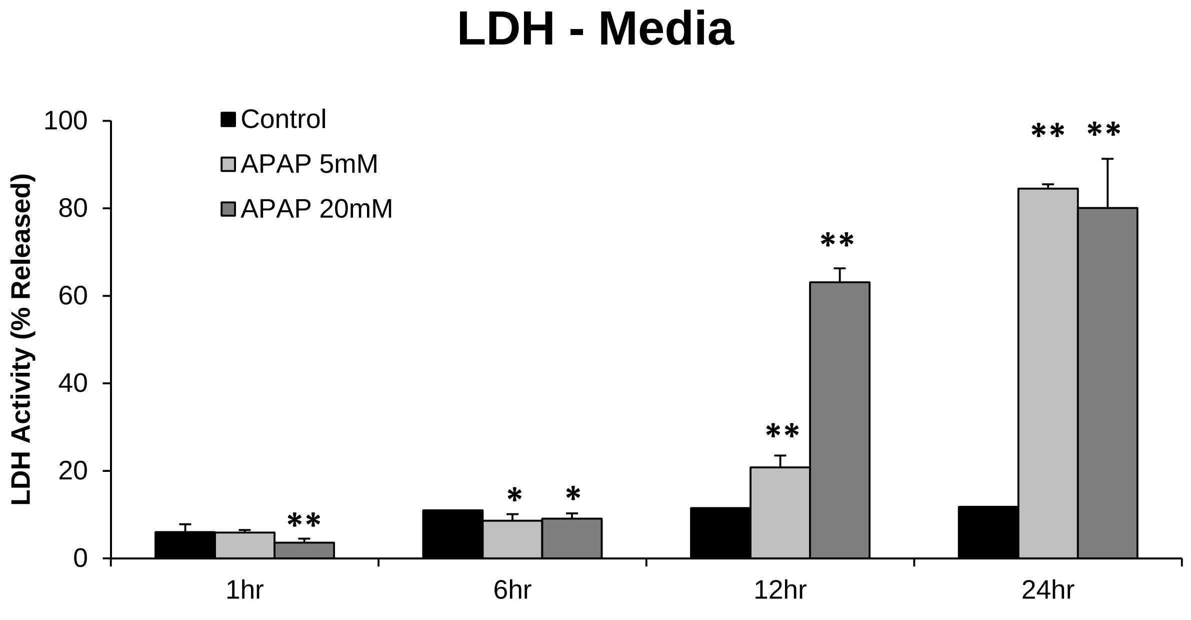
Supplementary Figure 1. Lactate Dehydrogenase (LDH) assay in hepaRG cells. HepRG cells were treated with 5 mM or 20 mM APAP and LDH assays were performed at different time points. Treatement with 5 mM APAP increased LDH at 12 h and 24 compared to control ($p \leq 0.0001$). The 20 mM APAP treatment also increased LDH activity with peak levels at 24 h time point ($p \leq 0.0001$). All experiments were run in triplicates.

Supplementary Figure 2. Top 10 pathways of 1,194 up-regulated genes (a) and 1,564 down-regulated genes (b) listed in IPA analysis. The y-axis (*left*) indicates the ratio of number of deregulated genes mapping to specific pathway, and the y-axis (*right*) indicates the *P* value calculated by Benjamini-Hochberg Multiple Testing Correction.

Supplementary Figure 3. MiRNAs suppressed the luciferase activities produced by the wild 3'-UTR of *CYP3A4* (a), *HNF1A* (b), *HNF4A* (c) or *NR1I2* (d), respectively. Constructs containing the wild or mutated 3'-UTR of *CYP3A4*, *HNF1A*, *HNF4A* or *NR1I2* were transiently transfected into HEK 293T and HepG2 cells, together with 40 nmol/L cognate miRNA mimic or miRNA negative control, respectively. Three independent experiments, each in triplicate, were conducted. * $P < 0.05$; ** $P < 0.001$ NC, miRNA negative control.

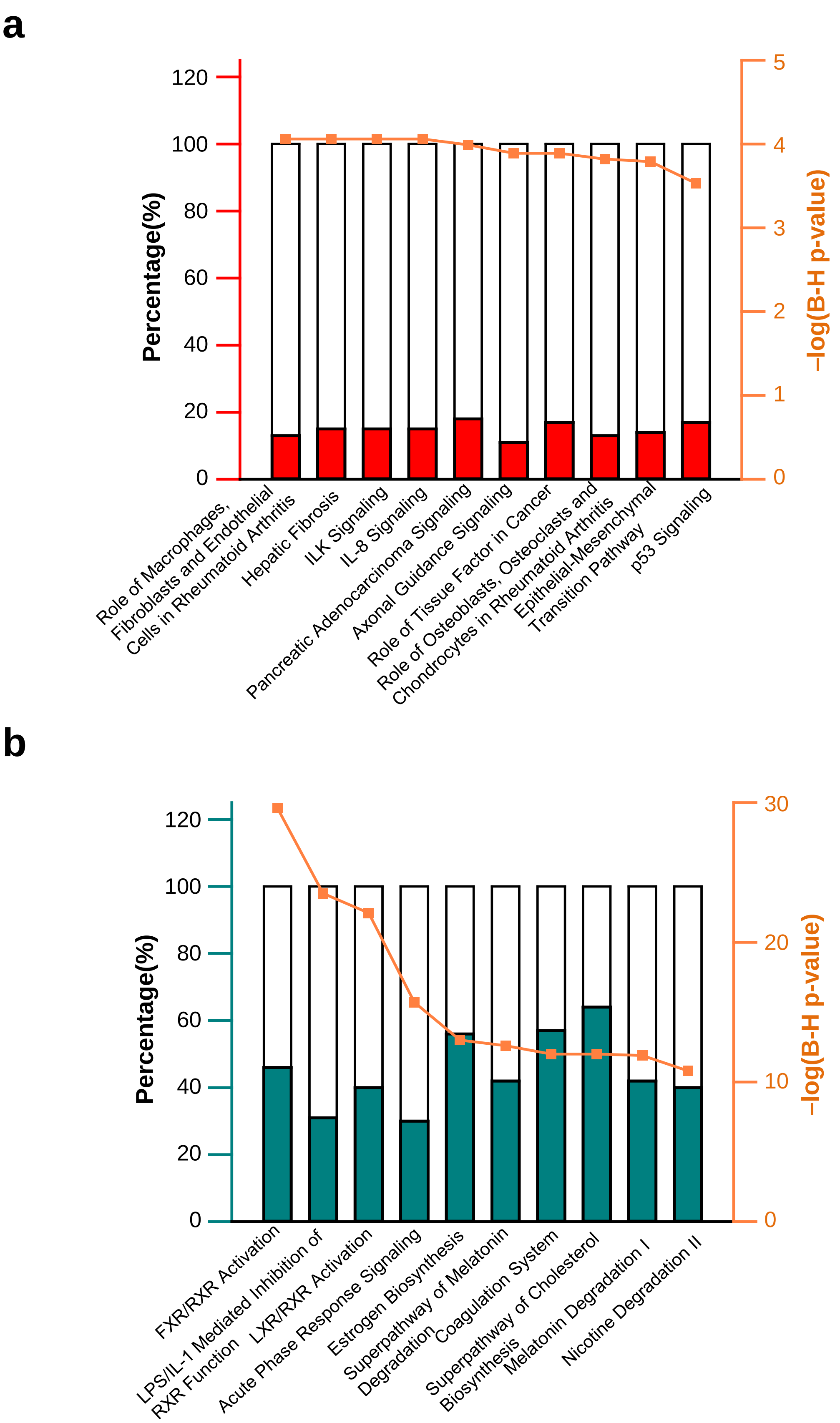
Supplementary Figure 4. The specific siRNAs reduced the mRNA and protein levels of HNF1A (a) , HNF4A (b) and NR1I2 (c), respectively. Each assay was carried out in triplicate. Data are shown as relative mRNA and protein levels normalized by GAPDH levels. ** $P<0.001$; NC, miRNA negative control.

Supplementary Figure 1

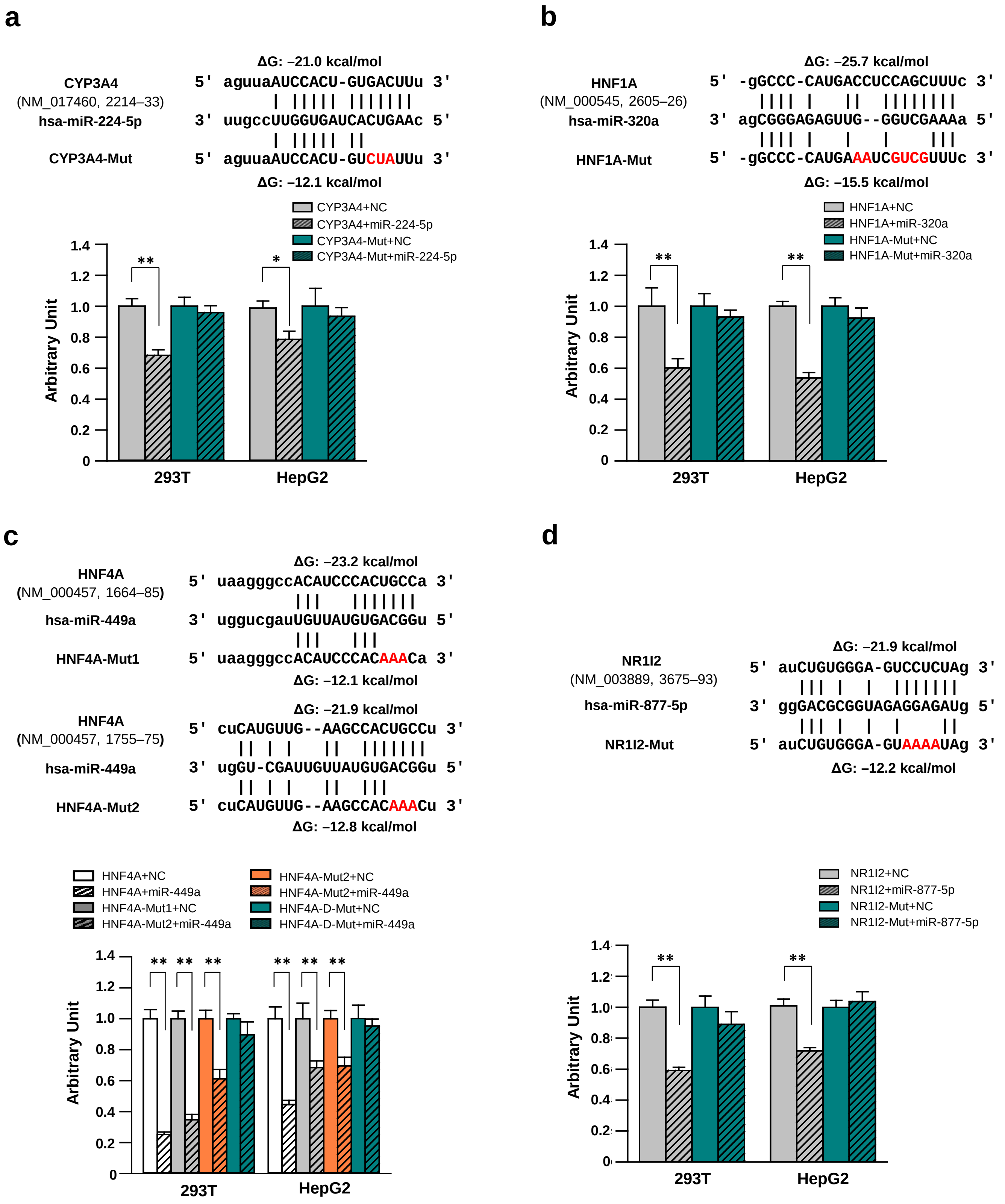


*** $p \leq 0.001$** **** $p \leq 0.0001$**

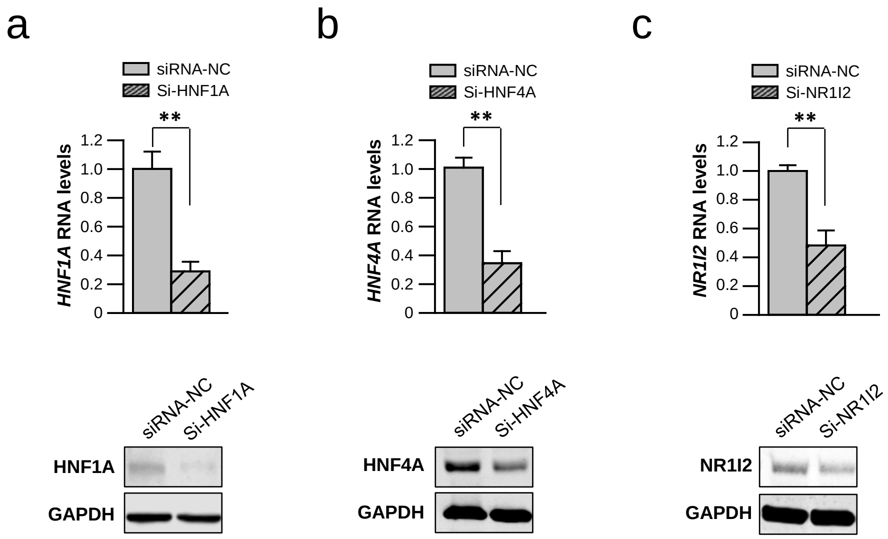
Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4



Supplementary Table 1 **Deregulated genes in HepaRG cells exposed to 10 mM APAP (Fold change>2)**

