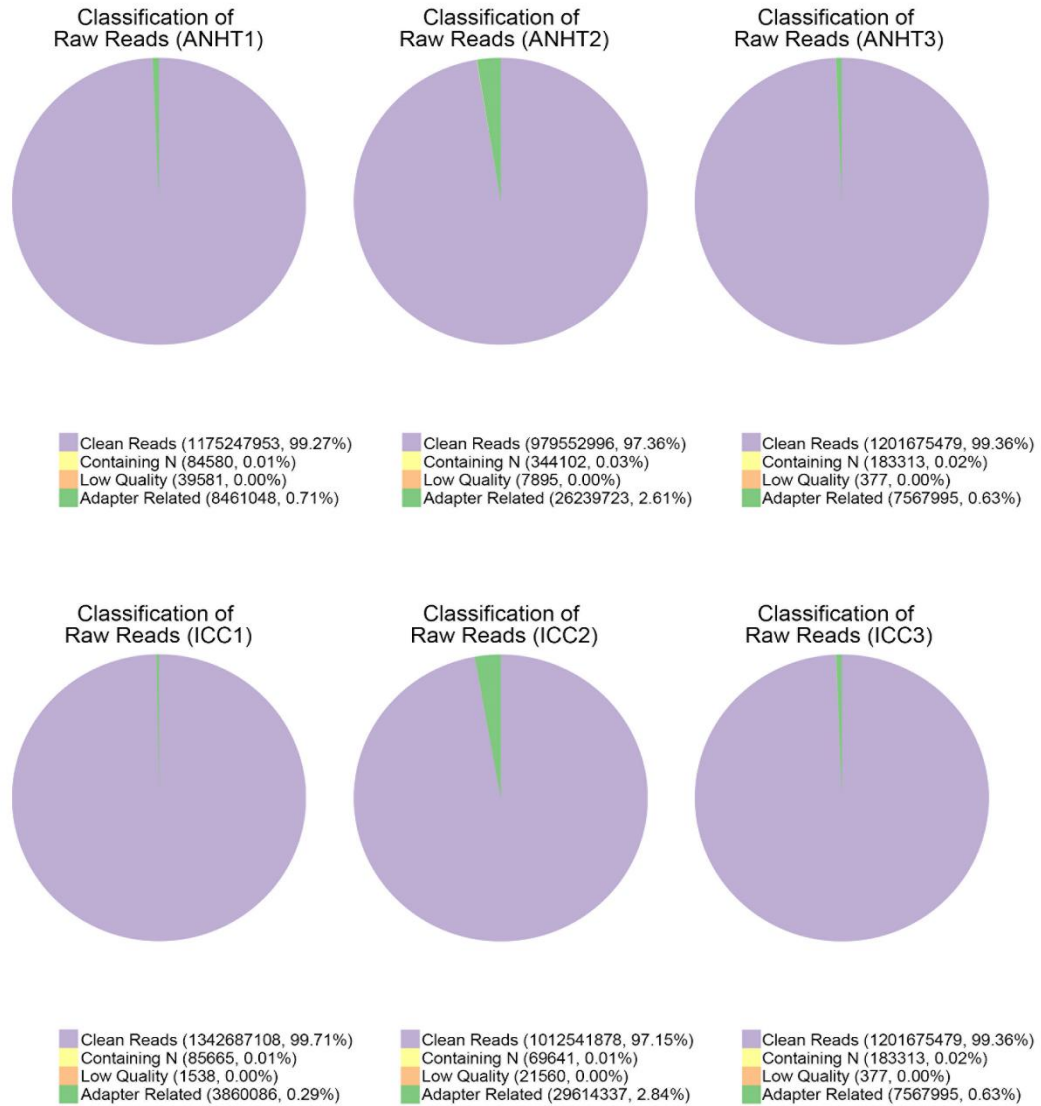


Figure S2. Raw reads information. Read pairs with connectors (Adapter Related: green region), read pairs with N content exceeding 10% of the length of the reads (Containing N: yellow region) and single-end sequencing read pairs with low quality (Quality score ≤ 10) bases exceeding 50% of the length of the read pairs (Low Quality: orange region) were removed. Clean reads were obtained (purple region).

Figure S3

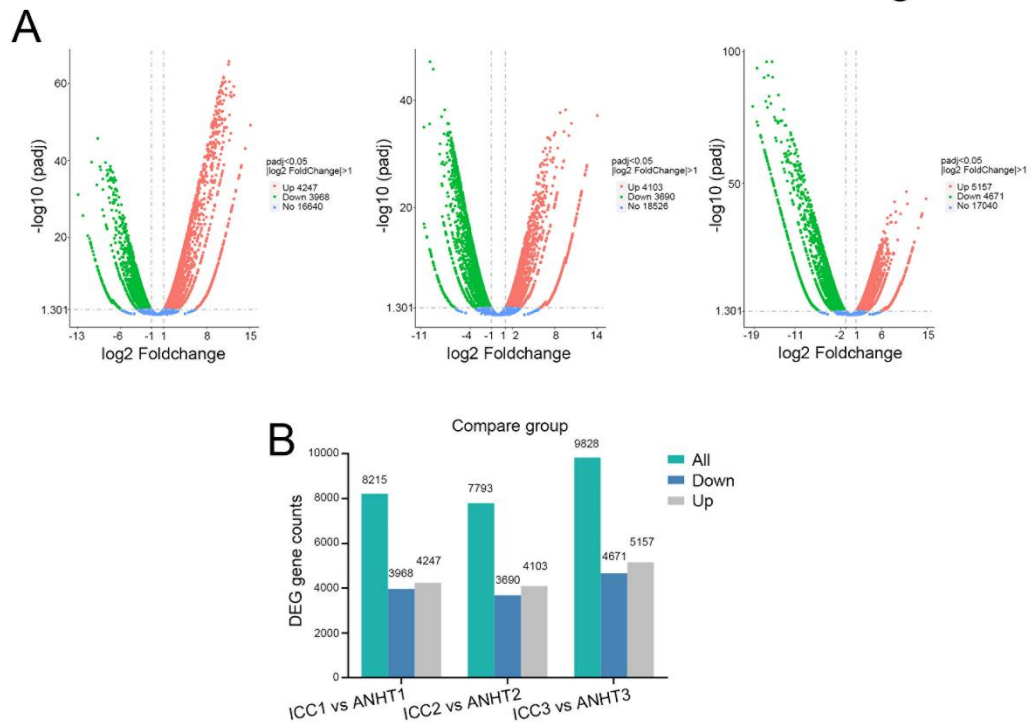


Figure S3. The differential expression analysis. (A-B) The volcano plot and column chart illustrate the gene expression difference between ANHT and ICC.

Figure S4

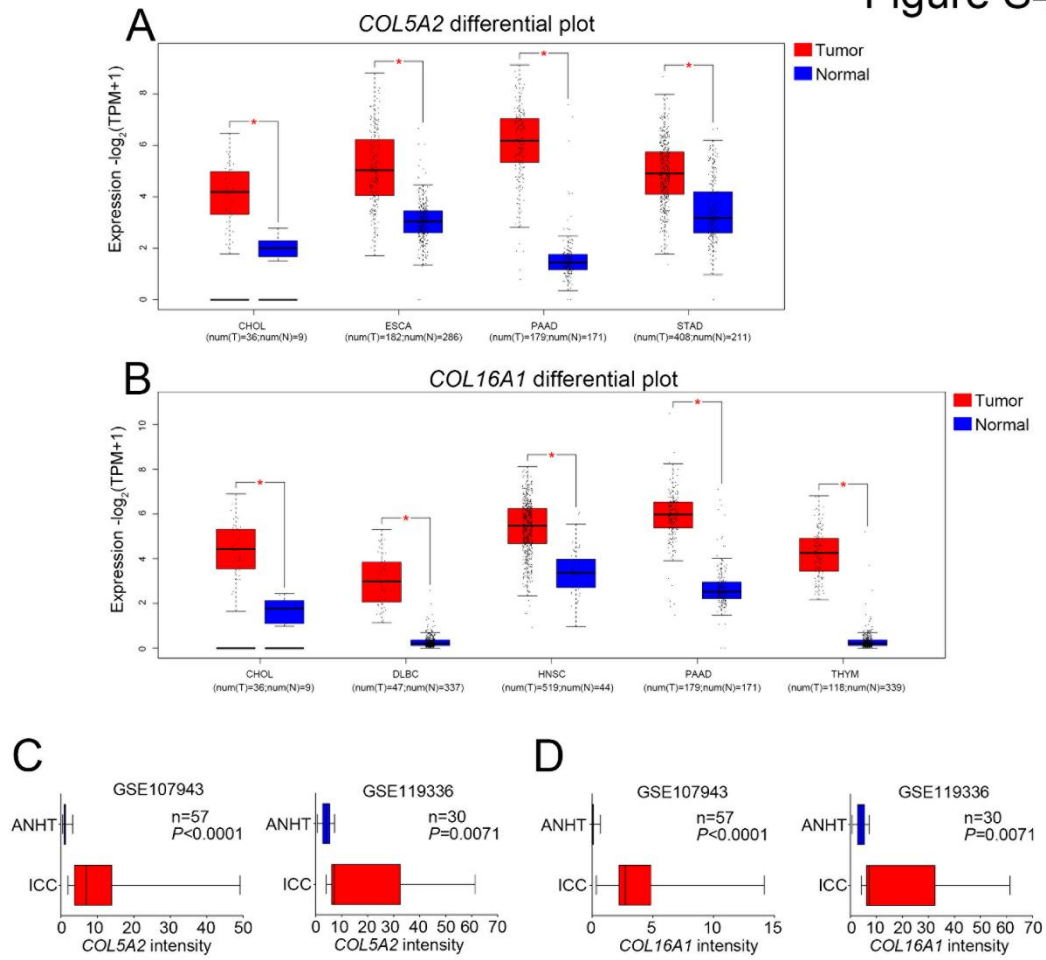


Figure S4. The expression of *COL5A2* and *COL16A1* are up-regulated in ICC. (A-B) The analysis of the expression of *COL5A2* and *COL16A1* from TCGA database. (C) The expression of *COL5A2* and *COL16A1* was analyzed according to the data from GSE107943 and GSE119336.

Figure S5

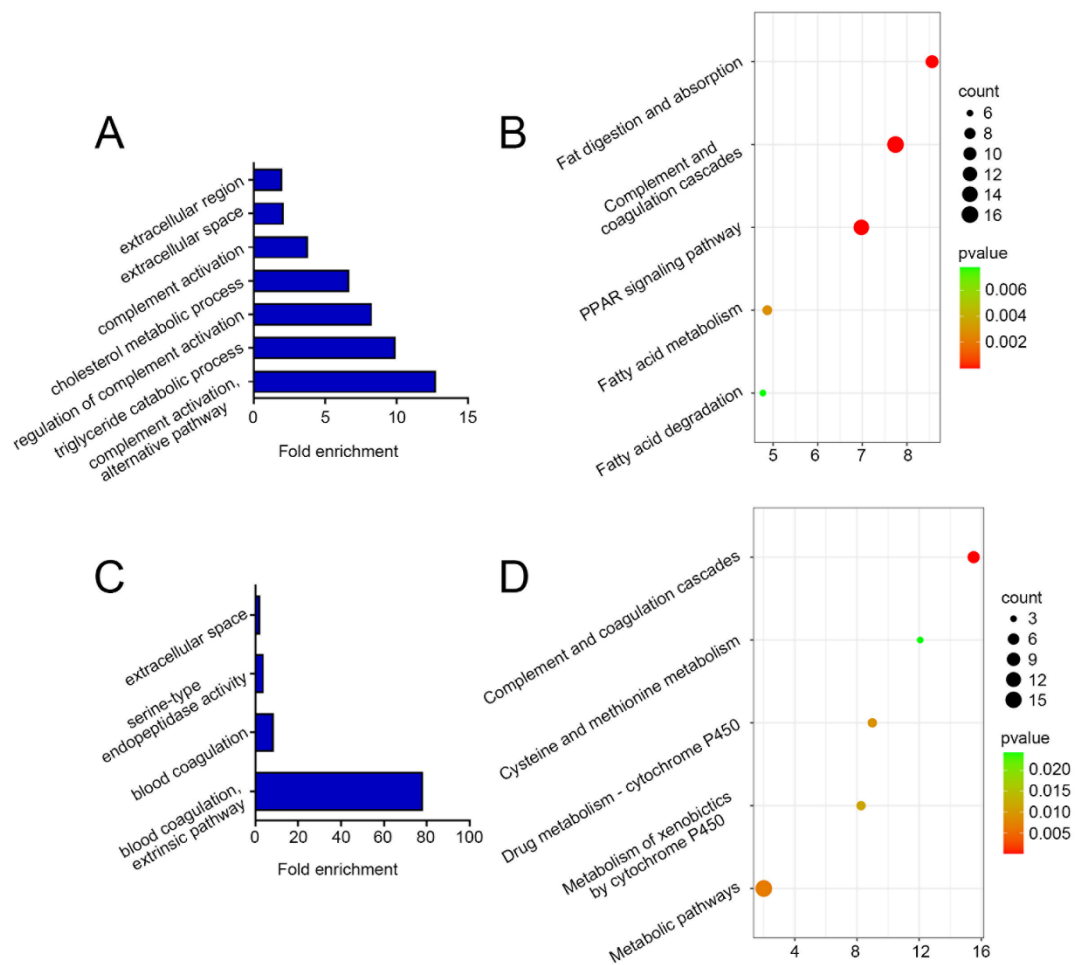


Figure S5. Enrichment of differentially downregulated genes in regions of differential chromosomal interaction and chromosomal structural variation. (A-B) Enrichment analysis of GO (A) and KEGG (B) terms for genes associated with differential intra-chromosomal interaction regions; (C-D) Enrichment analysis of GO (C) and KEGG (D) terms for genes associated with differential inter-chromosomal interaction regions.

Figure S6



Figure S6. TAD and TAD boundaries in three paired ANHT and ICC samples.

Figure S7

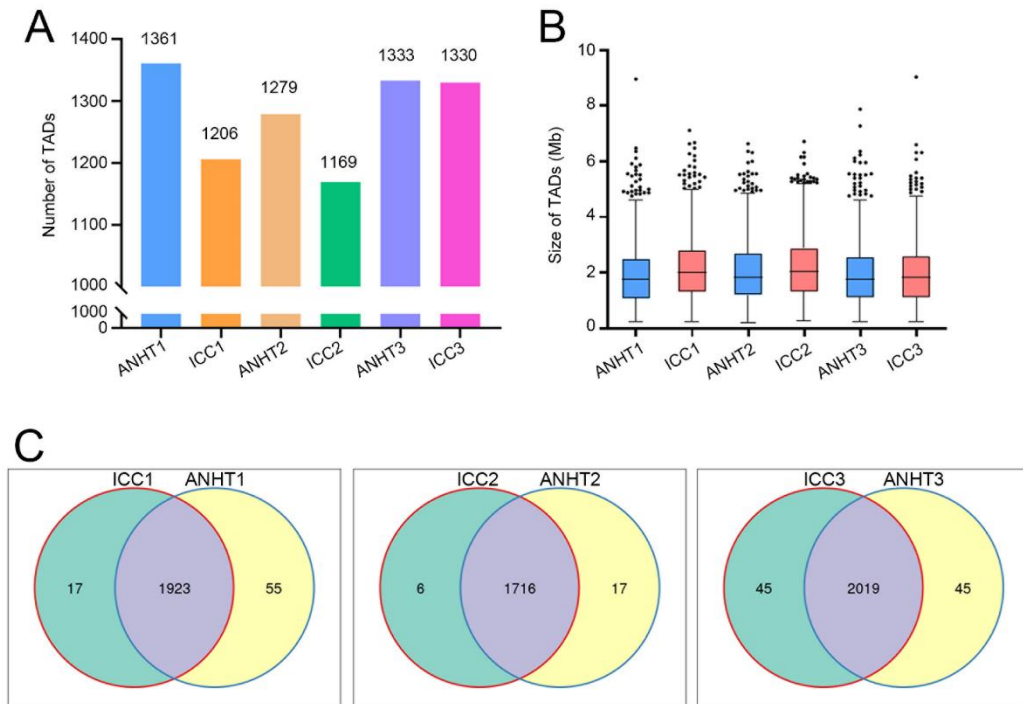


Figure S7. The number and size of TADs in three paired ANHT and ICC samples. (A-B) Chart of the number (A) and size (B) of TADs. c Venn diagram representing overlapping and specific TADs boundaries in ANHT and ICC.

Figure S8

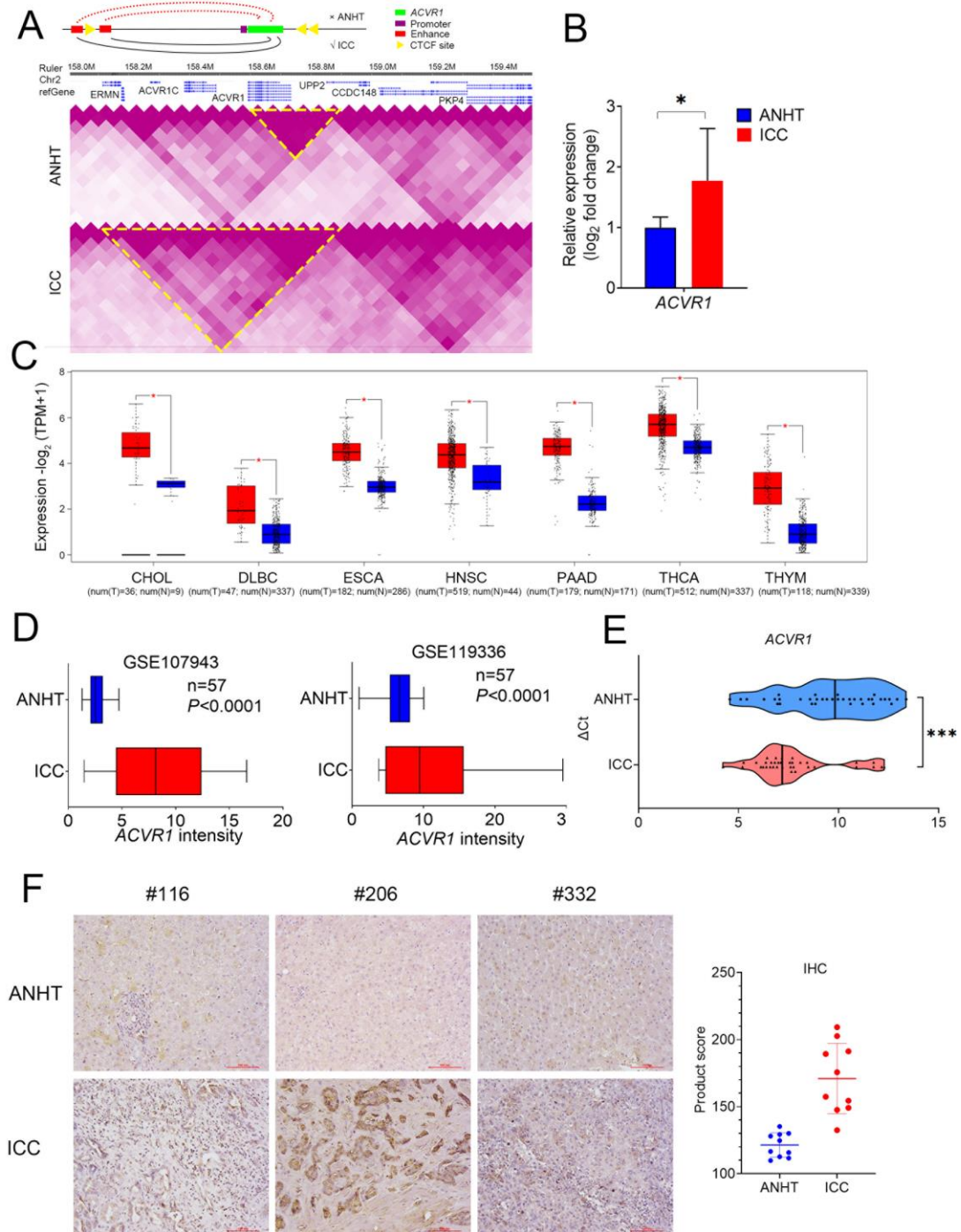


Figure S8. Fusion of topologically associated domain boundaries upregulates the expression of *ACVR1* in ICC. (A) The tumor-specific TAD boundary located on *ACVR1* (chr2:158,592,958-158,732,374) was visualized in a two-dimensional interaction matrix via WashU browser. With yellow triangles representing CTCF binding sites, and red, purple and

green squares representing enhancers, promoters, and targeted genes, respectively. The black lines indicate normal interactions within the same TAD boundary, while the red lines indicate failed interactions that are isolated by different TAD boundaries. (B) In RNA-seq analysis, the expression of *ACVR1* was up-regulated in ICC samples compared to ANHT samples. (C) The expression of *ACVR1* only highly expressed in CHOL, but also in ESCA, PAAD and THYM compared to those of corresponding normal tissues. (D) The expression of *ACVR1* was higher in ICC samples than those in ANHT samples in GSE107943 and GSE119336. (E) The mRNA expression levels of *HOPX* in ANHT and ICCs were validated by qRT-PCR (n=20), Student t test. (F) The expression of *ACVR1* was higher in ICC samples than that in ANHT as assessed by immunohistochemistry (n=10). *ACVR1* staining was measured by multiplying the numerical score of the staining intensity (none=1, weak=2, moderate=3, strong=4) with the staining percentage (0%–100%), resulting in an overall product score, Student t test. Data are presented as mean $\pm$ SD. * $P < 0.05$; ** $P < 0.01$.

Table S1. Clinical characteristics of the intrahepatic cholangiocarcinoma patients.

Patient ID	Gender	age (years)	pCIS +	WHO	pT	pN	TNM stage	HBV infection	Experimental type
ICC1	Male	49	CIS	I	T1	N0	T1N0M0	+	Hi-C and RNA-seq
ICC2	Female	64	CIS	III	T3	N0	T3N0M0	+	Hi-C and RNA-seq
ICC3	Male	45	CIS	II	T2	N0	T2N0M0	+	Hi-C and RNA-seq
ICC4	Male	52	CIS	III	T3	N0	T3N0M0	+	qRT-PCR
ICC5	Male	53	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC6	Male	48	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC7	Male	50	CIS	III	T3	N0	T3N0M0	+	qRT-PCR
ICC8	Female	69	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC9	Male	51	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC10	Female	52	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC11	Female	53	CIS	III	T3	N0	T3N0M0	+	qRT-PCR
ICC12	Male	57	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC13	Female	51	CIS	III	T3	N1	T3N1M1	+	qRT-PCR
ICC14	Female	64	CIS	III	T3	N0	T3N0M0	+	qRT-PCR
ICC15	Male	61	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC16	Male	50	CIS	III	T3	N0	T3N0M0	+	qRT-PCR
ICC17	Male	52	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC18	Female	64	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC19	Male	67	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC20	Female	62	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC21	Female	43	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC22	Male	48	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC23	Female	62	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC24	Female	39	CIS	III	T3	N1	T3N1M1	-	qRT-PCR
ICC25	Male	46	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC26	Male	57	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC27	Male	55	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC28	Female	54	CIS	III	T3	N1	T3N1M0	-	qRT-PCR
ICC29	Male	49	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC30	Male	45	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC31	Male	62	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC32	Female	54	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC33	Male	49	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC34	Female	54	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC35	Female	61	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC36	Male	36	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC37	Female	61	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC38	Female	41	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC39	Male	63	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC40	Male	55	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC41	Male	61	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC42	Female	54	CIS	III	T3	N1	T3N1M0	-	qRT-PCR
ICC43	Female	52	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC44	Female	63	CIS	III	T3	N1	T3N1M0	+	qRT-PCR
ICC45	Female	63	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC46	Male	52	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC47	Female	44	CIS	III	T3	N1	T3N1M0	-	qRT-PCR
ICC48	Female	54	CIS	III	T3	N0	T3N0M0	-	qRT-PCR
ICC49	Female	69	CIS	III	T3	N1	T3N1M0	-	qRT-PCR
ICC50	Male	56	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC51	Male	57	CIS	II	T2	N0	T2N0M0	+	qRT-PCR
ICC52	Male	54	CIS	II	T2	N1	T2N1M0	+	qRT-PCR
ICC53	Male	55	CIS	II	T2	N0	T2N0M0	-	qRT-PCR
ICC54	Male	52	CIS	II	T1	N0	T2N0M0	-	IHC or IF
ICC55	Male	52	CIS	III	T3	N0	T3N0M0	-	IHC or IF
ICC56	Male	67	CIS	III	T3	N0	T3N0M0	-	IHC or IF
ICC57	Female	62	CIS	III	T3	N0	T3N0M0	-	IHC or IF
ICC58	Female	39	CIS	III	T3	N1	T3N1M1	-	IHC or IF
ICC59	Female	43	CIS	II	T2	N0	T2N0M0	+	IHC or IF
ICC60	Male	57	CIS	II	T2	N0	T2N0M0	+	IHC or IF
ICC61	Male	46	CIS	II	T2	N0	T2N0M0	+	IHC or IF
ICC62	Male	46	CIS	III	T3	N0	T3N0M0	-	IHC or IF
ICC63	Female	54	CIS	II	T2	N0	T2N0M0	-	IHC or IF

Table S2. Summary of sequencing data for three paired ICC samples.

Sample	Raw bases(bp)	Clean bases(bp)	Effective rate(%)	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
ICC1	404748164700	402806132400	99.55	0.03	96.40	90.75	42.00
ANHT1	355813107600	352574385900	99.11	0.03	97.24	92.68	43.00
ICC2	313182108000	303762563400	96.98	0.03	97.56	93.42	43.00
ANHT2	302335526100	293865898800	97.43	0.03	97.43	93.06	43.00
ICC3	314024518500	308654965200	98.03	0.03	96.94	92.05	42.00
ANHT3	363634645800	360502643700	99.30	0.03	96.67	91.51	42.02

Table S3. Data filtering and deduplication results for three paired ICC samples.

Sample	Total pairs processed	Pairs with Singleton	Multiple pairs alignments	Unmapped pairs	Unique paired alignments	Unique paired alignment	valid interaction	Unique valid interaction	Invalid pairs	Dangling end pairs	Religation pairs	Self Cycle pairs	Dumped pairs	effect rate(%)
ICC1	154287(1.08)	19390004(14.44%)	154681437(11.52%)	25991881(1.94%)	968113749(72.10%)	968113749	891759716(92.11%)	668249585(69.03%)	76354033(7.89%)	304721803(15%)	25281421(2.61%)	712668(0.07%)	198877642(0.05%)	49.77%
ANHT1	1175247953	113339668(9.64%)	172572959(14.68%)	17954105(1.53%)	871383921(74.14%)	871383921	803598823(92.22%)	632043017(72.53%)	67785098(7.78%)	24085592(2.76%)	22719829(2.61%)	1141781(0.13%)	19837896(2.28%)	53.78%
ICC2	1012541878	126216317(12.47%)	136242552(13.65%)	27518476(2.72%)	720545337(7.16%)	720545333	688062166(95.49%)	563925984(78.26%)	32502367(4.51%)	15622096(2.17%)	8764138(1.22%)	5701320(0.08%)	7540031(1.05%)	55.68%
ANHT2	979552996	105858454(10.81%)	132929797(13.57%)	20781343(2.12%)	719983402(73.50%)	719983402	663512525(92.16%)	505655600(70.23%)	56470877(7.84%)	23822856(3.31%)	18059659(2.51%)	1009721(0.14%)	13578641(1.89%)	51.62%
ICC3	1028949884	105543221(10.26%)	138381479(13.45%)	17402192(1.69%)	767522992(74.60%)	767522992	748007979(97.46%)	591064803(77.01%)	19515013(2.54%)	55564300(7.2%)	60943300(7.9%)	299089(0.04%)	7565164(0.99%)	57.45%
ANHT3	1201678479	246541412(20.52%)	108896397(9.05%)	53177092(4.43%)	793060578(66.00%)	793060578	641751571(80.92%)	500154554(63.07%)	151309007(19.08%)	85440529(10.77%)	41496960(5.23%)	1653541(0.21%)	22717977(2.86%)	41.62%

Table S4. Summary of cis and trans interactions of three paired ICC samples.

Sample	Unique valid interaction	Trans interaction	Cis shortRange	Cis longRange	(Unique valid interaction)- (Trans interaction)
ICC1	668249585	364479519(54.54%)	57133949(8.55%)	246636117(36.91%)	303770066
ANHT1	632043017	205759451(32.55%)	78118113(12.36%)	348165453(55.09%)	271568417
ICC2	563925984	292357567(51.84%)	32093153(5.69%)	239475264(42.47%)	373255140
ANHT2	505655600	211423445(41.81%)	41636419(8.23%)	252595736(49.95%)	426283566
ICC3	591064803	217809663(36.85%)	45634059(7.72%)	327621081(55.43%)	294232155
ANHT3	500154554	201042620(40.20%)	62469398(12.49%)	236642536(47.31%)	299111934
Average	576848923.8	248812044.166667(49.75%)	52847515.1666667(10.57%)	275189364.5(55.03%)	328036879.666667(65.59%)

Table S6. Intrachromosomal and interchromosomal differential interaction numbers overlapped in three paired ICC samples.

Chrom	Chrom.1	diffContact.number
chr22	chr19	158
chr19	chr22	158
chr21	chr13	99
chr13	chr21	99
chr1	chr10	80
chr10	chr1	80
chr21	chr20	39
chr20	chr21	39
chr19	chr1	37
chr1	chr19	37
chr20	chr19	26
chr19	chr20	26
chr22	chr17	24
chr17	chr22	24
chr17	chr1	24
chr1	chr17	24
chr19	chr17	20
chr17	chr19	20
chr22	chr20	18
chr20	chr22	18
chr19	chr18	18
chr18	chr19	18
chr5	chr19	17
chr19	chr5	17
chr21	chr14	15
chr14	chr21	15
chr4	chr1	14
chr22	chr14	14
chr14	chr22	14
chr1	chr4	14
chr5	chr1	12
chr1	chr5	12
chr13	chr1	12
chr1	chr13	12
chr21	chr1	11
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chr19	chr11	8
chr11	chr19	8
chrY	chr13	7
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chr13	chrY	7
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chrX	chr11	6
chr9	chr11	6
chr4	chrX	6
chr4	chr13	6
chr21	chr18	6
chr20	chr17	6
chr18	chr21	6
chr17	chr20	6
chr16	chr10	6
chr13	chr4	6
chr11	chrX	6
chr11	chr9	6
chr10	chr16	6
chrX	chr13	5
chr9	chr4	5
chr8	chr2	5
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chr1	chr6	1
chr15	chrY	1
chr15	chrX	1
chr15	chr9	1
chr15	chr5	1
chr15	chr16	1
chr15	chr12	1
chr15	chr10	1
chr14	chrX	1
chr14	chr6	1
chr14	chr5	1
chr14	chr4	1
chr14	chr18	1
chr14	chr10	1
chr13	chr5	1
chr13	chr18	1
chr13	chr11	1
chr12	chrX	1
chr12	chr9	1
chr12	chr8	1
chr12	chr4	1
chr12	chr3	1
chr12	chr2	1
chr12	chr17	1
chr12	chr16	1
chr12	chr15	1
chr1	chr20	1
chr11	chr8	1
chr11	chr3	1
chr11	chr21	1
chr11	chr2	1
chr11	chr17	1
chr11	chr16	1
chr11	chr13	1
chr10	chrY	1
chr10	chr9	1
chr10	chr8	1
chr10	chr4	1
chr10	chr3	1
chr10	chr22	1
chr10	chr18	1
chr10	chr17	1
chr10	chr15	1
chr10	chr14	1

Table S7. Differentially expressed genes

gene_id	gene_name	ICC1	ANHT1	log2FoldChange	pvalue	padj
ENSG00000163631	ALB	3189.672131	2650170.792	9.698398319	1.22E-59	1.05E-56
ENSG00000198804	MT-CO1	398137.4622	971966.0613	1.287638951	0.002000843	0.008047781
ENSG00000198886	MT-ND4	106936.2693	339214.2998	1.665444266	7.61E-05	0.000440802
ENSG00000197249	SERPINA1	37553.10806	422084.0191	3.490520948	1.14E-14	2.67E-13
ENSG00000257017	HP	362.3401416	374536.0725	10.01298806	1.16E-61	1.80E-58
ENSG00000210082	MT-RNR2	80608.49018	288100.2251	1.837565067	1.41E-05	9.52E-05
ENSG00000130203	APOE	71245.48032	244609.6655	1.779608755	2.52E-05	0.000162579
ENSG00000198938	MT-CO3	109000.0039	275373.7901	1.337061725	0.001351997	0.005745986
ENSG00000125730	C3	34503.38422	223252.7632	2.693863037	6.88E-10	9.27E-09
ENSG00000198712	MT-CO2	110729.373	255044.4163	1.20370927	0.003801576	0.014098743
ENSG00000091513	TF	265.9184605	240261.6384	9.818648725	4.55E-60	4.04E-57
ENSG00000106927	AMBP	3718.436081	223660.431	5.910416658	1.91E-31	1.50E-29
ENSG00000136872	ALDOB	243.3682265	249568.5513	10.00125134	2.04E-61	2.67E-58
ENSG00000198899	MT-ATP6	69075.21534	200414.3681	1.536743662	0.000248332	0.001274478
ENSG00000198727	MT-CYB	49267.5623	180346.0559	1.872054561	9.93E-06	6.91E-05
ENSG00000118137	APOA1	201.3781318	207492.6116	10.00793619	2.28E-61	2.83E-58
ENSG00000171560	FGA	6114.980921	260777.4849	5.414295069	7.49E-28	4.70E-26
ENSG00000118271	TTR	87.07169561	146014.5171	10.7093038	6.90E-66	4.29E-62
ENSG00000198763	MT-ND2	51398.16998	145909.0637	1.505277643	0.000328234	0.001637547
ENSG00000171564	FGB	2125.923478	166840.6771	6.67230773	4.86E-37	5.18E-35
ENSG00000138207	RBP4	415.9941378	185874.6476	8.803067019	1.28E-52	4.68E-50
ENSG00000130208	APOC1	15595.40749	136522.4177	3.129932812	1.98E-12	3.70E-11
ENSG00000084674	APOB	167.1639751	123306.0098	9.525557757	1.28E-57	8.63E-55
ENSG00000091583	APOH	97.18043717	142476.6814	10.5156969	1.42E-64	5.05E-61
ENSG00000198786	MT-ND5	44118.33456	109289.6987	1.3087039	0.00169759	0.006932895
ENSG00000198888	MT-ND1	42527.37714	123420.4654	1.53711425	0.00024772	0.0012716
ENSG00000196616	ADH1B	93.29246006	160658.4051	10.74778629	2.78E-66	2.30E-62
ENSG00000110245	APOC3	164.0535968	120090.9646	9.514516137	1.63E-57	1.06E-54
ENSG00000212907	MT-ND4L	25348.76956	93283.91767	1.879706207	9.20E-06	6.44E-05
ENSG00000171557	FGG	3303.200861	152322.4358	5.527059818	1.16E-28	7.66E-27
ENSG00000145192	AHSG	94.84765097	104728.1926	10.10662409	1.53E-61	2.12E-58
ENSG00000109072	VTN	1642.25998	81909.08772	5.640148008	1.78E-29	1.23E-27
ENSG00000158874	APOA2	156.2776509	92892.96817	9.214024705	3.06E-55	1.55E-52
ENSG00000130649	CYP2E1	113.5099365	145329.0695	10.32051243	2.69E-63	6.07E-60
ENSG00000110169	HPX	76.96294991	93487.10853	10.24376703	3.24E-62	5.76E-59
ENSG00000145321	GC	1618.154565	83142.37906	5.683039771	8.70E-30	6.20E-28
ENSG00000198099	ADH4	30.30706789	96384.50727	11.62827202	8.10E-71	2.01E-66
ENSG00000115414	FN1	11787.52946	67994.37206	2.528138917	5.65E-09	6.68E-08
ENSG00000120885	CLU	12057.35459	79258.60445	2.716639198	5.16E-10	7.04E-09
ENSG00000117601	SERPINC1	78.51814188	68252.86169	9.761079711	1.10E-58	8.54E-56
ENSG00000175899	A2M	8509.192979	73533.25194	3.111280781	2.58E-12	4.75E-11
ENSG00000122194	PLG	59.07823066	68661.81544	10.1792514	2.43E-61	2.88E-58
ENSG00000021826	CPS1	66.07660199	94251.00327	10.47509993	9.60E-64	2.38E-60
ENSG00000182326	C1S	12329.51251	62748.70429	2.34745579	5.10E-08	5.26E-07
ENSG00000171766	GATM	632.9428926	25744.81996	5.345749852	3.44E-27	2.05E-25
ENSG00000198695	MT-ND6	20835.61374	45424.75469	1.124420535	0.006782518	0.02329411
ENSG00000055957	ITIH1	164.0535968	46011.17894	8.130446735	3.78E-47	8.54E-45
ENSG00000113889	KNG1	66.07660199	48154.97108	9.506278118	1.80E-56	1.12E-53
ENSG00000130707	ASS1	1269.014836	75129.20038	5.887435862	2.85E-31	2.21E-29
ENSG00000151655	ITIH2	726.254182	50208.74196	6.111045309	9.48E-33	8.27E-31
ENSG00000160862	AZGP1	134.5049993	58828.92118	8.771224395	8.02E-52	2.56E-49
ENSG00000113905	HRG	117.3979117	56427.92541	8.907142605	1.03E-52	3.82E-50
ENSG00000149131	SERPING1	15107.07843	48161.40117	1.672642246	7.15E-05	0.000418881
ENSG00000229314	ORM1	445.5427147	40341.12521	6.50009457	1.65E-35	1.64E-33
ENSG00000198848	CES1	27.97426007	29878.08208	10.05356047	1.14E-58	8.58E-56
ENSG00000134240	HMGCS2	43.52627316	48234.70421	10.10933468	2.55E-60	2.44E-57
ENSG00000180210	F2	48.19186435	35829.77377	9.533969111	3.82E-56	2.21E-53
ENSG00000139644	TMBIM6	8672.487728	33436.49412	1.946886729	4.61E-06	3.45E-05
ENSG00000172482	AGXT	45.08147069	41537.12203	9.843176843	2.62E-58	1.92E-55
ENSG00000158104	HPD	119.7306966	60791.38477	8.986247166	2.37E-53	9.82E-51
ENSG00000124253	PCK1	40.41587651	64621.14662	10.63787612	4.15E-64	1.15E-60
ENSG00000160868	CYP3A4	26.4190532	78793.0659	11.53463521	9.35E-70	1.16E-65
ENSG00000135744	AGT	525.6349081	32748.47444	5.960843398	1.34E-31	1.07E-29
ENSG00000255974	CYP2A6	14.75493478	15626.42968	10.03491133	1.38E-56	8.79E-54
ENSG00000198650	TAT	31.86227166	54505.32838	10.7339994	2.25E-64	7.00E-61
ENSG00000185624	P4HB	7399.56628	15576.27498	1.073819393	0.00970261	0.031748074
ENSG00000089220	PEBP1	3146.904459	32862.93005	3.38439602	5.50E-14	1.21E-12
ENSG00000125148	MT2A	2855.306692	25921.00444	3.182338789	9.81E-13	1.90E-11
ENSG00000167711	SERPINF2	251.9217637	34930.84713	7.114585391	7.20E-40	9.89E-38

ENSG00000111275	ALDH2	2693.567131	33814.58344	3.649984937	1.12E-15	2.96E-14
ENSG00000000971	CFH	1747.235177	35289.64618	4.335987812	3.03E-20	1.15E-18
ENSG00000143819	EPHX1	625.9445459	28572.77373	5.51214515	2.20E-28	1.43E-26
ENSG00000047457	CP	1520.177715	28040.36224	4.205065439	2.38E-19	8.33E-18
ENSG00000171759	PAH	188.936621	38297.64247	7.662145379	8.51E-44	1.51E-41
ENSG00000165092	ALDH1A1	1405.093795	31445.73813	4.483987096	2.93E-21	1.21E-19
ENSG00000106565	TMEM176B	5114.217388	19934.59026	1.962656166	3.94E-06	2.97E-05
ENSG00000106538	RARRES2	1223.136787	20855.37921	4.091603738	1.42E-18	4.69E-17
ENSG00000159403	C1R	6134.420773	29537.28729	2.267510178	1.32E-07	1.27E-06
ENSG00000175003	SLC22A1	21.75342271	18153.45521	9.695515118	1.89E-55	1.00E-52
ENSG00000121691	CAT	618.9461991	22095.10064	5.157449194	7.71E-26	4.28E-24
ENSG00000116133	DHCR24	2590.147123	18427.37707	2.830674538	1.20E-10	1.79E-09
ENSG00000132386	SERPINF1	1195.143401	18154.74123	3.92492972	1.85E-17	5.62E-16
ENSG00000123838	C4BPA	1110.385649	29650.45688	4.738744718	4.98E-23	2.28E-21
ENSG00000182871	COL18A1	2217.679575	16987.03681	2.937228702	2.91E-11	4.78E-10
ENSG00000169738	DCXR	640.7188335	26888.09004	5.390822525	1.64E-27	1.01E-25
ENSG00000162267	ITIH3	591.7304061	20265.09691	5.097579332	2.11E-25	1.15E-23
ENSG00000248144	ADH1C	112.7323414	32349.80884	8.162926452	3.89E-47	8.70E-45
ENSG00000151224	MAT1A	27.19665681	39157.98857	10.48424285	6.97E-62	1.16E-58
ENSG00000244414	CFHR1	48.19186435	24803.45472	9.003352996	3.62E-52	1.22E-49
ENSG00000141753	IGFBP4	3410.508839	20625.18197	2.596295613	2.47E-09	3.06E-08
ENSG00000106327	TFR2	73.85256557	19925.58813	8.07303301	5.24E-46	1.09E-43
ENSG00000116171	SCP2	870.8866787	19893.43768	4.513439272	2.30E-21	9.59E-20
ENSG00000243955	GSTA1	29.52946559	15908.06764	9.066560369	1.41E-51	4.43E-49
ENSG00000250722	SEPP1	94.07005552	12866.63487	7.093549364	6.23E-39	8.06E-37
ENSG00000138109	CYP2C9	272.9168088	30797.58501	6.817477647	1.06E-37	1.21E-35
ENSG00000228278	ORM2	166.3863805	19341.73592	6.859830922	9.89E-38	1.14E-35
ENSG00000099937	SERPIND1	24.86384483	20794.93636	9.69985538	6.22E-56	3.51E-53
ENSG00000169136	ATF5	1311.782509	8954.567862	2.770957198	2.75E-10	3.91E-09
ENSG00000151726	ACSL1	401.2198492	25382.16286	5.982781057	1.11E-31	8.90E-30
ENSG00000172831	CES2	516.3037789	10451.49291	4.338967863	4.48E-20	1.68E-18
ENSG00000176974	SHMT1	360.7849533	10411.62635	4.850366894	1.53E-23	7.33E-22
ENSG00000105398	SULT2A1	21.75342271	23462.13786	10.06560368	3.17E-58	2.19E-55
ENSG00000248527	MTATP6P1	7604.851107	25011.78965	1.717595473	4.68E-05	0.000286627
ENSG00000188488	SERPINA5	162.4984077	16743.97939	6.685839951	1.94E-36	2.01E-34
ENSG00000163586	FABP1	14.75493478	23835.08311	10.6440067	3.71E-61	4.19E-58
ENSG00000138356	AOX1	423.7700791	32228.92314	6.248458866	1.19E-33	1.07E-31
ENSG00000187758	ADH1A	42.7486742	26003.3096	9.243883338	7.78E-54	3.28E-51
ENSG00000166825	ANPEP	405.885414	9202.769352	4.502442001	3.73E-21	1.52E-19
ENSG00000132703	APCS	2485.171927	16848.14686	2.76109953	3.00E-10	4.24E-09
ENSG00000185432	METTL7A	1268.237242	17569.603	3.792034014	1.39E-16	3.91E-15
ENSG00000101856	PGRMC1	542.7419783	11751.65719	4.436094252	9.29E-21	3.66E-19
ENSG00000156096	UGT2B4	18.64299156	16790.27605	9.803960063	1.07E-55	5.79E-53
ENSG00000146678	IGFBP1	1094.833768	25834.84123	4.560355508	8.78E-22	3.76E-20
ENSG00000073849	ST6GAL1	2392.638235	15333.21756	2.679911147	8.62E-10	1.14E-08
ENSG00000138115	CYP2C8	20.97581587	25361.58657	10.23008554	4.55E-59	3.65E-56
ENSG00000100889	PCK2	484.4224205	17332.97568	5.160701662	8.36E-26	4.62E-24
ENSG00000145692	BHMT	18.64299156	38832.626	11.01359864	8.91E-65	3.69E-61
ENSG00000008394	MGST1	1013.9623986	18244.7625	4.169212854	4.29E-19	1.47E-17
ENSG00000131482	G6PC	51.30225638	31736.37821	9.268969549	2.69E-54	1.31E-51
ENSG00000136881	BAAT	104.1787948	18105.87255	7.439323172	1.28E-41	1.99E-39
ENSG00000125144	MT1G	15.53254811	8951.995826	9.157797318	3.99E-50	1.10E-47
ENSG00000139209	SLC38A4	6.978701584	23490.43026	11.68801695	7.36E-65	3.66E-61
ENSG00000127884	ECHS1	1277.568371	18066.00598	3.821655101	8.87E-17	2.53E-15
ENSG00000148672	GLUD1	1377.878003	17870.53124	3.696923951	5.78E-16	1.56E-14
ENSG00000163581	SLC2A2	6.978701584	16049.52963	11.13847759	9.83E-61	1.06E-57
ENSG00000002933	TMEM176A	2775.214505	13526.36215	2.285040399	1.10E-07	1.07E-06
ENSG00000135094	SDS	401.2198492	24304.47971	5.920188543	3.17E-31	2.45E-29
ENSG00000166347	CYB5A	657.0483092	14312.1192	4.444796911	7.42E-21	2.94E-19
ENSG00000183044	ABAT	116.6203166	15962.0804	7.094964427	3.28E-39	4.33E-37
ENSG00000169715	MT1E	814.1223119	12398.52429	3.928542647	2.13E-17	6.46E-16
ENSG00000159335	PTMS	2323.432365	10239.29993	2.13971443	5.86E-07	5.09E-06
ENSG000000080618	CPB2	43.52627316	17266.10274	8.627210854	3.27E-49	8.56E-47
ENSG00000099194	SCD	2937.731661	16063.67583	2.45096762	1.51E-08	1.68E-07
ENSG00000115884	SDC1	2097.930092	13419.62265	2.677219923	8.99E-10	1.18E-08
ENSG00000005421	PON1	27.97426007	10977.47431	8.609027169	7.49E-48	1.86E-45
ENSG00000160282	FTCD	26.4190532	18673.00652	9.457526501	3.69E-54	1.70E-51
ENSG00000179918	SEPHS2	1913.640303	8042.78104	2.071286822	1.27E-06	1.04E-05
ENSG000000083807	SLC27A5	65.29900539	14922.97779	7.833177403	5.71E-44	1.02E-41
ENSG00000109181	UGT2B10	10.08922402	15122.31059	10.52968443	3.06E-58	2.17E-55
ENSG00000120129	DUSP1	1367.769281	17345.83586	3.664553212	9.38E-16	2.48E-14

ENSG00000025423	<i>HSD17B6</i>	17.86538201	13742.41319	9.575967371	6.37E-54	2.73E-51
ENSG000000112245	<i>PTP4A1</i>	1769.785404	12654.44189	2.837894676	1.11E-10	1.68E-09
ENSG00000066813	<i>ACSM2B</i>	10.08922402	8424.728411	9.685715294	6.43E-52	2.13E-49
ENSG00000132855	<i>ANGPTL3</i>	9.31159843	21594.83961	11.15774382	1.13E-62	2.15E-59
ENSG00000105707	<i>HPN</i>	284.5807224	9425.250481	5.048927225	7.39E-25	3.85E-23
ENSG00000182551	<i>ADI1</i>	1085.502639	14989.85073	3.787374455	1.51E-16	4.22E-15
ENSG00000137204	<i>SLC22A7</i>	10.08922402	5770.387085	9.139760872	7.73E-48	1.90E-45
ENSG00000118520	<i>ARG1</i>	17.08777164	16241.14632	9.880673088	9.95E-56	5.49E-53
ENSG00000188338	<i>SLC38A3</i>	7.75633786	7453.784758	9.882455632	1.93E-52	6.94E-50
ENSG00000084234	<i>APLP2</i>	4817.176464	11135.65453	1.208897412	0.003710906	0.013811707
ENSG00000135929	<i>CYP27A1</i>	753.4699745	13444.05699	4.157017508	6.59E-19	2.22E-17
ENSG00000170509	<i>HSD17B13</i>	3.090401881	12804.906	11.95220575	1.32E-61	1.94E-58
ENSG00000165140	<i>FBP1</i>	635.2756749	15182.75344	4.578598642	9.20E-22	3.93E-20
ENSG00000225630	<i>MTND2P28</i>	4265.084693	11526.60403	1.43428612	0.000617209	0.002878184
ENSG00000113924	<i>HGD</i>	153.1672724	20666.33455	7.074720304	3.00E-39	4.01E-37
ENSG00000105697	<i>HAMP</i>	118.1755067	33073.83702	8.126912487	7.28E-47	1.61E-44
ENSG00000143878	<i>RHOB</i>	2108.038815	18383.65245	3.124362061	2.24E-12	4.17E-11
ENSG00000080910	<i>CFHR2</i>	19.42060034	13477.49346	9.428366931	6.05E-53	2.35E-50
ENSG00000140564	<i>FURIN</i>	2315.656425	7955.331811	1.780431434	2.61E-05	0.00016786
ENSG00000137106	<i>GRHPR</i>	1035.73662	12339.36746	3.574356012	3.67E-15	9.12E-14
ENSG00000142168	<i>SOD1</i>	1920.638649	14411.14259	2.907431441	4.38E-11	7.00E-10
ENSG00000171234	<i>UGT2B7</i>	131.39462	17741.92943	7.075585314	3.75E-39	4.93E-37
ENSG00000007933	<i>FMO3</i>	314.1293025	15955.65031	5.665931777	2.69E-29	1.83E-27
ENSG00000169764	<i>UGP2</i>	706.8143301	10784.5716	3.931221448	2.15E-17	6.51E-16
ENSG00000114771	<i>AADAC</i>	97.18043717	10558.23241	6.761423614	1.59E-36	1.65E-34
ENSG00000072778	<i>ACADVL</i>	3571.470806	11130.51046	1.639885661	9.93E-05	0.000560463
ENSG00000104635	<i>SLC39A14</i>	635.2756749	8557.188274	3.751381079	3.44E-16	9.39E-15
ENSG00000117594	<i>HSD11B1</i>	262.0304892	14924.26381	5.831020879	1.87E-30	1.36E-28
ENSG00000187048	<i>CYP4A11</i>	20.97581587	14826.52643	9.455625109	2.92E-53	1.19E-50
ENSG00000079557	<i>AFM</i>	2.312696499	13431.19681	12.41821722	3.00E-63	6.20E-60
ENSG00000103569	<i>AQP9</i>	109.621961	12568.27868	6.839276973	2.91E-37	3.13E-35
ENSG00000125166	<i>GOT2</i>	1006.188045	9070.30949	3.172066861	1.22E-12	2.33E-11
ENSG00000170099	<i>SERPINA6</i>	100.2908185	10342.18137	6.686208791	5.15E-36	5.20E-34
ENSG00000106804	<i>C5</i>	290.023882	11723.3648	5.336387688	6.31E-27	3.71E-25
ENSG00000179761	<i>PIPOX</i>	43.52627316	12617.14736	8.174657134	7.84E-46	1.60E-43
ENSG00000123384	<i>LRP1</i>	2787.65601	8483.885243	1.60561675	0.000137497	0.000749548
ENSG00000196177	<i>ACADSB</i>	127.5066458	14636.19576	6.841251619	2.11E-37	2.30E-35
ENSG00000132541	<i>HRSP12</i>	186.6038376	12160.61094	6.025023728	1.10E-31	8.88E-30
ENSG00000021852	<i>C8B</i>	24.86384483	15522.26222	9.277964233	9.03E-53	3.40E-50
ENSG00000183747	<i>ACSM2A</i>	17.08777164	12357.37171	9.486394268	8.95E-53	3.40E-50
ENSG00000116285	<i>ERRFI1</i>	549.7403251	18363.07616	5.061554416	3.93E-25	2.08E-23
ENSG00000141505	<i>ASGR1</i>	146.1689204	10001.38658	6.095053429	5.24E-32	4.34E-30
ENSG00000117592	<i>PRDX6</i>	1778.338939	12618.43338	2.826828301	1.29E-10	1.92E-09
ENSG00000142192	<i>APP</i>	3559.806896	7784.291406	1.128728103	0.006683612	0.022989813
ENSG00000101323	<i>HAO1</i>	8.533969895	9126.894285	10.03911292	5.70E-54	2.58E-51
ENSG00000138413	<i>IDH1</i>	1635.261634	8991.862386	2.458990755	1.41E-08	1.57E-07
ENSG00000166741	<i>NNMT</i>	5399.594402	12956.65614	1.262743966	0.002462497	0.009580196
ENSG00000119711	<i>ALDH6A1</i>	213.819642	12317.50515	5.847239855	1.79E-30	1.31E-28
ENSG00000101981	<i>F9</i>	3.090401881	11651.34778	11.81600702	1.39E-60	1.39E-57
ENSG00000125844	<i>RBP1</i>	3767.424505	7761.14308	1.042655093	0.012078423	0.038444001
ENSG00000100665	<i>SERPINA4</i>	17.86538201	11836.53439	9.360580386	2.61E-52	8.88E-50
ENSG00000104760	<i>FGL1</i>	746.4716279	16535.64447	4.469086354	4.92E-21	1.98E-19
ENSG00000115718	<i>PROC</i>	18.64299156	10364.04368	9.107926293	1.74E-50	5.10E-48
ENSG00000113790	<i>EHHADH</i>	80.8509296	8741.08886	6.753924934	2.49E-36	2.54E-34
ENSG00000170345	<i>FOS</i>	457.2066265	10392.33608	4.506102243	3.41E-21	1.40E-19
ENSG00000140263	<i>SORD</i>	144.613731	9735.180839	6.071550664	7.40E-32	6.11E-30
ENSG00000107537	<i>PHYH</i>	295.4670415	10099.12396	5.094420366	3.45E-25	1.83E-23
ENSG00000172955	<i>ADH6</i>	19.42060034	13672.96821	9.449141039	4.23E-53	1.70E-50
ENSG00000167315	<i>ACAA2</i>	800.9032128	9757.043146	3.606506768	2.70E-15	6.85E-14
ENSG00000147647	<i>DPYS</i>	6.201060061	9961.520022	10.61724933	2.76E-56	1.67E-53
ENSG00000161944	<i>ASGR2</i>	66.85419855	12515.55194	7.545480462	6.08E-42	9.76E-40
ENSG00000115310	<i>RTN4</i>	3486.713056	8449.162755	1.276899511	0.002224385	0.008855853
ENSG000000205403	<i>CFI</i>	1032.626243	11945.84592	3.531935393	6.85E-15	1.65E-13
ENSG00000075239	<i>ACAT1</i>	496.0863321	10258.5902	4.369704588	2.72E-20	1.04E-18
ENSG00000170458	<i>CD14</i>	4303.964395	11864.82679	1.462917957	0.00048339	0.002324366
ENSG00000130600	<i>H19</i>	496.0863321	10055.39934	4.340842762	4.28E-20	1.61E-18
ENSG00000157131	<i>C8A</i>	36.52787722	12672.44614	8.432966176	2.24E-47	5.15E-45
ENSG00000060971	<i>ACAA1</i>	766.6890737	9714.60455	3.663193141	1.19E-15	3.12E-14
ENSG00000112964	<i>GHR</i>	14.75493478	4876.604517	8.354891803	4.94E-44	8.96E-42
ENSG00000144381	<i>HSPD1</i>	2042.720915	8724.370625	2.094476303	9.76E-07	8.17E-06
ENSG00000214274	<i>ANG</i>	106.5115804	9676.024007	6.503452266	9.43E-35	9.01E-33

ENSG00000177606	<i>JUN</i>	1527.176061	4308.184523	1.496114154	0.000376588	0.001848001
ENSG00000185650	<i>ZFP36L1</i>	2943.174819	6161.336583	1.065824356	0.010381117	0.033596702
ENSG00000165795	<i>NDRG2</i>	478.2016676	9165.474828	4.260112107	1.61E-19	5.71E-18
ENSG00000122787	<i>AKR1D1</i>	3.868086451	5754.954868	10.48732874	5.85E-53	2.31E-50
ENSG00000113600	<i>C9</i>	2.312696499	10168.56893	12.01674936	3.08E-60	2.83E-57
ENSG00000224389	<i>C4B</i>	3782.976386	15420.66679	2.027227261	1.99E-06	1.58E-05
ENSG00000003989	<i>SLC7A2</i>	285.3583166	11116.36426	5.28307237	1.62E-26	9.42E-25
ENSG00000196620	<i>UGT2B15</i>	24.08624001	12377.948	8.996978087	2.51E-50	7.17E-48
ENSG00000186529	<i>CYP4F3</i>	46.63666774	8334.707146	7.477211682	8.41E-41	1.23E-38
ENSG00000163347	<i>CLDN1</i>	2067.603924	5608.348807	1.439543707	0.000603203	0.002819749
ENSG00000152558	<i>TMEM123</i>	1861.541502	9286.360528	2.318522285	7.58E-08	7.56E-07
ENSG00000137491	<i>SLCO2B1</i>	2181.910249	10037.39509	2.201642794	2.92E-07	2.65E-06
ENSG00000169439	<i>SDC2</i>	176.4951094	7629.969235	5.43285252	2.32E-27	1.39E-25
ENSG00000133835	<i>HSD17B4</i>	776.7977966	7105.273857	3.193039363	1.05E-12	2.03E-11
ENSG00000039537	<i>C6</i>	7.75633786	13971.32441	10.78887058	3.12E-59	2.59E-56
ENSG00000151790	<i>TDO2</i>	68.40939152	15708.73484	7.840215691	4.16E-44	7.61E-42
ENSG00000127948	<i>POR</i>	999.9672929	9616.867175	3.265427092	3.26E-13	6.64E-12
ENSG00000180432	<i>CYP8B1</i>	9.31159843	8368.143616	9.790047004	2.03E-52	7.09E-50
ENSG00000170315	<i>UBB</i>	2767.438565	7578.528512	1.453312101	0.000530836	0.002511618
ENSG00000160200	<i>CBS</i>	388.0007487	8162.380722	4.394356028	2.10E-20	8.10E-19
ENSG00000167244	<i>IGF2</i>	47.4142661	13851.72472	8.186281701	4.55E-46	9.51E-44
ENSG00000134538	<i>SLCO1B1</i>	5.423411881	7667.26376	10.42831286	3.13E-54	1.49E-51
ENSG00000139547	<i>RDH16</i>	19.42060034	9809.769888	8.970109812	1.62E-49	4.29E-47
ENSG00000169562	<i>GJB1</i>	195.9349709	6412.11011	5.031344701	1.39E-24	7.11E-23
ENSG00000100197	<i>CYP2D6</i>	18.64299156	5362.719353	8.157388571	2.14E-43	3.65E-41
ENSG00000165475	<i>CRYL1</i>	343.6778816	4132.000045	3.587158429	5.16E-15	1.27E-13
ENSG00000131187	<i>F12</i>	22.53102899	7530.945843	8.375834051	1.28E-45	2.59E-43
ENSG00000101474	<i>APMAP</i>	1450.971844	5420.590166	1.901317298	7.89E-06	5.61E-05
ENSG000000069535	<i>MAOB</i>	669.4898144	7410.060143	3.468068933	2.19E-14	4.99E-13
ENSG00000104870	<i>FCGRT</i>	2911.293463	6473.838978	1.152913605	0.005647665	0.019781949
ENSG00000261701	<i>HPR</i>	18.64299156	8081.361583	8.749013404	8.39E-48	2.02E-45
ENSG00000149476	<i>DAK</i>	387.2231546	5869.410478	3.921481511	3.34E-17	9.94E-16
ENSG00000140526	<i>ABHD2</i>	1135.268659	4097.277557	1.851488471	1.34E-05	9.11E-05
ENSG00000073060	<i>SCARB1</i>	678.0433493	3865.794301	2.511054301	8.79E-09	1.01E-07
ENSG00000135506	<i>OS9</i>	2212.236417	4800.729449	1.117686119	0.007308921	0.024753132
ENSG00000122786	<i>CALD1</i>	1405.093795	5478.46098	1.962986304	4.15E-06	3.12E-05
ENSG00000130005	<i>GAMT</i>	257.3649236	6111.181878	4.568803276	1.89E-21	7.90E-20
ENSG00000186910	<i>SERPINA11</i>	7.75633786	10569.80658	10.386354	3.25E-56	1.92E-53
ENSG00000169710	<i>FASN</i>	1265.126866	3172.630553	1.32628227	0.001569452	0.006492799
ENSG00000148584	<i>A1CF</i>	71.51977693	7035.828881	6.617432525	3.96E-35	3.84E-33
ENSG00000099834	<i>CDHR5</i>	106.5115804	5164.672568	5.597727464	3.67E-28	2.34E-26
ENSG00000148218	<i>ALAD</i>	532.633255	7222.301503	3.76088501	3.15E-16	8.62E-15
ENSG00000211445	<i>GPX3</i>	943.2029265	11157.51684	3.564102739	4.31E-15	1.06E-13
ENSG00000100714	<i>MTHFD1</i>	662.4914677	10308.7449	3.959532198	1.44E-17	4.42E-16
ENSG00000147257	<i>GPC3</i>	18.64299156	149.201868	2.990676437	1.31E-08	1.46E-07
ENSG00000184500	<i>PROS1</i>	332.7915631	7397.199962	4.473701398	6.71E-21	2.67E-19
ENSG00000186480	<i>INSIG1</i>	485.9776087	10792.2877	4.472565053	5.43E-21	2.18E-19
ENSG00000143162	<i>CREG1</i>	1736.34886	5964.575816	1.780270076	2.65E-05	0.000170461
ENSG00000163683	<i>SMIM14</i>	839.0053221	4848.312119	2.53051927	6.60E-09	7.69E-08
ENSG00000198734	<i>F5</i>	59.07823066	7635.113308	7.010481194	1.13E-37	1.28E-35
ENSG00000164237	<i>CMBL</i>	160.9432185	7942.47163	5.623728519	1.05E-28	6.99E-27
ENSG00000140374	<i>ETFA</i>	961.865184	4964.053746	2.367430722	4.49E-08	4.67E-07
ENSG00000172057	<i>ORMDL3</i>	2069.936706	5547.905957	1.422284534	0.000697737	0.003209149
ENSG00000167588	<i>GPD1</i>	17.08777164	5036.070759	8.191409295	4.14E-43	6.90E-41
ENSG00000103485	<i>QPRT</i>	321.1276503	5425.734239	4.077997343	3.26E-18	1.04E-16
ENSG00000173531	<i>MTS1</i>	199.822943	6400.535947	5.000410971	2.27E-24	1.15E-22
ENSG00000165672	<i>PRDX3</i>	1729.350514	6826.207933	1.980757984	3.39E-06	2.60E-05
ENSG00000214530	<i>STARD10</i>	821.1206585	8829.824108	3.426488843	3.71E-14	8.28E-13
ENSG00000113013	<i>HSPA9</i>	2016.282717	7408.774125	1.877455821	9.89E-06	6.88E-05
ENSG00000138293	<i>NCOA4</i>	1728.57292	5481.033016	1.664775285	8.10E-05	0.000466191
ENSG00000143416	<i>SELENBP1</i>	255.0321408	5529.901704	4.4377373	1.44E-20	5.60E-19
ENSG00000100652	<i>SLC10A1</i>	10.08922402	7480.791138	9.514278067	1.23E-50	3.69E-48
ENSG00000148702	<i>HABP2</i>	535.7436314	7318.752859	3.771625845	2.67E-16	7.32E-15
ENSG00000115738	<i>ID2</i>	1699.024346	7963.047919	2.228513134	2.18E-07	2.03E-06
ENSG00000004799	<i>PDK4</i>	44.30387198	8613.77307	7.598528885	1.55E-41	2.37E-39
ENSG00000173281	<i>PPP1R3B</i>	302.4653894	3744.908601	3.629459131	3.06E-15	7.70E-14
ENSG00000023330	<i>ALAS1</i>	853.7796093	11368.42381	3.734800856	3.96E-16	1.08E-14
ENSG00000159423	<i>ALDH4A1</i>	347.5658525	6657.739564	4.259114944	1.93E-19	6.82E-18
ENSG00000135535	<i>CD164</i>	1716.131415	4697.848003	1.452752347	0.000543785	0.002566126
ENSG00000074695	<i>LMAN1</i>	908.2111938	4537.095742	2.320478242	7.90E-08	7.87E-07
ENSG00000128928	<i>IVD</i>	1023.295115	7145.140418	2.803562644	1.84E-10	2.67E-09

ENSG00000124145	SDC4	1581.607644	5257.26587	1.73282012	4.25E-05	0.000261983
ENSG00000100024	UPB1	27.19665681	8436.302574	8.26963198	2.67E-45	5.27E-43
ENSG00000132840	BHMT2	101.0684138	9982.096311	6.623956327	1.52E-35	1.52E-33
ENSG00000181192	DHTKD1	361.5625475	6162.622601	4.090692216	2.57E-18	8.27E-17
ENSG00000166840	GLYATL1	6.201060061	5567.196228	9.777845476	5.28E-50	1.43E-47
ENSG00000116882	HAO2	2.312696499	4552.527959	10.8573895	1.47E-51	4.56E-49
ENSG00000131781	FMO5	99.51322321	8198.389229	6.362297875	1.19E-33	1.07E-31
ENSG00000137124	ALDH1B1	204.4885094	5474.602926	4.741701793	1.50E-22	6.66E-21
ENSG00000107372	ZFAND5	1464.968537	9426.536499	2.685735335	8.25E-10	1.10E-08
ENSG00000128311	TST	509.3054319	6758.048974	3.729628557	5.19E-16	1.40E-14
ENSG00000100380	ST13	1608.045842	6054.597082	1.912620176	6.97E-06	5.03E-05
ENSG00000072210	ALDH3A2	736.3629049	6954.809741	3.239268483	5.64E-13	1.12E-11
ENSG00000105852	PON3	95.62524639	7372.765619	6.266579401	6.43E-33	5.63E-31
ENSG00000152620	NADK2	170.2743533	6442.974544	5.240630843	5.94E-26	3.34E-24
ENSG00000121310	ECHDC2	705.259142	4538.38176	2.685697551	9.90E-10	1.30E-08
ENSG00000144908	ALDH1L1	32.63987315	8458.164882	8.011397348	5.48E-44	9.86E-42
ENSG00000138029	HADHB	1583.162833	5137.666188	1.698203427	5.93E-05	0.000352101
ENSG00000184232	OAF	1060.619629	5925.995274	2.481983648	1.11E-08	1.25E-07
ENSG00000106258	CYP3A5	93.29246006	6864.788475	6.199168465	2.29E-32	1.93E-30
ENSG00000189060	H1FO	1206.029718	2707.092005	1.166363057	0.005301281	0.018679239
ENSG00000063854	HAGH	681.9313197	4429.070223	2.699041446	8.30E-10	1.10E-08
ENSG00000161533	ACOX1	718.4782413	7040.972953	3.292497655	2.67E-13	5.48E-12
ENSG00000140093	SERPINA10	5.423411881	2381.729428	8.741651169	1.15E-41	1.81E-39
ENSG00000244731	C4A	1721.574573	6084.175498	1.821239006	1.77E-05	0.000117352
ENSG00000039068	CDH1	1065.285194	3890.228645	1.86846198	1.14E-05	7.83E-05
ENSG00000172340	SUCLG2	814.1223119	5998.012286	2.880942682	7.52E-11	1.16E-09
ENSG00000100664	EIF5	1173.370768	6482.841104	2.465817024	1.34E-08	1.49E-07
ENSG00000124713	GNMT	17.08777164	7748.282899	8.812977623	9.70E-48	2.32E-45
ENSG00000164405	UQCQRQ	2164.80318	5731.806543	1.404685368	0.000806912	0.003657667
ENSG00000106853	PTGR1	125.951456	3593.158467	4.832750016	6.49E-23	2.95E-21
ENSG00000128641	MYO1B	553.6282956	7203.011232	3.701265755	7.55E-16	2.02E-14
ENSG00000110243	APOA5	10.08922402	10960.75607	10.06535668	9.25E-55	4.60E-52
ENSG00000111897	SERINC1	1646.925545	4921.615149	1.579262564	0.000179046	0.000953137
ENSG00000124299	PEPD	766.6890737	4795.585377	2.644759608	1.62E-09	2.06E-08
ENSG00000079739	PGM1	689.7072605	5757.526905	3.061125144	6.79E-12	1.20E-10
ENSG00000178772	CPN2	13.19970438	6296.368482	8.882613217	3.07E-47	7.00E-45
ENSG00000105699	LSR	772.9098263	2184.96866	1.499043837	0.000396235	0.00193714
ENSG00000116005	PCYOX1	625.9445459	4474.080856	2.837193726	1.41E-10	2.08E-09
ENSG00000108187	PBLD	108.0667708	6498.273321	5.90821602	2.23E-30	1.62E-28
ENSG00000134294	SLC38A2	831.2293814	9912.651334	3.575723965	4.29E-15	1.06E-13
ENSG00000161031	PGLYRP2	24.08624001	7160.572635	8.207361046	1.96E-44	3.66E-42
ENSG00000073578	SDHA	1971.182262	5879.698623	1.576602578	0.000181707	0.000966268
ENSG00000198610	AKR1C4	39.63827699	8202.247283	7.687905719	4.93E-42	8.01E-40
ENSG00000140505	CYP1A2	1.534979634	9281.216455	12.43480291	1.16E-60	1.20E-57
ENSG00000165678	GHITM	2334.318682	5582.628445	1.257881741	0.002604167	0.010056956
ENSG00000119318	RAD23B	1506.958616	3868.366337	1.359987061	0.001184887	0.005099358
ENSG00000187097	ENTPD5	198.2677542	5680.36582	4.839469135	3.30E-23	1.54E-21
ENSG00000115486	GGCX	868.5538965	4306.898505	2.309762419	9.47E-08	9.34E-07
ENSG00000104325	DECRI	1162.484451	6136.90224	2.400148559	2.97E-08	3.15E-07
ENSG00000106400	ZNHIT1	1194.365807	4085.703394	1.774205185	2.89E-05	0.000184876
ENSG00000161013	MGAT4B	1621.264941	3333.382813	1.039784827	0.012581941	0.039847026
ENSG00000165471	MBL2	4.645755009	6886.650783	10.49057245	6.25E-54	2.73E-51
ENSG00000244067	GSTA2	10.08922402	7079.553495	9.434746651	4.84E-50	1.32E-47
ENSG00000187446	CHP1	1422.978458	5387.153696	1.920493719	6.48E-06	4.70E-05
ENSG00000166278	C2	1786.114879	4387.917644	1.296630631	0.00194791	0.007864208
ENSG00000211452	DIO1	5.423411881	3672.891588	9.366537253	2.65E-46	5.63E-44
ENSG00000117305	HMGCL	790.7944899	4947.335511	2.645050343	1.60E-09	2.04E-08
ENSG00000187134	AKR1C1	222.3731799	6584.436533	4.887119474	1.33E-23	6.37E-22
ENSG00000138823	MTTP	7.75633786	6072.601335	9.586801412	3.13E-50	8.83E-48
ENSG00000145703	IQGAP2	283.0255339	8913.415283	4.976277269	2.34E-24	1.18E-22
ENSG00000186115	CYP4F2	10.8668471	5042.500849	8.839541376	2.17E-46	4.66E-44
ENSG00000140107	SLC25A47	12.42208703	8067.215384	9.326803355	2.14E-50	6.19E-48
ENSG00000142178	SIK1	1037.291808	9904.935226	3.255145479	3.75E-13	7.59E-12
ENSG00000143418	CERS2	695.150419	3985.393983	2.519070335	8.08E-09	9.33E-08
ENSG00000147872	PLIN2	607.2822879	10056.68536	4.049325626	3.79E-18	1.20E-16
ENSG00000101577	LPIN2	1140.711817	4535.809724	1.991279888	3.13E-06	2.41E-05
ENSG00000120738	EGR1	373.2264599	6527.851737	4.127966201	1.44E-18	4.78E-17
ENSG00000138030	KHK	38.8606773	3524.999508	6.498013502	2.91E-33	2.59E-31
ENSG00000167798	C3P1	116.6203166	4623.258954	5.307319355	3.56E-26	2.03E-24
ENSG00000182199	SHMT2	1132.935877	4454.790585	1.975144886	3.72E-06	2.82E-05
ENSG00000143742	SRP9	1605.71306	3380.965483	1.074137071	0.009988893	0.032500842