Gene Symbol	Gene Locus	Gene Name	Fold changes (5mM APAP)	Fold changes (10 mM APAP)
A1CF	chr10:52559047-52645435	APOBEC1 complementation factor	0.271	0.031
AACS	chr12:125549924-125627871	acetoacetyl-CoA synthetase	1.832	2.205
AADAC	chr3:151347319-151546276	arylacetamide deacetylase	0.322	0.036
AAK1	chr2:69685126-70053596	AP2 associated kinase 1	1.743	2.861
AARS	chr16:70280724-70323438	alanyl-tRNA synthetase	2.252	3.467
AASS	chr7:121713388-121784344	aminoadipate-semialdehyde synthase	0.381	0.336
ABAT	chr16:8768443-8878432	4-aminobutyrate aminotransferase	0.366	0.126
ABCA1	chr9:107543177-107707472	ATP binding cassette subfamily A member 1	0.28	0.189
ABCA12	chr2:215796265-216003308	ATP binding cassette subfamily A member 12	0.722	0.227
ABCA3	chr16:2325783-2390747	ATP binding cassette subfamily A member 3	3.698	4.946
ABCA6	chr17:67074817-67138015	ATP binding cassette subfamily A member 6	0.212	0.04
ABCB4	chr7:87031171-87461646	ATP binding cassette subfamily B member 4	0.164	0.032
ABCB7	chrX:74270462-74376277	ATP binding cassette subfamily B member 7	0.579	0.342
ABCC2	chr10:101542178-101613520	ATP binding cassette subfamily C member 2	0.33	0.027
ABCC6	chr16:16243253-16317625	ATP binding cassette subfamily C member 6	0.318	0.126
ABCC6P1	chr16:18582506-18609629	ATP binding cassette subfamily C member 6 pseudogene 1	0.26	0.068
ABCC6P2	chr16:14908173-14918610	ATP binding cassette subfamily C member 6 pseudogene 2	0.239	0.096
ABCC9	chr12:21950323-22094668	ATP binding cassette subfamily C member 9	0.516	0.379
ABCG1	chr21:43619798-43718025	ATP binding cassette subfamily G member 1	3.271	5.315
ABCG2	chr4:89011415-89152474	ATP binding cassette subfamily G member 2 (Junior blood group)	0.395	0.118
ABCG5	chr2:44039610-44110328	ATP binding cassette subfamily G member 5	0.057	0.001
ABCG8	chr2:44039610-44110328	ATP binding cassette subfamily G member 8	0.033	0.001
ABHD14A	chr3:52002525-52023218	abhydrolase domain containing 14A	0.294	0.188
ABHD2	chr15:89631380-89745642	abhydrolase domain containing 2	0.563	0.425
ABHD3	chr18:19230857-19284893	abhydrolase domain containing 3	1.659	2.053
ABL1	chr9:133588305-133765535	ABL proto-oncogene 1, non-receptor tyrosine kinase	1.454	2.181
ABL2	chr1:179068322-179198819	ABL proto-oncogene 2, non-receptor tyrosine kinase	1.308	2.183
ABP1	chr7:150549564-150558379	amine oxidase, copper containing 1	0.42	0.119
ABRACL	chr6:139348013-139364439	ABRA C-terminal like	0.319	0.186
ABTB2	chr11:34127104-34379666	ankyrin repeat and BTB domain containing 2	2.111	3.447
ACAA1	chr3:38080695-38178733	acetyl-CoA acyltransferase 1	0.493	0.22
ACACB	chr12:109548959-109706030	acetyl-CoA carboxylase beta	0.421	0.32
ACAD9	chr3:128598332-128634437	acyl-CoA dehydrogenase family member 9	0.646	0.407
ACADL	chr2:210867304-211091474	acyl-CoA dehydrogenase, long chain	0.426	0.336
ACADM	chr1:76190042-76229355	acyl-CoA dehydrogenase, C-4 to C-12 straight chain	0.54	0.351
ACADS	chr12:121163570-121177811	acyl-CoA dehydrogenase, C-2 to C-3 short chain	0.622	0.416
ACADSB	chr10:124768428-124817806	acyl-CoA dehydrogenase, short/branched chain	0.531	0.275
ACAT1	chr11:107879341-108018891	acetyl-CoA acetyltransferase 1	0.582	0.3
ACAT2	chr6:160181290-160210735	acetyl-CoA acetyltransferase 2	0.284	0.202
ACBD7	chr10:15117473-15130775	acyl-CoA binding domain containing 7	1.405	2.043
ACER2	chr9:19408924-19455158	alkaline ceramidase 2	1.692	2.649
ACMSD	chr2:135595889-135716915	aminocarboxymuconate semialdehyde decarboxylase	0.173	0.02
ACO1	chr9:32324890-32450877	aconitase 1	0.477	0.359
ACOT1	chr14:73945188-74025651	acyl-CoA thioesterase 1	0.375	0.192
ACOT12	chr5:80256507-81047072	acyl-CoA thioesterase 12	0.144	0.057
ACOT2	chr14:74031643-74042509	acyl-CoA thioesterase 2	0.453	0.228
ACOT4	chr14:74058409-74062470	acyl-CoA thioesterase 4	0.638	0.308
ACOT7	chr1:6324331-6453826	acyl-CoA thioesterase 7	1.984	2.822
ACOX1	chr17:73937588-74002080	acyl-CoA oxidase 1, palmitoyl	0.52	0.314
ACOX2	chr3:58490862-58522929	acyl-CoA oxidase 2, branched chain	0.12	0.051
ACOXL	chr2:111490149-111926022	acyl-CoA oxidase-like	1.283	2.25
ACPP	chr3:132036210-132087146	acid phosphatase, prostate	0.229	0.204
ACRBP	chr12:6747241-6756668	acrosin binding protein	1.757	3.489
ACSF2	chr17:48503518-48552200	acyl-CoA synthetase family member 2	0.335	0.185
ACSL4	chrX:108884563-108976787	acyl-CoA synthetase long-chain family member 4	0.311	0.179
ACSL5	chr10:114133804-114188138	acyl-CoA synthetase long-chain family member 5	0.194	0.103
ACSM2A	chr16:20462738-20498991	acyl-CoA synthetase medium-chain family member 2A	0.199	0.026
ACSM2B	chr16:20529072-20593323	acyl-CoA synthetase medium-chain family member 2B	0.209	0.036
ACSM3	chr16:20775311-20860990	acyl-CoA synthetase medium-chain family member 3	0.255	0.043
ACSM5	chr16:20420855-20452618	acyl-CoA synthetase medium-chain family member 5	0.267	0.048
ACSS1	chr20:24986865-25038818	acyl-CoA synthetase short-chain family member 1	0.056	0.013
ACSS2	chr20:33460741-33515769	acyl-CoA synthetase short-chain family member 2	0.55	0.436
ACSS3	chr12:81471626-81651243	acyl-CoA synthetase short-chain family member 3	0.47	0.255
ACTL8	chr1:18081807-18153602	actin like 8	0.664	0.41
ACTN1	chr14:69312134-69446169	actinin alpha 1	2.139	2.208
ACTR3C	chr7:149944300-150035245	ARP3 actin-related protein 3 homolog C	0.636	0.256
ACY3	chr11:67410025-67418190	aminoacylase 3	0.237	0.032
ADA	chr20:43248162-43280376	adenosine deaminase	0.616	0.428
ADAMTS10	chr19:8645125-8675588	ADAM metallopeptidase with thrombospondin type 1 motif 10	0.485	0.218
ADAMTS20	chr12:43747699-43945724	ADAM metallopeptidase with thrombospondin type 1 motif 20	0.619	0.344
ADAMTS9	chr3:64501330-64997143	ADAM metallopeptidase with thrombospondin type 1 motif 9	1.252	2.23
ADAMTSL4	chr1:150518468-150544704	ADAMTS like 4	2.146	4.774
ADARB1	chr21:46494492-46646478	adenosine deaminase, RNA specific B1	1.612	2.865
ADAT3	chr19:1905370-1926012	adenosine deaminase, tRNA specific 3	1.795	2.75
ADC	chr1:33546713-33586481	antizyme inhibitor 2	1.578	2.551
ADCK3	chr1:227127180-227175246	aarF domain containing kinase 3	0.519	0.217
ADCY7	chr16:50279510-50402890	adenylate cyclase 7	2.529	3.574
ADH4	chr4:100010007-100273917	alcohol dehydrogenase 4 (class II), pi polypeptide	0.038	0.008
ADH5	chr4:99988727-100009947	alcohol dehydrogenase 5 (class III), chi polypeptide	0.451	0.326
ADH6	chr4:100010007-100273917	alcohol dehydrogenase 6 (class V)	0.115	0.007
ADM	chr11:10326634-10328939	adrenomedullin	1.796	2.328
ADORA2B	chr17:15848230-15879210	adenosine A2b receptor	1.738	2.818
ADRA1A	chr8:26605666-26729730	adrenoceptor alpha 1A	0.209	0.156
ADSSL1	chr14:105190533-105213647	adenylosuccinate synthase like 1	0.407	0.285
AFAP1	chr4:7755816-7941653	actin filament associated protein 1	3.758	8.601
AFAP1L1	chr5:148651400-148721799	actin filament associated protein 1 like 1	2.787	2.931
AFF4	chr5:132202207-132299473	AF4/FMR2 family member 4	1.531	2.115
AFM	chr4:74347405-74395600	afamin	0.177	0.021
AFMID	chr17:76170159-76203782	arylformamidase	0.535	0.278
AGBL2	chr11:47681142-47737024	ATP/GTP binding protein-like 2	0.614	0.322
AGBL5	chr2:27274490-27294567	ATP/GTP binding protein-like 5	0.595	0.49
AGL	chr1:100315632-100389579	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	0.498	0.282
AGMAT	chr1:15853351-15911605	agmatinase	0.303	0.057
AGMO	chr7:15198958-15601645	alkylglycerol monooxygenase	0.304	0.023
AGO2	chr8:141530258-141645694	argonaute 2, RISC catalytic component	1.668	2.373
AGPAT2	chr9:139567594-139581911	1-acylglycerol-3-phosphate O-acyltransferase 2	0.344	0.379
AGPAT5	chr8:6264112-6619021	1-acylglycerol-3-phosphate O-acyltransferase 5	2.019	4.034
AGPAT9	chr4:84457066-84527027	glycerol-3-phosphate acyltransferase 3	2.671	3.449
AGPHD1	chr15:78799905-78829715	hydroxylysine kinase	0.519	0.406
AGT	chr1:230838271-230850336	angiotensinogen	0.725	0.2
AGXT	chr2:241797144-241818536	alanine-glyoxylate aminotransferase	0.186	0.061

AGXT2	chr5:34997071-35048240	alanine--glyoxylate aminotransferase 2	0.12	0.015
AGXT2L1	chr4:109663018-109684235	ethanolamine-phosphate phospho-lyase	0.435	0.133
AHSG	chr3:186330849-186339107	alpha-2-HS-glycoprotein	0.302	0.082
AIFM1	chrX:129263337-129299861	apoptosis inducing factor, mitochondria associated 1	0.616	0.432
AIG1	chr6:143381589-143665270	androgen-induced 1	0.636	0.454
AK4	chr1:65613231-65697828	adenylate kinase 4	0.537	0.384
AKAP1	chr17:55162474-55198710	A-kinase anchoring protein 1	0.52	0.434
AKIRIN2	chr6:88384577-88411985	akirin 2	1.585	2.518
AKNA	chr9:117096083-117160753	AT-hook transcription factor	1.554	2.255
AKR1B10	chr7:134212253-134226166	aldo-keto reductase family 1, member B10 (aldose reductase)	0.406	0.033
AKR1C2	chr10:5005453-5326522	aldo-keto reductase family 1, member C2	0.479	0.205
AKR1C4	chr10:5005453-5326522	aldo-keto reductase family 1, member C4	0.177	0.018
AKR1C6P	chr10:4913858-4958540	aldo-keto reductase family 1, member C6, pseudogene	0.062	0.008
AKR1D1	chr7:137749922-137803050	aldo-keto reductase family 1, member D1	0.092	0.023
AKT3	chr1:243419242-244006886	v-akt murine thymoma viral oncogene homolog 3	2.071	2.561
ALAD	chr9:116148591-116163618	aminolevulinate dehydratase	0.603	0.345
ALB	chr4:74269971-74287129	albumin	0.527	0.099
ALDH1A1	chr9:75515577-75568233	aldehyde dehydrogenase 1 family member A1	0.294	0.061
ALDH1B1	chr9:38385772-38398662	aldehyde dehydrogenase 1 family member B1	0.605	0.403
ALDH1L1	chr3:125822307-125929011	aldehyde dehydrogenase 1 family member L1	0.337	0.122
ALDH3A1	chr17:19641280-19651750	aldehyde dehydrogenase 3 family member A1	0.173	0.048
ALDH3A2	chr17:19551554-19580917	aldehyde dehydrogenase 3 family member A2	0.698	0.418
ALDH4A1	chr1:19197920-19229328	aldehyde dehydrogenase 4 family member A1	0.598	0.289
ALDH5A1	chr6:24495018-24543479	aldehyde dehydrogenase 5 family member A1	0.763	0.404
ALDH6A1	chr14:74399694-74551196	aldehyde dehydrogenase 6 family member A1	0.476	0.218
ALDH7A1	chr5:125867007-125931283	aldehyde dehydrogenase 7 family member A1	0.495	0.227
ALDH9A1	chr1:165631448-165667900	aldehyde dehydrogenase 9 family member A1	0.713	0.434
ALDOB	chr9:104182697-104211853	aldolase, fructose-bisphosphate B	0.209	0.047
ALDOC	chr17:26900131-26904105	aldolase, fructose-bisphosphate C	0.418	0.343
ALG14	chr1:95392810-95538509	ALG14, UDP-N-acetylglucosaminyltransferase subunit	0.515	0.363
ALG1L	chr3:125635443-125656627	ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase-like	0.333	0.272
ALG8	chr11:77726760-77850699	ALG8, alpha-1,3-glucosyltransferase	0.641	0.428
ALKBH2	chr12:109525991-109531407	alkB homolog 2, alpha-ketoglutarate-dependent dioxygenase	0.496	0.35
ALKBH8	chr11:107373452-107436461	alkB homolog 8, tRNA methyltransferase	0.531	0.218
ALOXE3	chr17:7999217-8022234	arachidonate lipoxygenase 3	13.02	24.91
ALPK2	chr18:56148481-56296189	alpha kinase 2	6.067	4.708
ALPK3	chr15:85291739-85416713	alpha kinase 3	1.612	2.142
ALPL	chr1:21835857-21904905	alkaline phosphatase, liver/bone/kidney	0.078	0.022
ALX3	chr1:110574198-110613322	ALX homeobox 3	1.428	2.625
AMBP	chr9:116822404-116840752	alpha-1-microglobulin/bikunin precursor	0.736	0.167
AMD1	chr6:111195986-111216913	adenosylmethionine decarboxylase 1	1.867	3.414
AMDHD1	chr12:96337070-96362370	amidohydrolase domain containing 1	0.766	0.341
AMIGO3	chr3:49726949-49761384	adhesion molecule with Ig-like domain 3	1.345	2.166
AMN	chr14:103388992-103397352	amnion associated transmembrane protein	0.673	0.143
AMPD2	chr1:110162434-110174677	adenosine monophosphate deaminase 2	0.533	0.371
AMPD3	chr11:10471867-10529126	adenosine monophosphate deaminase 3	1.337	3.016
ANG	chr14:21151120-21168758	angiogenin, ribonuclease, RNase A family, 5	0.162	0.091
ANGPT1	chr8:108261709-108510254	angiopoietin 1	0.366	0.261
ANGPTL3	chr1:62920396-63154039	angiopoietin like 3	0.172	0.035
ANGPTL4	chr19:8429010-8439257	angiopoietin like 4	1.706	5.493
ANK2	chr4:113739132-114304896	ankyrin 2, neuronal	2.137	2.745
ANK3	chr10:61786055-62493284	ankyrin 3, node of Ranvier (ankyrin G)	0.4	0.163
ANKLE2	chr12:133302137-133338451	ankyrin repeat and LEM domain containing 2	1.509	2.049
ANKRD1	chr10:92631708-92699458	ankyrin repeat domain 1	4.91	3.6
ANKRD11	chr16:89333924-89557022	ankyrin repeat domain 11	1.896	3.198
ANKRD29	chr18:21178952-21242860	ankyrin repeat domain 29	0.833	0.403
ANKRD30BP3	chr10:45650109-45693809	ankyrin repeat domain 30B pseudogene 3	0.766	0.426
ANKRD33B	chr5:10564434-10657928	ankyrin repeat domain 33B	1.844	2.186
ANKRD36BP1	chr1:168195222-168283664	ankyrin repeat domain 36B pseudogene 1	0.742	0.472
ANKRD44	chr2:197851385-198175521	ankyrin repeat domain 44	0.685	0.37
ANKRD50	chr4:125584478-125633887	ankyrin repeat domain 50	1.706	2.341
ANKRD54	chr22:38225033-38245319	ankyrin repeat domain 54	1.49	2.199
ANKS4B	chr16:21245015-21263750	ankyrin repeat and sterile alpha motif domain containing 4B	0.211	0.03
ANLN	chr7:36363758-36493400	anillin actin binding protein	0.583	0.35
ANO3	chr11:26353677-26684836	anoctamin 3	0.72	0.428
ANP32A	chr15:69070874-69114510	acidic nuclear phosphoprotein 32 family member A	0.623	0.291
ANPEP	chr15:90328125-90358072	alanyl aminopeptidase, membrane	0.41	0.237
ANXA1	chr9:75766780-75785307	annexin A1	1.7	2.303
ANXA10	chr4:169013687-169246998	annexin A10	0.116	0.008
ANXA13	chr8:124693033-124749647	annexin A13	0.071	0.001
ANXA3	chr4:79472741-79531605	annexin A3	3.774	2.494
ANXA4	chr2:69685126-70053596	annexin A4	0.511	0.393
ANXA5	chr4:122589151-122618147	annexin A5	1.888	2.858
ANXA6	chr5:150478488-150537443	annexin A6	0.417	0.229
ANXA8	chr10:47096453-47174143	annexin A8-like 1	0.053	0.165
ANXA8L2	chr10:47746875-47769716	annexin A8-like 1	0.205	0.037
ANXA9	chr1:150954498-150980854	annexin A9	0.372	0.111
AOX1	chr2:201450730-201537620	aldehyde oxidase 1	0.418	0.097
AOX2P	chr2:201556882-201658941	aldehyde oxidase 2 pseudogene	0.311	0.165
AP1M2	chr19:10683346-10697991	adaptor related protein complex 1 mu 2 subunit	0.296	0.057
AP1S1	chr7:100797685-100804848	adaptor related protein complex 1 sigma 1 subunit	0.576	0.327
AP1S2	chrX:15843928-15873171	adaptor related protein complex 1 sigma 2 subunit	2.676	3.755
AP3M2	chr8:42010463-42028881	adaptor related protein complex 3 mu 2 subunit	1.958	2.484
AP5Z1	chr7:4815189-4835759	adaptor related protein complex 5 zeta 1 subunit	1.289	2.035
APBA1	chr9:72042448-72287289	amyloid beta precursor protein binding family A member 1	1.93	2.138
APBB1IP	chr10:26727149-26863674	amyloid beta precursor protein binding family B member 1 interacting protein	0.422	0.31
APCDD1L	chr20:57027922-57194948	adenomatosis polyposis coli down-regulated 1 like	4.723	6.55
APCS	chr1:159557615-159558661	amyloid P component, serum	0.325	0.03
APMAP	chr20:24943579-24973425	adipocyte plasma membrane associated protein	0.404	0.318
APOA1	chr11:116706464-116708338	apolipoprotein A-I	0.877	0.211
APOA2	chr1:161192082-161193418	apolipoprotein A2	0.487	0.041
APOA4	chr11:116691417-116694011	apolipoprotein A4	0.539	0.16
APOB	chr2:21224129-21266962	apolipoprotein B	0.459	0.075
APOBEC3A	chr22:39353526-39388784	apolipoprotein B mRNA editing enzyme catalytic subunit 3A	0.657	0.17
APOBEC3C	chr22:39410068-39416791	apolipoprotein B mRNA editing enzyme catalytic subunit 3C	0.439	0.279
APOBEC3G	chr22:39473009-39483748	apolipoprotein B mRNA editing enzyme catalytic subunit 3G	0.549	0.407
APOBEC3H	chr22:39493228-39500072	apolipoprotein B mRNA editing enzyme catalytic subunit 3H	0.133	0.089
APOC1	chr19:45417920-45422606	apolipoprotein C1	0.576	0.168
APOC3	chr11:116700623-116703787	apolipoprotein C3	0.564	0.15
APOE	chr19:45409038-45412650	apolipoprotein E	0.777	0.291
APOH	chr17:64208146-64225556	apolipoprotein H	0.681	0.148
APOL1	chr22:36649116-36663577	apolipoprotein L1	0.695	0.483
AQP11	chr11:77251026-77348851	aquaporin 11	0.523	0.404

AQP3	chr9:33441151-33447631	aquaporin 3 (Gill blood group)	0.793	0.216
AQP7	chr9:33384384-33402517	aquaporin 7	0.498	0.096
AQP7P3	chr9:42811681-42893137	aquaporin 7 pseudogene 3	0.482	0.182
AQP9	chr15:58430407-58478110	aquaporin 9	0.267	0.072
ARAP2	chr4:36059485-36246409	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	1.83	2.304
ARG1	chr6:131894343-131949379	arginase 1	0.075	0.014
ARG2	chr14:68086576-68141602	arginase 2	2.541	5.042
ARHGAP11A	chr15:32907690-32931868	Rho GTPase activating protein 11A	0.666	0.323
ARHGAP19	chr10:98757681-99052430	Rho GTPase activating protein 19	0.603	0.421
ARHGAP20	chr11:110447758-110583962	Rho GTPase activating protein 20	1.863	2.115
ARHGAP23	chr17:36584719-36668858	Rho GTPase activating protein 23	1.497	2.685
ARHGAP26	chr5:142149924-142608572	Rho GTPase activating protein 26	2.606	4.106
ARHGAP28	chr18:6729685-6915717	Rho GTPase activating protein 28	1.926	2.283
ARHGAP32	chr11:128834864-129149110	Rho GTPase activating protein 32	1.735	2.81
ARHGAP39	chr8:145754516-145911218	Rho GTPase activating protein 39	1.638	3.139
ARHGAP8	chr22:45064426-45258664	Rho GTPase activating protein 8	0.533	0.446
ARHGDIA	chr17:79825596-79829282	Rho GDP dissociation inhibitor alpha	1.543	2.143
ARHGEF10L	chr1:17866323-18024370	Rho guanine nucleotide exchange factor 10 like	0.548	0.415
ARHGEF16	chr1:3371146-3397677	Rho guanine nucleotide exchange factor 16	0.264	0.055
ARHGEF2	chr1:155916540-155953675	Rho/Rac guanine nucleotide exchange factor 2	8.114	10.63
ARHGEF39	chr9:35658286-35665278	Rho guanine nucleotide exchange factor 39	0.506	0.28
ARHGEF4	chr2:131594476-131804836	Rho guanine nucleotide exchange factor 4	2.243	5.065
ARID3B	chr15:74833547-74890472	AT-rich interaction domain 3B	1.639	2.645
ARIH2	chr3:48955220-49023842	ariadne RBR E3 ubiquitin protein ligase 2	1.582	2.208
ARL4C	chr2:235401517-235405751	ADP ribosylation factor like GTPase 4C	5.636	11.52
ARL4D	chr17:41476352-41485948	ADP ribosylation factor like GTPase 4D	1.623	2.357
ARL6IP5	chr3:69134089-69155239	ADP ribosylation factor like GTPase 6 interacting protein 5	0.548	0.352
ARL8A	chr1:202102531-202113871	ADP ribosylation factor like GTPase 8A	1.692	2.176
ARPC1B	chr7:98972297-99006305	actin related protein 2/3 complex subunit 1B	1.83	2.72
ARRB2	chr17:4613788-4624795	arrestin beta 2	0.637	0.419
ART4	chr12:14939411-14996548	ADP-ribosyltransferase 4 (Dombrock blood group)	0.358	0.043
ARVCF	chr22:19863039-20004309	armadillo repeat gene deleted in velocardiofacial syndrome	2.915	4.028
ASAP2	chr2:9346893-9613239	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	2.855	4.796
ASB13	chr10:5680819-5708558	ankyrin repeat and SOCS box containing 13	0.369	0.167
ASB4	chr7:95090878-95172810	ankyrin repeat and SOCS box containing 4	0.567	0.286
ASB8	chr12:48541514-48551377	ankyrin repeat and SOCS box containing 8	0.696	0.434
ASGR1	chr17:7076750-7082883	asialoglycoprotein receptor 1	0.194	0.044
ASGR2	chr17:7004640-7018620	asialoglycoprotein receptor 2	0.517	0.118
ASIC5	chr4:156750880-156841558	acid sensing ion channel subunit family member 5	0.637	0.327
ASNS	chr7:97481428-97501854	asparagine synthetase (glutamine-hydrolyzing)	12.93	28.77
ASPA	chr17:3377403-3403781	aspartoacylase	0.128	0.069
ASPHD2	chr22:26825279-26840978	aspartate beta-hydroxylase domain containing 2	2.36	2.592
ASPM	chr1:197053256-197115824	abnormal spindle microtubule assembly	0.453	0.217
ASTN2	chr9:119182459-120177317	astrotactin 2	0.628	0.34
ATF3	chr1:212738675-212794119	activating transcription factor 3	11.82	14.48
ATF4	chr22:39916568-39918691	activating transcription factor 4	2.392	3.773
ATF6B	chr6:32083044-32096017	activating transcription factor 6 beta	0.649	0.448
ATG4A	chrX:107334898-107397901	autophagy related 4A cysteine peptidase	0.752	0.494
ATG4B	chr2:242576799-242613274	autophagy related 4B cysteine peptidase	1.484	2.28
ATOH8	chr2:85973169-86018506	atonal bHLH transcription factor 8	0.615	0.415
ATP10D	chr4:47487245-47595551	ATPase phospholipid transporting 10D (putative)	1.545	2.546
ATP11A	chr13:113344374-113541482	ATPase phospholipid transporting 11A	1.556	2.323
ATP13A2	chr1:17312452-17338423	ATPase 13A2	2.735	4.994
ATP13A3	chr3:194123400-194234422	ATPase 13A3	1.574	2.021
ATP1A2	chr1:160085519-160114339	ATPase Na+/K+ transporting subunit alpha 2	0.357	0.274
ATP1B3	chr3:141595433-141645382	ATPase Na+/K+ transporting subunit beta 3	1.992	2.905
ATP2B1	chr12:89952794-90105729	ATPase plasma membrane Ca2+ transporting 1	1.167	2.207
ATP2B4	chr1:203595914-203713210	ATPase plasma membrane Ca2+ transporting 4	1.74	2.309
ATP5A1	chr18:43664109-43684199	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, car	0.542	0.347
ATP5B	chr12:57031958-57039852	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	0.567	0.436
ATP5C1	chr10:7830092-7849762	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide	0.596	0.42
ATP5G1	chr17:46970147-46973232	ATP synthase, H+ transporting, mitochondrial Fo complex subunit C1 (subunit	0.58	0.47
ATP5J	chr21:27011593-27144771	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F6	0.452	0.28
ATP5O	chr21:35275756-35288158	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0.541	0.362
ATP6V0E2	chr7:149564782-149577800	ATPase H+ transporting V0 subunit e2	0.621	0.206
ATP8B3	chr19:1782030-1812275	ATPase phospholipid transporting 8B3	0.42	0.291
ATXN2L	chr16:28829852-28848558	ataxin 2 like	1.717	2.309
ATXN7L1	chr7:105244824-105517915	ataxin 7 like 1	0.474	0.315
AUH	chr9:93975140-94124226	AU RNA binding protein/enoyl-CoA hydratase	0.487	0.273
AURKA	chr20:54944444-54967351	aurora kinase A	0.303	0.279
AURKB	chr17:8107825-8113944	aurora kinase B	0.619	0.33
AXIN1	chr16:337438-402676	axin 1	2.106	3.622
AZGP1P1	chr7:99578384-99585452	alpha-2-glycoprotein 1, zinc-binding pseudogene 1	0.273	0.176
B3GAT3	chr11:62382766-62389647	beta-1,3-glucuronyltransferase 3	1.826	2.67
B3GNT3	chr19:17905624-17924417	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	0.225	0.033
B4GALT2	chr1:44444873-44456854	beta-1,4-galactosyltransferase 2	1.918	2.149
BAAT	chr9:104117616-104147287	bile acid-CoA:amino acid N-acyltransferase	0.071	0.009
BACH2	chr6:90636246-91006627	BTB domain and CNC homolog 2	2.674	3.984
BAI2	chr1:32192549-32229675	adhesion G protein-coupled receptor B2	3.166	3.846
BAIAP2L2	chr22:38473903-38506676	BAI1 associated protein 2 like 2	0.643	0.469
BATF2	chr11:64755416-64764517	basic leucine zipper ATF-like transcription factor 2	0.327	0.275
BATF3	chr1:212859758-212873327	basic leucine zipper ATF-like transcription factor 3	2.835	5.484
BBOX1	chr11:27062508-27149354	gamma-butyrobetaine hydroxylase 1	0.238	0.033
BCAR3	chr1:94027262-94312706	breast cancer anti-estrogen resistance 3	1.516	2.75
BCAS4	chr20:49411466-49494544	breast carcinoma amplified sequence 4	2.292	2.543
BCHE	chr3:165490691-165555253	butyrylcholinesterase	0.529	0.229
BCKDHA	chr19:41903693-41930910	branched chain keto acid dehydrogenase E1, alpha polypeptide	0.443	0.315
BCKDHB	chr6:80816343-81180432	branched chain keto acid dehydrogenase E1, beta polypeptide	0.608	0.43
BCL2	chr18:60790578-60986979	B-cell CLL/lymphoma 2	2.208	3.922
BCL3	chr19:45243486-45263301	B-cell CLL/lymphoma 3	0.618	0.354
BCORL1	chrX:129115649-129192172	BCL6 corepressor-like 1	1.495	2.199
BDH1	chr3:197236653-197300194	3-hydroxybutyrate dehydrogenase, type 1	0.035	0.024
BDH2	chr4:103998781-104021024	3-hydroxybutyrate dehydrogenase, type 2	0.448	0.289
BDKRB2	chr14:96671070-96710792	bradykinin receptor B2	4.605	2.436
BEND7	chr10:13480483-13570589	BEN domain containing 7	2.248	3.145
BEX5	chrX:101408678-101410986	brain expressed X-linked 5	1.921	3.499
BGLAP	chr1:156182778-156262234	bone gamma-carboxyglutamate protein	0.692	0.446
BHLHE40	chr3:5021096-5026865	basic helix-loop-helix family member e40	1.358	2.169
BHLHE41	chr12:26272958-26278631	basic helix-loop-helix family member e41	2.712	3.856
BHMT2	chr5:78292796-78531831	betaine--homocysteine S-methyltransferase 2	0.49	0.135
BIK	chr22:43506753-43525718	BCL2 interacting killer	2.811	3.495
BIN1	chr2:127805598-127864903	bridging integrator 1	1.747	2.019
BIRC5	chr17:76210276-76221716	baculoviral IAP repeat containing 5	0.469	0.188

BIVM	chr13:103436630-103528351	basic, immunoglobulin-like variable motif containing	0.69	0.461
BLNK	chr10:97889150-98031357	B-cell linker	0.15	0.022
BNIP1	chr5:172571444-172591390	BCL2/adenovirus E1B 19kDa interacting protein 1	0.636	0.369
BPHL	chr6:3118891-3153804	biphenyl hydrolase-like (serine hydrolase)	0.5	0.337
BPNT1	chr1:220046618-220321383	3'(2'), 5'-bisphosphate nucleotidase 1	0.591	0.323
BRE	chr2:28004265-28561767	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.697	0.386
BRI3	chr7:97881690-98030427	brain protein I3	1.276	2.243
BRSK2	chr11:1411128-1483919	BR serine/threonine kinase 2	2.111	4.136
BRWD3	chrX:79924890-80065283	bromodomain and WD repeat domain containing 3	0.733	0.391
BSN	chr3:49591921-49710156	bassoon presynaptic cytomatrix protein	1.884	2.796
BTBD19	chr1:45266035-45452394	BTB domain containing 19	1.815	2.694
BTD	chr3:15643217-15696804	biotinidase	0.506	0.331
BTN3A2	chr6:26365397-26378548	butyrophilin subfamily 3 member A2	0.606	0.488
BTNL8	chr5:180326076-180378350	butyrophilin like 8	0.255	0.022
BUB1	chr2:111395407-111435687	BUB1 mitotic checkpoint serine/threonine kinase	0.607	0.397
BUB1B	chr15:40453209-40569688	BUB1 mitotic checkpoint serine/threonine kinase B	0.462	0.201
BUD31	chr7:99006600-99063824	BUD31 homolog	1.508	2.288
C10orf11	chr10:77542518-78317126	chromosome 10 open reading frame 11	0.451	0.252
C10orf54	chr10:73156690-73575704	chromosome 10 open reading frame 54	1.427	2.045
C11orf1	chr11:111744779-111754886	chromosome 11 open reading frame 1	0.654	0.44
C11orf35	chr11:532198-564025	lamin tail domain containing 2	0.59	0.374
C11orf54	chr11:93474789-93500422	chromosome 11 open reading frame 54	0.397	0.191
C12orf39	chr12:21679209-21685781	spexin hormone	2.121	3.46
C12orf44	chr12:52463694-52471279	autophagy related 101	1.543	2.091
C12orf75	chr12:105724413-105765296	chromosome 12 open reading frame 75	0.733	0.21
C14orf1	chr14:76117232-76127538	chromosome 14 open reading frame 1	0.316	0.152
C14orf105	chr14:57936054-57960609	chromosome 14 open reading frame 105	0.535	0.052
C14orf159	chr14:91580356-91691890	chromosome 14 open reading frame 159	0.366	0.214
C14orf93	chr14:23451961-23479360	chromosome 14 open reading frame 93	0.715	0.424
C15orf39	chr15:75494220-75504689	chromosome 15 open reading frame 39	1.783	2.683
C15orf52	chr15:40623624-40633168	chromosome 15 open reading frame 52	0.651	0.356
C15orf62	chr15:41060066-41106768	chromosome 15 open reading frame 62	0.472	0.324
C16orf62	chr16:19566665-19869950	chromosome 16 open reading frame 62	0.625	0.396
C16orf72	chr16:9185536-9213555	chromosome 16 open reading frame 72	1.871	2.598
C16orf93	chr16:30709024-30787628	coiled-coil domain containing 189	1.261	2.987
C17orf51	chr17:21430635-21476594	chromosome 17 open reading frame 51	1.721	2.153
C17orf53	chr17:42219273-42239944	chromosome 17 open reading frame 53	0.664	0.235
C17orf67	chr17:54869273-54911256	chromosome 17 open reading frame 67	2.05	2.491
C17orf75	chr17:30651762-30677062	chromosome 17 open reading frame 75	0.524	0.297
C19orf12	chr19:30189792-30206696	chromosome 19 open reading frame 12	0.466	0.267
C19orf60	chr19:18699430-18703224	chromosome 19 open reading frame 60	0.505	0.292
C19orf66	chr19:10196805-10213425	chromosome 19 open reading frame 66	0.576	0.388
C1orf111	chr1:162039483-162356896	chromosome 1 open reading frame 111	0.484	0.364
C1orf115	chr1:220863627-220872499	chromosome 1 open reading frame 115	0.479	0.229
C1orf131	chr1:231359508-231424376	chromosome 1 open reading frame 131	0.629	0.426
C1orf159	chr1:1015890-1051736	chromosome 1 open reading frame 159	2.951	6.048
C1orf220	chr1:178511426-178518731	chromosome 1 open reading frame 220	0.473	0.285
C1orf85	chr1:156262477-156265480	glycosylated lysosomal membrane protein	0.62	0.412
C1QL1	chr17:43037060-43045644	complement component 1, q subcomponent-like 1	1.641	2.879
C1RL	chr12:7247145-7311530	complement C1r subcomponent like	0.525	0.241
C2	chr6:31865561-31913449	complement component 2	0.778	0.349
C21orf33	chr21:45553462-45565605	chromosome 21 open reading frame 33	0.599	0.484
C21orf58	chr21:47720485-47865818	chromosome 21 open reading frame 58	0.618	0.44
C22orf23	chr22:38302070-38365319	chromosome 22 open reading frame 23	2.912	6.356
C2CD5	chr12:22601517-22697452	C2 calcium-dependent domain containing 5	0.764	0.48
C2orf47	chr2:200793633-200828847	chromosome 2 open reading frame 47	0.597	0.319
C2orf54	chr2:241825388-241836249	chromosome 2 open reading frame 54	0.009	0.001
C2orf72	chr2:231902268-231917323	chromosome 2 open reading frame 72	0.609	0.363
C2orf74	chr2:61372214-61392095	chromosome 2 open reading frame 74	0.658	0.437
C2orf88	chr2:191002485-191068210	chromosome 2 open reading frame 88	0.414	0.335
C4A	chr6:31949833-31970458	complement component 4B (Chido blood group)	0.708	0.413
C4BPA	chr1:207277574-207318317	complement component 4 binding protein alpha	0.759	0.148
C4BPB	chr1:207262211-207273337	complement component 4 binding protein beta	0.195	0.043
C4orf19	chr4:37455551-37687999	chromosome 4 open reading frame 19	0.872	0.449
C4orf32	chr4:113066552-113110267	chromosome 4 open reading frame 32	2.013	3.02
C4orf33	chr4:130014828-130033843	chromosome 4 open reading frame 33	0.513	0.226
C5	chr9:123714595-123836475	complement component 5	0.435	0.136
C5orf27	chr5:95187459-95195836	long intergenic non-protein coding RNA 1554	0.32	0.369
C5orf4	chr5:154197942-154256352	fatty acid hydroxylase domain containing 2	0.262	0.076
C5orf45	chr5:179224597-179285840	chromosome 5 open reading frame 45	2.393	3.074
C6	chr5:41142247-41261540	complement component 6	0.243	0.045
C6orf1	chr6:34214156-34216904	chromosome 6 open reading frame 1	3.172	7.17
C6orf141	chr6:49518112-49525753	chromosome 6 open reading frame 141	2.358	3.119
C6orf48	chr6:31802692-31807543	chromosome 6 open reading frame 48	3.239	5.908
C7orf10	chr7:40174574-40900366	succinyl-CoA:glutarate-CoA transferase	0.538	0.322
C8A	chr1:57320442-57383894	complement component 8 alpha subunit	0.338	0.07
C8B	chr1:57394882-57431717	complement component 8, beta polypeptide	0.514	0.187
C8G	chr9:139839380-139841613	complement component 8, gamma polypeptide	0.621	0.393
C8orf4	chr8:40010986-40012827	chromosome 8 open reading frame 4	0.783	0.403
C8orf47	chr8:99057974-99106890	glutamate rich 5	0.555	0.201
C9orf16	chr9:130922538-130926207	chromosome 9 open reading frame 16	1.976	3.046
C9orf3	chr9:97488950-97849500	chromosome 9 open reading frame 3	0.783	0.326
C9orf69	chr9:139006426-139016612	chromosome 9 open reading frame 69	2.14	2.02
C9orf91	chr9:117366345-117408703	chromosome 9 open reading frame 91	3.379	6.816
CA9	chr9:35673914-35681154	carbonic anhydrase 9	0.038	0.065
CABP1	chr12:121078421-121105127	calcium binding protein 1	3.496	7.811
CACNB2	chr10:18429605-18948181	calcium voltage-gated channel auxiliary subunit beta 2	0.488	0.382
CADM1	chr11:115044344-115375241	cell adhesion molecule 1	1.695	2.34
CALCRL	chr2:188206689-188313027	calcitonin receptor like receptor	0.495	0.443
CALN1	chr7:71244475-71877365	calneuron 1	1.736	3.239
CAMSAP1	chr9:138700332-138799268	calmodulin regulated spectrin associated protein 1	1.586	2.359
CAP2	chr6:17393625-17558023	CAP, adenylate cyclase-associated protein, 2 (yeast)	0.624	0.411
CAPN1	chr11:64948542-64979477	calpain 1	0.383	0.162
CARD16	chr11:104896133-104972158	caspase recruitment domain family member 16	0.424	0.182
CARD6	chr5:40841409-40855456	caspase recruitment domain family member 6	0.419	0.199
CARD8	chr19:48707321-48761450	caspase recruitment domain family member 8	0.464	0.358
CARD9	chr9:139256351-139294862	caspase recruitment domain family member 9	3.269	4.028
CASKIN2	chr17:73452663-73511627	CASK interacting protein 2	0.747	0.357
CASP1	chr11:104896133-104972158	caspase 1	0.405	0.234
CASP10	chr2:202047620-202094222	caspase 10	0.592	0.35
CASP14	chr19:15160212-15169109	caspase 14	0.081	0.024
CASP4	chr11:104813593-104839325	caspase 4	0.585	0.325
CASP8	chr2:202098165-202316319	caspase 8	0.676	0.472