ENSG00000168237	GLYCTK	178.8278929	5752.382832	5.006412315	2.36E-24	1.19E-22
ENSG00000135423	GLS2	56.74543914	7163.144671	6.976407585	1.85E-37	2.02E-35
ENSG00000138449	SLC40A1	1409.759359	4736.428545	1.748237261	3.69E-05	0.000230588
ENSG00000128309	MPST	829.6741933	5385.867678	2.698344937	8.04E-10	1.07E-08
ENSG00000104823	ECH1	1069.950758	3308.94847	1.628682326	0.000117427	0.000652797
ENSG00000152078	TMEM56	74.63016171	5333.140937	6.156405031	7.98E-32	6.57E-30
ENSG00000170540	ARL6IP1	1516.289744	4134.572081	1.447093483	0.000574442	0.002701561
ENSG00000162368	CMPK1	1281.456341	3633.025028	1.50326821	0.000357796	0.00176414
ENSG00000162496	DHRS3	1187.36746	3545.575798	1.57812317	0.000184918	0.000981241
ENSG00000115255	REEP6	177.2727039	5393.583787	4.926089909	9.42E-24	4.57E-22
ENSG00000112294	ALDH5A1	261.2528949	4351.909138	4.057389654	5.60E-18	1.77E-16
ENSG00000197894	ADH5	1179.59152	4191.156877	1.828923668	1.68E-05	0.000112198
ENSG00000147955	SIGMAR1	680.3761315	2709.664041	1.993464897	3.40E-06	2.61E-05
ENSG00000166035	LIPC	391.1111253	2356.009066	2.590238455	4.09E-09	4.94E-08
ENSG00000198417	MT1F	107.2891756	3369.39132	4.971072539	1.08E-23	5.21E-22
ENSG00000065054	SLC9A3R2	1199.031371	4153.862353	1.792449578	2.42E-05	0.000156197
ENSG00000100504	PYGL	267.473649	2402.305717	3.166255351	2.52E-12	4.66E-11
ENSG00000161267	BDH1	50.52465852	4827.735829	6.574249359	2.88E-34	2.70E-32
ENSG00000042445	RETSAT	873.997055	4621.972936	2.402608089	3.12E-08	3.31E-07
ENSG00000168306	ACOX2	31.08466991	3694.753896	6.886675072	2.12E-35	2.09E-33
ENSG00000116791	CRYZ	576.1785243	4215.591221	2.870830427	9.46E-11	1.44E-09
ENSG00000136868	SLC31A1	1027.960679	4099.849593	1.99562393	3.02E-06	2.33E-05
ENSG00000120053	GOT1	945.5357087	7424.206342	2.972838567	1.92E-11	3.25E-10
ENSG00000171236	LRG1	609.6150701	5990.296178	3.296349451	2.65E-13	5.46E-12
ENSG00000148834	GSTO1	2204.460476	4679.843749	1.08597324	0.009112243	0.029970199
ENSG00000149124	GLYAT	1.534979634	5623.781024	11.71203926	3.00E-55	1.55E-52
ENSG00000118514	ALDH8A1	15.53254811	4782.725196	8.25343451	2.20E-43	3.73E-41
ENSG00000009950	MLXIPL	55.19024445	3724.332312	6.072805283	1.04E-30	7.72E-29
ENSG00000139540	SLC39A5	4.645755009	2988.729966	9.28632904	6.02E-45	1.17E-42
ENSG00000111885	MAN1A1	1111.163243	4188.584841	1.914244107	7.06E-06	5.09E-05
ENSG00000166123	GPT2	206.8212926	7231.303629	5.126843181	2.78E-25	1.50E-23
ENSG00000057593	F7	3.090401881	6450.690652	10.96304541	3.43E-54	1.61E-51
ENSG00000129596	CDO1	19.42060034	5718.946362	8.191650117	1.04E-43	1.82E-41
ENSG00000146416	AIG1	436.9891793	3914.662989	3.162792942	1.93E-12	3.62E-11
ENSG00000164904	ALDH7A1	214.5972363	4922.901168	4.518893874	4.91E-21	1.98E-19
ENSG00000141232	TOB1	827.3414111	5884.842695	2.830229227	1.46E-10	2.14E-09
ENSG00000146085	MUT	195.9349709	5592.91659	4.834149519	3.39E-23	1.58E-21
ENSG00000100897	DCAF11	965.7531543	4337.762939	2.167048334	4.62E-07	4.08E-06
ENSG00000162882	HAAO	195.9349709	5009.064379	4.675092781	4.36E-22	1.89E-20
ENSG00000100003	SEC14L2	85.51650426	6192.201017	6.175768558	4.05E-32	3.36E-30
ENSG00000175336	APOF	6.201060061	6970.241958	10.10209821	1.99E-52	7.07E-50
ENSG00000167792	NDUFV1	1432.309587	3119.903811	1.123062349	0.007154567	0.024413338
ENSG00000187045	TMPRSS6	12.42208703	5096.513609	8.664253388	1.88E-45	3.76E-43
ENSG00000117335	CD46	1294.67544	2997.732093	1.211171999	0.003801641	0.014098743
ENSG00000115524	SF3B1	1552.836665	3715.330185	1.258492224	0.002634664	0.010152647
ENSG00000071537	SEL1L	1318.780855	2963.009604	1.16775287	0.005222492	0.018506565
ENSG00000259974	LINC00261	3.090401881	6295.082464	10.92781759	6.30E-54	2.73E-51
ENSG00000036473	OTC	4.645755009	5106.801754	10.05919708	1.05E-50	3.18E-48
ENSG00000116016	EPAS1	1212.25047	4249.027691	1.809311584	2.04E-05	0.000133707
ENSG00000008952	SEC62	1108.052867	4543.525832	2.035634433	1.95E-06	1.55E-05
ENSG00000160932	LY6E	2642.245924	6158.764547	1.220822675	0.003436953	0.012888573
ENSG00000062282	DGAT2	71.51977693	3531.429599	5.622984246	6.74E-28	4.25E-26
ENSG00000119927	GPAM	48.9694625	4376.343481	6.477609974	1.40E-33	1.25E-31
ENSG00000143149	ALDH9A1	669.4898144	4111.423756	2.61823694	2.35E-09	2.92E-08
ENSG00000151632	AKR1C2	260.4753007	6725.898522	4.689754998	2.69E-22	1.19E-20
ENSG00000166228	PCBD1	854.5572034	5546.619939	2.698149193	8.02E-10	1.07E-08
ENSG00000120915	EPHX2	143.0585416	5241.833653	5.194010536	1.48E-25	8.11E-24
ENSG00000186350	RXRA	1003.077669	4695.275967	2.226605458	2.33E-07	2.16E-06
ENSG00000093010	COMT	947.0908968	3612.448738	1.931228205	6.02E-06	4.39E-05
ENSG00000128016	ZFP36	1338.998301	3567.438105	1.413622975	0.000767245	0.003497133
ENSG00000162482	AKR7A3	88.62688686	5270.126051	5.891698978	4.17E-30	3.00E-28
ENSG00000123843	C4BPB	205.2661038	5311.278629	4.692535571	3.35E-22	1.47E-20
ENSG00000116678	LEPR	127.5066458	7465.358921	5.870003735	2.75E-30	2.00E-28
ENSG00000134352	IL6ST	1047.40053	4701.706057	2.166208396	4.62E-07	4.08E-06
ENSG00000184117	NIPSNAP1	411.328573	4070.271177	3.306305842	2.75E-13	5.63E-12
ENSG00000074416	MGLL	1227.802351	2838.26585	1.208816554	0.00388052	0.014361277
ENSG00000168509	HFE2	6.201060061	3416.973989	9.073629659	9.34E-45	1.80E-42
ENSG00000009724	MASP2	13.97732024	5549.191975	8.618639843	2.03E-45	4.04E-43
ENSG00000110092	CCND1	1387.986726	3305.090416	1.25159311	0.002793329	0.010697718
ENSG00000157557	ETS2	943.9805206	5308.706593	2.491344196	1.00E-08	1.14E-07
ENSG00000182919	C11orf54	253.4769522	3644.59919	3.845076396	1.42E-16	3.98E-15

ENSG00000139178	<i>C1RL</i>	866.2211143	3836.215885	2.146680411	6.14E-07	5.31E-06
ENSG00000215301	<i>DDX3X</i>	1705.245098	3543.003762	1.054915206	0.011350162	0.036410464
ENSG00000004142	<i>POLDIP2</i>	1170.260391	3257.507746	1.476809763	0.000453092	0.002190122
ENSG00000153904	<i>DDAH1</i>	387.2231546	2555.34187	2.72181321	7.71E-10	1.03E-08
ENSG00000005471	<i>ABCB4</i>	33.41747441	2740.528475	6.351718051	9.36E-32	7.65E-30
ENSG00000143653	<i>SCCPDH</i>	560.6266425	3215.069149	2.51942144	8.45E-09	9.72E-08
ENSG00000143627	<i>PKLR</i>	1.534979634	2818.975578	10.71569463	8.20E-48	2.00E-45
ENSG00000116785	<i>CFHR3</i>	2.312696499	3783.489144	10.59044519	1.44E-49	3.85E-47
ENSG00000109919	<i>MTCH2</i>	886.43856	2632.502956	1.570168377	0.000206005	0.001079994
ENSG00000125520	<i>SLC2A4RG</i>	924.5406691	2362.439157	1.353309724	0.001293729	0.005522178
ENSG00000176919	<i>C8G</i>	662.4914677	3504.423219	2.402938839	3.33E-08	3.51E-07
ENSG00000088812	<i>ATRN</i>	482.0896382	2739.242457	2.50603649	1.06E-08	1.21E-07
ENSG00000250799	<i>PRODH2</i>	15.53254811	2628.644901	7.389944904	5.38E-37	5.64E-35
ENSG00000139112	<i>GABARAPL1</i>	1601.82509	4463.792711	1.478458934	0.000437721	0.002123254
ENSG00000069275	<i>NUCKS1</i>	1051.288501	2298.138252	1.128176154	0.007019169	0.023974364
ENSG00000141485	<i>SLC13A5</i>	13.19970438	4886.892661	8.517017084	1.62E-44	3.08E-42
ENSG00000164344	<i>KLKB1</i>	22.53102899	4729.998455	7.70485372	1.24E-40	1.79E-38
ENSG00000143845	<i>ETNK2</i>	91.73726908	3082.609286	5.068346147	2.88E-24	1.44E-22
ENSG00000143278	<i>F13B</i>	2.312696499	4669.555605	10.89400611	7.83E-52	2.56E-49
ENSG00000221869	<i>CEBPD</i>	1950.187223	4615.542845	1.242814683	0.00294024	0.01118452
ENSG00000137642	<i>SORL1</i>	457.2066265	4803.301486	3.392696221	7.64E-14	1.65E-12
ENSG00000132837	<i>DMGDH</i>	6.201060061	5859.122333	9.851577858	1.49E-50	4.40E-48
ENSG00000116690	<i>PRG4</i>	5.423411881	3090.325395	9.117386893	1.89E-44	3.56E-42
ENSG00000204444	<i>APOM</i>	34.19507543	6256.501921	7.509542935	2.87E-40	4.01E-38
ENSG00000145476	<i>CYP4V2</i>	510.083026	3692.18186	2.855312213	1.18E-10	1.77E-09
ENSG00000157103	<i>SLC6A1</i>	25.64144922	2872.988338	6.800106935	2.18E-34	2.05E-32
ENSG00000128050	<i>PAICS</i>	744.1388457	2129.669882	1.516780921	0.000339498	0.001687644
ENSG00000006831	<i>ADIPOR2</i>	846.7812627	3071.035124	1.858471269	1.31E-05	8.94E-05
ENSG00000111666	<i>CHPT1</i>	280.6927512	2331.574722	3.053582511	1.12E-11	1.94E-10
ENSG00000103876	<i>FAH</i>	147.7241098	3006.734219	4.345901091	1.18E-19	4.28E-18
ENSG00000115425	<i>PECR</i>	168.7191642	3393.825664	4.329062336	1.28E-19	4.63E-18
ENSG00000101444	<i>AHCY</i>	1055.176471	4138.430135	1.97144207	3.89E-06	2.94E-05
ENSG00000143158	<i>MPC2</i>	825.7862229	2869.130284	1.796577892	2.45E-05	0.00015827
ENSG00000082153	<i>BZW1</i>	1161.706857	3233.073403	1.47652998	0.000454437	0.002196194
ENSG00000181061	<i>HIGD1A</i>	795.4600543	3626.594937	2.188539372	3.89E-07	3.47E-06
ENSG00000169242	<i>EFNA1</i>	1171.037985	3247.219602	1.47128806	0.000475117	0.002289904
ENSG00000100612	<i>DHRS7</i>	1024.072709	2125.811828	1.053564797	0.011734058	0.037511256
ENSG00000183549	<i>ACSM5</i>	57.52303638	4479.224928	6.279488064	2.49E-32	2.09E-30
ENSG00000102024	<i>PLS3</i>	1073.061134	3235.645439	1.592176664	0.00016414	0.00088162
ENSG00000178104	<i>PDE4DIP</i>	1196.698589	2476.894767	1.049360852	0.011964091	0.03811915
ENSG00000101076	<i>HNF4A</i>	205.2661038	3045.314762	3.890087356	9.00E-17	2.56E-15
ENSG00000117054	<i>ACADM</i>	326.5708096	3906.94688	3.579992169	5.96E-15	1.45E-13
ENSG00000168234	<i>TTC39C</i>	475.0912911	2960.437568	2.639156623	2.04E-09	2.56E-08
ENSG00000135069	<i>PSAT1</i>	164.8311914	3517.2834	4.414216378	3.41E-20	1.29E-18
ENSG00000179889	<i>PDXDC1</i>	773.6874204	2865.27223	1.888637779	9.83E-06	6.85E-05
ENSG00000067167	<i>TRAM1</i>	753.4699745	1877.610336	1.317082801	0.001767141	0.007196834
ENSG00000169692	<i>AGPAT2</i>	865.4435203	2343.148885	1.436763882	0.000660219	0.003058665
ENSG00000131724	<i>IL13RA1</i>	1349.107023	2948.863405	1.128052276	0.006927399	0.023742486
ENSG00000102910	<i>LONP2</i>	651.6051506	3519.855436	2.433176605	2.32E-08	2.50E-07
ENSG000000099860	<i>GADD45B</i>	802.4584009	4996.204198	2.638110687	1.76E-09	2.23E-08
ENSG00000169919	<i>GUSB</i>	1173.370768	2547.625762	1.118377593	0.00746979	0.025249779
ENSG00000074696	<i>PTPLAD1</i>	629.8325163	2627.358883	2.060306307	1.67E-06	1.34E-05
ENSG00000090512	<i>FETUB</i>	3.090401881	3456.84055	10.06306467	1.80E-47	4.26E-45
ENSG00000167969	<i>ECI1</i>	979.7498474	2957.865532	1.593912699	0.000162914	0.000876643
ENSG00000147853	<i>AK3</i>	656.2707151	4292.752306	2.709265336	7.47E-10	1.00E-08
ENSG00000139269	<i>INHBE</i>	10.8668471	592.8782362	5.751418506	6.24E-24	3.05E-22
ENSG00000145675	<i>PIK3R1</i>	160.1656239	4110.137738	4.680324856	5.72E-22	2.46E-20
ENSG00000132361	<i>CLUH</i>	922.9854809	3512.139328	1.927791656	6.25E-06	4.55E-05
ENSG00000052802	<i>MSMO1</i>	379.4472131	3899.230772	3.360722867	1.31E-13	2.77E-12
ENSG00000187017	<i>ESPN</i>	62.96621528	1566.393956	4.633609609	7.79E-21	3.08E-19
ENSG00000114200	<i>BCHE</i>	1.534979634	4094.705521	11.25426785	7.92E-52	2.56E-49
ENSG00000159921	<i>GNE</i>	507.7502437	3941.669368	2.95625421	3.10E-11	5.07E-10
ENSG000000090013	<i>BLVRB</i>	660.1586855	3014.450328	2.190751229	3.96E-07	3.54E-06
ENSG00000159228	<i>CBR1</i>	684.2641019	3524.999508	2.364742945	5.25E-08	5.40E-07
ENSG00000143365	<i>RORC</i>	129.8394304	3071.035124	4.562416313	4.72E-21	1.91E-19
ENSG00000117707	<i>PROX1</i>	113.5099365	4047.122851	5.154263266	4.71E-25	2.49E-23
ENSG00000173599	<i>PC</i>	189.7142155	4408.493933	4.537354676	4.15E-21	1.68E-19
ENSG00000095321	<i>CRAT</i>	400.442255	2595.208431	2.695734665	1.06E-09	1.38E-08
ENSG00000105221	<i>AKT2</i>	1207.584906	2435.742188	1.01212739	0.015285127	0.046723875
ENSG00000004864	<i>SLC25A13</i>	171.0519478	2560.485943	3.902786601	8.39E-17	2.41E-15
ENSG00000146701	<i>MDH2</i>	1272.125212	2874.274356	1.175847367	0.004934215	0.017587826

ENSG00000067082	<i>KLF6</i>	1660.144643	4700.420039	1.501389105	0.000357968	0.001764634
ENSG00000197444	<i>OGDHL</i>	155.5000563	4193.728913	4.75198267	1.82E-22	8.08E-21
ENSG00000126218	<i>F10</i>	33.41747441	5342.143063	7.314657617	8.05E-39	1.02E-36
ENSG00000189221	<i>MAOA</i>	25.64144922	4085.703394	7.308124782	4.00E-38	4.82E-36
ENSG00000159650	<i>UROCI</i>	0.757489584	3523.71349	11.93694364	3.30E-50	9.21E-48
ENSG00000139194	<i>RBP5</i>	129.0618355	2762.390782	4.418270589	4.43E-20	1.67E-18
ENSG00000164976	<i>KIAA1161</i>	118.9531016	1911.046806	4.00427555	3.06E-17	9.11E-16
ENSG00000065361	<i>ERBB3</i>	854.5572034	2321.286578	1.441500096	0.000631434	0.002939006
ENSG00000123561	<i>SERPINA7</i>	15.53254811	5162.100531	8.363557694	3.35E-44	6.17E-42
ENSG00000140479	<i>PCSK6</i>	87.84929125	3073.60716	5.126506939	1.21E-24	6.22E-23
ENSG00000198721	<i>ECI2</i>	283.8031281	2712.236077	3.255861354	6.78E-13	1.33E-11
ENSG00000160221	<i>C21orf33</i>	1125.93753	4086.989412	1.859766927	1.24E-05	8.46E-05
ENSG00000091262	<i>ABCC6</i>	192.0469988	2950.149423	3.940253843	4.17E-17	1.23E-15
ENSG00000091483	<i>FH</i>	526.4125022	3822.069686	2.859741997	1.12E-10	1.69E-09
ENSG00000162365	<i>CYP4A22</i>	7.75633786	4296.61036	9.08769525	1.65E-46	3.60E-44
ENSG00000105854	<i>PON2</i>	727.0317761	1669.275404	1.198938299	0.004367292	0.015782016
ENSG00000115457	<i>IGFBP2</i>	618.1686051	5998.012286	3.278109322	3.46E-13	7.04E-12
ENSG00000176907	<i>C8orf4</i>	901.9904413	3933.95326	2.124607836	7.49E-07	6.38E-06
ENSG00000124098	<i>FAM210B</i>	507.7502437	3442.694351	2.760990702	4.09E-10	5.67E-09
ENSG00000162817	<i>C1orf115</i>	253.4769522	3073.60716	3.599256165	5.48E-15	1.34E-13
ENSG00000129988	<i>LBP</i>	17.08777164	4264.459908	7.951478816	2.49E-41	3.75E-39
ENSG00000112697	<i>TMEM30A</i>	1266.682054	2635.074992	1.056683594	0.011358932	0.036429195
ENSG00000003436	<i>TFPI</i>	940.0925503	3802.779415	2.016001918	2.45E-06	1.92E-05
ENSG00000163527	<i>STT3B</i>	850.669233	1863.464137	1.131155065	0.007037293	0.024026361
ENSG00000122971	<i>ACADS</i>	538.0764137	3620.164847	2.749836345	4.59E-10	6.32E-09
ENSG00000140740	<i>UQCRC2</i>	1360.770934	3049.172816	1.163891486	0.005361597	0.018873034
ENSG00000133657	<i>ATP13A3</i>	551.2955133	3116.045757	2.498497834	1.11E-08	1.25E-07
ENSG00000119471	<i>HSDL2</i>	280.6927512	3158.484354	3.491494522	2.39E-14	5.43E-13
ENSG00000127241	<i>MASP1</i>	44.30387198	4277.320089	6.588607248	4.42E-34	4.11E-32
ENSG00000137700	<i>SLC37A4</i>	748.026816	3819.49765	2.351988122	6.00E-08	6.11E-07
ENSG00000072080	<i>SPP2</i>	6.978701584	5169.81664	9.50414998	1.69E-48	4.34E-46
ENSG00000112972	<i>HMGCS1</i>	215.3748307	1031.410424	2.258896361	2.88E-07	2.63E-06
ENSG00000075234	<i>TTC38</i>	579.2889007	4355.767192	2.91025597	5.57E-11	8.78E-10
ENSG00000147155	<i>EBP</i>	392.6663136	3089.039377	2.975314281	2.69E-11	4.44E-10
ENSG00000105835	<i>NAMPT</i>	970.4187186	3280.656072	1.757140007	3.49E-05	0.000219022
ENSG00000162433	<i>AK4</i>	69.96458431	2875.560374	5.358238757	4.93E-26	2.79E-24
ENSG00000196914	<i>ARHGEF12</i>	821.8982526	3382.251501	2.040748325	1.96E-06	1.56E-05
ENSG00000148730	<i>EIF4EBP2</i>	1505.403428	3676.749643	1.288184967	0.00209777	0.008406977
ENSG00000104408	<i>EIF3E</i>	1684.250059	3370.677338	1.000854054	0.016218746	0.049238664
ENSG00000180398	<i>MCFD2</i>	1076.949105	2844.69594	1.401186429	0.000863926	0.003855811
ENSG00000140284	<i>SLC27A2</i>	57.52303638	3972.533802	6.106302439	4.52E-31	3.43E-29
ENSG00000117500	<i>TMED5</i>	687.3744782	2375.299338	1.788706791	2.75E-05	0.000176124
ENSG00000130988	<i>RGN</i>	46.63666774	5940.141473	6.988584247	3.47E-37	3.72E-35
ENSG00000117118	<i>SDHB</i>	1018.62955	2861.414175	1.489949895	0.000409011	0.001993325
ENSG00000109758	<i>HGFAC</i>	16.31016037	5102.943699	8.277071289	1.18E-43	2.03E-41
ENSG00000063241	<i>ISOC2</i>	783.0185492	2624.786847	1.744877756	4.14E-05	0.000255949
ENSG00000112936	<i>C7</i>	279.9151569	5235.403562	4.224545433	3.78E-19	1.30E-17
ENSG00000072506	<i>HSD17B10</i>	771.3546382	2974.583767	1.947007293	5.42E-06	4.01E-05
ENSG00000176171	<i>BNIP3</i>	406.6630082	4085.703394	3.328217173	1.98E-13	4.14E-12
ENSG00000196502	<i>SULT1A1</i>	256.5873293	5298.418448	4.3672803	4.49E-20	1.68E-18
ENSG00000084110	<i>HAL</i>	6.201060061	4371.199409	9.428930627	2.12E-47	4.97E-45
ENSG00000122729	<i>ACO1</i>	696.7056072	4402.063843	2.659301382	1.38E-09	1.78E-08
ENSG00000162337	<i>LRP5</i>	406.6630082	2936.003224	2.851499693	1.38E-10	2.03E-09
ENSG00000149809	<i>TM7SF2</i>	187.3814321	2353.43703	3.649702375	3.53E-15	8.83E-14
ENSG00000106261	<i>ZKSCAN1</i>	674.1553789	2645.363136	1.972066599	4.29E-06	3.22E-05
ENSG00000117791	<i>2-Mar</i>	258.1425179	3104.471594	3.587371834	6.09E-15	1.48E-13
ENSG00000123684	<i>LPGAT1</i>	684.2641019	1381.20735	1.013111565	0.015736472	0.047914984
ENSG00000176720	<i>BOK</i>	391.1111253	2573.346123	2.717533854	8.15E-10	1.08E-08
ENSG00000204219	<i>TCEA3</i>	111.1771513	2385.587482	4.421656311	6.42E-20	2.37E-18
ENSG00000126522	<i>ASL</i>	234.8146891	4111.423756	4.129218587	1.94E-18	6.35E-17
ENSG00000108479	<i>GALK1</i>	320.3500561	1652.557169	2.366434286	6.66E-08	6.73E-07
ENSG00000133048	<i>CH13L1</i>	2345.982593	5200.681074	1.148449268	0.005865146	0.020484277
ENSG00000143252	<i>SDHC</i>	993.7465404	2038.362598	1.036326742	0.013182784	0.041106273
ENSG00000112992	<i>NNT</i>	506.9726496	4153.862353	3.034109535	1.07E-11	1.86E-10
ENSG00000122490	<i>PQLC1</i>	776.0202026	3152.054263	2.02191087	2.46E-06	1.93E-05
ENSG00000109180	<i>OCIAD1</i>	1259.683707	2649.221191	1.072399617	0.010217928	0.033115998
ENSG00000115107	<i>STEAP3</i>	192.8245932	3337.240868	4.112290707	3.08E-18	9.85E-17
ENSG00000170412	<i>GPRC5C</i>	238.7026607	3716.616203	3.95989586	2.59E-17	7.78E-16
ENSG00000105607	<i>GCDH</i>	408.9957906	4128.141991	3.334875538	1.77E-13	3.71E-12
ENSG00000157379	<i>DHRS1</i>	321.1276503	2779.109018	3.112826005	4.48E-12	8.05E-11
ENSG00000123453	<i>SARDH</i>	272.1392145	4002.112218	3.877638713	7.76E-17	2.23E-15

ENSG00000130173	<i>C19orf80</i>	2.312696499	949.1052639	8.595478615	7.65E-35	7.37E-33
ENSG00000148339	<i>SLC25A25</i>	145.3913257	4659.26746	5.000732536	3.71E-24	1.84E-22
ENSG00000197408	<i>CYP2B6</i>	1.39E-17	4323.61674	15.12322719	2.07E-52	7.13E-50
ENSG00000251164	<i>HULC</i>	11.64446802	2856.270103	7.921078913	9.23E-40	1.25E-37
ENSG00000078902	<i>TOLLIP</i>	735.5853109	2348.292958	1.674433384	8.12E-05	0.000467217
ENSG00000116962	<i>NID1</i>	748.026816	2118.095719	1.501402503	0.000389487	0.001906398
ENSG00000106049	<i>HIBADH</i>	558.2938602	3375.82141	2.595822292	3.31E-09	4.03E-08
ENSG00000198961	<i>PJA2</i>	691.2624486	2064.082959	1.577971697	0.00019967	0.001047887
ENSG00000185813	<i>PCYT2</i>	488.310391	2502.615128	2.357209076	6.28E-08	6.37E-07
ENSG00000204128	<i>C2orf72</i>	147.7241098	3630.452991	4.617845303	1.62E-21	6.83E-20
ENSG00000131844	<i>MCCC2</i>	572.2905538	3132.763992	2.452308752	1.92E-08	2.10E-07
ENSG00000088766	<i>CRLS1</i>	415.2165437	2336.718795	2.492122575	1.33E-08	1.48E-07
ENSG00000178537	<i>SLC25A20</i>	318.7948677	2422.882007	2.925449035	5.79E-11	9.10E-10
ENSG00000142494	<i>SLC47A1</i>	139.1705679	3045.314762	4.4502617	2.73E-20	1.04E-18
ENSG00000065809	<i>FAM107B</i>	916.7647284	2316.142505	1.336941151	0.001476399	0.0061529
ENSG00000237973	<i>hsa-mir-6723</i>	1294.67544	2990.015984	1.207453862	0.00390809	0.014439658
ENSG00000169083	<i>AR</i>	47.4142661	3409.257881	6.163776725	3.91E-31	3.00E-29
ENSG00000158864	<i>NDUFS2</i>	1067.617976	2404.877754	1.171437483	0.00514848	0.018275562
ENSG00000124486	<i>USP9X</i>	828.1190051	2489.754948	1.587906545	0.000178127	0.000948915
ENSG00000023228	<i>NDUFS1</i>	831.2293814	2977.155803	1.84042066	1.60E-05	0.000106804
ENSG00000159461	<i>AMFR</i>	1055.954065	2338.004813	1.146599829	0.006158648	0.02134912
ENSG00000154723	<i>ATP5J</i>	815.6775001	2528.33549	1.631925377	0.000118723	0.000659558
ENSG00000151552	<i>QDPR</i>	300.1326068	3802.779415	3.662747128	1.80E-15	4.65E-14
ENSG00000160113	<i>NR2F6</i>	412.8837612	1414.643821	1.776241933	3.52E-05	0.000220564
ENSG00000173334	<i>TRIB1</i>	1188.922649	3900.51679	1.713876763	5.21E-05	0.000313031
ENSG00000116704	<i>SLC35D1</i>	190.4918099	3076.179196	4.012325283	1.50E-17	4.57E-16
ENSG00000111713	<i>GYS2</i>	3.868086451	3604.73263	9.812430919	6.38E-48	1.60E-45
ENSG0000015479	<i>MATR3</i>	1174.148362	2403.591736	1.033463747	0.013309313	0.041417675
ENSG00000109929	<i>SC5D</i>	101.8460091	3940.38335	5.271929031	8.05E-26	4.47E-24
ENSG00000145826	<i>LECT2</i>	9.31159843	5245.691707	9.11628239	2.19E-47	5.08E-45
ENSG00000204370	<i>SDHD</i>	1061.397223	3086.467341	1.539847284	0.000263045	0.001343331
ENSG00000152700	<i>SAR1B</i>	677.2657552	2803.543361	2.049209677	1.88E-06	1.50E-05
ENSG00000163541	<i>SUCLG1</i>	879.4402134	2265.9878	1.365315264	0.001187021	0.005106163
ENSG00000187837	<i>HIST1H1C</i>	329.6811864	1117.573638	1.760740142	4.25E-05	0.000261818
ENSG00000196365	<i>LONP1</i>	856.8899856	1939.339204	1.178220235	0.005011429	0.017845138
ENSG00000117528	<i>ABCD3</i>	189.7142155	2510.331237	3.724970597	1.11E-15	2.91E-14
ENSG00000077147	<i>TM9SF3</i>	1007.743233	2336.718795	1.213215934	0.003804226	0.014104124
ENSG00000187244	<i>BCAM</i>	498.4191144	1165.156308	1.224807942	0.003749141	0.013932475
ENSG00000076770	<i>MBNL3</i>	116.6203166	2496.185038	4.418159915	5.69E-20	2.11E-18
ENSG00000116717	<i>GADD45A</i>	412.1061671	3456.84055	3.067917264	7.31E-12	1.29E-10
ENSG00000144224	<i>UBXN4</i>	854.5572034	2395.875627	1.48712659	0.000429411	0.002085795
ENSG00000023839	<i>ABCC2</i>	181.1606764	3233.073403	4.156494362	1.81E-18	5.93E-17
ENSG00000114054	<i>PCCB</i>	377.8920248	3023.452454	2.999663575	1.95E-11	3.30E-10
ENSG00000151914	<i>DST</i>	545.8523546	3006.734219	2.461291835	1.72E-08	1.89E-07
ENSG00000076555	<i>ACACB</i>	270.584026	3209.925077	3.567689291	8.14E-15	1.94E-13
ENSG00000198732	<i>SMOC1</i>	80.8509296	2907.710826	5.166027916	7.86E-25	4.09E-23
ENSG00000152332	<i>UHMK1</i>	588.6200297	1887.898481	1.68110431	7.89E-05	0.000455309
ENSG00000149547	<i>EI24</i>	657.8259033	3008.020237	2.192776597	3.81E-07	3.41E-06
ENSG00000138434	<i>SSFA2</i>	615.0582287	2650.507209	2.107198576	1.03E-06	8.56E-06
ENSG00000128849	<i>CGNL1</i>	401.9974433	1553.533775	1.949883941	6.23E-06	4.54E-05
ENSG00000163110	<i>PDLIM5</i>	935.4269859	2482.038839	1.407669653	0.000828371	0.003743483
ENSG00000138867	<i>GUCD1</i>	1043.51256	3116.045757	1.578120204	0.000186931	0.000990864
ENSG00000133135	<i>RNF128</i>	220.0403968	2592.636395	3.557716939	1.08E-14	2.54E-13
ENSG00000149150	<i>SLC43A1</i>	356.8969825	2460.176532	2.784674109	3.47E-10	4.85E-09
ENSG00000094631	<i>HDAC6</i>	787.6841136	2310.998433	1.552631855	0.000244035	0.001256314
ENSG00000065534	<i>MYLK</i>	872.4418668	2536.051599	1.539277337	0.000272455	0.001386825
ENSG00000090060	<i>PAPOLA</i>	841.3381043	1821.02554	1.113830882	0.007867787	0.026419054
ENSG00000122378	<i>FAM213A</i>	468.0929441	2887.134537	2.624389128	2.48E-09	3.07E-08
ENSG00000197903	<i>HIST1H2BK</i>	394.999096	806.3572511	1.029233157	0.015185719	0.046477165
ENSG00000147813	<i>NAPRT1</i>	555.9610779	2107.807575	1.922391158	7.52E-06	5.39E-05
ENSG00000180573	<i>HIST1H2AC</i>	275.2495915	730.4821804	1.407567883	0.001042593	0.00455905
ENSG00000067704	<i>IARS2</i>	846.7812627	2186.254678	1.36822621	0.001169726	0.00505451
ENSG00000164050	<i>PLXNB1</i>	908.2111938	2258.271691	1.313959398	0.001773192	0.007219115
ENSG00000114021	<i>NIT2</i>	454.8738441	2393.303591	2.395080244	4.02E-08	4.20E-07
ENSG00000156222	<i>SLC28A1</i>	0.757489584	1096.997348	10.25349511	9.45E-38	1.10E-35
ENSG00000123689	<i>GOS2</i>	199.822943	787.0669789	1.976932887	6.14E-06	4.47E-05
ENSG00000170385	<i>SLC30A1</i>	237.1474721	2017.786308	3.088135926	8.27E-12	1.45E-10
ENSG00000198189	<i>HSD17B11</i>	685.041696	3119.903811	2.186988399	4.12E-07	3.67E-06
ENSG00000166816	<i>LDHD</i>	156.2776509	3245.933584	4.375202394	7.31E-20	2.69E-18
ENSG00000110090	<i>CPT1A</i>	987.525788	3910.804934	1.985406897	3.38E-06	2.59E-05
ENSG00000112299	<i>VNN1</i>	503.8622732	2496.185038	2.308279454	1.08E-07	1.05E-06

ENSG00000106633	GCK	5.423411881	54.03631542	3.282259066	2.52E-06	1.97E-05
ENSG00000008513	ST3GAL1	992.9689464	3779.63109	1.928258933	6.17E-06	4.49E-05
ENSG00000082438	COBLL1	121.2858865	2960.437568	4.607710697	2.84E-21	1.17E-19
ENSG00000130396	MLLT4	622.0565755	2530.907526	2.024268299	2.51E-06	1.96E-05
ENSG00000164089	ETNPPL	16.31016037	2915.426935	7.469469353	1.12E-37	1.28E-35
ENSG00000165474	GJB2	96.40284179	857.7979766	3.151560739	1.04E-11	1.81E-10
ENSG00000011347	SYT7	7.75633786	995.4019163	6.97795564	5.33E-31	4.01E-29
ENSG00000110887	DAO	1.534979634	2100.091466	10.29099284	1.17E-44	2.23E-42
ENSG000000114378	HYAL1	386.4455604	2939.861279	2.926936778	5.23E-11	8.29E-10
ENSG00000125740	FOSB	28.75186299	1837.743775	5.991191753	7.39E-29	4.93E-27
ENSG00000177119	ANO6	620.5013873	2191.398751	1.820084662	2.05E-05	0.000134211
ENSG00000113282	CLINT1	573.845742	2111.665629	1.8793615	1.16E-05	7.99E-05
ENSG00000162407	PPAP2B	609.6150701	2680.085625	2.136030125	7.35E-07	6.28E-06
ENSG00000179295	PTPN11	675.7105671	1530.38545	1.179210925	0.005108062	0.018155426
ENSG00000168389	MFS2A	80.0733372	4330.04683	5.754429141	6.21E-29	4.16E-27
ENSG00000096696	DSP	876.3298372	2118.095719	1.273057988	0.002449243	0.009534209
ENSG00000249948	GBA3	4.645755009	2597.780467	9.084083065	1.91E-43	3.27E-41
ENSG00000164466	SFXN1	624.3893577	2936.003224	2.233060471	2.46E-07	2.27E-06
ENSG00000100075	SLC25A1	552.8507015	2749.530602	2.313909718	9.89E-08	9.69E-07
ENSG00000205213	LGR4	241.8130379	2779.109018	3.52187479	1.71E-14	3.92E-13
ENSG00000119396	RAB14	861.5555499	1841.601829	1.095787529	0.009003328	0.029666939
ENSG000000147100	SLC16A2	77.74054591	2431.884134	4.964725259	2.34E-23	1.10E-21
ENSG00000107562	XCLL12	659.3810914	3915.949007	2.569907517	4.35E-09	5.22E-08
ENSG00000156709	AIFM1	552.0731074	2379.157392	2.107213121	1.05E-06	8.75E-06
ENSG00000116761	CTH	32.63987315	5222.543381	7.315815507	7.93E-39	1.01E-36
ENSG00000213949	ITGA1	530.3004727	2437.028206	2.199918246	3.76E-07	3.37E-06
ENSG00000154305	MIA3	540.409196	2563.057979	2.245423506	2.22E-07	2.07E-06
ENSG00000137561	TTPA	14.75493478	2745.672547	7.526196723	6.78E-38	8.02E-36
ENSG000000000003	TSPAN6	265.1408662	2075.657122	2.968044003	3.84E-11	6.22E-10
ENSG00000099769	IGFALS	104.1787948	3901.802808	5.225106437	1.90E-25	1.03E-23
ENSG00000138796	HADH	265.9184605	3019.5944	3.504586852	2.03E-14	4.62E-13
ENSG00000001084	GCLC	351.4538233	2505.187165	2.832993436	1.90E-10	2.76E-09
ENSG00000122203	KIAA1191	1093.27858	2237.695402	1.033230821	0.013380686	0.041598117
ENSG00000130414	NDUFA10	933.8717978	2107.807575	1.174297342	0.00509011	0.018099383
ENSG00000151365	THRSP	0.757489584	2966.867659	11.68879506	2.33E-48	5.92E-46
ENSG00000154262	ABCA6	39.63827699	3031.168563	6.251789731	1.84E-31	1.45E-29
ENSG00000092148	HECTD1	325.7932154	2561.771961	2.974549243	2.96E-11	4.87E-10
ENSG00000135447	PPP1R1A	11.64446802	2721.238204	7.851212184	3.03E-39	4.03E-37
ENSG00000114779	ABHD14B	691.2624486	2628.644901	1.92677541	6.84E-06	4.94E-05
ENSG00000128590	DNAJB9	517.8589671	1880.182372	1.859926594	1.45E-05	9.79E-05
ENSG00000148803	FUOM	471.2033206	2836.979832	2.589555701	3.81E-09	4.61E-08
ENSG00000099977	DDT	214.5972363	5060.505103	4.558665714	2.61E-21	1.08E-19
ENSG00000141905	NFIC	818.0102823	2244.125492	1.45577843	0.000569438	0.002681072
ENSG00000100528	CNIH1	738.6956872	1759.296671	1.251753436	0.002958327	0.01124988
ENSG00000160867	FGFR4	758.135539	1935.48115	1.35197101	0.00134454	0.005717457
ENSG00000065154	OAT	497.6415203	4477.93891	3.169282126	1.70E-12	3.21E-11
ENSG00000160007	ARHGAP35	644.6068039	1783.731015	1.468172517	0.00052221	0.002473705
ENSG00000197142	ACSL5	1076.171511	3186.776752	1.566046552	0.000207876	0.001088887
ENSG00000128609	NDUFA5	710.7023005	1656.415223	1.220548	0.00375516	0.013949261
ENSG00000137414	FAM8A1	312.5741141	2323.858614	2.893667153	9.05E-11	1.38E-09
ENSG00000213398	LCAT	136.0601889	2753.388656	4.337459489	1.44E-19	5.16E-18
ENSG00000113328	CCNG1	611.9478524	2335.432777	1.931939785	6.69E-06	4.84E-05
ENSG00000108588	CCDC47	819.5654704	1661.559296	1.019445012	0.015044794	0.046074217
ENSG00000164406	LEAP2	28.75186299	2595.208431	6.489084254	1.85E-32	1.57E-30
ENSG00000150540	HNMT	486.7552028	3177.774625	2.706378298	8.39E-10	1.11E-08
ENSG000000243649	CFB	182.7158653	2186.254678	3.579747745	9.73E-15	2.30E-13
ENSG00000137364	TPMT	583.9544652	1889.184499	1.693564695	7.15E-05	0.000418843
ENSG00000159200	RCAN1	206.0436982	1846.745902	3.163060052	3.09E-12	5.65E-11
ENSG00000121057	AKAP1	482.0896382	1621.692735	1.749795304	4.33E-05	0.000266335
ENSG00000138095	LRPPRC	570.7353657	2118.095719	1.89158677	1.01E-05	7.00E-05
ENSG00000074964	ARHGEF10L	976.6394711	2103.94952	1.107062269	0.008174333	0.027267889
ENSG00000170430	MGMT	443.9875264	2528.33549	2.509198072	1.02E-08	1.16E-07
ENSG000000174080	CTSF	382.5575897	2404.877754	2.651745811	1.87E-09	2.36E-08
ENSG00000143375	CGN	229.3715289	1475.086671	2.684257151	1.70E-09	2.15E-08
ENSG00000230055	CISD3	580.8440888	2151.53219	1.888859527	1.03E-05	7.16E-05
ENSG00000250479	CHCHD10	730.9197464	2348.292958	1.683611294	7.55E-05	0.000437944
ENSG00000088926	F11	7.75633786	3470.986749	8.77984992	3.23E-44	6.00E-42
ENSG00000139318	DUSP6	877.8850253	2142.530063	1.287047276	0.002215951	0.008825101
ENSG00000118985	ELL2	747.249222	2633.788974	1.817261727	2.04E-05	0.000133801
ENSG00000108242	CYP2C18	195.9349709	1489.23287	2.925187172	8.15E-11	1.25E-09
ENSG00000158125	XDH	50.52465852	2911.568881	5.844718492	5.81E-29	3.90E-27

ENSG00000126777	<i>KTN1</i>	413.6613554	2129.669882	2.363686014	6.09E-08	6.19E-07
ENSG00000136636	<i>KCTD3</i>	305.5757663	1738.720382	2.507844497	1.24E-08	1.40E-07
ENSG00000173801	<i>JUP</i>	821.8982526	1759.296671	1.097801424	0.008864232	0.029259029
ENSG00000116754	<i>SRSF11</i>	838.227728	1944.483277	1.213804213	0.003856528	0.014285248
ENSG00000137171	<i>KLC4</i>	260.4753007	2062.796941	2.984676935	3.04E-11	4.99E-10
ENSG00000158109	<i>TPRG1L</i>	661.7138737	1860.892101	1.491485566	0.000433778	0.002106183
ENSG00000120137	<i>PANK3</i>	264.363272	1968.917621	2.896117327	9.89E-11	1.50E-09
ENSG00000206527	<i>PTPLB</i>	496.8639262	1459.654454	1.55439435	0.000262756	0.001342127
ENSG00000154556	<i>SORBS2</i>	53.63504947	2650.507209	5.623238304	1.72E-27	1.05E-25
ENSG00000091140	<i>DLD</i>	356.1193883	1552.247757	2.12344995	1.02E-06	8.47E-06
ENSG00000269190	<i>FBXO17</i>	121.2858865	601.8803635	2.30963463	2.74E-07	2.51E-06
ENSG00000116771	<i>AGMAT</i>	79.29573781	2308.426397	4.861038435	1.31E-22	5.84E-21
ENSG00000177189	<i>RPS6KA3</i>	548.962731	1571.538029	1.517118935	0.000355972	0.001755842
ENSG00000164040	<i>PGRMC2</i>	641.4964276	2098.805448	1.709807745	5.93E-05	0.000352261
ENSG00000171105	<i>INSR</i>	650.8275565	2217.119112	1.768092421	3.43E-05	0.000215682
ENSG00000187193	<i>MT1X</i>	41.19347589	1980.491783	5.582469612	1.24E-26	7.25E-25
ENSG00000025796	<i>SEC63</i>	445.5427147	1935.48115	2.118676391	9.74E-07	8.16E-06
ENSG00000158769	<i>F11R</i>	760.4683212	1763.154725	1.21301338	0.003893658	0.014405606
ENSG00000072042	<i>RDH11</i>	649.2723684	1541.959613	1.247649602	0.003082942	0.011691566
ENSG00000060566	<i>CREB3L3</i>	52.85745186	2489.754948	5.553990829	5.24E-27	3.09E-25
ENSG00000146648	<i>EGFR</i>	472.7585088	2674.941552	2.49995786	1.13E-08	1.27E-07
ENSG00000182512	<i>GLRX5</i>	620.5013873	1433.934092	1.208245165	0.004208943	0.015240864
ENSG00000125968	<i>ID1</i>	657.0483092	4992.346144	2.925367767	4.29E-11	6.88E-10
ENSG00000157399	<i>ARSE</i>	164.0535968	3843.931994	4.549150464	3.98E-21	1.62E-19
ENSG00000172164	<i>SNTB1</i>	223.1507742	2244.125492	3.329221185	3.07E-13	6.26E-12
ENSG00000167815	<i>PRDX2</i>	800.9032128	2115.523683	1.401129516	0.000899565	0.003989771
ENSG00000011105	<i>TSPAN9</i>	342.1226933	1629.408843	2.251259472	2.48E-07	2.28E-06
ENSG00000244474	<i>UGT1A4</i>	2.312696499	4234.881492	10.75304553	8.85E-51	2.72E-48
ENSG00000123124	<i>WWP1</i>	356.8969825	1845.459883	2.369911635	5.93E-08	6.04E-07
ENSG00000167701	<i>GPT</i>	58.30063355	2704.519969	5.532307135	6.36E-27	3.74E-25
ENSG00000186204	<i>CYP4F12</i>	34.19507543	1387.63744	5.33689601	1.72E-24	8.76E-23
ENSG00000130222	<i>GADD45G</i>	480.5344499	3500.565165	2.864496455	1.08E-10	1.64E-09
ENSG00000102531	<i>FNDCC3A</i>	625.9445459	2285.278071	1.868002143	1.28E-05	8.72E-05
ENSG00000101194	<i>SLC17A9</i>	583.1768711	1558.677848	1.418061527	0.000813427	0.003682645
ENSG00000182670	<i>TTC3</i>	566.8473952	1391.495495	1.295348949	0.002191023	0.008742098
ENSG00000110048	<i>OSBP</i>	668.7122204	1732.290291	1.373002703	0.001159529	0.005014807
ENSG00000154174	<i>TOMM70A</i>	539.6316019	1795.305178	1.733886747	4.87E-05	0.000294382
ENSG00000112414	<i>GPR126</i>	537.2988196	2665.939426	2.310524676	1.06E-07	1.03E-06
ENSG00000180185	<i>FAHD1</i>	404.3302257	983.8277532	1.282515447	0.002539287	0.009844639
ENSG00000005700	<i>IBTK</i>	406.6630082	1835.171739	2.173589876	5.42E-07	4.74E-06
ENSG00000123104	<i>ITPR2</i>	200.6005374	2233.837348	3.476183953	3.99E-14	8.90E-13
ENSG00000163702	<i>IL17RC</i>	432.3236145	1772.156852	2.03493538	2.45E-06	1.92E-05
ENSG00000119138	<i>KLF9</i>	262.0304892	2834.407795	3.434520436	5.58E-14	1.22E-12
ENSG00000114023	<i>FAM162A</i>	451.7634676	2278.847981	2.334280277	8.32E-08	8.25E-07
ENSG00000163050	<i>ADCK3</i>	559.8490484	1981.777801	1.823395956	2.05E-05	0.000134211
ENSG00000173674	<i>EIF1AX</i>	745.6940338	2075.657122	1.476709561	0.0004833	0.002324366
ENSG00000100934	<i>SEC23A</i>	435.433991	1588.256264	1.866542895	1.40E-05	9.46E-05
ENSG00000107897	<i>ACBD5</i>	416.7717319	1570.252011	1.913272175	8.72E-06	6.13E-05
ENSG00000160097	<i>FNDCC5</i>	12.42208703	1280.897938	6.67198022	8.53E-31	6.37E-29
ENSG00000106299	<i>WASL</i>	415.9941378	1275.753865	1.616340019	0.000156924	0.000846612
ENSG00000006756	<i>ARSD</i>	659.3810914	2932.14517	2.152514088	6.05E-07	5.23E-06
ENSG00000170873	<i>MTSS1</i>	325.0156212	2218.40513	2.770384536	4.32E-10	5.97E-09
ENSG00000169895	<i>SYAP1</i>	653.9379329	2079.515177	1.66878064	8.79E-05	0.000501126
ENSG0000013583	<i>HEBP1</i>	772.9098263	2067.941014	1.419629918	0.000777005	0.003536432
ENSG0000012504	<i>NR1H4</i>	110.3995562	2264.701782	4.356749104	1.72E-19	6.10E-18
ENSG00000105357	<i>MYH14</i>	213.819642	1410.785766	2.721188639	1.08E-09	1.41E-08
ENSG00000184999	<i>SLC22A10</i>	4.645755009	2201.686895	8.845422577	1.12E-41	1.77E-39
ENSG00000171130	<i>ATP6V0E2</i>	244.1458208	1045.556623	2.097764166	1.61E-06	1.30E-05
ENSG00000100577	<i>GSTZ1</i>	237.9250664	2687.801733	3.497051921	2.45E-14	5.56E-13
ENSG00000139344	<i>AMDHD1</i>	21.75342271	3531.429599	7.333627177	7.50E-38	8.79E-36
ENSG00000173905	<i>GOLIM4</i>	319.5724619	1700.139839	2.41088976	3.88E-08	4.07E-07
ENSG00000101346	<i>POFUT1</i>	543.5195724	1460.940472	1.426218444	0.000764905	0.003487107
ENSG00000104267	<i>CA2</i>	153.1672724	3086.467341	4.331504855	1.51E-19	5.39E-18
ENSG00000187735	<i>TCEA1</i>	520.9693435	1212.738978	1.218727213	0.003953063	0.014597143
ENSG00000174827	<i>PDZK1</i>	21.75342271	1432.648074	6.032117286	2.27E-28	1.47E-26
ENSG00000108582	<i>CPD</i>	440.0995558	1433.934092	1.703716433	6.89E-05	0.000404622
ENSG00000170271	<i>FAXDC2</i>	94.84765097	3141.766118	5.047737118	3.64E-24	1.81E-22
ENSG00000107186	<i>MPDZ</i>	83.96131282	2110.379611	4.649297016	2.79E-21	1.16E-19
ENSG00000073712	<i>FERMT2</i>	129.8394304	2028.074453	3.963825403	4.99E-17	1.46E-15
ENSG00000175189	<i>INHBC</i>	1.39E-17	1139.435945	13.19939903	1.71E-38	4.50E-36
ENSG00000163660	<i>CCNL1</i>	594.0631884	1631.980879	1.457682309	0.000585062	0.002744755

ENSG00000107566	ERLIN1	450.9858735	2497.471056	2.468922757	1.65E-08	1.83E-07
ENSG00000149084	HSD17B12	594.8407825	2102.663502	1.821370178	2.06E-05	0.000134834
ENSG00000109814	UGDH	468.0929441	1408.21373	1.588668127	0.000196033	0.001029442
ENSG00000166855	CLPX	407.4406023	2015.214272	2.305846167	1.21E-07	1.17E-06
ENSG00000182704	TSKU	307.9085489	4184.726787	3.763938056	4.00E-16	1.09E-14
ENSG00000165516	KLHDC2	553.6282956	1685.99364	1.60632841	0.000159087	0.000857911
ENSG00000072364	AFF4	461.0945971	2116.809701	2.198385765	4.04E-07	3.60E-06
ENSG00000181656	GPR88	6.201060061	208.3587455	5.038684683	2.55E-16	7.01E-15
ENSG00000162688	AGL	153.944867	1985.635856	3.687875552	2.39E-15	6.08E-14
ENSG00000168288	MMADHC	699.8159835	2031.932507	1.537585805	0.000287457	0.00145722
ENSG00000196739	COL27A1	450.9858735	1165.156308	1.36904253	0.001267052	0.005416681
ENSG00000153086	ACMSD	78.51814188	2951.435441	5.229724325	3.28E-25	1.76E-23
ENSG00000186951	PPARA	291.5790704	2990.015984	3.357549272	1.60E-13	3.37E-12
ENSG00000128602	SMO	157.0552455	1068.704949	2.765366297	7.85E-10	1.05E-08
ENSG00000080503	SMARCA2	846.0036686	1782.444997	1.07496204	0.010328456	0.03343498
ENSG00000124767	GLO1	510.083026	1966.345584	1.946388836	6.00E-06	4.38E-05
ENSG00000152990	GPR125	179.6054874	1646.127079	3.195134393	2.37E-12	4.40E-11
ENSG00000139684	ESD	687.3744782	2007.498163	1.546006943	0.000264158	0.001347904
ENSG00000163884	KLF15	51.30225638	2779.109018	5.75557243	2.62E-28	1.69E-26
ENSG00000085871	MGST2	545.0747605	2388.159518	2.131061906	8.11E-07	6.87E-06
ENSG00000153561	RMND5A	336.679534	1733.576309	2.363785242	6.61E-08	6.68E-07
ENSG00000171903	CYP4F11	76.18535388	1941.911241	4.669243125	3.21E-21	1.32E-19
ENSG00000197635	DPP4	137.6153784	1338.768752	3.280831895	9.83E-13	1.91E-11
ENSG00000171862	PTEN	708.3695183	1998.496037	1.496126151	0.000406815	0.001983404
ENSG00000128185	DGCR6L	716.145459	2260.843727	1.658317146	9.53E-05	0.000538777
ENSG00000103479	RBL2	419.8821085	1845.459883	2.135519812	8.14E-07	6.89E-06
ENSG00000186205	1-Mar	38.08307745	2006.212145	5.71394963	2.23E-27	1.34E-25
ENSG00000118004	COLEC11	1094.056174	2862.700193	1.387554435	0.000965632	0.004250301
ENSG00000165029	ABCA1	613.5030405	2118.095719	1.787362875	2.83E-05	0.00018119
ENSG00000141504	SAT2	496.0863321	3132.763992	2.658411195	1.57E-09	2.01E-08
ENSG00000162735	PEX19	438.5443675	1602.402463	1.86906946	1.36E-05	9.22E-05
ENSG00000168994	PXDC1	619.7237932	2200.400877	1.827807429	1.89E-05	0.000124753
ENSG00000084734	GCKR	206.8212926	1930.337078	3.221493482	1.41E-12	2.67E-11
ENSG00000198363	ASPH	679.5985375	1450.652327	1.093747073	0.009333605	0.030633403
ENSG00000106351	AGFG2	546.6299487	1364.489114	1.319458317	0.00183465	0.007452059
ENSG00000197594	ENPP1	39.63827699	2457.604495	5.949179208	2.84E-29	1.93E-27
ENSG00000105135	ILVBL	516.3037789	1439.078164	1.478559731	0.000499922	0.002398295
ENSG00000103423	DNAJA3	579.2889007	1387.63744	1.260028673	0.002840947	0.010860002
ENSG00000144852	NR1I2	3.090401881	2426.740061	9.552647413	1.12E-43	1.94E-41
ENSG00000167910	CYP7A1	1.39E-17	63.03848163	9.025563536	4.50E-11	7.18E-10
ENSG00000108389	MTMR4	507.7502437	1750.294544	1.785089716	3.00E-05	0.000190989
ENSG00000105379	ETFB	283.0255339	1833.885721	2.695263427	1.22E-09	1.59E-08
ENSG00000108515	ENO3	97.18043717	2968.153677	4.930726946	2.64E-23	1.24E-21
ENSG00000136052	SLC41A2	153.1672724	1853.175992	3.595578469	1.02E-14	2.41E-13
ENSG00000117143	UAP1	233.2595005	1878.896354	3.00908762	2.43E-11	4.03E-10
ENSG00000092621	PHGDH	115.8427216	2883.276483	4.635776799	1.79E-21	7.52E-20
ENSG00000160712	IL6R	571.5129598	2244.125492	1.973004847	4.36E-06	3.27E-05
ENSG00000116221	MRPL37	554.4058897	1621.692735	1.548208718	0.000268288	0.001367014
ENSG00000114480	GBE1	315.6844909	2044.792688	2.694828956	1.18E-09	1.53E-08
ENSG00000055917	PUM2	561.4042365	1666.703368	1.569610418	0.000221427	0.001150654
ENSG00000134716	CYP2J2	34.97267623	2798.399289	6.316507852	9.75E-32	7.92E-30
ENSG00000131979	GCH1	751.9147864	2199.114859	1.548077445	0.000259104	0.001325929
ENSG00000143164	DCAF6	461.8721912	1669.275404	1.85330376	1.60E-05	0.000107109
ENSG00000188641	DPYD	598.7287529	1453.224364	1.27904267	0.002464628	0.009586593
ENSG00000131910	NR0B2	103.4011996	1666.703368	4.008805296	4.10E-17	1.21E-15
ENSG00000121892	PDS5A	425.3252674	1266.751738	1.574131869	0.000225684	0.001171058
ENSG00000115963	RND3	209.1540757	4326.188776	4.369526561	5.54E-20	2.06E-18
ENSG00000157106	SMG1	538.0764137	1472.514635	1.452119433	0.000620973	0.002894108
ENSG00000107104	KANK1	237.1474721	2521.9054	3.409862795	8.47E-14	1.82E-12
ENSG00000137992	DBT	172.6071368	2119.381737	3.616976873	6.11E-15	1.48E-13
ENSG00000215644	GCCR	1.534979634	2483.324857	10.53280337	1.88E-46	4.07E-44
ENSG00000141027	NCOR1	860.7779559	2030.646489	1.238060849	0.003231592	0.012201309
ENSG00000132199	ENOSF1	451.7634676	1086.709203	1.266009052	0.002855946	0.010912304
ENSG00000161813	LARP4	202.1557262	1713.00002	3.082070209	1.04E-11	1.80E-10
ENSG00000112893	MAN2A1	403.5526316	1404.355676	1.798679709	2.80E-05	0.00017919
ENSG00000171503	ETFDH	124.3962662	2449.888387	4.298136273	3.45E-19	1.19E-17
ENSG00000119431	HDHD3	264.363272	1270.609793	2.264274775	2.40E-07	2.21E-06
ENSG00000205339	IPO7	660.1586855	1561.249884	1.241601047	0.003210084	0.012138543
ENSG00000197312	DDI2	295.4670415	1422.359929	2.266633424	2.19E-07	2.04E-06
ENSG00000166391	MOGAT2	1.39E-17	2411.307844	14.28083012	3.93E-46	8.28E-44
ENSG00000147471	PROSC	622.0565755	1440.364183	1.211089094	0.004065125	0.014940451

ENSG00000187824	TMEM220	91.73726908	2134.813955	4.538324651	1.38E-20	5.40E-19
ENSG00000143921	ABCG8	0.757489584	1607.546536	10.80475496	8.35E-42	1.33E-39
ENSG00000102038	SMARCA1	90.95967356	1913.618842	4.39278747	1.31E-19	4.73E-18
ENSG00000038210	PI4K2B	161.7208131	1349.056897	3.059230447	1.67E-11	2.84E-10
ENSG00000138041	SMEK2	451.7634676	1397.925585	1.629301942	0.000137776	0.000750806
ENSG00000168303	MPLKIP	349.1210408	969.6815539	1.473350664	0.000570618	0.002685609
ENSG00000089057	SLC23A2	391.8887195	2667.225444	2.766361743	4.21E-10	5.83E-09
ENSG00000017427	IGF1	52.85745186	2365.011193	5.479837058	1.77E-26	1.03E-24
ENSG00000100348	TXN2	799.3480246	1776.014906	1.151574693	0.006057804	0.021087775
ENSG00000117620	SLC35A3	193.6021877	1361.917078	2.813532731	3.65E-10	5.09E-09
ENSG00000135318	NT5E	49.74706056	1511.095178	4.920874836	1.99E-22	8.81E-21
ENSG00000152952	PLOD2	440.0995558	1086.709203	1.303734913	0.002133758	0.00854156
ENSG00000117859	OSBPL9	423.7700791	1828.741648	2.109098401	1.09E-06	9.05E-06
ENSG00000137710	RDX	349.1210408	1894.328571	2.439383692	2.71E-08	2.90E-07
ENSG00000145391	SETD7	412.1061671	1855.748028	2.170499046	5.73E-07	4.99E-06
ENSG00000198478	SH3BGRL2	56.74543914	1824.883594	5.003676221	3.27E-23	1.53E-21
ENSG00000169905	TOR1AIP2	620.5013873	1873.752282	1.594173724	0.000174312	0.000930127
ENSG00000177943	MAMDC4	181.9382708	1122.71771	2.624490426	4.08E-09	4.93E-08
ENSG00000204653	ASPDH	4.645755009	2313.570469	8.916931223	3.30E-42	5.39E-40
ENSG00000176105	YES1	202.1557262	985.1137714	2.283967808	2.29E-07	2.13E-06
ENSG00000214717	ZBED1	837.4501339	1776.014906	1.084406654	0.009734664	0.031769311
ENSG00000145247	OCIAD2	712.2574887	1648.699115	1.210659266	0.004013181	0.014783994
ENSG00000160870	CYP3A7	8.533969895	4054.83896	8.868652738	3.13E-45	6.13E-43
ENSG00000165609	NUDT5	350.6762292	1057.130786	1.591499856	0.0002016	0.001057346
ENSG00000173230	GOLGB1	616.6134169	1256.463594	1.026715242	0.014712904	0.045174704
ENSG00000181513	ACBD4	297.0222299	1716.858074	2.530530579	9.33E-09	1.07E-07
ENSG00000100239	PPP6R2	726.254182	1508.523142	1.054405644	0.011971986	0.038139413
ENSG00000165688	PMPCB	653.9379329	1629.408843	1.316900702	0.001812379	0.007366585
ENSG00000105819	PMPCB	545.8523546	1491.804907	1.450200738	0.000634095	0.002950286
ENSG00000112293	GPLD1	12.42208703	918.2408288	6.191812439	2.31E-27	1.39E-25
ENSG00000165410	CFL2	280.6927512	1948.341331	2.794536124	3.53E-10	4.93E-09
ENSG00000132561	MATN2	88.62688686	691.9016356	2.9626765	1.43E-10	2.11E-09
ENSG00000198585	NUDT16	566.0698011	1427.504002	1.334184899	0.001611205	0.006618161
ENSG00000147475	ERLIN2	445.5427147	1406.927712	1.658559565	0.000103292	0.000580973
ENSG00000137563	GGH	279.1375627	1459.654454	2.385952186	5.77E-08	5.89E-07
ENSG00000007847	ITCH	359.229765	1643.555042	2.193364849	4.65E-07	4.11E-06
ENSG00000106460	TMEM106B	533.4108491	1169.014362	1.131715469	0.007245973	0.024560026
ENSG00000152782	PANK1	15.53254811	3047.886798	7.603427622	1.44E-38	1.79E-36
ENSG00000189077	TMEM120A	661.7138737	1603.688481	1.276897172	0.002481249	0.009645206
ENSG000000064115	TM7SF3	778.3529848	1710.427983	1.135683786	0.00680994	0.023378599
ENSG00000169814	BTD	213.819642	1414.643821	2.7251283	1.02E-09	1.34E-08
ENSG00000156261	CCT8	567.6249893	1329.766626	1.227913239	0.003672901	0.013676396
ENSG000000213563	C8orf82	468.8705382	1451.938345	1.630385109	0.000134807	0.000736565
ENSG00000123472	ATPAF1	499.1967086	1295.044137	1.375025232	0.001189291	0.005115043
ENSG00000083123	BCKDHB	120.5082916	1886.612463	3.966993864	5.70E-17	1.65E-15
ENSG00000161573	CCL16	3.090401881	1352.914952	8.709744856	1.83E-37	2.02E-35
ENSG00000196083	IL1RAP	151.6120831	2040.934634	3.749511399	1.02E-15	2.69E-14
ENSG00000178078	STAP2	272.9168088	825.6475232	1.596495581	0.00021422	0.001117877
ENSG00000161395	PGAP3	297.7998242	886.0903756	1.572591946	0.000259394	0.001326319
ENSG00000107745	MICU1	541.1867901	1922.620969	1.828576131	1.94E-05	0.000128142
ENSG00000168216	LMBRD1	496.0863321	1435.22011	1.532300074	0.00031894	0.001594698
ENSG00000129422	MTUS1	510.8606201	1765.726762	1.788945119	2.94E-05	0.00018771
ENSG00000115594	IL1R1	858.4451737	1921.334951	1.162149221	0.00558819	0.019615092
ENSG00000134389	CFHR5	3.868086451	2439.600242	9.24920201	9.78E-44	1.72E-41
ENSG00000183077	AFMID	273.694403	1644.84106	2.586658642	4.98E-09	5.93E-08
ENSG00000153879	CEBPG	370.1160832	861.656031	1.218752088	0.00417338	0.015119355
ENSG00000228253	MT-ATP8	702.1487657	1574.110065	1.164489664	0.005608119	0.019679487
ENSG00000139508	SLC46A3	277.5823742	1837.743775	2.726297435	8.57E-10	1.13E-08
ENSG00000137714	FDX1	415.9941378	1581.826174	1.926559801	7.79E-06	5.54E-05
ENSG00000162896	PIGR	297.7998242	1095.71133	1.878903662	1.37E-05	9.30E-05
ENSG00000157184	CPT2	356.1193883	1938.053186	2.443681277	2.57E-08	2.75E-07
ENSG00000114416	FXR1	533.4108491	1346.484861	1.335605007	0.001596062	0.006579071
ENSG00000162599	NFIA	196.7125654	1368.347169	2.79735031	4.35E-10	6.02E-09
ENSG00000140450	ARRDC4	148.5017045	587.7341634	1.983564429	7.14E-06	5.14E-05
ENSG00000137880	GCHFR	361.5625475	1553.533775	2.102768903	1.24E-06	1.02E-05
ENSG00000198947	DMD	77.74054591	2024.216399	4.70002591	1.60E-21	6.76E-20
ENSG00000181035	SLC25A42	179.6054874	1610.118572	3.16322752	3.68E-12	6.68E-11
ENSG00000167772	ANGPTL4	181.1606764	2507.759201	3.789999471	4.73E-16	1.28E-14
ENSG00000131620	ANO1	466.5377559	2139.958027	2.197149995	3.99E-07	3.56E-06
ENSG00000156110	ADK	195.1573765	1936.767168	3.309979389	4.57E-13	9.12E-12
ENSG00000115363	EVA1A	47.4142661	2407.44979	5.661841822	1.62E-27	9.98E-26