CASZ1	chr1:10696665-10856733	castor zinc finger 1	1.334	2.132
CAT	chr11:34460463-34493607	catalase	0.497	0.288
CATSPERG	chr19:38826442-38861589	cation channel sperm associated auxiliary subunit gamma	2.728	7.469
CAV1	chr7:116164838-116201239	caveolin 1	0.437	0.258
CBFA2T2	chr20:32077927-32238326	CBFA2/RUNX1 translocation partner 2	1.581	2.289
CBFB	chr16:67062827-67134960	core-binding factor, beta subunit	2.009	3.05
CBL	chr11:119076985-119178859	Cbl proto-oncogene	1.6	2.415
CBLN3	chr14:24894567-24898931	cerebellin 3 precursor	0.32	0.259
CBR1	chr21:37441939-37498938	carbonyl reductase 1	0.731	0.445
CBR4	chr4:169908741-169931468	carbonyl reductase 4	0.556	0.318
CBX2	chr17:77751973-77762148	chromobox 2	1.742	2.067
CBX4	chr17:77806954-77813213	chromobox 4	2.865	5.201
CCBP2	chr3:42850963-42910229	atypical chemokine receptor 2	0.304	0.16
CCDC120	chrX:48910960-48927510	coiled-coil domain containing 120	0.539	0.307
CCDC125	chr5:68575686-68628568	coiled-coil domain containing 125	0.579	0.299
CCDC136	chr7:128431463-128462187	coiled-coil domain containing 136	3.605	5.87
CCDC150	chr2:197504355-197627123	coiled-coil domain containing 150	0.815	0.448
CCDC152	chr5:42756919-42812024	coiled-coil domain containing 152	0.413	0.242
CCDC163P	chr1:45959597-45965751	coiled-coil domain containing 163, pseudogene	1.413	2.856
CCDC170	chr6:151815174-151942328	coiled-coil domain containing 170	0.189	0.036
CCDC34	chr11:27359649-27384795	coiled-coil domain containing 34	0.578	0.181
CCDC51	chr3:48473579-48481529	coiled-coil domain containing 51	0.657	0.35
CCDC53	chr12:102406658-102455909	coiled-coil domain containing 53	0.663	0.4
CCDC58	chr3:122078435-122102074	coiled-coil domain containing 58	0.522	0.326
CCDC68	chr18:52568506-52626739	coiled-coil domain containing 68	0.697	0.302
CCDC85B	chr11:65657289-65667997	coiled-coil domain containing 85B	4.946	12.03
CCDC92	chr12:124247041-124800570	coiled-coil domain containing 92	2.076	3.485
CCL14	chr17:34310691-34329170	C-C motif chemokine ligand 14	0.199	0.048
CCL15	chr17:34310691-34329170	C-C motif chemokine ligand 15	0.199	0.048
CCL2	chr17:32582295-32584220	C-C motif chemokine ligand 2	0.285	0.086
CCL20	chr2:228678557-228682280	C-C motif chemokine ligand 20	4.346	2.177
CCL5	chr17:34198283-34207377	C-C motif chemokine ligand 5	0.957	2.78
CCND1	chr11:69455805-69490165	cyclin D1	2.486	2.653
CCND2	chr12:4382901-4414522	cyclin D2	2.087	2.432
CCNI	chr4:77968228-77997989	cyclin I	1.667	2.486
CCNJL	chr5:159678561-159739573	cyclin J like	2.646	4.052
CCNYL1	chr2:208576194-208621429	cyclin Y like 1	1.797	2.647
CCRN4L	chr4:139936941-140098270	nocturnin	1.98	2.059
CCSAP	chr1:229456751-229478688	centriole, cilia and spindle associated protein	1.956	2.548
CCSER2	chr10:86088334-86278276	coiled-coil serine rich protein 2	1.676	2.456
CD1D	chr1:158147809-158156216	CD1d molecule	0.337	0.119
CD200	chr3:112051408-112081658	CD200 molecule	5.178	10.75
CD247	chr1:167399876-167487847	CD247 molecule	2.18	5.891
CD274	chr9:5450502-5470567	CD274 molecule	2.507	4.2
CD302	chr2:160569009-160761267	CD302 molecule	0.665	0.384
CD44	chr11:35160416-35253949	CD44 molecule (Indian blood group)	4.325	6.299
CD70	chr19:6582520-6591224	CD70 molecule	1.735	2.859
CD74	chr5:149781199-149792499	CD74 molecule	0.485	0.374
CDC14B	chr9:99262092-99382112	cell division cycle 14B	0.678	0.414
CDC20B	chr5:54408622-54469005	cell division cycle 20B	0.126	0.104
CDC25C	chr5:137620958-137667516	cell division cycle 25C	0.489	0.345
CDC42EP1	chr22:37956470-37965432	CDC42 effector protein 1	1.737	2.095
CDCA3	chr12:6957971-6960456	cell division cycle associated 3	0.349	0.279
CDCP1	chr3:45123768-45187914	CUB domain containing protein 1	2.656	4.327
CDH1	chr16:68771194-68869444	cadherin 1	0.252	0.054
CDH10	chr5:24487208-24645085	cadherin 10	0.389	0.295
CDK1	chr10:62538088-62554778	cyclin-dependent kinase 1	0.747	0.379
CDK18	chr1:205473683-205502163	cyclin-dependent kinase 18	0.705	0.346
CDK5	chr7:150750898-150755052	cyclin-dependent kinase 5	0.59	0.332
CDK5RAP2	chr9:123151146-123342448	CDK5 regulatory subunit associated protein 2	0.699	0.449
CDKN1A	chr6:36644236-36655116	cyclin-dependent kinase inhibitor 1A	1.437	2.197
CDKN2B	chr9:21967137-22121093	cyclin-dependent kinase inhibitor 2B	1.578	2.791
CDKN2C	chr1:51434366-51440309	cyclin-dependent kinase inhibitor 2C	0.388	0.278
CDKN2D	chr19:10677137-10679655	cyclin-dependent kinase inhibitor 2D	1.523	2.832
CDNF	chr10:14860272-14880017	cerebral dopamine neurotrophic factor	0.666	0.364
CDR2L	chr17:72983726-73001892	cerebellar degeneration related protein 2 like	3.427	5.65
CDRT4	chr17:15339235-15466945	CMT1A duplicated region transcript 4	1.616	2.141
CDYL	chr6:4706392-4955778	chromodomain protein, Y-like	2.118	3.341
CEACAM1	chr19:42901299-43156507	carcinoembryonic antigen related cell adhesion molecule 1	0.528	0.075
CEBPG	chr19:33864574-33873592	CCAAT/enhancer binding protein gamma	2.437	3.085
CENPF	chr1:214776531-214837914	centromere protein F	0.288	0.293
CENPI	chrX:100353200-100418635	centromere protein I	0.658	0.165
CENPO	chr2:25013135-25142693	centromere protein O	0.864	0.356
CEP164	chr11:117192312-117283982	centrosomal protein 164	1.628	2.135
CEP170B	chr14:105331640-105363108	centrosomal protein 170B	1.784	2.92
CEP19	chr3:196433147-196559518	centrosomal protein 19	1.757	2.048
CERS5	chr12:50523383-50561158	ceramide synthase 5	1.535	2.189
CES2	chr16:66968346-66978994	carboxylesterase 2	0.519	0.309
CES5A	chr16:55880065-55989943	carboxylesterase 5A	0.582	0.082
CETN4P	chr4:123621577-123670522	centrin 4, pseudogene	3.619	5.905
CFB	chr6:31913720-31919861	complement factor B	0.746	0.471
CFHR2	chr1:196912933-196928356	complement factor H related 2	0.13	0.027
CFHR5	chr1:196946666-196978803	complement factor H related 5	0.565	0.121
CFI	chr4:110661847-110723335	complement factor I	0.548	0.162
CGB7	chr19:49557530-49562927	chorionic gonadotropin beta subunit 7	2.81	3.639
CGNL1	chr15:57668702-57844419	cingulin-like 1	0.575	0.483
CGREF1	chr2:27309610-27341995	cell growth regulator with EF-hand domain 1	0.303	0.121
CHAC1	chr15:41245545-41254871	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	17.53	35.5
CHCHD1	chr10:75541807-75543406	coiled-coil-helix-coiled-coil-helix domain containing 1	0.59	0.429
CHD3	chr17:7759620-7816075	chromodomain helicase DNA binding protein 3	0.465	0.299
CHN2	chr7:29234120-29553944	chimerin 2	0.374	0.158
CHPF	chr2:220403635-220408487	chondroitin polymerizing factor	1.782	3.382
CHRD	chr3:184097773-184107617	chordin	0.508	0.178
CHRDL2	chr11:74407473-74442186	chordin-like 2	0.822	0.254
CHRNA5	chr15:78857861-78913637	cholinergic receptor nicotinic alpha 5 subunit	3.009	3.867
CHRNA7	chr15:32322685-32463562	cholinergic receptor nicotinic alpha 7 subunit	2.582	3.077
CHST1	chr11:45669238-45687593	carbohydrate sulfotransferase 1	1.763	3.036
CHST11	chr12:104849340-105155792	carbohydrate (chondroitin 4) sulfotransferase 11	2.753	6.68
CHST13	chr3:126242946-126262134	carbohydrate (chondroitin 4) sulfotransferase 13	0.402	0.106
CHST3	chr10:73724119-73773322	carbohydrate (chondroitin 6) sulfotransferase 3	2.753	6.473
CHST4	chr16:71481500-71645739	carbohydrate sulfotransferase 4	0.382	0.062
CHST8	chr19:34112860-34264414	carbohydrate sulfotransferase 8	3.956	10.42
CHSY1	chr15:101715927-101792181	chondroitin sulfate synthase 1	1.959	2.437

CHSY3	chr5:129240233-129522351	chondroitin sulfate synthase 3	1.248	2.372
CIDEB	chr14:24759803-24787242	cell death-inducing DFFA-like effector b	0.523	0.453
CIDEC	chr3:9906149-10149915	cell death inducing DFFA like effector c	0.235	0.035
CIDECP	chr3:9906149-10149915	cell death-inducing DFFA-like effector c pseudogene	1.541	2.522
CIRBP	chr19:1267469-1279246	cold inducible RNA binding protein	1.62	2.097
CISD3	chr17:36861831-36906081	CDGSH iron sulfur domain 3	0.652	0.47
CIT	chr12:120123594-120315116	citron rho-interacting serine/threonine kinase	0.467	0.243
CIZ1	chr9:130928343-131017527	CDKN1A interacting zinc finger protein 1	1.318	2.014
CKAP2L	chr2:113493941-113522254	cytoskeleton associated protein 2 like	0.668	0.26
CLDN1	chr3:190023489-190040235	claudin 1	1.791	2.07
CLDN14	chr21:37832919-37948867	claudin 14	0.026	0.05
CLDN16	chr3:190040351-190129978	claudin 16	0.452	0.261
CLDN3	chr7:73183326-73184600	claudin 3	0.442	0.135
CLDN7	chr17:7146905-7166512	claudin 7	0.471	0.2
CLDN9	chr16:3054821-3064506	claudin 9	2.273	3.018
CLDND2	chr19:51870291-51872377	claudin domain containing 2	0.544	0.36
CLEC2B	chr12:10004967-10022458	C-type lectin domain family 2 member B	0.338	0.158
CLGN	chr4:141309606-141348815	calmegin	2.601	2.605
CLIC4	chr1:25071759-25170815	chloride intracellular channel 4	1.859	3.217
CLIP1	chr12:122755979-122907497	CAP-Gly domain containing linker protein 1	1.572	2.1
CLIP2	chr7:73703800-73820273	CAP-Gly domain containing linker protein 2	1.723	2.466
CLMN	chr14:95648275-95786245	calmin (calponin-like, transmembrane)	0.504	0.273
CLPX	chr15:65440555-65477675	caseinolytic mitochondrial matrix peptidase chaperone subunit	0.595	0.415
CLRN3	chr10:129676113-129691211	clarin 3	0.085	0.004
CLSTN3	chr12:7247145-7311530	calsyntenin 3	0.404	0.2
CLUH	chr17:2592679-2616754	clustered mitochondria (cluA/CLU1) homolog	0.567	0.401
CMBL	chr5:10250281-10308168	carboxymethylenebutenolidase homolog (Pseudomonas)	0.526	0.255
CMIP	chr16:81478774-81745367	c-Maf inducing protein	2.079	3.244
CMPK1	chr1:47799468-47844511	cytidine/uridine monophosphate kinase 1	0.592	0.386
CNGA1	chr4:47937993-48018684	cyclic nucleotide gated channel alpha 1	0.414	0.314
CNIH4	chr1:224544532-224567119	cornichon family AMPA receptor auxiliary protein 4	1.615	2.407
CNNM4	chr2:97426638-97477628	cyclin and CBS domain divalent metal cation transport mediator 4	2.951	5.294
CNTLN	chr9:17048973-17503917	centlein	0.687	0.297
CNTNAP2	chr7:145813452-148118088	contactin associated protein-like 2	1.866	2.473
CNTNAP4	chr16:76267777-76669564	contactin associated protein like 4	0.459	0.283
COA3	chr17:40949635-40950743	cytochrome c oxidase assembly factor 3	0.515	0.319
COA4	chr11:73583712-73681332	cytochrome c oxidase assembly factor 4 homolog	0.662	0.457
COBL	chr7:51083908-51384540	cordon-bleu WH2 repeat protein	0.751	0.353
COG4	chr16:70514414-70557458	component of oligomeric golgi complex 4	0.668	0.481
COG7	chr16:23399813-23464585	component of oligomeric golgi complex 7	0.645	0.459
COL12A1	chr6:75794041-75915970	collagen type XII alpha 1	2.252	3.763
COL18A1	chr21:46825096-46962385	collagen type XVIII alpha 1	0.488	0.208
COL21A1	chr6:55921387-56112378	collagen type XXI alpha 1	0.617	0.484
COL28A1	chr7:7310420-7575460	collagen type XXVIII alpha 1	0.291	0.285
COL4A1	chr13:110801309-110959519	collagen type IV alpha 1	1.611	3.592
COL4A2	chr13:110959630-111165438	collagen type IV alpha 2	1.636	3.351
COL4A5	chrX:107682995-107940775	collagen type IV alpha 5	0.554	0.355
COL5A1	chr9:137533563-137736688	collagen type V alpha 1	1.619	2.731
COLQ	chr3:15491639-15643180	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcho	0.379	0.208
COPA	chr1:160246598-160328742	coatomer protein complex subunit alpha	0.311	0.326
COQ5	chr12:120941059-120966964	coenzyme Q5, methyltransferase	0.584	0.341
COQ6	chr14:74399694-74551196	coenzyme Q6, monooxygenase	0.555	0.417
CORIN	chr4:47596017-47840059	corin, serine peptidase	2.187	8.786
CORO1C	chr12:109038884-109125326	coronin 1C	1.831	2.038
COX14	chr12:50478852-50514240	COX14 cytochrome c oxidase assembly factor	0.43	0.451
COX6A2	chr16:31439051-31439749	cytochrome c oxidase subunit 6A2	0.394	0.262
COX6B1	chr19:36139124-36149686	cytochrome c oxidase subunit 6B1	0.522	0.361
COX7A2	chr6:75947390-75953644	cytochrome c oxidase subunit 7A2	0.526	0.424
COX7C	chr5:85913704-85916749	cytochrome c oxidase subunit 7C	0.622	0.459
CP	chr3:148847370-148939843	ceruloplasmin (ferroxidase)	0.346	0.176
CPA4	chr7:129932973-129964020	carboxypeptidase A4	10.63	28.01
CPA6	chr8:68334404-68658621	carboxypeptidase A6	0.292	0.348
CPB2	chr13:46626982-46679211	carboxypeptidase B2	0.39	0.061
CPEB2	chr4:15004014-15071777	cytoplasmic polyadenylation element binding protein 2	1.719	2.941
CPED1	chr7:120628750-120937730	cadherin like and PC-esterase domain containing 1	0.352	0.237
CPM	chr12:69201970-69357020	carboxypeptidase M	0.955	0.414
CPN2	chr3:194060493-194072111	carboxypeptidase N subunit 2	0.281	0.114
CPNE4	chr3:131253576-131753844	copine 4	2.082	5.392
CPT2	chr1:53656295-53686289	carnitine palmitoyltransferase 2	0.602	0.395
CRADD	chr12:94071150-94244531	CASP2 and RIPK1 domain containing adaptor with death domain	0.597	0.248
CRB3	chr19:6464259-6481798	crumbs 3, cell polarity complex component	0.524	0.104
CREB3L3	chr19:4153597-4173051	cAMP responsive element binding protein 3-like 3	0.075	0.014
CREB5	chr7:28338939-28865513	cAMP responsive element binding protein 5	5.663	5.798
CREM	chr10:35415768-35501886	cAMP responsive element modulator	1.853	2.304
CRHR1	chr17:43697709-43913194	corticotropin releasing hormone receptor 1	0.57	0.341
CRIP3	chr6:43265713-43276530	cysteine rich protein 3	0.356	0.266
CRISPLD1	chr8:75860887-75946793	cysteine rich secretory protein LCCL domain containing 1	0.698	0.357
CRMP1	chr4:5712891-5894785	collapsin response mediator protein 1	1.445	2.394
CRP	chr1:159682077-159726405	C-reactive protein, pentraxin-related	0.221	0.071
CRY1	chr12:107385141-107487635	cryptochrome circadian clock 1	1.678	2.203
CRYAB	chr11:111779349-111782473	crystallin alpha B	0.521	0.189
CRYBB2	chr22:25615611-25627836	crystallin beta B2	0.845	2.301
CRYL1	chr13:20977804-21100012	crystallin lambda 1	0.684	0.476
CRYM	chr16:21269838-21329912	crystallin mu	0.963	0.229
CRYZ	chr1:75171073-75232360	crystallin zeta	0.414	0.141
CSF1	chr1:110453232-110473616	colony stimulating factor 1	2.175	3.677
CSGALNACT2	chr10:43633892-43680756	chondroitin sulfate N-acetylgalactosaminyltransferase 2	2.034	3.063
CSMD3	chr8:113235158-114449376	CUB and Sushi multiple domains 3	0.463	0.275
CSPG4	chr15:75931425-76008618	chondroitin sulfate proteoglycan 4	0.531	0.391
CSPG5	chr3:47603727-47621730	chondroitin sulfate proteoglycan 5	3.95	6.3
CSRNP1	chr3:39183341-39195102	cysteine and serine rich nuclear protein 1	1.751	2.81
CSRNP2	chr12:51454987-51477454	cysteine and serine rich nuclear protein 2	2.031	3.137
CSRNP3	chr2:166326156-166545917	cysteine and serine rich nuclear protein 3	0.576	0.453
CSRP1	chr1:201452657-201476387	cysteine and glycine rich protein 1	1.643	2.437
CST7	chr20:24922507-24942898	cystatin F	0.071	0.044
CTH	chr1:70876854-70911330	cystathionine gamma-lyase	1.462	2.21
CTPS2	chrX:16606121-16731059	CTP synthase 2	0.628	0.291
CTSO	chr4:156845269-156875048	cathepsin O	0.506	0.34
CTSS	chr1:150702671-150738433	cathepsin S	0.508	0.096
CTXN1	chr19:7989380-7991051	cortexin 1	5.833	8.958
CUEDC2	chr10:104183001-104196246	CUE domain containing 2	0.674	0.439
CUL2	chr10:35297465-35389841	cullin 2	0.678	0.441
CUTC	chr10:101419262-101515894	cutC copper transporter	0.869	0.449

CUX2	chr12:111471827-111788479	cut like homeobox 2	0.575	0.249
CX3CL1	chr16:57406413-57418962	C-X3-C motif chemokine ligand 1	3.603	2.286
CXADR	chr21:18885223-18965897	coxsackie virus and adenovirus receptor	0.788	0.495
CXCL1	chr4:74735108-74737019	C-X-C motif chemokine ligand 1	0.359	0.043
CXCL10	chr4:76932332-77033955	C-X-C motif chemokine ligand 10	0.315	0.038
CXCL13	chr4:78432906-78532988	C-X-C motif chemokine ligand 13	0.096	0.118
CXCL2	chr4:74962750-74964999	C-X-C motif chemokine ligand 2	0.274	0.052
CXCL3	chr4:74902305-74904512	C-X-C motif chemokine ligand 3	0.566	0.297
CXorf48	chrX:134290460-134305751	cancer/testis antigen 55	0.659	0.246
CYB5A	chr18:71920526-71959251	cytochrome b5 type A	0.289	0.1
CYB5RL	chr1:54635323-54665746	cytochrome b5 reductase like	0.568	0.382
CYBA	chr16:88709443-88729558	cytochrome b-245 alpha chain	0.381	0.321
CYGB	chr17:74523429-74553748	cytoglobin	0.21	0.184
CYLD	chr16:50775816-50835846	CYLD lysine 63 deubiquitinase	1.483	2.262
CYP1A1	chr15:75011882-75017979	cytochrome P450 family 1 subfamily A member 1	0.318	0.086
CYP1B1	chr2:38294745-38303323	cytochrome P450 family 1 subfamily B member 1	1.717	2.828
CYP21A1P	chr6:31971726-31981050	cytochrome P450 family 21 subfamily A member 1, pseudogene	0.15	0.048
CYP21A2	chr6:32006092-32077151	cytochrome P450 family 21 subfamily A member 2	0.151	0.042
CYP2A6	chr19:41344771-41357163	cytochrome P450 family 2 subfamily A member 6	0.245	0.101
CYP2B6	chr19:41430169-41524301	cytochrome P450 family 2 subfamily B member 6	0.167	0.057
CYP2B7P1	chr19:41430169-41524301	cytochrome P450 family 2 subfamily B member 7, pseudogene	0.167	0.057
CYP2C18	chr10:96442636-96495947	cytochrome P450 family 2 subfamily C member 18	0.238	0.041
CYP2C19	chr10:96522462-96612671	cytochrome P450 family 2 subfamily C member 19	0.253	0.049
CYP2C8	chr10:96796528-96829254	cytochrome P450 family 2 subfamily C member 8	0.215	0.07
CYP2C9	chr10:96698384-96749148	cytochrome P450 family 2 subfamily C member 9	0.178	0.052
CYP2E1	chr10:135238569-135392077	cytochrome P450 family 2 subfamily E member 1	0.267	0.094
CYP2J2	chr1:60358931-60394390	cytochrome P450 family 2 subfamily J member 2	0.607	0.313
CYP39A1	chr6:46517444-46646658	cytochrome P450 family 39 subfamily A member 1	0.458	0.202
CYP3A4	chr7:99354582-99381904	cytochrome P450 family 3 subfamily A member 4	0.207	0.044
CYP3A5	chr7:99211435-99277643	cytochrome P450 family 3 subfamily A member 5	0.377	0.138
CYP3A7	chr7:99282301-99332819	cytochrome P450 family 3 subfamily A member 7	0.129	0.013
CYP4B1	chr1:47264669-47285021	cytochrome P450 family 4 subfamily B member 1	0.226	0.105
CYP4F22	chr19:15599615-15663254	cytochrome P450 family 4 subfamily F member 22	0.286	0.146
CYP4X1	chr1:47489239-47516423	cytochrome P450 family 4 subfamily X member 1	0.098	0.019
CYP51A1	chr7:91741462-91764059	cytochrome P450 family 51 subfamily A member 1	0.525	0.393
CYP7B1	chr8:65500285-65711444	cytochrome P450 family 7 subfamily B member 1	0.834	0.494
CYP8B1	chr3:42913683-42917633	cytochrome P450 family 8 subfamily B member 1	0.09	0.005
CYR61	chr1:86046443-86049648	cysteine rich angiogenic inducer 61	2.754	2.702
CYTH2	chr19:48972392-48985608	cytohesin 2	1.672	2.749
CYTH3	chr7:6201405-6312242	cytohesin 3	2.571	5.589
CYYR1	chr21:27778278-27945581	cysteine and tyrosine rich 1	3.034	5.226
DAAM2	chr6:39760158-39902290	dishevelled associated activator of morphogenesis 2	0.329	0.219
DAB1	chr1:57462084-58716211	DAB1, reelin adaptor protein	0.388	0.131
DACH2	chrX:85403454-86087605	dachshund family transcription factor 2	1.395	3.229
DACT1	chr14:59100785-59115038	dishevelled-binding antagonist of beta-catenin 1	2.288	4.098
DACT3	chr19:47150868-47220384	dishevelled-binding antagonist of beta-catenin 3	2.811	5.658
DAGLB	chr7:6448208-6488045	diacylglycerol lipase beta	1.862	2.074
DAO	chr12:109270653-109294797	D-amino-acid oxidase	0.189	0.011
DARS	chr2:136664253-136765351	aspartyl-tRNA synthetase	0.558	0.336
DARS2	chr1:173768687-173828196	aspartyl-tRNA synthetase 2, mitochondrial	0.626	0.468
DBH	chr9:136501484-136525168	dopamine beta-hydroxylase	0.061	0.029
DBI	chr2:120124503-120130122	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protei	0.532	0.341
DBN1	chr5:176883613-176924602	drebrin 1	3.192	6.473
DBT	chr1:100598626-100715613	dihydrolipoamide branched chain transacylase E2	0.465	0.351
DCAF11	chr14:24583277-24594451	DDB1 and CUL4 associated factor 11	0.453	0.309
DCAF6	chr1:167885912-168045083	DDB1 and CUL4 associated factor 6	0.616	0.386
DCBLD1	chr6:117803652-117923705	discoidin, CUB and LCCL domain containing 1	2.103	4.514
DCBLD2	chr3:98433176-98620543	discoidin, CUB and LCCL domain containing 2	1.617	2.234
DCLK1	chr13:35516377-36705967	doublecortin like kinase 1	6.652	10.59
DCT	chr13:95090241-95157244	dopachrome tautomerase	2.821	4.069
DCUN1D3	chr16:20866186-20936330	defective in cullin neddylation 1 domain containing 3	1.65	2.377
DDC	chr7:50526128-50633154	dopa decarboxylase	0.18	0.019
DDIT3	chr12:57881735-57914300	DNA damage inducible transcript 3	4.953	9.093
DDIT4	chr10:74033676-74035797	DNA damage inducible transcript 4	2.964	4.35
DDO	chr6:110712754-110736753	D-aspartate oxidase	0.532	0.191
DDT	chr22:24309025-24322019	D-dopachrome tautomerase	0.546	0.408
DDTL	chr22:24309025-24322019	D-dopachrome tautomerase-like	0.391	0.362
DECR1	chr8:91013579-91064227	2,4-dienoyl-CoA reductase 1, mitochondrial	0.408	0.128
DENND1C	chr19:6464259-6481798	DENN domain containing 1C	0.601	0.107
DEPDC1	chr1:68939834-68962799	DEP domain containing 1	0.581	0.376
DEPDC7	chr11:33037409-33055128	DEP domain containing 7	0.426	0.265
DERA	chr12:16064185-16190315	deoxyribose-phosphate aldolase	0.629	0.416
DESI2	chr1:244816351-244872339	desumoylating isopeptidase 2	1.696	2.533
DFFB	chr1:3773844-3802277	DNA fragmentation factor subunit beta	0.367	0.186
DGAT2	chr11:75479777-75512581	diacylglycerol O-acyltransferase 2	0.424	0.351
DGCR5	chr22:18957996-18982142	DiGeorge syndrome critical region gene 5 (non-protein coding)	4.64	8.66
DGKH	chr13:42614171-42817141	diacylglycerol kinase eta	1.526	2.269
DGKZ	chr11:46354454-46402104	diacylglycerol kinase zeta	1.714	2.633
DHCR24	chr1:55315299-55352921	24-dehydrocholesterol reductase	0.488	0.184
DHCR7	chr11:71145456-71159477	7-dehydrocholesterol reductase	0.498	0.354
DHDH	chr19:49436938-49448226	dihydrodiol dehydrogenase	1.547	3.306
DHODH	chr16:72042582-72060891	dihydroorotate dehydrogenase (quinone)	0.496	0.396
DHRS1	chr14:24759803-24787242	dehydrogenase/reductase (SDR family) member 1	0.486	0.337
DHRS2	chr14:24105572-24114848	dehydrogenase/reductase (SDR family) member 2	0.256	0.198
DHRS3	chr1:12627938-12682999	dehydrogenase/reductase (SDR family) member 3	0.554	0.382
DHTKD1	chr10:12110933-12165348	dehydrogenase E1 and transketolase domain containing 1	0.476	0.347
DHX34	chr19:47852531-47886062	DEAH-box helicase 34	1.726	2.69
DHX58	chr17:40253421-40264861	DEXH-box helicase 58	0.648	0.431
DIAPH2	chrX:95939661-96860069	diaphanous related formin 2	0.525	0.372
DIAPH3	chr13:60239720-60738119	diaphanous related formin 3	0.995	0.4
DIO1	chr1:54359860-54376759	deiodinase, iodothyronine type I	0.291	0.076
DIRAS3	chr1:68167148-68698405	DIRAS family GTP binding RAS like 3	0.778	0.317
DKK1	chr10:54074040-54077493	dickkopf WNT signaling pathway inhibitor 1	0.363	0.337
DKK2	chr4:107842958-107957453	dickkopf WNT signaling pathway inhibitor 2	3.047	8.697
DLD	chr7:107531573-107643804	dihydrolipoamide dehydrogenase	0.561	0.328
DLGAP4	chr20:34995443-35157040	discs large homolog associated protein 4	2.922	5.938
DLGAP5	chr14:55613239-55658396	discs large homolog associated protein 5	0.261	0.165
DMGDH	chr5:78292796-78531831	dimethylglycine dehydrogenase	0.497	0.148
DNAAF3	chr19:55669678-55678090	dynein (axonemal) assembly factor 3	2.137	4.468
DNAJB1	chr19:14625578-14629201	DnaJ heat shock protein family (Hsp40) member B1	1.837	2.269
DNAJB2	chr2:220144039-220151622	DnaJ heat shock protein family (Hsp40) member B2	1.536	2.098
DNAJB9	chr7:108210188-108215294	DnaJ heat shock protein family (Hsp40) member B9	1.279	2.348
DNAJC1	chr10:22044718-22292671	DnaJ heat shock protein family (Hsp40) member C1	2.066	3.076