ENSG00000124588	NQO2	505.4174614	1133.005855	1.16433266	0.005795242	0.020261745
ENSG00000165801	ARHGEF40	528.7452845	1620.406717	1.615416296	0.000150248	0.000812892
ENSG00000138768	USO1	501.5294909	1495.662961	1.576070309	0.000212753	0.001111387
ENSG00000143314	MRPL24	713.8126768	1463.512508	1.035630954	0.013651168	0.042327817
ENSG00000176422	SPRYD4	188.1590266	1658.98726	3.139290829	5.09E-12	9.11E-11
ENSG00000149260	CAPN5	140.7257574	1373.491241	3.285557875	8.90E-13	1.74E-11
ENSG00000106771	TMEM245	623.6117636	1647.413097	1.401244051	0.000933077	0.004120759
ENSG00000170439	METTL7B	95.62524639	2267.273818	4.565374977	8.40E-21	3.32E-19
ENSG00000146039	SLC17A4	46.63666774	824.3615051	4.139582546	4.84E-17	1.42E-15
ENSG00000060762	MPC1	531.0780668	2233.837348	2.072211318	1.55E-06	1.26E-05
ENSG00000146904	EPHA1	178.0502984	396.1174457	1.152864614	0.008016104	0.026840936
ENSG00000111181	SLC6A12	94.84765097	1832.599703	4.270084913	8.23E-19	2.77E-17
ENSG00000172456	FGGY	69.18698793	756.2025434	3.447468617	3.84E-13	7.74E-12
ENSG00000164442	CITED2	517.8589671	1323.336535	1.353265379	0.001408796	0.005961122
ENSG00000125652	ALKBH7	630.6101104	1553.533775	1.300503873	0.002083207	0.008351307
ENSG00000126524	SBDS	579.2889007	1329.766626	1.198575475	0.004490042	0.016181457
ENSG00000053254	FOXN3	558.2938602	1358.059024	1.282191625	0.002400147	0.009478179
ENSG00000140961	OSGIN1	38.08307745	835.9356683	4.451037179	1.27E-18	4.22E-17
ENSG00000066583	ISOC1	340.5675049	1540.673594	2.177047355	5.63E-07	4.90E-06
ENSG00000116044	NFE2L2	385.6679663	2178.53857	2.497470844	1.26E-08	1.41E-07
ENSG00000144040	SFXN5	203.710915	1651.271151	3.01807655	2.33E-11	3.88E-10
ENSG00000133027	PEMT	93.29246006	1440.364183	3.946463772	1.32E-16	3.72E-15
ENSG00000154122	ANKH	679.5985375	1769.584816	1.380438761	0.001093565	0.004756004
ENSG00000100614	PPM1A	422.992485	1266.751738	1.582063785	0.000212662	0.001111381
ENSG00000121671	CRY2	342.1226933	1579.254137	2.206156914	4.12E-07	3.66E-06
ENSG00000196781	TLE1	572.2905538	1166.442326	1.027063119	0.014635411	0.044970102
ENSG00000173992	CCS	555.1834838	1143.294	1.041919305	0.013332018	0.041477946
ENSG00000187546	AGMO	15.53254811	1265.46572	6.335351549	2.54E-29	1.74E-27
ENSG00000177706	FAM20C	387.2231546	1615.262644	2.060097607	1.95E-06	1.56E-05
ENSG00000066027	PPP2R5A	535.7436314	1214.024996	1.179922511	0.005212995	0.018484697
ENSG00000141179	PCTP	353.0090117	1626.836807	2.203807475	4.22E-07	3.74E-06
ENSG00000016391	CHDH	403.5526316	1810.737395	2.165326257	6.01E-07	5.20E-06
ENSG00000107164	FUBP3	463.4273794	1131.719837	1.287790405	0.002371866	0.009372454
ENSG00000198682	PAPSS2	216.9300194	2439.600242	3.490470758	2.94E-14	6.61E-13
ENSG00000055208	TAB2	547.4075428	1320.764499	1.270423797	0.002642439	0.010171569
ENSG00000157224	CLDN12	134.5049993	1131.719837	3.071409126	1.81E-11	3.07E-10
ENSG00000146233	CYP39A1	3.868086451	1781.158979	8.79539479	2.23E-40	3.17E-38
ENSG00000069431	ABCC9	58.30063355	1814.595449	4.956607965	7.34E-23	3.32E-21
ENSG00000178445	GLDC	143.8361363	2415.165898	4.068279663	8.76E-18	2.72E-16
ENSG00000029363	BCLAF1	493.7535498	1300.188209	1.396556859	0.001003392	0.004406239
ENSG00000053371	AKR7A2	381.0024014	1078.993094	1.501414261	0.000442848	0.002145613
ENSG00000086696	HSD17B2	109.621961	2784.25309	4.664891373	1.31E-21	5.55E-20
ENSG00000168827	CLFM1	308.6861431	1028.838387	1.73628667	5.50E-05	0.000328563
ENSG00000128607	KLHDC10	335.1243456	1073.849022	1.679551532	9.33E-05	0.000528226
ENSG00000123179	EBPL	446.3203088	1508.523142	1.75662656	4.14E-05	0.000255736
ENSG00000095203	EPB41L4B	30.30706789	2088.517303	6.100087452	1.16E-29	8.16E-28
ENSG00000151239	TWF1	443.2099323	941.3891551	1.086494965	0.010194937	0.033054401
ENSG00000111077	TENC1	524.857314	1642.269024	1.645394448	0.000114852	0.000640488
ENSG00000172466	TNF24	475.8688853	1250.033503	1.393019114	0.00104519	0.004568799
ENSG00000065150	IPO5	697.4832012	1849.317938	1.406549597	0.000865561	0.003862393
ENSG00000256043	CTSO	475.8688853	1475.086671	1.631834955	0.000132752	0.000726131
ENSG00000163959	SLC51A	57.52303638	1085.423185	4.234594493	5.80E-18	1.83E-16
ENSG00000093144	ECHDC1	580.0664948	1242.317394	1.098508835	0.009103003	0.029943772
ENSG00000005187	ACSM3	17.08777164	1490.518889	6.434991648	3.25E-30	2.35E-28
ENSG00000112237	CCNC	356.8969825	866.8001036	1.279788317	0.00269263	0.010356751
ENSG00000185189	NRBP2	605.7270997	1527.813413	1.334487352	0.001605599	0.006603868
ENSG00000101974	ATP11C	97.18043717	1103.427438	3.503232781	8.19E-14	1.76E-12
ENSG00000145020	AMT	164.0535968	1253.891557	2.933055607	8.54E-11	1.31E-09
ENSG00000108924	HLF	57.52303638	2125.811828	5.204287512	1.32E-24	6.74E-23
ENSG00000138075	ABCG5	3.090401881	1377.349296	8.73556634	1.20E-37	1.35E-35
ENSG00000163605	PPP4R2	331.2363747	1066.132913	1.685976934	8.81E-05	0.000501962
ENSG00000111726	CMAS	325.7932154	1143.294	1.810671563	2.64E-05	0.000169351
ENSG00000120158	RCL1	247.2561979	2174.680515	3.135973573	4.11E-12	7.43E-11
ENSG00000170145	SIK2	433.8788028	1836.457757	2.081173227	1.46E-06	1.19E-05
ENSG00000130779	CLIP1	421.4372967	1125.289746	1.416552697	0.000863931	0.003855811
ENSG00000134463	ECHDC3	49.74706056	1131.719837	4.503828278	1.41E-19	5.05E-18
ENSG00000214855	APOC1P1	18.64299156	423.1238299	4.493881115	2.63E-17	7.88E-16
ENSG00000085719	CPNE3	686.5968842	1419.787893	1.047945259	0.012609069	0.039847026
ENSG00000139197	PEX5	370.8936774	1122.71771	1.597498781	0.000192362	0.00101857
ENSG00000186301	MST1P2	132.9498097	1175.444453	3.142854554	6.65E-12	1.18E-10
ENSG00000099246	RAB18	535.7436314	1440.364183	1.426539857	0.000774125	0.003524618

ENSG00000166311	<i>SMPD1</i>	492.9759557	1432.648074	1.53878386	0.000301054	0.001519948
ENSG00000152894	<i>PTPRK</i>	454.09625	1095.71133	1.270481601	0.002736784	0.010503826
ENSG00000176209	<i>SMIM19</i>	303.2429837	1075.13504	1.825437023	2.39E-05	0.000154908
ENSG00000155380	<i>SLC16A1</i>	215.3748307	2020.358344	3.228822458	1.27E-12	2.43E-11
ENSG00000134759	<i>ELP2</i>	509.3054319	1350.342915	1.406430688	0.000910087	0.004030697
ENSG00000110436	<i>SLC1A2</i>	5.423411881	3824.641723	9.424944033	9.71E-47	2.14E-44
ENSG00000129151	<i>BBOX1</i>	0.757489584	1017.264224	10.14463955	5.93E-37	6.17E-35
ENSG00000170017	<i>ALCAM</i>	196.7125654	1176.730471	2.579716605	6.80E-09	7.91E-08
ENSG00000180767	<i>CHST13</i>	18.64299156	708.6198717	5.237679453	2.87E-22	1.26E-20
ENSG00000163320	<i>CGGBP1</i>	492.1983616	1017.264224	1.04711082	0.013055988	0.040767574
ENSG00000119139	<i>TJP2</i>	422.992485	1621.692735	1.938406234	6.92E-06	4.99E-05
ENSG00000164120	<i>HPGD</i>	45.08147069	2854.984085	5.980375936	1.20E-29	8.39E-28
ENSG00000023697	<i>DERA</i>	304.7981721	1304.046264	2.096514703	1.40E-06	1.14E-05
ENSG00000179094	<i>PER1</i>	453.3186559	1971.489657	2.120314934	9.59E-07	8.04E-06
ENSG00000205364	<i>MT1M</i>	33.41747441	1142.007982	5.088908305	9.38E-23	4.22E-21
ENSG00000196411	<i>EPHB4</i>	332.0139689	1021.122279	1.620369661	0.000162028	0.000872822
ENSG00000182327	<i>GLTPD2</i>	28.75186299	2560.485943	6.469652214	2.54E-32	2.13E-30
ENSG00000172828	<i>CES3</i>	22.53102899	390.9733724	4.108485509	2.46E-15	6.26E-14
ENSG00000160285	<i>LSS</i>	410.5509788	1322.050517	1.686758854	8.12E-05	0.000467017
ENSG00000129946	<i>SHC2</i>	339.0123165	1105.999475	1.705472976	7.34E-05	0.000429002
ENSG00000169018	<i>FEM1B</i>	353.0090117	873.2301942	1.306246281	0.00218259	0.00871458
ENSG00000167699	<i>GLOD4</i>	761.2459152	1584.39821	1.057324088	0.01168793	0.037402278
ENSG00000112337	<i>SLC17A2</i>	2.312696499	1167.728344	8.894515622	5.03E-37	5.30E-35
ENSG00000141295	<i>SCRN2</i>	446.3203088	1187.018616	1.410857478	0.000904536	0.00401039
ENSG00000016864	<i>GLT8D1</i>	475.8688853	983.8277532	1.047560377	0.013100998	0.040887157
ENSG00000109787	<i>KLF3</i>	419.1045143	1426.217983	1.766429641	3.84E-05	0.000239494
ENSG00000127914	<i>AKAP9</i>	150.8344885	1179.302507	2.965677009	6.26E-11	9.79E-10
ENSG00000109686	<i>SH3D19</i>	213.819642	1570.252011	2.875675733	1.47E-10	2.16E-09
ENSG00000171227	<i>TMEM37</i>	388.0007487	1607.546536	2.050296588	2.19E-06	1.73E-05
ENSG00000079385	<i>TEACAM1</i>	125.951456	1115.001601	3.144629998	6.93E-12	1.23E-10
ENSG00000139793	<i>MBNL2</i>	478.9792617	1322.050517	1.464427229	0.000576185	0.002706177
ENSG00000113742	<i>CPEB4</i>	370.1160832	1656.415223	2.161554364	6.58E-07	5.66E-06
ENSG00000139410	<i>SDSL</i>	342.1226933	1478.944726	2.111487721	1.17E-06	9.67E-06
ENSG00000145012	<i>LPP</i>	457.9842206	1405.641694	1.617518499	0.000151515	0.000819385
ENSG00000124839	<i>RAB17</i>	115.0651266	1698.853821	3.882368221	2.01E-16	5.57E-15
ENSG000000055163	<i>CYFIP2</i>	786.9068195	1984.349838	1.334216622	0.001546607	0.006408957
ENSG00000119125	<i>GDA</i>	212.2644532	1675.705495	2.979967296	3.87E-11	6.26E-10
ENSG00000117114	<i>LPHN2</i>	248.8113865	1358.059024	2.447714349	2.85E-08	3.04E-07
ENSG00000102897	<i>LYRM1</i>	252.6993579	1094.425311	2.114009539	1.28E-06	1.05E-05
ENSG00000114315	<i>HES1</i>	381.0024014	1491.804907	1.968751529	5.18E-06	3.85E-05
ENSG00000172893	<i>DHCR7</i>	283.8031281	981.255717	1.789170892	3.58E-05	0.000224459
ENSG00000140396	<i>NCOA2</i>	360.7849533	1027.552369	1.50957831	0.000419765	0.002040536
ENSG000000081041	<i>CXCL2</i>	207.598887	1963.773548	3.240857693	1.09E-12	2.09E-11
ENSG00000172845	<i>SP3</i>	376.3368365	815.3593781	1.115047678	0.008582443	0.028415694
ENSG00000141646	<i>SMAD4</i>	499.1967086	1009.548116	1.015764271	0.016020692	0.048714743
ENSG00000115760	<i>BIRC6</i>	389.555937	1145.866036	1.556140643	0.000268669	0.001368677
ENSG00000178425	<i>NT5DC1</i>	227.0387459	1045.556623	2.202506452	5.38E-07	4.71E-06
ENSG00000188559	<i>RALGAP2</i>	297.7998242	1262.893684	2.083752141	1.62E-06	1.31E-05
ENSG000000099260	<i>PALMD</i>	105.7339853	911.8107382	3.106540753	1.55E-11	2.64E-10
ENSG00000124120	<i>TPAL</i>	212.2644532	1149.72409	2.436524662	3.76E-08	3.94E-07
ENSG00000061794	<i>MRPS35</i>	489.8655793	1054.55875	1.10590294	0.008890658	0.029334567
ENSG00000049319	<i>SRD5A2</i>	1.39E-17	1145.866036	13.2075169	3.27E-38	3.98E-36
ENSG00000075292	<i>ZNF638</i>	353.7866058	1346.484861	1.92778074	7.93E-06	5.63E-05
ENSG00000131069	<i>ACSS2</i>	478.2016676	1000.545989	1.06481485	0.011686752	0.037402278
ENSG00000132356	<i>PRKAA1</i>	381.0024014	1206.308887	1.662314278	0.000106173	0.000595967
ENSG00000112304	<i>ACOT13</i>	256.5873293	1244.889431	2.277822321	2.07E-07	1.94E-06
ENSG00000106780	<i>MEGF9</i>	242.5906322	1364.489114	2.491036439	1.74E-08	1.91E-07
ENSG00000198730	<i>CTR9</i>	304.0205779	717.6219988	1.238587174	0.00377835	0.014023886
ENSG00000052841	<i>TTC17</i>	576.1785243	1228.171195	1.091688054	0.009514131	0.031172385
ENSG00000052795	<i>FNIP2</i>	234.8146891	1057.130786	2.169832958	7.15E-07	6.11E-06
ENSG00000144655	<i>CSRNP1</i>	500.7518968	1826.169612	1.866326925	1.34E-05	9.09E-05
ENSG00000168575	<i>SLC20A2</i>	249.5889808	1211.45296	2.278419848	2.08E-07	1.94E-06
ENSG00000147419	<i>CCDC25</i>	300.1326068	1311.762372	2.127269312	1.05E-06	8.78E-06
ENSG00000162729	<i>IGSF8</i>	597.1735647	1278.325901	1.097805483	0.009102106	0.029943772
ENSG00000102743	<i>SLC25A15</i>	53.63504947	2389.445537	5.473651505	2.01E-26	1.16E-24
ENSG00000105518	<i>TMEM205</i>	363.89533	1064.846895	1.548628033	0.000298518	0.001509905
ENSG00000228716	<i>DHFR</i>	244.9234151	1151.010109	2.231796184	3.47E-07	3.12E-06
ENSG00000065485	<i>PDIA5</i>	307.9085489	1266.751738	2.040015639	2.70E-06	2.10E-05
ENSG00000137274	<i>BPHL</i>	73.07496939	986.3997895	3.752103791	3.43E-15	8.57E-14
ENSG000000244734	<i>HBB</i>	78.51814188	915.6687926	3.541310968	7.00E-14	1.52E-12
ENSG00000013441	<i>CLK1</i>	598.7287529	1323.336535	1.143974684	0.006655464	0.022912177

ENSG00000242265	PEG10	42.7486742	299.6660672	2.805150556	5.31E-09	6.31E-08
ENSG00000068878	PSME4	381.7799955	934.9590645	1.291783425	0.002434193	0.009484447
ENSG00000172380	GNG12	387.2231546	945.2472095	1.287153991	0.002462598	0.009580196
ENSG00000023909	GCLM	405.1078199	1121.431692	1.468591117	0.000571172	0.002687711
ENSG00000108510	MED13	313.3517083	1063.560877	1.762536048	4.30E-05	0.000264742
ENSG00000139531	SUOX	234.0370948	1219.169068	2.380342242	6.87E-08	6.91E-07
ENSG00000169251	NMD3	273.694403	1134.291873	2.050540763	2.44E-06	1.91E-05
ENSG00000213512	GBP7	2.312696499	878.3742668	8.483758205	4.84E-34	4.47E-32
ENSG00000120896	SORBS3	581.6216829	1205.022869	1.050677213	0.012610656	0.039847026
ENSG00000166183	ASPG	1.534979634	2375.299338	10.46864228	5.64E-46	1.16E-43
ENSG00000179152	TCAIM	253.4769522	906.6666657	1.838076607	2.24E-05	0.000145395
ENSG00000100941	PNN	280.6927512	1060.98884	1.917759376	9.57E-06	6.68E-05
ENSG00000169047	IRS1	265.1408662	1216.597032	2.197374968	5.16E-07	4.53E-06
ENSG00000144895	EIF2A	415.9941378	1066.132913	1.357398935	0.001411914	0.005973034
ENSG00000144674	GOLGA4	154.7224617	911.8107382	2.557901687	1.10E-08	1.24E-07
ENSG00000113580	NR3C1	458.7618147	1442.936219	1.652847887	0.000110602	0.000618592
ENSG00000134363	FST	121.2858865	2173.394497	4.161867488	3.00E-18	9.61E-17
ENSG00000079785	DDX1	475.8688853	1112.429565	1.224780227	0.003831021	0.014199227
ENSG00000143248	RG55	279.9151569	973.5396083	1.797673555	3.31E-05	0.000208774
ENSG00000166681	NGFRAP1	407.4406023	870.658158	1.095182733	0.009941462	0.032380426
ENSG00000185361	TNFAIP8L1	380.2248072	1062.274859	1.481834127	0.000515551	0.002454489
ENSG00000067064	IDI1	365.4505183	1017.264224	1.476532453	0.000540358	0.002551151
ENSG00000115504	EHBP1	213.0420476	1234.601286	2.534001847	1.18E-08	1.33E-07
ENSG00000169967	MAP3K2	325.7932154	1087.995221	1.739153577	5.46E-05	0.000326648
ENSG00000113369	ARRDC3	234.8146891	483.5666882	1.041623307	0.015677625	0.047776773
ENSG00000157326	DHRS4	217.7076138	1160.012235	2.412870611	4.74E-08	4.91E-07
ENSG00000167107	ACSF2	255.809735	1207.594905	2.238321138	3.19E-07	2.90E-06
ENSG00000141429	GALNT1	488.310391	1067.418931	1.127974504	0.007561961	0.025519695
ENSG00000130164	LDLR	707.5919242	1500.807033	1.084557446	0.009905675	0.032276553
ENSG00000153823	PID1	44.30387198	1071.276985	4.591329763	6.70E-20	2.47E-18
ENSG00000124782	RREB1	463.4273794	1126.575764	1.281218456	0.002490646	0.009678705
ENSG00000137713	PPP2R1B	265.9184605	1460.940472	2.457179029	2.43E-08	2.61E-07
ENSG00000172602	RND1	165.608786	1597.258391	3.268616257	9.34E-13	1.82E-11
ENSG00000073417	PDE8A	255.0321408	947.8192458	1.893289952	1.32E-05	8.99E-05
ENSG00000122042	UBL3	450.2082794	1229.457213	1.449023136	0.000656477	0.00304303
ENSG00000131791	PRKAB2	112.7323414	1081.56513	3.260487062	1.74E-12	3.27E-11
ENSG00000122884	P4HA1	491.4207675	1318.192463	1.423226289	0.000794157	0.003605257
ENSG00000137133	HINT2	398.8870668	1031.410424	1.370196642	0.001293999	0.005522381
ENSG00000185728	YTHDF3	394.2215019	986.3997895	1.32279661	0.001867782	0.007565797
ENSG00000073169	SELO	400.442255	1197.306761	1.57974019	0.000218344	0.001136054
ENSG00000145545	SRD5A1	212.2644532	1566.393956	2.882651623	1.42E-10	2.09E-09
ENSG00000106404	CLDN15	89.40448245	397.403464	2.150281417	2.20E-06	1.73E-05
ENSG00000111530	CAND1	431.5460204	999.2599707	1.211018657	0.004333737	0.015667642
ENSG00000132424	PNISR	401.2198492	1175.444453	1.550358114	0.000282332	0.00143343
ENSG00000121039	RDH10	380.2248072	1100.855402	1.533297376	0.000333609	0.001661359
ENSG00000127418	FGFRL1	332.0139689	999.2599707	1.589148997	0.000214741	0.00111942
ENSG00000185950	IRS2	215.3748307	2456.318477	3.510696562	2.32E-14	5.27E-13
ENSG00000164172	MOCS2	431.5460204	1408.21373	1.705912232	6.70E-05	0.000394984
ENSG00000068078	FGFR3	512.7469376	1336.196716	1.356428705	0.001373673	0.005825397
ENSG00000138792	ENPEP	124.7875316	1642.269024	3.843270525	4.14E-16	1.12E-14
ENSG00000103381	CPPED1	289.2462877	830.7915957	1.521659681	0.000398621	0.00194651
ENSG00000129636	ITFG1	398.1094726	974.8256264	1.291616249	0.00239023	0.009440514
ENSG00000214456	PLIN5	111.1771513	1266.751738	3.50849746	5.85E-14	1.28E-12
ENSG00000182985	CADM1	353.7866058	1319.478481	1.898552685	1.07E-05	7.40E-05
ENSG00000139428	MMAB	222.3731799	1365.775133	2.617860853	3.97E-09	4.80E-08
ENSG00000188706	ZDHHC9	263.5856777	882.2323212	1.742280383	5.57E-05	0.000332145
ENSG00000137216	TMEM63B	368.5608949	1085.423185	1.557864701	0.000266907	0.001360813
ENSG00000167363	FN3K	167.1639751	1333.62468	2.994915187	4.05E-11	6.50E-10
ENSG00000081377	CDC14B	131.39462	1567.679975	3.575206946	1.67E-14	3.83E-13
ENSG00000167635	ZNF146	229.3715289	587.7341634	1.356836704	0.001652528	0.006772232
ENSG00000115042	FAHD2A	194.3797821	1616.548662	3.055015834	1.51E-11	2.58E-10
ENSG00000185658	BRWD1	237.9250664	982.5417351	2.045306373	2.91E-06	2.25E-05
ENSG00000160972	PPP1R16A	439.3219617	969.6815539	1.141917987	0.006982078	0.023857514
ENSG00000198836	OPA1	184.2710543	1095.71133	2.570999661	8.31E-09	9.57E-08
ENSG00000176623	RMDN1	437.7667734	1041.698569	1.250377444	0.003229855	0.012196604
ENSG00000203880	PCMTD2	365.4505183	1071.276985	1.551162592	0.000287649	0.001457892
ENSG00000205436	EXOC3L4	98.73562788	970.967572	3.295881265	1.31E-12	2.49E-11
ENSG00000154639	CXADR	80.07333372	970.967572	3.597653603	2.59E-14	5.86E-13
ENSG00000114520	SNX4	160.9432185	1260.321648	2.968026088	5.59E-11	8.79E-10
ENSG00000156011	PSD3	65.29900539	1689.851694	4.690684097	3.49E-21	1.43E-19
ENSG00000008294	SPAG9	430.7684263	1054.55875	1.291319861	0.00237296	0.009375284

ENSG00000133142	<i>TCEAL4</i>	446.3203088	1000.545989	1.164324425	0.005940297	0.020707725
ENSG00000116574	<i>RHOU</i>	328.125998	927.2429557	1.498234078	0.000473613	0.002283095
ENSG00000250056	<i>LINC01018</i>	1.534979634	1628.122825	9.92376958	6.07E-42	9.76E-40
ENSG00000109084	<i>TMEM97</i>	102.6236044	844.9377953	3.039682364	4.06E-11	6.52E-10
ENSG00000242612	<i>DECRC2</i>	269.0288375	1235.887304	2.199078196	5.08E-07	4.46E-06
ENSG00000162928	<i>PEX13</i>	293.1342588	1031.410424	1.814432944	2.73E-05	0.000174765
ENSG00000172425	<i>TTC36</i>	3.868086451	1846.745902	8.847561078	9.15E-41	1.33E-38
ENSG00000103942	<i>HOMER2</i>	130.6170252	1130.433819	3.112041115	1.08E-11	1.88E-10
ENSG00000101972	<i>STAG2</i>	421.4372967	941.3891551	1.159143667	0.006189631	0.021450542
ENSG00000069956	<i>MAPK6</i>	146.1689204	708.6198717	2.276193072	3.31E-07	2.99E-06
ENSG00000118482	<i>PHF3</i>	263.5856777	985.1137714	1.901395511	1.17E-05	8.04E-05
ENSG00000103067	<i>ESRP2</i>	125.1738611	1156.154181	3.205838057	3.40E-12	6.21E-11
ENSG00000085721	<i>RRN3</i>	373.2264599	928.5289738	1.314506324	0.002017405	0.00810713
ENSG00000181788	<i>SIAH2</i>	321.9052445	1069.990967	1.732395144	5.82E-05	0.000346336
ENSG00000171793	<i>CTPS1</i>	243.3682265	1071.276985	2.137420912	1.03E-06	8.60E-06
ENSG000000082146	<i>STRADB</i>	204.4885094	1403.069658	2.777608444	5.60E-10	7.61E-09
ENSG00000100852	<i>ARHGAP5</i>	168.7191642	826.9335413	2.292121478	2.32E-07	2.15E-06
ENSG00000066455	<i>GOLGA5</i>	296.2446357	828.2195595	1.482712748	0.000554494	0.002614179
ENSG00000137776	<i>SLTM</i>	366.2281124	1012.120152	1.466153979	0.000599831	0.002806628
ENSG00000152270	<i>PDE3B</i>	80.07333372	1073.849022	3.742935912	3.14E-15	7.91E-14
ENSG00000069667	<i>RORA</i>	90.95967356	1922.620969	4.399558001	1.18E-19	4.28E-18
ENSG00000120686	<i>UFM1</i>	496.8639262	1054.55875	1.085443861	0.010196262	0.033054401
ENSG00000099330	<i>OCELL1</i>	245.7010094	709.9058899	1.530100639	0.00040398	0.001971127
ENSG00000112851	<i>ERBB2IP</i>	370.1160832	931.1010101	1.330565563	0.001780421	0.007246172
ENSG00000204178	<i>TMEM57</i>	405.1078199	1253.891557	1.629648738	0.000139718	0.000759721
ENSG00000205702	<i>CYP2D7P</i>	14.75493478	1068.704949	6.164980917	5.30E-28	3.36E-26
ENSG00000123358	<i>NR4A1</i>	125.951456	1224.313141	3.279545584	1.09E-12	2.09E-11
ENSG00000198077	<i>CYP2A7</i>	0.757489584	1284.755992	10.48141077	2.01E-39	2.70E-37
ENSG00000124198	<i>ARFGEF2</i>	372.4488657	861.656031	1.209690962	0.004411959	0.015924956
ENSG00000136051	<i>KIAA1033</i>	436.9891793	958.1073908	1.13227468	0.007484686	0.025286377
ENSG00000073008	<i>PVR</i>	367.0057066	846.2238134	1.204852989	0.004614697	0.016572502
ENSG00000166033	<i>HTRA1</i>	627.4997341	1266.751738	1.013236384	0.015967288	0.04857018
ENSG00000133315	<i>MACROD1</i>	205.2661038	1004.404043	2.289929342	2.11E-07	1.97E-06
ENSG00000144824	<i>PHLDB2</i>	206.8212926	1035.268478	2.322708471	1.38E-07	1.32E-06
ENSG00000170088	<i>TMEM192</i>	276.0271857	1396.639567	2.338447162	1.02E-07	9.95E-07
ENSG00000111816	<i>FRK</i>	73.07496939	743.3423619	3.344004638	1.15E-12	2.20E-11
ENSG00000155666	<i>KDM8</i>	93.29246006	594.1642544	2.669102596	5.76E-09	6.77E-08
ENSG00000111700	<i>SLCO1B3</i>	5.423411881	2274.989926	8.675504561	3.56E-41	5.29E-39
ENSG00000138032	<i>PPM1B</i>	433.1012087	901.5225931	1.057349361	0.0124677	0.039566481
ENSG00000138640	<i>FAM13A</i>	103.4011996	1761.868707	4.088909807	1.22E-17	3.75E-16
ENSG00000158793	<i>NIT1</i>	413.6613554	1117.573638	1.433485742	0.000773227	0.003521818
ENSG00000261012	<i>RP11-116D2.1</i>	1.534979634	1581.826174	9.882153633	1.23E-41	1.92E-39
ENSG00000173848	<i>NET1</i>	237.1474721	878.3742668	1.888360411	1.44E-05	9.73E-05
ENSG00000008311	<i>AASS</i>	26.4190532	1959.915494	6.20549967	4.41E-30	3.17E-28
ENSG00000140905	<i>GCSH</i>	92.51486458	1023.694315	3.465911875	1.42E-13	2.99E-12
ENSG00000135317	<i>SNX14</i>	366.2281124	895.0925025	1.288900225	0.002452475	0.009545297
ENSG00000092439	<i>TRPM7</i>	122.0634815	787.0669789	2.687380074	3.19E-09	3.90E-08
ENSG00000100697	<i>DICER1</i>	394.999096	918.2408288	1.21666538	0.004177718	0.01513
ENSG00000122779	<i>TRIM24</i>	187.3814321	670.0393268	1.837400574	2.66E-05	0.000170986
ENSG00000100519	<i>PSMC6</i>	433.8788028	922.0988832	1.087316639	0.010212555	0.033102903
ENSG00000139597	<i>N4BP2L1</i>	399.6646609	1652.557169	2.047418489	2.18E-06	1.72E-05
ENSG00000078070	<i>MCCC1</i>	191.2694043	1129.147801	2.560625865	9.20E-09	1.05E-07
ENSG00000213853	<i>EMP2</i>	301.6877952	1233.315268	2.03085855	2.88E-06	2.23E-05
ENSG00000171988	<i>JMJD1C</i>	203.710915	1072.563004	2.395607742	6.05E-08	6.15E-07
ENSG00000077097	<i>TOP2B</i>	377.8920248	896.3785206	1.245756765	0.003416024	0.012815891
ENSG00000111142	<i>METAP2</i>	276.0271857	919.526847	1.735503133	5.92E-05	0.00035187
ENSG00000120437	<i>ACAT2</i>	214.5972363	974.8256264	2.18271658	6.71E-07	5.76E-06
ENSG00000119707	<i>RBM25</i>	372.4488657	1008.262098	1.43635403	0.000752875	0.003437939
ENSG00000166260	<i>COX11</i>	316.4620851	761.346616	1.266067645	0.002995312	0.0113794
ENSG00000170242	<i>USP47</i>	271.3616203	1010.834134	1.896653144	1.22E-05	8.38E-05
ENSG00000073803	<i>MAP3K13</i>	273.694403	573.5879633	1.066956428	0.012888354	0.040289278
ENSG00000109519	<i>GRPEL1</i>	431.5460204	1067.418931	1.306204227	0.002124388	0.008509534
ENSG000000256162	<i>SMLR1</i>	5.423411881	1009.548116	7.503431366	1.35E-32	1.15E-30
ENSG00000172594	<i>SMPDL3A</i>	291.5790704	1100.855402	1.916101564	9.62E-06	6.70E-05
ENSG00000198814	<i>GK</i>	331.2363747	1054.55875	1.670230541	0.000101225	0.000569863
ENSG00000119673	<i>ACOT2</i>	222.3731799	1233.315268	2.47069355	2.38E-08	2.57E-07
ENSG00000114062	<i>UBE3A</i>	338.2347224	936.2450826	1.468414966	0.000594134	0.002780494
ENSG00000112159	<i>MDN1</i>	367.0057066	1066.132913	1.538094908	0.000326377	0.001629263
ENSG00000160202	<i>CRYAA</i>	0.757489584	414.1217019	8.848272749	1.15E-27	7.16E-26
ENSG00000135378	<i>PRRG4</i>	183.4934598	832.0776139	2.180058662	7.64E-07	6.50E-06
ENSG00000100522	<i>GNPNAT1</i>	135.2825941	1144.580018	3.079401395	1.66E-11	2.82E-10

ENSG00000136153	<i>LMO7</i>	368.5608949	1275.753865	1.790937801	3.08E-05	0.000195539
ENSG00000181704	<i>YIPF6</i>	320.3500561	825.6475232	1.365417046	0.001399011	0.005925772
ENSG00000144283	<i>PKP4</i>	418.3269202	911.8107382	1.123775265	0.007989761	0.026759938
ENSG00000146477	<i>SLC22A3</i>	30.30706789	907.9526838	4.898384713	3.45E-21	1.42E-19
ENSG00000070018	<i>LRP6</i>	90.95967356	1349.056897	3.888465842	2.87E-16	7.87E-15
ENSG00000113615	<i>SEC24A</i>	334.3467515	1037.840514	1.633699651	0.00014096	0.000765973
ENSG00000165272	<i>AQP3</i>	374.004054	1211.45296	1.695189075	7.88E-05	0.000454881
ENSG00000167676	<i>PLIN4</i>	31.08466991	1008.262098	5.013168674	5.45E-22	2.35E-20
ENSG00000111058	<i>ACSS3</i>	80.07333372	1666.703368	4.377095636	2.19E-19	7.67E-18
ENSG00000109618	<i>SEPSECS</i>	74.63016171	1211.45296	4.018247444	7.04E-17	2.03E-15
ENSG00000196504	<i>PRPF40A</i>	380.2248072	923.3849013	1.279700936	0.002619795	0.010100046
ENSG00000138398	<i>PPIG</i>	255.0321408	965.8234995	1.920434803	1.01E-05	6.99E-05
ENSG00000125246	<i>CLYBL</i>	219.2628025	1385.065404	2.658402397	2.45E-09	3.04E-08
ENSG00000163686	<i>ABHD6</i>	160.9432185	979.9696989	2.605075007	5.81E-09	6.83E-08
ENSG00000164209	<i>SLC25A46</i>	308.6861431	816.6453962	1.403087399	0.001070415	0.004669211
ENSG00000139289	<i>PHLDA1</i>	363.89533	2017.786308	2.470693201	1.77E-08	1.94E-07
ENSG00000160325	<i>CACFD1</i>	282.2479397	814.0733599	1.527653435	0.000383285	0.001878265
ENSG00000114790	<i>ARHGEF26</i>	9.31159843	1180.588525	6.964747662	1.55E-31	1.23E-29
ENSG00000160293	<i>VAV2</i>	323.4604329	740.7703256	1.195002866	0.005211035	0.018481774
ENSG00000088205	<i>DDX18</i>	350.6762292	835.9356683	1.252844925	0.003337192	0.012556146
ENSG00000110074	<i>FOXRED1</i>	297.0222299	1113.715583	1.906184896	1.08E-05	7.49E-05
ENSG00000162378	<i>ZYG11B</i>	236.3698778	891.2344481	1.91406281	1.10E-05	7.59E-05
ENSG00000125901	<i>MRPS26</i>	488.310391	1158.726217	1.246377371	0.003227497	0.01218955
ENSG00000073734	<i>ABCB11</i>	5.423411881	1540.673594	8.113235036	4.89E-37	5.20E-35
ENSG00000090661	<i>CERS4</i>	213.819642	1207.594905	2.496843021	1.73E-08	1.91E-07
ENSG00000080819	<i>CPOX</i>	297.0222299	770.348743	1.374443817	0.001338906	0.005697398
ENSG00000170608	<i>FOXA3</i>	78.51814188	1193.448706	3.923514108	2.63E-16	7.24E-15
ENSG00000009765	<i>IYD</i>	1.534979634	1817.167485	10.08224247	4.10E-43	6.89E-41
ENSG00000175198	<i>PCCA</i>	156.2776509	1563.82192	3.321691628	4.92E-13	9.80E-12
ENSG00000119787	<i>ATL2</i>	173.3847314	893.8064844	2.364979088	1.01E-07	9.89E-07
ENSG00000257093	<i>KIAA1147</i>	227.0387459	866.8001036	1.932034162	9.48E-06	6.62E-05
ENSG00000136478	<i>TEX2</i>	375.5592423	1023.694315	1.446272545	0.000693167	0.003190493
ENSG00000102081	<i>FMR1</i>	279.9151569	954.2493364	1.76880307	4.36E-05	0.000267935
ENSG00000154265	<i>ABCA5</i>	65.29900539	920.8128651	3.814836688	2.22E-15	5.69E-14
ENSG00000186318	<i>BACE1</i>	311.0189257	1174.158435	1.916023759	9.67E-06	6.73E-05
ENSG00000105676	<i>ARMC6</i>	337.4571282	1801.735268	2.416091065	3.60E-08	3.78E-07
ENSG00000114796	<i>KLHL24</i>	406.6630082	906.6666657	1.15639723	0.006488151	0.022375884
ENSG00000114166	<i>KAT2B</i>	363.89533	1050.700696	1.529335553	0.000352506	0.001741166
ENSG00000163029	<i>SMC6</i>	144.613731	571.0159269	1.980177055	7.52E-06	5.39E-05
ENSG00000105176	<i>URI1</i>	352.2314175	761.346616	1.111641447	0.008908075	0.029380337
ENSG00000136381	<i>IREB2</i>	203.710915	771.6347612	1.920586404	1.10E-05	7.59E-05
ENSG00000116406	<i>EDEM3</i>	195.9349709	792.2110515	2.014657427	4.49E-06	3.37E-05
ENSG00000184470	<i>TXNRD2</i>	273.694403	1314.334408	2.263064293	2.34E-07	2.16E-06
ENSG00000151135	<i>C12orf23</i>	246.4786037	632.7447998	1.359564668	0.00157251	0.006503282
ENSG00000198670	<i>LPA</i>	1.534979634	1235.887304	9.526134579	5.08E-39	6.61E-37
ENSG00000115364	<i>MRPL19</i>	324.238027	937.5311007	1.531340796	0.000352858	0.001742556
ENSG00000013375	<i>PGM3</i>	199.822943	659.7511815	1.722402908	7.92E-05	0.000457075
ENSG00000111271	<i>ACAD10</i>	318.0172735	934.9590645	1.55531386	0.000292225	0.001480103
ENSG00000153201	<i>RANBP2</i>	293.1342588	950.391282	1.696419516	8.41E-05	0.000480779
ENSG00000196549	<i>MME</i>	5.423411881	686.757563	6.947659819	1.31E-28	8.62E-27
ENSG00000205981	<i>DNAJC19</i>	357.6745767	874.5162124	1.28943405	0.002509056	0.009745676
ENSG00000171703	<i>TCEA2</i>	260.4753007	715.0499625	1.456319269	0.000711769	0.003265831
ENSG00000196715	<i>VKORC1L1</i>	417.5493261	954.2493364	1.192083607	0.00499979	0.017808796
ENSG00000145824	<i>CXCL14</i>	638.3860512	1480.230744	1.21309989	0.003967697	0.014638134
ENSG00000175866	<i>BAIAP2</i>	212.2644532	1039.126532	2.290621302	2.04E-07	1.91E-06
ENSG00000134365	<i>CFHR4</i>	1.39E-17	1572.824047	13.66440257	1.43E-41	2.21E-39
ENSG00000113407	<i>TARS</i>	548.1851369	1112.429565	1.020737058	0.015341374	0.046849716
ENSG00000106733	<i>NMRK1</i>	375.5592423	884.8043574	1.235939477	0.003731504	0.013880057
ENSG00000198162	<i>MAN1A2</i>	238.7026607	905.3806475	1.922619712	9.86E-06	6.86E-05
ENSG00000204228	<i>HSD17B8</i>	177.2727039	869.3721398	2.293026826	2.27E-07	2.11E-06
ENSG00000115109	<i>EPB41L5</i>	112.7323414	928.5289738	3.04040673	3.38E-11	5.50E-10
ENSG00000104324	<i>CPQ</i>	415.9941378	963.2514633	1.21101006	0.004314493	0.015607151
ENSG00000145626	<i>UGT3A1</i>	3.090401881	1518.811287	8.876605006	1.09E-38	1.36E-36
ENSG00000215845	<i>TSTD1</i>	410.5509788	997.9739526	1.281090075	0.002616632	0.010094801
ENSG00000080493	<i>SLC4A4</i>	238.7026607	1449.366309	2.601387444	4.50E-09	5.38E-08
ENSG00000119547	<i>ONECUT2</i>	5.423411881	1022.408297	7.521691395	9.93E-33	8.60E-31
ENSG00000136783	<i>NIPSNAP3A</i>	258.9201121	875.8022305	1.757479215	4.99E-05	0.000300303
ENSG00000168904	<i>LRRC28</i>	166.3863805	650.7490543	1.966567078	7.89E-06	5.61E-05
ENSG00000117480	<i>FAAH</i>	232.4819062	865.5140854	1.895733271	1.33E-05	9.04E-05
ENSG00000134709	<i>HOOK1</i>	69.96458431	928.5289738	3.727516755	5.63E-15	1.37E-13
ENSG00000005469	<i>CROT</i>	124.3962662	646.8909998	2.377174406	1.22E-07	1.18E-06

ENSG00000138942	<i>RNF185</i>	444.7651205	995.4019163	1.16192296	0.006112835	0.02125374
ENSG00000198130	<i>HIBCH</i>	97.18043717	1709.141965	4.134468201	7.17E-18	2.23E-16
ENSG00000127831	<i>VIL1</i>	40.41587651	850.0818678	4.389778205	2.10E-18	6.84E-17
ENSG00000136021	<i>SCYL2</i>	258.9201121	640.4609089	1.306043482	0.002386576	0.009427581
ENSG00000090905	<i>TNRC6A</i>	419.8821085	870.658158	1.051802843	0.013071264	0.040804607
ENSG00000124333	<i>VAMP7</i>	250.3665751	682.8995085	1.447031086	0.000780689	0.003552548
ENSG00000141338	<i>ABCA8</i>	15.53254811	1522.669341	6.602267081	3.04E-31	2.35E-29
ENSG00000101460	<i>MAP1LC3A</i>	328.125998	887.3763937	1.434839648	0.000796287	0.003614264
ENSG00000084073	<i>ZMPSTE24</i>	325.7932154	797.3551241	1.290822679	0.002523728	0.009795012
ENSG00000199488	<i>RNU1-70P</i>	1.534979634	1018.550243	9.247128753	5.52E-37	5.77E-35
ENSG00000110013	<i>SIAE</i>	417.5493261	910.52472	1.124422575	0.008077448	0.027020857
ENSG00000172497	<i>ACOT12</i>	0.757489584	749.7724527	9.704519033	9.18E-34	8.39E-32
ENSG00000119950	<i>MXI1</i>	258.9201121	1072.563004	2.049835193	2.64E-06	2.06E-05
ENSG00000163251	<i>FZD5</i>	113.5099365	1084.137167	3.254008646	1.93E-12	3.62E-11
ENSG00000144035	<i>NAT8</i>	7.75633786	1652.557169	7.709248709	2.59E-36	2.63E-34
ENSG00000166275	<i>C10orf32</i>	258.9201121	1269.323775	2.292812636	1.69E-07	1.60E-06
ENSG00000064225	<i>ST3GAL6</i>	90.95967356	1301.474227	3.83666519	6.24E-16	1.68E-14
ENSG00000138802	<i>SEC24B</i>	290.023882	1054.55875	1.8618334	1.73E-05	0.000114913
ENSG00000239305	<i>RNF103</i>	348.3434466	783.2089245	1.168486874	0.005987195	0.020865358
ENSG00000101670	<i>LIPG</i>	314.1293025	1324.622553	2.075614692	1.81E-06	1.45E-05
ENSG00000183864	<i>TOB2</i>	517.081373	1049.414677	1.020865256	0.015453707	0.047146421
ENSG00000196372	<i>ASB13</i>	311.7965199	1104.713456	1.824475551	2.32E-05	0.000150342
ENSG00000142484	<i>TM4SF5</i>	14.75493478	1518.811287	6.672021036	1.20E-31	9.57E-30
ENSG00000168792	<i>ABHD15</i>	343.6778816	766.4906886	1.156807398	0.006667679	0.022950444
ENSG00000164187	<i>LMBRD2</i>	124.3962662	565.8718541	2.184158209	1.03E-06	8.56E-06
ENSG00000126602	<i>TRAP1</i>	370.8936774	1008.262098	1.442388452	0.000729514	0.003341702
ENSG00000131373	<i>HACL1</i>	184.2710543	596.7362907	1.694404402	0.000104028	0.000584716
ENSG00000143257	<i>NR1I3</i>	3.868086451	1953.485403	8.928622028	2.30E-41	3.49E-39
ENSG00000123200	<i>ZC3H13</i>	276.0271857	1271.895811	2.203477757	4.77E-07	4.21E-06
ENSG00000086619	<i>ERO1LB</i>	132.1722149	801.2131785	2.598415851	8.36E-09	9.62E-08
ENSG00000089050	<i>RBBP9</i>	237.9250664	760.0605978	1.67494393	0.000112447	0.000627499
ENSG00000138593	<i>SECISBP2L</i>	199.822943	815.3593781	2.02787637	3.63E-06	2.77E-05
ENSG00000224877	<i>C17orf89</i>	462.6497853	1192.162688	1.365270419	0.00131054	0.005585532
ENSG00000142748	<i>FCN3</i>	22.53102899	1512.381196	6.059898911	1.32E-28	8.65E-27
ENSG00000243818	<i>RP11-372E1.4</i>	1.39E-17	1239.745358	13.32111307	4.79E-39	6.27E-37
ENSG000000067900	<i>ROCK1</i>	289.2462877	672.6113632	1.216985932	0.004441869	0.016023609
ENSG00000135540	<i>NHSL1</i>	107.2891756	655.893127	2.610289466	9.48E-09	1.08E-07
ENSG00000151729	<i>SLC25A4</i>	356.1193883	1220.455087	1.776534875	3.67E-05	0.000229862
ENSG00000148943	<i>LIN7C</i>	233.2595005	781.9229064	1.744405164	5.82E-05	0.000346388
ENSG00000132485	<i>ZRANB2</i>	349.898635	784.4949426	1.164429483	0.006257742	0.021656388
ENSG00000147642	<i>SYBU</i>	139.9481627	1774.728888	3.663271625	3.90E-15	9.67E-14
ENSG00000153339	<i>TRAPPC8</i>	171.0519478	911.8107382	2.413274328	6.01E-08	6.12E-07
ENSG00000165030	<i>NFIL3</i>	313.3517083	1545.817667	2.301962445	1.43E-07	1.37E-06
ENSG00000117151	<i>CTBS</i>	300.910201	747.2004163	1.311679677	0.002182541	0.00871458
ENSG00000111249	<i>CUX2</i>	3.090401881	564.5858359	7.449083362	2.24E-28	1.45E-26
ENSG00000133195	<i>SLC39A11</i>	447.0979029	990.2578439	1.146903992	0.006729118	0.023120297
ENSG00000109184	<i>DCUN1D4</i>	114.2875316	787.0669789	2.782231187	1.03E-09	1.35E-08
ENSG00000132329	<i>RAMP1</i>	325.0156212	835.9356683	1.362430085	0.001449548	0.006051143
ENSG00000014123	<i>UFL1</i>	216.9300194	963.2514633	2.149898501	9.93E-07	8.30E-06
ENSG00000145439	<i>CBR4</i>	174.9399204	1403.069658	3.002601998	3.23E-11	5.25E-10
ENSG00000065548	<i>ZC3H15</i>	378.6696189	817.9314144	1.110679064	0.008938904	0.029469949
ENSG00000107902	<i>LHPP</i>	209.9316701	853.9399222	2.023418124	3.90E-06	2.95E-05
ENSG00000014824	<i>SLC30A9</i>	272.1392145	664.8952542	1.288252018	0.002687287	0.010337797
ENSG00000102967	<i>DHODH</i>	115.0651266	933.6730464	3.018863517	4.17E-11	6.69E-10
ENSG00000096092	<i>TMEM14A</i>	202.1557262	734.3402348	1.860174744	2.08E-05	0.000135909
ENSG00000173598	<i>NUDT4</i>	343.6778816	857.7979766	1.319157559	0.002023715	0.008131173
ENSG00000158828	<i>PINK1</i>	171.8295423	976.1116445	2.505037734	1.88E-08	2.06E-07
ENSG00000120054	<i>CPN1</i>	1.39E-17	1502.093051	13.59802367	4.44E-41	6.56E-39
ENSG00000141198	<i>TOM1L1</i>	62.18861847	1028.838387	4.045112965	8.92E-17	2.54E-15
ENSG00000183048	<i>SLC25A10</i>	94.07005552	711.191908	2.916483645	2.62E-10	3.73E-09
ENSG00000169762	<i>TAPT1</i>	192.0469988	1054.55875	2.456190753	3.26E-08	3.45E-07
ENSG00000043093	<i>DCUN1D1</i>	185.8262432	824.3615051	2.148407461	1.05E-06	8.73E-06
ENSG00000176641	<i>RNF152</i>	53.63504947	1934.195132	5.168722786	2.88E-24	1.44E-22
ENSG00000163714	<i>U2SURP</i>	292.3566646	805.0712329	1.460871278	0.000664123	0.003072171
ENSG00000198265	<i>HELZ</i>	357.6745767	807.6432692	1.174680409	0.005842266	0.020414667
ENSG00000150907	<i>FOXO1</i>	305.5757663	1496.948979	2.291856638	1.61E-07	1.53E-06
ENSG00000163825	<i>RTP3</i>	2.312696499	702.1897809	8.160823498	1.05E-31	8.51E-30
ENSG00000165997	<i>ARL5B</i>	102.6236044	1018.550243	3.309254168	1.05E-12	2.03E-11
ENSG00000078674	<i>PCM1</i>	256.5873293	848.7958497	1.72534681	6.56E-05	0.000386504
ENSG00000102471	<i>NDFIP2</i>	321.9052445	952.9633183	1.565305217	0.000267849	0.001365057
ENSG00000096401	<i>CDC5L</i>	171.0519478	754.9165253	2.140889038	1.28E-06	1.05E-05

ENSG00000205707	LYRM5	73.85256557	927.2429557	3.647646148	1.61E-14	3.70E-13
ENSG00000075711	DLG1	259.6977064	789.6390152	1.603760941	0.000206822	0.001083822
ENSG00000143630	HCN3	66.85419855	776.7788338	3.535575625	1.00E-13	2.14E-12
ENSG00000157625	TAB3	158.6104347	681.6134903	2.102400089	1.98E-06	1.58E-05
ENSG00000178401	DNAJC22	255.809735	839.7937227	1.714342355	7.57E-05	0.000438951
ENSG00000168118	RAB4A	377.8920248	837.2216864	1.147269428	0.006932651	0.023757208
ENSG00000036257	CUL3	353.7866058	898.9505569	1.344948275	0.0016408	0.006730829
ENSG00000186522	10-Sep	278.3599685	946.5332276	1.765124975	4.38E-05	0.000269407
ENSG00000183098	GPC6	114.2875316	639.1748907	2.481996762	3.97E-08	4.15E-07
ENSG00000137449	CPEB2	153.944867	672.6113632	2.126257467	1.67E-06	1.35E-05
ENSG00000148450	MSRB2	351.4538233	832.0776139	1.242977651	0.003468299	0.012994359
ENSG00000181904	C5orf24	283.8031281	784.4949426	1.466341747	0.000649408	0.003013635
ENSG00000130193	THEM6	234.8146891	772.9207793	1.718120345	7.62E-05	0.000441102
ENSG00000106034	CPED1	128.2842407	886.0903756	2.78669547	8.33E-10	1.10E-08
ENSG000000095209	TMEM38B	131.39462	309.9542149	1.237066202	0.004919722	0.017538682
ENSG00000116138	DNAJC16	244.9243151	882.2323212	1.848163336	2.14E-05	0.00013947
ENSG00000158373	HIST1H2BD	144.613731	371.6830975	1.360850996	0.00204892	0.008225798
ENSG00000140948	ZCCHC14	240.2578493	751.0584708	1.643688867	0.000146208	0.000792759
ENSG00000172009	THOP1	486.7552028	1211.45296	1.315171519	0.001928528	0.00779661
ENSG00000139218	SCAF11	328.9035922	717.6219988	1.125141589	0.008338129	0.02776436
ENSG00000143776	CDC42BPA	257.3649236	870.658158	1.757668313	4.87E-05	0.000294065
ENSG000000254211	CTB-43E15.4	20.19820843	1536.81554	6.239671661	1.95E-29	1.35E-27
ENSG00000165959	CLMN	309.4637373	1250.033503	2.013584924	3.44E-06	2.64E-05
ENSG00000185608	MRPL40	448.6530911	982.5417351	1.130611562	0.007631222	0.025728976
ENSG00000044446	PHKA2	335.9019398	990.2578439	1.559305282	0.000279697	0.00142165
ENSG00000166471	TMEM41B	257.3649236	574.8739815	1.158890586	0.00678663	0.023305015
ENSG00000109819	PPARGC1A	176.4951094	1692.42373	3.260330588	9.91E-13	1.92E-11
ENSG00000187079	TEAD1	213.0420476	745.9143982	1.807113082	3.39E-05	0.000213292
ENSG000000066468	FGFR2	357.6745767	1042.984587	1.543568939	0.000316441	0.001582523
ENSG00000109107	ALDOC	193.6021877	757.4885616	1.967272074	7.08E-06	5.10E-05
ENSG00000185127	C6orf120	208.3764814	635.3168362	1.607536546	0.000214928	0.001119684
ENSG00000114857	NKTR	300.1326068	954.2493364	1.668241167	0.000108048	0.000605807
ENSG00000143850	PLEKHA6	278.3599685	758.7745797	1.446179851	0.000758042	0.003458992
ENSG00000143382	ADAMTSL4	231.7043119	888.6624118	1.938637849	8.54E-06	6.01E-05
ENSG00000171365	CLCN5	70.74218064	1009.548116	3.83228132	1.25E-15	3.27E-14
ENSG000000061987	MON2	192.8245932	839.7937227	2.121866805	1.38E-06	1.12E-05
ENSG00000075643	MOCOS	128.2842407	677.7554358	2.400055075	9.14E-08	9.02E-07
ENSG00000113492	AGXT2	0.757489584	1373.491241	10.57775704	3.92E-40	5.41E-38
ENSG00000106333	PCOLCE	248.0337922	1377.349296	2.472574472	2.22E-08	2.39E-07
ENSG00000151892	GFRA1	15.53254811	1440.364183	6.522103291	1.15E-30	8.49E-29
ENSG00000235142	RP1-60O19.1	82.40612126	691.9016356	3.067497467	4.33E-11	6.93E-10
ENSG00000205358	MT1H	1.39E-17	70.75461835	9.191911381	7.81E-12	1.38E-10
ENSG00000196660	SLC30A10	13.19970438	1194.734724	6.484878688	1.33E-29	9.29E-28
ENSG00000106025	TSPAN12	69.18698793	682.8995085	3.30038913	2.91E-12	5.35E-11
ENSG00000095637	SORBS1	69.18698793	1423.645947	4.360127429	5.31E-19	1.80E-17
ENSG00000015171	ZMYND11	408.9957906	850.0818678	1.055187672	0.012720396	0.039847026
ENSG00000144891	AGTR1	34.19507543	1445.508255	5.395838138	6.62E-25	3.47E-23
ENSG00000070159	PTPN3	166.3863805	865.5140854	2.37796956	8.97E-08	8.87E-07
ENSG00000135070	ISCA1	382.5575897	857.7979766	1.164597275	0.00622096	0.021538092
ENSG00000125798	FOXA2	19.42060034	888.6624118	5.505741434	3.55E-24	1.76E-22
ENSG00000166200	COPS2	244.9234151	707.3338535	1.529435359	0.000398422	0.001945917
ENSG00000106384	MOGAT3	1.39E-17	126.0535149	10.02417873	1.86E-16	5.16E-15
ENSG00000174738	NR1D2	154.7224617	506.7150163	1.710464913	0.000104104	0.000585009
ENSG00000229807	XIST	237.9250664	2824.119651	3.568423894	8.71E-15	2.07E-13
ENSG00000173898	SPTBN2	209.9316701	1331.052644	2.663720386	2.24E-09	2.80E-08
ENSG00000146476	C6orf211	192.8245932	613.4545271	1.668849859	0.000131167	0.000718095
ENSG00000102763	VWA8	172.6071368	1139.435945	2.721710155	1.30E-09	1.68E-08
ENSG00000138018	EPT1	346.7882583	753.6305071	1.119406841	0.008609237	0.028496814
ENSG00000083223	ZCCHC6	186.6038376	1145.866036	2.617429181	4.51E-09	5.39E-08
ENSG00000114698	PLSCR4	239.480255	1042.984587	2.122031411	1.22E-06	1.00E-05
ENSG00000081923	ATP8B1	132.1722149	392.2593907	1.568220324	0.00038484	0.001884768
ENSG00000136444	RSAD1	412.8837612	938.8171189	1.184769394	0.005269818	0.018610588
ENSG000000164038	SLC9B2	96.40284179	1203.736851	3.640323956	1.11E-14	2.61E-13
ENSG00000153721	CNKSR3	148.5017045	1361.917078	3.19583192	2.94E-12	5.40E-11
ENSG00000161653	NAGS	90.18207801	754.9165253	3.063352714	4.02E-11	6.47E-10
ENSG00000110871	COQ5	353.7866058	743.3423619	1.070766009	0.011850523	0.037771832
ENSG00000197977	ELOVL2	24.08624001	1652.557169	6.092051546	6.72E-29	4.49E-27
ENSG00000100320	RBFOX2	326.5708096	736.9122711	1.173669772	0.005959265	0.020770935
ENSG00000178814	OPLAH	311.0189257	1105.999475	1.829754731	2.29E-05	0.000148693
ENSG00000100814	CCNB1IP1	346.0106641	1063.560877	1.619563172	0.000160017	0.000862553
ENSG00000147576	ADHFE1	88.62688686	999.2599707	3.492907235	1.04E-13	2.21E-12

ENSG00000165156	ZHX1	122.8410764	834.6496502	2.762903294	1.09E-09	1.43E-08
ENSG00000115084	SLC35F5	262.8080835	661.0371996	1.330166517	0.002003286	0.008055601
ENSG00000106617	PRKAG2	258.9201121	776.7788338	1.584398404	0.000243738	0.001255044
ENSG00000213930	GALT	215.3748307	661.0371996	1.61715742	0.000193304	0.001018857
ENSG00000153707	PTPRD	56.74543914	407.6916104	2.841689266	1.63E-09	2.07E-08
ENSG00000055609	KMT2C	363.1177358	758.7745797	1.062863374	0.012234868	0.038887166
ENSG00000133026	MYH10	169.4967587	1156.154181	2.768935331	7.43E-10	9.97E-09
ENSG00000146433	TMEM181	214.5972363	576.1599997	1.424141509	0.001020872	0.004471149
ENSG00000107957	SH3PXD2A	604.1719115	1332.338662	1.140701289	0.00675336	0.023200381
ENSG00000075651	PLD1	177.2727039	832.0776139	2.229778301	4.61E-07	4.08E-06
ENSG00000144115	THNSL2	207.598887	540.15149	1.378853414	0.001482879	0.006176801
ENSG00000109756	RAPGEF2	301.6877952	808.9292874	1.422462093	0.000924689	0.004085894
ENSG00000198142	SOWAHC	150.8344885	1202.450833	2.993718788	4.33E-11	6.93E-10
ENSG00000135655	USP15	270.584026	811.5013236	1.583944185	0.000232408	0.001203686
ENSG000000091039	OSBPL8	279.1375627	662.3232178	1.246048361	0.003622229	0.013501875
ENSG00000144827	ABHD10	247.2561979	843.6517771	1.769991424	4.43E-05	0.000271807
ENSG00000076826	CAMSAP3	129.8394304	582.5900906	2.164439503	1.18E-06	9.73E-06
ENSG00000101752	MIB1	223.9283686	554.2976903	1.306975978	0.002474993	0.009623899
ENSG00000143507	DUSP10	230.1491232	857.7979766	1.897356037	1.33E-05	9.02E-05
ENSG00000169139	UBE2V2	251.9217637	739.4843074	1.552932781	0.000322733	0.001612043
ENSG00000198252	STYX	172.6071368	668.7533087	1.953023029	8.67E-06	6.10E-05
ENSG00000170802	FOXN2	193.6021877	451.4162319	1.220631894	0.005006089	0.017828678
ENSG00000156052	GNAQ	276.0271857	729.1961622	1.400958234	0.001103758	0.004797931
ENSG00000164292	RHOBTB3	174.1623259	1269.323775	2.864507823	2.18E-10	3.14E-09
ENSG00000162772	ATF3	268.2512433	577.4460179	1.105592244	0.009811308	0.031994236
ENSG00000170855	TRIAP1	353.7866058	792.2110515	1.162612364	0.006321261	0.021855712
ENSG00000253352	TUG1	264.363272	808.9292874	1.612902251	0.000184271	0.000978017
ENSG00000211456	SACMIL	316.4620851	742.0563437	1.229047755	0.003924266	0.014495117
ENSG00000134313	KIDINS220	289.2462877	645.6049816	1.157873218	0.006761618	0.02322554
ENSG00000117009	KMO	34.97267623	1710.427983	5.606295267	1.26E-26	7.39E-25
ENSG00000113594	LIFR	70.74218064	1400.497621	4.30447239	1.01E-18	3.36E-17
ENSG00000187164	KIAA1598	285.3583166	709.9058899	1.314343933	0.002156394	0.00861691
ENSG00000057294	PKP2	66.07660199	585.162127	3.143810418	2.80E-11	4.61E-10
ENSG00000135241	PNPLA8	192.0469988	488.7107611	1.346758136	0.001940489	0.007841142
ENSG00000074935	TUBE1	83.96131282	1102.14142	3.712164645	4.58E-15	1.13E-13
ENSG000000225968	ELFN1	27.97426007	535.0074172	4.250433165	7.22E-17	2.08E-15
ENSG00000158321	AUTS2	133.7274045	771.6347612	2.527296091	1.84E-08	2.02E-07
ENSG00000157087	ATP2B2	2.312696499	798.6411422	8.346485758	4.78E-33	4.21E-31
ENSG00000149742	SLC22A9	3.868086451	744.62838	7.53728065	3.23E-31	2.49E-29
ENSG00000166912	MTMR10	293.9118531	789.6390152	1.425301108	0.000899112	0.003988476
ENSG00000177425	PAWR	276.0271857	884.8043574	1.679975915	9.99E-05	0.000563063
ENSG00000110628	SLC22A18	325.0156212	1270.609793	1.966429887	5.68E-06	4.17E-05
ENSG00000138821	SLC39A8	229.3715289	1037.840514	2.177082254	6.96E-07	5.96E-06
ENSG00000205726	ITSN1	194.3797821	758.7745797	1.963940259	7.32E-06	5.26E-05
ENSG00000157216	SSBP3	309.4637373	765.2046704	1.30560686	0.002226662	0.008863499
ENSG00000166415	WDR72	78.51814188	1296.330155	4.042801414	4.39E-17	1.29E-15
ENSG00000018510	AGPS	344.4554758	802.4991967	1.219771684	0.004152848	0.015119355
ENSG00000105088	OLFM2	302.4653894	961.9654451	1.668693962	0.000105369	0.000591732
ENSG00000101413	RPRD1B	298.5774184	652.0350725	1.126384116	0.008454725	0.028066587
ENSG00000121690	DEPDC7	10.08922402	1221.741105	6.90012187	2.49E-31	1.94E-29
ENSG00000108439	PNPO	109.621961	870.658158	2.987890048	7.22E-11	1.12E-09
ENSG00000198677	TTC37	220.0403968	889.94843	2.015194213	4.11E-06	3.09E-05
ENSG00000106070	GRB10	365.4505183	766.4906886	1.068223296	0.012108223	0.038524051
ENSG00000180011	ZADH2	306.3533605	739.4843074	1.270854161	0.002928115	0.011143516
ENSG00000171492	LRRC8D	248.0337922	529.8633443	1.094535176	0.010732801	0.034653647
ENSG00000116833	NR5A2	154.7224617	712.4779262	2.202055658	6.77E-07	5.80E-06
ENSG00000118898	PPL	243.3682265	612.168509	1.330188336	0.00197294	0.007949005
ENSG00000091436	MLTK	347.5658525	715.0499625	1.040373577	0.014530997	0.044698999
ENSG00000184402	SS18L1	174.9399204	973.5396083	2.475371058	2.59E-08	2.77E-07
ENSG00000019995	ZRANB1	262.8080835	1035.268478	1.977291374	5.33E-06	3.94E-05
ENSG00000109576	AADAT	17.86538201	1381.20735	6.261425166	2.03E-29	1.40E-27
ENSG00000144357	UBR3	145.3913257	1060.98884	2.866140968	2.53E-10	3.61E-09
ENSG00000130881	LRP3	107.2891756	1226.885177	3.513657479	5.69E-14	1.25E-12
ENSG00000151276	MAGI1	107.2891756	793.4970697	2.885016502	3.00E-10	4.24E-09
ENSG00000136536	7-Mar	318.0172735	810.2153055	1.348739103	0.001607807	0.006610762
ENSG00000142892	PIGK	210.7092645	439.8420675	1.061093502	0.014097082	0.04359624
ENSG00000233377	MTND4P20	36.52787722	1255.177575	5.097335207	4.87E-23	2.24E-21
ENSG00000101605	MYOM1	100.2908185	1977.919747	4.299781422	5.20E-19	1.77E-17
ENSG00000117595	IRF6	41.97107512	655.893127	3.961397883	8.72E-16	2.32E-14
ENSG00000165169	DYNLT3	144.613731	618.5985999	2.095630731	2.30E-06	1.81E-05
ENSG00000120907	ADRA1A	1.534979634	1080.279112	9.332007846	1.35E-37	1.51E-35

ENSG00000170522	ELOVL6	59.8558277	1251.319521	4.382554874	4.73E-19	1.61E-17
ENSG00000237949	LINC00844	0.757489584	811.5013236	9.818645424	1.36E-34	1.29E-32
ENSG00000136933	RABEPK	346.0106641	789.6390152	1.1899715	0.005224507	0.018511064
ENSG00000100033	PRODH	10.08922402	2168.250425	7.727664542	2.30E-37	2.49E-35
ENSG00000188647	PTAR1	185.0486487	772.9207793	2.0615073	2.82E-06	2.19E-05
ENSG00000167196	FBXO22	250.3665751	565.8718541	1.175875672	0.006176549	0.02140819
ENSG00000111911	HINT3	236.3698778	598.0223089	1.338534316	0.001896465	0.007670729
ENSG00000139405	RITA1	297.0222299	628.8867453	1.081773309	0.011239863	0.036075258
ENSG00000110921	MVK	162.4984077	541.4375082	1.735386889	7.67E-05	0.000443828
ENSG00000103449	SALL1	173.3847314	1099.569384	2.66385394	2.75E-09	3.39E-08
ENSG00000165424	ZCCHC24	367.0057066	889.94843	1.277527296	0.002718428	0.010443049
ENSG00000172943	PHF8	308.6861431	673.8973813	1.125942949	0.008372376	0.027850027
ENSG00000124006	OBSL1	406.6630082	1039.126532	1.353104694	0.001480976	0.006169908
ENSG00000189233	NUGGC	185.8262432	790.9250334	2.088678476	1.98E-06	1.58E-05
ENSG00000174567	GOLT1A	78.51814188	875.8022305	3.477097212	1.71E-13	3.58E-12
ENSG00000164258	NDUFS4	407.4406023	828.2195595	1.023097873	0.015898268	0.048389842
ENSG00000116191	RALGPS2	87.07169561	915.6687926	3.392385776	4.00E-13	8.04E-12
ENSG00000066855	MTFR1	146.9465151	581.3040725	1.982870287	7.75E-06	5.51E-05
ENSG00000186106	ANKRD46	108.8443659	906.6666657	3.056606461	2.83E-11	4.66E-10
ENSG00000107679	PLEKHA1	252.6993579	709.9058899	1.489605167	0.000563303	0.002653696
ENSG00000065243	PKN2	146.9465151	614.7405453	2.063541781	3.40E-06	2.61E-05
ENSG00000206560	ANKRD28	201.3781318	643.0329452	1.674202075	0.000119347	0.000662026
ENSG00000110330	BIRC2	321.9052445	873.2301942	1.439259993	0.000776397	0.003534311
ENSG00000125149	C16orf70	199.0453486	625.0286908	1.650036247	0.000152571	0.000824741
ENSG00000088256	GNAI1	338.2347224	699.6177446	1.048146301	0.013739542	0.04255936
ENSG00000204682	CASC10	7.75633786	497.7128887	5.978131197	6.21E-24	3.05E-22
ENSG00000059769	DNAJC25	86.29409995	1042.984587	3.593108153	2.80E-14	6.32E-13
ENSG00000197323	TRIM33	219.2628025	488.7107611	1.15568689	0.00738331	0.024984639
ENSG00000154059	IMPACT	223.1507742	601.8803635	1.430787071	0.000939109	0.004144577
ENSG00000122257	RBBP6	258.9201121	718.908017	1.472716248	0.000636551	0.002958961
ENSG00000115365	LANCL1	184.2710543	558.1557449	1.597994882	0.000249172	0.001278524
ENSG00000068305	MEF2A	226.2611516	545.2955628	1.268415278	0.00324126	0.012230381
ENSG00000169093	ASMTL	313.3517083	653.3210906	1.059580396	0.012830374	0.040133267
ENSG00000158711	ELK4	230.1491232	621.1706362	1.431770074	0.000908583	0.004026894
ENSG00000149212	SESN3	169.4967587	947.8192458	2.482312061	2.57E-08	2.75E-07
ENSG00000110429	FBXO3	202.1557262	650.7490543	1.685851953	0.000107969	0.000605496
ENSG00000133678	TMEM254	222.3731799	949.1052639	2.092825985	1.76E-06	1.41E-05
ENSG00000153130	SCOC	237.1474721	770.348743	1.699058735	8.95E-05	0.000509202
ENSG00000164068	RNF123	223.1507742	700.9037628	1.65049375	0.000142472	0.000773511
ENSG00000105856	HBP1	265.1408662	650.7490543	1.294797077	0.002570399	0.009940448
ENSG00000111339	ART4	76.18535388	761.346616	3.318503208	1.83E-12	3.44E-11
ENSG00000106688	SLC1A1	300.1326068	824.3615051	1.457175193	0.000678394	0.00312829
ENSG00000196850	PPTC7	287.6910993	742.0563437	1.366496075	0.001473399	0.006142456
ENSG00000058063	ATP11B	241.8130379	605.738418	1.324200313	0.002143843	0.008570888
ENSG00000085760	MTIF2	195.9349709	565.8718541	1.529318835	0.000443499	0.002148347
ENSG00000173210	ABLIM3	286.1359108	1394.067531	2.283923661	1.85E-07	1.74E-06
ENSG00000124523	SIRT5	202.1557262	1058.416804	2.38750356	6.97E-08	7.01E-07
ENSG00000151090	THRB	38.8606773	727.9101441	4.222375648	2.56E-17	7.70E-16
ENSG00000138709	LARP1B	160.1656239	1019.836261	2.669579067	2.84E-09	3.50E-08
ENSG00000145349	CAMK2D	294.6894473	825.6475232	1.485816052	0.000548627	0.002587499
ENSG00000215908	CROCCP2	252.6993579	652.0350725	1.366944496	0.001530963	0.006350481
ENSG00000164403	SHROOM1	102.6236044	848.7958497	3.046254077	3.70E-11	6.02E-10
ENSG00000161243	FBXO27	18.64299156	131.1975941	2.805281453	1.04E-07	1.01E-06
ENSG00000011405	PIK3C2A	185.0486487	619.8846181	1.743231275	6.73E-05	0.000396122
ENSG00000112701	SENP6	320.3500561	663.609236	1.050266498	0.013636658	0.042293377
ENSG00000164039	BDH2	100.2908185	892.5204662	3.15184094	9.84E-12	1.71E-10
ENSG00000029993	HMGB3	230.9267175	631.4587817	1.450602126	0.000790959	0.003593362
ENSG00000154734	ADAMTS1	209.1540757	601.8803635	1.524179259	0.000443954	0.002149712
ENSG00000163687	DNASE1L3	36.52787722	1340.05477	5.191728613	1.09E-23	5.26E-22
ENSG00000114030	KPNA1	241.0354436	618.5985999	1.359148185	0.001616927	0.006639472
ENSG00000135617	PRADC1	221.5955855	644.3189634	1.539153345	0.000368072	0.001810494
ENSG00000164117	FBXO8	252.6993579	583.8761088	1.207682333	0.005049043	0.017966208
ENSG00000125629	INSIG2	264.363272	986.3997895	1.899029942	1.22E-05	8.35E-05
ENSG00000047346	FAM214A	227.8163402	776.7788338	1.768927816	4.78E-05	0.000289284
ENSG00000112249	ASCC3	251.9217637	519.5751986	1.043826141	0.015137992	0.046348211
ENSG00000162460	TMEM82	0.757489584	1206.308887	10.39052286	9.43E-39	1.19E-36
ENSG00000162852	CNST	154.7224617	699.6177446	2.175780842	9.06E-07	7.62E-06
ENSG00000166037	CEP57	203.710915	1041.698569	2.353487094	9.91E-08	9.70E-07
ENSG00000166016	ABTB2	120.5082916	658.4651633	2.448513486	5.39E-08	5.54E-07
ENSG00000107854	TNKS2	311.0182527	734.3402348	1.23898879	0.003731467	0.013880057
ENSG00000124587	PEX6	254.2545465	748.4864345	1.557096674	0.000305285	0.001539744

ENSG00000135100	<i>HNF1A</i>	109.621961	542.7235264	2.306098496	3.06E-07	2.78E-06
ENSG00000163684	<i>RPP14</i>	356.8969825	751.0584708	1.073039165	0.011579609	0.037079513
ENSG00000165215	<i>CLDN3</i>	117.3979117	468.1344692	1.994097321	8.04E-06	5.70E-05
ENSG00000115290	<i>GRB14</i>	41.19347589	914.3827744	4.467563614	6.51E-19	2.20E-17
ENSG00000156968	<i>MPV17L</i>	64.52140874	546.5815811	3.079715698	6.05E-11	9.47E-10
ENSG00000101849	<i>TBL1X</i>	210.7092645	1109.857529	2.396217877	5.89E-08	6.00E-07
ENSG00000144481	<i>TRPM8</i>	1.534979634	1462.22649	9.768736608	8.44E-41	1.23E-38
ENSG00000136152	<i>COG3</i>	220.8179912	817.9314144	1.88838015	1.52E-05	0.000102053
ENSG00000129514	<i>FOXA1</i>	286.1359108	676.4694177	1.240826594	0.003749235	0.013932475
ENSG00000023287	<i>RB1CC1</i>	272.9168088	677.7554358	1.311771432	0.002260171	0.008986811
ENSG00000138688	<i>KIAA1109</i>	143.0585416	986.3997895	2.784298806	7.61E-10	1.02E-08
ENSG00000100116	<i>GCAT</i>	48.9694625	1050.700696	4.419337207	5.08E-19	1.73E-17
ENSG00000174032	<i>SLC25A30</i>	243.3682265	983.8277532	2.014578665	3.82E-06	2.89E-05
ENSG00000180694	<i>TMEM64</i>	259.6977064	585.162127	1.171466166	0.00639358	0.022089579
ENSG00000120833	<i>SOC2</i>	118.175067	1451.938345	3.617366512	1.10E-14	2.58E-13
ENSG000000213995	<i>CARKD</i>	363.1177358	1013.40617	1.480286177	0.000530966	0.002511618
ENSG00000139132	<i>FGD4</i>	161.7208131	730.4821804	2.174288303	8.86E-07	7.47E-06
ENSG00000105829	<i>BET1</i>	195.1573765	437.270031	1.163173699	0.007233498	0.024554698
ENSG00000116750	<i>UCHL5</i>	188.936621	533.721399	1.497379656	0.000588391	0.002758025
ENSG00000052723	<i>SIKE1</i>	236.3698778	529.8633443	1.163985527	0.006686516	0.022989813
ENSG00000141664	<i>ZCCHC2</i>	236.3698778	938.8171189	1.989093983	5.06E-06	3.76E-05
ENSG00000166482	<i>MFAP4</i>	443.9875264	1041.698569	1.230027212	0.003728181	0.013871848
ENSG00000100557	<i>C14orf105</i>	125.951456	348.5347671	1.467235522	0.000939304	0.004144577
ENSG00000134900	<i>TPP2</i>	246.4786037	709.9058899	1.5255446	0.00040398	0.001971127
ENSG00000166387	<i>PPFIBP2</i>	243.3682265	730.4821804	1.585071455	0.000241603	0.001245341
ENSG00000108387	<i>4-Sep</i>	216.9300194	905.3806475	2.060519808	2.61E-06	2.03E-05
ENSG00000013561	<i>RNF14</i>	365.4505183	769.0627249	1.073055687	0.011665238	0.037344087
ENSG00000106069	<i>CHN2</i>	87.07169561	833.363632	3.256521198	2.68E-12	4.94E-11
ENSG00000162551	<i>ALPL</i>	43.52627316	1165.156308	4.737976043	6.61E-21	2.64E-19
ENSG00000138592	<i>USP8</i>	199.0453486	601.8803635	1.595599216	0.000246762	0.001267727
ENSG00000175806	<i>MSRA</i>	166.3863805	801.2131785	2.266611424	3.19E-07	2.89E-06
ENSG00000103150	<i>MLYCD</i>	152.3896778	865.5140854	2.504630318	2.18E-08	2.37E-07
ENSG00000171497	<i>PPID</i>	213.0420476	846.2238134	1.989119993	5.52E-06	4.06E-05
ENSG00000153936	<i>HS2ST1</i>	173.3847314	506.7150163	1.546311103	0.000394776	0.001930389
ENSG00000121361	<i>KCNJ8</i>	141.5033522	1087.995221	2.94146725	9.63E-11	1.46E-09
ENSG00000106078	<i>COBL</i>	117.3979117	749.7724527	2.67351453	3.79E-09	4.58E-08
ENSG00000132849	<i>INADL</i>	214.5972363	627.6007271	1.547499064	0.000348894	0.001725036
ENSG00000158290	<i>CUL4B</i>	272.1392145	573.5879633	1.075173287	0.012046029	0.038350718
ENSG00000172469	<i>MANEA</i>	155.5000563	601.8803635	1.951497357	9.58E-06	6.68E-05
ENSG000000205765	<i>C5orf51</i>	119.7306966	324.1004176	1.43539566	0.001255319	0.005372064
ENSG00000049246	<i>PER3</i>	115.0651266	502.8569617	2.126222934	2.15E-06	1.70E-05
ENSG00000156006	<i>NAT2</i>	0.757489584	1091.853275	10.24671468	1.06E-37	1.21E-35
ENSG00000185100	<i>ADSSL1</i>	119.7306966	426.9818847	1.833025256	3.69E-05	0.000230757
ENSG00000123213	<i>NLN</i>	279.9151569	994.1158982	1.827844953	2.45E-05	0.000158349
ENSG00000081307	<i>UBA5</i>	209.1540757	464.2764145	1.14975562	0.007765307	0.02615976
ENSG00000137177	<i>KIF13A</i>	261.2528949	675.1833995	1.369268098	0.001431054	0.006003845
ENSG00000141425	<i>RPRD1A</i>	237.9250664	572.3019451	1.265666569	0.003306121	0.012448666
ENSG00000172086	<i>KRCC1</i>	170.2743533	500.2849252	1.553984504	0.000372108	0.001828898
ENSG00000198060	<i>5-Mar</i>	335.1243456	707.3338535	1.077291281	0.011354504	0.036419693
ENSG00000110315	<i>RNF141</i>	253.4769522	622.4566544	1.295548406	0.002540895	0.009849337
ENSG00000003393	<i>ALS2</i>	166.3863805	658.4651633	1.983570356	6.74E-06	4.88E-05
ENSG00000180530	<i>NRIP1</i>	60.63342469	641.7469271	3.400709216	9.08E-13	1.77E-11
ENSG000000241935	<i>HOGA1</i>	59.8558277	1045.556623	4.123397907	2.50E-17	7.54E-16
ENSG00000116667	<i>C1orf21</i>	276.0271857	934.9590645	1.759512118	4.75E-05	0.000289284
ENSG00000167700	<i>MFSD3</i>	232.4819062	654.6071088	1.492857477	0.000541714	0.002556837
ENSG00000143842	<i>SOX13</i>	165.608786	399.9755006	1.271265079	0.003662483	0.013643737
ENSG00000163069	<i>SGCB</i>	311.0189257	676.4694177	1.120581203	0.008653288	0.028623567
ENSG00000234456	<i>MAGI2-AS3</i>	44.30387198	893.8064844	4.330058637	3.81E-18	1.21E-16
ENSG00000137500	<i>CCDC90B</i>	384.112778	812.7873418	1.080995478	0.010884312	0.035047232
ENSG00000143756	<i>FBXO28</i>	258.1425179	607.0244362	1.233036533	0.00404605	0.014885224
ENSG00000113851	<i>CRBN</i>	217.7076138	587.7341634	1.432084036	0.000957278	0.004217149
ENSG00000090539	<i>CHRD</i>	313.3517083	1012.120152	1.691020706	8.52E-05	0.000486927
ENSG00000166479	<i>TMX3</i>	277.5823742	610.8824908	1.137481924	0.007950749	0.026658014
ENSG00000159256	<i>MORC3</i>	255.809735	734.3402348	1.520779993	0.00042433	0.002061922
ENSG00000071794	<i>HLTF</i>	152.3896778	519.5751986	1.768513542	5.80E-05	0.000345005
ENSG00000124374	<i>PAIP2B</i>	99.51322321	652.0350725	2.710176902	3.01E-09	3.69E-08
ENSG000000042781	<i>USH2A</i>	1.39E-17	518.2891804	12.06305598	5.82E-30	4.17E-28
ENSG00000063176	<i>SPHK2</i>	155.5000563	361.3949507	1.21575216	0.005698947	0.019947518
ENSG00000123739	<i>PLA2G12A</i>	154.7224617	887.3763937	2.518717699	1.75E-08	1.92E-07
ENSG00000138604	<i>GLCE</i>	115.8427216	537.5794536	2.21282985	7.81E-07	6.63E-06
ENSG00000106823	<i>ECM2</i>	46.63666774	793.4970697	4.084536925	1.11E-16	3.14E-15

ENSG00000124615	MOCS1	97.18043717	902.8086113	3.21376136	4.60E-12	8.26E-11
ENSG00000005882	PDK2	101.0684138	655.893127	2.696345995	3.73E-09	4.52E-08
ENSG00000147592	LACTB2	201.3781318	437.270031	1.117936609	0.010091712	0.032758195
ENSG00000163701	IL17RE	41.19347589	160.7760419	1.960537854	5.14E-05	0.000309227
ENSG00000170775	GPR37	15.53254811	43.74811345	1.484153491	0.01296303	0.040502341
ENSG00000166483	WEE1	122.0634815	504.1429799	2.044826682	4.79E-06	3.57E-05
ENSG00000153914	SREK1	279.1375627	771.6347612	1.46640105	0.000644983	0.002994781
ENSG00000153207	AHCTF1	151.6120831	658.4651633	2.117604769	1.74E-06	1.40E-05
ENSG00000112339	HBS1L	192.8245932	554.2976903	1.522578865	0.000470393	0.002268973
ENSG00000170677	SOCS6	166.3863805	834.6496502	2.325589	1.65E-07	1.57E-06
ENSG00000175110	MRPS22	234.0370948	595.4502726	1.346617527	0.001795552	0.00730536
ENSG00000198948	MFAP3L	13.19970438	1203.736851	6.495707527	1.12E-29	7.90E-28
ENSG00000136997	MYC	293.1342588	1080.279112	1.88121237	1.40E-05	9.48E-05
ENSG00000118922	KLF12	95.62524639	1001.832007	3.387135101	3.96E-13	7.97E-12
ENSG00000009564	BTAF1	237.1474721	733.0542167	1.627476193	0.000171123	0.000914089
ENSG00000175906	ARL4D	27.97426007	785.7809608	4.804917771	1.56E-20	6.07E-19
ENSG00000072415	MPP5	102.6236044	487.4247429	2.246138545	6.38E-07	5.50E-06
ENSG00000132437	DDC	1.534979634	889.94843	9.052425154	1.45E-35	1.46E-33
ENSG00000164830	OXR1	125.1738611	775.4928156	2.629749142	6.12E-09	7.16E-08
ENSG00000197785	ATAD3A	265.1408662	551.7256539	1.056685538	0.013701728	0.042463059
ENSG00000108064	TFAM	274.4719973	689.3295993	1.328003615	0.001935116	0.007821972
ENSG00000117643	MAN1C1	365.4505183	911.8107382	1.318660254	0.001955945	0.007886927
ENSG00000163032	VSNL1	34.97267623	649.4630361	4.209391229	4.71E-17	1.38E-15
ENSG00000004866	ST7	203.710915	519.5751986	1.350089066	0.001874864	0.007590771
ENSG00000135111	TBX3	60.63342469	816.6453962	3.74836767	6.71E-15	1.62E-13
ENSG00000152583	SPARCL1	353.0090117	744.62838	1.076432618	0.011392858	0.03652386
ENSG00000164494	PDSS2	181.9382708	546.5815811	1.586135689	0.000280671	0.001425437
ENSG00000182902	SLC25A18	38.08307745	1035.268478	4.75954599	1.04E-20	4.10E-19
ENSG000000244005	NFS1	248.8113865	587.7341634	1.239539249	0.004001601	0.014743522
ENSG00000154727	GABPA	149.2792991	551.7256539	1.884839769	1.95E-05	0.000128532
ENSG00000109445	ZNF330	243.3682265	684.1855266	1.490622959	0.0005515	0.002600555
ENSG00000138459	SLC35A5	213.0420476	522.147235	1.292640312	0.002780726	0.010654378
ENSG00000174684	B3GNT1	261.2528949	657.1791451	1.330281058	0.001940296	0.007841142
ENSG00000138381	ASNSD1	213.0420476	677.7554358	1.668886705	0.000123672	0.00067886
ENSG00000150656	CNDP1	6.201060061	1252.605539	7.625913486	4.30E-34	4.02E-32
ENSG00000196323	ZBTB44	311.0189257	740.7703256	1.25156479	0.003421685	0.012833255
ENSG00000166669	ATF7IP2	118.9531016	643.0329452	2.433021766	6.28E-08	6.37E-07
ENSG00000119938	PPP1R3C	14.75493478	576.1599997	5.273770966	8.81E-22	3.77E-20
ENSG00000036054	TBC1D23	191.2694043	563.2998177	1.557491268	0.000341189	0.001695036
ENSG00000189180	ZNF33A	174.1623259	533.721399	1.614758833	0.000221031	0.001149313
ENSG00000164347	GFM2	121.2858865	621.1706362	2.355140272	1.61E-07	1.53E-06
ENSG00000131375	CAPN7	182.7158653	549.1536175	1.586759278	0.000286342	0.001452161
ENSG000000095539	SEMA4G	127.5066458	904.0946294	2.82447416	5.03E-10	6.88E-09
ENSG00000066739	ATG2B	242.5906322	610.8824908	1.331769204	0.002045922	0.008215087
ENSG00000182400	TRAPPC6B	170.2743533	455.2742867	1.417998243	0.0011428	0.004952795
ENSG00000140262	TCF12	257.3649236	529.8633443	1.041285915	0.015418219	0.047043927
ENSG00000163602	RYBP	255.0321408	589.0201816	1.207085246	0.004916835	0.017530905
ENSG00000064545	TMEM161A	235.5922834	567.1578723	1.266849249	0.003326794	0.012520816
ENSG00000147027	TMEM47	252.6993579	697.0457083	1.463234293	0.000703591	0.003234279
ENSG000000047932	GOPC	187.3814321	524.7192714	1.484758586	0.000638358	0.002965682
ENSG00000127955	GNAI1	174.1623259	520.8612168	1.579577489	0.00030153	0.001522039
ENSG00000081913	PHLPP1	110.3995562	671.325345	2.602659067	9.69E-09	1.11E-07
ENSG00000122741	DCAF10	181.9382708	567.1578723	1.639439904	0.000177821	0.00094763
ENSG00000006042	TMEM98	132.9498097	443.7001223	1.737501941	8.89E-05	0.000505986
ENSG00000121964	GTDC1	200.6005374	1667.989386	3.05479122	1.45E-11	2.48E-10
ENSG00000107949	BCCIP	252.6993579	693.1876538	1.45522811	0.000753576	0.003440511
ENSG00000170502	NUDT9	245.7010094	761.346616	1.631012915	0.000167896	0.00089827
ENSG00000163428	LRRC58	108.0667708	685.4715448	2.663511343	5.01E-09	5.96E-08
ENSG00000120925	RNF170	157.0552455	522.147235	1.732168717	8.31E-05	0.000475429
ENSG00000175287	PHYHD1	40.41587651	591.592218	3.86685162	5.17E-15	1.27E-13
ENSG00000256612	CYP2B7P	3.868086451	480.9946517	6.906884205	8.14E-26	4.50E-24
ENSG00000130935	NOL11	216.1524251	500.2849252	1.210048172	0.005047904	0.017965918
ENSG00000152484	USP12	185.8262432	697.0457083	1.906414676	1.41E-05	9.52E-05
ENSG00000164741	DLC1	170.2743533	654.6071088	1.941797656	1.03E-05	7.13E-05
ENSG00000136689	IL1RN	177.2727039	637.8888725	1.846416648	2.54E-05	0.000163292
ENSG00000100417	PMM1	290.023882	703.4757991	1.277833029	0.002849816	0.010890558
ENSG00000135525	MAP7	83.18371705	673.8973813	3.01593811	8.78E-11	1.34E-09
ENSG00000162702	ZNF281	178.0502984	792.2110515	2.152644038	1.10E-06	9.09E-06
ENSG00000136160	EDNRB	73.07496939	1134.291873	3.953632769	1.74E-16	4.84E-15
ENSG00000185745	IFIT1	199.0453486	978.6836807	2.296875349	2.04E-07	1.91E-06
ENSG00000142082	SIRT3	293.9118531	610.8824908	1.055054727	0.013467961	0.041811911

ENSG00000136371	<i>MTHFS</i>	72.29737318	406.4055921	2.488458982	7.45E-08	7.44E-07
ENSG00000137960	<i>GIPC2</i>	60.63342469	520.8612168	3.099654509	5.31E-11	8.39E-10
ENSG00000154153	<i>FAM134B</i>	41.19347589	1010.834134	4.612225129	7.01E-20	2.58E-18
ENSG00000114541	<i>FRMD4B</i>	263.5856777	622.4566544	1.239161525	0.003960961	0.014621964
ENSG00000067208	<i>EVI5</i>	115.8427216	486.1387246	2.067747539	4.09E-06	3.08E-05
ENSG00000148429	<i>USP6NL</i>	272.1392145	658.4651633	1.274234114	0.002964872	0.011273043
ENSG00000122912	<i>SLC25A16</i>	133.7274045	812.7873418	2.602246681	7.44E-09	8.61E-08
ENSG00000156256	<i>USP16</i>	195.9349709	495.1408523	1.336717872	0.002065278	0.008287452
ENSG00000176542	<i>KIAA2018</i>	106.5115804	695.7596901	2.705886044	2.85E-09	3.50E-08
ENSG00000170011	<i>MYRIP</i>	10.08922402	560.7277813	5.776691118	2.23E-23	1.05E-21
ENSG00000197969	<i>VPS13A</i>	101.8460091	690.6156175	2.759715434	1.47E-09	1.88E-08
ENSG00000177200	<i>CHD9</i>	170.2743533	614.7405453	1.851159931	2.48E-05	0.00015981
ENSG00000086205	<i>FOLH1</i>	33.41747441	829.5055776	4.627705441	1.32E-19	4.75E-18
ENSG00000172059	<i>KLF11</i>	160.9432185	877.0882486	2.445076667	3.95E-08	4.13E-07
ENSG00000120756	<i>PLS1</i>	115.0651266	471.992524	2.034857114	5.61E-06	4.11E-05
ENSG00000065057	<i>NTHL1</i>	203.710915	605.738418	1.57141299	0.000306485	0.001544545
ENSG00000129214	<i>SHBG</i>	7.75633786	2078.229158	8.039885886	9.72E-39	1.22E-36
ENSG00000135297	<i>MTO1</i>	257.3649236	670.0393268	1.379855951	0.001335024	0.005682494
ENSG00000074276	<i>CDHR2</i>	76.96294991	1220.455087	3.984604124	9.94E-17	2.82E-15
ENSG00000122376	<i>FAM35A</i>	134.5049993	740.7703256	2.460055912	4.19E-08	4.36E-07
ENSG00000106993	<i>CDC37L1</i>	166.3863805	900.236575	2.43471019	4.59E-08	4.76E-07
ENSG00000168724	<i>DNAJC21</i>	306.3533605	636.6028544	1.054758923	0.013350451	0.041524899
ENSG00000118873	<i>RAB3GAP2</i>	223.9283686	529.8633443	1.241946985	0.004054867	0.014915452
ENSG00000164080	<i>RAD54L2</i>	216.1524251	649.4630361	1.58648117	0.000253456	0.00129756
ENSG00000125430	<i>HS3ST3B1</i>	126.7290509	1243.603412	3.293228038	9.24E-13	1.80E-11
ENSG00000165650	<i>PDZD8</i>	165.608786	430.8399396	1.378480296	0.001673402	0.006844258
ENSG00000134987	<i>WDR36</i>	168.7191642	500.2849252	1.567210879	0.000347085	0.001721913
ENSG00000005812	<i>FBXL3</i>	241.8130379	726.6241259	1.586676124	0.000246251	0.001266411
ENSG00000113163	<i>COL4A3BP</i>	280.6927512	700.9037628	1.319706109	0.002132524	0.008540747
ENSG00000198887	<i>SMC5</i>	208.3764814	522.147235	1.32456485	0.002164734	0.008648847
ENSG00000141084	<i>RANBP10</i>	297.7998242	699.6177446	1.231747183	0.004023261	0.014810153
ENSG00000175311	<i>ANKS4B</i>	35.75027683	535.0074172	3.898148287	4.58E-15	1.13E-13
ENSG00000133731	<i>IMPA1</i>	261.2528949	713.7639443	1.449424457	0.00075661	0.003453092
ENSG00000143412	<i>ANXA9</i>	88.62688686	661.0371996	2.89685048	3.37E-10	4.73E-09
ENSG00000241399	<i>CD302</i>	23.30863474	824.3615051	5.135850953	3.90E-22	1.70E-20
ENSG00000163788	<i>SNRK</i>	290.023882	601.8803635	1.052842659	0.013650191	0.042327817
ENSG00000076258	<i>FMO4</i>	23.30863474	797.3551241	5.087801992	8.34E-22	3.58E-20
ENSG00000065613	<i>SLK</i>	227.0387459	640.4609089	1.495502564	0.0005454	0.002573256
ENSG00000258289	<i>CHURC1</i>	131.39462	505.4289981	1.942344328	1.23E-05	8.44E-05
ENSG00000126106	<i>TMEM53</i>	113.5099365	582.5900906	2.35812584	1.65E-07	1.57E-06
ENSG00000120837	<i>NFYB</i>	255.0321408	712.4779262	1.481572213	0.000587069	0.002753652
ENSG00000127990	<i>SGCE</i>	185.8262432	492.5688158	1.405570292	0.001255076	0.00537195
ENSG00000111907	<i>TPD52L1</i>	38.8606773	811.5013236	4.379188869	2.42E-18	7.81E-17
ENSG00000164190	<i>NIPBL</i>	260.4753007	726.6241259	1.479481361	0.000582699	0.002734704
ENSG00000196455	<i>PIK3R4</i>	219.2628025	628.8867453	1.519442234	0.000450285	0.00217867
ENSG00000133818	<i>RRAS2</i>	176.4951094	609.5964726	1.787313488	4.39E-05	0.000269805
ENSG00000166821	<i>PEX11A</i>	56.74543914	650.7490543	3.516183713	2.11E-13	4.39E-12
ENSG00000039560	<i>RAI14</i>	224.7059629	542.7235264	1.271539849	0.003283708	0.012377398
ENSG00000164163	<i>ABCE1</i>	288.4686935	654.6071088	1.181729595	0.005877068	0.020518966
ENSG00000113658	<i>SMAD5</i>	205.2661038	502.8569617	1.29194894	0.002842598	0.010864644
ENSG00000089335	<i>ZNF302</i>	150.0568938	369.1110608	1.297581083	0.003079549	0.011680481
ENSG00000047634	<i>SCML1</i>	73.85256557	572.3019451	2.951569115	2.26E-10	3.24E-09
ENSG00000187630	<i>DHRS4L2</i>	195.9349709	468.1344692	1.255818237	0.003778635	0.014023886
ENSG00000156928	<i>MALSU1</i>	251.9217637	553.0116721	1.133787172	0.008267179	0.027548027
ENSG00000100722	<i>ZC3H14</i>	171.0519478	607.0244362	1.826371794	3.22E-05	0.000203012
ENSG00000036549	<i>ZZZ3</i>	143.8361363	482.2806699	1.744335106	8.08E-05	0.000465666
ENSG00000158169	<i>FANCC</i>	120.5082916	551.7256539	2.193398669	9.70E-07	8.13E-06
ENSG00000170293	<i>CMTM8</i>	74.63016171	515.7171439	2.786317232	1.86E-09	2.35E-08
ENSG00000087076	<i>HSD17B14</i>	216.9300194	653.3210906	1.589847347	0.000252956	0.001295268
ENSG00000148057	<i>IDNK</i>	132.1722149	742.0563437	2.487772395	3.22E-08	3.41E-07
ENSG00000165322	<i>ARHGAP12</i>	240.2578493	510.573071	1.086969101	0.01142229	0.036613492
ENSG00000121749	<i>TBC1D15</i>	225.4835572	627.6007271	1.476153724	0.000629961	0.0029327
ENSG00000197496	<i>SLC2A10</i>	64.52140874	662.3232178	3.356769417	1.49E-12	2.81E-11
ENSG00000172869	<i>DMXL1</i>	185.8262432	581.3040725	1.644494516	0.000169778	0.000907492
ENSG00000204099	<i>NEU4</i>	25.64144922	959.3934089	5.217846619	4.63E-23	2.13E-21
ENSG00000134318	<i>ROCK2</i>	164.8311914	646.8909998	1.971526325	7.94E-06	5.63E-05
ENSG00000178075	<i>GRAMD1C</i>	41.19347589	650.7490543	3.976928868	1.06E-15	2.80E-14
ENSG00000196600	<i>SLC22A25</i>	1.39E-17	483.5666882	11.96303302	3.00E-29	2.03E-27
ENSG00000256340	<i>ABCC6P1</i>	46.63666774	731.7681985	3.967713667	6.32E-16	1.70E-14
ENSG00000166780	<i>C16orf45</i>	137.6153784	384.5432808	1.481403133	0.000814375	0.003686268
ENSG00000186715	<i>MST1L</i>	94.84765097	802.4991967	3.078863341	2.61E-11	4.32E-10

ENSG00000093217	XYLB	17.86538201	639.1748907	5.14989582	1.28E-21	5.44E-20
ENSG00000148498	PARD3	267.473649	555.5837085	1.054105924	0.014190748	0.043825924
ENSG00000156162	DPY19L4	188.1590266	511.8590892	1.442996182	0.000912464	0.004040492
ENSG00000121210	KIAA0922	243.3682265	550.4396357	1.176869573	0.006130992	0.021259181
ENSG00000100867	DHRS2	8.533969895	1201.164815	7.113524422	2.62E-32	2.18E-30
ENSG00000032219	ARID4A	113.5099365	605.738418	2.414330386	8.69E-08	8.61E-07
ENSG00000111647	UHRF1BP1L	63.74381204	498.998907	2.965794461	2.62E-10	3.73E-09
ENSG00000029725	RABEP1	251.9217637	711.191908	1.496659707	0.000528556	0.002502811
ENSG00000067334	DNTTIP2	174.9399204	477.1365969	1.446683701	0.000935407	0.004130316
ENSG00000179456	ZBTB18	222.3731799	540.15149	1.279733903	0.002972051	0.011296886
ENSG00000145725	PPIP5K2	162.4984077	535.0074172	1.718154063	8.90E-05	0.000506515
ENSG00000138138	ATAD1	269.8064318	704.7618172	1.384662472	0.001289862	0.005506617
ENSG00000196700	ZNF512B	249.5889808	527.2913079	1.078503871	0.012204183	0.038799562
ENSG00000011295	TTC19	262.8080835	650.7490543	1.307539722	0.002371182	0.009371241
ENSG00000143369	ECM1	151.6120831	1078.993094	2.830028329	3.75E-10	5.23E-09
ENSG000000251322	SHANK3	174.1623259	698.3317264	2.002522513	5.45E-06	4.01E-05
ENSG00000137871	ZNF280D	216.9300194	544.0095446	1.325730262	0.002201484	0.008778742
ENSG00000116752	BCAS2	175.7175149	433.4119761	1.3016567	0.002867227	0.010952041
ENSG00000117155	SSX2IP	86.29409995	293.2359749	1.762868451	0.00010287	0.000578864
ENSG00000169174	PCSK9	120.5082916	397.403464	1.720150856	0.000105371	0.000591732
ENSG00000009694	TENM1	1.534979634	670.0393268	8.643000939	1.32E-32	1.13E-30
ENSG00000139631	CSAD	188.1590266	528.5773261	1.489355347	0.000619713	0.00288932
ENSG00000130513	GDF15	300.1326068	1278.325901	2.090021401	1.57E-06	1.28E-05
ENSG00000167740	CYB5D2	210.7092645	747.2004163	1.825471907	2.75E-05	0.000176173
ENSG00000163697	APBB2	211.4868589	511.8590892	1.274498956	0.003327302	0.01252083
ENSG00000173638	SLC19A1	132.1722149	396.1174457	1.582337093	0.000350514	0.001732015
ENSG00000179833	SERTAD2	233.2595005	540.15149	1.210823205	0.004871863	0.017388017
ENSG00000166833	NAV2	213.0420476	680.3274722	1.67435049	0.000118975	0.000660513
ENSG00000128585	MKLN1	136.0601889	551.7256539	2.018477533	5.60E-06	4.11E-05
ENSG00000155906	RMND1	181.1606764	563.2998177	1.635768683	0.000182011	0.000967468
ENSG00000113161	HMGCR	181.9382708	482.2806699	1.40560607	0.001249804	0.005350305
ENSG00000107643	MAPK8	168.7191642	434.6979944	1.364516673	0.001827432	0.0074254
ENSG00000174804	FZD4	227.0387459	950.391282	2.064842201	2.40E-06	1.89E-05
ENSG00000144909	OSBPL11	185.0486487	500.2849252	1.434035679	0.000981861	0.004316264
ENSG00000122482	ZNF644	132.1722149	416.6937385	1.655378772	0.000183326	0.000973835
ENSG00000145833	DDX46	192.0469988	522.147235	1.442215547	0.000921831	0.004074869
ENSG00000272520	CTD-2044J15.2	52.07985416	758.7745797	3.861183299	1.78E-15	4.59E-14
ENSG00000168672	FAM84B	187.3814321	496.4268705	1.404809262	0.001213587	0.005207823
ENSG00000047188	YTHDC2	189.7142155	527.2913079	1.473975177	0.000715562	0.003281418
ENSG00000107864	CPEB3	61.41102161	886.0903756	3.847756165	1.60E-15	4.14E-14
ENSG00000241186	TDGF1	1.534979634	70.75461835	5.401429166	9.47E-11	1.44E-09
ENSG00000186918	ZNF395	254.2545465	558.1557449	1.133852181	0.008162228	0.027238478
ENSG00000170456	DENND5B	187.3814321	603.1663817	1.685734041	0.000111812	0.000624797
ENSG00000163848	ZNF148	168.7191642	441.1280858	1.385696143	0.001528394	0.006340884
ENSG00000139977	NAA30	143.8361363	403.8335555	1.488279456	0.000742614	0.003395449
ENSG00000198515	CNGA1	17.08777164	502.8569617	4.867581882	2.82E-19	9.78E-18
ENSG00000164463	CREBRF	189.7142155	601.8803635	1.664818725	0.000139522	0.000758824
ENSG00000128513	POT1	79.29573781	205.7867078	1.373971854	0.002629844	0.010137215
ENSG00000151233	GXYLT1	123.6186713	487.4247429	1.977938549	8.87E-06	6.23E-05
ENSG00000122121	XPNPEP2	2.312696499	1223.027123	8.961261899	1.64E-37	1.82E-35
ENSG00000159261	CLDN14	13.19970438	613.4545271	5.523327963	7.90E-23	3.57E-21
ENSG00000100815	TRIP11	168.7191642	505.4289981	1.581966481	0.000306775	0.001545689
ENSG00000145604	SKP2	113.5099365	326.6724544	1.523678269	0.000607832	0.002839254
ENSG00000082258	CCNT2	158.6104347	652.0350725	2.038405107	3.84E-06	2.91E-05
ENSG00000160145	KALRN	115.0651266	658.4651633	2.51511601	2.76E-08	2.95E-07
ENSG00000127980	PEX1	135.2825941	405.1195738	1.581226576	0.000345044	0.0017125
ENSG00000104611	SH2D4A	104.9563901	497.7128887	2.243883169	7.05E-07	6.03E-06
ENSG00000135597	REPS1	207.598887	619.8846181	1.577455618	0.000274418	0.00139653
ENSG00000138078	PREPL	204.4885094	470.7065057	1.202119612	0.005662139	0.019824266
ENSG00000160323	ADAMTS13	24.86384483	1080.279112	5.433222219	1.51E-24	7.71E-23
ENSG00000117479	SLC19A2	54.412647	747.2004163	3.775959697	6.60E-15	1.60E-13
ENSG00000145217	SLC26A1	53.63504947	488.7107611	3.184256786	2.38E-11	3.95E-10
ENSG00000153234	NR4A2	162.4984077	520.8612168	1.679501314	0.000126273	0.000692219
ENSG00000060642	PIGV	180.3830819	591.592218	1.712657832	8.80E-05	0.000501559
ENSG00000119986	AVPI1	205.2661038	820.5034506	1.998202216	5.08E-06	3.78E-05
ENSG00000032742	IFT88	49.74706056	228.9350457	2.198810881	3.11E-06	2.40E-05
ENSG00000174327	SLC16A13	55.19024445	497.7128887	3.16945336	3.05E-11	5.00E-10
ENSG00000106330	MOSPD3	178.0502984	414.1217019	1.216975772	0.00513924	0.018249893
ENSG00000259976	RP11-553L6.5	182.7158653	612.168509	1.743452024	6.49E-05	0.000383285
ENSG00000170185	USP38	221.5955855	657.1791451	1.567660725	0.000292418	0.001480555
ENSG00000140465	CYP1A1	1.39E-17	1219.169068	13.29696936	7.26E-39	9.31E-37

ENSG00000151553	<i>FAM160B1</i>	191.2694043	553.0116721	1.530902829	0.000435065	0.002112019
ENSG00000112874	<i>NUDT12</i>	63.74381204	582.5900906	3.18919861	1.38E-11	2.36E-10
ENSG00000147573	<i>TRIM55</i>	11.64446802	771.6347612	6.033069228	4.47E-26	2.54E-24
ENSG00000070961	<i>ATP2B1</i>	173.3847314	389.6873541	1.167536834	0.007292147	0.02469969
ENSG00000072163	<i>LIMS2</i>	112.7323414	567.1578723	2.32930647	2.21E-07	2.06E-06
ENSG00000107669	<i>ATE1</i>	177.2727039	460.4183597	1.376141712	0.001566715	0.006483633
ENSG00000152382	<i>TADA1</i>	113.5099365	549.1536175	2.272869123	4.25E-07	3.77E-06
ENSG00000162972	<i>C2orf47</i>	125.951456	625.0286908	2.309677188	2.68E-07	2.45E-06
ENSG00000138308	<i>PLA2G12B</i>	5.423411881	877.0882486	7.300536595	3.98E-31	3.04E-29
ENSG00000138670	<i>RASGEF1B</i>	227.0387459	814.0733599	1.841504129	2.35E-05	0.000152468
ENSG00000110435	<i>PDHX</i>	168.7191642	546.5815811	1.694873978	0.000113055	0.000630746
ENSG00000151718	<i>WWC2</i>	135.2825941	582.5900906	2.105254396	2.28E-06	1.79E-05
ENSG00000139116	<i>KIF21A</i>	83.18371705	533.721399	2.679550743	6.19E-09	7.25E-08
ENSG00000134255	<i>CEPT1</i>	165.608786	527.2913079	1.669868918	0.000136561	0.00074484
ENSG00000109466	<i>KLHL2</i>	222.3731799	617.3125817	1.472338541	0.000653785	0.00303225
ENSG00000109794	<i>FAM149A</i>	101.8460091	914.3827744	3.164580979	7.45E-12	1.31E-10
ENSG00000189056	<i>RELN</i>	169.4967587	761.346616	2.166289777	9.48E-07	7.96E-06
ENSG00000038219	<i>BOD1L1</i>	192.8245932	461.704378	1.258938065	0.003785683	0.014045848
ENSG00000136574	<i>GATA4</i>	98.73562788	505.4289981	2.354099712	1.98E-07	1.85E-06
ENSG00000140092	<i>FBLN5</i>	318.0172735	713.7639443	1.165904193	0.006319479	0.021854828
ENSG00000205189	<i>ZBTB10</i>	141.5033522	471.992524	1.736799283	8.20E-05	0.000469841
ENSG00000108094	<i>CUL2</i>	199.822943	417.9797568	1.064037013	0.014012248	0.04336086
ENSG00000163626	<i>COX18</i>	297.7998242	622.4566544	1.063178544	0.012896062	0.040308303
ENSG00000102753	<i>KPNA3</i>	246.4786037	508.0010346	1.042826825	0.015402026	0.047006062
ENSG00000126231	<i>PROZ</i>	7.75633786	306.0961595	5.27697899	3.14E-19	1.09E-17
ENSG00000115361	<i>ACADL</i>	1.39E-17	571.0159269	12.20280469	6.10E-31	4.58E-29
ENSG00000143952	<i>VPS54</i>	226.2611516	473.2785422	1.064105545	0.01338393	0.041602999
ENSG00000124383	<i>MPHOSPH10</i>	186.6038376	425.6958665	1.189092977	0.006377755	0.022037969
ENSG00000164742	<i>ADCY1</i>	38.8606773	1093.139293	4.80895622	3.03E-21	1.25E-19
ENSG00000138315	<i>OIT3</i>	0.757489584	958.1073908	10.05821289	2.52E-36	2.57E-34
ENSG00000137806	<i>NDUFAF1</i>	227.0387459	536.2934354	1.239457204	0.004044704	0.014882476
ENSG00000198839	<i>ZNF277</i>	155.5000563	372.9691158	1.261219925	0.004078349	0.014984091
ENSG00000112234	<i>FBXL4</i>	129.0618355	537.5794536	2.057113271	4.04E-06	3.04E-05
ENSG00000156017	<i>C9orf41</i>	117.3979117	424.4098482	1.852663353	3.27E-05	0.000206185
ENSG00000245848	<i>CEBPA</i>	36.52787722	100.3331108	1.453602183	0.003966767	0.014636876
ENSG00000148634	<i>HERC4</i>	276.80478	596.7362907	1.107731063	0.009797536	0.03195771
ENSG00000166225	<i>FRS2</i>	86.29409995	333.1025464	1.946715406	1.82E-05	0.000120711
ENSG00000118518	<i>RNF146</i>	199.822943	495.1408523	1.308390588	0.00255643	0.00989875
ENSG00000135776	<i>ABCB10</i>	172.6071368	475.8505787	1.462142609	0.000842895	0.003802897
ENSG00000188070	<i>C11orf95</i>	217.7076138	462.9903962	1.087966888	0.011771299	0.037606122
ENSG00000146373	<i>RNF217</i>	120.5082916	466.848451	1.952448156	1.17E-05	8.03E-05
ENSG00000073754	<i>CD5L</i>	17.08777164	1364.489114	6.307546568	2.68E-29	1.83E-27
ENSG00000177683	<i>THAP5</i>	145.3913257	360.1089323	1.307494249	0.002837651	0.01084907
ENSG00000108559	<i>NUP88</i>	243.3682265	513.1451075	1.075670597	0.01258376	0.039847026
ENSG00000151461	<i>UPF2</i>	172.6071368	421.8378116	1.288360175	0.003244165	0.012239484
ENSG00000128915	<i>NARG2</i>	187.3814321	446.2721588	1.251183639	0.003890706	0.01439683
ENSG00000198455	<i>ZXDB</i>	115.0651266	249.5113443	1.115463812	0.012402908	0.039380975
ENSG00000171444	<i>MCC</i>	86.29409995	680.3274722	2.97676328	1.35E-10	2.00E-09
ENSG00000165912	<i>PACSLN3</i>	136.0601889	729.1961622	2.420771531	6.82E-08	6.88E-07
ENSG00000164855	<i>TMEM184A</i>	150.8344885	375.5411525	1.315040802	0.002774498	0.010633792
ENSG00000105793	<i>GTPBP10</i>	97.18043717	480.9946517	2.305498353	3.74E-07	3.35E-06
ENSG00000171723	<i>GPHN</i>	95.62524639	767.7767067	3.003295883	7.35E-11	1.13E-09
ENSG00000124568	<i>SLC17A1</i>	5.423411881	802.4991967	7.172329405	3.25E-30	2.35E-28
ENSG00000066248	<i>NGEF</i>	213.819642	578.7320361	1.435800119	0.00093032	0.004109311
ENSG00000118777	<i>ABCG2</i>	50.52465852	866.8001036	4.09680663	7.27E-17	2.09E-15
ENSG00000145708	<i>CRHBP</i>	8.533969895	825.6475232	6.572741344	1.99E-28	1.30E-26
ENSG00000147202	<i>DIAPH2</i>	186.6038376	504.1429799	1.433051538	0.001009247	0.004428036
ENSG00000008869	<i>HEATR5B</i>	178.8278929	493.854834	1.464671268	0.000799575	0.003628525
ENSG00000120549	<i>KIAA1217</i>	244.1458208	527.2913079	1.110297007	0.009732677	0.031767054
ENSG00000078177	<i>N4BP2</i>	72.29737318	344.6767119	2.250844429	1.06E-06	8.83E-06
ENSG00000052126	<i>PLEKHA5</i>	66.07660199	376.8271708	2.509009643	7.45E-08	7.44E-07
ENSG00000184731	<i>FAM110C</i>	101.0684138	709.9058899	2.810496743	8.95E-10	1.18E-08
ENSG00000115464	<i>USP34</i>	115.8427216	500.2849252	2.109121296	2.36E-06	1.86E-05
ENSG00000182568	<i>SATB1</i>	184.2710543	446.2721588	1.275313995	0.00330102	0.012434468
ENSG00000198420	<i>FAM115A</i>	158.6104347	574.8739815	1.856730166	2.40E-05	0.0001552
ENSG00000155313	<i>USP25</i>	182.7158653	460.4183597	1.332544125	0.002235464	0.008895688
ENSG00000176018	<i>LYSMD3</i>	102.6236044	558.1557449	2.441590306	6.96E-08	7.00E-07
ENSG00000197442	<i>MAP3K5</i>	200.6005374	456.5603049	1.185781672	0.006338137	0.021907161
ENSG00000153714	<i>LURAP1L</i>	116.6203166	979.9696989	3.069331027	2.24E-11	3.74E-10
ENSG00000156253	<i>RWDD2B</i>	190.4918099	411.5496653	1.110619532	0.010803147	0.034835687
ENSG00000101695	<i>RNF125</i>	200.6005374	664.8952542	1.728006995	7.16E-05	0.000419218

ENSG00000080546	SESN1	197.4901598	673.8973813	1.769934873	4.90E-05	0.00029556
ENSG00000234155	RP11-30P6.6	6.201060061	444.9861406	6.133016964	1.73E-23	8.24E-22
ENSG00000011566	MAP4K3	188.1590266	405.1195738	1.105669531	0.01074109	0.034675906
ENSG00000144320	KIAA1715	156.2776509	520.8612168	1.735765984	7.86E-05	0.000454244
ENSG00000164168	TMEM184C	178.8278929	565.8718541	1.661023447	0.000148158	0.000802103
ENSG00000183628	DGCR6	96.40284179	677.7554358	2.81173106	8.95E-10	1.18E-08
ENSG00000069869	NEDD4	31.08466991	774.2067975	4.632130908	2.11E-19	7.43E-18
ENSG00000162851	TFB2M	97.18043717	405.1195738	2.057879956	5.29E-06	3.91E-05
ENSG00000170482	SLC23A1	20.19820843	470.7065057	4.532834153	1.23E-17	3.79E-16
ENSG00000165494	PCF11	244.1458208	504.1429799	1.045541969	0.014842826	0.045528625
ENSG00000215781	AC011043.1	192.8245932	425.6958665	1.141817454	0.008622287	0.028536212
ENSG00000187867	PALM3	4.645755009	544.0095446	6.828711317	4.66E-27	2.76E-25
ENSG00000198862	LTN1	71.51977693	407.6916104	2.508586537	5.82E-08	5.93E-07
ENSG00000215256	DHRS4-AS1	48.9694625	374.2551341	2.9303209	7.14E-10	9.61E-09
ENSG00000175455	CCDC14	174.1623259	428.267903	1.297250295	0.00288657	0.011020638
ENSG00000157741	UBN2	138.3929732	398.6894823	1.525388987	0.000532968	0.002519861
ENSG00000116990	MYCL	116.6203166	509.2870528	2.125205273	2.03E-06	1.62E-05
ENSG00000119912	IDE	225.4835572	550.4396357	1.286922406	0.002805928	0.010742659
ENSG00000182165	TP53TG1	206.0436982	444.9861406	1.110146346	0.010175632	0.03299613
ENSG00000001631	KRIT1	104.1787948	384.5432808	1.882512412	2.74E-05	0.00017547
ENSG00000071189	SNX13	150.0568938	421.8378116	1.490166986	0.000701315	0.003224415
ENSG00000138660	APIAR	229.3715289	535.0074172	1.221255371	0.004507352	0.016225149
ENSG00000123191	ATP7B	48.19186435	653.3210906	3.756957007	1.41E-14	3.27E-13
ENSG00000151240	DIP2C	207.598887	603.1663817	1.538018209	0.000388169	0.001900323
ENSG00000149313	AASDHPPT	216.9300194	564.5858359	1.379281831	0.00144078	0.006016564
ENSG00000131732	ZCCHC9	213.0420476	531.1493625	1.317296694	0.002308986	0.009175035
ENSG00000121274	PAPD5	108.0667708	374.2551341	1.790606958	6.54E-05	0.000385914
ENSG00000148985	PGAP2	177.2727039	441.1280858	1.314407299	0.002495898	0.009697598
ENSG00000172345	STAR2	206.8212926	457.8463232	1.145809819	0.008052967	0.026953474
ENSG00000184012	TMPRSS2	40.41587651	1058.416804	4.705979897	1.59E-20	6.15E-19
ENSG00000039319	ZFYVE16	213.0420476	488.7107611	1.197182901	0.005633243	0.019742562
ENSG00000170989	S1PR1	160.1656239	363.9669874	1.183369036	0.006689801	0.022997925
ENSG00000126773	PCNXL4	178.8278929	375.5411525	1.069644805	0.014167759	0.043782129
ENSG00000139835	G RTP1	92.51486458	700.9037628	2.919478295	2.38E-10	3.41E-09
ENSG00000149573	MPZL2	85.51650426	471.992524	2.462426772	7.43E-08	7.42E-07
ENSG00000162664	ZNF326	128.2842407	502.8569617	1.969510402	9.53E-06	6.65E-05
ENSG00000164211	STARD4	175.7175149	372.9691158	1.085026349	0.012796569	0.040032563
ENSG00000128052	KDR	225.4835572	487.4247429	1.111550502	0.010152164	0.032928623
ENSG00000177485	ZBTB33	104.1787948	408.9776287	1.971366543	1.17E-05	8.02E-05
ENSG00000129292	PHF20L1	143.8361363	381.9712441	1.408002595	0.001417117	0.005992251
ENSG00000136874	STX17	108.8443659	280.3757899	1.363741865	0.002313244	0.009190485
ENSG00000162065	TBC1D24	104.1787948	288.0919009	1.466017792	0.001081488	0.004712552
ENSG00000135218	CD36	51.30225638	429.5539213	3.062137324	1.47E-10	2.15E-09
ENSG00000107789	MINPP1	204.4885094	587.7341634	1.522396205	0.000445213	0.002154971
ENSG00000198146	ZNF770	26.4190532	425.6958665	4.002861249	5.19E-15	1.27E-13
ENSG00000065183	WDR3	151.6120831	600.5943453	1.984909081	7.01E-06	5.05E-05
ENSG00000164252	AGGF1	175.7175149	435.9840127	1.310191003	0.002728687	0.010475983
ENSG00000148426	PROSER2	186.6038376	551.7256539	1.563145636	0.000324952	0.001622801
ENSG00000156735	BAG4	166.3863805	361.3949507	1.11821483	0.010813008	0.034835687
ENSG00000127329	PTPRB	191.2694043	563.2998177	1.557491268	0.000341189	0.001695036
ENSG00000257702	LBX2-AS1	132.9498097	388.4013358	1.545510202	0.000475367	0.002290664
ENSG00000101049	SGK2	64.52140874	663.609236	3.359567539	1.40E-12	2.66E-11
ENSG00000168538	TRAPPC11	202.1557262	491.2827976	1.280374374	0.003094335	0.011731192
ENSG00000172296	SPTLC3	27.97426007	293.2359749	3.383152757	2.49E-11	4.12E-10
ENSG00000171385	KCND3	4.645755009	943.9611914	7.623697608	9.91E-33	8.60E-31
ENSG00000168300	PCMTD1	148.5017045	468.1344692	1.655384678	0.000166872	0.000893877
ENSG00000111052	LIN7A	35.75027683	574.8739815	4.001816938	1.01E-15	2.67E-14
ENSG00000187889	C1orf168	1.39E-17	549.1536175	12.14649326	1.54E-30	1.14E-28
ENSG00000158571	PFKFB1	6.978701584	497.7128887	6.127677279	6.21E-24	3.05E-22
ENSG00000112200	ZNF451	203.710915	447.5581771	1.134875199	0.008893971	0.029341605
ENSG00000171174	RBKS	133.7274045	510.573071	1.931588397	1.31E-05	8.92E-05
ENSG00000179387	ELMOD2	168.7191642	396.1174457	1.23046293	0.004859139	0.017347587
ENSG00000154274	C4orf19	115.8427216	307.382178	1.406580961	0.001604645	0.006601035
ENSG00000180155	LYNX1	163.2760023	963.2514633	2.559509764	1.06E-08	1.21E-07
ENSG00000132744	ACY3	48.19186435	433.4119761	3.165012821	4.76E-11	7.57E-10
ENSG00000039123	SKIV2L2	135.2825941	564.5858359	2.059973851	3.67E-06	2.79E-05
ENSG00000178567	EPM2AIP1	131.39462	380.6852258	1.533525485	0.000514088	0.002454489
ENSG00000006757	PNPLA4	208.3764814	617.3125817	1.566067933	0.000302919	0.001528739
ENSG00000167220	HDHD2	146.1689204	399.9755006	1.451245632	0.000972158	0.004278149
ENSG00000145780	FEM1C	158.6104347	496.4268705	1.645104219	0.000171007	0.000913668
ENSG00000174306	ZHX3	105.7339853	517.0031621	2.288096988	3.76E-07	3.37E-06

ENSG00000134962	<i>KLB</i>	2.312696499	880.946303	8.487976034	4.58E-34	4.25E-32
ENSG00000169891	<i>REPS2</i>	41.97107512	444.9861406	3.401798955	2.43E-12	4.50E-11
ENSG00000145743	<i>FBXL17</i>	160.9432185	448.8441954	1.478722066	0.000747015	0.003413061
ENSG00000156398	<i>SFXN2</i>	130.6170252	730.4821804	2.482153525	3.27E-08	3.45E-07
ENSG00000114812	<i>VIPR1</i>	13.97732024	1032.696442	6.192888919	1.19E-27	7.39E-26
ENSG00000170634	<i>ACYP2</i>	163.2760023	384.5432808	1.234962555	0.004665887	0.016734578
ENSG00000174720	<i>LARP7</i>	188.936621	501.5709434	1.407763432	0.001216457	0.005219235
ENSG00000159267	<i>H LCS</i>	163.2760023	451.4162319	1.466220782	0.000793461	0.003602752
ENSG00000183735	<i>TBK1</i>	176.4951094	433.4119761	1.295291553	0.003039386	0.011535187
ENSG00000134852	<i>CLOCK</i>	111.1771513	423.1238299	1.92673638	1.70E-05	0.000113564
ENSG00000168874	<i>ATOH8</i>	22.53102899	1234.601286	5.767143162	1.62E-26	9.42E-25
ENSG00000113522	<i>RAD50</i>	214.5972363	444.9861406	1.051504223	0.015030429	0.046041571
ENSG00000196792	<i>STRN3</i>	108.0667708	470.7065057	2.121335778	2.50E-06	1.96E-05
ENSG00000197498	<i>RPF2</i>	175.7175149	406.4055921	1.20885946	0.005610502	0.019685069
ENSG00000197165	<i>SULT1A2</i>	8.533969895	841.0797408	6.599454798	1.30E-28	8.56E-27
ENSG00000138035	<i>PNPT1</i>	157.0552455	329.2444912	1.06702888	0.014757413	0.045300173
ENSG00000153922	<i>CHD1</i>	181.9382708	536.2934354	1.558726365	0.000353301	0.001744396
ENSG00000083520	<i>DIS3</i>	174.9399204	452.7022502	1.370859711	0.001687502	0.006898497
ENSG00000019169	<i>MARCO</i>	87.07169561	994.1158982	3.510961888	7.56E-14	1.63E-12
ENSG00000135870	<i>RC3H1</i>	171.0519478	434.6979944	1.344722306	0.002070085	0.008304061
ENSG00000173597	<i>SULT1B1</i>	12.42208703	751.0584708	5.901899099	2.62E-25	1.42E-23
ENSG00000135917	<i>SLC19A3</i>	13.97732024	668.7533087	5.566092651	1.10E-23	5.32E-22
ENSG00000122873	<i>CISD1</i>	181.1606764	378.1131892	1.060805906	0.01453387	0.044698999
ENSG00000259347	<i>RP11-798K3.2</i>	0.757489584	237.9371765	8.049049765	2.70E-22	1.19E-20
ENSG00000145388	<i>METTL14</i>	96.40284179	489.9967793	2.343817898	2.38E-07	2.20E-06
ENSG00000242193	<i>RP11-568K15.1</i>	88.62688686	414.1217019	2.222300431	9.85E-07	8.24E-06
ENSG00000135093	<i>USP30</i>	78.51814188	428.267903	2.445173106	1.01E-07	9.89E-07
ENSG00000157181	<i>C1orf27</i>	117.3979117	456.5603049	1.957987358	1.17E-05	8.05E-05
ENSG00000140691	<i>ARMC5</i>	166.3863805	600.5943453	1.850874669	2.49E-05	0.000160615
ENSG00000205865	<i>FAM99B</i>	1.39E-17	270.0876416	11.1229753	1.82E-23	8.62E-22
ENSG00000124370	<i>MCEE</i>	161.7208131	576.1599997	1.831960184	3.01E-05	0.000191378
ENSG00000154719	<i>MRPL39</i>	163.2760023	416.6937385	1.350775822	0.001990005	0.008012566
ENSG00000091428	<i>RAPGEF4</i>	32.63987315	394.8314273	3.590700198	5.42E-13	1.07E-11
ENSG00000144840	<i>RABL3</i>	153.944867	407.6916104	1.404098188	0.00138559	0.005871924
ENSG00000162897	<i>FCAMR</i>	3.090401881	102.905152	4.994322608	1.26E-12	2.40E-11
ENSG00000109667	<i>SLC2A9</i>	107.2831756	913.0967563	3.087536189	2.11E-11	3.53E-10
ENSG00000185875	<i>THNSL1</i>	29.52946559	451.4162319	3.927705869	8.07E-15	1.93E-13
ENSG00000108055	<i>SMC3</i>	183.4934598	399.9755006	1.12343442	0.009916247	0.032306767
ENSG00000183323	<i>CCDC125</i>	174.9399204	455.2742867	1.379031461	0.001566998	0.006483725
ENSG00000158825	<i>CDA</i>	46.63666774	479.7086334	3.358586127	3.47E-12	6.33E-11
ENSG00000249096	<i>RP11-290F5.1</i>	127.5066458	681.6134903	2.417004925	7.33E-08	7.33E-07
ENSG00000250436	<i>RP11-622A1.2</i>	0.757489584	560.7277813	9.285429866	9.27E-31	6.89E-29
ENSG00000134982	<i>APC</i>	80.07333372	324.1004176	2.014959905	1.06E-05	7.34E-05
ENSG00000101846	<i>STS</i>	241.0354436	581.3040725	1.269452188	0.003186661	0.012059144
ENSG00000172731	<i>LRRC20</i>	126.7290509	425.6958665	1.746813363	8.66E-05	0.000494573
ENSG00000121486	<i>TRMT1L</i>	156.2776509	442.414104	1.500312131	0.000613281	0.002862016
ENSG00000181744	<i>C3orf58</i>	117.3979117	511.8590892	2.122895413	2.10E-06	1.67E-05
ENSG00000156453	<i>PCDH1</i>	141.5033522	589.0201816	2.056293257	3.53E-06	2.70E-05
ENSG00000167136	<i>ENDOG</i>	111.9547464	551.7256539	2.299487416	3.51E-07	3.16E-06
ENSG00000151292	<i>CSNK1G3</i>	122.8410764	358.822914	1.545227581	0.000515073	0.002454489
ENSG00000196236	<i>XPNPEP3</i>	139.9481627	607.0244362	2.115651552	2.02E-06	1.60E-05
ENSG00000259417	<i>RP11-2E17.1</i>	3.090401881	658.4651633	7.670962102	5.95E-30	4.25E-28
ENSG00000196428	<i>TSC22D2</i>	137.6153784	426.9818847	1.632395724	0.000211797	0.001107092
ENSG00000196636	<i>ACN9</i>	78.51814188	225.0769895	1.51737418	0.000875348	0.003900462
ENSG00000118246	<i>FASTKD2</i>	141.5033522	420.5517933	1.570355142	0.000355157	0.001752864
ENSG00000164327	<i>RICTOR</i>	191.2694043	501.5709434	1.390072703	0.001365517	0.005797731
ENSG00000150787	<i>PTS</i>	223.9283686	478.4226152	1.09464073	0.011172646	0.035878052
ENSG00000095951	<i>HIVEP1</i>	167.1639751	475.8505787	1.508332685	0.000564492	0.002658792
ENSG00000174992	<i>ZG16</i>	1.39E-17	491.2827976	11.98586732	2.04E-29	1.40E-27
ENSG00000132763	<i>MMACHC</i>	54.412647	450.1302136	3.044930808	1.54E-10	2.26E-09
ENSG00000144228	<i>SPOPL</i>	99.51322321	347.2487487	1.801385796	6.07E-05	0.000359945
ENSG00000139517	<i>LNX2</i>	120.5082916	363.9669874	1.593386466	0.000328188	0.001637547
ENSG00000171100	<i>MTM1</i>	80.07333372	443.7001223	2.4679872	8.32E-08	8.25E-07
ENSG00000012174	<i>MBTPS2</i>	101.0684138	406.4055921	2.005936867	8.78E-06	6.16E-05
ENSG00000146802	<i>TMEM168</i>	122.8410764	281.6618084	1.196026735	0.007209902	0.024554698
ENSG00000108061	<i>SHOC2</i>	146.1689204	420.5517933	1.523600311	0.000531022	0.002511618
ENSG00000169372	<i>CRADD</i>	77.74054591	424.4098482	2.446453735	9.76E-08	9.60E-07
ENSG00000134480	<i>CCNH</i>	174.1623259	435.9840127	1.32300617	0.002422972	0.009484447
ENSG00000091831	<i>ESR1</i>	53.63504947	736.9122711	3.776672067	6.30E-15	1.53E-13
ENSG00000249173	<i>LINC01093</i>	1.39E-17	812.7873418	12.71207853	1.32E-34	1.26E-32
ENSG00000155744	<i>FAM126B</i>	169.4967587	437.270031	1.366397464	0.001692598	0.006914781

ENSG00000138587	MNS1	6.201060061	28.31577365	2.163591984	0.004621058	0.016580972
ENSG00000196922	ZNF252P	129.0618355	295.8080118	1.195509868	0.006977814	0.023849499
ENSG00000011258	MBTD1	81.62852544	371.6830975	2.184833154	1.68E-06	1.35E-05
ENSG00000213996	TM6SF2	3.090401881	326.6724544	6.659916336	6.50E-23	2.95E-21
ENSG00000183527	PSMG1	157.0552455	362.680969	1.206531303	0.005895063	0.020570236
ENSG00000186908	ZDHHC17	125.1738611	433.4119761	1.790517592	5.71E-05	0.000340502
ENSG00000123454	DBH	120.5082916	882.2323212	2.870510935	3.00E-10	4.24E-09
ENSG00000240935	PLGLA	1.534979634	671.325345	8.645766874	1.23E-32	1.05E-30
ENSG00000151611	MMAA	111.9547464	555.5837085	2.309538881	3.13E-07	2.84E-06
ENSG00000174010	KLHL15	57.52303638	497.7128887	3.109875179	5.44E-11	8.58E-10
ENSG00000065559	MAP2K4	205.2661038	482.2806699	1.231685755	0.004370342	0.015786202
ENSG00000162927	PUS10	48.19186435	401.2615189	3.053842563	2.09E-10	3.01E-09
ENSG00000237037	NDUFA6-AS1	29.52946559	518.2891804	4.126964728	4.43E-16	1.20E-14
ENSG00000102796	DHRS12	185.0486487	459.1323415	1.310220907	0.002565396	0.009927281
ENSG00000076351	SLC46A1	146.9465151	358.822914	1.286999027	0.00345773	0.012958668
ENSG000000092607	TBX15	10.8668471	914.3827744	6.376397673	2.47E-28	1.59E-26
ENSG00000253797	UTP14C	142.2809469	384.5432808	1.433350444	0.001114626	0.004839131
ENSG00000256847	CCND2P1	1.39E-17	325.386436	11.39161341	2.80E-25	1.50E-23
ENSG00000075336	TIMM21	157.8328401	330.5305096	1.065532407	0.015177624	0.046458108
ENSG00000114107	CEP70	52.07985416	340.8186568	2.706743136	1.26E-08	1.41E-07
ENSG00000188536	HBA2	39.63827699	424.4098482	3.415730021	2.86E-12	5.26E-11
ENSG00000139324	TMTC3	96.40284179	317.6703255	1.718731399	0.000131684	0.000720607
ENSG00000069702	TGFBR3	48.9694625	411.5496653	3.06733134	1.26E-10	1.89E-09
ENSG00000182107	TMEM30B	60.63342469	452.7022502	2.897358543	7.16E-10	9.62E-09
ENSG00000185808	PIGP	174.9399204	410.263647	1.228880636	0.004800551	0.017177899
ENSG00000163083	INHBB	91.73726908	757.4885616	3.043629802	4.51E-11	7.19E-10
ENSG00000109511	ANXA10	2.312696499	708.6198717	8.173972607	8.30E-32	6.81E-30
ENSG00000186212	SOWAHB	14.75493478	663.609236	5.477603329	3.58E-23	1.66E-21
ENSG00000219607	PPP1R3G	31.86227166	969.6815539	4.921399058	1.34E-21	5.69E-20
ENSG00000154114	TBCEL	169.4967587	417.9797568	1.301320879	0.00300283	0.011405157
ENSG00000116747	TROVE2	118.1755067	303.5241226	1.359635177	0.002210657	0.008808254
ENSG00000135220	UGT2A3	120.5082916	500.2849252	2.052223745	4.29E-06	3.22E-05
ENSG00000137054	POLR1E	195.1573765	482.2806699	1.304492251	0.002617432	0.010094801
ENSG00000183971	NPW	59.07823066	1096.997348	4.211501155	6.29E-18	1.97E-16
ENSG00000135336	ORC3	142.2809469	354.9648589	1.317911092	0.002744246	0.010525961
ENSG00000174485	DENND4A	108.8443659	421.8378116	1.952900546	1.39E-05	9.38E-05
ENSG00000163811	WDR43	146.1689204	380.6852258	1.379950366	0.001690535	0.006907487
ENSG00000166266	CUL5	114.2875316	457.8463232	2.000736432	7.75E-06	5.51E-05
ENSG00000162616	DNAJB4	79.29573781	392.2593907	2.304305553	5.04E-07	4.43E-06
ENSG00000177707	PVRL3	34.19507543	414.1217019	3.592629795	5.40E-13	1.07E-11
ENSG00000180875	GREM2	1.39E-17	839.7937227	12.75923005	6.02E-35	5.83E-33
ENSG00000197822	OCLN	100.2908185	327.9584728	1.707739575	0.00014359	0.000779072
ENSG00000107282	APBA1	38.8606773	580.0180543	3.894762244	3.26E-15	8.19E-14
ENSG00000260105	AOC4P	1.534979634	743.3423619	8.792761339	1.08E-33	9.77E-32
ENSG00000152749	GPR180	66.85419855	159.4900227	1.252237805	0.007361279	0.024913477
ENSG00000153132	CLGN	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000156869	FRRS1	25.64144922	381.9712441	3.889409275	2.59E-14	5.86E-13
ENSG00000066557	LRRC40	104.1787948	363.9669874	1.80319467	5.89E-05	0.000349913
ENSG00000101004	NINL	157.0552455	515.7171439	1.714295399	9.69E-05	0.000547623
ENSG00000161048	NAPEPLD	94.07005552	456.5603049	2.277160232	5.54E-07	4.84E-06
ENSG00000110344	UBE4A	133.7274045	357.5368956	1.417680769	0.001364714	0.005795313
ENSG00000178803	ADORA2A-AS1	2.312696499	357.5368956	7.187247327	7.08E-25	3.69E-23
ENSG00000106819	ASPN	252.6993579	563.2998177	1.155931839	0.007192364	0.024525476
ENSG00000034693	PEX3	72.29737318	297.0940303	2.036585475	9.49E-06	6.62E-05
ENSG00000179588	ZFPM1	150.0568938	347.2487487	1.209519558	0.005813321	0.020322095
ENSG00000168944	CEP120	115.8427216	338.24662	1.54458127	0.000529828	0.002508357
ENSG00000133028	SCO1	177.2727039	390.9733724	1.140320863	0.008605604	0.028488585
ENSG00000064300	NGFR	20.19820843	862.9420492	5.407134519	1.55E-23	7.41E-22
ENSG00000102189	EEA1	134.5049993	370.3970791	1.460291802	0.000906837	0.004019873
ENSG00000120798	NR2C1	153.1672724	351.1068038	1.195884418	0.006267383	0.021686731
ENSG00000197580	BCO2	23.30863474	616.0265635	4.715623947	2.72E-19	9.46E-18
ENSG00000143196	DPT	143.0585416	617.3125817	2.108212563	2.13E-06	1.69E-05
ENSG00000213066	FGFR10P	109.621961	390.9733724	1.833051795	4.03E-05	0.000249962
ENSG00000186687	LYRM7	87.84929125	443.7001223	2.334501602	2.86E-07	2.61E-06
ENSG00000101343	CRNKL1	151.6120831	316.3843071	1.060406215	0.016045526	0.048772356
ENSG00000163960	UBXN7	168.7191642	378.1131892	1.16336974	0.007747994	0.026104974
ENSG00000115808	STRN	121.2858865	318.9563439	1.393723757	0.001688631	0.006900844
ENSG00000088451	TGDS	85.51650426	461.704378	2.430638803	1.06E-07	1.03E-06
ENSG00000070778	PTPN21	111.1771513	399.9755006	1.845587278	3.72E-05	0.000232254
ENSG00000143409	FAM63A	173.3847314	446.2721588	1.363097845	0.0017319	0.007060256
ENSG00000137834	SMAD6	75.40775781	437.270031	2.53338429	3.99E-08	4.17E-07

ENSG00000168813	ZNF507	65.29900539	345.9627303	2.402798612	2.33E-07	2.16E-06
ENSG00000184779	RPS17	195.1573765	915.6687926	2.229307392	4.40E-07	3.89E-06
ENSG00000134853	PDGFRA	187.3814321	564.5858359	1.590386856	0.000258853	0.001324917
ENSG00000155792	DEPTOR	100.2908185	277.8037528	1.468369831	0.001067219	0.004656086
ENSG00000015520	NPC1L1	279.9151569	601.8803635	1.103999632	0.009845775	0.032102418
ENSG00000164690	SHH	56.74543914	571.0159269	3.327643503	2.89E-12	5.32E-11
ENSG00000076321	KLHL20	88.62688686	360.1089323	2.02072986	8.06E-06	5.71E-05
ENSG00000159459	UBR1	157.0552455	325.386436	1.050028748	0.016493108	0.049900937
ENSG000000260549	MT1L	24.86384483	455.2742867	4.186804332	3.71E-16	1.01E-14
ENSG00000005436	GCFC2	68.40939152	387.1153174	2.497909444	7.14E-08	7.16E-07
ENSG00000122591	FAM126A	72.29737318	235.3651392	1.700690519	0.000207469	0.001086984
ENSG00000096717	SIRT1	139.1705679	491.2827976	1.818535503	4.01E-05	0.000248774
ENSG00000056998	GYG2	6.201060061	924.6709195	7.188032966	6.34E-31	4.75E-29
ENSG00000152939	MARVELD2	98.73562788	306.0961595	1.630757119	0.000306021	0.001542831
ENSG00000167074	TEF	122.0634815	582.5900906	2.253437402	5.20E-07	4.56E-06
ENSG00000102908	FEAT5	107.2891756	387.1153174	1.849740692	3.67E-05	0.00022952
ENSG00000100372	SLC25A17	152.3896778	340.8186568	1.160327009	0.008572325	0.02839354
ENSG00000137513	NARS2	114.2875316	461.704378	2.012839846	6.82E-06	4.93E-05
ENSG00000185278	ZBTB37	171.0519478	369.1110608	1.108821226	0.010904357	0.03509359
ENSG00000001561	ENPP4	84.73890855	212.2168019	1.322722572	0.003746927	0.013931169
ENSG00000026103	FAS	181.9382708	520.8612168	1.516610544	0.000511899	0.00244866
ENSG00000100592	DAAM1	104.9563901	508.0010346	2.273395146	4.98E-07	4.38E-06
ENSG00000144724	PTPRG	192.0469988	424.4098482	1.143278917	0.008400846	0.027911112
ENSG00000167964	RAB26	40.41587651	478.4226152	3.560590255	3.97E-13	7.99E-12
ENSG00000048649	RSF1	153.1672724	430.8399396	1.491052457	0.000682609	0.003145975
ENSG000000248709	CTC-505O3.2	1.39E-17	672.6113632	12.43900973	1.23E-32	1.05E-30
ENSG00000182566	CLEC4G	2.312696499	814.0733599	8.374093841	3.06E-33	2.72E-31
ENSG00000087258	GNAO1	20.19820843	586.4481452	4.849951057	9.78E-20	3.57E-18
ENSG000000166575	TMEM135	71.51977693	465.5624327	2.700040114	5.94E-09	6.97E-08
ENSG00000176531	PHLDB3	91.73726908	286.8058824	1.642784473	0.000292728	0.001481824
ENSG00000108375	RNF43	110.3995562	325.386436	1.558023391	0.000466734	0.002252995
ENSG00000115841	RMDN2	44.30387198	572.3019451	3.686960835	4.98E-14	1.10E-12
ENSG00000169750	RAC3	41.97107512	124.7674951	1.568091246	0.001348494	0.005732309
ENSG00000130653	PNPLA7	101.0684138	524.7192714	2.374484507	1.70E-07	1.61E-06
ENSG00000115368	WDR75	166.3863805	347.2487487	1.060623805	0.015616842	0.047614894
ENSG000000079134	THOC1	106.5115804	284.2338454	1.414667458	0.001639574	0.006726907
ENSG00000019991	HGF	82.40612126	695.7596901	3.075518488	3.88E-11	6.27E-10
ENSG000000241644	INMT	303.2429837	618.5985999	1.028090939	0.015939237	0.048490789
ENSG00000113119	TMCO6	131.39462	545.2955628	2.051854002	4.02E-06	3.03E-05
ENSG00000173409	ARV1	118.1755067	311.2402333	1.395841093	0.001661987	0.006807629
ENSG00000121879	PIK3CA	115.0651266	351.1068038	1.608105473	0.0003144	0.001577627
ENSG000000066422	ZBTB11	94.84765097	306.0961595	1.688632025	0.000190205	0.001007577
ENSG00000178026	FAM211B	85.51650426	473.2785422	2.466351469	6.92E-08	6.96E-07
ENSG00000155324	GRAMD3	89.40448245	489.9967793	2.452382483	7.94E-08	7.91E-07
ENSG000000205269	TMEM170B	52.07985416	369.1110608	2.821762213	3.18E-09	3.89E-08
ENSG000000067248	DHX29	83.18371705	474.5645605	2.510101038	4.67E-08	4.84E-07
ENSG000000214313	AZGP1P1	0.757489584	577.4460179	9.327808153	4.57E-31	3.46E-29
ENSG00000148935	GAS2	0.757489584	308.6681964	8.424390624	8.79E-25	4.54E-23
ENSG00000108176	DNAJC12	109.621961	542.7235264	2.306098496	3.06E-07	2.78E-06
ENSG00000161544	CYGB	304.0205779	623.7426726	1.036343452	0.015019452	0.046013618
ENSG00000180488	FAM73A	32.63987315	311.2402333	3.247587454	5.49E-11	8.65E-10
ENSG00000112144	ICK	91.73726908	249.5113443	1.441888476	0.001476364	0.0061529
ENSG00000151229	SLC2A13	73.85256557	231.5070831	1.646210148	0.000347035	0.001721913
ENSG00000196865	NHLRC2	99.51322321	425.6958665	2.095164872	3.41E-06	2.61E-05
ENSG00000144306	SCRN3	114.2875316	383.2572625	1.744245802	9.30E-05	0.000527116
ENSG000000183421	PLPK4	153.1672724	448.8441954	1.550102128	0.000416871	0.00202845
ENSG00000166819	PLIN1	5.423411881	470.7065057	6.402780523	8.70E-25	4.50E-23
ENSG00000162881	OXER1	47.4142661	309.9542149	2.704857658	1.50E-08	1.67E-07
ENSG00000107554	DNMBP	96.40284179	366.5390241	1.925108939	1.98E-05	0.000130093
ENSG00000159086	PAXBP1	101.0684138	365.2530058	1.851951683	3.93E-05	0.000244481
ENSG00000085365	SCAMP1	174.1623259	381.9712441	1.132240504	0.009191931	0.030204317
ENSG00000011198	ABHD5	87.07169561	227.649027	1.384834656	0.002296672	0.009129023
ENSG000000182923	CEP63	89.40448245	273.9456972	1.613726167	0.000355512	0.001754269
ENSG00000132196	HSD17B7	125.951456	348.5347671	1.467235522	0.000939304	0.004144577
ENSG00000173889	PHC3	171.8295423	397.403464	1.208805397	0.005626649	0.019722232
ENSG00000173041	ZNF680	66.07660199	380.6852258	2.523701455	6.25E-08	6.34E-07
ENSG00000184517	ZFP1	55.19024445	461.704378	3.061131021	1.26E-10	1.88E-09
ENSG00000100344	PNPLA3	24.08624001	439.8420675	4.182642989	7.53E-16	2.02E-14
ENSG00000152409	JMY	139.9481627	353.6788405	1.336502522	0.002446432	0.009526253
ENSG000000156218	ADAMTSL3	62.96621528	464.2764145	2.879431063	7.44E-10	9.97E-09
ENSG00000113318	MSH3	108.8443659	416.6937385	1.935203658	1.64E-05	0.000109751