DNAJC17	chr15:41060066-41106768	DnaJ heat shock protein family (Hsp40) member C17	0.518	0.229
DNAJC22	chr12:49740987-49751545	DnaJ heat shock protein family (Hsp40) member C22	0.589	0.254
DNAJC28	chr21:34860015-34864129	DnaJ heat shock protein family (Hsp40) member C28	0.722	0.34
DNAJC6	chr1:65713909-65881552	DnaJ heat shock protein family (Hsp40) member C6	3.55	6.997
DNAJC7	chr17:40118704-40190044	DnaJ heat shock protein family (Hsp40) member C7	0.744	0.473
DNALI1	chr1:38022519-38061586	dynein axonemal light intermediate chain 1	0.684	0.438
DNER	chr2:230222344-230579286	delta/notch like EGF repeat containing	0.412	0.328
DNM1P41	chr15:85045805-85123412	dynamin 1 pseudogene 41	1.69	2.207
DNMT3L	chr21:45663024-45682099	DNA (cytosine-5-)-methyltransferase 3-like	1.35	3.527
DNPH1	chr6:43193366-43197211	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	0.507	0.272
DOCK11	chrX:117629840-117820123	dedicator of cytokinesis 11	2.863	2.904
DOCK5	chr8:25042214-25273233	dedicator of cytokinesis 5	1.733	2.766
DOLPP1	chr9:131843382-131852717	dolichyldiphosphatase 1	0.705	0.426
DOPEY2	chr21:37529005-37666769	dopey family member 2	2.261	3.581
DPP4	chr2:162848719-162931052	dipeptidyl peptidase 4	0.669	0.3
DPYD	chr1:97487823-98386615	dihydropyrimidine dehydrogenase	0.477	0.269
DPYS	chr8:105391651-105482804	dihydropyrimidinase	0.229	0.067
DPYSL3	chr5:146770370-146889619	dihydropyrimidinase like 3	2.144	3.018
DRAP1	chr11:65686727-65689048	DR1 associated protein 1	2.02	3.109
DSE	chr6:116580059-116759546	dermatan sulfate epimerase	1.693	2.298
DTNB	chr2:25599889-25896516	dystrobrevin beta	1.71	2.191
DTX4	chr11:58939659-58980494	deltex 4, E3 ubiquitin ligase	0.61	0.418
DUSP10	chr1:221874763-221915832	dual specificity phosphatase 10	2.407	3.752
DUSP12	chr1:161718341-161726952	dual specificity phosphatase 12	1.464	2.049
DUSP18	chr22:31049846-31063906	dual specificity phosphatase 18	1.709	2.375
DUSP4	chr8:29190578-29208267	dual specificity phosphatase 4	2.117	5.773
DUSP5	chr10:112257624-112271302	dual specificity phosphatase 5	14.32	24.98
DUSP6	chr12:89741836-89746296	dual specificity phosphatase 6	4.797	9.828
DUSP7	chr3:52082936-52090461	dual specificity phosphatase 7	1.836	2.789
DUSP8	chr11:1489691-1785501	dual specificity phosphatase 8	3.764	4.114
DUSP9	chrX:152890864-152916781	dual specificity phosphatase 9	0.109	0.038
DVL3	chr3:183873141-183891391	dishevelled segment polarity protein 3	1.478	2.549
DYNC2LI1	chr2:44001177-44037539	dynein cytoplasmic 2 light intermediate chain 1	0.695	0.472
E2F7	chr12:77415025-77459893	E2F transcription factor 7	2.102	2.373
E2F8	chr11:19245609-19263202	E2F transcription factor 8	0.778	0.044
EBP	chrX:48380129-48387105	emopamil binding protein (sterol isomerase)	0.47	0.212
EBPL	chr13:50234809-50265754	emopamil binding protein like	0.5	0.285
ECE1	chr1:21543739-21672034	endothelin converting enzyme 1	1.379	2.09
ECH1	chr19:39306061-39322497	enoyl-CoA hydratase 1, peroxisomal	0.612	0.463
ECHDC2	chr1:53361581-53387446	enoyl-CoA hydratase domain containing 2	0.394	0.177
ECHDC3	chr10:11784355-11806065	enoyl-CoA hydratase domain containing 3	0.577	0.316
ECHS1	chr10:135175986-135186908	enoyl-CoA hydratase, short chain, 1, mitochondrial	0.602	0.362
ECI2	chr6:4068592-4135831	enoyl-CoA delta isomerase 2	0.466	0.3
ECM2	chr9:95059196-95432547	extracellular matrix protein 2	0.219	0.033
ECT2	chr3:172468347-172546450	epithelial cell transforming 2	0.735	0.406
EDA	chrX:68835910-69259321	ectodysplasin A	1.53	2.414
EDN2	chr1:41944445-41950344	endothelin 2	0.071	0.018
EDNRA	chr4:148279018-148466106	endothelin receptor type A	1.585	2.282
EDNRB	chr13:78469615-78549674	endothelin receptor type B	0.482	0.408
EFCAB11	chr14:90263468-90421089	EF-hand calcium binding domain 11	0.696	0.296
EFNA1	chr1:155100348-155107386	ephrin A1	0.291	0.171
EGFL8	chr6:32120578-32145888	EGF like domain multiple 8	0.632	0.244
EGFR	chr7:55086362-55279462	epidermal growth factor receptor	2.332	3.645
EGR1	chr5:137801180-137805004	early growth response 1	4.951	8.461
EGR2	chr10:64571755-64578927	early growth response 2	3.392	3.304
EHBP1	chr2:62900985-63275656	EH domain binding protein 1	0.485	0.37
EHBP1L1	chr11:65333590-65360117	EH domain binding protein 1 like 1	1.588	2.094
EHD4	chr15:42188093-42264858	EH domain containing 4	2.095	2.474
EHHADH	chr3:184880688-184971886	enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	0.263	0.065
EHMT2	chr6:31847536-31865466	euchromatic histone-lysine N-methyltransferase 2	0.624	0.399
EIF1	chr17:39845126-39847898	eukaryotic translation initiation factor 1	1.803	3.028
EIF2S2	chr20:32581299-32700091	eukaryotic translation initiation factor 2 subunit beta	1.89	2.392
EIF4A3	chr17:78109012-78120982	eukaryotic translation initiation factor 4A3	1.71	2.117
EIF4B	chr12:53400061-53435993	eukaryotic translation initiation factor 4B	0.671	0.483
EIF4EBP1	chr8:37887848-37917883	eukaryotic translation initiation factor 4E binding protein 1	2.541	3.894
EIF4EBP2	chr10:72163860-72188374	eukaryotic translation initiation factor 4E binding protein 2	1.4	2.411
ELMO1	chr7:36892510-37488895	engulfment and cell motility 1	0.3	0.108
ELMSAN1	chr14:74181786-74256662	ELM2 and Myb/SANT domain containing 1	2.013	3.457
ELOVL7	chr5:60047571-60140176	ELOVL fatty acid elongase 7	1.606	2.21
EMB	chr5:49678949-49779711	embigin	0.179	0.108
EMILIN3	chr20:39969412-39995498	elastin microfibril interfacer 3	0.279	0.192
EML1	chr14:100259738-100408395	echinoderm microtubule associated protein like 1	2.562	3.327
EML5	chr14:89029252-89259225	echinoderm microtubule associated protein like 5	1.664	3.439
EML6	chr2:54951688-55199156	echinoderm microtubule associated protein like 6	1.936	2.681
EMP2	chr16:10622278-10674539	epithelial membrane protein 2	0.382	0.183
EMX1	chr2:73143230-73163973	empty spiracles homeobox 1	0.471	0.328
ENC1	chr5:73923230-73937249	ectodermal-neural cortex 1	1.936	2.31
ENDOD1	chr11:94822973-94865815	endonuclease domain containing 1	1.985	2.254
ENKUR	chr10:25137553-25351640	enkurin, TRPC channel interacting protein	0.277	0.136
ENOSF1	chr18:596997-712662	enolase superfamily member 1	0.585	0.417
ENOX1	chr13:43787665-44361116	ecto-NOX disulfide-thiol exchanger 1	2.465	3.435
ENPEP	chr4:111397193-111484493	glutamyl aminopeptidase	0.482	0.111
EPB41	chr1:29213586-29450421	erythrocyte membrane protein band 4.1	0.749	0.461
EPB41L4B	chr9:111934253-112083021	erythrocyte membrane protein band 4.1 like 4B	0.736	0.468
EPB49	chr8:21906452-21940036	dematin actin binding protein	0.648	0.422
EPHA2	chr1:16450831-16513739	EPH receptor A2	3.114	2.598
EPHA5	chr4:66185280-66559104	EPH receptor A5	1.928	3.729
EPHB2	chr1:23037330-23241874	EPH receptor B2	3.982	9.123
EPHX2	chr8:27348518-27472328	epoxide hydrolase 2	0.427	0.193
EPS8L2	chr11:706119-727727	EPS8 like 2	0.437	0.16
EPS8L3	chr1:110292701-110306644	EPS8 like 3	0.436	0.086
ERAP2	chr5:96208994-96385073	endoplasmic reticulum aminopeptidase 2	0.392	0.267
ERC2	chr3:55542335-56502436	ELKS/RAB6-interacting/CAST family member 2	1.299	2.48
EREG	chr4:75230859-75254477	epiregulin	4.385	7.46
ERI2	chr16:20775311-20860990	ERI1 exoribonuclease family member 2	0.705	0.371
ERN1	chr17:62116519-62207510	endoplasmic reticulum to nucleus signaling 1	2.144	4.274
ERP27	chr12:15066975-15091463	endoplasmic reticulum protein 27	0.631	0.142
ERVMER34-1	chr4:53608564-53617807	endogenous retrovirus group MER34 member 1	2.672	4.514
ESCO2	chr8:27590832-27662424	establishment of sister chromatid cohesion N-acetyltransferase 2	0.624	0.057
ESD	chr13:47345390-47371819	esterase D	0.51	0.308
ESPL1	chr12:53662082-53687427	extra spindle pole bodies like 1, separase	0.337	0.225
ESPN	chr1:6484847-6580121	espin	0.15	0.07
ESRP2	chr16:68119006-68271538	epithelial splicing regulatory protein 2	0.269	0.111

ESRRG	chr1:216676587-217311097	estrogen related receptor gamma	0.423	0.239
ESYT1	chr12:56521985-56538460	extended synaptotagmin protein 1	2.171	2.542
ETFA	chr15:76352298-76603810	electron transfer flavoprotein alpha subunit	0.65	0.408
ETFB	chr19:51848408-51869672	electron transfer flavoprotein beta subunit	0.625	0.243
ETNK2	chr1:204100176-204121307	ethanolamine kinase 2	0.168	0.069
ETS1	chr11:128328655-128457453	ETS proto-oncogene 1, transcription factor	1.543	2.295
ETV1	chr7:13930855-14031050	ETS variant 1	0.522	0.368
EVA1B	chr1:36771993-36795049	eva-1 homolog B (C. elegans)	1.836	2.97
EVC	chr4:5712891-5894785	EvC ciliary complex subunit 1	1.429	2.231
EVC2	chr4:5564145-5711275	EvC ciliary complex subunit 2	1.843	2.454
EVPLL	chr17:18281063-18292960	envoplakin-like	0.234	0.105
EXT1	chr8:118811347-119124104	exostosin glycosyltransferase 1	1.647	2.268
EXTL1	chr1:26335416-26363108	exostosin-like glycosyltransferase 1	0.326	0.181
EXTL3	chr8:28558989-28611207	exostosin like glycosyltransferase 3	1.327	2.102
EYA1	chr8:72109667-72448026	EYA transcriptional coactivator and phosphatase 1	0.569	0.379
EZH2	chr7:148504463-148581441	enhancer of zeste 2 polycomb repressive complex 2 subunit	2.171	2.701
F10	chr13:113777107-113805079	coagulation factor X	0.417	0.144
F11	chr4:187181417-187422212	coagulation factor XI	0.271	0.041
F12	chr5:176829133-176836708	coagulation factor XII	0.754	0.197
F13B	chr1:197007888-197036397	coagulation factor XIII B chain	0.226	0.045
F2	chr11:46740742-46761056	coagulation factor II, thrombin	0.559	0.135
F3	chr1:94994731-95007413	coagulation factor III, tissue factor	2.287	3.101
F5	chr1:169481191-169555840	coagulation factor V	0.362	0.048
F9	chrX:138612894-138647837	coagulation factor IX	0.604	0.11
FABP1	chr2:88422507-88427650	fatty acid binding protein 1	0.056	0.031
FADS1	chr11:61567096-61634825	fatty acid desaturase 1	0.835	0.425
FADS3	chr11:61640991-61659062	fatty acid desaturase 3	2.412	2.71
FAH	chr15:80445130-80489121	fumarylacetoacetate hydrolase (fumarylacetoacetase)	0.309	0.168
FAM109A	chr12:111798454-111806955	family with sequence similarity 109 member A	1.704	2.271
FAM110B	chr8:58907069-59062551	family with sequence similarity 110 member B	2.362	4.032
FAM115C	chr7:143317885-143427571	TRPM8 channel associated factor 2	0.867	0.458
FAM127B	chrX:134184962-134186221	family with sequence similarity 127 member B	1.695	2.477
FAM131A	chr3:184053655-184079439	family with sequence similarity 131 member A	1.813	2.344
FAM134A	chr2:220036618-220050197	family with sequence similarity 134 member A	1.574	2.426
FAM134B	chr5:16473146-16617167	family with sequence similarity 134 member B	0.745	0.416
FAM13A	chr4:89630939-90032516	family with sequence similarity 13 member A	0.286	0.19
FAM13B	chr5:137225124-137369557	family with sequence similarity 13 member B	1.911	2.56
FAM13C	chr10:60936347-61123601	family with sequence similarity 13 member C	0.338	0.174
FAM162A	chr3:122103022-122128961	family with sequence similarity 162 member A	0.566	0.372
FAM167A	chr8:11197145-11332199	family with sequence similarity 167 member A	2.201	5.744
FAM168B	chr2:131805447-131851004	family with sequence similarity 168 member B	1.344	2.126
FAM171A2	chr17:42430901-42441235	family with sequence similarity 171 member A2	2.784	4.589
FAM184A	chr6:119280995-119470358	family with sequence similarity 184 member A	0.842	0.369
FAM189A2	chr9:71939487-72007483	family with sequence similarity 189 member A2	2.712	3.948
FAM195A	chr16:691830-699220	MAPK regulated co-repressor interacting protein 2	0.422	0.37
FAM195B	chr17:79780292-79791167	MAPK regulated co-repressor interacting protein 1	2.866	5.016
FAM198B	chr4:159045731-159094202	family with sequence similarity 198 member B	0.318	0.169
FAM20A	chr17:66507920-66597593	family with sequence similarity 20 member A	0.354	0.116
FAM211A	chr17:16342300-16395505	leucine rich repeat containing 75A	3.06	7.955
FAM212B	chr1:112264576-112310199	family with sequence similarity 212 member B	1.948	2.524
FAM213A	chr10:82167584-82196870	family with sequence similarity 213 member A	0.678	0.307
FAM219A	chr9:34398111-34458568	family with sequence similarity 219 member A	1.951	2.668
FAM220A	chr7:6369038-6388590	family with sequence similarity 220 member A	1.535	2.116
FAM222A	chr12:110151812-110211292	family with sequence similarity 222 member A	4.68	10.48
FAM227A	chr22:38974032-39069855	family with sequence similarity 227 member A	1.684	2.507
FAM3C	chr7:120988904-121038465	family with sequence similarity 3 member C	2.043	3.179
FAM43A	chr3:194406545-194409766	family with sequence similarity 43 member A	3.521	7.5
FAM47E	chr4:77135192-77232283	family with sequence similarity 47 member E	0.466	0.346
FAM49A	chr2:16730729-16847134	family with sequence similarity 49 member A	2.483	5.858
FAM53A	chr4:1618559-1686016	family with sequence similarity 53 member A	1.751	2.256
FAM53B	chr10:126306753-126480439	family with sequence similarity 53 member B	1.427	2.445
FAM5C	chr1:190066782-190446759	BMP/retinoic acid inducible neural specific 3	0.375	0.303
FAM63A	chr1:150954498-150980854	family with sequence similarity 63 member A	0.377	0.241
FAM65B	chr6:24804512-25004893	family with sequence similarity 65 member B	0.067	0.015
FAM69B	chr9:139607023-139622636	family with sequence similarity 69 member B	2.972	6.838
FAM72D	chr1:143875655-144094409	family with sequence similarity 72 member D	1.871	2.927
FAM78B	chr1:166039255-166135958	family with sequence similarity 78 member B	0.769	0.437
FAM86B1	chr8:11973290-12293852	family with sequence similarity 86 member B1	2.24	3.907
FAM86B3P	chr8:8086091-8102387	family with sequence similarity 86, member A pseudogene	1.763	2.305
FAM86DP	chr3:75463422-75484278	family with sequence similarity 86, member D, pseudogene	1.919	3.419
FAM86JP	chr3:125635443-125656627	family with sequence similarity 86, member A pseudogene	1.755	2.595
FAM89A	chr1:231152644-231175995	family with sequence similarity 89 member A	2.126	2.907
FAM96A	chr15:64364760-64386207	family with sequence similarity 96 member A	0.441	0.278
FAM98C	chr19:38893774-38916945	family with sequence similarity 98 member C	0.606	0.421
FANCD2	chr3:9906149-10149915	Fanconi anemia complementation group D2	0.934	0.219
FANCE	chr6:35420106-35434990	Fanconi anemia complementation group E	2.383	3.439
FARP1	chr13:98794877-99102023	FERM, ARH/RhoGEF and pleckstrin domain protein 1	1.534	2.264
FARS2	chr6:5108652-5771816	phenylalanyl-tRNA synthetase 2, mitochondrial	0.633	0.492
FASN	chr17:80036213-80056106	fatty acid synthase	0.342	0.254
FASTKD2	chr2:207602290-207660911	FAST kinase domains 2	0.607	0.427
FASTKD3	chr5:7859268-7869169	FAST kinase domains 3	0.665	0.344
FBLIM1	chr1:16084795-16113447	filamin binding LIM protein 1	2.505	3.005
FBLN7	chr2:112895961-112945993	fibulin 7	0.419	0.225
FBXL7	chr5:15500304-15939903	F-box and leucine-rich repeat protein 7	2.01	3.004
FBXO2	chr1:11708417-11723384	F-box protein 2	0.712	0.484
FBXO25	chr8:356807-495781	F-box protein 25	0.679	0.392
FBXO36	chr2:230628549-230878020	F-box protein 36	0.608	0.364
FBXO42	chr1:16573245-16679003	F-box protein 42	2.152	2.981
FBXW4	chr10:103370420-103454743	F-box and WD repeat domain containing 4	1.439	2.159
FCGR1A	chr1:149754244-149783928	Fc fragment of IgG receptor Ia	4.279	7.991
FCGR1B	chr1:120926127-120935944	Fc fragment of IgG receptor Ib	4.008	7.562
FCGRT	chr19:50015535-50029685	Fc fragment of IgG receptor and transporter	0.6	0.234
FDFT1	chr8:11660189-11696848	farnesyl-diphosphate farnesyltransferase 1	0.465	0.33
FDPS	chr1:155274495-155300909	farnesyl diphosphate synthase	0.45	0.216
FEM1C	chr5:114856398-114880591	fem-1 homolog C	1.448	2.064
FETUB	chr3:186358148-186370797	fetuin B	0.254	0.074
FGA	chr4:155499904-155511897	fibrinogen alpha chain	0.234	0.038
FGB	chr4:155484128-155493915	fibrinogen beta chain	0.205	0.03
FGD4	chr12:32552474-32798984	FYVE, RhoGEF and PH domain containing 4	0.621	0.471
FGF13	chrX:137713733-138287647	fibroblast growth factor 13	2.25	2.104
FGFR1	chr8:38268222-38326352	fibroblast growth factor receptor 1	3.082	8.96
FGFR2	chr10:123237843-123357972	fibroblast growth factor receptor 2	1.696	2.72
FGG	chr4:155525285-155533918	fibrinogen gamma chain	0.253	0.051