ENSG00000157796	WDR19	110.3995562	289.3779194	1.38887783	0.001800581	0.007324621
ENSG00000185269	NOTUM	5.423411881	469.4204875	6.398834355	9.13E-25	4.71E-23
ENSG00000196693	ZNF33B	94.07005552	324.1004176	1.782921367	8.01E-05	0.000461964
ENSG00000112394	SLC16A10	5.423411881	362.680969	6.026742613	3.24E-22	1.42E-20
ENSG00000163781	TOPBP1	109.621961	237.9371765	1.116793192	0.012755795	0.039920082
ENSG00000151287	TEX30	75.40775781	333.1025464	2.140926611	3.03E-06	2.34E-05
ENSG00000180917	CMTR2	109.621961	239.2231952	1.124566595	0.012272918	0.038998132
ENSG00000188215	DCUN1D3	186.6038376	410.263647	1.135833625	0.009086587	0.029901645
ENSG00000022267	FHL1	208.3764814	430.8399396	1.047317146	0.015660866	0.047737409
ENSG00000102786	INTS6	137.6153784	366.5390241	1.412241888	0.001412092	0.005973034
ENSG00000104691	UBXN8	68.40939152	453.9882684	2.727747647	4.83E-09	5.75E-08
ENSG00000126838	PZP	10.08922402	1250.033503	6.933147433	1.44E-31	1.14E-29
ENSG00000165879	FRAT1	133.7274045	288.0919009	1.106212426	0.01241315	0.03940846
ENSG00000131269	ABCB7	122.8410764	376.8271708	1.615839856	0.00028308	0.001436496
ENSG00000213463	SYNJ2BP	156.2776509	343.3906936	1.134857208	0.009426688	0.030910332
ENSG00000205885	C1RL-AS1	110.3995562	259.7994931	1.233376866	0.00567504	0.019866637
ENSG00000137040	RANBP6	165.608786	363.9669874	1.135195775	0.009454885	0.030994614
ENSG00000104883	PEX11G	50.52465852	371.6830975	2.875396091	1.53E-09	1.96E-08
ENSG00000213516	RBMXL1	173.3847314	388.4013358	1.162769074	0.007479643	0.025272774
ENSG00000164199	GPR98	1.39E-17	219.9329146	10.82672983	1.66E-21	6.96E-20
ENSG00000166477	LEO1	107.2891756	262.3715303	1.288760966	0.003877315	0.014351552
ENSG00000271122	RP11-379H18.1	100.2908185	272.6596787	1.44141465	0.001310594	0.005585532
ENSG00000158715	SLC45A3	62.18861847	277.8037528	2.156603463	3.60E-06	2.75E-05
ENSG00000145332	KLHL8	106.5115804	358.822914	1.750758418	8.95E-05	0.000509055
ENSG00000004766	CCDC132	75.40775781	214.7888395	1.508111557	0.000978166	0.004300781
ENSG00000205544	TMEM256	186.6038376	405.1195738	1.117634438	0.010225456	0.033131756
ENSG00000189046	ALKBH2	108.0667708	257.2274559	1.24980022	0.005157502	0.01830497
ENSG00000160801	PTH1R	13.97732024	765.2046704	5.760437757	4.80E-25	2.53E-23
ENSG00000139144	PIK3C2G	0.757489584	311.2402333	8.436358587	7.07E-25	3.69E-23
ENSG00000142273	CBLC	37.30547743	192.9265189	2.365908732	1.21E-06	9.95E-06
ENSG00000154511	FAM69A	115.0651266	360.1089323	1.644618907	0.000229314	0.0011894
ENSG00000197579	TOPORS	128.2842407	447.5581771	1.801472038	4.86E-05	0.000293876
ENSG00000138162	TACC2	125.951456	378.1131892	1.584719606	0.000362451	0.001785673
ENSG00000174990	CA5A	1.39E-17	356.2508773	11.52231548	3.51E-26	2.01E-24
ENSG00000175087	PDIK1L	81.62852544	196.7845757	1.26771313	0.005892356	0.020563676
ENSG00000164631	ZNF12	118.1755067	249.5113443	1.077029589	0.015502396	0.047283354
ENSG00000225470	JPX	178.8278929	416.6937385	1.219624294	0.005169648	0.018345461
ENSG00000151332	MBIP	84.73890855	340.8186568	2.005938231	9.58E-06	6.68E-05
ENSG00000163728	TTC14	137.6153784	318.9563439	1.21169121	0.006077422	0.021135349
ENSG00000172007	RAB33B	130.6170252	325.386436	1.315697808	0.00301234	0.01143778
ENSG00000113494	PRLR	20.97581587	387.1153174	4.196704681	7.74E-16	2.07E-14
ENSG00000108551	RASD1	148.5017045	538.8654718	1.858347473	2.50E-05	0.000160917
ENSG00000175600	SUGCT	30.30706789	371.6830975	3.610063721	6.70E-13	1.32E-11
ENSG00000169288	MRPL1	125.951456	361.3949507	1.51949496	0.000611462	0.002854063
ENSG00000115947	ORC4	161.7208131	336.9606016	1.058243566	0.015609386	0.047597998
ENSG00000140043	PTGR2	92.51486458	284.2338454	1.617633917	0.000333057	0.001658943
ENSG00000163104	SMARCAD1	125.1738611	320.2423623	1.354057221	0.002208171	0.008799757
ENSG00000160339	FCN2	0.757489584	769.0627249	9.741162787	5.04E-34	4.64E-32
ENSG00000135945	REV1	137.6153784	318.9563439	1.21169121	0.006077422	0.021135349
ENSG00000077458	FAM76B	124.3962662	363.9669874	1.547628047	0.000477873	0.00230185
ENSG00000104490	NCALD	142.2809469	352.3928222	1.307422311	0.0029154	0.011105415
ENSG00000133138	TBC1D8B	20.19820843	223.7909708	3.460487389	4.00E-11	6.45E-10
ENSG00000132613	MTSS1L	41.97107512	372.9691158	3.147155644	7.21E-11	1.12E-09
ENSG00000177888	ZBTB41	85.51650426	214.7888395	1.326938123	0.003803532	0.014103652
ENSG00000251637	RP11-119D9.1	2.312696499	447.5581771	7.511151444	4.08E-27	2.42E-25
ENSG000000089177	KIF16B	122.0634815	348.5347671	1.512420633	0.00065838	0.003050714
ENSG00000116641	DOCK7	121.2858865	331.816528	1.450733469	0.001076271	0.004692287
ENSG00000166126	AMN	20.19820843	246.9393071	3.602433206	6.35E-12	1.13E-10
ENSG00000217128	FNIP1	114.2875316	357.5368956	1.644051154	0.000221971	0.001152354
ENSG00000005243	COPZ2	110.3995562	288.0919009	1.382454256	0.001870291	0.007574722
ENSG00000185010	F8	104.9563901	336.9606016	1.681283911	0.000181028	0.000963272
ENSG00000154655	L3MBTL4	97.18043717	255.9414373	1.395547958	0.00195171	0.007873682
ENSG00000112208	BAG2	115.0651266	277.8037528	1.270367153	0.00439969	0.015882976
ENSG00000117834	SLC5A9	9.31159843	321.5283808	5.088577087	1.59E-18	5.23E-17
ENSG00000164074	C4orf29	139.9481627	360.1089323	1.362488909	0.001975518	0.007955525
ENSG00000259494	MRPL46	101.0684138	347.2487487	1.779044966	7.77E-05	0.000449043
ENSG00000123636	BAZ2B	115.0651266	383.2572625	1.734475102	0.000103542	0.000582246
ENSG00000258867	LINC01146	16.31016037	321.5283808	4.289168536	1.78E-15	4.59E-14
ENSG00000163827	LRRC2	16.31016037	252.0833815	3.938243805	2.39E-13	4.95E-12
ENSG00000243696	RP5-966M1.6	31.86227166	393.545409	3.620630021	3.69E-13	7.47E-12
ENSG00000211455	STK38L	108.0667708	286.8058824	1.406773875	0.001670822	0.006837056

ENSG00000136143	SUCLA2	115.0651266	397.403464	1.786753379	6.43E-05	0.000380038
ENSG00000164134	NAA15	121.2858865	306.0961595	1.334368226	0.002566788	0.009930069
ENSG00000214357	NEURL1B	137.6153784	461.704378	1.745165547	7.60E-05	0.000440225
ENSG00000138606	SHF	36.52787722	694.4736719	4.243525881	2.88E-17	8.62E-16
ENSG00000137033	IL33	42.7486742	497.7128887	3.536922133	3.84E-13	7.74E-12
ENSG00000163710	PCOLCE2	41.97107512	173.6362337	2.044599947	2.39E-05	0.000154934
ENSG00000127995	CASD1	101.8460091	250.7973629	1.298711195	0.00395452	0.014600354
ENSG00000198690	FAN1	98.73562788	240.5092138	1.282989482	0.00450753	0.016225149
ENSG00000134897	BIVM	130.6170252	329.2444912	1.33269794	0.002644222	0.010176857
ENSG00000137267	TUBB2A	81.62852544	240.5092138	1.557058333	0.000670774	0.003094874
ENSG00000147003	TMEM27	3.868086451	585.162127	7.189647804	9.89E-29	6.57E-27
ENSG00000013503	POLR3B	93.29246006	239.2231952	1.35694872	0.002567315	0.009930069
ENSG00000155545	MIER3	123.6186713	353.6788405	1.515307892	0.000666718	0.003083603
ENSG00000135999	EPC2	92.51486458	267.5156045	1.530209494	0.000667314	0.003084628
ENSG00000165060	FANX	108.0667708	421.8378116	1.963230952	1.23E-05	8.41E-05
ENSG00000126091	ST3GAL3	122.0634815	273.9456972	1.165117716	0.008541834	0.028303863
ENSG00000127954	STEAP4	13.19970438	460.4183597	5.10939297	5.07E-20	1.89E-18
ENSG00000155330	C16orf87	139.9481627	331.816528	1.244474522	0.004808668	0.017204468
ENSG00000144445	KANSL1L	92.51486458	352.3928222	1.927644534	1.98E-05	0.000130093
ENSG00000088899	LZTS3	77.74054591	289.3779194	1.894104835	3.80E-05	0.000236789
ENSG00000207652	MIR621	13.19970438	630.1727635	5.562112888	4.23E-23	1.95E-21
ENSG00000163319	MRPS18C	162.4984077	338.24662	1.056823335	0.016035626	0.048748225
ENSG00000162543	UBXN10	94.07005552	619.8846181	2.718273505	3.19E-09	3.90E-08
ENSG00000180776	ZDHHC20	27.97426007	73.32666296	1.384939152	0.008182193	0.027290447
ENSG00000010379	SLC6A13	3.090401881	441.1280858	7.093157624	6.79E-26	3.81E-24
ENSG00000004700	RECCQL	88.62688686	191.6405	1.1110419	0.015343879	0.046851612
ENSG00000203724	C1orf53	50.52465852	201.9286512	1.995486356	2.37E-05	0.000153365
ENSG00000113810	SMC4	40.41587651	138.913712	1.777211495	0.000250178	0.001283154
ENSG00000132846	ZBED3	76.96294991	307.382178	1.995631986	1.40E-05	9.44E-05
ENSG00000111846	GCNT2	92.51486458	374.2551341	2.014458827	8.34E-06	5.88E-05
ENSG00000196632	WNK3	0.757489584	141.4857511	7.299528559	1.68E-17	5.12E-16
ENSG00000188833	ENTPD8	6.978701584	375.5411525	5.721426303	3.59E-21	1.47E-19
ENSG00000145734	BDP1	103.4011996	325.386436	1.652381084	0.00021975	0.001143132
ENSG00000179941	BBS10	68.40939152	213.5028207	1.639696233	0.000366417	0.001803423
ENSG00000105821	DNAJC2	52.85745186	222.5049521	2.070470993	1.29E-05	8.75E-05
ENSG00000164219	PGGT1B	116.6203166	257.2274559	1.140041057	0.010761202	0.034727301
ENSG00000103528	SYT17	36.52787722	313.8122702	3.097752851	2.54E-10	3.63E-09
ENSG00000070269	TMEM260	104.9563901	294.5219933	1.48713942	0.000909508	0.004030277
ENSG00000178301	AQP11	28.75186299	365.2530058	3.660532032	3.49E-13	7.08E-12
ENSG00000111110	PPM1H	57.52303638	231.5070831	2.005942221	1.78E-05	0.000118463
ENSG00000099889	ARVCF	97.95803254	412.8356836	2.073611977	4.55E-06	3.40E-05
ENSG00000228794	LINC01128	102.6236044	282.9478269	1.461703296	0.001191306	0.005122822
ENSG00000163293	NIPAL1	22.53102899	335.6745832	3.888537621	5.52E-14	1.21E-12
ENSG00000149582	TMEM25	118.1755067	312.5262518	1.401788049	0.001603912	0.006599111
ENSG00000115816	CEBPZ	20.19820843	318.9563439	3.971507249	4.15E-14	9.23E-13
ENSG00000130545	CRB3	94.07005552	245.6532884	1.383242437	0.00219124	0.008742098
ENSG00000148516	ZEB1	135.2825941	285.5198639	1.0766151	0.014591355	0.044851363
ENSG00000139874	SSTR1	17.08777164	340.8186568	4.306570853	1.14E-15	2.99E-14
ENSG00000089048	ESF1	51.30225638	217.360877	2.079709575	1.11E-05	7.66E-05
ENSG00000133488	SEC14L4	32.63987315	378.1131892	3.528297267	1.29E-12	2.46E-11
ENSG00000133641	C12orf29	72.29737318	352.3928222	2.282776221	7.43E-07	6.33E-06
ENSG00000198157	HMGN5	25.64144922	168.4921572	2.709092711	8.75E-08	8.66E-07
ENSG00000152942	RAD17	133.7274045	289.3779194	1.112636	0.012019573	0.038281202
ENSG00000136682	CBWD2	115.0651266	264.9435674	1.202010708	0.006855668	0.023516097
ENSG00000138081	FBXO11	79.29573781	276.5177343	1.800019428	7.81E-05	0.000451098
ENSG00000113240	CLK4	108.0667708	370.3970791	1.77566148	7.55E-05	0.000437944
ENSG00000135424	ITGA7	86.29409995	209.6447643	1.278944174	0.004832369	0.017279317
ENSG00000177853	ZNF518A	113.5099365	249.5113443	1.135071837	0.011486511	0.036795621
ENSG00000169519	METTL15	97.95803254	252.0833815	1.362162245	0.002457596	0.009563732
ENSG00000099810	MTAP	108.8443659	316.3843071	1.538001116	0.000589256	0.002758704
ENSG00000188582	PAQR9	53.63504947	204.500689	1.927781032	3.83E-05	0.000238961
ENSG00000084764	MAPRE3	138.3929732	327.9584728	1.243712545	0.004586913	0.016479867
ENSG00000137720	C11orf1	156.276509	376.8271708	1.268872978	0.003751701	0.013938493
ENSG00000066651	TRMT11	88.62688686	280.3757899	1.659769159	0.000260755	0.001332457
ENSG00000133424	LARGE	105.7339853	367.8250424	1.797053716	6.44E-05	0.000380489
ENSG00000174136	RGMB	62.96621528	596.7362907	3.24147348	6.64E-12	1.18E-10
ENSG00000137070	IL11RA	146.9465151	356.2508773	1.276623397	0.003666979	0.013656391
ENSG00000109458	GAB1	99.51322321	307.382178	1.625502272	0.000282361	0.00143343
ENSG00000156958	GALK2	104.1787948	230.2210644	1.142631103	0.01071505	0.034609821
ENSG00000162804	SNED1	69.18698793	313.8122702	2.178859381	2.40E-06	1.89E-05
ENSG00000241058	NSUN6	39.63827699	415.4077202	3.384807084	4.34E-12	7.82E-11

ENSG00000103154	NECAB2	1.39E-17	221.2189333	10.83513745	1.50E-21	6.35E-20
ENSG00000180346	TIGD2	48.19186435	360.1089323	2.897773128	1.49E-09	1.91E-08
ENSG00000060749	QSER1	115.0651266	253.3694001	1.137592126	0.010693828	0.034549656
ENSG00000126953	TIMM8A	84.73890855	214.7888395	1.340094792	0.003402	0.012767516
ENSG00000136630	HLX	156.2776509	340.8186568	1.124013666	0.009969371	0.03244582
ENSG00000115648	MLPH	42.7486742	473.2785422	3.464312459	1.07E-12	2.07E-11
ENSG00000133103	COG6	70.74218064	320.2423623	2.176106995	2.19E-06	1.73E-05
ENSG00000229005	HNF4A-AS1	1.39E-17	402.5475372	11.69853575	2.15E-27	1.30E-25
ENSG00000110060	PUS3	99.51322321	318.9563439	1.678811146	0.000181898	0.000967073
ENSG00000086712	TXLNG	108.0667708	277.8037528	1.36078122	0.002366302	0.009368341
ENSG00000196678	ERI2	41.19347589	307.382178	2.89510207	2.37E-09	2.94E-08
ENSG00000118007	STAG1	43.52627316	199.3566135	2.191459757	4.82E-06	3.59E-05
ENSG00000166582	CENPV	87.07169561	249.5113443	1.517074698	0.000823246	0.003721678
ENSG00000163510	CWC22	93.29246006	304.8101411	1.706375994	0.000154587	0.000834549
ENSG00000134532	SOX5	19.42060034	334.3885648	4.095893301	8.01E-15	1.92E-13
ENSG00000162105	SHANK2	104.9563901	432.1259579	2.040064126	5.98E-06	4.36E-05
ENSG00000162600	OMA1	74.63016171	333.1025464	2.155852854	2.53E-06	1.98E-05
ENSG00000151657	KIN	75.40775781	312.5262518	2.048965365	7.90E-06	5.61E-05
ENSG00000161558	TMEM143	102.6236044	325.386436	1.663256613	0.000196072	0.001029442
ENSG00000185716	C16orf52	84.73890855	264.9435674	1.642737034	0.000319375	0.001596553
ENSG00000165832	TRUB1	117.3979117	322.8143992	1.458014272	0.001026834	0.004494094
ENSG00000174373	RALGAPA1	105.7339853	335.6745832	1.665133877	0.000210121	0.001099487
ENSG00000139117	CPNE8	79.29573781	280.3757899	1.820002208	6.77E-05	0.000398282
ENSG00000162623	TYW3	113.5099365	254.6554187	1.164501469	0.009529251	0.031213698
ENSG00000133858	ZFC3H1	122.8410764	258.5134745	1.072346915	0.016070052	0.048817351
ENSG00000067533	RRP15	104.1787948	226.3630083	1.11825988	0.01260455	0.039847026
ENSG00000170085	SIMC1	117.3979117	259.7994931	1.144813489	0.010410394	0.03368268
ENSG00000164073	MFSD8	113.5099365	331.816528	1.546212545	0.000507112	0.002426696
ENSG00000128655	PDE11A	6.978701584	493.854834	6.116452767	7.47E-24	3.64E-22
ENSG00000111615	KRR1	68.40939152	267.5156045	1.964931288	2.08E-05	0.00013551
ENSG00000126759	CFP	56.74543914	574.8739815	3.337356604	2.52E-12	4.66E-11
ENSG00000131725	WDR44	91.73726908	327.9584728	1.83616156	5.23E-05	0.000314262
ENSG00000091656	ZFHX4	78.51814188	268.8016231	1.773395924	9.85E-05	0.000555684
ENSG00000176399	DMRTA1	0.757489584	504.1429799	9.131990365	1.16E-29	8.16E-28
ENSG00000109654	TRIM2	55.96784183	335.6745832	2.581205075	4.73E-08	4.90E-07
ENSG000000269624	AL138847.1	0.757489584	424.4098482	8.883667856	6.25E-28	3.95E-26
ENSG00000131471	AOC3	108.8443659	306.0961595	1.490322937	0.000891587	0.003957213
ENSG00000124564	SLC17A3	11.64446802	428.267903	5.183810481	3.04E-20	1.16E-18
ENSG00000119326	CTNNAL1	101.8460091	320.2423623	1.651231731	0.000247605	0.001271272
ENSG00000197841	ZNF181	50.52465852	273.9456972	2.435347758	2.58E-07	2.37E-06
ENSG00000088386	SLC15A1	57.52303638	343.3906936	2.574539141	4.11E-08	4.29E-07
ENSG000000227242	NBPF13P	21.75342271	255.9414373	3.547769181	6.13E-12	1.09E-10
ENSG00000146147	MLIP	1.39E-17	86.18688029	9.476198975	2.65E-13	5.46E-12
ENSG00000095596	CYP26A1	3.090401881	565.8718541	7.452365243	2.15E-28	1.40E-26
ENSG00000168566	SNRNP48	109.621961	334.3885648	1.607567725	0.000335005	0.001666645
ENSG000000021488	SLC7A9	6.978701584	246.9393071	5.116806559	3.05E-17	9.11E-16
ENSG00000196233	LCOR	115.0651266	329.2444912	1.515381379	0.000662624	0.003066238
ENSG00000163818	LZTFL1	76.96294991	320.2423623	2.054744281	7.71E-06	5.49E-05
ENSG00000232667	AC004862.6	1.39E-17	334.3885648	11.43097319	1.51E-25	8.23E-24
ENSG000000087299	L2HGDH	36.52787722	254.6554187	2.79650148	1.02E-08	1.16E-07
ENSG00000118298	CA14	10.08922402	245.6532884	4.586335319	1.53E-15	3.97E-14
ENSG00000180745	CLRN3	19.42060034	241.7952325	3.628314443	4.80E-12	8.59E-11
ENSG00000146700	SRCRB4D	2.312696499	16.74147634	2.778673814	0.005247305	0.018541622
ENSG00000159899	NPR2	88.62688686	439.8420675	2.309211393	3.91E-07	3.49E-06
ENSG00000216775	RP1-152L7.5	48.9694625	138.913712	1.501123946	0.001810349	0.007359541
ENSG00000184979	USP18	120.5082916	344.6767119	1.514844283	0.000627912	0.002924254
ENSG00000236882	C5orf27	2.312696499	84.90085893	5.114269303	4.39E-12	7.88E-11
ENSG00000165983	PTER	93.29246006	304.8101411	1.706375994	0.000154587	0.000834549
ENSG00000243156	MICAL3	76.96294991	333.1025464	2.111529571	4.30E-06	3.23E-05
ENSG00000187325	TAF9B	71.51977693	241.7952325	1.75513042	0.00012891	0.00070605
ENSG00000042062	FAM65C	57.52303638	522.147235	3.17900491	2.22E-11	3.70E-10
ENSG00000135437	RDH5	6.978701584	459.1323415	6.01129729	3.81E-23	1.76E-21
ENSG000000164850	GPBR1	32.63987315	378.1131892	3.528297267	1.29E-12	2.46E-11
ENSG00000160963	COL26A1	17.08777164	141.4857511	3.038804237	1.70E-08	1.87E-07
ENSG00000078114	NEBL	42.7486742	198.0705946	2.208050019	5.18E-06	3.85E-05
ENSG00000107736	CDH23	41.97107512	402.5475372	3.257230975	1.66E-11	2.83E-10
ENSG000000088179	PTPN4	108.8443659	286.8058824	1.396443468	0.00183756	0.007461321
ENSG00000117262	GPR89A	92.51486458	239.2231952	1.369005833	0.002567315	0.009930069
ENSG00000134760	DSG1	1.39E-17	500.2849252	12.01205843	1.33E-29	9.29E-28
ENSG00000178826	TMEM139	39.63827699	151.7739068	1.932790366	8.26E-05	0.000472952
ENSG00000182600	C2orf82	17.08777164	450.1302136	4.707808904	3.09E-18	9.88E-17

ENSG00000174405	LIG4	99.51322321	288.0919009	1.532028449	0.000635717	0.002956175
ENSG00000081026	MAGI3	46.63666774	268.8016231	2.523199248	1.19E-07	1.15E-06
ENSG00000167232	ZNF91	86.29409995	219.9329146	1.348029549	0.002995591	0.0113794
ENSG00000154359	LONRF1	107.2891756	298.3800488	1.47423625	0.00095385	0.004205029
ENSG00000214944	ARHGEF28	108.0667708	308.6681964	1.51272142	0.000719889	0.003300653
ENSG00000170899	GSTA4	63.74381204	209.6447643	1.715093081	0.000238055	0.001230628
ENSG00000176894	PXMP2	20.19820843	347.2487487	4.0940819	7.46E-15	1.79E-13
ENSG00000271738	RP11-137H2.6	41.19347589	363.9669874	3.138805126	1.14E-10	1.71E-09
ENSG00000179454	KLHL28	91.73726908	231.5070831	1.33388319	0.003302115	0.012435464
ENSG00000132952	USPL1	110.3995562	254.6554187	1.204535589	0.007478765	0.025272774
ENSG00000125247	TMTC4	92.51486458	307.382178	1.730551869	0.000119973	0.000662026
ENSG00000126653	NSRP1	117.3979117	279.0897714	1.248106753	0.004827178	0.017263239
ENSG00000213160	KLHL23	70.74218064	162.0620612	1.193917499	0.01017343	0.032993294
ENSG00000155970	MICU3	20.19820843	226.3630083	3.476966641	3.12E-11	5.11E-10
ENSG00000145715	RASA1	87.07169561	299.660672	1.781230794	8.68E-05	0.000495228
ENSG00000134508	CABLES1	95.62524639	232.7931018	1.282077686	0.004745267	0.016994758
ENSG00000100294	MCAT	139.9481627	325.386436	1.216251248	0.005786498	0.020234018
ENSG00000177465	ACOT4	109.621961	280.3757899	1.353484904	0.002536438	0.009835127
ENSG00000176225	RTTN	81.62852544	225.0769895	1.461424795	0.001395193	0.005910604
ENSG00000249364	RP11-434D9.1	1.39E-17	545.2955628	12.13632371	1.76E-30	1.29E-28
ENSG00000071205	ARHGAP10	129.0618355	329.2444912	1.349959827	0.00225931	0.008984825
ENSG00000151458	ANKRD50	45.85906927	255.9414373	2.476681616	2.48E-07	2.28E-06
ENSG00000144120	TMEM177	104.9563901	263.6575488	1.327485182	0.003098851	0.011744729
ENSG00000171954	CYP4F22	18.64299156	81.0427944	2.110959866	0.000135269	0.000738765
ENSG00000058056	USP13	58.30063355	237.9371765	2.026125278	1.46E-05	9.80E-05
ENSG00000106524	ANKMY2	101.0684138	245.6532884	1.279866304	0.004423063	0.015962718
ENSG00000203832	NBPF20	119.7306966	271.3736602	1.179319677	0.008164549	0.027242565
ENSG00000188676	IDO2	20.19820843	313.8122702	3.948057257	5.71E-14	1.25E-12
ENSG00000148690	FRA10AC1	106.5115804	318.9563439	1.580894284	0.000399661	0.001951205
ENSG00000120688	WBP4	108.0667708	236.6511578	1.129565047	0.011747918	0.037542017
ENSG00000254685	FPGT	71.51977693	187.7824431	1.390573967	0.002820484	0.010792201
ENSG00000197859	ADAMTSL2	140.7257574	335.6745832	1.253161312	0.004558591	0.016392594
ENSG00000138399	FASTKD1	125.1738611	281.6618084	1.168917087	0.008367931	0.027842695
ENSG00000146938	NLGN4X	0.757489584	41.17606037	5.521174694	2.10E-08	2.28E-07
ENSG000000009413	REV3L	79.29573781	272.6596787	1.779755974	9.44E-05	0.000534143
ENSG000000035115	SH3YL1	82.40612126	353.6788405	2.099564441	4.20E-06	3.16E-05
ENSG00000246082	NUDT16P1	80.07333372	258.5134745	1.688868455	0.000213874	0.001116513
ENSG00000055147	FAM114A2	123.6186713	259.7994931	1.070410092	0.01606932	0.048817351
ENSG00000164180	TMEM161B	75.40775781	273.9456972	1.858941221	4.83E-05	0.000292458
ENSG00000254235	RP11-115J16.1	0.757489584	214.7888395	7.901451736	2.73E-21	1.13E-19
ENSG00000105926	MPP6	54.412647	237.9371765	2.125447347	6.00E-06	4.38E-05
ENSG00000182463	TSHZ2	97.18043717	389.6873541	2.001863003	9.18E-06	6.43E-05
ENSG00000109193	SULT1E1	0.757489584	415.4077202	8.852744919	1.03E-27	6.42E-26
ENSG00000118804	FAM47E-STBD1	27.19665681	241.7952325	3.14544274	5.11E-10	6.99E-09
ENSG00000155158	TTC39B	116.6203166	321.5283808	1.461833303	0.001064008	0.004643706
ENSG00000108272	DHRS11	77.74054591	183.9243862	1.24054116	0.006941883	0.023782287
ENSG00000134909	ARHGAP32	79.29573781	293.2359749	1.884680566	3.68E-05	0.000230421
ENSG00000173276	ZBTB21	73.85256557	214.7888395	1.538120087	0.000851118	0.003832238
ENSG000000085274	MYNN	89.40448245	217.360877	1.280062022	0.004565027	0.016413097
ENSG00000183579	ZNRF3	69.96458431	432.1259579	2.624195354	1.72E-08	1.89E-07
ENSG00000087842	PIR	80.8509296	231.5070831	1.515830465	0.000914715	0.004049019
ENSG00000240038	AMY2B	76.96294991	195.4985568	1.343018001	0.00345964	0.012963872
ENSG00000151623	NR3C2	30.30706789	284.2338454	3.22318524	1.18E-10	1.77E-09
ENSG00000100350	FOXRED2	119.7306966	263.6575488	1.137719431	0.010859003	0.034970266
ENSG00000147894	C9orf72	86.29409995	309.9542149	1.842835632	4.87E-05	0.000294382
ENSG00000165185	KIAA1958	40.41587651	241.7952325	2.576377727	1.01E-07	9.91E-07
ENSG00000164070	HSPA4L	99.51322321	357.5368956	1.843496792	3.98E-05	0.000247444
ENSG00000160124	CCDC58	76.96294991	271.3736602	1.815939795	7.67E-05	0.000443828
ENSG00000151413	NUBPL	64.52140874	254.6554187	1.978119775	1.86E-05	0.000123068
ENSG00000186448	ZNF197	108.0667708	234.0791205	1.113805844	0.012707012	0.039847026
ENSG00000161326	DUSP14	115.8427216	263.6575488	1.185288524	0.007994009	0.02677056
ENSG00000142182	DNMT3L	1.39E-17	149.201868	10.26723488	6.30E-18	1.97E-16
ENSG00000119509	INVS	119.7306966	272.6596787	1.186137906	0.007878733	0.026448664
ENSG00000119778	ATAD2B	62.96621528	194.2125379	1.622504113	0.000491038	0.002360685
ENSG00000256802	RP11-680F8.1	70.74218064	198.0705946	1.483228137	0.00133267	0.005673777
ENSG00000093134	VNN3	7.75633786	465.5624327	5.881811575	2.83E-23	1.33E-21
ENSG00000134612	FOLH1B	0.757489584	345.9627303	8.588901365	7.20E-26	4.02E-24
ENSG00000147119	CHST7	170.2743533	351.1068038	1.043263708	0.016448384	0.049893164
ENSG00000127989	MTERF	53.63504947	140.1997316	1.383474206	0.003792122	0.014067641
ENSG00000117000	RLF	95.62524639	217.360877	1.183164523	0.009120097	0.029992063
ENSG00000173530	TNFRSF10D	115.8427216	501.5709434	2.112824369	2.29E-06	1.80E-05

ENSG00000000457	SCYL3	98.73562788	237.9371765	1.267484336	0.004905183	0.01749689
ENSG00000243444	PALM2	2.312696499	306.0961595	6.963206151	2.29E-23	1.08E-21
ENSG00000225241	RP11-640M9.2	79.29573781	245.6532884	1.629334798	0.000350249	0.001731045
ENSG00000261572	RP11-384L8.1	5.423411881	185.2104052	5.05757789	5.79E-16	1.56E-14
ENSG00000166432	ZMAT1	52.85745186	308.6681964	2.542514154	6.66E-08	6.72E-07
ENSG00000162694	EXTL2	48.9694625	203.2146701	2.049619259	1.74E-05	0.000115922
ENSG00000021461	CYP3A43	1.39E-17	402.5475372	11.69853575	2.15E-27	1.30E-25
ENSG00000144331	ZNF385B	18.64299156	318.9563439	4.086268527	9.80E-15	2.32E-13
ENSG00000269430	LRR32DN	15.53254811	479.7086334	4.936095069	1.39E-19	5.00E-18
ENSG00000164684	ZNF704	88.62688686	289.3779194	1.705346638	0.000153986	0.000831773
ENSG00000175105	ZNF654	86.29409995	239.2231952	1.469271784	0.001161857	0.005023128
ENSG00000249242	TMEM150C	27.19665681	385.8292991	3.819402804	6.59E-14	1.43E-12
ENSG00000145194	ECE2	62.18861847	151.7739068	1.28488124	0.006130968	0.021259181
ENSG00000154258	ABCA9	51.30225638	393.545409	2.935858096	7.32E-10	9.83E-09
ENSG00000172824	CES4A	69.18698793	257.2274559	1.892100719	4.18E-05	0.000258142
ENSG00000075407	ZNF37A	92.51486458	276.5177343	1.577941361	0.000450795	0.002180713
ENSG00000164161	HHIP	5.423411881	536.2934354	6.590938855	4.20E-26	2.39E-24
ENSG00000184374	COLEC10	23.30863474	528.5773261	4.494783618	8.00E-18	2.48E-16
ENSG00000146216	TBTK1	24.08624001	64.32450474	1.410964899	0.008470153	0.028088813
ENSG00000184454	NCMAP	38.08307745	218.6468958	2.516722363	2.58E-07	2.37E-06
ENSG00000105849	TWISTNB	80.07333372	173.6362337	1.11496273	0.015262054	0.046664823
ENSG00000167799	NUDT8	70.74218064	204.500689	1.529296816	0.000955048	0.004208815
ENSG00000260065	CTA-445C9.15	132.1722149	439.8420675	1.733359213	9.12E-05	0.000517798
ENSG00000182796	TMEM198B	98.73562788	239.2231952	1.275257739	0.004702117	0.016847501
ENSG00000102362	SYTL4	69.18698793	374.2551341	2.432907457	1.55E-07	1.48E-06
ENSG00000170365	SMAD1	62.18861847	218.6468958	1.811277065	9.83E-05	0.000554795
ENSG00000171914	TLN2	76.96294991	225.0769895	1.546184154	0.000764561	0.00348618
ENSG00000169193	CCDC126	45.85906927	180.0663291	1.969627661	4.27E-05	0.000263015
ENSG00000247903	RP11-421F16.3	99.51322321	216.0748583	1.117193092	0.013591439	0.042158395
ENSG00000044459	CNTLN	77.74054591	281.6618084	1.855127245	5.28E-05	0.000316943
ENSG00000167165	UGT1A6	44.30387198	471.992524	3.409000456	2.36E-12	4.39E-11
ENSG00000197885	NKIRAS1	75.40775781	263.6575488	1.803736589	7.92E-05	0.000456994
ENSG00000134864	GGACT	59.07823066	295.8080118	2.321020732	7.60E-07	6.46E-06
ENSG00000183354	KIAA2026	100.2908185	279.0897714	1.475030663	0.001024357	0.004485622
ENSG00000164749	HNF4G	40.41587651	294.5219933	2.860863294	3.56E-09	4.32E-08
ENSG00000055955	ITIH4	84.73890855	281.6618084	1.730984422	0.000146778	0.000795675
ENSG00000205133	TRIQQ	38.08307745	232.7931018	2.607128754	9.53E-08	9.39E-07
ENSG00000143434	SEMA6C	42.7486742	235.3651392	2.456823545	2.89E-07	2.63E-06
ENSG00000253313	C1orf210	6.201060061	108.0492338	4.091930445	7.24E-11	1.12E-09
ENSG00000182224	CYB5D1	93.29246006	267.5156045	1.518152381	0.000749904	0.003425001
ENSG00000185436	IFNLR1	87.84929125	363.9669874	2.04879357	6.86E-06	4.96E-05
ENSG00000165269	AQP7	10.08922402	261.0855117	4.674200366	4.13E-16	1.12E-14
ENSG00000110693	SOX6	88.62688686	276.5177343	1.639786379	0.000311198	0.001567339
ENSG00000242110	AMACR	13.97732024	349.8207854	4.631425913	5.04E-17	1.48E-15
ENSG00000175984	DENND2C	26.4190532	131.1975941	2.305520449	5.75E-06	4.21E-05
ENSG00000169744	LDB2	101.8460091	317.6703255	1.639601448	0.000267715	0.001364654
ENSG00000120057	SFRP5	12.42208703	619.8846181	5.625013115	2.21E-23	1.05E-21
ENSG00000125675	GRIA3	0.757489584	64.32450474	6.16350562	2.69E-11	4.45E-10
ENSG00000205143	ARID3C	3.090401881	294.5219933	6.510493827	6.48E-22	2.79E-20
ENSG00000130812	ANGPTL6	18.64299156	430.8399396	4.51994723	1.85E-17	5.62E-16
ENSG00000140386	SCAPER	56.74543914	203.2146701	1.837562232	0.000100383	0.000565507
ENSG00000144451	SPAG16	81.62852544	180.0663291	1.139690734	0.013146855	0.041014821
ENSG000000007001	UPP2	1.534979634	129.9115743	6.277157006	8.55E-17	2.44E-15
ENSG00000101417	PXMP4	73.85256557	191.6405	1.373682569	0.002938606	0.011180017
ENSG00000116194	ANGPTL1	12.42208703	318.9563439	4.666586058	5.20E-17	1.52E-15
ENSG00000145390	USP53	55.19024445	257.2274559	2.217448029	2.45E-06	1.92E-05
ENSG00000160233	LRR33	19.42060034	354.9648589	4.182019654	2.27E-15	5.81E-14
ENSG00000087237	CETP	86.29409995	421.8378116	2.287348773	5.46E-07	4.77E-06
ENSG00000080709	KCNN2	11.64446802	425.6958665	5.175121986	3.55E-20	1.34E-18
ENSG00000223991	AC104809.2	1.39E-17	271.3736602	11.12982591	1.67E-23	7.97E-22
ENSG00000198924	DCLRE1A	55.96784183	225.0769895	2.004765969	2.07E-05	0.00013548
ENSG00000058729	RIOK2	73.85256557	268.8016231	1.861611469	5.26E-05	0.000315866
ENSG00000151014	CCR4L	63.74381204	433.4119761	2.762539395	3.30E-09	4.03E-08
ENSG00000203778	FAM229B	78.51814188	217.360877	1.467070061	0.001424896	0.006003845
ENSG00000119698	PPP4R4	1.39E-17	51.46426629	8.733404515	1.25E-09	1.61E-08
ENSG00000126814	TRMT5	95.62524639	236.6511578	1.305781519	0.003988678	0.014698086
ENSG00000132423	COQ3	62.18861847	154.3459455	1.309109605	0.005063522	0.018009995
ENSG00000169432	SCN9A	3.090401881	277.8037528	6.426213245	2.41E-21	1.01E-19
ENSG00000154642	C21orf91	83.18371705	237.9371765	1.514371671	0.000881843	0.003924477
ENSG00000102221	JADE3	59.07823066	225.0769895	1.926927415	3.87E-05	0.000240766
ENSG00000109906	ZBTB16	41.97107512	475.8505787	3.498526716	6.43E-13	1.27E-11

ENSG00000211454	AKR7L	31.08466991	264.9435674	3.085445606	6.61E-10	8.92E-09
ENSG00000171428	NAT1	85.51650426	246.9393071	1.528090422	0.000739197	0.003381864
ENSG00000163590	PPM1L	45.85906927	192.9265189	2.069098659	1.66E-05	0.000110978
ENSG00000141441	GAREM	118.1755067	264.9435674	1.163576484	0.008686721	0.028726512
ENSG00000114248	LRRC31	1.39E-17	34.74592196	8.167995064	2.40E-07	2.21E-06
ENSG00000174796	THAP6	95.62524639	225.0769895	1.233468641	0.006434811	0.022213505
ENSG00000180089	TMEM86B	32.63987315	243.0812511	2.891124055	4.72E-09	5.63E-08
ENSG00000117010	ZNF684	18.64299156	315.0982886	4.068716863	1.27E-14	2.95E-13
ENSG00000251685	RP11-813N20.1	2.312696499	331.816528	7.079571394	3.92E-24	1.93E-22
ENSG00000256185	RP11-612B6.2	67.63179505	258.5134745	1.932024822	2.63E-05	0.000169203
ENSG00000153902	LGI4	34.19507543	84.90085893	1.307742747	0.009128294	0.030011078
ENSG00000167992	VWCE	2.312696499	109.3352541	5.478806414	4.01E-14	8.94E-13
ENSG00000111727	HCFC2	40.41587651	209.6447643	2.370627845	9.53E-07	7.99E-06
ENSG00000102595	UGGT2	81.62852544	219.9329146	1.428084354	0.001875249	0.007591095
ENSG00000156298	TSPAN7	28.75186299	243.0812511	3.073267775	7.76E-10	1.04E-08
ENSG00000071243	ING3	58.30063355	153.0599261	1.389968757	0.002953275	0.011232386
ENSG00000090612	ZNF268	67.63179505	226.3630083	1.740500745	0.000177443	0.000945819
ENSG00000146587	RBAK	39.63827699	223.7909708	2.492720383	2.52E-07	2.32E-06
ENSG00000119862	LGALS1	74.63016171	240.5092138	1.686140976	0.000252766	0.001294557
ENSG00000112357	PEX7	62.96621528	141.4857511	1.16579431	0.013240693	0.041219616
ENSG00000273290	CTC-297N7.8	90.18207801	246.9393071	1.451574685	0.001346778	0.005725994
ENSG00000180667	YOD1	44.30387198	194.2125379	2.128298434	9.14E-06	6.41E-05
ENSG00000264575	LINC00526	39.63827699	145.3438097	1.8703772	0.00013723	0.00074832
ENSG00000196159	FAT4	25.64144922	280.3757899	3.443440243	1.20E-11	2.06E-10
ENSG00000197429	IPP	107.2891756	226.3630083	1.075873177	0.016078996	0.048830112
ENSG00000181031	RPH3AL	55.96784183	309.9542149	2.466231611	1.69E-07	1.60E-06
ENSG00000067445	TRO	49.74706056	258.5134745	2.374041817	5.09E-07	4.47E-06
ENSG00000168477	TNXB	87.84929125	295.8080118	1.749736	0.000118389	0.000657851
ENSG00000113971	NPHP3	96.40284179	312.5262518	1.695185725	0.000161347	0.000869342
ENSG00000052344	PRSS8	9.31159843	106.7632134	3.498925207	2.85E-09	3.50E-08
ENSG00000145241	CENPC	63.74381204	241.7952325	1.920842964	3.81E-05	0.000237794
ENSG00000225791	TRAM2-AS1	66.85419855	240.5092138	1.844566941	6.94E-05	0.000407364
ENSG00000182700	IGIP	62.18861847	281.6618084	2.176494405	3.07E-06	2.37E-05
ENSG00000102781	KATNAL1	89.40448245	210.9307831	1.236759094	0.006683246	0.022989813
ENSG00000165923	AGBL2	22.53102899	78.47075096	1.793074595	0.00091912	0.004065619
ENSG00000163291	PAQR3	41.19347589	122.1954553	1.56495222	0.001284291	0.005486602
ENSG00000168769	TET2	73.85256557	216.0748583	1.546728376	0.000806979	0.003657667
ENSG00000186732	MPPED1	0.757489584	293.2359749	8.350419834	2.70E-24	1.35E-22
ENSG00000136011	STAB2	1.534979634	417.9797568	7.962314564	8.70E-28	5.45E-26
ENSG00000134138	MEIS2	62.96621528	180.0663291	1.513453063	0.001153984	0.004991694
ENSG00000188868	ZNF563	17.08777164	70.75461835	2.040038163	0.000242489	0.001249652
ENSG00000186642	PDE2A	65.29900539	342.1046752	2.386624381	2.81E-07	2.56E-06
ENSG00000135144	DTX1	88.62688686	299.6660672	1.755730861	9.95E-05	0.000560812
ENSG00000165633	VSTM4	59.07823066	367.8250424	2.63528636	2.17E-08	2.36E-07
ENSG00000166743	ACSM1	6.201060061	657.1791451	6.695441415	2.10E-27	1.28E-25
ENSG00000228695	CES1P1	0.757489584	192.9265189	7.746658311	2.50E-20	9.59E-19
ENSG00000083097	DOPEY1	50.52465852	216.0748583	2.093126383	9.32E-06	6.52E-05
ENSG00000102543	CDADC1	73.85256557	263.6575488	1.833745119	6.75E-05	0.000397161
ENSG00000150764	DIXDC1	92.51486458	248.2253257	1.422277571	0.001723683	0.00703368
ENSG00000229644	NAMPTL	41.97107512	257.2274559	2.611313549	6.85E-08	6.90E-07
ENSG00000264920	RP11-6N17.4	48.9694625	200.6426324	2.031251751	2.00E-05	0.000131081
ENSG00000121989	ACVR2A	42.7486742	201.9286512	2.235867374	2.91E-06	2.25E-05
ENSG00000070759	TESK2	89.40448245	201.9286512	1.173864765	0.0101282	0.032868051
ENSG00000120832	MTERFD3	49.74706056	239.2231952	2.262203439	1.65E-06	1.33E-05
ENSG00000197013	ZNF429	34.97267623	127.3395348	1.859711313	0.00017584	0.000938078
ENSG00000156463	SH3RF2	14.75493478	196.7845757	3.724388559	5.45E-12	9.74E-11
ENSG00000205609	EIF3CL	27.19665681	562.0137995	4.361931598	2.50E-17	7.54E-16
ENSG00000113595	TRIM23	75.40775781	250.7973629	1.731620785	0.000151922	0.00082141
ENSG00000226733	RP11-397G17.1	33.41747441	90.04494392	1.425562629	0.005426586	0.019085579
ENSG00000166352	C11orf74	45.85906927	144.0577902	1.647942072	0.000669438	0.003089859
ENSG00000233593	RP4-665J23.1	28.75186299	254.6554187	3.140349301	3.26E-10	4.57E-09
ENSG00000256937	RP11-436I9.5	10.08922402	120.9094353	3.564229054	9.67E-10	1.27E-08
ENSG00000142677	IL22RA1	8.533969895	160.7760419	4.212971305	6.17E-13	1.22E-11
ENSG00000213096	ZNF254	48.19186435	159.4900227	1.723296725	0.000300224	0.001517299
ENSG00000171097	CCBL1	73.85256557	160.7760419	1.12047334	0.015192792	0.046493087
ENSG00000227117	CTA-85E5.10	3.868086451	91.33096499	4.511286428	5.87E-11	9.20E-10
ENSG00000103316	CRYM	4.645755009	149.201868	4.963028334	7.77E-15	1.86E-13
ENSG00000151948	GLT1D1	15.53254811	541.4375082	5.110698139	9.28E-21	3.66E-19
ENSG00000157077	ZFYVE9	55.19024445	237.9371765	2.10502837	7.55E-06	5.40E-05
ENSG00000180354	MTURN	131.39462	379.3992075	1.52864482	0.000530599	0.002511052
ENSG00000140832	MARVELD3	20.19820843	199.3566135	3.293763987	3.17E-10	4.46E-09

ENSG00000259479	<i>CTD-2008A1.2</i>	11.64446802	249.5113443	4.404637265	3.22E-15	8.09E-14
ENSG00000007516	<i>BAIAP3</i>	43.52627316	186.4964241	2.095304874	1.26E-05	8.60E-05
ENSG00000198865	<i>CCDC152</i>	12.42208703	151.7739068	3.59563618	1.15E-10	1.72E-09
ENSG00000188985	<i>DHFRP1</i>	49.74706056	146.6298291	1.556395816	0.001196727	0.005144354
ENSG00000162572	<i>SCNN1D</i>	58.30063355	132.4836138	1.181828779	0.013974012	0.043264084
ENSG00000095932	<i>C19orf77</i>	6.978701584	760.0605978	6.738380649	3.30E-28	2.11E-26
ENSG00000105609	<i>LILRB5</i>	62.96621528	408.9776287	2.696509884	9.35E-09	1.07E-07
ENSG00000248740	<i>RP11-328K4.1</i>	1.534979634	343.3906936	7.678805398	7.69E-26	4.28E-24
ENSG00000151150	<i>ANK3</i>	41.19347589	322.8143992	2.96575164	1.01E-09	1.33E-08
ENSG00000268230	<i>CTD-2619J13.8</i>	28.75186299	183.9243862	2.671127866	8.10E-08	8.05E-07
ENSG00000139160	<i>METTL20</i>	36.52787722	163.3480804	2.156213046	1.01E-05	7.03E-05
ENSG00000112425	<i>EPM2A</i>	37.30547743	181.3523481	2.276699189	3.13E-06	2.41E-05
ENSG00000267056	<i>AC005336.4</i>	5.423411881	135.0556532	4.602248686	2.84E-13	5.82E-12
ENSG00000050555	<i>LAMC3</i>	43.52627316	360.1089323	3.044227119	2.86E-10	4.06E-09
ENSG00000135249	<i>RINT1</i>	76.96294991	185.2104052	1.26506513	0.005865484	0.020484277
ENSG00000176595	<i>ZBTBD11</i>	17.08797164	398.6894823	4.532772286	4.36E-17	1.29E-15
ENSG00000105784	<i>RUNDC3B</i>	7.75633786	216.0748583	4.774716467	4.96E-16	1.34E-14
ENSG00000125551	<i>PLGLB2</i>	22.53102899	317.6703255	3.809028359	1.67E-13	3.51E-12
ENSG00000213759	<i>UGT2B11</i>	1.534979634	42.46208706	4.666107167	1.33E-07	1.28E-06
ENSG00000134317	<i>GRHL1</i>	12.42208703	141.4857511	3.494436539	3.83E-10	5.34E-09
ENSG00000197272	<i>IL27</i>	21.75342271	151.7739068	2.794256113	6.17E-08	6.27E-07
ENSG00000170949	<i>ZNF160</i>	92.51486458	205.7867078	1.151893787	0.011229183	0.036050291
ENSG00000182903	<i>ZNF721</i>	61.41102161	261.0855117	2.085204005	7.35E-06	5.28E-05
ENSG00000184675	<i>AMER1</i>	119.7306966	309.9542149	1.371029679	0.002122847	0.008504735
ENSG00000087301	<i>TXNDC16</i>	34.19507543	172.3502146	2.32839397	2.41E-06	1.89E-05
ENSG00000198270	<i>TMEM116</i>	63.74381204	187.7824431	1.556286511	0.000882611	0.003927193
ENSG00000144426	<i>NBEAL1</i>	24.08624001	164.6340996	2.765454519	7.89E-08	7.86E-07
ENSG00000085465	<i>OVGP1</i>	31.08466991	300.9520857	3.269230889	6.41E-11	1.00E-09
ENSG00000136457	<i>CHAD</i>	6.978701584	213.5028207	4.906994298	6.60E-16	1.77E-14
ENSG00000104938	<i>CLEC4M</i>	3.090401881	308.6681964	6.578153445	2.31E-22	1.02E-20
ENSG00000203727	<i>SAMD5</i>	26.4190532	419.265775	3.980908293	6.97E-15	1.68E-13
ENSG00000237517	<i>DGCR5</i>	17.08777164	524.7192714	4.928967948	1.09E-19	3.98E-18
ENSG00000105550	<i>FGF21</i>	1.39E-17	66.89655057	9.111133693	2.09E-11	3.50E-10
ENSG00000210194	<i>MT-TE</i>	38.8606773	195.4985568	2.326298664	1.97E-06	1.57E-05
ENSG00000115468	<i>EFHD1</i>	57.52303638	189.0684621	1.713930868	0.000245906	0.001264899
ENSG00000185946	<i>RNPC3</i>	51.30225638	174.9222528	1.76648799	0.00019128	0.001013052
ENSG00000079156	<i>OSBPL6</i>	39.63827699	117.0513752	1.558283371	0.001597982	0.006579071
ENSG00000164647	<i>STEAP1</i>	19.42060034	209.6447643	3.422564561	6.87E-11	1.07E-09
ENSG00000176273	<i>SLC35G1</i>	38.08307745	127.3395348	1.737260957	0.000397992	0.001944199
ENSG00000123607	<i>TTC21B</i>	73.85256557	226.3630083	1.613805821	0.000450984	0.002181205
ENSG00000128918	<i>ALDH1A2</i>	57.52303638	168.4921572	1.547794368	0.00108891	0.004736586
ENSG00000137875	<i>BCL2L10</i>	3.090401881	160.7760419	5.637567809	2.33E-16	6.42E-15
ENSG00000172935	<i>MRGPRF</i>	15.53254811	92.616986	2.564510289	2.60E-06	2.02E-05
ENSG00000102048	<i>ASB9</i>	16.31016037	291.9499564	4.149987798	1.25E-14	2.90E-13
ENSG00000259673	<i>IQCH-AS1</i>	66.85419855	173.6362337	1.374767852	0.003196281	0.012090026
ENSG00000165895	<i>ARHGAP42</i>	28.75186299	306.0961595	3.405695134	1.09E-11	1.89E-10
ENSG00000137941	<i>TTL7</i>	17.08777164	84.90085893	2.302661377	2.77E-05	0.000177121
ENSG00000130962	<i>PRRG1</i>	50.52465852	205.7867078	2.02277748	1.81E-05	0.000120006
ENSG00000104218	<i>CSPP1</i>	70.74218064	169.7781763	1.260982703	0.006831716	0.023440406
ENSG00000158301	<i>GPRASP2</i>	41.97107512	194.2125379	2.206082488	5.23E-06	3.88E-05
ENSG00000145348	<i>TBCK</i>	101.0684138	254.6554187	1.331768952	0.003046855	0.011560004
ENSG00000186260	<i>MKL2</i>	48.19186435	163.3480804	1.757759231	0.000222649	0.001155554
ENSG00000163002	<i>NUP35</i>	66.85419855	177.494291	1.406454841	0.002521841	0.009789217
ENSG00000144820	<i>GPR128</i>	1.534979634	348.5347671	7.700250997	5.53E-26	3.12E-24
ENSG00000198718	<i>FAM179B</i>	58.30063355	149.201868	1.353161502	0.003862998	0.014306721
ENSG00000147996	<i>CBWD5</i>	48.9694625	146.6298291	1.579060283	0.000984438	0.004326825
ENSG00000121207	<i>LRAT</i>	33.41747441	433.4119761	3.691347407	1.38E-13	2.92E-12
ENSG00000122008	<i>POLK</i>	72.29737318	225.0769895	1.636235725	0.000372517	0.001830548
ENSG00000145331	<i>TRMT10A</i>	25.64144922	199.3566135	2.951633583	5.32E-09	6.31E-08
ENSG00000119042	<i>SATB2</i>	45.85906927	126.0535149	1.455470188	0.002614377	0.010090113
ENSG00000111879	<i>FAM184A</i>	14.75493478	183.9243862	3.626934131	1.96E-11	3.30E-10
ENSG00000165478	<i>HEPACAM</i>	1.39E-17	480.9946517	11.95534056	3.47E-29	2.34E-27
ENSG00000085552	<i>IGSF9</i>	3.868086451	86.18688029	4.427742622	1.53E-10	2.24E-09
ENSG00000153291	<i>SLC25A27</i>	4.645755009	239.2231952	5.643765513	4.66E-19	1.59E-17
ENSG00000109762	<i>SNX25</i>	107.2891756	226.3630083	1.075873177	0.016078996	0.048830112
ENSG00000138678	<i>AGPAT9</i>	20.19820843	419.265775	4.365908018	1.45E-16	4.04E-15
ENSG00000157426	<i>AASDH</i>	52.85745186	133.7696335	1.336803311	0.005326906	0.018761549
ENSG00000162409	<i>PRKAA2</i>	40.41587651	135.0556532	1.736605433	0.000354063	0.001747815
ENSG00000246695	<i>RASSF8-AS1</i>	66.07660199	156.9179841	1.245639913	0.007284865	0.024678388
ENSG00000109956	<i>B3GAT1</i>	87.07169561	277.8037528	1.671978039	0.000229938	0.001192137
ENSG00000146521	<i>C6orf123</i>	11.64446802	351.1068038	4.897278925	2.34E-18	7.57E-17

ENSG00000165841	CYP2C19	38.08307745	146.6298291	1.940613881	7.32E-05	0.000428279
ENSG00000173611	SCAI	52.07985416	153.0599261	1.552341204	0.001046633	0.004574304
ENSG00000184956	MUC6	83.18371705	381.9712441	2.197032414	1.51E-06	1.22E-05
ENSG00000213071	LPAL2	4.645755009	236.6511578	5.628176597	6.11E-19	2.06E-17
ENSG00000081052	COL4A4	40.41587651	119.6234153	1.56168558	0.001335175	0.005682494
ENSG00000269386	RAB11B-AS1	42.7486742	249.5113443	2.54099446	1.15E-07	1.11E-06
ENSG00000162733	DDR2	80.07333372	254.6554187	1.667183623	0.000259502	0.001326326
ENSG00000131773	KHDRBS3	51.30225638	185.2104052	1.84889467	9.51E-05	0.000537625
ENSG00000079150	FKBP7	69.96458431	163.3480804	1.221227923	0.008508574	0.028201174
ENSG00000186998	EMID1	49.74706056	137.6276924	1.465050713	0.002354518	0.009345505
ENSG00000176055	MBLAC2	43.52627316	196.7845757	2.172734649	5.57E-06	4.09E-05
ENSG00000138036	DYNC2LI1	62.96621528	173.6362337	1.461021572	0.00177854	0.007239701
ENSG00000186377	CYP4X1	8.533969895	137.6276924	3.98883676	1.11E-11	1.91E-10
ENSG00000128802	GDF2	1.39E-17	398.6894823	11.6846455	2.70E-27	1.62E-25
ENSG00000101871	MID1	46.63666774	249.5113443	2.415803213	3.85E-07	3.44E-06
ENSG00000204583	LRCOL1	7.75633786	264.9435674	5.06875042	6.90E-18	2.15E-16
ENSG00000148357	HMCN2	10.08922402	171.0641955	4.06449904	1.87E-12	3.51E-11
ENSG00000184788	SATL1	27.97426007	149.201868	2.408818911	2.07E-06	1.65E-05
ENSG00000152284	TCF7L1	81.62852544	210.9307831	1.367817748	0.002929578	0.011147375
ENSG00000163738	MTHFD2L	60.63342469	200.6426324	1.723814029	0.000241245	0.001243757
ENSG00000149289	ZC3H12C	79.29573781	219.9329146	1.469841664	0.001287314	0.005497629
ENSG00000150893	FREM2	1.39E-17	135.0556532	10.12362204	4.67E-17	1.37E-15
ENSG00000165626	BEND7	61.41102161	181.3523481	1.559713658	0.000783127	0.003562991
ENSG00000145934	TENM2	47.4142661	343.3906936	2.852609359	2.45E-09	3.04E-08
ENSG00000105865	DUS4L	41.19347589	101.6191314	1.299166784	0.00833992	0.02776436
ENSG00000239911	PRKAG2-AS1	28.75186299	176.2082719	2.609330208	1.65E-07	1.57E-06
ENSG00000223956	RP4-710M16.2	0.757489584	225.0769895	7.968921373	9.21E-22	3.93E-20
ENSG00000169856	ONECUT1	37.30547743	177.494291	2.245693233	4.32E-06	3.24E-05
ENSG00000152217	SETBP1	100.2908185	230.2210644	1.197428101	0.007543497	0.025464298
ENSG00000047597	XK	5.423411881	27.0297426	2.28548408	0.00288962	0.011020638
ENSG00000187566	NHLRC1	32.63987315	142.7717707	2.123802457	1.64E-05	0.000109769
ENSG00000104332	SFRP1	26.4190532	185.2104052	2.802631794	2.96E-08	3.14E-07
ENSG00000108381	ASPA	20.97581587	277.8037528	3.71815012	1.25E-12	2.38E-11
ENSG00000164300	SERINC5	19.42060034	163.3480804	3.062757285	5.46E-09	6.45E-08
ENSG00000242732	RGAG4	76.18535388	250.7973629	1.71684739	0.000176781	0.000942897
ENSG00000150756	FAM173B	73.85256557	164.6340996	1.154663591	0.012886032	0.040287084
ENSG00000161896	IP6K3	6.201060061	60.46643496	3.255473577	4.89E-07	4.31E-06
ENSG00000154175	ABI3BP	77.74054591	250.7973629	1.687746843	0.000237331	0.001227139
ENSG00000180596	HIST1H2BC	17.86538201	56.60836376	1.655037447	0.003629461	0.013526804
ENSG00000089847	ANKRD24	82.40612126	186.4964241	1.176628583	0.010802704	0.034835687
ENSG00000171119	NRTN	14.75493478	68.18257328	2.196595161	0.000120421	0.000662026
ENSG00000162461	SLC25A34	26.4190532	276.5177343	3.380588141	2.53E-11	4.19E-10
ENSG00000156374	PCGF6	59.8558277	187.7824431	1.646874332	0.000452603	0.002188183
ENSG00000146122	DAAM2	45.08147069	180.0663291	1.994224206	3.33E-05	0.000209672
ENSG00000104643	MTMR9	69.18698793	159.4900227	1.20285707	0.009483301	0.031079567
ENSG00000175595	ERCC4	51.30225638	138.913712	1.434171529	0.002618028	0.010094801
ENSG00000157214	STEAP2	28.75186299	119.6234153	2.050925878	5.86E-05	0.000348312
ENSG00000185664	PMEL	17.86538201	113.1933148	2.653495533	9.72E-07	8.15E-06
ENSG00000185038	MROH2A	1.39E-17	194.2125379	10.64738726	2.50E-20	9.59E-19
ENSG00000183281	PLGLB1	15.53254811	298.3800488	4.251265613	3.56E-15	8.88E-14
ENSG00000180957	PITPNB	66.85419855	195.4985568	1.545767249	0.000877442	0.003908334
ENSG00000224837	GCSHP5	19.42060034	169.7781763	3.118426212	2.96E-09	3.63E-08
ENSG00000269837	RP11-15H20.5	55.96784183	181.3523481	1.693293363	0.000321737	0.001607715
ENSG00000148123	LPPR1	1.39E-17	113.1933148	9.86905794	1.57E-15	4.09E-14
ENSG00000272091	RP4-758J24.5	31.08466991	159.4900227	2.353577403	2.58E-06	2.01E-05
ENSG00000146950	SHROOM2	47.4142661	204.500689	2.105141964	9.90E-06	6.89E-05
ENSG00000105251	SHD	4.645755009	132.4836138	4.791695611	7.04E-14	1.53E-12
ENSG00000154309	DISP1	76.18535388	313.8122702	2.040114513	8.55E-06	6.02E-05
ENSG00000145945	FAM50B	111.1771513	248.2253257	1.15754062	0.009408684	0.030855368
ENSG00000087884	AAMDC	77.74054591	180.0663291	1.209973192	0.00856063	0.028358585
ENSG00000169570	DTWD2	45.08147069	144.0577902	1.672538618	0.000538655	0.00254385
ENSG00000078487	ZCWPW1	63.74381204	183.9243862	1.526352805	0.001124564	0.004877165
ENSG00000182150	ERCC6L2	52.07985416	150.4878874	1.527907668	0.001300295	0.00554544
ENSG00000230551	CTB-89H12.4	69.18698793	165.9201188	1.259845566	0.006305941	0.021811044
ENSG00000135541	AHI1	70.74218064	190.3544811	1.425930717	0.002084407	0.008354769
ENSG00000110723	EXPH5	9.31159843	357.5368956	5.241679141	1.57E-19	5.60E-18
ENSG00000171408	PDE7B	27.97426007	289.3779194	3.364051879	3.22E-11	5.25E-10
ENSG00000133800	LYVE1	26.4190532	343.3906936	3.692968162	4.04E-13	8.10E-12
ENSG00000180190	TDRP	76.96294991	237.9371765	1.626312546	0.000394028	0.001927109
ENSG00000182890	GLUD2	24.86384483	93.90300695	1.910500005	0.000274638	0.001397364
ENSG00000180592	SKIDA1	9.31159843	93.90300695	3.313934368	1.97E-08	2.15E-07

ENSG00000137968	SLC44A5	23.30863474	70.75461835	1.595287022	0.003780774	0.014029729
ENSG00000138639	ARHGAP24	59.07823066	194.2125379	1.714244405	0.00025933	0.001326265
ENSG00000137601	NEK1	50.52465852	172.3502146	1.767103281	0.000178248	0.000949092
ENSG00000107560	RAB11FIP2	64.52140874	181.3523481	1.488591828	0.001480631	0.006169501
ENSG00000065320	NTN1	10.8668471	234.0791205	4.411041973	3.90E-15	9.67E-14
ENSG00000157992	KRTCAP3	24.86384483	147.9158486	2.565486278	6.28E-07	5.42E-06
ENSG00000226015	CCT8P1	6.978701584	190.3544811	4.741507746	6.69E-15	1.61E-13
ENSG00000120156	TEK	69.18698793	190.3544811	1.457936517	0.001574633	0.006510982
ENSG00000114739	ACVR2B	55.19024445	159.4900227	1.52820438	0.001185234	0.005099358
ENSG00000182156	ENPP7	5.423411881	270.0876416	5.601601949	2.07E-19	7.27E-18
ENSG00000173175	ADCY5	97.95803254	212.2168019	1.113904821	0.01354958	0.042044295
ENSG00000173166	RAPH1	17.08777164	128.6255546	2.901424153	8.01E-08	7.97E-07
ENSG00000236155	RP11-231P20.2	1.534979634	201.9286512	6.913086678	9.43E-21	3.71E-19
ENSG00000175556	LONRF3	59.07823066	213.5028207	1.850797817	7.51E-05	0.000437836
ENSG00000260001	TGFBR3L	13.19970438	119.6234153	3.165817045	1.53E-08	1.69E-07
ENSG00000152977	ZIC1	0.757489584	38.60400605	5.428347569	4.11E-08	4.28E-07
ENSG00000250510	GPR162	45.85906927	115.7653551	1.332736587	0.006407112	0.02213018
ENSG00000206530	WDR52	31.86227166	137.6276924	2.105534688	2.65E-05	0.000170332
ENSG00000169291	SHE	59.8558277	227.649027	1.924492386	3.95E-05	0.000245263
ENSG00000155542	SETD9	59.8558277	185.2104052	1.626987695	0.000513389	0.002454489
ENSG00000186352	ANKRD37	68.40939152	198.0705946	1.531507101	0.000909926	0.00430697
ENSG00000185973	TMLHE	57.52303638	155.6319648	1.433320279	0.002583102	0.009984913
ENSG00000168679	SLC16A4	41.19347589	284.2338454	2.782184117	9.18E-09	1.05E-07
ENSG00000196782	MAML3	48.9694625	160.7760419	1.711849726	0.000345049	0.0017125
ENSG00000162989	KCNJ3	1.39E-17	42.46208706	8.456589381	2.10E-08	2.28E-07
ENSG00000121350	PYROXD1	27.19665681	132.4836138	2.277950566	7.77E-06	5.53E-05
ENSG00000143502	SUSD4	35.75027683	106.7632134	1.574057836	0.001747336	0.007118511
ENSG00000182263	FIGN	20.19820843	177.494291	3.126271983	2.48E-09	3.07E-08
ENSG00000172817	CYP7B1	24.08624001	225.0769895	3.216380652	3.96E-10	5.49E-09
ENSG00000145777	TSLP	16.31016037	137.6276924	3.065577308	1.39E-08	1.55E-07
ENSG00000109189	USP46	63.74381204	142.7717707	1.161171115	0.01327961	0.041330417
ENSG00000198944	SOWAHA	1.534979634	60.46643496	5.175078124	1.10E-09	1.43E-08
ENSG00000083535	PIBF1	59.07823066	145.3438097	1.296321077	0.005875206	0.020515347
ENSG00000019102	VSIG2	4.645755009	33.45989316	2.809533643	0.000186219	0.000987511
ENSG00000114120	SLC25A36	90.18207801	222.5049521	1.301318112	0.004026504	0.014819895
ENSG00000024752	CKMT2-AS1	41.19347589	97.76106944	1.243381375	0.010923125	0.035149439
ENSG00000174469	CNTNAP2	1.534979634	190.3544811	6.827971903	3.48E-20	1.32E-18
ENSG00000166922	SCG5	13.19970438	241.7952325	4.180509192	4.10E-14	9.14E-13
ENSG00000070371	CLTCL1	32.63987315	201.9286512	2.623648864	9.64E-08	9.48E-07
ENSG00000209082	MT-TL1	49.74706056	246.9393071	2.307984306	9.99E-07	8.35E-06
ENSG00000143028	SYPL2	6.978701584	232.7931018	5.031732942	1.03E-16	2.93E-15
ENSG00000266964	FXYP1	1.39E-17	111.9072946	9.85258755	1.87E-15	4.80E-14
ENSG00000186466	AQP7P1	6.978701584	190.3544811	4.741507746	6.69E-15	1.61E-13
ENSG00000154065	ANKRD29	48.19186435	122.1954553	1.339290305	0.00522641	0.018515167
ENSG00000256771	ZNF253	48.19186435	127.3395348	1.398733571	0.003525051	0.01316729
ENSG00000162595	DIRAS3	6.201060061	120.9094353	4.254029936	9.51E-12	1.67E-10
ENSG00000184925	LCN12	13.97732024	113.1933148	3.004438685	7.39E-08	7.38E-07
ENSG00000104154	SLC30A4	39.63827699	127.3395348	1.679724786	0.00065472	0.003035452
ENSG00000136842	TMOD1	17.86538201	203.2146701	3.497161009	3.22E-11	5.25E-10
ENSG00000112494	UNC93A	0.757489584	186.4964241	7.697779933	5.47E-20	2.03E-18
ENSG00000143067	ZNF697	45.85906927	126.0535149	1.455470188	0.002614377	0.010090113
ENSG00000267194	RP1-193H18.2	38.8606773	111.9072946	1.521982099	0.002201389	0.008778742
ENSG00000147124	ZNF41	40.41587651	101.6191314	1.326566206	0.00833992	0.02776436
ENSG00000205978	NYNRIN	41.97107512	164.6340996	1.967839365	4.86E-05	0.000293851
ENSG00000179476	C14orf28	48.9694625	141.4857511	1.527573297	0.00143949	0.006013199
ENSG00000269486	CTC-360G5.9	1.534979634	33.45989316	4.323257978	2.59E-06	2.01E-05
ENSG00000165682	CLC1B	6.978701584	235.3651392	5.047578691	8.66E-17	2.47E-15
ENSG00000260552	RP11-49I11.1	39.63827699	101.6191314	1.354496084	0.006842984	0.023475827
ENSG00000065665	SEC61A2	52.07985416	140.1997316	1.425812456	0.002696242	0.01036696
ENSG00000136895	GARNL3	22.53102899	129.9115743	2.519667467	1.04E-06	8.69E-06
ENSG00000225830	ERCC6	48.19186435	131.1975941	1.441761954	0.002575691	0.009959364
ENSG00000106526	ACTR3C	32.63987315	187.7824431	2.518917853	3.27E-07	2.96E-06
ENSG00000065621	GSTO2	7.75633786	99.04709015	3.650140783	3.05E-09	3.74E-08
ENSG00000204611	ZNF616	38.8606773	93.90300695	1.269162396	0.010719151	0.034616811
ENSG00000100068	LRP5L	71.51977693	168.4921572	1.234278925	0.00817127	0.027261331
ENSG00000172878	METAP1D	45.85906927	138.913712	1.595519556	0.000995816	0.00437606
ENSG00000254607	RP11-115C10.1	1.39E-17	198.0705946	10.67575154	1.61E-20	6.24E-19
ENSG00000251424	RP11-468N14.3	1.39E-17	199.3566135	10.68508371	1.45E-20	5.63E-19
ENSG00000108448	TRIM16L	48.9694625	156.9179841	1.676829494	0.000464398	0.002242153
ENSG00000151304	SRFBP1	41.97107512	96.47504867	1.197407625	0.015683452	0.047788672
ENSG00000197763	TXNRD3	34.19507543	110.6212744	1.689135105	0.000700431	0.003220944

ENSG00000101204	CHRNA4	1.39E-17	173.6362337	10.48590472	2.83E-19	9.82E-18
ENSG00000132970	WASF3	16.31016037	178.78031	3.442759213	1.55E-10	2.26E-09
ENSG00000150054	MPP7	19.42060034	54.03631542	1.468552529	0.010235822	0.03314806
ENSG00000119943	PYROXD2	62.96621528	163.3480804	1.372954031	0.003316575	0.012484246
ENSG00000123552	USP45	45.85906927	122.1954553	1.410659703	0.003618164	0.013488747
ENSG00000089682	RBM41	38.08307745	127.3395348	1.737260957	0.000397992	0.001944199
ENSG00000170917	NUDT6	27.19665681	147.9158486	2.436802524	1.51E-06	1.23E-05
ENSG00000249790	RP11-20D14.6	3.868086451	25.74371105	2.688333859	0.000589	0.002758025
ENSG00000158296	SLC13A3	11.64446802	249.5113443	4.404637265	3.22E-15	8.09E-14
ENSG00000135547	HEY2	15.53254811	149.201868	3.25185106	1.67E-09	2.12E-08
ENSG00000162924	REL	34.97267623	120.9094353	1.785016494	0.000344079	0.001708708
ENSG00000230461	PROX1-AS1	30.30706789	182.6383671	2.58537174	2.26E-07	2.10E-06
ENSG00000165655	ZNF503	76.18535388	169.7781763	1.154243635	0.011637827	0.037261135
ENSG00000136098	NEK3	68.40939152	150.4878874	1.135364166	0.016030979	0.04874006
ENSG00000144649	FAM198A	4.645755009	55.32233968	3.533298117	5.99E-07	5.19E-06
ENSG00000196876	SCN8A	5.423411881	135.0556532	4.602248686	2.84E-13	5.82E-12
ENSG00000263400	CTC-297N7.5	2.312696499	172.3502146	6.134920526	5.75E-18	1.81E-16
ENSG00000258429	PDF	41.97107512	114.479335	1.444037648	0.003216002	0.012155612
ENSG00000090534	THPO	48.9694625	167.206138	1.768391468	0.000221861	0.001152354
ENSG00000241388	HNF1A-AS1	20.97581587	83.6148375	1.987090724	0.000212723	0.001111387
ENSG00000164306	PRIMPOL	46.63666774	119.6234153	1.355809422	0.005548996	0.019488526
ENSG00000235109	ZSCAN31	24.86384483	111.9072946	2.163319709	3.17E-05	0.000200692
ENSG00000118965	WDR35	42.7486742	129.9115743	1.599937702	0.001096601	0.004768371
ENSG00000120279	MYCT1	48.9694625	150.4878874	1.616504445	0.000727855	0.003334715
ENSG00000151631	AKR1C6P	1.39E-17	154.3459455	10.31610546	3.20E-18	1.02E-16
ENSG00000188931	C1orf192	29.52946559	155.6319648	2.391977495	1.74E-06	1.39E-05
ENSG00000214900	C14orf182	32.63987315	97.76106944	1.577877376	0.002040217	0.008193503
ENSG00000230623	RP11-469A15.2	18.64299156	123.4814752	2.717901808	2.74E-07	2.51E-06
ENSG00000197417	SHPK	48.9694625	169.7781763	1.790401946	0.000178227	0.000949092
ENSG00000232637	WI2-3658N16.1	34.19507543	88.75892278	1.371783679	0.006020558	0.020972804
ENSG00000174326	SLC16A11	19.42060034	104.1911725	2.41452975	5.47E-06	4.03E-05
ENSG00000138079	SLC3A1	5.423411881	399.9755006	6.167917105	3.63E-23	1.68E-21
ENSG00000128536	CDHR3	13.97732024	140.1997316	3.312894136	2.26E-09	2.81E-08
ENSG00000186017	ZNF566	49.74706056	113.1933148	1.183289316	0.014689257	0.045107669
ENSG00000244503	RP11-278L15.6	6.978701584	27.0297426	1.929911063	0.006127713	0.02125374
ENSG000000066185	ZMYND12	24.86384483	133.7696335	2.420560835	2.72E-06	2.11E-05
ENSG00000072201	LNX1	13.97732024	97.76106944	2.793178149	6.35E-07	5.48E-06
ENSG00000272005	RP11-91J19.4	30.30706789	99.04709015	1.703218329	0.000711242	0.003264016
ENSG00000235477	RP11-122G18.5	42.7486742	133.7696335	1.642127158	0.000783401	0.003563586
ENSG00000235501	RP4-639F20.1	32.63987315	169.7781763	2.373586075	1.40E-06	1.14E-05
ENSG00000168077	SCARA3	70.74218064	204.500689	1.529296816	0.000955048	0.004208815
ENSG00000257337	RP11-983P16.4	40.41587651	186.4964241	2.201912221	5.34E-06	3.95E-05
ENSG000000222009	BTBD19	50.52465852	126.0535149	1.316096198	0.006430266	0.022200899
ENSG00000081386	ZNF510	61.41102161	137.6276924	1.161935333	0.015000965	0.045962647
ENSG00000206535	LNP1	34.19507543	117.0513752	1.770578253	0.000384783	0.001884768
ENSG00000107890	ANKRD26	22.53102899	97.76106944	2.109825651	5.02E-05	0.000302407
ENSG00000272341	RP1-151F17.2	17.08777164	138.913712	3.012354885	2.41E-08	2.59E-07
ENSG00000120519	SLC10A7	37.30547743	147.9158486	1.982855645	5.04E-05	0.000303341
ENSG00000213373	LINC00671	0.757489584	261.0855117	8.182939114	3.55E-23	1.65E-21
ENSG00000259820	AC083843.1	19.42060034	151.7739068	2.956797204	1.95E-08	2.13E-07
ENSG00000235609	AF127936.7	15.53254811	163.3480804	3.382453352	3.50E-10	4.90E-09
ENSG00000165113	GKAP1	41.97107512	132.4836138	1.65459739	0.000679204	0.003130865
ENSG00000144648	ACKR2	6.978701584	127.3395348	4.161865145	1.29E-11	2.21E-10
ENSG00000149557	FEZ1	65.29900539	162.0620612	1.309189252	0.004693865	0.016822786
ENSG00000168913	ENHO	3.090401881	81.0427944	4.650132239	6.99E-11	1.08E-09
ENSG00000140876	NUDT7	7.75633786	186.4964241	4.562436375	1.02E-14	2.41E-13
ENSG00000167384	ZNF180	31.86227166	88.75892278	1.473290878	0.004126239	0.015119355
ENSG00000017621	MAGIX	35.75027683	96.47504867	1.428011545	0.00468342	0.016795038
ENSG00000096872	IFT74	62.18861847	142.7717707	1.19672663	0.010221378	0.033122861
ENSG00000079689	SCGN	3.868086451	57.89438766	3.854496483	7.11E-08	7.13E-07
ENSG00000228709	AP001065.15	0.757489584	57.89438766	6.011803941	1.30E-10	1.93E-09
ENSG00000189014	FAM35DP	1.39E-17	77.18472911	9.317236682	1.52E-12	2.87E-11
ENSG00000204613	TRIM10	20.97581587	55.32233968	1.392055467	0.012147795	0.038625234
ENSG00000255468	RP11-867G23.8	10.8668471	82.32881599	2.904622762	9.01E-07	7.59E-06
ENSG00000241635	UGT1A8	9.31159843	231.5070831	4.614857213	1.61E-15	4.18E-14
ENSG00000115423	DNAH6	1.534979634	137.6276924	6.360337123	2.59E-17	7.78E-16
ENSG00000240602	RP11-64D22.2	9.31159843	136.3416728	3.851451299	3.90E-11	6.30E-10
ENSG00000197121	PGAP1	18.64299156	124.7674951	2.732837569	2.14E-07	2.00E-06
ENSG00000162391	FAM151A	1.39E-17	52.75029095	8.768945747	6.95E-10	9.35E-09
ENSG00000164291	ARSK	45.85906927	136.3416728	1.568576231	0.001168291	0.005049185
ENSG00000231770	TMEM44-AS1	47.4142661	110.6212744	1.2192487	0.013505876	0.041913917

ENSG00000005108	THSD7A	28.75186299	90.04494392	1.641529679	0.001457271	0.006082364
ENSG00000197056	ZMYM1	38.08307745	88.75892278	1.217024968	0.014133375	0.043681301
ENSG00000222011	FAM185A	38.8606773	122.1954553	1.648762799	0.000804773	0.003650114
ENSG00000188001	TPRG1	35.75027683	129.9115743	1.85693837	0.000193418	0.001018857
ENSG00000213971	RP11-15H20.6	27.19665681	119.6234153	2.130750592	2.82E-05	0.000180347
ENSG00000197044	ZNF441	20.97581587	87.47290157	2.052093639	0.000122726	0.000673812
ENSG00000139352	ASCL1	4.645755009	447.5581771	6.547210187	4.19E-25	2.22E-23
ENSG00000205683	DPF3	37.30547743	96.47504867	1.366813921	0.00724203	0.024554698
ENSG00000163071	SPATA18	45.08147069	311.2402333	2.783395481	7.22E-09	8.37E-08
ENSG00000185332	TMEM105	3.868086451	54.03631542	3.755176067	1.95E-07	1.83E-06
ENSG00000103226	NOMO3	44.30387198	113.1933148	1.349969116	0.005217114	0.018492778
ENSG00000171714	ANO5	14.75493478	131.1975941	3.139869855	6.87E-09	7.99E-08
ENSG00000234906	APOC2	3.090401881	101.6191314	4.97619674	1.51E-12	2.85E-11
ENSG00000196911	KPNA5	48.19186435	110.6212744	1.195849008	0.013505876	0.041913917
ENSG00000036672	USP2	11.64446802	146.6298291	3.638105727	8.31E-11	1.28E-09
ENSG00000144642	RBMS3	53.63504947	180.0663291	1.744297023	0.000249746	0.001281206
ENSG00000140835	CHST4	79.29573781	210.9307831	1.409575058	0.002035766	0.00817695
ENSG00000007908	SELE	13.19970438	92.616986	2.79700897	6.73E-07	5.77E-06
ENSG00000099974	DDTL	35.75027683	295.8080118	3.043462735	4.97E-10	6.80E-09
ENSG00000166004	KIAA1731	23.30863474	129.9115743	2.471014862	1.69E-06	1.36E-05
ENSG00000164169	PRMT10	23.30863474	123.4814752	2.397835896	3.75E-06	2.84E-05
ENSG00000204186	ZDBF2	44.30387198	144.0577902	1.697561795	0.000430434	0.002090355
ENSG00000196208	GREB1	10.8668471	105.477193	3.261709235	2.18E-08	2.36E-07
ENSG00000058404	CAMK2B	4.645755009	144.0577902	4.912444069	1.52E-14	3.50E-13
ENSG00000101955	SRPX	20.19820843	232.7931018	3.517359589	1.92E-11	3.24E-10
ENSG00000225765	AC068535.3	1.39E-17	77.18472911	9.317236682	1.52E-12	2.87E-11
ENSG00000239887	C1orf226	20.19820843	162.0620612	2.995121175	1.11E-08	1.25E-07
ENSG00000113805	CNTN3	1.39E-17	110.6212744	9.835926953	2.22E-15	5.69E-14
ENSG000000091622	PITPNM3	41.19347589	119.6234153	1.534286157	0.001672817	0.006844095
ENSG00000255277	ABCC6P2	13.19970438	78.47075096	2.558161206	6.53E-06	4.73E-05
ENSG00000144395	CCDC150	10.8668471	142.7717707	3.698140516	1.36E-10	2.01E-09
ENSG00000184227	ACOT1	17.08777164	117.0513752	2.765496883	3.20E-07	2.90E-06
ENSG00000168116	KIAA1586	41.97107512	99.04709015	1.235328466	0.012036012	0.038323734
ENSG00000204147	ASAH2B	17.86538201	104.1911725	2.534047234	3.19E-06	2.46E-05
ENSG00000183666	GUSBP1	66.85419855	150.4878874	1.168471737	0.012612062	0.039847026
ENSG00000108830	RND2	10.08422402	99.04709015	3.276745593	2.26E-08	2.44E-07
ENSG00000042317	SPATA7	33.41747441	87.47290157	1.383799478	0.007412425	0.025072921
ENSG00000170962	PDGFD	62.96621528	155.6319648	1.303185606	0.005478885	0.019253173
ENSG000000017373	SRCIN1	23.30863474	100.3331108	2.098601955	5.26E-05	0.000315836
ENSG00000151320	AKAP6	10.8668471	78.47075096	2.835464379	1.82E-06	1.46E-05
ENSG00000256223	ZNF10	31.86227166	96.47504867	1.593427746	0.001741377	0.007096561
ENSG00000124279	FASTKD3	47.4142661	109.3352541	1.202393453	0.014618718	0.044924362
ENSG00000198908	BHLHB9	11.64446802	95.18041139	2.330537464	0.000104403	0.000586561
ENSG00000165521	EML5	22.53102899	120.9094353	2.416144943	2.95E-06	2.28E-05
ENSG00000146021	KLHL3	48.19186435	196.7845757	2.026280658	2.07E-05	0.000134923
ENSG00000245750	RP11-279F6.1	1.534979634	101.6191314	5.923100599	9.32E-15	2.21E-13
ENSG00000215915	ATAD3C	26.4190532	131.1975941	2.305520449	5.75E-06	4.21E-05
ENSG00000141449	GREB1L	2.312696499	36.03195036	3.880018036	7.63E-06	5.44E-05
ENSG00000154330	PGM5	57.52303638	162.0620612	1.491692429	0.001619818	0.006650245
ENSG00000215386	LINC00478	14.75493478	118.3373953	2.991151156	7.63E-08	7.61E-07
ENSG00000072657	TRHDE	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000204923	FBXO48	23.30863474	95.18902784	2.022747168	0.000112314	0.000626895
ENSG00000097096	SYDE2	12.42208703	108.0492338	3.10577629	3.23E-08	3.42E-07
ENSG00000196268	ZNF493	38.08307745	90.04494392	1.237755429	0.012845498	0.040175519
ENSG00000222033	LINC01124	18.64299156	64.32450474	1.778096069	0.001512582	0.006285775
ENSG00000164398	ACSL6	18.64299156	231.5070831	3.624132245	5.35E-12	9.56E-11
ENSG00000123612	ACVR1C	11.64446802	172.3502146	3.871127105	4.15E-12	7.49E-11
ENSG00000237125	HAND2-AS1	63.74381204	195.4985568	1.614352744	0.000545609	0.002573754
ENSG00000198707	CEP290	34.97267623	108.0492338	1.622917003	0.00111534	0.004841384
ENSG00000165630	PRPF18	33.41747441	90.04494392	1.425562629	0.005426586	0.019085579
ENSG00000205571	SMN2	33.41747441	95.18902784	1.505628168	0.003233442	0.012206441
ENSG00000197016	ZNF470	20.19820843	113.1933148	2.477738216	2.88E-06	2.23E-05
ENSG00000182983	ZNF662	17.08777164	88.75892278	2.36670231	1.53E-05	0.00010247
ENSG00000164035	EMCN	38.8606773	113.1933148	1.538452489	0.001830875	0.007438115
ENSG00000186567	CEACAM19	37.30547743	118.3373953	1.661222726	0.000708766	0.003254455
ENSG00000213240	NOTCH2NL	33.41747441	86.18688029	1.362455616	0.008225538	0.027420298
ENSG00000137872	SEMA6D	32.63987315	176.2082719	2.427186488	8.30E-07	7.02E-06
ENSG00000169122	FAM110B	20.19820843	124.7674951	2.618076292	6.65E-07	5.71E-06
ENSG00000146414	SHPRH	7.75633786	133.7696335	4.083336222	5.57E-12	9.94E-11
ENSG00000171451	DSEL	36.52787722	91.33096499	1.318118651	0.009522412	0.031195406
ENSG00000063127	SLC6A16	34.19507543	140.1997316	2.030721543	4.20E-05	0.000259186

ENSG00000234502	<i>FYTTD1P1</i>	1.39E-17	167.206138	10.43149563	5.94E-19	2.01E-17
ENSG00000164188	<i>RANBP3L</i>	1.39E-17	207.0727266	10.73984353	6.20E-21	2.48E-19
ENSG00000267391	<i>RP11-1151B14.3</i>	3.090401881	141.4857511	5.45329138	3.28E-15	8.21E-14
ENSG00000235169	<i>SMIM1</i>	27.97426007	127.3395348	2.180395544	1.94E-05	0.000128017
ENSG00000185621	<i>LMLN</i>	50.52465852	129.9115743	1.359556683	0.00476158	0.017045814
ENSG00000154263	<i>ABCA10</i>	33.41747441	159.4900227	2.249631311	5.30E-06	3.93E-05
ENSG00000140470	<i>ADAMTS17</i>	9.31159843	84.90085893	3.168701116	9.30E-08	9.17E-07
ENSG00000128965	<i>CHAC1</i>	52.07985416	174.9222528	1.744843629	0.00023545	0.001218935
ENSG00000198932	<i>GPRASP1</i>	45.85906927	133.7696335	1.541120129	0.001485929	0.006188466
ENSG00000073756	<i>PTGS2</i>	9.31159843	110.6212744	3.550093475	1.54E-09	1.97E-08
ENSG00000162687	<i>KCNT2</i>	6.978701584	149.201868	4.390288512	7.66E-13	1.50E-11
ENSG00000170647	<i>TMEM133</i>	44.30387198	123.4814752	1.475371431	0.002245371	0.008932249
ENSG00000258604	<i>AL161668.5</i>	1.39E-17	178.78031	10.52800124	1.55E-19	5.54E-18
ENSG00000225177	<i>RP11-390P2.4</i>	16.31016037	51.46426629	1.648162485	0.005639186	0.019755035
ENSG00000156413	<i>FUT6</i>	14.75493478	140.1997316	3.235543346	2.26E-09	2.81E-08
ENSG00000272335	<i>RP11-53O19.3</i>	44.30387198	118.3373953	1.414032376	0.003418953	0.012824945
ENSG00000205362	<i>MT1A</i>	1.39E-17	200.6426324	10.69435591	1.30E-20	5.08E-19
ENSG00000260244	<i>RP11-588K22.2</i>	63.74381204	154.3459455	1.273554091	0.006698565	0.023021686
ENSG00000226306	<i>NPY6R</i>	1.39E-17	33.45989316	8.113740193	3.48E-07	3.13E-06
ENSG00000173406	<i>DAB1</i>	1.39E-17	93.90300695	9.599767846	5.19E-14	1.14E-12
ENSG00000099954	<i>CECR2</i>	1.534979634	167.206138	6.641013411	5.24E-19	1.78E-17
ENSG00000238102	<i>RP11-19D2.1</i>	1.39E-17	51.46426629	8.733404515	1.25E-09	1.61E-08
ENSG00000241360	<i>PDXP</i>	16.31016037	81.0427944	2.302276283	2.96E-05	0.000188939
ENSG00000259203	<i>RP11-209K10.2</i>	22.53102899	59.18041139	1.386624423	0.012528859	0.039735203
ENSG00000126016	<i>AMOT</i>	22.53102899	109.3352541	2.271099952	1.25E-05	8.59E-05
ENSG00000176124	<i>DLEU1</i>	34.97267623	99.04709015	1.497533033	0.002743804	0.01052589
ENSG00000197557	<i>TTC30A</i>	24.86384483	97.76106944	1.968529563	0.000168126	0.000899046
ENSG00000178297	<i>TMPRSS9</i>	7.75633786	34.74592196	2.141502611	0.001436097	0.006003845
ENSG00000197863	<i>ZNF790</i>	45.85906927	115.7653551	1.332736587	0.006407112	0.02213018
ENSG00000185267	<i>CDNF</i>	10.8668471	153.0599261	3.798460169	4.03E-11	6.49E-10
ENSG00000272430	<i>RP11-38L15.8</i>	3.090401881	34.74592196	3.43060899	1.06E-05	7.33E-05
ENSG00000183748	<i>MRC1L1</i>	16.31016037	52.75029095	1.683703717	0.004015113	0.014784539
ENSG00000175707	<i>C1orf172</i>	34.19507543	82.32881599	1.263412884	0.012477797	0.039593368
ENSG00000256967	<i>RP11-273B20.1</i>	14.75493478	75.89870716	2.351057422	3.75E-05	0.000233823
ENSG00000135537	<i>LACE1</i>	27.97426007	87.47290157	1.639126866	0.001534991	0.006364004
ENSG00000170743	<i>SYT9</i>	1.39E-17	176.2082719	10.50710652	1.97E-19	6.96E-18
ENSG00000271992	<i>RP11-42O15.3</i>	3.090401881	200.6426324	5.956969834	2.66E-18	8.54E-17
ENSG00000234076	<i>TPRG1-AS1</i>	0.757489584	60.46643496	6.074411443	7.60E-11	1.17E-09
ENSG00000267675	<i>RP11-1151B14.2</i>	3.868086451	100.3331108	4.64676996	1.14E-11	1.97E-10
ENSG00000132854	<i>KANK4</i>	1.39E-17	144.0577902	10.21665062	1.27E-17	3.88E-16
ENSG00000169418	<i>NPR1</i>	31.86227166	104.1911725	1.704324992	0.000744056	0.003401418
ENSG00000179636	<i>TPPP2</i>	1.39E-17	158.2040034	10.35170177	1.88E-18	6.16E-17
ENSG00000166148	<i>AVPR1A</i>	4.645755009	97.76106944	4.353590855	9.54E-11	1.45E-09
ENSG00000155008	<i>APOOL</i>	15.53254811	70.75461835	2.176527557	0.000146896	0.000795966
ENSG00000188529	<i>SRSF10</i>	13.97732024	120.9094353	3.099497442	2.50E-08	2.69E-07
ENSG00000073150	<i>PANX2</i>	6.201060061	252.0833815	5.313399074	4.60E-18	1.46E-16
ENSG00000189337	<i>KAZN</i>	44.30387198	132.4836138	1.576813336	0.001060734	0.00463186
ENSG00000132164	<i>SLC6A11</i>	3.868086451	276.5177343	6.108451238	2.08E-20	8.02E-19
ENSG00000217648	<i>RP1-95L4.4</i>	19.42060034	95.18902784	2.284291635	1.85E-05	0.000122431
ENSG00000138735	<i>PDE5A</i>	40.41587651	120.9094353	1.577100089	0.001220719	0.005235717
ENSG00000164197	<i>RNF180</i>	26.4190532	114.479335	2.109022968	3.34E-05	0.000210616
ENSG00000177694	<i>NAALADL2</i>	7.75633786	78.47075096	3.314553895	1.26E-07	1.21E-06
ENSG00000204335	<i>SP5</i>	20.97581587	73.32666296	1.797905926	0.000871067	0.003884867
ENSG00000084453	<i>SLCO1A2</i>	0.757489584	141.4857511	7.299528559	1.68E-17	5.12E-16
ENSG00000168661	<i>ZNF30</i>	14.75493478	54.03631542	1.861662376	0.001400255	0.005929017
ENSG00000116668	<i>SWT1</i>	34.19507543	96.47504867	1.491920547	0.002916468	0.011105415
ENSG00000238097	<i>RP11-513G11.3</i>	1.39E-17	128.6255546	10.05329737	1.16E-16	3.28E-15
ENSG00000273151	<i>RP11-449P15.2</i>	25.64144922	167.206138	2.698045497	9.63E-08	9.47E-07
ENSG00000197893	<i>NRAP</i>	6.978701584	102.905152	3.85476231	5.90E-10	7.99E-09
ENSG00000245017	<i>RP11-181C3.1</i>	9.31159843	180.0663291	4.252502729	2.34E-13	4.85E-12
ENSG00000128573	<i>FOXP2</i>	10.08922402	114.479335	3.485454775	2.29E-09	2.85E-08
ENSG00000273259	<i>RP11-986E7.7</i>	7.75633786	48.89221631	2.633089873	5.82E-05	0.000346144
ENSG00000255284	<i>AP006621.5</i>	14.75493478	56.60836376	1.928629809	0.000977512	0.004298667
ENSG00000243989	<i>ACY1</i>	25.64144922	86.18688029	1.742748847	0.000922377	0.0040764
ENSG00000197603	<i>C5orf42</i>	43.52627316	113.1933148	1.375433986	0.005217114	0.018492778
ENSG00000226124	<i>FTCDNL1</i>	26.4190532	92.616986	1.803574663	0.000442375	0.00214374
ENSG00000240291	<i>RP11-499P20.2</i>	11.64446802	120.9094353	3.360057984	2.47E-09	3.06E-08
ENSG00000146411	<i>SLC2A12</i>	4.645755009	180.0663291	5.234129658	1.76E-16	4.90E-15
ENSG00000143869	<i>GDF7</i>	1.534979634	191.6405	6.837680899	3.11E-20	1.18E-18
ENSG00000230306	<i>BANF1P2</i>	0.757489584	84.90085893	6.5633857	2.65E-13	5.46E-12
ENSG00000078018	<i>MAP2</i>	47.4142661	108.0492338	1.185338953	0.015822937	0.048172355

ENSG00000170214	ADRA1B	9.31159843	144.0577902	3.93081714	1.58E-11	2.68E-10
ENSG00000164309	CMYA5	14.75493478	158.2040034	3.409731725	2.78E-10	3.95E-09
ENSG00000081051	AFP	1.39E-17	158.2040034	10.35170177	1.88E-18	6.16E-17
ENSG00000146374	RSPO3	23.30863474	178.78031	2.931376884	1.24E-08	1.39E-07
ENSG00000204790	CBWD6	29.52946559	90.04494392	1.603214732	0.001942548	0.007846908
ENSG00000213901	SLC23A3	13.97732024	127.3395348	3.174192261	1.14E-08	1.29E-07
ENSG00000143199	ADCY10	0.757489584	132.4836138	7.204753265	6.31E-17	1.82E-15
ENSG00000235200	RP4-763G1.2	1.39E-17	252.0833815	11.02348583	8.41E-23	3.79E-21
ENSG00000135315	KIAA1009	16.31016037	83.6148375	2.347297893	1.86E-05	0.000122957
ENSG00000118094	TREH	0.757489584	185.2104052	7.687802349	6.13E-20	2.27E-18
ENSG00000198780	FAM169A	20.97581587	205.7867078	3.285410818	3.45E-10	4.84E-09
ENSG00000213430	HSPD1P1	19.42060034	100.3331108	2.360146422	9.35E-06	6.53E-05
ENSG00000232561	GTF2IP1	25.64144922	114.479335	2.15189229	3.34E-05	0.000210616
ENSG00000271359	RP11-84C13.1	13.19970438	133.7696335	3.326943533	2.43E-09	3.02E-08
ENSG00000189320	FAM180A	16.31016037	183.9243862	3.483662146	9.40E-11	1.43E-09
ENSG00000006638	TBXA2R	38.08077745	163.3480804	2.096286617	1.87E-05	0.000123516
ENSG00000152760	TCTEX1D1	3.090401881	156.9179841	5.602547578	3.86E-16	1.05E-14
ENSG00000001630	CYP51A1	11.64446802	42.46208706	1.852530668	0.0032271	0.01218955
ENSG00000041515	MYO16	52.85745186	132.4836138	1.322876796	0.005728899	0.020043889
ENSG00000130518	KIAA1683	29.52946559	88.75892278	1.582484272	0.002434526	0.009484447
ENSG00000148225	WDR31	27.97426007	68.18257328	1.280149233	0.014956827	0.045844363
ENSG000000231574	RP11-91K9.1	8.533969895	60.46643496	2.80357776	9.46E-06	6.60E-05
ENSG00000226085	UQCRRF51P1	29.52946559	81.0427944	1.451427057	0.005394739	0.018987006
ENSG00000154914	USP43	35.75027683	162.0620612	2.17574005	1.10E-05	7.61E-05
ENSG00000225489	RP11-390F4.3	17.86538201	79.75677272	2.148907034	9.77E-05	0.00055195
ENSG00000254231	CTD-2284J15.1	14.75493478	93.90300695	2.657797802	2.23E-06	1.76E-05
ENSG00000001626	CFTR	38.08307745	180.0663291	2.236785649	4.65E-06	3.48E-05
ENSG00000145723	GIN1	42.7486742	99.04709015	1.208931718	0.014408269	0.044442484
ENSG00000129535	NRL	22.53102899	69.46859588	1.617513096	0.003132914	0.011864784
ENSG00000266010	GATA6-AS1	20.19820843	84.90085893	2.063214871	0.00011993	0.000662026
ENSG00000144218	AFF3	37.30547743	178.78031	2.256102769	3.68E-06	2.79E-05
ENSG00000157502	MUM1L1	3.090401881	52.75029095	4.031559673	5.07E-08	5.23E-07
ENSG00000237310	GS1-124K5.4	27.19665681	84.90085893	1.636583	0.001620943	0.006651567
ENSG00000187187	ZNF546	27.97426007	87.47290157	1.639126866	0.001534991	0.006364004
ENSG00000224093	RP5-1033H22.2	28.75186299	83.6148375	1.534763614	0.003276705	0.012352876
ENSG000000228923	AP000355.2	1.39E-17	84.90085893	9.454534595	3.28E-13	6.67E-12
ENSG00000169894	MUC3A	13.97732024	205.7867078	3.866240762	2.33E-12	4.34E-11
ENSG00000263535	AK4P1	9.31159843	174.9222528	4.210711086	4.03E-13	8.09E-12
ENSG00000172782	FADS6	1.39E-17	249.5113443	11.00869598	1.10E-22	4.91E-21
ENSG00000264569	RP13-650J16.1	2.312696499	93.90300695	5.259502554	7.30E-13	1.43E-11
ENSG00000150625	GPM6A	3.090401881	132.4836138	5.358516087	1.03E-14	2.41E-13
ENSG00000246859	STARD4-AS1	11.64446802	82.32881599	2.806146019	1.94E-06	1.55E-05
ENSG00000154269	ENPP3	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000198796	ALPK2	29.52946559	128.6255546	2.117206115	2.28E-05	0.000148196
ENSG00000168309	FAM107A	33.41747441	96.47504867	1.524969036	0.002916468	0.011105415
ENSG00000129317	PUS7L	24.86384483	61.75245837	1.306606023	0.014653994	0.045004945
ENSG00000266680	RP5-1148A21.3	13.97732024	42.46208706	1.591970127	0.008356463	0.02780826
ENSG00000121270	ABCC11	2.312696499	70.75461835	4.851646088	9.47E-11	1.44E-09
ENSG00000139865	TTC6	13.19970438	75.89870716	2.510142324	1.09E-05	7.52E-05
ENSG00000138722	MMRN1	10.08922402	153.0599261	3.904154496	1.49E-11	2.56E-10
ENSG00000148795	CYP17A1	5.423411881	136.3416728	4.615911423	2.47E-13	5.10E-12
ENSG00000183287	CCBE1	5.423411881	164.6340996	4.887770781	5.77E-15	1.40E-13
ENSG00000260704	LINC00543	22.53102899	78.47075096	1.793074595	0.00091912	0.004065619
ENSG00000152402	GUCY1A2	34.97267623	101.6191314	1.534482611	0.002243768	0.008927303
ENSG00000260404	RP11-384K6.6	30.30706789	75.89870716	1.319612559	0.012145152	0.038625234
ENSG000000062524	LTK	41.97107512	117.0513752	1.476065331	0.002474866	0.009623899
ENSG00000197050	ZNF420	17.08777164	64.32450474	1.902781298	0.000640504	0.002974539
ENSG00000213533	TMEM110	20.97581587	82.32881599	1.964755533	0.000244393	0.001257375
ENSG00000146166	LGSN	1.39E-17	149.201868	10.26723488	6.30E-18	1.97E-16
ENSG00000114547	ROPN1B	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000166262	FAM227B	17.86538201	66.89655057	1.895571287	0.000726766	0.003330341
ENSG00000198829	SUCNR1	47.4142661	135.0556532	1.506943788	0.001549286	0.006417918
ENSG00000142556	ZNF614	44.30387198	110.6212744	1.316838129	0.006728098	0.023119988
ENSG00000246090	RP11-696N14.1	3.868086451	72.04064071	4.169406185	2.74E-09	3.39E-08
ENSG00000188818	ZDHHC11	14.75493478	214.7888395	3.850630587	1.02E-12	1.98E-11
ENSG00000188206	HNRNPU-AS1	11.64446802	86.18688029	2.872140262	9.92E-07	8.30E-06
ENSG00000151338	MIPOL1	11.64446802	48.89221631	2.055523613	0.000759269	0.003463958
ENSG00000197776	KLHDC1	31.86227166	82.32881599	1.364920083	0.007925241	0.026586836
ENSG00000153993	SEMA3D	10.8668471	54.03631542	2.298050451	0.000180546	0.000960915
ENSG00000167608	TMC4	19.42060034	88.75892278	2.183495636	4.28E-05	0.000263235
ENSG00000262445	CTD-2545H1.2	1.39E-17	45.03413956	8.541243594	7.89E-09	9.12E-08

ENSG00000122483	CCDC18	20.97581587	55.32233968	1.392055467	0.012147795	0.038625234
ENSG00000176428	VPS37D	16.31016037	61.75245837	1.910631835	0.000661742	0.00306287
ENSG00000268869	ESPNP	2.312696499	75.89870716	4.952762174	3.02E-11	4.96E-10
ENSG00000154736	ADAMTS5	20.19820843	91.33096499	2.168423057	4.53E-05	0.000278013
ENSG00000250588	IQCJ-SCHIP1	23.30863474	72.04064071	1.62123818	0.002075695	0.008323881
ENSG00000210176	MT-TH	46.63666774	127.3395348	1.445918751	0.002924253	0.011130522
ENSG00000185437	SH3BGR	22.53102899	72.04064071	1.669890785	0.002075695	0.008323881
ENSG00000169085	C8orf46	7.75633786	93.90300695	3.573275393	7.06E-09	8.20E-08
ENSG00000240875	LINC00886	20.19820843	88.75892278	2.127255803	6.85E-05	0.000402856
ENSG00000264868	CTB-167B5.2	0.757489584	155.6319648	7.436919856	2.45E-18	7.89E-17
ENSG00000163449	TMEM169	13.97732024	47.60619097	1.756585343	0.003196233	0.012090026
ENSG00000197933	ZNF823	19.42060034	63.03848163	1.690483645	0.00259576	0.010027607
ENSG00000222040	ADRA2B	3.868086451	186.4964241	5.540472475	8.98E-17	2.56E-15
ENSG00000140459	CYP11A1	41.19347589	124.7674951	1.594979986	0.001077572	0.004697132
ENSG00000132141	CCT6B	8.533969895	109.3352541	3.657089128	6.15E-10	8.31E-09
ENSG00000241224	RP11-59E19.1	0.757489584	122.1954553	7.088219355	2.99E-16	8.20E-15
ENSG00000185070	FLRT2	32.63987315	118.3373953	1.853201172	0.000236019	0.001221119
ENSG00000132122	SPATA6	21.75342271	68.18257328	1.640944223	0.002565378	0.009927281
ENSG00000146215	CRIP3	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000165716	FAM69B	19.42060034	74.61268511	1.933325172	0.000504622	0.002418505
ENSG00000188092	GPR89B	25.64144922	160.7760419	2.641503755	1.89E-07	1.78E-06
ENSG00000080200	CRYBG3	8.533969895	41.17606037	2.250341011	0.000660415	0.003059005
ENSG00000156886	ITGAD	48.9694625	117.0513752	1.254265944	0.009185361	0.030186718
ENSG00000241570	RP11-372E1.6	4.645755009	48.89221631	3.355375776	2.75E-06	2.13E-05
ENSG00000132677	RHBG	1.534979634	108.0492338	6.011534992	3.16E-15	7.94E-14
ENSG00000179988	PSTK	27.97426007	86.18688029	1.617783003	0.001727643	0.007045211
ENSG00000176771	NCKAP5	9.31159843	79.75677272	3.078635963	2.29E-07	2.13E-06
ENSG00000180881	CAPS2	17.86538201	48.89221631	1.444019919	0.011440165	0.036662951
ENSG00000197888	UGT2B17	16.31016037	255.9414373	3.960148133	1.75E-13	3.67E-12
ENSG00000181315	ZNF322	19.42060034	72.04064071	1.882782647	0.000676858	0.003122365
ENSG00000250303	RP11-356J5.12	8.533969895	132.4836138	3.933919582	2.17E-11	3.62E-10
ENSG00000230409	TCEA1P2	20.97581587	106.7632134	2.339309487	1.01E-05	7.01E-05
ENSG00000111319	SCNN1A	10.8668471	77.18472911	2.811654712	2.17E-06	1.72E-05
ENSG00000122481	RWDD3	17.08777164	68.18257328	1.986691988	0.000334323	0.001663919
ENSG00000172995	ARPP21	1.534979634	82.32881599	5.619722518	6.65E-12	1.18E-10
ENSG00000177034	MTX3	21.75342271	74.61268511	1.770784081	0.001103785	0.004797931
ENSG00000228826	RP11-344P13.4	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000272143	FGF14-AS2	31.08466991	81.0427944	1.377721045	0.006946155	0.023793644
ENSG00000148200	NR6A1	32.63987315	81.0427944	1.307598284	0.01112167	0.035728205
ENSG00000253426	RP11-10A14.4	3.090401881	70.75461835	4.454525307	7.62E-10	1.02E-08
ENSG00000198300	PEG3	13.19970438	131.1975941	3.298954757	3.14E-09	3.84E-08
ENSG00000118407	FILIP1	13.19970438	64.32450474	2.271769373	7.64E-05	0.000442406
ENSG00000247796	CTD-2366F13.1	13.97732024	64.32450474	2.190035261	0.000138064	0.000751552
ENSG00000130234	ACE2	2.312696499	182.6383671	6.218521354	1.78E-18	5.84E-17
ENSG00000150722	PPP1R1C	2.312696499	111.9072946	5.512322257	2.85E-14	6.43E-13
ENSG00000173275	ZNF449	27.97426007	72.04064071	1.359446567	0.009230716	0.030319735
ENSG00000226453	RP11-379B8.1	8.533969895	32.17386395	1.895382403	0.005911861	0.020617274
ENSG00000156049	GNAI4	11.64446802	126.0535149	3.420120022	1.08E-09	1.41E-08
ENSG00000260274	RP11-817O13.8	16.31016037	77.18472911	2.231994652	5.57E-05	0.000332187
ENSG00000127472	PLA2G5	24.86384483	101.6191314	2.024314973	0.000103578	0.000582321
ENSG00000113389	NPR3	39.63827699	93.90300695	1.240681116	0.013003216	0.040617686
ENSG00000168135	KCNJ4	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000249042	CTD-2015H6.3	21.75342271	59.18041139	1.436975194	0.009265254	0.030425141
ENSG00000168621	GDNF	1.534979634	249.5113443	7.218213764	1.00E-22	4.50E-21
ENSG00000168152	THAP9	17.08777164	109.3352541	2.667198488	9.17E-07	7.71E-06
ENSG00000040608	RTN4R	28.75186299	91.33096499	1.661966472	0.001299147	0.005542449
ENSG00000271239	RP11-238F2.1	1.39E-17	64.32450474	9.054654516	3.48E-11	5.65E-10
ENSG00000176387	HSD11B2	13.97732024	45.03413956	1.676624339	0.004688294	0.016805242
ENSG00000164619	BMPER	6.978701584	129.9115743	4.190692849	9.71E-12	1.70E-10
ENSG00000184985	SORCS2	20.19820843	108.0492338	2.410697482	5.44E-06	4.01E-05
ENSG00000230333	AC004538.3	1.39E-17	73.32666296	9.243355124	3.82E-12	6.93E-11
ENSG00000163815	CLEC3B	10.8668471	142.7717707	3.698140516	1.36E-10	2.01E-09
ENSG00000177432	NAPIL5	38.8606773	122.1954553	1.648762799	0.000804773	0.003650114
ENSG00000179528	LBX2	20.97581587	77.18472911	1.871787483	0.000492806	0.002368729
ENSG00000267444	SMUG1P1	1.39E-17	101.6191314	9.713582814	1.12E-14	2.62E-13
ENSG00000152779	SLC16A12	2.312696499	158.2040034	6.011436477	3.28E-17	9.78E-16
ENSG00000253598	SLC10A5	2.312696499	69.46859588	4.825219558	1.20E-10	1.79E-09
ENSG00000224122	POU6F2-AS1	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000176049	JAKMIP2	10.08922402	78.47075096	2.941158705	8.04E-07	6.82E-06
ENSG00000243710	WDR65	14.75493478	79.75677272	2.422499397	1.96E-05	0.000128617
ENSG00000196326	AKR1CL1	13.97732024	81.0427944	2.522899058	9.02E-06	6.33E-05

ENSG00000248050	<i>RP11-422N16.3</i>	1.39E-17	78.47075096	9.341046348	1.21E-12	2.32E-11
ENSG00000135913	<i>USP37</i>	20.19820843	56.60836376	1.479280129	0.00753465	0.025441342
ENSG00000071991	<i>CDH19</i>	2.312696499	96.47504867	5.298447103	4.13E-13	8.27E-12
ENSG00000237188	<i>RP11-337C18.8</i>	10.08922402	51.46426629	2.333516871	0.000138966	0.000756129
ENSG00000189157	<i>FAM47E</i>	6.978701584	54.03631542	2.926686049	7.20E-06	5.18E-05
ENSG00000189419	<i>SPATA41</i>	2.312696499	73.32666296	4.903089832	4.74E-11	7.55E-10
ENSG00000272760	<i>RP11-5C23.1</i>	16.31016037	70.75461835	2.106669351	0.000146896	0.000795966
ENSG00000197619	<i>ZNF615</i>	20.19820843	79.75677272	1.973149717	0.000244362	0.001257375
ENSG00000118596	<i>SLC16A7</i>	17.86538201	97.76106944	2.442234998	7.26E-06	5.22E-05
ENSG00000178662	<i>CSRP3</i>	2.312696499	29.60180421	3.597276321	5.75E-05	0.000342588
ENSG00000106689	<i>LHX2</i>	48.9694625	110.6212744	1.172822796	0.015840954	0.048221298
ENSG00000225265	<i>RP11-378J18.3</i>	10.8668471	42.46208706	1.951007412	0.001866265	0.007562114
ENSG00000099365	<i>STX1B</i>	12.42208703	70.75461835	2.495670465	1.33E-05	9.05E-05
ENSG00000257315	<i>ZBED6</i>	2.312696499	73.32666296	4.903089832	4.74E-11	7.55E-10
ENSG00000216588	<i>IGSF23</i>	3.868086451	81.0427944	4.339061959	4.13E-10	5.72E-09
ENSG00000268925	<i>AL161645.2</i>	1.39E-17	110.6212744	9.835926953	2.22E-15	5.69E-14
ENSG00000267809	<i>NDUFV2P1</i>	34.19507543	79.75677272	1.217677593	0.015368674	0.046921557
ENSG00000233554	<i>RP11-326F20.5</i>	10.08922402	75.89870716	2.893139823	1.16E-06	9.58E-06
ENSG00000176714	<i>CCDC121</i>	12.42208703	41.17606037	1.716082674	0.006493106	0.022381135
ENSG00000244479	<i>OR2A1-AS1</i>	16.31016037	55.32233968	1.752262636	0.002863026	0.010937675
ENSG00000169752	<i>NRG4</i>	11.64446802	57.89438766	2.298894123	0.000153941	0.000831773
ENSG000000237361	<i>LINC01071</i>	1.39E-17	37.31797838	8.27074258	1.17E-07	1.13E-06
ENSG00000185652	<i>NTF3</i>	3.868086451	91.33096499	4.511286428	5.87E-11	9.20E-10
ENSG00000196597	<i>ZNF782</i>	10.08922402	48.89221631	2.259694683	0.000266845	0.001360778
ENSG00000214796	<i>RP11-480I12.5</i>	4.645755009	27.0297426	2.502650885	0.001197455	0.005144813
ENSG00000085741	<i>WNT11</i>	15.53254811	187.7824431	3.583454058	2.95E-11	4.85E-10
ENSG00000225792	<i>AC004540.4</i>	1.534979634	56.60836376	5.080117639	3.13E-09	3.84E-08
ENSG00000259706	<i>HSP90B2P</i>	1.39E-17	32.17386395	8.057364981	7.40E-07	6.31E-06
ENSG00000175161	<i>CADM2</i>	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000152042	<i>NBPF11</i>	22.53102899	82.32881599	1.862232978	0.000537939	0.00254095
ENSG0000008226	<i>DLEC1</i>	9.31159843	91.33096499	3.273909303	3.28E-08	3.46E-07
ENSG00000170323	<i>FABP4</i>	3.090401881	51.46426629	3.996018441	8.72E-08	8.63E-07
ENSG00000261469	<i>RP11-96D1.6</i>	1.39E-17	108.0492338	9.802017206	3.77E-15	9.37E-14
ENSG00000136573	<i>BLK</i>	45.08147069	127.3395348	1.494699515	0.001974966	0.007954589
ENSG00000233006	<i>AC034220.3</i>	14.75493478	73.32666296	2.30138508	5.21E-05	0.000312995
ENSG00000046889	<i>PREX2</i>	11.64446802	81.0427944	2.783459599	2.30E-06	1.81E-05
ENSG00000003096	<i>KLHL13</i>	6.978701584	57.89438766	3.026006465	2.87E-06	2.22E-05
ENSG00000143994	<i>ABHD1</i>	6.201060061	32.17386395	2.34727822	0.001516645	0.006294242
ENSG00000196437	<i>ZNF569</i>	22.53102899	60.46643496	1.417588584	0.010901385	0.035088568
ENSG00000229214	<i>LINC00242</i>	6.978701584	45.03413956	2.664297223	6.40E-05	0.000378303
ENSG00000197768	<i>C9orf173</i>	3.868086451	69.46859588	4.117028497	5.33E-09	6.32E-08
ENSG00000113946	<i>CLDN16</i>	10.08922402	43.74811345	2.099649671	0.000812684	0.003680623
ENSG00000255545	<i>RP11-627G23.1</i>	3.090401881	96.47504867	4.901326321	3.73E-12	6.75E-11
ENSG00000250786	<i>SNHG18</i>	24.86384483	68.18257328	1.449297364	0.006676975	0.022976078
ENSG00000246985	<i>SOCS2-AS1</i>	17.86538201	96.47504867	2.423149988	8.34E-06	5.88E-05
ENSG00000240891	<i>PLCXD2</i>	20.19820843	60.46643496	1.574240614	0.004091611	0.015030593
ENSG00000260886	<i>RP11-432I5.1</i>	1.39E-17	110.6212744	9.835926953	2.22E-15	5.69E-14
ENSG00000224652	<i>LINC00885</i>	1.39E-17	39.89003337	8.366656493	4.11E-08	4.28E-07
ENSG00000170498	<i>KISS1</i>	0.757489584	29.60180421	5.046392718	1.09E-06	9.03E-06
ENSG00000229740	<i>U91324.1</i>	1.39E-17	57.89438766	8.902952836	1.70E-10	2.48E-09
ENSG00000267385	<i>CTB-50L17.14</i>	6.201060061	70.75461835	3.481824619	5.50E-08	5.64E-07
ENSG00000150527	<i>CTAGE5</i>	14.75493478	54.03631542	1.861662376	0.001400255	0.005929017
ENSG00000261578	<i>RP11-21L23.2</i>	10.8668471	177.494291	4.012009737	2.42E-12	4.48E-11
ENSG00000232040	<i>SCAND3</i>	17.08777164	59.18041139	1.782722959	0.0014637	0.00610612
ENSG00000105792	<i>C7orf63</i>	10.8668471	87.47290157	2.991960868	3.84E-07	3.43E-06
ENSG00000165874	<i>FAM35BP</i>	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000226491	<i>FTOP1</i>	2.312696499	25.74371105	3.39652492	0.000240916	0.001242834
ENSG00000182836	<i>PLCXD3</i>	5.423411881	108.0492338	4.280643851	1.73E-11	2.93E-10
ENSG00000172748	<i>ZNF596</i>	5.423411881	28.31577365	2.35230539	0.002142368	0.008567747
ENSG00000205835	<i>GMNC</i>	3.090401881	96.47504867	4.901326321	3.73E-12	6.75E-11
ENSG00000250328	<i>CTC-210G5.1</i>	0.757489584	88.75892278	6.627426632	1.16E-13	2.46E-12
ENSG00000228291	<i>RP11-445P17.6</i>	1.39E-17	60.46643496	8.965560338	9.92E-11	1.50E-09
ENSG00000215105	<i>TTC3P1</i>	13.97732024	46.32016539	1.717158747	0.003870034	0.014326736
ENSG00000156876	<i>SASS6</i>	14.75493478	52.75029095	1.826975703	0.002011027	0.008084116
ENSG00000120693	<i>SMAD9</i>	22.53102899	144.0577902	2.668678865	2.22E-07	2.07E-06
ENSG00000205361	<i>MT1DP</i>	1.534979634	32.17386395	4.266882767	3.68E-06	2.79E-05
ENSG00000067840	<i>PDZD4</i>	38.08307745	99.04709015	1.375082677	0.005440776	0.019132781
ENSG00000139914	<i>FITM1</i>	10.08922402	45.03413956	2.141355951	0.000518548	0.002457766
ENSG00000231806	<i>PCAT7</i>	0.757489584	29.60180421	5.046392718	1.09E-06	9.03E-06
ENSG00000168772	<i>CXXC4</i>	3.090401881	37.31797838	3.533356506	4.01E-06	3.03E-05
ENSG00000267390	<i>RP11-635N19.1</i>	16.31016037	50.17824141	1.611723521	0.006686163	0.022989813

ENSG00000186648	<i>LRRC16B</i>	18.64299156	50.17824141	1.420407104	0.013710255	0.042473934
ENSG00000005981	<i>ASB4</i>	1.39E-17	37.31797838	8.27074258	1.17E-07	1.13E-06
ENSG00000169507	<i>SLC38A11</i>	9.31159843	74.61268511	2.982571585	5.82E-07	5.06E-06
ENSG00000196482	<i>ESRRG</i>	5.423411881	32.17386395	2.535991626	0.000660977	0.003060465
ENSG00000122756	<i>CNTFR</i>	0.757489584	110.6212744	6.944778058	1.87E-15	4.80E-14
ENSG00000257151	<i>PWAR6</i>	27.97426007	87.47290157	1.639126866	0.001534991	0.006364004
ENSG00000134548	<i>C12orf39</i>	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000163501	<i>IHH</i>	5.423411881	83.6148375	3.911166568	1.29E-09	1.66E-08
ENSG00000150672	<i>DLG2</i>	7.75633786	114.479335	3.858849965	2.86E-10	4.05E-09
ENSG00000253958	<i>CLDN23</i>	17.08777164	51.46426629	1.581531297	0.005639186	0.019755035
ENSG00000173320	<i>STOX2</i>	25.64144922	87.47290157	1.764092709	0.000815388	0.003690182
ENSG00000241506	<i>PSMC1P1</i>	23.30863474	64.32450474	1.458030157	0.008470153	0.028088813
ENSG00000170264	<i>FAM161A</i>	12.42208703	47.60619097	1.924963682	0.00195502	0.007884475
ENSG00000147231	<i>CXorf57</i>	10.8668471	33.45989316	1.608158223	0.013705036	0.042463059
ENSG00000165995	<i>CACNB2</i>	15.53254811	60.46643496	1.950176514	0.000784949	0.003568669
ENSG00000158731	<i>OR10J6P</i>	2.312696499	57.89438766	4.562687544	1.84E-09	2.33E-08
ENSG00000181856	<i>SLC2A4</i>	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000188611	<i>ASAH2</i>	0.757489584	65.61052772	6.192021575	2.09E-11	3.50E-10
ENSG00000230102	<i>RP11-407B7.1</i>	1.534979634	33.45989316	4.323257978	2.59E-06	2.01E-05
ENSG00000245573	<i>BDNF-AS</i>	16.31016037	51.46426629	1.648162485	0.005639186	0.019755035
ENSG00000213424	<i>KRT222</i>	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000254343	<i>RP11-760H22.2</i>	12.42208703	83.6148375	2.736299007	1.38E-06	1.13E-05
ENSG00000141150	<i>RASL10B</i>	5.423411881	149.201868	4.745861529	4.27E-14	9.48E-13
ENSG00000152268	<i>SPON1</i>	14.75493478	60.46643496	2.023590294	0.000480429	0.002311918
ENSG00000077616	<i>NAALAD2</i>	2.312696499	42.46208706	4.116324089	8.61E-07	7.27E-06
ENSG00000272129	<i>RP11-250B2.6</i>	3.868086451	73.32666296	4.194898771	2.21E-09	2.76E-08
ENSG00000099984	<i>GSTT2</i>	25.64144922	153.0599261	2.570592011	3.79E-07	3.39E-06
ENSG00000159398	<i>CES5A</i>	1.39E-17	91.33096499	9.559742781	7.72E-14	1.67E-12
ENSG00000100170	<i>SLC5A1</i>	3.090401881	132.4836138	5.358516087	1.03E-14	2.41E-13
ENSG00000185532	<i>PRKG1</i>	24.08624001	77.18472911	1.673547065	0.001490418	0.00620508
ENSG00000120341	<i>SEC16B</i>	3.090401881	91.33096499	4.822356708	9.54E-12	1.67E-10
ENSG00000244062	<i>RP11-404G16.2</i>	1.39E-17	51.46426629	8.733404515	1.25E-09	1.61E-08
ENSG00000182993	<i>C12orf60</i>	17.86538201	51.46426629	1.517842108	0.008232207	0.027438849
ENSG00000264098	<i>CTD-2350C19.1</i>	20.97581587	73.32666296	1.797905926	0.000871067	0.003884867
ENSG00000232724	<i>AC111186.1</i>	3.090401881	19.31354564	2.586619364	0.006966163	0.023812952
ENSG00000176381	<i>PRR18</i>	3.090401881	111.9072946	5.115201476	2.70E-13	5.54E-12
ENSG00000198221	<i>MLLT4-AS1</i>	8.533969895	29.60180421	1.775559035	0.009730816	0.031767054
ENSG00000230882	<i>AC005077.14</i>	1.39E-17	84.90085893	9.454534595	3.28E-13	6.67E-12
ENSG00000249201	<i>CTD-3080P12.3</i>	1.39E-17	66.89655057	9.111133693	2.09E-11	3.50E-10
ENSG00000228146	<i>CASP16</i>	1.39E-17	77.18472911	9.317236682	1.52E-12	2.87E-11
ENSG00000174564	<i>IL20RB</i>	16.31016037	63.03848163	1.940321507	0.000471263	0.002272212
ENSG00000160191	<i>PDE9A</i>	31.86227166	114.479335	1.840057769	0.000262593	0.001341574
ENSG00000204876	<i>AC021218.2</i>	10.08922402	50.17824141	2.297077907	0.000172494	0.000920821
ENSG00000176912	<i>C18orf56</i>	10.08922402	42.46208706	2.056701738	0.001019268	0.004464912
ENSG00000253944	<i>RP11-156K13.1</i>	3.090401881	108.0492338	5.064631132	5.29E-13	1.05E-11
ENSG00000149294	<i>NCAM1</i>	34.19507543	90.04494392	1.392514139	0.005426586	0.019085579
ENSG00000260006	<i>RP11-469M7.1</i>	24.86384483	65.61052772	1.393902629	0.009889231	0.032239878
ENSG00000144057	<i>ST6GAL2</i>	7.75633786	81.0427944	3.361025859	7.14E-08	7.16E-07
ENSG00000226964	<i>RHEBP2</i>	0.757489584	47.60619097	5.730055702	2.27E-09	2.83E-08
ENSG00000179314	<i>WSCD1</i>	4.645755009	30.8878343	2.694490385	0.000342416	0.00170079
ENSG00000223749	<i>MIR503HG</i>	27.97426007	84.90085893	1.596118623	0.001944944	0.007854035
ENSG00000112175	<i>BMP5</i>	21.75342271	100.3331108	2.197605331	3.89E-05	0.00024173
ENSG00000272502	<i>RP11-713M15.2</i>	9.31159843	47.60619097	2.335371119	0.000162828	0.000876371
ENSG00000266258	<i>RP11-4104.1</i>	10.08922402	83.6148375	3.03265228	3.29E-07	2.98E-06
ENSG00000232451	<i>AC016768.1</i>	0.757489584	78.47075096	6.449897453	9.72E-13	1.89E-11
ENSG00000174358	<i>SLC6A19</i>	0.757489584	117.0513752	7.026221206	6.77E-16	1.81E-14
ENSG00000205866	<i>FAM99A</i>	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000204710	<i>SPDYC</i>	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000260802	<i>LINC00890</i>	1.39E-17	163.3480804	10.39783718	9.85E-19	3.29E-17
ENSG00000141469	<i>SLC14A1</i>	19.42060034	56.60836376	1.535519962	0.00753465	0.025441342
ENSG00000236136	<i>ADORA2BP</i>	0.757489584	65.61052772	6.192021575	2.09E-11	3.50E-10
ENSG00000225766	<i>RP11-468E2.9</i>	6.201060061	74.61268511	3.558318302	2.95E-08	3.13E-07
ENSG00000226121	<i>AHCTF1P1</i>	3.868086451	60.46643496	3.917103985	4.35E-08	4.52E-07
ENSG00000089163	<i>SIRT4</i>	12.42208703	37.31797838	1.574501665	0.01458372	0.044833439
ENSG00000147041	<i>SYTL5</i>	1.534979634	84.90085893	5.664052381	4.39E-12	7.88E-11
ENSG00000248485	<i>PCP4L1</i>	1.39E-17	99.04709015	9.676633236	1.97E-14	4.50E-13
ENSG00000166405	<i>RIC3</i>	20.19820843	84.90085893	2.063214871	0.00011993	0.000662026
ENSG00000183154	<i>RP11-863K10.7</i>	6.978701584	68.18257328	3.261618834	3.24E-07	2.94E-06
ENSG00000259802	<i>CTD-2256P15.2</i>	14.75493478	42.46208706	1.514619337	0.012652254	0.039847026
ENSG00000141434	<i>MEP1B</i>	1.39E-17	51.46426629	8.733404515	1.25E-09	1.61E-08
ENSG00000273079	<i>GRIN2B</i>	0.757489584	81.0427944	6.496369417	6.26E-13	1.23E-11

ENSG00000256863	RP11-959F10.6	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000145075	CCDC39	10.08922402	47.60619097	2.221316954	0.000332559	0.001656794
ENSG00000102098	SCML2	5.423411881	23.17164641	2.064165063	0.009732694	0.031767054
ENSG00000231487	AP006285.7	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000152527	PLEKHH2	24.86384483	72.04064071	1.528594697	0.003962214	0.014622247
ENSG00000171368	TPPP	26.4190532	73.32666296	1.467035674	0.006246459	0.021620352
ENSG00000173930	SLCO4C1	1.39E-17	54.03631542	8.80363242	5.21E-10	7.11E-09
ENSG00000233270	SNRPEP4	17.08777164	60.46643496	1.81368712	0.001239274	0.005307973
ENSG00000130948	HSD17B3	12.42208703	64.32450474	2.3584136	4.03E-05	0.000250047
ENSG00000117322	CR2	27.19665681	75.89870716	1.475075871	0.004313863	0.015607142
ENSG00000249267	LINC00939	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000222019	URAHP	7.75633786	83.6148375	3.406047469	4.94E-08	5.10E-07
ENSG00000269155	AL009178.1	10.8668471	34.74592196	1.662413094	0.008764824	0.028953975
ENSG00000270820	RP11-355B11.2	17.08777164	46.32016539	1.429904785	0.013240194	0.041219616
ENSG00000151687	ANKAR	19.42060034	54.03631542	1.468552529	0.010235822	0.03314806
ENSG00000175548	ALG10B	8.533969895	28.31577365	1.711696167	0.016051556	0.048778755
ENSG00000156750	AQP7P3	1.39E-17	65.61052772	9.08317047	2.69E-11	4.45E-10
ENSG00000154874	CCDC144B	0.757489584	21.88561332	4.612369121	1.96E-05	0.000128617
ENSG00000148053	NTRK2	10.8668471	82.32881599	2.904622762	9.01E-07	7.59E-06
ENSG00000261829	RP11-223I10.1	3.868086451	63.03848163	3.977107183	2.12E-08	2.30E-07
ENSG00000229944	AC004797.1	17.08777164	63.03848163	1.873690319	0.000754736	0.003445174
ENSG00000123965	PMS2P5	16.31016037	61.75245837	1.910631835	0.000661742	0.00306287
ENSG00000242220	TCP10L	2.312696499	122.1954553	5.639102958	5.57E-15	1.36E-13
ENSG00000233058	LINC00884	10.08922402	47.60619097	2.221316954	0.000332559	0.001656794
ENSG00000206685	RNU6-1189P	1.39E-17	47.60619097	8.621204597	4.20E-09	5.05E-08
ENSG00000235105	RP11-329A14.1	9.31159843	57.89438766	2.617119358	1.78E-05	0.000118357
ENSG00000269976	RP11-130L8.2	2.312696499	133.7696335	5.769563383	8.93E-16	2.37E-14
ENSG00000236682	AC068282.3	28.75186299	70.75461835	1.294135072	0.013372773	0.04157872
ENSG00000176945	MUC20	22.53102899	77.18472911	1.769264928	0.001051845	0.004595468
ENSG00000187240	DYNC2H1	13.97732024	70.75461835	2.327292126	4.83E-05	0.000292332
ENSG00000108556	CHRNE	12.42208703	48.89221631	1.96334141	0.001317417	0.005612682
ENSG00000234949	AC104667.3	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000265158	LRRRC37A7P	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000251364	CTD-2516F10.2	24.08624001	68.18257328	1.494875589	0.004943748	0.017616754
ENSG00000064692	SNCAIP	17.08777164	50.17824141	1.545092333	0.006686163	0.022989813
ENSG00000154928	EPHB1	10.08922402	55.32233968	2.437617023	5.93E-05	0.000352261
ENSG00000069712	KIAA1107	4.645755009	46.32016539	3.277571453	4.66E-06	3.48E-05
ENSG00000141622	RNF165	2.312696499	50.17824141	4.356700258	1.65E-08	1.83E-07
ENSG00000127081	ZNF484	11.64446802	41.17606037	1.808264876	0.003980794	0.014671208
ENSG00000204837	RP11-204M4.2	1.534979634	15.45544135	3.213844342	0.002133716	0.00854156
ENSG00000214960	ISPD	2.312696499	37.31797838	3.930477288	4.01E-06	3.03E-05
ENSG00000196967	ZNF585A	25.64144922	64.32450474	1.321204387	0.014764309	0.04531015
ENSG00000183230	CTNNA3	1.39E-17	79.75677272	9.364469441	9.72E-13	1.89E-11
ENSG00000235903	CPB2-AS1	0.757489584	54.03631542	5.912483525	3.92E-10	5.45E-09
ENSG00000197723	HSPB9	5.423411881	56.60836376	3.349226499	3.67E-07	3.30E-06
ENSG00000091536	MYO15A	6.201060061	48.89221631	2.949495565	8.67E-06	6.10E-05
ENSG00000272009	RP1-313I6.12	7.75633786	30.8878343	1.972204481	0.00406587	0.014940451
ENSG00000168079	SCARA5	11.64446802	88.75892278	2.914516814	6.06E-07	5.24E-06
ENSG00000157168	NRG1	17.86538201	64.32450474	1.839092109	0.000998515	0.004387147
ENSG00000213494	CCL14	4.645755009	87.47290157	4.193336288	5.95E-10	8.06E-09
ENSG00000133477	FAM83F	0.757489584	46.32016539	5.690629107	4.20E-09	5.05E-08
ENSG00000164849	GPR146	1.534979634	74.61268511	5.477922849	3.78E-11	6.13E-10
ENSG00000197099	RP11-573D15.8	1.534979634	42.46208706	4.666107167	1.33E-07	1.28E-06
ENSG00000204949	FAM83A-AS1	1.39E-17	38.60400605	8.319496464	5.79E-08	5.91E-07
ENSG00000267270	AC139100.2	6.201060061	33.45989316	2.403653431	0.00115274	0.00498805
ENSG00000273062	RP11-428K3.1	8.533969895	56.60836376	2.708617275	2.21E-05	0.000143729
ENSG00000164061	BSN	9.31159843	46.32016539	2.295944524	0.000415	0.002020136
ENSG00000254154	RP4-798P15.3	1.534979634	70.75461835	5.401429166	9.47E-11	1.44E-09
ENSG00000267296	CEBPA-AS1	3.090401881	16.74147634	2.381553033	0.014485426	0.044569852
ENSG00000243694	RP11-6B4.1	1.39E-17	75.89870716	9.293027466	2.40E-12	4.45E-11
ENSG00000228055	LINC00864	1.39E-17	56.60836376	8.870599853	2.96E-10	4.19E-09
ENSG00000158023	WDR66	12.42208703	70.75461835	2.495670465	1.33E-05	9.05E-05
ENSG00000241764	AC002467.7	15.53254811	46.32016539	1.566394179	0.009083827	0.02989652
ENSG00000184601	C14orf180	1.39E-17	146.6298291	10.24216444	9.55E-18	2.95E-16
ENSG00000267596	CCL15	3.090401881	52.75029095	4.031559673	5.07E-08	5.23E-07
ENSG00000183134	PTGDR2	3.868086451	39.89003337	3.31820014	9.35E-06	6.53E-05
ENSG00000204176	SYT15	23.30863474	64.32450474	1.458030157	0.008470153	0.028088813
ENSG00000253196	RP11-706C16.7	1.39E-17	93.90300695	9.599767846	5.19E-14	1.14E-12
ENSG00000170500	LONRF2	18.64299156	106.7632134	2.508200239	3.69E-06	2.80E-05
ENSG00000165972	CCDC38	1.39E-17	81.0427944	9.387518312	7.79E-13	1.52E-11
ENSG00000254827	SLC22A18AS	27.97426007	84.90085893	1.596118623	0.001944944	0.007854035