FGGY	chr1:59762488-60228402	FGGY carbohydrate kinase domain containing	0.538	0.265
FGL1	chr8:17721899-17753047	fibrinogen like 1	0.72	0.137
FH	chr1:241660856-241683085	fumarate hydratase	0.57	0.364
FHDC1	chr4:153839553-153900848	FH2 domain containing 1	1.754	2.285
FHL1	chrX:135225773-135338641	four and a half LIM domains 1	1.854	2.205
FHL2	chr2:105977274-106055230	four and a half LIM domains 2	2.581	3.119
FICD	chr12:108908937-108915189	FIC domain containing	2.2	4.464
FIGN	chr2:164459119-164592671	fidgetin	0.605	0.298
FILIP1	chr6:76005489-76203503	filamin A interacting protein 1	0.401	0.222
FILIP1L	chr3:99273152-99897476	filamin A interacting protein 1-like	3.702	3.52
FKBP5	chr6:35541361-35704724	FK506 binding protein 5	0.684	0.471
FKBP8	chr19:18642567-18654383	FK506 binding protein 8	0.625	0.497
FKRP	chr19:47222767-47261832	fukutin related protein	1.577	2.042
FLJ46906	chr6:138725335-139018519	uncharacterized LOC441172	3.052	5.691
FLNA	chrX:153576754-153603006	filamin A	2.872	2.482
FLNB	chr3:57994117-58157982	filamin B	2.562	3.527
FLOT2	chr17:27206352-27224715	flotillin 2	0.624	0.387
FLRT2	chr14:85996487-86094270	fibronectin leucine rich transmembrane protein 2	2.094	2.825
FLT1	chr13:28874482-29069265	fms related tyrosine kinase 1	0.99	2.48
FMNL1	chr17:43299291-43324958	formin like 1	0.253	0.308
FMNL2	chr2:153191668-153617998	formin like 2	3.534	6.361
FMNL3	chr12:50017196-50101256	formin like 3	1.972	4.255
FMO3	chr1:171060010-171086959	flavin containing monooxygenase 3	0.242	0.055
FMO4	chr1:171283346-171311223	flavin containing monooxygenase 4	0.365	0.147
FMO5	chr1:146626681-146767447	flavin containing monooxygenase 5	0.154	0.014
FN3K	chr17:80693451-80709073	fructosamine 3 kinase	0.51	0.334
FNBP1	chr9:132649465-132805473	formin binding protein 1	2.013	3.188
FOLR1	chr11:71900601-71907367	folate receptor 1 (adult)	0.536	0.303
FOS	chr14:75745480-75748937	FBJ murine osteosarcoma viral oncogene homolog	4.838	5.944
FOSL1	chr11:65657289-65667997	FOS like antigen 1	11.84	18.99
FOXA2	chr20:22541179-22566101	forkhead box A2	0.509	0.316
FOXF1	chr16:86544132-86548070	forkhead box F1	2.46	3.329
FOXK2	chr17:80477593-80562663	forkhead box K2	1.818	3.048
FOXO3B	chr17:18561741-18585572	forkhead box O3B pseudogene	1.444	2.268
FOXP4	chr6:41514128-41570122	forkhead box P4	1.801	3.612
FOXQ1	chr6:1312674-1314993	forkhead box Q1	3.224	2.012
FOXRED1	chr11:126138934-126148027	FAD-dependent oxidoreductase domain containing 1	0.592	0.391
FPR1	chr19:52249022-52255150	formyl peptide receptor 1	0.201	0.217
FRAT1	chr10:99078984-99081672	frequently rearranged in advanced T-cell lymphomas 1	0.469	0.21
FRAT2	chr10:99092253-99094458	frequently rearranged in advanced T-cell lymphomas 2	0.511	0.314
FRK	chr6:116252829-116567088	fyn related Src family tyrosine kinase	0.295	0.091
FRMD5	chr15:44163008-44487478	FERM domain containing 5	2.957	7.633
FRMD6	chr14:51921229-52197444	FERM domain containing 6	2.465	3.713
FSIP2	chr2:186289622-186698126	fibrous sheath interacting protein 2	0.73	0.371
FSTL1	chr3:120113060-120169918	follistatin like 1	0.534	0.24
FSTL3	chr19:676388-685215	follistatin like 3	2.189	4.069
FSTL5	chr4:162304913-163124576	follistatin like 5	0.775	0.471
FUK	chr16:70488370-70514177	fucokinase	0.696	0.409
FUOM	chr10:135156169-135171539	fucose mutarotase	0.463	0.351
FXYD5	chr19:35645624-35660788	FXYD domain containing ion transport regulator 5	2.229	3.742
FYN	chr6:111981534-112194655	FYN proto-oncogene, Src family tyrosine kinase	0.107	0.001
FZD1	chr7:90893782-90898132	frizzled class receptor 1	1.39	2.227
FZD4	chr11:86534447-86711989	frizzled class receptor 4	0.54	0.356
FZD7	chr2:202899223-202904324	frizzled class receptor 7	2.536	5.35
G0S2	chr1:209848669-209849735	G0/G1 switch 2	0.471	0.403
G6PC	chr17:41052813-41066450	glucose-6-phosphatase catalytic subunit	0.109	0.034
GAB3	chrX:153903526-153979348	GRB2 associated binding protein 3	1.426	2.218
GABRA3	chrX:151334677-151654766	gamma-aminobutyric acid type A receptor alpha3 subunit	1.331	2.277
GADD45A	chr1:68150859-68154021	growth arrest and DNA damage inducible alpha	1.938	3.126
GALNT10	chr5:153569697-153825382	polypeptide N-acetylgalactosaminyltransferase 10	1.78	3.288
GALNT15	chr3:16216047-16273367	polypeptide N-acetylgalactosaminyltransferase 15	0.124	0.05
GALNT18	chr11:11292420-11643570	polypeptide N-acetylgalactosaminyltransferase 18	2.162	2.913
GALNT5	chr2:158114073-158169951	polypeptide N-acetylgalactosaminyltransferase 5	0.206	0.075
GALT	chr9:34646480-34662689	galactose-1-phosphate uridylyltransferase	0.585	0.417
GAMT	chr19:1383877-1401757	guanidinoacetate N-methyltransferase	0.465	0.135
GAREM	chr18:29843483-30050447	GRB2 associated regulator of MAPK1 subtype 1	2.132	3.132
GARS	chr7:30634004-30673651	glycyl-tRNA synthetase	2.794	4.112
GAS1	chr9:89559276-89562104	growth arrest specific 1	0.434	0.256
GAS2	chr11:22649821-22834547	growth arrest specific 2	0.218	0.078
GAS5	chr1:173830655-173856528	growth arrest specific 5 (non-protein coding)	3.492	7.609
GATAD2A	chr19:19496622-19619741	GATA zinc finger domain containing 2A	1.977	2.833
GATM	chr15:45650586-45672842	glycine amidinotransferase	0.457	0.149
GBA3	chr4:22694547-22821192	glucosylceramidase beta 3 (gene/pseudogene)	0.241	0.011
GBP2	chr1:89570415-89591818	guanylate binding protein 2	0.477	0.215
GBP4	chr1:89597433-89664633	guanylate binding protein 4	0.251	0.102
GC	chr4:72607406-72671237	group-specific component (vitamin D binding protein)	0.659	0.127
GCC1	chr7:127219396-127225661	GRIP and coiled-coil domain containing 1	2.36	3.5
GCHFR	chr15:41056284-41059911	GTP cyclohydrolase I feedback regulator	0.407	0.409
GCKR	chr2:27714749-27750318	glucokinase (hexokinase 4) regulator	0.291	0.118
GCLM	chr1:94348983-94394199	glutamate-cysteine ligase modifier subunit	2.759	3.118
GCNT2	chr6:10521567-10629601	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.419	0.168
GCNT3	chr15:59903868-59949737	glucosaminyl (N-acetyl) transferase 3, mucin type	1.016	0.176
GDA	chr9:74729510-74868453	guanine deaminase	0.748	0.211
GDF11	chr12:56137041-56211540	growth differentiation factor 11	3.584	5.464
GDF15	chr19:18496967-18499986	growth differentiation factor 15	8.279	16.48
GDI2	chr10:5807185-5855512	GDP dissociation inhibitor 2	0.667	0.471
GDPD5	chr11:75145684-75236938	glycerophosphodiester phosphodiesterase domain containing 5	2.33	4.051
GDPGP1	chr15:90777486-90785312	GDP-D-glucose phosphorylase 1	0.454	0.336
GEM	chr8:95261484-95274547	GTP binding protein overexpressed in skeletal muscle	2.731	4.78
GFPT1	chr2:69546900-69614386	glutamine--fructose-6-phosphate transaminase 1	1.635	2.223
GFRA1	chr10:117816434-118033126	GDNF family receptor alpha 1	0.319	0.257
GGN	chr19:38874559-38880594	gametogenetin	1.621	2.457
GGT8P	chr2:91963332-91978189	gamma-glutamyltransferase 8 pseudogene	0.185	0.095
GHDC	chr17:40341104-40346550	GH3 domain containing	0.604	0.407
GHR	chr5:42423496-42722173	growth hormone receptor	0.443	0.318
GIMAP2	chr7:150382793-150390728	GTPase, IMAP family member 2	0.517	0.163
GINS1	chr20:25388322-25429191	GINS complex subunit 1	0.899	0.158
GINS3	chr16:58426297-58440048	GINS complex subunit 3	0.937	0.344
GIPC2	chr1:78511225-78604178	GIPC PDZ domain containing family member 2	0.551	0.308
GIT1	chr17:27900486-27948441	GIT ArfGAP 1	1.925	4.68
GJA3	chr13:20712394-20735183	gap junction protein alpha 3	3.234	4.518
GJB1	chrX:70430034-70948962	gap junction protein beta 1	0.131	0.011
GJB2	chr13:20761603-20767114	gap junction protein beta 2	0.551	0.214

GJB5	chr1:35220647-35224113	gap junction protein beta 5	13.31	81.92
GKAP1	chr9:86354335-86432752	G kinase anchoring protein 1	1.901	2.534
GLDC	chr9:6532463-6645692	glycine decarboxylase	0.435	0.172
GLIPR1L1	chr12:75728462-75784685	GLI pathogenesis related 1 like 1	0.71	0.253
GLIPR2	chr9:36136741-36163903	GLI pathogenesis related 2	2.404	4.163
GLIS2	chr16:4365852-4389659	GLIS family zinc finger 2	1.307	3.086
GLIS3	chr9:3824127-4300046	GLIS family zinc finger 3	2.815	5.064
GLRX	chr5:95149552-95158577	glutaredoxin	0.363	0.167
GLS2	chr12:56862300-56882181	glutaminase 2	0.314	0.182
GLT25D1	chr19:17666510-17693967	collagen beta(1-O)galactosyltransferase 1	1.725	2.344
GLT25D2	chr1:183904965-184006863	collagen beta(1-O)galactosyltransferase 2	1.448	2.079
GLUD1	chr10:88809958-88854776	glutamate dehydrogenase 1	0.522	0.403
GLUD2	chrX:120181461-120183796	glutamate dehydrogenase 2	0.384	0.115
GLUL	chr1:182350838-182361341	glutamate-ammonia ligase	0.435	0.246
GLYAT	chr11:58466955-58499480	glycine-N-acyltransferase	0.036	0.004
GLYATL1	chr11:58695101-58825925	glycine-N-acyltransferase like 1	0.027	0.005
GMPR2	chr14:24701647-24708447	guanosine monophosphate reductase 2	0.626	0.481
GNA12	chr7:2767740-2883959	G protein subunit alpha 12	1.683	2.823
GNAL	chr18:11689013-11908865	G protein subunit alpha L	0.605	0.439
GNB2	chr7:100271362-100276792	G protein subunit beta 2	1.671	2.915
GNG11	chr7:93551015-93555826	G protein subunit gamma 11	1.536	2.889
GNMT	chr6:42928499-42981719	glycine N-methyltransferase	0.165	0.092
GNPDA1	chr5:141380233-141392620	glucosamine-6-phosphate deaminase 1	1.37	2.233
GNPDA2	chr4:44703416-44728651	glucosamine-6-phosphate deaminase 2	1.296	2.609
GOLGA2P5	chr12:100550158-100593392	golgin A2 pseudogene 5	0.323	0.246
GOLT1A	chr1:204167287-204183220	golgi transport 1A	0.447	0.181
GORASP2	chr2:171784947-171823643	golgi reassembly stacking protein 2	1.394	2.03
GPAM	chr10:113909621-113975231	glycerol-3-phosphate acyltransferase, mitochondrial	0.213	0.155
GPC1	chr2:241374260-241407538	glypican 1	1.793	2.518
GPC2	chr7:99767000-99775004	glypican 2	2.424	3.491
GPC5	chr13:92050883-93519487	glypican 5	1.717	2.223
GPCPD1	chr20:5525018-5591672	glycerophosphocholine phosphodiesterase 1	1.148	2.23
GPER	chr7:1018659-1177893	G protein-coupled estrogen receptor 1	0.237	0.202
GPI	chr19:34850684-34893318	glucose-6-phosphate isomerase	0.592	0.427
GPM6B	chrX:13788040-13956831	glycoprotein M6B	0.493	0.402
GPR1	chr2:207040041-207082771	G protein-coupled receptor 1	10.85	11.96
GPR126	chr6:142623036-142767403	adhesion G protein-coupled receptor G6	0.637	0.33
GPR133	chr12:131438443-131626090	adhesion G protein-coupled receptor D1	1.358	2.238
GPR137C	chr14:53019865-53104431	G protein-coupled receptor 137C	2.95	2.979
GPR157	chr1:9160348-9252396	G protein-coupled receptor 157	1.603	2.677
GPR161	chr1:168048779-168106905	G protein-coupled receptor 161	2.856	4.256
GPR56	chr16:57653909-57698944	adhesion G protein-coupled receptor G1	2.59	7.376
GPR64	chrX:19007382-19140755	adhesion G protein-coupled receptor G2	2.296	2.615
GPR87	chr3:150804675-151176497	G protein-coupled receptor 87	0.689	0.295
GPR88	chr1:101003727-101007583	G protein-coupled receptor 88	0.267	0.145
GPRC5C	chr17:72427097-72448123	G protein-coupled receptor class C group 5 member C	0.661	0.437
GPRIN1	chr5:175953699-176037137	G protein regulated inducer of neurite outgrowth 1	3.579	6.06
GPSM1	chr9:139221931-139254057	G-protein signaling modulator 1	2.452	2.874
GPX2	chr14:65381078-65569413	glutathione peroxidase 2	0.107	0.01
GRAMD1B	chr11:123301319-123498481	GRAM domain containing 1B	0.313	0.263
GRAMD1C	chr3:113557680-113666341	GRAM domain containing 1C	0.47	0.293
GRAMD3	chr5:125695787-125830209	GRAM domain containing 3	0.374	0.084
GRB10	chr7:50657759-50861181	growth factor receptor bound protein 10	2.076	3.777
GRB7	chr17:37894108-37903539	growth factor receptor bound protein 7	0.321	0.159
GRHL1	chr2:10091791-10142412	grainyhead like transcription factor 1	1.932	2.767
GRHPR	chr9:37422459-37472483	glyoxylate reductase/hydroxypyruvate reductase	0.467	0.329
GRIA3	chrX:122318095-122624766	glutamate ionotropic receptor AMPA type subunit 3	0.58	0.335
GRK5	chr10:120967196-121215131	G protein-coupled receptor kinase 5	1.411	2.237
GRK6	chr5:176853494-176883287	G protein-coupled receptor kinase 6	1.86	2.213
GRTP1	chr13:113978211-114018463	growth hormone regulated TBC protein 1	0.279	0.173
GSN	chr9:124030379-124095123	gelsolin	0.23	0.112
GSTA4	chr6:52842745-52860178	glutathione S-transferase alpha 4	0.652	0.373
GSTK1	chr7:142960521-142966222	glutathione S-transferase kappa 1	0.555	0.336
GSTM1	chr1:110198697-110236367	Glutathione S-Transferase Mu 1	0.322	0.140
GSTO1	chr10:106013951-106027222	glutathione S-transferase omega 1	0.328	0.126
GTF2A1	chr14:81641795-81689666	general transcription factor IIA subunit 1	1.628	2.169
GTF2I	chr7:74072029-74175022	general transcription factor IIi	0.577	0.317
GTF2IRD1	chr7:73867515-74016928	GTF2I repeat domain containing 1	2.345	2.988
GTF2IRD1P1	chr7:66117918-66309846	GTF2I repeat domain containing 1 pseudogene 1	1.554	2.291
GTF3C6	chr6:111279762-111289091	general transcription factor IIIC subunit 6	0.545	0.313
GTPBP2	chr6:43543877-43596936	GTP binding protein 2	3.709	5.829
GTSE1	chr22:46690546-46729084	G2 and S-phase expressed 1	0.384	0.391
GYG2	chrX:2746793-2801206	glycogenin 2	0.141	0.01
GYPC	chr2:127413444-127454251	glycophorin C (Gerbich blood group)	1.578	2.516
GYS2	chr12:21689122-21757865	glycogen synthase 2	0.118	0.041
H1F0	chr22:38201113-38203443	H1 histone family member 0	1.689	2.029
H1FX	chr3:129033613-129043412	H1 histone family member X	1.667	2.345
H2AFJ	chr12:14927269-14930936	H2A histone family member J	1.529	2.335
H2AFY2	chr10:71812356-71930285	H2A histone family member Y2	0.67	0.321
H2AFZ	chr4:100869243-100871512	H2A histone family member Z	1.781	2.349
H6PD	chr1:9293675-9331428	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase	0.643	0.448
HAAO	chr2:42989628-43030907	3-hydroxyanthranilate 3,4-dioxygenase	0.552	0.133
HABP2	chr10:115310589-115423829	hyaluronan binding protein 2	0.285	0.044
HABP4	chr9:99192128-99259567	hyaluronan binding protein 4	1.983	2.824
HADH	chr4:108910869-108956331	hydroxyacyl-CoA dehydrogenase	0.769	0.425
HAL	chr12:96366439-96390143	histidine ammonia-lyase	0.262	0.091
HAMP	chr19:35773409-35776045	hepcidin antimicrobial peptide	0.669	0.075
HAO1	chr20:7826328-7921179	hydroxyacid oxidase 1	0.116	0.01
HAO2	chr1:119904920-119936755	hydroxyacid oxidase 2	0.026	0.008
HAP1	chr17:39873997-39890898	huntingtin-associated protein 1	5.634	16.73
HBEGF	chr5:139712427-139726188	heparin binding EGF like growth factor	4.853	8.747
HCFC1R1	chr16:3072625-3077756	host cell factor C1 regulator 1	2.339	3.004
HCFC2	chr12:104458235-104504663	host cell factor C2	0.655	0.267
HCG9	chr6:29914520-29946177	HLA complex group 9 (non-protein coding)	2.537	3.597
HCN4	chr15:73612199-73661605	hyperpolarization activated cyclic nucleotide gated potassium channel 4	13.02	20.23
HDAC11	chr3:13521714-13547924	histone deacetylase 11	1.305	2.052
HDAC9	chr7:18126571-19161426	histone deacetylase 9	3.456	2.393
HDGF	chr1:156711898-156737161	hepatoma-derived growth factor	0.461	0.276
HDHD3	chr9:116135696-116139264	haloacid dehalogenase like hydrolase domain containing 3	0.557	0.393
HDX	chrX:83572881-83757487	highly divergent homeobox	2.824	3.681
HEATR3	chr16:50099879-50140332	HEAT repeat containing 3	0.571	0.271
HECA	chr6:139456248-139501946	hdc homolog, cell cycle regulator	1.8	2.463
HELZ	chr17:65056517-65241799	helicase with zinc finger	0.653	0.467