ENSG00000259370	<i>RP11-1069G10.1</i>	1.534979634	65.61052772	5.292688256	3.13E-10	4.40E-09
ENSG00000110244	<i>APOA4</i>	1.39E-17	126.0535149	10.02417873	1.86E-16	5.16E-15
ENSG00000178821	<i>TMEM52</i>	6.201060061	56.60836376	3.160513092	1.23E-06	1.02E-05
ENSG00000243083	<i>LINC00870</i>	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000260855	<i>RP11-439E19.10</i>	6.201060061	34.74592196	2.457908303	0.000877744	0.003908334
ENSG00000203280	<i>CTA-221G9.11</i>	10.08922402	56.60836376	2.47071221	4.81E-05	0.000291355
ENSG00000145362	<i>ANK2</i>	20.19820843	52.75029095	1.377626023	0.016342315	0.04960169
ENSG00000228620	<i>RP3-434P1.6</i>	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000206077	<i>ZDHHC11B</i>	6.201060061	104.1911725	4.03952288	1.18E-10	1.77E-09
ENSG00000256528	<i>AP006285.1</i>	1.39E-17	32.17386395	8.057364981	7.40E-07	6.31E-06
ENSG00000234432	<i>RP11-1275H24.1</i>	6.978701584	28.31577365	1.996732374	0.004621058	0.016580972
ENSG00000273477	<i>RP11-196O16.1</i>	3.868086451	23.17164641	2.537082065	0.001665133	0.006814897
ENSG00000205771	<i>CATSPER2P1</i>	13.97732024	51.46426629	1.86878526	0.001496038	0.006224308
ENSG00000273247	<i>RP11-83A24.2</i>	11.64446802	46.32016539	1.977719289	0.00140429	0.005943066
ENSG00000226699	<i>RP11-122K13.7</i>	1.534979634	36.03195036	4.429801113	1.30E-06	1.06E-05
ENSG00000197380	<i>DACT3</i>	15.53254811	79.75677272	2.349085617	3.46E-05	0.000217538
ENSG00000165828	<i>PRAP1</i>	1.534979634	36.03195036	4.429801113	1.30E-06	1.06E-05
ENSG00000185304	<i>RGPD2</i>	19.42060034	81.0427944	2.052438421	0.000135269	0.000738765
ENSG00000227258	<i>SMIM2-AS1</i>	9.31159843	55.32233968	2.551671188	2.74E-05	0.000175639
ENSG00000196653	<i>ZNF502</i>	8.533969895	28.31577365	1.711696167	0.016051556	0.048778755
ENSG00000223922	<i>ASS1P2</i>	1.39E-17	128.6255546	10.05329737	1.16E-16	3.28E-15
ENSG00000100399	<i>CHADL</i>	12.42208703	70.75461835	2.495670465	1.33E-05	9.05E-05
ENSG00000176115	<i>AQP7P4</i>	1.39E-17	78.47075096	9.341046348	1.21E-12	2.32E-11
ENSG00000196263	<i>ZNF471</i>	8.533969895	63.03848163	2.863580958	6.24E-06	4.54E-05
ENSG00000198106	<i>SNX29P2</i>	6.201060061	43.74811345	2.789450553	3.15E-05	0.000199236
ENSG00000102349	<i>KLF8</i>	24.86384483	61.75245837	1.306606023	0.014653994	0.045004945
ENSG00000196724	<i>ZNF418</i>	11.64446802	38.60400605	1.715437751	0.006068669	0.02111377
ENSG00000259881	<i>RP11-830F9.5</i>	2.312696499	47.60619097	4.280939305	2.95E-08	3.13E-07
ENSG00000151743	<i>AMN1</i>	13.19970438	45.03413956	1.758358452	0.002909732	0.011088834
ENSG00000159289	<i>GOLGA6A</i>	1.39E-17	59.18041139	8.934596177	1.30E-10	1.93E-09
ENSG00000233392	<i>AC104809.4</i>	3.090401881	73.32666296	4.50596905	3.88E-10	5.40E-09
ENSG00000270157	<i>RP5-894A10.6</i>	9.31159843	33.45989316	1.827906714	0.008204261	0.027353041
ENSG00000170959	<i>DCDC1</i>	1.534979634	74.61268511	5.477922849	3.78E-11	6.13E-10
ENSG00000131409	<i>LRRC4B</i>	20.19820843	63.03848163	1.634243812	0.00259576	0.010027607
ENSG00000235652	<i>RP11-545I5.3</i>	4.645755009	24.45767899	2.358939008	0.003149424	0.011921861
ENSG00000007062	<i>PROM1</i>	5.423411881	97.76106944	4.13642405	9.54E-11	1.45E-09
ENSG00000261705	<i>RP11-61A14.2</i>	17.08777164	54.03631542	1.651759203	0.003389794	0.012727088
ENSG00000070601	<i>FRMPD1</i>	1.534979634	30.8878343	4.20821472	7.53E-06	5.39E-05
ENSG00000231948	<i>HS1BP3-IT1</i>	3.090401881	122.1954553	5.241982176	5.39E-14	1.18E-12
ENSG00000260966	<i>RP11-690D19.3</i>	14.75493478	57.89438766	1.960982792	0.000817574	0.003697518
ENSG00000163322	<i>FAM175A</i>	13.19970438	42.46208706	1.673704239	0.008356463	0.02780826
ENSG00000273328	<i>RP11-141M3.5</i>	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000273281	<i>RP11-339B21.14</i>	10.8668471	57.89438766	2.397370867	8.00E-05	0.004461113
ENSG00000259108	<i>CTD-3098H1.2</i>	1.39E-17	55.32233968	8.837504666	3.92E-10	5.45E-09
ENSG00000135976	<i>ANKRD36</i>	6.978701584	41.17606037	2.535377218	0.000137515	0.000749548
ENSG00000182648	<i>LINC01006</i>	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000261238	<i>AC009166.5</i>	2.312696499	28.31577365	3.533413453	8.17E-05	0.000468565
ENSG00000207770	<i>MIR568</i>	7.75633786	34.74592196	2.141502611	0.001436097	0.006003845
ENSG00000181997	<i>AQP7P2</i>	1.39E-17	66.89655057	9.111133693	2.09E-11	3.50E-10
ENSG00000149634	<i>SPATA25</i>	9.31159843	42.46208706	2.170755903	0.001019268	0.004464912
ENSG00000182851	<i>GPIHBP1</i>	3.090401881	21.88561332	2.766131942	0.002370371	0.009369526
ENSG00000205795	<i>CYS1</i>	12.42208703	92.616986	2.883653197	3.74E-07	3.35E-06
ENSG00000129244	<i>ATP1B2</i>	14.75493478	65.61052772	2.141200426	0.000201115	0.001055249
ENSG00000152582	<i>SPEF2</i>	9.31159843	75.89870716	3.007193988	4.82E-07	4.25E-06
ENSG0000018869	<i>ZNF582</i>	16.31016037	52.75029095	1.683703717	0.004015113	0.014784539
ENSG00000163239	<i>TDRD10</i>	8.533969895	64.32450474	2.892671937	5.08E-06	3.78E-05
ENSG00000230328	<i>RP11-35N6.6</i>	0.757489584	61.75245837	6.104724969	5.84E-11	9.16E-10
ENSG00000207778	<i>MIR122</i>	1.39E-17	131.1975941	10.0818399	8.55E-17	2.44E-15
ENSG00000156042	<i>TTC18</i>	7.75633786	45.03413956	2.514751141	0.000118807	0.00065973
ENSG00000149050	<i>ZNF214</i>	6.201060061	24.45767899	1.953058796	0.010811714	0.034835687
ENSG00000267824	<i>AC137056.1</i>	1.39E-17	34.74592196	8.167995064	2.40E-07	2.21E-06
ENSG00000136866	<i>ZFP37</i>	6.201060061	30.8878343	2.288610173	0.001998931	0.008041993
ENSG00000188672	<i>RHCE</i>	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000101405	<i>OXT</i>	3.868086451	92.616986	4.53143776	4.87E-11	7.73E-10
ENSG00000188107	<i>EYS</i>	5.423411881	46.32016539	3.060404648	1.44E-05	9.73E-05
ENSG00000160111	<i>CPAMD8</i>	24.86384483	70.75461835	1.502643539	0.004513216	0.016238563
ENSG00000264016	<i>CTC-297N7.9</i>	1.534979634	45.03413956	4.75076138	7.22E-08	7.22E-07
ENSG00000213937	<i>CLDN9</i>	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000224769	<i>AC069213.1</i>	3.090401881	16.74147634	2.381553033	0.014485426	0.044569852
ENSG00000272909	<i>CTD-2555O16.4</i>	6.978701584	57.89438766	3.026006465	2.87E-06	2.22E-05
ENSG00000231690	<i>LINC00574</i>	1.534979634	27.0297426	4.01637522	2.30E-05	0.000149015

ENSG00000230953	RP4-631H13.6	4.645755009	25.74371105	2.432583662	0.001648699	0.006758769
ENSG00000254990	RP11-108O10.2	1.39E-17	38.60400605	8.319496464	5.79E-08	5.91E-07
ENSG00000003987	MTMR7	3.090401881	46.32016539	3.844391928	3.56E-07	3.20E-06
ENSG00000134042	MRO	6.201060061	36.03195036	2.510196567	0.000211448	0.001105499
ENSG00000100626	GALNT16	3.090401881	60.46643496	4.228174264	8.28E-09	9.54E-08
ENSG00000171433	GLOD5	1.39E-17	61.75245837	8.995873864	7.60E-11	1.17E-09
ENSG00000239467	AC007405.6	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000128271	ADORA2A	8.533969895	36.03195036	2.05830075	0.002205393	0.008790097
ENSG00000248884	CTC-537E7.3	1.39E-17	37.31797838	8.27074258	1.17E-07	1.13E-06
ENSG00000149548	CCDC15	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000165659	DACH1	3.868086451	69.46859588	4.117028497	5.33E-09	6.32E-08
ENSG00000206127	GOLGA80	3.868086451	24.45767899	2.614689205	0.001173602	0.005059824
ENSG00000107518	ATRNL1	3.868086451	81.0427944	4.339061959	4.13E-10	5.72E-09
ENSG00000241316	RP11-81N13.1	5.423411881	47.60619097	3.099831243	1.12E-05	7.71E-05
ENSG000000064309	CDON	10.08922402	47.60619097	2.221316954	0.00032559	0.001656794
ENSG00000236255	AC009404.2	10.08922402	37.31797838	1.870854937	0.003217043	0.012155612
ENSG00000247627	MTND4P12	8.533969895	57.89438766	2.740970258	1.78E-05	0.000118357
ENSG00000271868	RP11-1293J14.1	2.312696499	41.17606037	4.072058297	1.58E-06	1.28E-05
ENSG00000164512	ANKRD55	8.533969895	47.60619097	2.459222019	0.000162828	0.000876371
ENSG00000179399	GPC5	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000153822	KCNJ16	20.19820843	74.61268511	1.877085339	0.000504622	0.002418505
ENSG00000166473	PKD1L2	0.757489584	28.31577365	4.98252985	1.61E-06	1.30E-05
ENSG00000218819	TDRI15	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000262003	RP11-676J12.7	1.39E-17	66.89655057	9.111133693	2.09E-11	3.50E-10
ENSG00000249746	RP11-254I22.3	0.757489584	34.74592196	5.276846169	1.67E-07	1.58E-06
ENSG00000223723	BX842568.2	1.534979634	61.75245837	5.20539165	8.49E-10	1.12E-08
ENSG00000232710	RP4-669P10.16	3.090401881	36.03195036	3.482897254	7.63E-06	5.44E-05
ENSG00000261098	RP11-819C21.1	10.08922402	45.03413956	2.141355951	0.000518548	0.002457766
ENSG00000120332	TNN	17.08777164	50.17824141	1.545092333	0.006686163	0.022989813
ENSG00000272327	RP11-1002K11.1	21.75342271	61.75245837	1.498252882	0.006027957	0.020995639
ENSG00000229484	RP5-888M10.2	0.757489584	36.03195036	5.329134433	1.17E-07	1.13E-06
ENSG00000224251	RP11-499O7.7	0.757489584	33.45989316	5.222591298	2.40E-07	2.21E-06
ENSG00000272452	RP11-391M1.4	18.64299156	59.18041139	1.65803773	0.00330135	0.012434468
ENSG00000166402	TUB	18.64299156	56.60836376	1.594041407	0.005296084	0.01866357
ENSG00000224183	SDHDP6	10.08922402	33.45989316	1.713852549	0.008204261	0.027353041
ENSG00000138152	BTBD16	3.868086451	60.46643496	3.917103985	4.35E-08	4.52E-07
ENSG00000268164	CTD-2337J16.1	13.19970438	74.61268511	2.485519921	1.29E-05	8.80E-05
ENSG00000179869	ABCA13	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000177788	RP5-1061H20.4	4.645755009	38.60400605	3.015289914	4.27E-05	0.000262923
ENSG00000267680	ZNF224	7.75633786	39.89003337	2.34016404	0.000404469	0.001972354
ENSG00000100012	SEC14L3	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000245146	LINC01024	13.97732024	38.60400605	1.454877209	0.014931034	0.045776594
ENSG000000064655	EYA2	17.86538201	83.6148375	2.216977516	5.38E-05	0.000322162
ENSG00000137727	ARHGAP20	7.75633786	38.60400605	2.293004011	0.000668181	0.003084628
ENSG00000260259	RP11-368I7.4	1.534979634	39.89003337	4.576174279	3.45E-07	3.11E-06
ENSG00000177692	DNAJC28	6.201060061	33.45989316	2.403653431	0.00115274	0.00498805
ENSG00000258457	RP11-298I3.4	4.645755009	25.74371105	2.432583662	0.001648699	0.006758769
ENSG00000205106	CTD-2210P24.4	10.8668471	50.17824141	2.191383581	0.000336783	0.001674819
ENSG00000272316	XXbac-BPGBPG55C20.2	10.08922402	37.31797838	1.870854937	0.003217043	0.012155612
ENSG00000237886	RP11-611D20.2	13.97732024	41.17606037	1.547704334	0.010138421	0.032888339
ENSG00000184828	ZBTB7C	10.8668471	52.75029095	2.263363777	0.000221986	0.001152354
ENSG00000250696	RP11-704M14.1	6.978701584	38.60400605	2.442550093	0.000300744	0.001518689
ENSG00000179639	FCER1A	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000224934	RP11-441O15.3	6.978701584	75.89870716	3.416081095	6.38E-08	6.47E-07
ENSG00000166104	hsa-mir-7162	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000213171	LINGO4	1.534979634	48.89221631	4.869100112	2.21E-08	2.38E-07
ENSG00000261189	RP3-512B11.3	1.534979634	30.8878343	4.20821472	7.53E-06	5.39E-05
ENSG00000163749	CCDC158	1.534979634	23.17164641	3.795056203	0.000109596	0.000613237
ENSG00000178082	TWF1P1	4.645755009	32.17386395	2.753158431	0.000252157	0.001291708
ENSG00000197558	SSPO	10.8668471	50.17824141	2.191383581	0.000336783	0.001674819
ENSG00000235092	AC011747.7	5.423411881	61.75245837	3.47450051	1.12E-07	1.09E-06
ENSG00000236810	RP5-886K2.3	3.868086451	25.74371105	2.688333859	0.000589	0.002758025
ENSG00000229729	RP11-159G9.5	6.201060061	41.17606037	2.702236828	5.36E-05	0.000321225
ENSG00000124343	XG	1.534979634	99.04709015	5.886151022	1.63E-14	3.75E-13
ENSG00000139292	LGR5	6.201060061	50.17824141	2.986878789	6.75E-06	4.88E-05
ENSG00000103034	NDRG4	12.42208703	54.03631542	2.107391505	0.000498242	0.002390697
ENSG00000162620	LRR1Q3	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000259065	RP5-1021I20.1	10.08922402	36.03195036	1.820395684	0.004060649	0.014927886
ENSG00000227218	RP11-203J24.8	7.75633786	25.74371105	1.710297758	0.015305394	0.046750705
ENSG00000112530	PACRG	7.75633786	55.32233968	2.811012213	1.17E-05	8.03E-05
ENSG00000261058	RP11-252E2.2	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08

ENSG00000206549	PRSS50	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000254539	RP4-791M13.3	10.08922402	37.31797838	1.870854937	0.003217043	0.012155612
ENSG00000259359	RP11-327J17.2	1.39E-17	33.45989316	8.113740193	3.48E-07	3.13E-06
ENSG00000259721	RP11-758N13.1	2.312696499	51.46426629	4.393139222	1.24E-08	1.40E-07
ENSG00000169629	RGPDP8	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000176204	LRRTM4	1.39E-17	86.18688029	9.476198975	2.65E-13	5.46E-12
ENSG00000224417	RP11-503C24.6	0.757489584	39.89003337	5.475507598	2.93E-08	3.11E-07
ENSG00000226416	MRPL23-AS1	1.534979634	23.17164641	3.795056203	0.000109596	0.000613237
ENSG00000180998	GPR137C	3.090401881	20.59957972	2.679165917	0.003385132	0.012711505
ENSG00000235510	BX842568.1	1.39E-17	42.46208706	8.456589381	2.10E-08	2.28E-07
ENSG00000270705	RP11-736N17.9	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000256139	RP11-968O1.5	8.533969895	33.45989316	1.951757615	0.004613369	0.016570127
ENSG00000141431	ASXL3	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000128591	FLNC	14.75493478	41.17606037	1.470353545	0.015229728	0.046577967
ENSG00000220848	RPS18P9	10.08922402	34.74592196	1.768107421	0.00512978	0.018219588
ENSG00000177098	SCN4B	7.75633786	30.8878343	1.972204481	0.00406587	0.014940451
ENSG00000248334	WHAMMP2	8.533969895	38.60400605	2.157513886	0.001356148	0.005759922
ENSG00000231437	RP11-88H9.2	3.090401881	78.47075096	4.603660275	1.31E-10	1.95E-09
ENSG00000121410	A1BG	0.757489584	33.45989316	5.222591298	2.40E-07	2.21E-06
ENSG00000229419	RALGAPA1P	4.645755009	32.17386395	2.753158431	0.000252157	0.001291708
ENSG00000250387	RP11-136K7.2	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627
ENSG00000133636	NTS	15.53254811	43.74811345	1.484153491	0.01296303	0.040502341
ENSG00000245248	USP2-AS1	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000167780	SOAT2	3.868086451	24.45767899	2.614689205	0.001173602	0.005059824
ENSG00000240303	ACAD11	1.534979634	18.02751115	3.43463054	0.000884859	0.003929458
ENSG00000165443	PHYHIP1L	0.757489584	45.03413956	5.650094699	5.75E-09	6.76E-08
ENSG00000226251	RP11-151I1.3	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000146352	CLVS2	1.39E-17	60.46643496	8.965560338	9.92E-11	1.50E-09
ENSG00000198075	SULT1C4	14.75493478	48.89221631	1.717612282	0.003476403	0.013016873
ENSG00000145536	ADAMTS16	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000161132	XXbac-B444P24.10	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000101746	NOL4	1.39E-17	38.60400605	8.319496464	5.79E-08	5.91E-07
ENSG00000247317	RP11-273G15.2	6.201060061	68.18257328	3.428478444	1.04E-07	1.01E-06
ENSG00000176402	GJC3	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000258001	RP11-756H6.1	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000185186	LINC00313	4.645755009	61.75245837	3.691667315	1.12E-07	1.09E-06
ENSG00000232426	RP11-508M1.7	1.39E-17	50.17824141	8.696965551	1.68E-09	2.14E-08
ENSG00000124003	MOGAT1	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000177138	FAM9B	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000237658	RP5-968D22.3	0.757489584	25.74371105	4.845641317	5.45E-06	4.01E-05
ENSG00000111404	RERGL	1.534979634	36.03195036	4.429801113	1.30E-06	1.06E-05
ENSG00000165028	NIPSNAP3B	7.75633786	27.0297426	1.780364981	0.01172386	0.037483475
ENSG00000101850	GPR143	3.868086451	19.31354564	2.275549085	0.006966163	0.023812952
ENSG00000230590	FTX	10.8668471	41.17606037	1.906741619	0.002322339	0.009220726
ENSG00000250327	RP11-173M11.2	3.090401881	28.31577365	3.136292671	8.17E-05	0.000468565
ENSG00000206172	HBA1	3.090401881	20.59957972	2.679165917	0.003385132	0.012711505
ENSG00000231327	AC016700.5	6.201060061	32.17386395	2.34727822	0.001516645	0.006294242
ENSG00000204314	PRRT1	5.423411881	38.60400605	2.798123109	0.000121298	0.000666266
ENSG00000184414	RP11-44M6.3	1.534979634	33.45989316	4.323257978	2.59E-06	2.01E-05
ENSG00000226450	CYP2D8P	6.978701584	25.74371105	1.85984384	0.008135331	0.027159656
ENSG00000258913	RP11-260M19.2	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000228477	RP3-342P20.2	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000062370	ZNF112	10.8668471	42.46208706	1.951007412	0.001866265	0.007562114
ENSG00000161860	SYCE2	6.978701584	34.74592196	2.291048693	0.000877744	0.003908334
ENSG00000235899	RP11-345L23.1	0.757489584	36.03195036	5.329134433	1.17E-07	1.13E-06
ENSG00000187105	HEATR4	10.08922402	38.60400605	1.919608821	0.002551039	0.009879412
ENSG00000242600	MBL1P	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000225418	AKRIC5P	1.39E-17	45.03413956	8.541243594	7.89E-09	9.12E-08
ENSG00000130294	KIF1A	1.534979634	24.45767899	3.872663343	7.35E-05	0.000429002
ENSG00000256667	KLRAP1	7.75633786	33.45989316	2.087247739	0.002409866	0.009484447
ENSG00000188573	FBLN1	3.090401881	24.45767899	2.925759484	0.001173602	0.005059824
ENSG00000233280	CRYBG3	2.312696499	25.74371105	3.39652492	0.000240916	0.001242834
ENSG00000223764	RP11-54O7.3	13.97732024	56.60836376	2.005980598	0.000588514	0.002758025
ENSG00000237413	RP11-183M13.1	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000267586	LINC00907	2.312696499	48.89221631	4.319317034	2.21E-08	2.38E-07
ENSG00000240401	AC012358.8	6.201060061	29.60180421	2.227454852	0.003489554	0.013062179
ENSG00000256234	RP11-283G6.4	10.8668471	34.74592196	1.662413094	0.008764824	0.028953975
ENSG00000260686	CTB-36H16.2	6.978701584	29.60180421	2.060595242	0.002639002	0.010161486
ENSG00000128606	LRRC17	3.868086451	38.60400605	3.271040111	1.26E-05	8.62E-05
ENSG00000255145	RP11-60I3.5	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000228445	UGT1A2P	1.39E-17	48.89221631	8.659582326	2.27E-09	2.83E-08

ENSG00000134259	NGF	2.312696499	48.89221631	4.319317034	2.21E-08	2.38E-07
ENSG00000124780	KCNK17	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000237674	GSTA7P	1.39E-17	36.03195036	8.220283328	1.67E-07	1.58E-06
ENSG00000255798	RP11-817J15.3	1.39E-17	101.6191314	9.713582814	1.12E-14	2.62E-13
ENSG00000141639	MAPK4	7.75633786	32.17386395	2.030872528	0.003128224	0.011850635
ENSG00000105877	DNAH11	7.75633786	41.17606037	2.385831136	0.000315485	0.001578376
ENSG00000261617	RP11-243A14.1	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000175894	TSPEAR	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000171885	AQP4	6.978701584	47.60619097	2.744258226	3.04E-05	0.00019315
ENSG00000254614	AP003068.23	10.8668471	43.74811345	1.993955345	0.001501162	0.00624145
ENSG00000206052	DOK6	6.201060061	66.89655057	3.401046932	1.29E-07	1.24E-06
ENSG00000124749	COL21A1	6.201060061	27.0297426	2.096770673	0.006127713	0.02125374
ENSG00000232721	RP11-403I13.5	3.090401881	60.46643496	4.228174264	8.28E-09	9.54E-08
ENSG00000179873	NLRP11	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000256678	RP11-611O2.2	5.423411881	34.74592196	2.64662171	0.000372105	0.001828898
ENSG00000160460	SPTBN4	4.645755009	27.0297426	2.502650885	0.001197455	0.005144813
ENSG00000123496	IL13RA2	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000231683	RP1-27K12.2	1.39E-17	54.03631542	8.80363242	5.21E-10	7.11E-09
ENSG00000152932	RAB3C	3.090401881	21.88561332	2.766131942	0.002370371	0.009369526
ENSG00000162032	SPSB3	3.868086451	27.0297426	2.758401081	0.000419448	0.002039395
ENSG00000256383	AC020910.2	9.31159843	30.8878343	1.712863456	0.013149317	0.041017354
ENSG00000272505	RP11-981G7.6	9.31159843	41.17606037	2.126490111	0.001279883	0.005468709
ENSG00000223396	RP510P7	11.64446802	36.03195036	1.616224615	0.011463391	0.036726295
ENSG00000229896	RP11-456H18.2	5.423411881	28.31577365	2.35230539	0.002142368	0.008567747
ENSG00000136546	SCN7A	2.312696499	48.89221631	4.319317034	2.21E-08	2.38E-07
ENSG00000196972	LINC00087	8.533969895	36.03195036	2.05830075	0.002205393	0.008790097
ENSG00000233215	AP000472.2	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000046653	GPM6B	3.868086451	30.8878343	2.950240581	0.000111734	0.000624501
ENSG00000235961	PNMA6C	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000222001	AC106876.2	4.645755009	28.31577365	2.569472195	0.000872039	0.003887807
ENSG00000197991	PCDH20	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000251169	AC005355.2	6.978701584	24.45767899	1.786199186	0.010811714	0.034835687
ENSG00000226321	AC104809.3	1.534979634	33.45989316	4.323257978	2.59E-06	2.01E-05
ENSG00000135517	MIP	2.312696499	30.8878343	3.658431642	4.06E-05	0.000251823
ENSG00000186952	TMEM232	6.201060061	24.45767899	1.953058796	0.010811714	0.034835687
ENSG00000109927	TECTA	13.19970438	41.17606037	1.629438447	0.010138421	0.032888339
ENSG00000225507	AC069282.6	0.757489584	38.60400605	5.428347569	4.11E-08	4.28E-07
ENSG00000171790	SLFN1	6.978701584	25.74371105	1.85984384	0.008135331	0.027159656
ENSG00000198185	ZNF334	1.534979634	46.32016539	4.791295788	5.34E-08	5.49E-07
ENSG00000272518	RP11-26J3.3	5.423411881	25.74371105	2.215416857	0.003904919	0.014430085
ENSG00000263096	RP11-515O17.2	2.312696499	15.45544135	2.664061264	0.007864773	0.026412502
ENSG00000184434	LRRC19	0.757489584	39.89003337	5.475507598	2.93E-08	3.11E-07
ENSG00000184564	SLITRK6	1.39E-17	60.46643496	8.965560338	9.92E-11	1.50E-09
ENSG00000256811	RP11-7M8.2	1.39E-17	28.31577365	7.873678745	2.40E-06	1.89E-05
ENSG00000253953	PCDHGB4	14.75493478	50.17824141	1.754995506	0.00289507	0.011038037
ENSG00000260963	RP11-297L17.2	7.75633786	46.32016539	2.555285549	9.35E-05	0.000529119
ENSG00000188626	GOLGA8M	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000272549	RP11-351J23.2	3.090401881	39.89003337	3.629270419	2.15E-06	1.70E-05
ENSG00000179914	ITLN1	5.423411881	42.46208706	2.935216027	4.11E-05	0.000253912
ENSG00000173114	LRRN3	9.31159843	54.03631542	2.517798942	4.24E-05	0.000261576
ENSG00000230371	KARSP2	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000271681	RP11-1259L22.2	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000130876	SLC7A10	2.312696499	42.46208706	4.116324089	8.61E-07	7.27E-06
ENSG00000182912	C21orf90	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000183729	NPBWR1	2.312696499	46.32016539	4.24151271	5.34E-08	5.49E-07
ENSG00000118402	ELOVL4	15.53254811	46.32016539	1.566394179	0.009083827	0.02989652
ENSG00000158445	KCNB1	1.534979634	43.74811345	4.7090551	9.80E-08	9.61E-07
ENSG00000223459	FAM115B	6.978701584	25.74371105	1.85984384	0.008135331	0.027159656
ENSG00000264696	AC108078.1	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000108947	EFNB3	1.39E-17	56.60836376	8.870599853	2.96E-10	4.19E-09
ENSG00000036448	MYOM2	3.868086451	41.17606037	3.363867236	5.19E-06	3.86E-05
ENSG00000260015	RP11-510M2.5	13.97732024	45.03413956	1.676624339	0.004688294	0.016805242
ENSG00000232650	RP5-834N19.1	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000181619	GPR135	7.75633786	29.60180421	1.91104916	0.005290723	0.018647325
ENSG00000255240	RP11-142C4.6	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000272864	RP11-17E13.2	1.534979634	25.74371105	3.946307997	4.96E-05	0.000298911
ENSG00000148541	FAM13C	5.423411881	36.03195036	2.698909973	0.000211448	0.001105499
ENSG00000233110	RP11-301L8.2	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000236524	RP11-134F2.2	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000249863	RP11-177C12.1	5.423411881	27.0297426	2.28548408	0.00288962	0.011020638
ENSG00000229886	RP5-1132H15.3	1.39E-17	32.17386395	8.057364981	7.40E-07	6.31E-06

ENSG00000131183	SLC34A1	0.757489584	28.31577365	4.98252985	1.61E-06	1.30E-05
ENSG00000157653	C9orf43	4.645755009	27.0297426	2.502650885	0.001197455	0.005144813
ENSG00000240915	RP11-659E9.2	1.39E-17	41.17606037	8.412323589	2.93E-08	3.11E-07
ENSG00000250934	RP11-71E19.1	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000257877	RP3-462E2.3	3.090401881	32.17386395	3.319978907	2.06E-05	0.000134408
ENSG00000228065	RP11-222A11.1	5.423411881	23.17164641	2.064165063	0.009732694	0.031767054
ENSG00000167614	TTYH1	6.978701584	39.89003337	2.489710122	0.000231229	0.001198079
ENSG00000224511	LINC00365	1.39E-17	29.60180421	7.937541613	1.61E-06	1.30E-05
ENSG00000246523	RP11-736K20.6	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000262881	RP11-669E14.4	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000186231	KLHL32	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000235949	AC061961.2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000060709	RIMBP2	6.201060061	43.74811345	2.789450553	3.15E-05	0.000199236
ENSG00000176222	ZNF404	8.533969895	34.74592196	2.006012486	0.002817474	0.010785202
ENSG00000164100	NDST3	1.39E-17	51.46426629	8.733404515	1.25E-09	1.61E-08
ENSG00000262801	U91319.1	1.39E-17	34.74592196	8.167995064	2.40E-07	2.21E-06
ENSG00000235890	TSPEAR-AS1	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000231100	RP11-740C1.2	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000144488	ESPNL	4.645755009	29.60180421	2.633335064	0.000636793	0.002958961
ENSG00000243384	RP11-475O23.2	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000237118	CYP2F2P	6.978701584	27.0297426	1.929911063	0.006127713	0.002125374
ENSG00000232284	GNG12-AS1	2.312696499	30.8878343	3.658431642	4.06E-05	0.000251823
ENSG00000170890	PLA2G1B	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000165072	MAMDC2	12.42208703	41.17606037	1.716082674	0.006493106	0.022381135
ENSG00000151360	ALLC	3.868086451	38.60400605	3.271040111	1.26E-05	8.62E-05
ENSG00000157578	LCA5L	5.423411881	23.17164641	2.064165063	0.009732694	0.031767054
ENSG00000231993	RP1-85F18.5	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000234899	SOX9-AS1	8.533969895	52.75029095	2.606963169	5.29E-05	0.000316952
ENSG00000131386	GALNT15	4.645755009	32.17386395	2.753158431	0.000252157	0.001291708
ENSG00000224616	RP11-305E17.6	2.312696499	15.45544135	2.664061264	0.007864773	0.026412502
ENSG00000176635	HORMAD2	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000188517	COL25A1	1.39E-17	30.8878343	7.998696934	1.09E-06	9.03E-06
ENSG00000226853	AC010894.3	6.201060061	25.74371105	2.02670345	0.008135331	0.027159656
ENSG00000257718	RP11-396F22.1	3.868086451	21.88561332	2.455061663	0.002370371	0.009369526
ENSG00000210184	MT-TS2	9.31159843	39.89003337	2.080823015	0.001608974	0.006611185
ENSG00000233008	RP11-475O6.1	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000233967	RP11-250B2.3	3.868086451	29.60180421	2.88908526	0.000214972	0.001119684
ENSG00000204152	TIMM23B	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000189292	FAM150B	0.757489584	68.18257328	6.24741631	9.96E-12	1.73E-10
ENSG00000225603	RP11-325P15.1	0.757489584	27.0297426	4.915708539	2.40E-06	1.89E-05
ENSG00000205578	POM121B	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000233483	CTD-2020K17.4	5.423411881	28.31577365	2.35230539	0.002142368	0.008567747
ENSG00000134121	CHL1	3.868086451	16.74147634	2.070482753	0.014485426	0.044569852
ENSG00000257878	RP11-256L6.3	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000100505	TRIM9	2.312696499	16.74147634	2.778673814	0.005247305	0.018541622
ENSG00000227392	HPN-AS1	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000272555	RP11-459I19.1	1.534979634	25.74371105	3.946307997	4.96E-05	0.000298911
ENSG00000227712	RP11-418J17.3	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000164946	FREM1	9.31159843	37.31797838	1.984909102	0.003217043	0.012155612
ENSG00000251448	RP11-71E19.2	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000248319	RP11-205M3.3	1.39E-17	37.31797838	8.27074258	1.17E-07	1.13E-06
ENSG00000203900	RP11-261N11.8	1.39E-17	29.60180421	7.937541613	1.61E-06	1.30E-05
ENSG00000153165	RGPD3	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000255090	RP11-820L6.1	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000220204	RP1-53C18.3	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000236267	AP006216.5	1.39E-17	43.74811345	8.499537315	1.09E-08	1.23E-07
ENSG00000213062	AL021068.1	0.757489584	32.17386395	5.166216086	3.48E-07	3.13E-06
ENSG00000236816	ANKRD20A7P	1.39E-17	30.8878343	7.998696934	1.09E-06	9.03E-06
ENSG00000204789	ZNF204P	2.312696499	36.03195036	3.880018036	7.63E-06	5.44E-05
ENSG00000124440	HIF3A	0.757489584	28.31577365	4.98252985	1.61E-06	1.30E-05
ENSG00000139220	PPFIA2	1.534979634	36.03195036	4.429801113	1.30E-06	1.06E-05
ENSG00000226580	RPL39P40	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000262061	RP11-1260E13.4	6.201060061	37.31797838	2.560655819	0.000159961	0.000862434
ENSG00000081181	ARG2	6.201060061	33.45989316	2.403653431	0.00115274	0.00498805
ENSG00000231609	AC009501.4	3.868086451	29.60180421	2.88908526	0.000214972	0.001119684
ENSG00000230628	RP4-781K5.6	1.39E-17	50.17824141	8.696965551	1.68E-09	2.14E-08
ENSG00000237742	RP11-624M8.1	0.757489584	21.88561332	4.612369121	1.96E-05	0.000128617
ENSG00000183844	FAM3B	2.312696499	52.75029095	4.428680455	7.10E-09	8.24E-08
ENSG00000184845	DRD1	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000117281	CD160	13.97732024	38.60400605	1.454877209	0.014931034	0.045776594
ENSG00000204334	ERICH2	2.312696499	18.02751115	2.884847462	0.003515158	0.013136257

ENSG00000159263	<i>SIM2</i>	4.645755009	25.74371105	2.432583662	0.001648699	0.006758769
ENSG00000253549	<i>RP11-317J10.2</i>	6.978701584	27.0297426	1.929911063	0.006127713	0.02125374
ENSG00000245711	<i>NADK2-AS1</i>	1.534979634	28.31577365	4.083196531	1.58E-05	0.000105369
ENSG00000150045	<i>KLRF1</i>	6.978701584	33.45989316	2.236793821	0.00115274	0.00498805
ENSG00000119147	<i>C2orf40</i>	2.312696499	36.03195036	3.880018036	7.63E-06	5.44E-05
ENSG00000214439	<i>FAM185BP</i>	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000260645	<i>RP11-250B2.5</i>	0.757489584	27.0297426	4.915708539	2.40E-06	1.89E-05
ENSG00000273193	<i>RP11-523G9.3</i>	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG000000082175	<i>PGR</i>	8.533969895	29.60180421	1.775559035	0.009730816	0.031767054
ENSG00000235078	<i>AC142528.1</i>	6.201060061	33.45989316	2.403653431	0.00115274	0.00498805
ENSG00000215018	<i>COL28A1</i>	0.757489584	36.03195036	5.329134433	1.17E-07	1.13E-06
ENSG00000152672	<i>CLEC4F</i>	10.08922402	34.74592196	1.768107421	0.00512978	0.018219588
ENSG00000188396	<i>TCTEX1D4</i>	2.312696499	15.45544135	2.664061264	0.007864773	0.026412502
ENSG00000228791	<i>THRB-AS1</i>	2.312696499	15.45544135	2.664061264	0.007864773	0.026412502
ENSG00000152092	<i>ASTN1</i>	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000142549	<i>IGLN5</i>	1.534979634	42.46208706	4.666107167	1.33E-07	1.28E-06
ENSG00000267183	<i>AC010525.6</i>	1.534979634	18.02751115	3.43463054	0.000884859	0.003929458
ENSG00000144230	<i>GPR17</i>	3.090401881	28.31577365	3.136292671	8.17E-05	0.000468565
ENSG00000262756	<i>AC009133.21</i>	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000167014	<i>C15orf43</i>	1.39E-17	46.32016539	8.581778002	5.75E-09	6.76E-08
ENSG00000249684	<i>RP11-423H2.3</i>	2.312696499	21.88561332	3.163252723	0.000739506	0.003381864
ENSG00000109991	<i>P2RX3</i>	0.757489584	21.88561332	4.612369121	1.96E-05	0.000128617
ENSG00000154529	<i>CNTNAP3B</i>	3.090401881	19.31354564	2.586619364	0.006966163	0.023812952
ENSG00000147206	<i>NXF3</i>	1.534979634	28.31577365	4.083196531	1.58E-05	0.000105369
ENSG00000165125	<i>TRPV6</i>	2.312696499	39.89003337	4.026391201	2.15E-06	1.70E-05
ENSG00000251393	<i>RP1-240K6.3</i>	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000166206	<i>GABRB3</i>	1.39E-17	42.46208706	8.456589381	2.10E-08	2.28E-07
ENSG00000164929	<i>BAALC</i>	6.201060061	32.17386395	2.34727822	0.001516645	0.006294242
ENSG00000267566	<i>RP11-104J23.1</i>	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000267395	<i>AC074212.6</i>	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000262294	<i>RP11-1260E13.2</i>	3.090401881	19.31354564	2.586619364	0.006966163	0.023812952
ENSG00000228697	<i>RP5-968D22.1</i>	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000186458	<i>DEFB132</i>	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000271420	<i>RP5-1057J7.7</i>	3.868086451	19.31354564	2.275549085	0.006966163	0.023812952
ENSG00000267454	<i>ZNF582-AS1</i>	5.423411881	24.45767899	2.141772203	0.007167784	0.024445015
ENSG00000249976	<i>RP11-580P21.1</i>	1.39E-17	57.89438766	8.902952836	1.70E-10	2.48E-09
ENSG00000225119	<i>LINC00999</i>	5.423411881	25.74371105	2.215416857	0.003904919	0.014430085
ENSG00000273174	<i>RP11-434H6.6</i>	3.868086451	21.88561332	2.455061663	0.002370371	0.009369526
ENSG00000257696	<i>RP11-175P13.2</i>	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000226824	<i>RP4-756H11.3</i>	7.75633786	38.60400605	2.293004011	0.000668181	0.003084628
ENSG00000173212	<i>MAB21L3</i>	2.312696499	23.17164641	3.245273125	0.000506526	0.002424359
ENSG00000225077	<i>LINC00337</i>	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000197083	<i>ZNF300P1</i>	2.312696499	32.17386395	3.717099689	2.06E-05	0.000134408
ENSG00000237522	<i>NONOP2</i>	3.090401881	21.88561332	2.766131942	0.002370371	0.009369526
ENSG00000033122	<i>LRRC7</i>	1.534979634	30.8878343	4.20821472	7.53E-06	5.39E-05
ENSG00000272894	<i>RP5-1159O4.1</i>	4.645755009	23.17164641	2.281331868	0.004368548	0.015782016
ENSG00000269305	<i>AL158147.2</i>	0.757489584	28.31577365	4.98252985	1.61E-06	1.30E-05
ENSG00000226803	<i>RP11-203B9.4</i>	3.090401881	16.74147634	2.381553033	0.014485426	0.044569852
ENSG00000228812	<i>RP11-157P1.5</i>	3.868086451	20.59957972	2.368095638	0.003385132	0.012711505
ENSG00000186399	<i>GOLGA8R</i>	0.757489584	16.74147634	4.227790211	0.000193974	0.001018857
ENSG00000171827	<i>ZNF570</i>	3.868086451	16.74147634	2.070482753	0.014485426	0.044569852
ENSG00000141665	<i>FBXO15</i>	7.75633786	27.0297426	1.780364981	0.01172386	0.037483475
ENSG00000262006	<i>RP11-700H6.4</i>	3.090401881	32.17386395	3.319978907	2.06E-05	0.000134408
ENSG00000215124	<i>RP3-420J14.1</i>	1.39E-17	28.31577365	7.873678745	2.40E-06	1.89E-05
ENSG00000198523	<i>PLN</i>	5.423411881	23.17164641	2.064165063	0.009732694	0.031767054
ENSG00000248445	<i>CTB-118N6.3</i>	7.75633786	27.0297426	1.780364981	0.01172386	0.037483475
ENSG00000196553	<i>LINC00238</i>	1.39E-17	41.17606037	8.412323589	2.93E-08	3.11E-07
ENSG00000198691	<i>ABCA4</i>	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000224747	<i>AP001065.7</i>	1.39E-17	28.31577365	7.873678745	2.40E-06	1.89E-05
ENSG00000232653	<i>GOLGA8N</i>	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000186976	<i>EFCAB6</i>	3.868086451	20.59957972	2.368095638	0.003385132	0.012711505
ENSG00000147223	<i>RIPPLY1</i>	1.39E-17	30.8878343	7.998696934	1.09E-06	9.03E-06
ENSG00000227477	<i>STK4-AS1</i>	3.868086451	25.74371105	2.688333859	0.000589	0.002758025
ENSG00000099869	<i>IGF2-AS</i>	1.39E-17	28.31577365	7.873678745	2.40E-06	1.89E-05
ENSG00000257660	<i>RP11-579D7.4</i>	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000168546	<i>GFRA2</i>	6.978701584	25.74371105	1.85984384	0.008135331	0.027159656
ENSG00000164616	<i>FBXL21</i>	1.39E-17	34.74592196	8.167995064	2.40E-07	2.21E-06
ENSG00000256433	<i>RP1-102E24.8</i>	3.090401881	20.59957972	2.679165917	0.003385132	0.012711505
ENSG00000253428	<i>CTB-43E15.2</i>	6.201060061	25.74371105	2.02670345	0.008135331	0.027159656
ENSG00000197181	<i>PIWIL2</i>	2.312696499	21.88561332	3.163252723	0.000739506	0.003381864
ENSG00000237767	<i>RP11-101E14.2</i>	1.39E-17	36.03195036	8.220283328	1.67E-07	1.58E-06

ENSG00000196335	STK31	4.645755009	20.59957972	2.112345441	0.008458934	0.028066587
ENSG00000230633	RP11-37E23.5	6.978701584	27.0297426	1.929911063	0.006127713	0.02125374
ENSG00000144681	STAC	5.423411881	25.74371105	2.215416857	0.003904919	0.014430085
ENSG00000187627	RGPD1	0.757489584	47.60619097	5.730055702	2.27E-09	2.83E-08
ENSG00000249456	RP11-298J20.4	3.090401881	16.74147634	2.381553033	0.014485426	0.044569852
ENSG00000152580	IGSF10	3.090401881	19.31354564	2.586619364	0.006966163	0.023812952
ENSG00000116031	CD207	7.75633786	37.31797838	2.244250127	0.000860935	0.003844508
ENSG00000223519	KIF28P	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG000000044012	GUCA2B	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000065325	GLP2R	3.868086451	36.03195036	3.171826975	2.31E-05	0.000149892
ENSG00000235033	RP11-61I13.3	2.312696499	16.74147634	2.778673814	0.005247305	0.018541622
ENSG00000165985	C1QL3	7.75633786	39.89003337	2.34016404	0.000404469	0.001972354
ENSG00000230921	HAO2-IT1	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000164627	KIF6	3.868086451	23.17164641	2.537082065	0.001665133	0.006814897
ENSG00000197838	CYP2A13	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000270060	RP11-390K5.6	6.201060061	25.74371105	2.02670345	0.008135331	0.027159656
ENSG00000157021	FAM92A1P1	6.201060061	27.0297426	2.096770673	0.006127713	0.02125374
ENSG00000182057	Z83851.3	3.090401881	20.59957972	2.679165917	0.003385132	0.012711505
ENSG00000206384	COL6A6	1.39E-17	42.46208706	8.456589381	2.10E-08	2.28E-07
ENSG00000248676	RP11-766F14.1	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000232150	ST13P4	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000224043	CCNT2-AS1	6.201060061	27.0297426	2.096770673	0.006127713	0.02125374
ENSG00000159905	ZNF221	0.757489584	23.17164641	4.694389523	1.27E-05	8.64E-05
ENSG00000104413	ESRP1	3.868086451	42.46208706	3.408133028	3.89E-06	2.94E-05
ENSG00000260618	RP11-23N2.4	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000129965	INS-IGF2	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000258818	RNASE4	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000132698	RAB25	1.534979634	30.8878343	4.20821472	7.53E-06	5.39E-05
ENSG00000238018	AC093110.3	4.645755009	20.59957972	2.112345441	0.008458934	0.028066587
ENSG00000233590	RP11-153K11.3	4.645755009	29.60180421	2.633335064	0.000636793	0.002958961
ENSG00000251675	CTC-458I2.2	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000227070	RP11-191G24.1	2.312696499	20.59957972	3.076286698	0.001084588	0.004718613
ENSG00000166323	C11orf65	1.534979634	30.8878343	4.20821472	7.53E-06	5.39E-05
ENSG00000255495	FAM85A	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000230647	AC022816.2	0.757489584	36.03195036	5.329134433	1.17E-07	1.13E-06
ENSG00000148948	LRRC4C	4.645755009	33.45989316	2.809533643	0.000186219	0.000987511
ENSG00000099957	P2RX6	3.868086451	32.17386395	3.008908628	8.10E-05	0.000466191
ENSG00000227370	RP4-669P10.19	3.090401881	37.31797838	3.533356506	4.01E-06	3.03E-05
ENSG00000265511	RP11-524F11.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000174473	GALNTL6	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000155066	PROM2	7.75633786	27.0297426	1.780364981	0.01172386	0.037483475
ENSG00000178115	GOLGA8Q	2.312696499	23.17164641	3.245273125	0.000506526	0.002424359
ENSG00000235357	RP1-159G19.1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000244694	PTCHD4	0.757489584	34.74592196	5.276846169	1.67E-07	1.58E-06
ENSG00000205312	AC022596.2	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000251165	F11-AS1	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000246022	ALDH1L1-AS2	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000181227	RP4-682C21.2	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000183908	LRRC55	1.39E-17	36.03195036	8.220283328	1.67E-07	1.58E-06
ENSG00000260500	CTD-3193O13.1	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000247137	RP11-727A23.5	6.978701584	24.45767899	1.786199186	0.010811714	0.034835687
ENSG00000173258	ZNF483	3.868086451	37.31797838	3.222286227	1.70E-05	0.000113564
ENSG00000246763	RGMB-AS1	5.423411881	21.88561332	1.982144661	0.01323105	0.041205082
ENSG00000135298	BAI3	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000134569	LRP4	4.645755009	34.74592196	2.863788515	0.000137915	0.000751397
ENSG00000253955	CTB-33O18.3	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000233585	AC115617.2	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000260400	RP11-119F7.5	4.645755009	28.31577365	2.569472195	0.000872039	0.003887807
ENSG00000235720	RP11-340I6.6	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000253939	RP11-44K6.3	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000183778	B3GALT5	0.757489584	43.74811345	5.608388419	7.89E-09	9.12E-08
ENSG00000147082	CCNB3	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627
ENSG00000236849	RP11-151D14.1	1.534979634	14.16940643	3.089334671	0.005281544	0.01863638
ENSG00000260284	TPSP2	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000130528	HRC	0.757489584	18.02751115	4.333963859	0.000120499	0.000662026
ENSG00000261978	CTD-2529O21.2	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000181072	CHRM2	1.39E-17	29.60180421	7.937541613	1.61E-06	1.30E-05
ENSG00000165953	SERPINA12	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000153666	GOLGA8I	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000205360	MT1CP	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000214252	AZGP1P2	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05

ENSG00000237836	PHKA2-AS1	4.645755009	21.88561332	2.199311466	0.006072876	0.021125448
ENSG00000243055	GK-AS1	1.534979634	32.17386395	4.266882767	3.68E-06	2.79E-05
ENSG00000100312	ACR	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000184616	AC004166.6	6.201060061	25.74371105	2.02670345	0.008135331	0.027159656
ENSG00000243896	OR2A7	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000253525	CTD-2114J12.1	1.534979634	18.02751115	3.43463054	0.000884859	0.003929458
ENSG00000165449	SLC16A9	0.757489584	24.45767899	4.771996663	8.28E-06	5.84E-05
ENSG00000189108	IL1RAPL2	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000106809	OGN	3.868086451	24.45767899	2.614689205	0.001173602	0.005059824
ENSG00000267726	CTD-2526M8.2	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000116147	TNR	3.090401881	39.89003337	3.629270419	2.15E-06	1.70E-05
ENSG00000228888	RP4-764O22.2	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000114349	GNAT1	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000227467	RP11-169D4.1	0.757489584	24.45767899	4.771996663	8.28E-06	5.84E-05
ENSG00000183166	CALN1	1.39E-17	38.60400605	8.319496464	5.79E-08	5.91E-07
ENSG00000272456	CTD-2342N23.3	4.645755009	19.31354564	2.019798888	0.011803031	0.937668763
ENSG00000255471	RP11-736K20.5	1.534979634	28.31577365	4.083196531	1.58E-05	0.000105369
ENSG00000263006	ROCK1P1	2.312696499	20.59957972	3.076286698	0.001084588	0.004718613
ENSG00000183833	MAATS1	1.534979634	18.02751115	3.43463054	0.000884859	0.003929458
ENSG00000103184	SEC14L5	6.201060061	28.31577365	2.163591984	0.004621058	0.016580972
ENSG00000166856	GPR182	2.312696499	18.02751115	2.884847462	0.003515158	0.013136257
ENSG00000197254	AP000445.1	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000255423	EBLN2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000136197	C7orf25	3.090401881	18.02751115	2.487726681	0.010033723	0.032582726
ENSG00000185689	C6orf201	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627
ENSG00000241754	RP11-280H21.1	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000236842	RP11-399K21.10	1.534979634	14.16940643	3.089334671	0.005281544	0.01863638
ENSG00000182329	AC079354.1	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000186094	AGBL4	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000146151	HMGCLL1	2.312696499	30.8878343	3.658431642	4.06E-05	0.000251823
ENSG00000236754	AC004019.13	0.757489584	25.74371105	4.845641317	5.45E-06	4.01E-05
ENSG00000272510	RP4-680D5.8	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000068615	REEP1	3.090401881	27.0297426	3.069471361	0.000116677	0.000648917
ENSG00000243069	ARHGEF26-AS1	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000264924	RP11-799B12.2	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000198939	ZFP2	6.201060061	27.0297426	2.096770673	0.006127713	0.02125374
ENSG00000257817	RP4-601P9.2	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000228327	RP11-206L10.2	2.312696499	23.17164641	3.245273125	0.000506526	0.002424359
ENSG00000133661	SFTPD	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000230870	FBXW11P1	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000224080	UBE2FP1	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000120440	TTL2	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000176928	GCNT4	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000128285	MCHR1	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000123572	NRK	1.534979634	20.59957972	3.626069776	0.000376589	0.001848001
ENSG00000233376	RP5-881L22.6	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000184160	ADRA2C	3.090401881	29.60180421	3.200155539	5.75E-05	0.000342588
ENSG00000227999	MTND5P1	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627
ENSG00000273350	RP4-539M6.20	0.757489584	23.17164641	4.694389523	1.27E-05	8.64E-05
ENSG00000255191	RP11-626H12.1	3.090401881	23.17164641	2.848152344	0.001665133	0.006814897
ENSG00000121570	DPPA4	1.534979634	19.31354564	3.533523223	0.000575412	0.002703923
ENSG00000135409	AMHR2	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000230435	AC004160.4	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000257410	RP11-2H8.2	4.645755009	23.17164641	2.281331868	0.004368548	0.015782016
ENSG00000179930	ZNF648	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000270720	RP11-84C13.2	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000116183	PAPPA2	1.39E-17	34.74592196	8.167995064	2.40E-07	2.21E-06
ENSG00000254042	CTC-558O2.1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000266852	MIR4482-1	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000184313	MROH7	2.312696499	24.45767899	3.322880266	0.000348534	0.001723599
ENSG00000239445	ST3GAL6-AS1	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000270589	RP11-348N5.7	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000163217	BMP10	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000233836	RP11-255H23.2	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000100362	PVALB	2.312696499	34.74592196	3.827729772	1.06E-05	7.33E-05
ENSG00000253357	CTB-78F1.2	1.39E-17	29.60180421	7.937541613	1.61E-06	1.30E-05
ENSG00000214264	RP11-356J5.5	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000227411	BAATP1	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000083307	GRHL2	0.757489584	33.45989316	5.222591298	2.40E-07	2.21E-06
ENSG00000233695	GAS6-AS1	6.201060061	30.8878343	2.288610173	0.001998931	0.008041993
ENSG00000134343	ANO3	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026

ENSG00000260396	AC012065.7	0.757489584	25.74371105	4.845641317	5.45E-06	4.01E-05
ENSG00000231170	AC002451.3	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000236341	RP5-1103B4.3	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000236417	CTSLP1	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000272574	RP11-359K18.4	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000257139	RP11-320P7.2	2.312696499	25.74371105	3.39652492	0.000240916	0.001242834
ENSG00000272787	KB-226F1.2	4.645755009	29.60180421	2.633335064	0.000636793	0.002958961
ENSG00000150526	MIA2	1.534979634	14.16940643	3.089334671	0.005281544	0.01863638
ENSG00000241362	RPL36AP43	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000259985	RP11-549B18.1	0.757489584	18.02751115	4.333963859	0.000120499	0.000662026
ENSG00000112309	B3GAT2	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000145794	MEGF10	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000168356	SCN11A	3.090401881	30.8878343	3.261310861	4.06E-05	0.000251823
ENSG00000268593	CTD-2611O12.6	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG000000091138	SLC26A3	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000157423	HYDIN	2.312696499	27.0297426	3.466592142	0.000116677	0.000648917
ENSG00000257259	RP11-767I20.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000062096	ARSF	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000229425	AJ006998.2	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000258545	RP4-755D9.1	5.423411881	21.88561332	1.982144661	0.01323105	0.041205082
ENSG00000270513	RP11-116B13.1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000248890	HHIP-AS1	3.868086451	16.74147634	2.070482753	0.014485426	0.044569852
ENSG00000230490	RP11-141M1.3	0.757489584	24.45767899	4.771996663	8.28E-06	5.84E-05
ENSG00000187545	PRAMEF10	1.39E-17	39.89003337	8.366656493	4.11E-08	4.28E-07
ENSG00000234770	GULOP	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000146469	VIP	0.757489584	19.31354564	4.432856543	7.55E-05	0.000437944
ENSG00000095464	PDE6C	3.868086451	16.74147634	2.070482753	0.014485426	0.044569852
ENSG00000263082	CTD-2034I21.2	1.39E-17	30.8878343	7.998696934	1.09E-06	9.03E-06
ENSG00000122477	LRRRC39	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000162069	CCDC64B	3.090401881	28.31577365	3.136292671	8.17E-05	0.000468565
ENSG00000234840	RP11-399D6.2	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000143171	RXRG	0.757489584	16.74147634	4.227790211	0.000193974	0.001018857
ENSG00000229017	RP11-439L18.3	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000133169	BEX1	1.39E-17	30.8878343	7.998696934	1.09E-06	9.03E-06
ENSG00000229808	RP11-456P18.2	2.312696499	15.45544135	2.664061264	0.007864773	0.026412502
ENSG00000233942	AC004012.1	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000167741	GGT6	2.312696499	18.02751115	2.884847462	0.003515158	0.013136257
ENSG00000260987	RP11-423G4.7	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000161055	SCGB3A1	4.645755009	23.17164641	2.281331868	0.004368548	0.015782016
ENSG00000233936	RP11-399H11.2	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000224037	RP4-781K5.7	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000231467	RP5-1170K4.7	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000258551	RP11-661P17.1	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000132874	SLC14A2	0.757489584	23.17164641	4.694389523	1.27E-05	8.64E-05
ENSG00000244265	SIAH2-AS1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000228842	PCDH9-AS2	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000198010	DLGAP2	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000133958	UNC79	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000262995	CTD-2194A8.2	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000234235	BOK-AS1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000204706	MAMDC2-AS1	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000230645	AC016682.1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000269952	RP11-324I22.3	1.534979634	19.31354564	3.533523223	0.000575412	0.002703923
ENSG00000232354	VIPR1-AS1	3.090401881	20.59957972	2.679165917	0.003385132	0.012711505
ENSG00000258999	RP11-114N19.3	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000175093	SPSB4	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000140538	NTRK3	1.534979634	19.31354564	3.533523223	0.000575412	0.002703923
ENSG00000256969	RP11-320N7.2	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000258460	RP11-168L7.1	0.757489584	23.17164641	4.694389523	1.27E-05	8.64E-05
ENSG00000016402	IL20RA	1.534979634	29.60180421	4.147059399	1.09E-05	7.51E-05
ENSG00000231628	RP3-355L5.4	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000127129	EDN2	4.645755009	23.17164641	2.281331868	0.004368548	0.015782016
ENSG00000232287	SLC6A1-AS1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000217258	AC007249.3	0.757489584	19.31354564	4.432856543	7.55E-05	0.000437944
ENSG00000237337	RP11-567C20.2	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000228705	LINC00659	0.757489584	18.02751115	4.333963859	0.000120499	0.000662026
ENSG00000223704	RP1-90L6.2	5.423411881	21.88561332	1.982144661	0.01323105	0.041205082
ENSG00000258819	RP11-7F17.3	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000228653	HNRNPCP7	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000266304	RP11-484N16.1	1.39E-17	27.0297426	7.806857434	3.61E-06	2.75E-05
ENSG00000250266	RP11-789C1.1	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05

ENSG00000258442	RP11-474N8.5	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000205832	C16orf96	1.534979634	15.45544135	3.213844342	0.002133716	0.00854156
ENSG00000244256	RN7SL130P	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000256020	RP5-1154L15.2	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000257940	RP11-248E9.6	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000236548	RP11-510H23.1	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000267076	CCDC58P3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000262769	RP11-1113L8.1	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000177511	ST8SIA3	1.534979634	16.74147634	3.328456892	0.001369576	0.00580901
ENSG00000150627	WDR17	3.090401881	18.02751115	2.487726681	0.010033723	0.032582726
ENSG00000235310	RP11-250H24.4	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000112761	WSP3	0.757489584	19.31354564	4.432856543	7.55E-05	0.000437944
ENSG00000227038	AC005077.12	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000165194	PCDH19	1.534979634	19.31354564	3.533523223	0.000575412	0.002703923
ENSG00000229291	RP4-580N22.2	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000227240	RP11-563D10.1	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000186479	RGS7BP	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000233255	AC019181.2	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000254198	RP11-598P20.3	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000213754	RP11-284B18.3	0.757489584	16.74147634	4.227790211	0.000193974	0.001018857
ENSG00000234329	RP11-767N6.2	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000108602	ALDH3A1	1.534979634	24.45767899	3.872663343	7.35E-05	0.000429002
ENSG00000103546	SLC6A2	1.39E-17	25.74371105	7.736790212	5.45E-06	4.01E-05
ENSG00000243431	RPL5P30	1.534979634	18.02751115	3.43463054	0.000884859	0.003929458
ENSG00000260541	LA16c-429E7.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000232855	AF131217.1	3.868086451	16.74147634	2.070482753	0.014485426	0.044569852
ENSG00000203403	AC020907.2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000259298	RP11-562A8.4	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000125787	GNRH2	1.39E-17	29.60180421	7.937541613	1.61E-06	1.30E-05
ENSG00000109182	CWH43	1.39E-17	32.17386395	8.057364981	7.40E-07	6.31E-06
ENSG00000179915	NRXN1	3.090401881	21.88561332	2.766131942	0.002370371	0.009369526
ENSG00000130413	STK33	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000180481	GLIPR1L2	1.534979634	20.59957972	3.626069776	0.000376589	0.001848001
ENSG00000230314	ELOVL2-AS1	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000273143	RP11-525A16.4	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000241592	RP11-372E1.7	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000232546	RP11-458F8.1	2.312696499	16.74147634	2.778673814	0.005247305	0.018541622
ENSG00000250413	RP11-448G15.1	0.757489584	19.31354564	4.432856543	7.55E-05	0.000437944
ENSG00000132938	MTUS2	0.757489584	20.59957972	4.525403096	4.78E-05	0.000289284
ENSG00000261241	RP11-883G14.1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000270093	AP000473.8	3.090401881	16.74147634	2.381553033	0.014485426	0.044569852
ENSG00000249352	7SK	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000108231	LGI1	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000263508	RP11-963H4.3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000228798	AP000473.5	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000142449	FBN3	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000258561	RP11-72M17.1	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000102468	HTR2A	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000197353	LYPD2	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000240006	RP11-200A1.1	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000261097	LINC00563	1.534979634	14.16940643	3.089334671	0.005281544	0.01863638
ENSG00000251443	RP11-113I22.1	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000272167	RP11-53A1.2	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000237907	RP5-1013A22.2	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000137648	TMPRSS4	1.534979634	21.88561332	3.713035801	0.000164371	0.00088162
ENSG00000241886	RP11-242C19.2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000226435	ANKRD18DP	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000175928	LRRN1	0.757489584	18.02751115	4.333963859	0.000120499	0.000662026
ENSG00000243406	MRPS31P5	2.312696499	18.02751115	2.884847462	0.003515158	0.013136257
ENSG00000156885	COX6A2	1.534979634	28.31577365	4.083196531	1.58E-05	0.000105369
ENSG00000231969	AC144449.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000169302	STK32A	3.868086451	18.02751115	2.176656401	0.010033723	0.032582726
ENSG00000214049	UCA1	2.312696499	19.31354564	2.983740146	0.002364823	0.009363974
ENSG00000273199	AP000692.10	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000257526	RP11-20E24.1	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000087495	PHACTR3	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000261616	RP11-6O2.3	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000273407	RP11-757A13.1	1.39E-17	21.88561332	7.503518016	1.96E-05	0.000128617
ENSG00000224714	RP11-179K3.2	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000225083	GRTP1-AS1	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627
ENSG00000262248	RP11-235E17.5	0.757489584	15.45544135	4.113177661	0.000315208	0.001577627

ENSG00000268686	AC010524.2	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000254632	RP11-21L23.4	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000240618	RP11-206L10.5	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000258603	RP3-414A15.10	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000210077	MT-TV	0.757489584	21.88561332	4.612369121	1.96E-05	0.000128617
ENSG00000272054	RP11-423P10.2	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000248587	GDNF-AS1	1.39E-17	24.45767899	7.663145558	8.28E-06	5.84E-05
ENSG00000253888	RP11-521M14.1	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000271936	RP11-443B20.1	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000183798	EMILIN3	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000254237	RP11-115J16.2	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000255362	RP11-619A14.3	1.534979634	12.88337194	2.953055648	0.008390282	0.027879739
ENSG00000241544	RP11-6F2.5	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000263606	RP11-737O24.3	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000248114	AC114812.9	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000205754	SLCO1B7	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000268297	CLEC4GP1	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000269353	AC092071.1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000234509	AP000253.1	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000229312	RP11-470P21.2	1.39E-17	16.74147634	7.118939107	0.000193974	0.001018857
ENSG00000251049	RP11-685F15.1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000224477	RP1-81D8.3	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000268162	HBCBP	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000250564	RP11-215P8.4	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000228639	AC005152.3	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000106714	CNTNAP3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000143839	REN	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000241549	GUSBP2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000196381	ZNF781	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000223975	AP001048.4	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000171587	DSCAM	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000134201	GSTM5	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000227802	DNAJB3	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000267259	CTD-2008P7.9	1.39E-17	18.02751115	7.225112755	0.000120499	0.000662026
ENSG00000267541	RP11-380M21.2	1.39E-17	23.17164641	7.585538418	1.27E-05	8.64E-05
ENSG00000128313	APOL5	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000230910	RP3-525N10.2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000171864	PRND	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000273319	RP11-138A9.2	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000127249	ATP13A4	0.757489584	14.16940643	3.988667991	0.00085757	0.003832238
ENSG00000159197	KCNE2	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000128310	GALR3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000257046	LST3	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000249908	CTD-2589H19.4	1.39E-17	19.31354564	7.324005438	7.55E-05	0.000437944
ENSG00000261235	RP11-510J16.5	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000205488	CALML3-AS1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000221390	MIR1295A	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000229782	AC118754.4	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000175785	PRIMA1	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489
ENSG00000232131	NCOA7-AS1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000205041	CTC-425O23.2	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000171402	XAGE3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000136928	GABBR2	1.39E-17	20.59957972	7.416551991	4.78E-05	0.000289284
ENSG00000228057	SEC63P1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000271452	RP11-342K6.2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000110975	SYT10	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000228925	AC016722.4	1.534979634	11.59733845	2.802547756	0.013412089	0.04164886
ENSG00000252447	snoU13	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000235286	AP000925.2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000235724	AC009299.2	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000267363	CTD-3162L10.4	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000255385	RP11-313I2.2	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000161649	CD300LG	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000186510	CLCNKA	1.534979634	14.16940643	3.089334671	0.005281544	0.01863638
ENSG00000260743	RP11-255C15.3	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000248705	AC114812.10	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000121351	IAPP	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000260948	RP11-552M11.8	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000107295	SH3GL2	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000259433	CTD-2651B20.4	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000227310	RP11-144G6.10	1.39E-17	15.45544135	7.004326556	0.000517265	0.002454489

ENSG00000187987	ZSCAN23	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000234650	PCCA-AS1	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000212293	SNORA16	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000127083	OMD	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000258590	NBEAP1	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000253190	AC084082.3	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000244383	RP11-475O23.3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000095713	CRTAC1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000131379	C3orf20	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000155754	ALS2CR11	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000272507	U6	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000204365	C10orf126	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000260372	AQP4-AS1	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000162753	SLC9C2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000227678	RP11-394G3.3	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000252172	RNU6-720P	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000228751	AC004022.8	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000226622	AC092155.4	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000226851	AC004112.4	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000227192	RP1-45I4.3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000203857	HSD3B1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000236378	RP11-394G3.2	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000224177	LINC00570	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000205622	AF064858.6	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000187736	NHEJ1	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000206150	RNASE13	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000120952	PRAMEF2	1.39E-17	14.16940643	6.879816886	0.00085757	0.003832238
ENSG00000171495	MROH2B	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000224201	PNMA6A	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000255710	RP11-667M19.9	0.757489584	10.3113069	3.5338229	0.004174171	0.015119355
ENSG00000242973	RP11-446F17.3	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000145832	SLC25A48	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000235904	RBMS3-AS3	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000253406	AC012613.2	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000185559	DLK1	0.757489584	12.88337194	3.852388967	0.00143701	0.006003845
ENSG00000071909	MYO3B	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000229775	RP11-298H24.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000259762	RP11-158M2.4	0.757489584	11.59733845	3.701881076	0.002434933	0.009484447
ENSG00000134551	PRH2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000273030	RP11-285F16.1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000153498	SPACA7	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000124302	CHST8	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000225431	AP001626.1	1.39E-17	12.88337194	6.743537863	0.00143701	0.006003845
ENSG00000231083	AC011747.6	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000270244	RP11-123J14.4	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000210117	MT-TW	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000253199	RP11-421P23.1	1.39E-17	11.59733845	6.593029971	0.002434933	0.009484447
ENSG00000204055	RP11-247A12.2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000242366	UGT1A1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000165186	PTCHD1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000214105	CTD-2116F7.1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000239265	CLRN1-AS1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000248373	RP11-556I14.1	1.39E-17	10.3113069	6.424971795	0.004174171	0.015119355
ENSG00000182545	RNASE10	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000222406	RNA5SP314	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000237845	RP5-940F7.2	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000233244	CYP4F59P	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000179796	LRRC3B	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000151952	TMEM132D	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026
ENSG00000173610	UGT2A1	1.39E-17	9.025278763	6.234723377	0.012730848	0.039847026

Table S8. Differentially expressed genes in the intrachromosomal differential interaction regions and their enrichment

gene_id	gene_name	ICC1	ANHT1	ICC2	ANHT2	ICC3	ANHT3
ENSG00000000971	<i>CFH</i>	12.47589435	246.3210112	27.25633513	119.8938872	2.132136612	146.7420972
ENSG00000003436	<i>TFPI</i>	4.657799219	18.45378238	3.72230474	16.8049085	0.492979756	16.1365691
ENSG00000007001	<i>UPP2</i>	0.031785748	2.496947086	0.193295883	41.76449145	0.107746945	4.35846613
ENSG00000007933	<i>FMO3</i>	5.265419745	261.9109046	4.432831729	173.9925275	0.954535103	285.1891845
ENSG00000008226	<i>DLEC1</i>	0.061998982	0.622494829	0.083240163	1.872480238	0.095528819	3.222534737
ENSG00000009724	<i>MASP2</i>	0.198991792	74.20428504	1.459816861	90.61323592	0.206109438	91.30171755
ENSG00000011347	<i>SYT7</i>	0.063155019	9.504830315	0.240036925	21.77230404	0.99012981	16.62423954
ENSG00000019169	<i>MARCO</i>	2.418705833	27.1809289	4.595230073	16.13202453	0.114937849	3.719476002
ENSG00000021826	<i>CPS1</i>	0.368978238	512.9927445	3.013931706	176.7779095	0.057199298	418.0446717
ENSG00000021852	<i>C8B</i>	0.533840996	323.327783	4.173943442	152.7429028	0.043780833	236.6739788
ENSG00000023330	<i>ALAS1</i>	19.56899096	254.8251601	18.03078629	56.90638336	5.323738958	78.9713982
ENSG00000036672	<i>USP2</i>	0.144983075	1.836452288	0.521806392	3.367631524	0.491461881	2.822801972
ENSG00000042445	<i>RETSAT</i>	11.914128	61.61694566	8.856669306	25.34007392	12.79586574	47.22443522
ENSG00000044012	<i>guca2b</i>	0.078718975	1.959227831	0.205160059	2.767406738	0.86723206	3.53256766
ENSG00000047457	<i>CP</i>	12.10951606	218.4694111	4.135285565	80.11619748	1.637580781	76.43890237
ENSG00000049246	<i>PER3</i>	0.828058372	3.546785232	0.815625157	6.929196377	1.680211932	10.82612589
ENSG00000055955	<i>ITIH4</i>	0.843195235	2.931107245	0.433533029	4.355701619	0	3.575109669
ENSG00000055957	<i>ITIH1</i>	2.079251791	575.7217182	33.547576	407.0349405	0.04383223	698.8373879
ENSG00000060971	<i>ACAA1</i>	6.289397989	77.71253344	6.704888271	51.38240118	2.768649945	145.226014
ENSG00000062282	<i>DGAT2</i>	0.517280473	25.39761241	2.365725978	12.16531555	0.030232261	51.73337478
ENSG00000064225	<i>ST3GAL6</i>	0.829591339	11.76541551	0.766152753	14.75314302	1.203392696	13.41566726
ENSG00000065485	<i>MIR7110</i>	4.338021073	17.86777497	4.254907632	16.15245355	4.298832407	17.73442466
ENSG00000072080	<i>SPP2</i>	0.334353403	232.3136977	3.001499777	106.1811306	0.062965952	209.8754763
ENSG00000073734	<i>ABCB11</i>	0.063864608	17.00217798	0.134742085	12.44478795	0.015463391	7.248320735
ENSG00000073754	<i>CD5L</i>	0.363562434	31.58103154	1.612461167	12.91576669	0	3.243940389
ENSG00000073849	<i>st6gal1</i>	15.16521792	95.24809064	4.54623123	51.969077	4.547932795	68.66012066
ENSG00000074964	<i>ARHGEF10L</i>	7.156785754	15.24119209	16.36299846	53.25720326	10.56172197	40.22409239
ENSG00000075239	<i>ACAT1</i>	5.108542904	104.4319704	4.277168393	25.14900697	2.339347491	73.4090278
ENSG00000076258	<i>FMO4</i>	0.560133829	18.00726533	1.557162405	10.17409545	1.708861413	19.7367189
ENSG00000078902	<i>TOLLIP</i>	7.069313967	22.31110398	12.3783903	28.11098739	8.753324995	40.02710711
ENSG00000079739	<i>PGM1</i>	9.766734486	80.02083453	6.468410751	29.79106587	4.751851033	68.80848722
ENSG00000080910	<i>CFHR2</i>	0.884525573	626.9448895	7.183120408	241.0612823	0	425.1890685
ENSG00000082146	<i>STRADB</i>	3.66742528	24.60090195	7.782539919	17.60687846	6.424731488	24.9360922
ENSG00000082438	<i>COBLL1</i>	0.415886976	9.797664813	0.741614914	6.670705367	1.006315128	8.340236303
ENSG00000084234	<i>APLP2</i>	37.53178831	85.03557742	23.1721452	64.14145442	29.51636844	79.68292799
ENSG00000084674	<i>APOB</i>	0.643379508	472.7089194	10.06353813	200.7684347	0.094005177	299.4564477
ENSG00000084734	<i>GCKR</i>	3.820507603	34.84554982	1.296502121	52.12457608	1.087657337	57.59577288
ENSG00000084764	<i>MAPRE3</i>	2.33685437	5.389257172	3.068800656	8.478033348	3.592281282	9.371273014
ENSG00000085465	<i>OVGP1</i>	0.629119522	5.72498765	1.229724452	3.621662964	1.159591339	7.789986887
ENSG00000085552	<i>IGSF9</i>	0.035494885	0.739871167	0.345363097	7.000389444	2.761347092	7.763703836
ENSG00000085741	<i>WNT11</i>	0.391463793	4.445288844	0.102024619	2.958854576	0.663489623	2.016975325
ENSG00000086205	<i>folh1</i>	0.51616098	12.33051231	0.501794465	2.030613642	0.395760108	7.189949426
ENSG00000087884	<i>AAMDC</i>	2.297759489	5.267378479	0.84049103	3.061096532	1.434800577	4.783824256
ENSG00000090512	<i>FETUB</i>	0.092875945	97.08632143	0.484112867	35.95694036	0.37386034	71.66423204
ENSG00000090534	<i>THPO</i>	1.52151653	4.96265248	0.490348612	5.4783815	0.24956218	7.831293598
ENSG00000090539	<i>CHRD</i>	2.676314361	8.690725501	1.64047471	47.9046258	1.534081718	46.19285793
ENSG00000091428	<i>RAPGEF4</i>	0.269069175	3.134036078	0.855191701	1.949531965	0.42267467	5.137458055
ENSG00000091513	<i>TF</i>	1.805187403	1594.582206	11.55449957	669.1415499	0.153445047	1505.693392
ENSG00000092607	<i>TBX15</i>	0.160519697	13.65652194	0.075088797	2.864985819	0.04185598	5.171693905
ENSG00000092621	<i>PHGDH</i>	1.203719828	29.15305399	0.994891266	23.99455351	3.97409572	62.42328694
ENSG00000093217	<i>XYLB</i>	0.202300253	6.800024923	0.962789318	3.586907195	0.163984881	12.5576694
ENSG00000099260	<i>PALMD</i>	0.723968218	6.287059087	0.752751271	4.47905989	0.241545152	5.447922455
ENSG00000099834	<i>CDHR5</i>	1.589562331	75.80284349	1.201719883	36.53652133	3.002628883	104.427674
ENSG00000099869	<i>IGF2-AS</i>	0	0.560963078	0.014240269	0.633887689	0.236149773	0.844568845
ENSG00000109906	<i>ZBTB16</i>	0.398264647	4.244878332	0.435691451	10.90278776	0.750018166	5.136169074
ENSG00000109927	<i>TECTA</i>	0.103809626	0.303965441	0.058354388	0.461552094	0.056923806	0.304478935
ENSG00000109929	<i>SC5D</i>	1.080738272	40.24249038	1.665054862	27.48622579	1.187766821	46.56227971
ENSG00000109956	<i>B3GAT1</i>	0.452470469	1.382091615	0.132218251	0.766420277	1.115475595	4.019964085
ENSG00000110074	<i>FOXRED1</i>	3.106985219	11.19105431	3.637393196	11.08339794	3.344057483	18.97149736
ENSG00000110169	<i>HPX</i>	1.203678389	1463.58376	21.58842067	991.7856046	0.52647929	2028.381563
ENSG00000110243	<i>APOA5</i>	0.290992126	321.4978002	5.645818516	432.3871684	0	773.0291765
ENSG00000110244	<i>APOA4</i>	0	4.87357923	0.249960317	6.74343601	0	46.33404391
ENSG00000110245	<i>Apoc3</i>	10.69060043	7882.873713	116.3046691	15703.4554	0.045988412	19874.22973
ENSG00000110436	<i>SLC1A2</i>	0.026678015	17.63120343	0.11919282	4.247254543	0.012918973	7.347857871
ENSG00000110628	<i>SLC22A18</i>	3.571495905	13.58661478	3.863037332	21.97261604	7.349373828	22.56873926
ENSG00000110723	<i>EXPH5</i>	0.052009844	1.874280678	0.026356909	1.226573981	0.135899722	2.54288256
ENSG00000113790	<i>ehhadh</i>	0.98989949	105.7203767	1.633074072	54.76674382	1.550670536	94.64483669
ENSG00000113805	<i>CNTN3</i>	0	1.230557292	0.015982326	1.681569285	0.31960551	0.886733562
ENSG00000113889	<i>kng1</i>	1.030376663	731.9164744	8.14353782	322.4547923	0	571.5322956
ENSG00000113905	<i>HRG</i>	1.365006631	633.7964122	10.49510654	370.2547431	0.015738378	572.6449692

ENSG00000113924	HGD	2.898800538	393.8237591	3.106837197	196.2022262	10.29360332	294.8660424
ENSG00000114021	NIT2	5.812980407	30.26606545	8.074543105	20.1601733	3.871845724	32.94653092
ENSG00000114023	FAM162A	6.789713974	34.15231636	3.713489025	28.39959052	7.958893004	41.72128288
ENSG00000114054	PCCB	2.932522212	22.81821184	3.7346921	9.1030119	2.760110664	18.18948208
ENSG00000114200	BCHE	0.030496579	75.52308373	1.351180689	23.85474079	0.051688468	57.80876702
ENSG00000114248	LRRC31	0	0.634050623	0	0.344970185	0.012793435	0.702554413
ENSG00000114315	HES1	10.71181246	41.12525636	9.345428735	28.64406894	41.60287475	95.60965374
ENSG00000114378	HYAL1	7.262353287	53.35728985	2.059592141	51.66899474	3.738452616	66.58717095
ENSG00000114541	FRMD4B	1.548365149	3.532566415	1.540789735	4.973250394	1.530850277	4.374914814
ENSG00000114698	PLSCR4	3.235299606	14.02580822	2.743039014	11.04163863	3.099773445	12.08499726
ENSG00000114771	aadac	3.380951676	359.8209126	6.192562054	135.1527288	0.167135343	201.9688848
ENSG00000114779	ABHD14B	12.63712245	47.2710975	8.421103251	45.62859257	6.627161461	80.87654035
ENSG00000114790	ARHGEF26	0.094178814	12.22612243	0.632224887	17.06621267	0.457102527	10.18874862
ENSG00000114812	VIPR1	0.114653579	7.956392224	0.210276548	10.23351603	0.05397935	9.252814115
ENSG00000114857	NKTR	1.007621033	3.126394054	2.760224621	6.803777131	1.944241615	4.731559357
ENSG00000115042	FAHD2A	1.908014564	16.22088904	1.909817428	14.90281503	2.987826117	21.46790941
ENSG00000115107	STEAP3	2.403108427	40.25123521	5.197562292	41.32983681	12.54015096	38.6484572
ENSG00000115290	GRB14	0.807260574	17.5064744	11.15209728	27.76755707	2.307196332	29.14946703
ENSG00000115361	ACADL	0	7.405438666	0.260814933	8.028889076	0.427063732	11.53012102
ENSG00000115363	EVA1A	1.044718996	49.87248717	1.309315947	21.73553928	0.812774788	30.00250795
ENSG00000115423	DNAH6	0.006955043	0.578814168	0.090632348	0.342311462	0.091357474	0.601105194
ENSG00000115425	PECR	3.086738753	60.62873471	3.130657398	41.58911376	3.542032678	64.82899388
ENSG00000115457	IGFBP2	7.640298286	71.52414579	63.07735757	181.9712742	4.611691306	88.89056084
ENSG00000115504	EHBP1	1.458058549	8.538695817	2.523426295	5.618367677	2.117526041	4.694712744
ENSG00000115648	MLPH	0.337735205	3.580271141	0.152136259	6.904079482	0.916940628	9.386801094
ENSG00000115718	PROC	0.414386783	236.1293087	6.70902174	370.6227567	3.336122886	471.7532911
ENSG00000115841	RMDN2	0.423027559	5.422760687	0.524031937	2.037981245	0.418242335	3.398307712
ENSG00000115963	RND3	3.308233934	68.42537784	3.680550914	33.62664839	7.202803837	20.75517285
ENSG00000116005	PCYOX1	6.091974038	43.20892493	4.522444339	17.20630202	13.53243785	29.7387462
ENSG00000116016	EPAS1	9.616759299	33.10506944	10.58163059	30.92104795	10.21850407	21.63627755
ENSG00000116133	DHCR24	33.8839723	235.8709191	72.13877643	150.4263783	22.76922407	219.9750537
ENSG00000116138	DNAJC16	1.629987481	5.856490749	1.43034632	3.878086025	0.999951231	6.376058418
ENSG00000116171	SCP2	6.088725544	136.163872	10.17107241	84.00957154	5.519528628	136.0065252
ENSG00000116194	ANGPTL1	0.207149111	5.327568245	0.491889781	5.121979497	0.257470238	6.908847431
ENSG00000116285	ERRFI1	7.690332389	249.3663563	37.41323543	290.8416887	22.89089126	181.8375935
ENSG00000116678	LEPR	0.639893132	37.03996784	1.407576718	33.0875396	0.559656132	19.96868721
ENSG00000116690	PRG4	0.055835915	34.78577492	0.574001283	9.749272537	0.094635955	26.34051886
ENSG00000116704	SLC35D1	1.5371657	24.44283237	2.185726061	9.14520774	1.163492676	17.52375435
ENSG00000116761	CTH	0.817646888	122.9801486	1.505215332	32.30368435	0.115485399	104.1561136
ENSG00000116785	CFHR3	0.047872898	73.0292195	2.439906933	110.769237	0.027046495	131.2867675
ENSG00000116791	CRYZ	8.24518095	58.71940474	15.13624768	46.5360702	12.55967078	50.20335619
ENSG00000116882	HAO2	0.075112246	137.8726996	1.218062707	135.1112252	0	230.9978887
ENSG00000116990	MYCL	1.280422804	5.715510489	2.05544861	4.436155733	0.165122459	7.386813248
ENSG00000117009	KMO	0.331954186	16.3518173	0.679760903	6.765834742	0.087073249	10.9951614
ENSG00000117010	ZNF684	0.371137045	5.893518813	0.712018146	2.663868026	0.825612297	3.649712878
ENSG00000117118	SDHB	24.07026112	66.06649343	18.48982119	41.97460235	9.026355908	71.57347484
ENSG00000117143	UAP1	4.030134115	31.36695707	11.00706313	26.68657863	5.392002843	38.97420977
ENSG00000117305	HMGCL	8.073411435	49.70482317	7.66315246	34.35392107	2.54807338	58.05025245
ENSG00000117479	SLC19A2	0.857717324	11.56993816	2.446719531	22.23258132	2.582015684	12.48977954
ENSG00000117480	FAAH	4.960231228	17.7229043	9.941985526	33.68560056	2.223712	38.99822353
ENSG00000117528	ABCD3	1.458451471	18.60717171	6.345756598	16.78208997	4.216805744	19.270077
ENSG00000117592	PRDX6	43.20304891	303.039033	48.69210082	218.5406019	51.30095735	340.9472527
ENSG00000117594	HSD11B1	9.978017017	555.9425325	12.2665221	211.9851696	20.5915374	387.7297805
ENSG00000117601	SERPINC1	2.479044941	2200.657376	20.91131434	1343.079784	0.022589883	2338.174853
ENSG00000117620	SLC35A3	1.762038683	12.40455153	3.140023853	6.988710802	3.688416526	9.624389994
ENSG00000117643	MAN1C1	2.340898325	5.750001677	0.81526884	4.417197462	0.304858171	11.92345003
ENSG00000117791	MARC2	5.806360253	68.13602469	7.219574566	41.33544019	15.29993621	114.9619664
ENSG00000117834	SLC5A9	0.113990631	4.0299718	0.198057495	3.788814764	1.563180088	7.440592346
ENSG00000118004	COLEC11	24.69610142	62.87821117	8.36098588	73.57393549	5.324491403	40.2617468
ENSG00000118094	TREH	0.014773728	3.309315039	0.064172983	3.505802358	0.43819829	4.542648308
ENSG00000118137	APOA1	8.118557697	8282.945656	218.6128827	20166.86219	0.223741374	22989.33153
ENSG00000118298	CA14	0.159181336	3.638041817	0.159562996	1.054650199	0.996167952	4.314514633
ENSG00000119147	c2orf40	0.080979716	1.175705501	0	0.379584566	0.34313008	1.794577738
ENSG00000120341	SEC16B	0.025482027	0.703587079	0.066412122	0.660677562	0.172757336	0.889407031
ENSG00000121310	ECHDC2	3.580433118	22.43719921	3.369688847	49.86025504	2.764056336	47.34907831
ENSG00000121671	CRY2	3.161317987	14.48158242	9.885643581	28.54402149	5.146087698	24.75950592
ENSG00000121690	DEPDC7	0.183685498	20.88048828	0.773328823	11.82230168	0.215534384	19.82080356
ENSG00000121691	CAT	10.7834883	375.2597763	12.33222204	112.520385	3.498307019	334.8161835
ENSG00000123612	ACVR1C	0.07666432	1.065350109	0.026640686	0.476147453	0.060637684	0.815493596
ENSG00000123689	G0S2	13.72955284	51.66219092	9.381689965	54.18109441	1.517617589	202.3979066
ENSG00000123838	C4BPA	26.27959304	690.4869484	27.07852236	248.2612128	5.547246196	439.8550838
ENSG00000123843	C4BPB	3.708228638	93.79255462	5.301529685	75.52428368	0.185582314	103.1747285

ENSG00000124003	MOGAT1	0	1.116086847	0.03895692	2.049412566	0.038001875	3.726574239
ENSG00000124370	MCEE	5.671837898	20.16653475	3.670394313	9.918954907	5.419666365	18.08434884
ENSG00000124374	PAIP2B	0.868202975	5.902782298	0.3446127	1.65766738	0.291765308	5.224682009
ENSG00000124839	RAB17	1.355915012	20.1902514	2.099812993	32.9184854	11.86535638	39.96084326
ENSG00000125551	PLGLB2	0.583791656	8.010918833	0.670183459	6.74343601	0.388718377	17.29209806
ENSG00000126106	TMEM53	1.835852109	9.110308355	1.909371336	10.47644264	0.755981171	13.10769947
ENSG00000127241	masp1	0.210278031	19.78057825	0.315534569	12.83595379	0.777597747	13.63666657
ENSG00000127249	ATP13A4	0.007815604	0.133733673	0.020369292	0.261023571	0.033116551	0.649501048
ENSG00000127472	PLA2G5	0.450663869	2.215263287	0.908307405	8.52370829	0.229148243	1.587946601
ENSG00000128641	MYO1B	3.393798369	42.97824699	16.1987509	34.33652575	5.087456588	28.08054072
ENSG00000128655	PDE11A	0.033841979	2.246104686	0.013066683	1.434288588	0.21350133	1.474933835
ENSG00000129151	BBOX1	0.019072739	23.46794544	0.314817445	11.0634497	11.03942119	32.74618219
ENSG00000131373	HACL1	3.469654297	11.17999718	2.502898627	5.853831441	3.360397804	8.881873314
ENSG00000131781	FMO5	0.97318108	77.82832564	2.352248476	52.46405604	1.536372382	46.73756393
ENSG00000131791	PRKAB2	1.205005854	11.26011026	4.703313148	12.16412111	4.157655645	12.08829701
ENSG00000131910	NR0B2	5.041010647	81.95707633	13.45590877	220.1664773	1.619221744	176.8263345
ENSG00000132196	HSD17B7	1.743518411	4.803855376	2.999645028	9.454545832	1.641710471	8.068485042
ENSG00000132677	RHBG	0.027774958	1.814630565	0.14477607	6.761868866	0.047075608	12.2564648
ENSG00000132703	APCS	154.6883972	1034.267195	17.67987859	768.1745806	45.71814295	915.6297538
ENSG00000132744	ACY3	2.169010537	18.95072539	0.816537036	22.93935377	1.684944656	37.97298884
ENSG00000132855	ANGPTL3	0.173520843	377.7098882	4.195744155	119.6150679	0.012254143	120.335921
ENSG00000133048	CHI3L1	39.61774967	86.7462782	59.43134149	241.7372417	6.04167362	37.86269409
ENSG00000133315	MACROD1	5.714115838	27.33077103	14.01285435	48.91573563	7.015775477	51.97295572
ENSG00000133800	LYVE1	0.414467163	5.552968654	1.161503608	6.392355273	0.135963464	1.33329723
ENSG00000134240	HMGCS2	0.932227399	1066.472207	8.400390745	534.0704273	0	1664.320117
ENSG00000134365	CFHR4	0	30.70254498	0.266383992	16.39659982	0	21.13663766
ENSG00000134389	CFHR5	0.083059788	49.02004136	0.51953576	17.95806329	0	31.97250527
ENSG00000134716	CYP2J2	0.660133642	53.20188163	0.996775981	30.14191853	0.253074691	62.4088266
ENSG00000135378	PRRG4	1.903604184	8.552999355	1.668511484	6.393460217	4.162641508	9.731844172
ENSG00000135617	PRADC1	9.051675101	26.03052446	8.240814437	22.19294985	6.73673033	28.64551667
ENSG00000135744	AGT	13.43599936	812.5645686	85.77024781	999.5061397	48.62209646	1350.559433
ENSG00000135917	SLC19A3	0.15873787	7.133405517	0.114918892	3.704840454	0.059787524	11.08095346
ENSG00000135929	CYP27A1	14.6515462	256.193751	42.15444303	240.1781097	3.311042313	371.8752805
ENSG00000136546	SCN7A	0.017212268	0.339145423	0.104671455	1.694297559	0	0.657980799
ENSG00000136630	HLX	2.200066189	4.674825637	2.423601724	5.601494355	2.873543295	10.76260539
ENSG00000136689	ILIRN	3.175353263	11.13618841	1.843227032	9.437910902	0.623809642	16.19274334
ENSG00000137491	SLCO2B1	13.43866108	60.83530103	10.93910636	24.08015643	0.602973342	56.50597485
ENSG00000137642	SORL1	1.365227209	14.0388851	0.982413833	14.49627241	1.304393	15.89168067
ENSG00000137700	SLC37A4	7.057640977	35.09827913	5.959690782	39.98151161	7.584058567	51.74436886
ENSG00000137713	PPP2R1B	2.244861352	12.35800448	3.292880012	22.00397219	1.736459468	16.13322716
ENSG00000137714	FDX1	7.49050582	28.0466428	5.921548999	22.62290268	4.844705612	38.2261431
ENSG00000137941	TLL7	0.093607113	0.457634776	0.185875831	0.595479363	0.132211777	0.807538705
ENSG00000137960	GIPC2	0.851662833	7.452049792	0.205521529	7.505955171	0.080193234	9.849636802
ENSG00000137992	DBT	0.889761909	10.65866395	1.210032324	3.705369831	1.652515031	6.813719375
ENSG00000138029	HADHB	22.24114845	70.66277169	18.38344331	39.5746529	28.79264027	69.81239569
ENSG00000138030	KHK	0.767895887	65.48274839	5.923896144	41.95144432	1.158336879	94.36894064
ENSG00000138075	ABCG5	0.050532504	21.04678773	0.417048486	32.13238195	0.010705904	37.05977903
ENSG00000138079	SLC3A1	0.050362308	3.480595087	0.056252551	0.644972696	0.158523435	1.996969127
ENSG00000138356	AOX1	4.41849949	329.9804641	5.537215312	116.3522069	0.337143432	222.3123839
ENSG00000138413	idh1	20.0284684	108.2696441	19.85563477	60.20991327	5.306191852	106.9304049
ENSG00000142082	SIRT3	3.29743528	6.675173398	2.495759107	7.844656481	3.67482949	10.46558444
ENSG00000142748	FCN3	0.563855992	39.67232931	2.82603958	49.36602815	0.349189353	23.50118386
ENSG00000143028	SYPL2	0.09322138	3.280874687	0.070862376	0.983173909	0.158000355	1.684969664
ENSG00000143171	RXRG	0.018560517	0.375334893	0	0.228376634	0	0.370184815
ENSG00000143196	DPT	4.631108723	19.64712792	2.194500433	34.87443825	0.222989723	18.14962674
ENSG00000143199	ADCY10	0.007655193	1.226531994	0.046552853	1.628189937	0.11028529	2.252043052
ENSG00000143257	NR1I3	0.071097168	33.59894184	0.827654787	23.34493891	0.168703027	37.577399
ENSG00000143278	F13B	0.038363452	108.3426501	0.616568782	30.75006821	0	36.05766307
ENSG00000143365	rorc	1.17599716	27.6483383	1.804037322	24.47859796	3.500698504	35.81335818
ENSG00000143369	ECM1	2.601521566	18.25416506	2.466622297	14.08745929	4.587097708	13.71556776
ENSG00000143416	SELENBP1	4.211330389	89.71057659	2.9245262	148.2872726	4.091708692	152.227835
ENSG00000143434	SEMA6C	0.431447618	2.317335006	1.110309325	11.51891709	1.759158318	11.79820623
ENSG00000143627	PKLR	0.035901626	61.20828308	0.49902951	32.24768798	0.030424725	84.67277722
ENSG00000143630	HCN3	0.980730316	10.71454206	1.852613756	13.20991824	1.826524462	19.50355664
ENSG00000143819	EPHX1	14.45140806	648.6492612	24.70154971	468.9535944	36.53364244	804.2980646
ENSG00000143839	REn	0	0.3493009	0	0.39470965	0	0.63980065
ENSG00000143845	ETNK2	1.152636839	37.69998736	1.528371819	57.76098239	2.81900653	63.37113254
ENSG00000143869	GDF7	0.022583003	2.617119073	0.117713172	2.084032813	0.612412718	4.729328929
ENSG00000143878	RHOB	51.08695147	441.6809918	262.2512653	901.5205832	107.7623945	335.0499581
ENSG00000143921	ABCG8	0.017634232	34.28878445	0.382991105	25.69653979	0.029888154	40.79839493
ENSG00000143994	ABHD1	0.19805334	1.100296334	0.589912368	3.232667624	0.119885505	4.84360421
ENSG00000144035	NAT8	0.496253731	99.19560683	2.026253469	84.00277587	1.556030296	53.69477975
ENSG00000144040	SFXN5	1.051214631	8.466233966	1.193100026	9.80526129	0.711242084	13.2800088
ENSG00000144115	THNSL2	1.842806171	4.796680074	1.154454019	6.401049398	7.509754612	19.243538

ENSG00000144230	<i>gpr17</i>	0.070378477	0.602126973	0.091711386	1.639152314	0.357852172	1.637627772
ENSG00000144331	<i>ZNF385B</i>	0.212407811	3.414258896	0.23066018	4.884863769	0.022500545	5.810367879
ENSG00000144357	<i>UBR3</i>	0.823341598	5.936077065	2.346740301	5.780870255	2.379366192	5.150888518
ENSG00000144648	<i>ACKR2</i>	0.060151142	1.323325134	0.089581683	0.981799401	0.050974904	1.999498893
ENSG00000144649	<i>FAM198A</i>	0.063924591	0.712640808	0.120323979	1.142378726	0.243777158	3.895710526
ENSG00000144655	<i>CSRNP1</i>	9.080285243	32.29845601	4.509499811	31.58808805	5.092866039	30.11109088
ENSG00000144820	<i>ADGRG7</i>	0.022974934	4.842605615	0.049898377	4.361557488	0	2.596632476
ENSG00000144827	<i>ABHD10</i>	4.729079577	15.87422033	5.784141865	13.2893235	4.271305041	15.35807469
ENSG00000144852	<i>NR1I2</i>	0.034934197	25.63587811	0.212442269	34.23412251	0.103617079	40.77460879
ENSG00000144891	<i>AGTR1</i>	0.553997803	23.62522882	1.749051443	14.10828411	0.103057413	15.65324044
ENSG00000144908	<i>ALDH1L1</i>	0.137162286	35.08230273	0.300876471	21.42781532	0.476574841	41.19458762
ENSG00000145020	<i>AMT</i>	2.122564575	15.62729582	4.520403456	15.6303266	2.645750334	21.4410136
ENSG00000145192	<i>AHSG</i>	2.376724253	2530.077337	19.51985052	517.4089711	0.18618173	1557.632138
ENSG00000148935	<i>GAS2</i>	0.013316868	4.971630839	0.219810197	4.822063126	0.440128257	7.060575159
ENSG00000148943	<i>LIN7C</i>	2.90712803	9.481024442	4.136679737	11.17169278	3.500063442	12.14621547
ENSG00000149124	<i>GLYAT</i>	0.016736192	113.8470191	0.843289674	65.86797615	0	131.2665072
ENSG00000149131	<i>SERPING1</i>	242.3456402	759.8482189	67.04759426	725.8097929	87.46679374	948.9278309
ENSG00000149150	<i>SLC43A1</i>	5.784641853	39.57197397	15.87325817	38.59205078	0.833933611	54.30498112
ENSG00000149212	<i>SESN3</i>	0.929028139	5.195508042	0.830710292	2.310130803	0.675927654	3.848958243
ENSG00000149260	<i>CAPN5</i>	1.364279251	12.66213741	0.827660797	12.5665669	8.267472378	21.94044456
ENSG00000149476	<i>TKFC</i>	2.674384304	41.0085096	5.86610002	47.8828714	3.700642728	69.33421453
ENSG00000149547	<i>EI24</i>	10.69336651	48.15249994	13.75075043	29.3579693	18.65124729	42.958848
ENSG00000149582	<i>TMEM25</i>	1.257965959	3.212913058	1.306990915	3.212248977	1.159699819	9.281535612
ENSG00000149742	<i>SLC22A9</i>	0.099481855	17.91999814	0.276557845	11.99586463	0	15.87312367
ENSG00000149809	<i>TM7SF2</i>	3.130257284	39.25462144	8.553512966	47.29062054	1.378950652	69.14754726
ENSG00000150672	<i>DLG2</i>	0.023367632	0.404389849	0.048213698	0.266987926	0.029704244	0.252449984
ENSG00000150722	<i>PPP1R1C</i>	0.028591702	1.289803467	0.173872214	0.770619791	0.024229952	1.726603238
ENSG00000150787	<i>PTS</i>	4.143988182	6.688361695	2.947881312	12.32508356	4.249799417	9.083602095
ENSG00000151090	<i>THRB</i>	0.259016071	4.751026256	0.318776659	2.949914495	0.292669851	4.412633603
ENSG00000151360	<i>ALLC</i>	0.073950005	0.86275006	0.016060917	1.852322657	0.015667177	1.474914166
ENSG00000151365	<i>THRSP</i>	0.040030007	143.654352	1.217154866	165.4956374	0	203.8551651
ENSG00000152078	<i>TMEM56</i>	0.603154105	40.95663281	1.174833752	42.62043786	1.156793081	32.95520057
ENSG00000152270	<i>PDE3B</i>	0.448984698	5.831812349	0.721598126	4.908914749	0.04185398	5.275920531
ENSG00000152580	<i>IGSF10</i>	0.016029753	0.093506892	0.024370083	0.21132538	0.006792183	0.079927343
ENSG00000152672	<i>CLEC4F</i>	0.246843623	0.797494783	0.049487093	0.467272435	0	0.94677571
ENSG00000152760	<i>TCTEX1D1</i>	0.060639004	2.876983868	0.092189665	0.906013257	0.025694171	4.409378809
ENSG00000153086	<i>ACMSD</i>	1.670566464	60.24163914	0.791615798	31.6487491	1.88762202	34.02018391
ENSG00000153165	<i>RGPD3</i>	0	0.441557187	0.050770645	0.45493335	0.127352525	0.596675578
ENSG00000153561	<i>RMND5A</i>	2.921661018	14.48321165	5.046352494	11.49748902	6.456207959	15.31413885
ENSG00000153823	<i>PID1</i>	0.75438238	18.10207268	4.781741858	13.18668488	5.457719881	14.32617436
ENSG00000153904	<i>DDAH1</i>	3.747362738	24.28235188	3.330575674	12.60786931	2.742945071	24.78282756
ENSG00000154305	<i>MIA3</i>	3.095190242	14.30071173	4.267824615	9.089374671	4.155378913	12.33582397
ENSG00000154309	<i>DISP1</i>	0.745283851	3.214507115	0.412020851	2.634971189	0.667474267	2.604102409
ENSG00000154511	<i>FAM69A</i>	2.610846016	7.952227183	1.887488487	5.070676145	1.191375009	5.704930558
ENSG00000156869	<i>FRS1</i>	0.374801152	5.585746198	0.29409618	2.550257508	0.543034763	4.963447909
ENSG00000157087	<i>ATP2B2</i>	0.013869718	4.666049241	0.469920478	6.639448446	1.790503278	4.656571726
ENSG00000157103	<i>SLC6A1</i>	0.316240321	33.30212888	0.824196233	28.46777814	2.411972163	55.92183628
ENSG00000157131	<i>C8A</i>	0.877669798	305.7571078	4.73078546	217.8078311	0	347.6447082
ENSG00000157184	<i>cpt2</i>	6.052311083	32.39260762	4.21353278	14.13623259	2.365435122	25.40092609
ENSG00000158109	<i>TPRG1L</i>	16.02198545	43.81981657	9.927656176	31.82460429	10.29469839	35.4629079
ENSG00000158125	<i>XDH</i>	0.474856539	27.41539683	0.338138577	22.24931757	0.310058031	20.45557773
ENSG00000158825	<i>CDA</i>	2.830449887	28.3153435	3.264452325	66.39448446	0.206780709	54.74929629
ENSG00000158874	<i>APOA2</i>	9.54823686	5587.829342	169.2694237	5285.455193	0.084287756	6524.787457
ENSG00000159423	<i>ALDH4A1</i>	5.468118508	102.6465406	12.00333804	105.056862	1.533845124	143.4858232
ENSG00000159650	<i>UROC1</i>	0.01411692	60.1694522	0.233015976	63.6240858	0.035890025	116.048992
ENSG00000160097	<i>FNDC5</i>	0.239542419	23.19569089	0.182088539	12.21079652	0.076124813	13.43703659
ENSG00000160124	<i>CCDC58</i>	2.610846016	8.834409086	2.71243689	8.137697407	3.809241746	9.305080857
ENSG00000160145	<i>KALRN</i>	0.26673486	1.52834171	0.13670077	0.991689865	0.362645574	1.687205345
ENSG00000160712	<i>IL6R</i>	5.149248568	20.11129377	4.634295018	32.7406948	3.961876661	37.23815293
ENSG00000160801	<i>PTH1R</i>	0.272831514	15.78254522	0.933269834	31.89185231	1.199403143	22.33305112
ENSG00000161267	<i>BDH1</i>	0.33523813	30.11756436	0.779617232	20.90561371	0.16608721	40.58033223
ENSG00000162267	<i>ITIH3</i>	5.7226076	194.5563119	6.536709257	190.8431683	0.235417794	196.7961498
ENSG00000162365	<i>CYP4A22</i>	0.160010992	83.15949034	1.278879934	100.3266919	0	265.7354744
ENSG00000162407	<i>PLPP3</i>	6.667881426	28.82105311	9.469110918	26.86371352	4.482869644	20.80542308
ENSG00000162433	<i>AK4</i>	0.514727362	21.57031504	0.835070207	12.61235213	2.359706797	24.38715817
ENSG00000162460	<i>TMEM82</i>	0.030917913	45.1126709	0.725213815	56.24890744	0.078603877	126.8243436
ENSG00000162461	<i>SLC25A34</i>	0.485396724	4.919340538	0.217232075	1.784002907	0.349022538	8.752119118
ENSG00000162482	<i>AKR7A3</i>	3.050567451	175.1923481	4.130435884	185.6485679	2.0961034	258.9473091
ENSG00000162496	<i>DHRS3</i>	22.7316399	66.36380279	15.5671697	87.4215314	6.753497454	99.48159258
ENSG00000162543	<i>UBXN10</i>	0.953232956	6.324892809	0.080613062	1.853506801	0.121529599	4.037944868
ENSG00000162551	<i>ALPL</i>	0.841984847	21.97476501	1.530668299	25.81814195	0.766392152	30.39875659
ENSG00000162572	<i>SCNN1D</i>	0.852335818	1.870727928	1.541784217	7.716836339	0.643152223	12.18694398

ENSG00000162595	<i>DIRAS3</i>	0.166734211	3.482892405	0.12415667	2.972682955	0.504637159	7.44272238
ENSG00000162599	<i>NFIA</i>	1.033099665	7.154371277	1.937698264	7.932469015	0.637391266	9.023629417
ENSG00000162688	<i>AGL</i>	1.075418433	13.38298494	2.066998544	9.686793114	1.076632669	13.93811229
ENSG00000162735	<i>PEX19</i>	5.699264404	20.41855992	5.875552311	12.98084978	8.552628129	22.74458324
ENSG00000162804	<i>sned1</i>	0.29043549	1.312338139	0.282351683	3.537178269	0.838009555	2.551529888
ENSG00000162817	<i>C1orf115</i>	4.282307647	51.19185919	7.249068911	35.09530681	6.289538505	46.93863196
ENSG00000162881	<i>OXR1</i>	1.548706387	10.01022098	2.157327965	33.46525907	0.995649115	56.98406302
ENSG00000162882	<i>HAAO</i>	4.223709073	104.4529958	8.357073847	180.7295273	2.118402372	282.8370873
ENSG00000162896	<i>PIGR</i>	3.898370172	14.23316786	0.849004459	9.400898396	0.782685776	21.06229784
ENSG00000162897	<i>FCAMR</i>	0.051714144	1.608884478	0.134779153	0.727215108	0	0.623152926
ENSG00000162927	<i>PUS10</i>	0.343972394	2.981094079	0.747060417	2.321333759	0.739156577	3.154578457
ENSG00000162972	<i>MAIP1</i>	4.369630217	21.87708903	5.178775537	14.54780053	6.891068998	19.09437896
ENSG00000162989	<i>KCNJ3</i>	0	0.476198523	0	0.09783706	0	1.110116012
ENSG00000163032	<i>VSNL1</i>	0.52720971	9.631453867	0.106514093	5.237026648	0.114293141	10.59657656
ENSG00000163239	<i>TDRD10</i>	0.191037513	1.350770297	0.37718821	4.151723722	0.161894165	1.558716107
ENSG00000163581	<i>SLC2A2</i>	0.110026873	266.9985461	2.87950579	123.1007632	0.034965728	235.4242172
ENSG00000163586	<i>FABP1</i>	0.324631809	550.5500861	6.071770728	294.2772726	0	358.9014739
ENSG00000163605	<i>PPP4R2</i>	3.112527696	10.16146173	5.353218999	13.29691608	4.153546274	10.67384839
ENSG00000163686	<i>ABHD6</i>	2.671225013	15.52103946	1.319563892	11.20915391	0.565930397	14.97324861
ENSG00000163687	<i>NDASE1L3</i>	0.686715534	24.19759955	2.088031493	19.96950329	0.113860763	11.98432182
ENSG00000163701	<i>IL17RE</i>	0.532666189	1.95422606	0.497675482	4.928866215	4.982504125	11.77648465
ENSG00000163702	<i>IL17RC</i>	5.403416117	22.18874068	4.469371222	48.29057706	8.12309322	67.92385823
ENSG00000163815	<i>CLEC3B</i>	0.595414657	7.343447438	0.66505279	7.400997304	0.864998326	4.382586203
ENSG00000163825	<i>RTP3</i>	0.106726484	30.21545337	0.432684273	18.38492414	0	33.70335181
ENSG00000163827	<i>LRRC2</i>	0.175542475	2.548616673	0.225121381	1.322418748	0.014167899	2.05623113
ENSG00000163884	<i>KLF15</i>	1.006569145	55.46947709	1.820579417	70.19282322	1.440335096	70.59429628
ENSG00000163958	<i>ZDHHC19</i>	0.193236958	0.691358896	0.067149427	2.071970624	0.049127423	2.40878894
ENSG00000163959	<i>SLC51A</i>	0.648148813	11.65681335	0.316248049	7.834641932	0.398786345	10.24138357
ENSG00000164050	<i>PLXNB1</i>	5.344291988	13.10433615	12.17387037	35.9487576	11.88257095	35.73749696
ENSG00000164061	<i>BSN</i>	0.034757642	0.16220329	0.110716886	0.300389422	0.213550627	0.659533588
ENSG00000164068	<i>RNF123</i>	1.7328624	5.342117218	3.404974768	8.362611129	1.655410167	7.854886971
ENSG00000164080	<i>RAD54L2</i>	1.036543529	3.096055239	1.42777568	4.994944037	0.678016673	4.428185284
ENSG00000165478	<i>HEPACAM</i>	0	7.140449068	0.085300291	4.83259034	0	6.36458782
ENSG00000165912	<i>PAC3IN3</i>	2.86889475	15.06169744	1.513204536	12.96739221	3.487666231	25.54436644
ENSG00000166016	<i>ABTB2</i>	1.455311715	7.526460585	2.027796581	7.292280918	2.851004102	6.973737028
ENSG00000166311	<i>SMPD1</i>	10.12886996	29.5491687	8.547566579	18.2239156	6.112620836	21.85124671
ENSG00000166387	<i>PPFIBP2</i>	1.485551565	4.317655718	1.829715413	4.380744148	1.047724763	6.278283658
ENSG00000166391	<i>MOGAT2</i>	0	34.18189922	0.48870047	34.87626067	0	49.49500223
ENSG00000166405	<i>RIC3</i>	0.158685186	0.626603044	0.121950337	0.654419813	0.35688202	0.862242164
ENSG00000166575	<i>TMEM135</i>	0.725087449	4.486865924	1.086777846	3.529499316	1.26270861	4.224613384
ENSG00000166741	<i>NNMT</i>	106.693175	252.3191714	17.44127585	302.0436737	16.35879807	131.3055305
ENSG00000166840	<i>LOC100287413</i>	0.06911063	58.17387267	0.382751736	27.22693279	0	54.50399797
ENSG00000167244	<i>IGF2</i>	0.404028328	112.8241623	2.878178978	140.9256379	2.779086511	193.8231256
ENSG00000167799	<i>NUDT8</i>	2.803783112	7.880329807	2.546488384	25.93022589	4.42810725	21.44687688
ENSG00000167992	<i>VWCE</i>	0.028955778	1.276199121	0.109005766	6.939063518	0.196307897	2.534652161
ENSG00000168237	<i>GLYCTK</i>	2.117873839	68.22299154	2.444670659	67.80227342	0.689663063	121.5553936
ENSG00000168306	<i>ACOX2</i>	0.474945298	54.42521299	1.237818518	44.18269917	0.516014053	107.0330062
ENSG00000168309	<i>FAM107A</i>	0.370945234	1.030403427	0.375966123	4.703993349	0.104785473	0.98351865
ENSG00000168356	<i>SCN11A</i>	0.024397263	0.22770779	0.026493739	0.214424636	0.046519621	0.233161182
ENSG00000168389	<i>MFSD2A</i>	1.131563059	61.73567069	1.443839003	69.84411943	0.089900597	77.32535926
ENSG00000168509	<i>HFE2</i>	0.141248003	83.39909842	0.63107199	46.81896105	0	87.3989024
ENSG00000168874	<i>ATO8H</i>	0.216567872	11.55028652	0.477074799	24.21382971	1.422355878	9.474379539
ENSG00000169174	<i>PCSK9</i>	1.365346551	4.375177171	1.589424213	9.535895082	0.192843137	10.2571953
ENSG00000169242	<i>EFNA1</i>	26.6719669	72.70059604	28.8473305	60.22281436	37.89662484	122.9624487
ENSG00000169291	<i>SHE</i>	0.411994656	1.532917054	0.561060871	1.575612092	0.193444444	0.990127067
ENSG00000169764	<i>UGP2</i>	6.326978396	94.64991993	10.72201249	48.01848048	13.61965595	70.81303454
ENSG00000169814	<i>BTD</i>	3.273425729	21.71005867	1.818690753	8.385601043	2.666533267	19.18984514
ENSG00000170011	<i>MYRIP</i>	0.104042569	5.427998666	0.146008836	3.22156401	0.29842344	3.458504593
ENSG00000170145	<i>SIK2</i>	2.561806034	10.65660138	2.063014664	10.09398612	3.488227606	11.1071694
ENSG00000170293	<i>CMTM8</i>	3.68276065	24.96982885	7.615911879	23.57187012	3.799410592	54.75613606
ENSG00000170385	<i>SLC30A1</i>	2.55838108	20.95354169	3.975285351	12.91773292	4.598101868	16.25249296
ENSG00000170634	<i>ACYP2</i>	1.883974704	4.403304361	1.332383157	3.311605788	1.026938652	4.767732836
ENSG00000170743	<i>SYT9</i>	0	2.118723359	0	0.891254844	0.042126047	1.553256955
ENSG00000170959	<i>DCDC5</i>	0.007142132	0.322189508	0.003102344	0.244808249	0.072630938	0.611339407
ENSG00000170989	<i>S1PR1</i>	3.045278551	6.736679855	3.722409152	11.72800121	1.621050334	6.994455849
ENSG00000171174	<i>RBKS</i>	1.951727327	7.304848809	0.852914347	3.03564946	1.433454049	6.664724303
ENSG00000171227	<i>TMEM37</i>	9.718908469	39.86894004	12.73612524	44.15082314	15.56896347	58.41135219
ENSG00000171793	<i>CTPS1</i>	2.46870046	10.59234171	5.86588617	15.60467924	1.849631683	12.15994981
ENSG00000172340	<i>SUCLG2</i>	15.23922937	110.3416191	14.32242957	38.68364429	9.834048863	76.21314662
ENSG00000172425	<i>TTC36</i>	0.232880219	104.0405318	2.468223945	161.2025396	0.157882912	231.5401458
ENSG00000172456	<i>FGGY</i>	0.641289839	6.900781636	1.284646485	3.832629529	1.387419219	7.7494557
ENSG00000172482	<i>AGXT</i>	0.569128129	529.5303955	7.205815737	746.0759753	0.017863182	1069.089513

ENSG00000172893	<i>DHCR7</i>	4.010410107	13.40820055	4.946330123	20.87020499	3.685816435	35.67478184
ENSG00000172995	<i>ARPP21</i>	0.004656681	0.4635985	0	0.057297824	0.011838872	0.33280686
ENSG00000173406	<i>DAB1</i>	0	0.68016432	0.031221146	0.821227773	0.055835535	1.772036872
ENSG00000173531	<i>MST1</i>	2.255475158	71.56511752	6.263757751	125.0967731	1.441380308	124.5380649
ENSG00000173599	<i>PC</i>	1.887103819	42.28099275	5.028446401	43.41506476	1.229652695	55.00707769
ENSG00000173898	<i>SPTBN2</i>	1.343309012	8.286312294	3.152221063	11.39002603	3.921097599	15.91093337
ENSG00000173992	<i>CCS</i>	13.201974	26.26886784	13.82898214	46.44561995	5.360568396	61.31272042
ENSG00000174080	<i>CTSF</i>	7.529622213	47.20438447	13.97079079	37.8805998	5.280790886	58.82448908
ENSG00000174567	<i>golt1a</i>	4.136903899	43.82360197	8.122243405	75.69892769	12.58584621	53.69993478
ENSG00000174827	<i>PDZK1</i>	0.540635349	34.69855515	0.887162097	22.59640073	6.329392755	33.28035622
ENSG00000175161	<i>CADM2</i>	0	0.102447611	0.008173544	0.157110584	0.011959749	0.117280775
ENSG00000176720	<i>BOK</i>	8.459141093	55.20018136	7.410458762	62.189112	18.72571769	122.0563595
ENSG00000176771	<i>NCKAP5</i>	0.049235441	0.474848474	0.102655259	0.406760952	0.075103967	0.433711555
ENSG00000178075	<i>GRAMD1C</i>	0.312580183	4.731448754	0.637103597	4.226507604	0.519601994	7.073569864
ENSG00000178301	<i>AQP11</i>	0.666877196	8.665044876	0.425989689	2.896074981	0.548521215	9.4539269
ENSG00000178537	<i>SLC25A20</i>	9.294453345	69.66481996	6.525687997	34.5554195	1.450414492	67.95522164
ENSG00000178772	<i>CPN2</i>	0.248323531	118.2020009	1.24044596	98.97573534	0	154.7992355
ENSG00000178821	<i>TMEM52</i>	0.235860619	2.017918627	0.332966796	5.70061482	0.149909528	7.497287575
ENSG00000179528	<i>LBX2</i>	0.625320336	2.244739666	0.43877374	2.536553463	1.161760482	5.396476185
ENSG00000179914	<i>ITLN1</i>	0.190135785	1.626717275	0.110119627	2.339513033	0	2.422800956
ENSG00000180210	<i>F2</i>	1.087340576	798.7222996	15.64228793	544.915247	0.046854076	1036.889265
ENSG00000180432	<i>CYP8B1</i>	0.117035887	107.6942949	1.617545634	136.244659	0	144.8296757
ENSG00000180767	<i>CHST13</i>	0.525379858	22.51544569	6.869134932	30.66020598	3.918037881	66.58257069
ENSG00000180875	<i>GREM2</i>	0	11.44765193	0.029371836	4.694935395	0.105056501	8.035673693
ENSG00000180902	<i>D2HGDH</i>	3.026781137	6.106976058	4.292271785	15.38222591	6.322060681	18.70236238
ENSG00000181061	<i>HIGD1A</i>	23.66718456	106.2641245	19.8031276	56.71785844	10.14125078	66.3121219
ENSG00000181656	<i>gpr88</i>	0.107694594	3.392379699	0.128643761	0.946514937	0.159714553	3.378532914
ENSG00000182551	<i>ADI1</i>	11.22475956	153.2547829	17.26329651	80.05161996	7.642860472	183.5982858
ENSG00000182568	<i>SATB1</i>	0.809839443	1.8923521	0.484257325	2.384852239	0.745715562	2.94838881
ENSG00000182704	<i>TSKU</i>	4.277464497	57.58397537	3.39976689	39.59381274	4.376903396	49.72807058
ENSG00000182919	<i>C11orf54</i>	2.353884461	33.04767157	3.165074171	24.81243461	2.693604879	28.10877254
ENSG00000182983	<i>ZNF662</i>	0.145947914	0.745956005	0.422638217	1.026175045	0.147241809	0.900991081
ENSG00000183134	<i>PTGDR2</i>	0.081166197	0.782802882	0.070512697	0.713360027	0.082540859	0.998284233
ENSG00000183281	<i>PLGLB1</i>	0.291895828	5.26709805	0.202866344	8.08112848	0.234997928	6.719314256
ENSG00000184232	<i>OAF</i>	19.354458	106.0647974	10.38668018	115.3013964	11.42363153	160.866166
ENSG00000184313	<i>MROH7</i>	0.015575087	0.153443447	0.009020515	0.228145965	0.043996868	0.474590674
ENSG00000184454	<i>NCMAP</i>	0.547251567	3.014950761	0.188187818	1.322675404	0.521737527	2.823445029
ENSG00000184500	<i>PROS1</i>	4.386221307	95.02653469	4.687014851	52.25248544	3.384081964	72.16035611
ENSG00000184999	<i>SLC22A10</i>	0.08792372	39.02510591	0.343724664	40.64670714	0	33.95196148
ENSG00000185038	<i>MROH2A</i>	0	1.965222887	0.029073777	2.735431538	0.007090255	4.296898661
ENSG00000185304	<i>RGPD2</i>	0.166531638	0.652804022	0.150460404	0.866467008	0.028225347	0.65321485
ENSG00000185436	<i>IFNLRI</i>	0.983243655	4.202385503	0.597102037	1.594083619	0.954593504	3.680943953
ENSG00000186094	<i>AGBL4</i>	0.018698367	0.145431741	0	0.087646781	0.010563916	0.258982082
ENSG00000186205	<i>MARC1</i>	0.564789924	28.5532684	1.287977799	16.71169996	3.001405945	36.23834994
ENSG00000186377	<i>CYP4X1</i>	0.1757727	2.659671766	0.124937663	1.516757198	0.406249214	4.939909304
ENSG00000186642	<i>PDE2A</i>	0.536564845	2.707544017	0.596883798	4.152208284	0.626612921	2.50140199
ENSG00000187017	<i>ESPN</i>	0.869223011	21.66957716	0.665709192	31.9451613	0.988622144	51.03982827
ENSG00000187048	<i>CYP4A11</i>	0.302025889	216.6612916	2.991170376	205.540883	0	374.6420689
ENSG00000187627	<i>Rgpd1</i>	0.006839649	0.393659798	0.011883817	0.528993161	0.01738872	0.295565987
ENSG00000187889	<i>C1orf168</i>	0	6.737594425	0.801908809	8.362340975	0.034384601	8.395916259
ENSG00000188001	<i>TPRG1</i>	0.202077017	0.774354749	0.218371205	0.944328572	0.054298641	1.376225625
ENSG00000188641	<i>DPYD</i>	5.232842687	12.60023916	3.294296004	9.412369901	1.415413324	13.8799543
ENSG00000196083	<i>IL1RAP</i>	0.906014718	12.08999099	4.637481083	11.53537954	2.336600466	9.743275142
ENSG00000196208	<i>GREB1</i>	0.049589121	0.486566758	0.102729903	1.374549812	0.022628389	1.56598393
ENSG00000196482	<i>ESRRG</i>	0.030235901	0.167977225	0.022514808	0.197406652	0.003660475	0.373315055
ENSG00000196549	<i>MME</i>	0.034389149	4.080845665	0.034143301	4.680435228	0.083265659	8.622527683
ENSG00000196600	<i>SLC22A25</i>	0	7.325955986	0.032644071	9.247062439	0.021229192	12.96959076
ENSG00000196660	<i>SLC30A10</i>	0.138460811	11.77007393	0.672192534	4.595645797	3.858356016	12.50826904
ENSG00000197099	<i>RP11-573D15.8</i>	0.034593469	0.88789905	0.045079336	0.456056815	0.043974197	3.104811031
ENSG00000197312	<i>DDI2</i>	1.409547058	6.662218147	1.752701861	4.723905837	1.102630529	6.976775849
ENSG00000197580	<i>BCO2</i>	0.207667823	5.157853406	0.342779578	13.44540222	1.096988567	12.05747943
ENSG00000197635	<i>DPP4</i>	1.594966822	15.19284082	1.18185137	4.799094334	0.254428203	9.18470726
ENSG00000197885	<i>nkiras1</i>	1.205700582	4.320050774	0.764988575	1.905035252	0.436260206	2.634405459
ENSG00000198130	<i>HIBCH</i>	0.764509629	13.0619524	1.169147544	4.642345266	1.076232708	7.655479714
ENSG00000198585	<i>NUDT16</i>	4.654116812	11.52956723	3.306522525	8.99076894	6.55523321	11.19806437
ENSG00000198734	<i>F5</i>	0.466144343	60.63378016	5.310114422	46.71605265	0.216989748	37.78869143
ENSG00000203832	<i>NBPF20</i>	0.422442023	0.949690818	0.525354761	1.744503895	0.470790863	1.216695973
ENSG00000204099	<i>NEU4</i>	0.302376936	11.31908501	0.364374144	21.91196813	0.247982345	30.28385318
ENSG00000204128	<i>C2orf72</i>	2.20881234	53.58912296	11.82081012	35.11498524	9.007638319	73.48452159
ENSG00000204178	<i>TMEM57</i>	5.999644627	18.09037976	3.65783723	13.12488301	3.002109514	15.9389931
ENSG00000204219	<i>TCEA3</i>	1.804937644	38.57961368	0.603981876	19.24756974	4.056243336	45.93208956
ENSG00000204370	<i>SDHD</i>	28.91333895	82.52533034	15.68934051	38.23394998	19.55705881	73.70020981

ENSG00000204710	SPDYC	0	1.549119533	0	5.334867641	0	6.463105626
ENSG00000205106	DKFZp779M0652	1.013764555	4.392979738	1.258146435	11.58281247	0.981841962	10.831756
ENSG00000205835	GMNC	0.049416644	1.441318779	0	1.08579247	0	1.211469707
ENSG00000205865	FAM99B	0	14.38779248	0.191316082	62.01338331	0	56.0744995
ENSG00000205981	DNAJC19	5.700759707	13.86238376	3.392750094	9.744227425	6.374819766	14.35410719
ENSG00000206384	COL6A6	0	0.247860035	0.008389366	0.347980143	0.024551093	0.192604121
ENSG00000206549	PRSS50	0	0.24697192	0.165514264	1.59074466	0.148001895	0.633316184
ENSG00000211452	DIO1	0.144157142	91.49173279	0.822977731	42.35332893	0.052356658	37.71959406
ENSG00000213171	LINGO4	0.027816057	0.822119018	0.012082525	0.513391214	0.153222119	0.809060332
ENSG00000213512	gpb7	0.057451379	20.3462996	0.299463461	15.3163107	0	28.64633107
ENSG00000213533	TMEM110	0.213241874	0.816515892	0.342005041	1.210994006	0.145959033	1.199579695
ENSG00000214530	STARD10	12.75584768	135.2910849	20.97465756	151.0974988	10.45565755	225.0633875
ENSG00000214595	eml6	0.03910295	0.126722522	0.070771827	0.292120486	0.063513881	0.254550188
ENSG00000215915	ATAD3C	0.390050939	1.875396434	0.112951552	1.454350196	1.061758614	4.262990981
ENSG00000218819	TDRD15	0	0.202569308	0.019964231	0.740568869	0	0.152780432
ENSG00000222040	ADRA2B	0.071682777	3.233689697	0.18682208	3.628865504	1.202797589	3.24064169
ENSG00000223991		0	6.577773247	0.052230514	6.305615911	0	15.08885936
ENSG00000226321	CROCC2	0.017774292	0.359435685	0.092647924	0.734215825	0	0.502213666
ENSG00000230921	HAO2-IT1	0	3.05578119	0	1.593705938	0	3.013851937
ENSG00000231609	LOC100132215	0.101108495	0.72348745	0.421619812	1.528444457	0.119957725	1.04190141
ENSG00000231948	HS1BP3-IT1	0.156650761	11.57475067	1.769163578	43.7817583	0.531012861	3.645086482
ENSG00000231969	LOC101929231	0	0.715300278	0.039947996	0.808288563	0.038968654	0.687848302
ENSG00000232284	GNG12-AS1	0.040688509	0.506345894	0.070695847	0.405287316	0.068962709	0.428303297
ENSG00000232287	SLC6A1-AS1	0	1.251775487	0.139817986	2.121757478	0.068195145	1.872475932
ENSG00000235169	SMIM1	1.67488235	7.586231821	0.684727074	9.438336407	2.588270236	20.2231887
ENSG00000236267		0	7.464040263	0.122603159	3.224901455	0	6.098600291
ENSG00000236341		0	1.557947459	0	0.812528765	0	1.920713017
ENSG00000237188		0.168860688	0.808222095	0.37238422	2.123399523	0.396278255	0.993093924
ENSG00000239887	C1orf226	0.230420108	2.052833685	0.19107731	4.565758547	1.162737099	4.108251185
ENSG00000241399	CD302	0.355004329	12.20616418	0.478564296	2.646697632	0.404587814	5.045853352
ENSG00000241635	UGT1A1	0.070651809	1.64854221	0.122756758	1.469582428	0.10477891	2.035413578
ENSG00000243384		0	7.519236527	0.116648148	9.912850935	0	12.05110225
ENSG00000243696		0.297673655	3.542316495	0.562460191	9.274493683	0.037839396	12.25748457
ENSG00000243710	cfap57	0.157618594	0.800075672	0.064861724	1.195724885	0.056241433	1.282283607
ENSG00000243818	LOC100507389	0	34.20968722	0.237826321	35.72957194	0	47.77540534
ENSG00000243989	ACY1	0.399110219	1.299879811	0.660944257	2.258102544	0.264238088	2.446088517
ENSG00000244414	CFHR1	1.240656914	641.761875	4.497086089	268.614046	0	533.5374163
ENSG00000244474	UGT1A4	0.055902333	95.45219908	0.372330528	11.92267295	0	28.83405048
ENSG00000244734	HBB	3.78672323	44.14743527	3.809121034	35.80341269	0.506691662	8.480026712
ENSG00000246022	ALDH1L1-AS2	0	0.349521129	0	0.972205559	0	0.718177602
ENSG00000248485	pcp4l1	0	3.95293821	0.086011626	1.276233149	0	1.590702869
ENSG00000251364	LOC100506258	0.184527611	0.543331298	0.120230527	0.567626906	0.145207556	0.492904897
ENSG00000254539		0.648955972	2.439593746	0.75170268	2.661678425	0.64161508	3.235815716
ENSG00000254607	LOC101929427	0	23.16454326	0.084005868	14.27776884	0.081946429	13.3396022
ENSG00000254827	SLC22A18AS	0.923026369	2.707544017	0.481124516	2.271463224	0.58107468	2.191610439
ENSG00000255284	LOC171391	0.754408764	3.037358161	2.351688348	7.956490363	1.917964301	9.440936254
ENSG00000255468	LOC102724064	0.427229348	3.038075364	1.16648148	3.272099064	0.879274543	4.31121082
ENSG00000255471		0.077167863	1.32042787	0.033519583	0.678219139	0.098093509	1.090191242
ENSG00000257702	LBX2-AS1	3.653179935	10.59372069	2.879821121	11.93125452	2.962103893	26.4236287
ENSG00000260855		0.108283936	0.568490665	0.211659946	0.832732773	0.160588567	1.327313009
ENSG00000261572		0.173964356	5.566859407	1.165864621	4.674224617	0.042121591	11.8134177
ENSG00000261578		0.156949713	2.406562263	0.00973923	1.418824084	0.104505155	1.490629695
ENSG00000261829		0.392936691	5.990101563	1.706808186	6.216252677	1.33197206	15.80466308
ENSG00000269624		0.025921251	13.30624225	0.247708422	3.599536789	0	6.20391364
ENSG00000272510		0	2.112823366	0.471986726	3.103734638	0.115103944	2.934731065
ENSG00000272574		0	2.605676024	0.72760726	4.580195151	0.788632962	7.578892685
ENSG00000273174		0.415886976	2.199580007	0.650339232	3.2165593	0.211465299	2.764920214

Table S9. Differential intrachromosomal interaction regions of cell migration signaling

[illegible]

chr2-47000000_chr2-79000000
chr2-47000000_chr2-80000000
chr2-47000000_chr2-82000000
chr2-47000000_chr2-84000000
chr2-47000000_chr2-85000000
chr2-47000000_chr2-88000000
chr2-47000000_chr2-91000000
chr2-47000000_chr2-95000000
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chr2-47000000_chr3-117000000
chr2-47000000_chr8-76000000
chr2-47000000_chr14-107000000
chr2-47000000_chr15-88000000
chr2-47000000_chr17-35000000

chr2-47000000_chr2-191000000
chr2-47000000_chr2-192000000
chr2-47000000_chr2-193000000
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chr2-47000000_chr4-166000000
chr2-47000000_chr8-105000000
chr2-47000000_chr9-170000000
chr2-47000000_chrX-125000000

chr2-47000000_chr2-122000000
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chr2-47000000_chr17-7000000
chr2-47000000_chr17-8000000
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chr2-47000000_chr22-20000000
chr2-47000000_chr22-29000000
chr2-47000000_chr22-49000000
chr2-47000000_chrX-0

Table S13. Differentially expressed genes in the interchromosomal differential interaction regions and their enrichment

gene_id	gene_name	ICC1	ANHT1	ICC2	ANHT2	ICC3	ANHT3
ENSG00000065328	<i>MCM10</i>	0.52152	0.03597395	0.281579073	0	1.552126878	0.073018339
ENSG00000109674	<i>NEIL3</i>	0.40553	0.088409112	0.924475531	0.027870342	1.632471077	0.01922667
ENSG00000151025	<i>GPR158</i>	0.39692	0.008465007	0.4907247	0.021348263	0.637604844	0.029454682
ENSG00000151725	<i>CENPU</i>	4.93486	0.636235682	3.799404715	0.304311224	4.716875801	0.591628057
ENSG00000153132	<i>CLGN</i>	13.1424	0.087668419	1.749828988	0.154766325	2.461849409	0.366059308
ENSG00000170312	<i>CDK1</i>	3.42223	0.217500211	2.897422731	0.042194086	5.334453154	0.291080672
ENSG00000182010	<i>RTKN2</i>	0.18154	0.041098014	0.2211596	0.008637237	0.656187529	0.059584957
ENSG00000134871	<i>COL4A2</i>	8.73652	3.193309642	13.14672516	1.642045613	25.76022489	9.971382805

[illegible][illegible]

chr1-153000000_chr5-89000000
chr1-153000000_chr5-98000000
chr1-153000000_chr5-100000000
chr1-153000000_chr5-103000000
chr1-153000000_chr5-105000000
chr1-153000000_chr5-121000000
chr1-153000000_chr5-128000000
chr1-153000000_chr5-164000000
chr1-153000000_chr6-28000000
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chr1-153000000_chr12-59000000

chr1-153000000_chr17-79000000
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chr1-153000000_chr20-3000000

chr1-153000000_chr12-80000000
chr1-153000000_chr12-81000000
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chr1-153000000_chr21-33000000
chr1-153000000_chr22-42000000
chr1-153000000_chr22-47000000
chr1-153000000_chrX-3000000

Table S12. The common compartment switch regions identified in the three paired ANHT and ICC.

Chrom	cbins 1	cbins 2
chr10	11000000	12000000
chr10	3000000	4000000
chr10	4000000	5000000
chr10	7000000	8000000
chr11	35000000	36000000
chr11	58000000	59000000
chr12	68000000	69000000
chr12	69000000	70000000
chr12	92000000	93000000
chr12	93000000	94000000
chr13	24000000	25000000
chr14	22000000	23000000
chr14	31000000	32000000
chr14	52000000	53000000
chr14	53000000	54000000
chr16	75000000	76000000
chr18	43000000	44000000
chr18	56000000	57000000
chr18	60000000	61000000
chr2	106000000	107000000
chr2	11000000	12000000
chr2	160000000	161000000
chr2	161000000	162000000
chr2	230000000	231000000
chr4	151000000	152000000
chr4	25000000	26000000
chr4	57000000	58000000
chr5	157000000	158000000
chr5	158000000	159000000
chr5	170000000	171000000
chr5	32000000	33000000
chr6	20000000	21000000
chr6	46000000	47000000
chr6	52000000	53000000
chr8	37000000	38000000
chr8	95000000	96000000

Table S13. Differentially expressed genes in the compartment transition regions

gene_id	gene_name	ICC1	ANHT1	ICC2	ANHT2	ICC3	ANHT3
ENSG000000157131	<i>C8A</i>	0.877669798	305.7571078	4.73078546	217.8078311	0	347.6447082
ENSG000000021852	<i>C8B</i>	0.533840996	323.327783	4.173943442	152.7429028	0.043780833	236.6739788
ENSG000000101474	<i>APMAP</i>	34.52827898	125.5631813	32.47514862	121.7225923	31.01361791	131.168367
ENSG000000103546	<i>SLC6A2</i>	0	0.267632028	0	0.151211955	0	0.157276031
ENSG000000132855	<i>ANGPTL3</i>	0.173520843	377.7098882	4.195744155	119.6150679	0.012254143	120.335921
ENSG000000134716	<i>CYP2J2</i>	0.660133642	53.20188163	0.996775981	30.14191853	0.253074691	62.4088266
ENSG000000156006	<i>NAT2</i>	0.035548584	46.94783018	0.71030075	28.80625492	0.120502162	62.15632665
ENSG000000159398	<i>CES5A</i>	0	1.619963134	0	0.644562197	0	3.266730796
ENSG000000162599	<i>NFIA</i>	1.033099665	7.154371277	1.937698264	7.932469015	0.637391266	9.023629417
ENSG000000171428	<i>NAT1</i>	1.540341551	4.423544968	0.79775128	3.827054017	1.154739598	5.169520696
ENSG000000183044	<i>ABAT</i>	0.699333754	93.12017458	2.648047038	31.63892283	0.359676199	64.99463669
ENSG000000187889	<i>C1orf168</i>	0	6.737594425	0.801908809	8.362340975	0.034384601	8.395916259
ENSG000000198848	<i>CES1</i>	0.528036273	578.2832802	7.826189161	388.4811517	0.094920583	1207.351788
ENSG000000269624	<i>AL138847.1</i>	0.025921251	13.30624225	0.247708422	3.599536789	0	6.20391364
ENSG000000057593	<i>F7</i>	0.728240076	73.50268194	0.839792838	67.70644494	0.661665551	97.16248268
ENSG000000143278	<i>F13B</i>	0.856137985	32.78367641	0.616568782	30.75006821	0	36.05766307
ENSG000000126218	<i>F10</i>	2.541782518	146.1521651	2.720634861	142.6339757	4.665520471	148.3275247

Table 14. The number and size of TAD on each chromosome.

Chr	ICC1	ANHT1	ICC2	ANHT2	ICC3	ANHT3
Number						
chr1	101	123	95	111	113	118
chr2	109	120	104	113	114	114
chr3	85	91	81	87	93	92
chr4	71	86	76	80	79	88
chr5	72	83	76	82	83	83
chr6	79	85	75	82	83	86
chr7	74	78	70	74	79	76
chr8	70	67	59	69	69	68
chr9	50	56	45	47	48	53
chr10	55	62	60	59	66	56
chr11	51	62	50	63	58	64
chr12	60	69	56	64	65	66
chr13	37	44	38	40	42	42
chr14	34	47	33	39	39	40
chr15	37	40	37	38	40	42
chr16	35	36	35	34	35	35
chr17	35	34	28	31	35	35
chr18	31	37	30	34	36	37
chr19	19	19	18	19	23	19
chr20	27	30	24	28	32	29
chr21	14	18	12	17	15	17
chr22	13	13	15	15	17	14
chrX	46	58	51	51	62	55
chrY	1	3	1	2	4	4
Total	1206	1361	1169	1279	1330	1333

Table S15. Tumor-specific TAD boundaries of ICC samples.

chr	binstart	binend	samples
chr1	104040000	104320000	HCC1; HCC2
chr3	145920000	146320000	HCC2; HCC3
chr5	6271000	6478000	HCC2; HCC3
chr5	16480000	16760000	HCC3; HCC2
chr5	86320000	86720000	HCC1; HCC2; HCC3

Table S16. The CTCF bonding site and EnhancerAtals of *HOPX*

Target genes	EnhancerAtlas ID	EnhancerAtlas Coordinate
<i>HOXP</i>	HS102-17085	chr4:57252320-57253520
<i>HOXP</i>	HS102-17086	chr4:57333910-57335100
<i>HOXP</i>	HS102-17087	chr4:57371680-57372710
<i>HOXP</i>	HS102-17088	chr4:57506820-57509110

Table S17. The CTCF bonding site and EnhancerAtals of ACVR1		
Target genes	CTCF motif	CTCF bonding site
<i>ACVR1</i>	TCAATAGGAGGC	chr2: 158077375-158077386
<i>ACVR1</i>	CCACAAGGAGGC	chr2: 158753853-158753864
<i>ACVR1</i>	ACAGCAGGGGGC	chr2: 158758047-158758058

Table 18. PCR primer sequences for selected genes.

Gene	Forward primer	Reverse primer	Application
<i>GAPDH</i>	ATCACTGCCACCCAGAAGAC	CTTCACCACCTTCTTGATGTC	RT-PCR
<i>S100A3</i>	CGACTGAGTTTCGGGAAT	ACTCGTGGCAGTAGAGAC	RT-PCR
<i>MAPK12</i>	AGGCAGGCAGACAGTGAGA	TTGAACAGCGTCTTGCCT	RT-PCR
<i>HOPX</i>	GACAAGCACCCGGATTCCA	GTCTGTGACGGATCTGCACTC	RT-PCR
<i>ACVR1</i>	GAGAAGCCCAAGGTCAACCC	GCGGGGTCTTACAGGTCATC	RT-PCR

Table S19. Antibodies information

	Item number	Company
HOPX	11419-1-AP	Proteintech
ACVR1	67417-1-Ig	Proteintech

Supplemental Materials and Methods

Genome-wide intrachromosomal contact matrix

The resolution represents a specific window size. The chromosomes are equally divided according to the resolution and the final effective contacts are counted according to the resolution to obtain the observation matrix. The maximum likelihood method was used to standardize the observation interaction matrix. Finally, the interaction information was visually displayed in the whole genome, obtained and a set of standardized interaction heat map of the whole genome.

Genome-wide interchromosomal contact matrix

Divide the observed number of interactions between a certain pair of chromosomes by the expected number of interactions between all chromosomes, and use this data to plot the degree of interaction between different chromosomes across the entire genome.

Sequence quality checking and filtering

The following reads were removed:

(a) Reads with $\geq 10\%$ unidentified nucleotides (N); (b) Read with aligned to the adapter; (c) Reads with $> 50\%$ bases having phred quality < 5 . Clean reads were aligned to the NT database using Blast mem v 2.2.26. Reference genome and gene model annotation files were downloaded from genome website directly. Bowtie2 was used to build index of the reference genome and align clean reads to the reference genome. Then valid paired reads were obtained by filtering with HiC-Pro. The iterative correction (ICE) method was applied to normalize interaction matrices to eliminate the bias of raw matrices. Observed interaction matrix was an interaction matrix after the statistics of the finally valid contacts according to a certain resolution. Building and normalizing observed interaction matrix with pastis.

Immunofluorescence

Sections were blocked with PBS (pH 7.5) containing 1% BSA for 0.5 h. Add the

ZNF738 antibody diluted to an appropriate concentration on the sample, put it in an enamel box to ensure that the sample is completely covered by the antibody solution for 0.5 h. The sample slides were rinsed with PBS and then soaked in PBS solution for 1 min. Add the secondary antibody dropwise to the sample and incubate in the dark for 0.5 h. Rinse the sample slides with PBS and rinse again with distilled water. Wipe off excess water in the sample while keeping the sample moist, add a drop of glycerol, cover with a coverslip, and examine under a fluorescence microscope. Antibodies used are listed in Table S22.