HERC5	chr4:89378199-89427321	HECT and RLD domain containing E3 ubiquitin protein ligase 5	1.869	2.231
HES4	chr1:934230-944881	hes family bHLH transcription factor 4	1.166	2.491
HES6	chr2:239146907-239148681	hes family bHLH transcription factor 6	2.609	5.523
HES7	chr17:8023907-8027639	hes family bHLH transcription factor 7	2.048	3.664
HEXIM2	chr17:43236391-43247696	hexamethylene bisacetamide inducible 2	0.464	0.204
HEY2	chr6:126070731-126082415	hes related family bHLH transcription factor with YRPW motif 2	2.576	3.446
HFE	chr6:26086547-26098258	hemochromatosis	0.382	0.333
HFE2	chr1:145413122-145417545	hemochromatosis type 2 (juvenile)	0.09	0.006
HGD	chr3:120347014-120401418	homogentisate 1,2-dioxygenase	0.41	0.047
HHLA3	chr1:70820492-70833705	HERV-H LTR-associating 3	1.387	2.032
HIBCH	chr2:191069351-191236391	3-hydroxyisobutyryl-CoA hydrolase	0.499	0.204
HIC2	chr22:21771649-21805750	hypermethylated in cancer 2	1.303	2.143
HILPDA	chr7:128095883-128104700	hypoxia inducible lipid droplet associated	1.665	2.014
HIST1H1T	chr6:26105991-26109945	histone cluster 1, H1t	4.383	4.959
HIST1H2AD	chr6:26146343-26199521	histone cluster 1, H2ad	5.757	7.155
HIST1H2AE	chr6:26217147-26217711	histone cluster 1, H2ae	3.347	3.454
HIST1H2AG	chr6:27100816-27114637	histone cluster 1, H2ag	3.646	4.732
HIST1H2AI	chr6:27775844-27780258	histone cluster 1, H2ai	3.521	2.659
HIST1H2AK	chr6:27801740-27824183	histone cluster 1, H2ak	1.938	3.457
HIST1H2BC	chr6:26112743-26140256	histone cluster 1, H2bc	3.594	3.645
HIST1H2BE	chr6:26146343-26199521	histone cluster 1, H2be	2.148	4.247
HIST1H2BG	chr6:26214352-26217023	histone cluster 1, H2bg	5.592	5.663
HIST1H2BJ	chr6:27090228-27100616	histone cluster 1, H2bj	1.578	2.781
HIST1H2BN	chr6:27801740-27824183	histone cluster 1, H2bn	3.717	7.199
HIST1H2BO	chr6:27861202-27926219	histone cluster 1, H2bo	1.345	3.378
HIST1H4C	chr6:26102081-26105297	histone cluster 1, H4c	2.972	5.165
HIST1H4D	chr6:26146343-26199521	histone cluster 1, H4d	4.784	5.248
HIST1H4E	chr6:26204728-26210036	histone cluster 1, H4e	3.334	3.227
HIST1H4H	chr6:26280826-26285745	histone cluster 1, H4h	2.625	3.23
HIST1H4I	chr6:27100816-27114637	histone cluster 1, H4i	3.084	5.982
HIST1H4J	chr6:27791628-27800624	histone cluster 1, H4j	3.952	4.036
HIST1H4K	chr6:27791628-27800624	histone cluster 1, H4k	2.957	4.227
HIST2H2AC	chr1:149858524-149858961	histone cluster 2, H2ac	1.706	2.768
HIST2H2BC	chr1:149814992-149823161	histone cluster 2, H2bc (pseudogene)	2.026	3.803
HIST2H2BE	chr1:149856009-149858232	histone cluster 2, H2be	1.729	2.451
HIVEP2	chr6:143072603-143267446	human immunodeficiency virus type I enhancer binding protein 2	1.627	2.501
HJURP	chr2:234745426-234763212	Holliday junction recognition protein	0.319	0.142
HKDC1	chr10:70980058-71027315	hexokinase domain containing 1	0.853	0.336
HLA-DRA	chr6:32407618-32412826	major histocompatibility complex, class II, DR alpha	0.755	0.44
HLA-DRB1	chr6:32485153-32557613	major histocompatibility complex, class II, DR beta 1	0.607	0.259
HM13	chr20:30102240-30161066	histocompatibility (minor) 13	1.859	2.81
HMGA1	chr6:34204576-34214008	high mobility group AT-hook 1	4.556	8.912
HMGA2	chr12:66151799-66360071	high mobility group AT-hook 2	1.456	2.133
HMGCR	chr5:74632328-74657926	3-hydroxy-3-methylglutaryl-CoA reductase	0.564	0.425
HMGCS1	chr5:43287571-43313658	3-hydroxy-3-methylglutaryl-CoA synthase 1	0.251	0.176
HMGCS2	chr1:120290618-120311555	3-hydroxy-3-methylglutaryl-CoA synthase 2	0.106	0.014
HMGN3	chr6:79910929-79946517	high mobility group nucleosomal binding domain 3	0.531	0.36
HMMR	chr5:162887516-162918953	hyaluronan mediated motility receptor	0.219	0.22
HMOX1	chr22:35777059-35790207	heme oxygenase 1	1.545	2.585
HN1	chr17:73131343-73150775	hematological and neurological expressed 1	1.981	2.057
HNF1A	chr12:121415244-121454300	HNF1 homeobox A	0.298	0.07
HNF4A	chr20:42984440-43061485	hepatocyte nuclear factor 4 alpha	0.146	0.02
HNF4G	chr8:76319764-76479061	hepatocyte nuclear factor 4 gamma	0.826	0.404
HNMT	chr2:138721807-138773934	histamine N-methyltransferase	0.224	0.059
HNRNPA1	chr12:54674461-54680871	heterogeneous nuclear ribonucleoprotein A1	0.533	0.333
HNRNPD	chr4:83273759-83295202	heterogeneous nuclear ribonucleoprotein D	0.6	0.398
HOMER1	chr5:78654651-78809700	homer scaffolding protein 1	2.819	4.666
HOMER3	chr19:19040009-19052041	homer scaffolding protein 3	2.715	4.899
HOOK1	chr1:60280532-60342050	hook microtubule-tethering protein 1	0.738	0.341
HOXA3	chr7:27145808-27170399	homeobox A3	0.26	0.05
HOXB13	chr17:46802126-46806111	homeobox B13	0.598	0.305
HPD	chr12:122277432-122326517	4-hydroxyphenylpyruvate dioxygenase	0.278	0.066
HPGD	chr4:175411122-175444086	hydroxyprostaglandin dehydrogenase 15-(NAD)	0.621	0.093
HPX	chr11:6452267-6462254	hemopexin	0.872	0.196
HRCT1	chr9:35906086-35907847	histidine rich carboxyl terminus 1	0.472	0.138
HRG	chr3:186383797-186396023	histidine rich glycoprotein	0.535	0.119
HRH1	chr3:11178778-11305146	histamine receptor H1	1.769	2.17
HRSP12	chr8:99114566-99129418	reactive intermediate imine deaminase A homolog	0.474	0.147
HS6ST1	chr2:129023047-129076171	heparan sulfate 6-O-sulfotransferase 1	1.814	2.7
HSBP1L1	chr18:77724581-77793936	heat shock factor binding protein 1-like 1	0.352	0.143
HSD11B1	chr1:209859524-209908429	hydroxysteroid (11-beta) dehydrogenase 1	0.49	0.25
HSD11B1L	chr19:5678430-5688534	hydroxysteroid (11-beta) dehydrogenase 1-like	2.144	2.697
HSD11B2	chr16:67463721-67471806	hydroxysteroid (11-beta) dehydrogenase 2	0.451	0.28
HSD17B11	chr4:88257690-88312455	hydroxysteroid (17-beta) dehydrogenase 11	0.425	0.144
HSD17B2	chr16:82068857-82132139	hydroxysteroid (17-beta) dehydrogenase 2	0.118	0.012
HSD17B3	chr9:98997588-99145992	hydroxysteroid (17-beta) dehydrogenase 3	0.689	0.403
HSD17B4	chr5:118748685-118878030	hydroxysteroid (17-beta) dehydrogenase 4	0.445	0.174
HSD17B6	chr12:57157095-57181574	hydroxysteroid (17-beta) dehydrogenase 6	0.48	0.148
HSD17B7	chr1:162760495-162782608	hydroxysteroid (17-beta) dehydrogenase 7	0.319	0.358
HSD17B7P2	chr10:38645307-38667511	hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2	0.271	0.222
HSD17B8	chr6:33172413-33174608	hydroxysteroid (17-beta) dehydrogenase 8	0.497	0.324
HSDL1	chr16:84155743-84178800	hydroxysteroid dehydrogenase like 1	2.042	3.185
HSPA12A	chr10:118430702-118502085	heat shock protein family A (Hsp70) member 12A	2.373	3.445
HSPA13	chr21:15743436-15755509	heat shock protein family A (Hsp70) member 13	3.547	6.907
HSPA5	chr9:127997126-128003666	heat shock protein family A (Hsp70) member 5	1.538	2.7
HSPA8	chr11:122928199-122932901	heat shock protein family A (Hsp70) member 8	0.574	0.216
HSPB1	chr7:75924225-75933614	heat shock protein family B (small) member 1	0.556	0.438
HSPB2	chr11:111783459-111797595	heat shock protein family B (small) member 2	0.397	0.036
HSPB6	chr19:36239261-36248616	heat shock protein family B (small) member 6	2.575	4.71
HSPB8	chr12:119616594-119632551	heat shock protein family B (small) member 8	0.923	0.458
HSPE1	chr2:198351303-198418423	heat shock protein family E (Hsp10) member 1	0.534	0.339
HSPG2	chr1:22138757-22263778	heparan sulfate proteoglycan 2	1.409	2.161
HTR7P1	chr12:13080639-13236383	5-hydroxytryptamine receptor 7 pseudogene 1	1.643	2.247
HULC	chr6:8435855-8789203	hepatocellular carcinoma up-regulated long non-coding RNA	0.077	0.032
HYAL1	chr3:50337319-50349812	hyaluronoglucosaminidase 1	0.318	0.173
HYOU1	chr11:118914895-118927927	hypoxia up-regulated 1	1.99	2.884
IARS	chr9:94972489-95056038	isoleucyl-tRNA synthetase	1.875	2.206
IARS2	chr1:220046618-220321383	isoleucyl-tRNA synthetase 2, mitochondrial	0.708	0.478
ICA1	chr7:8152814-8302242	islet cell autoantigen 1	0.906	0.485
ICOSLG	chr21:45642608-45660888	inducible T-cell co-stimulator ligand	3.632	13.42
ID2	chr2:8822112-8824583	inhibitor of DNA binding 2, HLH protein	0.439	0.229
IDH1	chr2:209100952-209119806	isocitrate dehydrogenase (NADP(+)) 1, cytosolic	0.51	0.418
IDH3B	chr20:2639040-2644865	isocitrate dehydrogenase 3 (NAD(+)) beta	0.642	0.43

IDI1	chr10:1064846-1178548	isopentenyl-diphosphate delta isomerase 1	0.574	0.291
IER2	chr19:13261266-13265720	immediate early response 2	1.88	2.185
IER3	chr6:30710975-30712327	immediate early response 3	3.08	4.538
IFFO2	chr1:19230773-19283187	intermediate filament family orphan 2	1.968	2.766
IFI27	chr14:94571201-94583033	interferon alpha inducible protein 27	0.572	0.38
IFI44	chr1:79115286-79129877	interferon induced protein 44	0.611	0.295
IFIT1	chr10:91152302-91168626	interferon induced protein with tetratricopeptide repeats 1	0.302	0.244
IFIT2	chr10:91061705-91069033	interferon induced protein with tetratricopeptide repeats 2	0.643	0.442
IFITM2	chr11:309531-311834	interferon induced transmembrane protein 2	0.353	0.081
IFITM3	chr11:319672-320914	interferon induced transmembrane protein 3	0.385	0.306
IFNE	chr9:21454134-21559820	interferon, epsilon	2.512	5.231
IFRD1	chr7:112063198-112130943	interferon related developmental regulator 1	2.876	4.948
IFT27	chr22:37154245-37172292	intraflagellar transport 27	0.623	0.414
IGFBP1	chr7:45927958-45933267	insulin like growth factor binding protein 1	2.562	2.18
IGFBP3	chr7:45951843-45960871	insulin like growth factor binding protein 3	5.6	12.48
IGFBP7	chr4:57843827-58071465	insulin like growth factor binding protein 7	1.405	2.741
IKBKE	chr1:206643585-206670223	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	0.163	0.046
IL15	chr4:142557748-142656251	interleukin 15	1.42	2.327
IL15RA	chr10:5994333-6021549	interleukin 15 receptor subunit alpha	1.732	2.52
IL17RE	chr3:9906149-10149915	interleukin 17 receptor E	0.351	0.226
IL18	chr11:112013932-112034840	interleukin 18	1.761	2.193
IL1B	chr2:113587336-113594356	interleukin 1 beta	2.382	2.826
IL1R2	chr2:102608305-102644884	interleukin 1 receptor type 2	0.163	0.051
IL1RAP	chr3:190231839-190374986	interleukin 1 receptor accessory protein	1.611	2.635
IL22RA1	chr1:24446190-24469775	interleukin 22 receptor subunit alpha 1	0.381	0.065
IL31RA	chr5:55147203-55218789	interleukin 31 receptor A	2.698	3.791
IL32	chr16:3096602-3125579	interleukin 32	0.449	0.107
IL6	chr7:22766765-22771621	interleukin 6	4.421	7.618
IL6R	chr1:154377668-154441926	interleukin 6 receptor	0.684	0.418
IL8	chr4:74606222-74609433	C-X-C motif chemokine ligand 8	0.536	0.323
IMPDH1	chr7:128032330-128090404	IMP (inosine 5'-monophosphate) dehydrogenase 1	2.383	3.781
INADL	chr1:62207703-62629591	PATJ, crumbs cell polarity complex component	0.68	0.32
INE2	chrX:15645440-15805927	inactivation escape 2 (non-protein coding)	1.32	2.277
INHBB	chr2:121103718-121109383	inhibin beta B	1.804	2.194
INPP4A	chr2:99061320-99207496	inositol polyphosphate-4-phosphatase type I A	1.532	2.109
INSIG1	chr7:155089485-155101947	insulin induced gene 1	0.374	0.258
INSR	chr19:7112265-7294331	insulin receptor	0.615	0.395
INTS1	chr7:1468098-1544081	integrator complex subunit 1	1.439	2.102
IPO8	chr12:30781914-30848997	importin 8	0.592	0.326
IQCB1	chr3:121488425-121553926	IQ motif containing B1	1.588	2.22
IQCD	chr12:113623394-113658882	IQ motif containing D	3.15	4.082
IQGAP2	chr5:75699105-76003957	IQ motif containing GTPase activating protein 2	0.275	0.027
IQGAP3	chr1:156495196-156542396	IQ motif containing GTPase activating protein 3	0.467	0.306
IRAK2	chr3:10206554-10285430	interleukin 1 receptor associated kinase 2	2.076	3.214
IRF6	chr1:209958856-209979520	interferon regulatory factor 6	0.175	0.064
IRF7	chr11:572809-640705	interferon regulatory factor 7	2.077	2.692
IRF8	chr16:85932773-85956211	interferon regulatory factor 8	2.597	3.314
IRS2	chr13:110406181-110442998	insulin receptor substrate 2	2.009	3.321
ISOC2	chr19:55964345-55973049	isochorismatase domain containing 2	0.38	0.329
ITFG1	chr16:47189273-47735440	integrin alpha FG-GAP repeat containing 1	0.686	0.494
ITFG3	chr16:284796-316119	family with sequence similarity 234 member A	1.535	2.067
ITGA11	chr15:68588494-68724546	integrin subunit alpha 11	3.758	6.512
ITGA2	chr5:52285122-52391113	integrin subunit alpha 2	3.135	6.21
ITGA3	chr17:48133339-48167950	integrin subunit alpha 3	2.627	4.191
ITGA6	chr2:173292313-173371181	integrin subunit alpha 6	1.825	2.398
ITGAM	chr16:31265166-31344213	integrin subunit alpha M	0.311	0.087
ITGB3	chr17:45329813-45399861	integrin subunit beta 3	4.832	8.484
ITIH1	chr3:52811601-52826084	inter-alpha-trypsin inhibitor heavy chain 1	0.722	0.227
ITIH2	chr10:7745197-7791483	inter-alpha-trypsin inhibitor heavy chain 2	0.533	0.092
ITIH4	chr3:52847005-52931597	inter-alpha-trypsin inhibitor heavy chain family member 4	0.643	0.195
ITPA	chr20:3189312-3204516	inosine triphosphatase	0.611	0.446
ITPKA	chr15:41785389-41795757	inositol-trisphosphate 3-kinase A	2.428	3.087
ITPR1	chr3:4535031-4889524	inositol 1,4,5-trisphosphate receptor type 1	1.972	2.639
ITPRIP	chr10:106069453-106098251	inositol 1,4,5-trisphosphate receptor interacting protein	3.434	8.664
IYD	chr6:150690027-150725765	iodotyrosine deiodinase	0.306	0.06
JAG1	chr20:10618206-10654694	jagged 1	3.266	4.864
JARID2	chr6:15245750-15522273	jumonji and AT-rich interaction domain containing 2	1.612	2.668
JDP2	chr14:75894508-75939423	Jun dimerization protein 2	2.834	4.635
JHDM1D	chr7:139784545-139876767	lysine demethylase 7A	1.535	2.342
JKAMP	chr14:59919111-60043549	JNK1/MAPK8-associated membrane protein	0.707	0.439
JOSD1	chr22:39081547-39097357	Josephin domain containing 1	1.982	2.793
JPH1	chr8:75146938-75233676	junctophilin 1	3.25	5.047
JUN	chr1:59246459-59249943	jun proto-oncogene	2.77	2.946
JUND	chr19:18390562-18392432	jun D proto-oncogene	2.656	3.384
KANK1	chr9:470293-746106	KN motif and ankyrin repeat domains 1	0.303	0.136
KANSL3	chr2:97258891-97304116	KAT8 regulatory NSL complex subunit 3	1.588	2.041
KBTBD4	chr11:47487488-47606116	kelch repeat and BTB domain containing 4	0.735	0.484
KBTBD7	chr13:41759055-41768779	kelch repeat and BTB domain containing 7	0.469	0.228
KC6	chr18:38958108-39144845	keratoconus gene 6	0.47	0.25
KCNC3	chr19:50815529-50832634	potassium voltage-gated channel subfamily C member 3	2.248	4.128
KCNH7	chr2:163175541-163695264	potassium voltage-gated channel subfamily H member 7	0.669	0.159
KCNH8	chr3:19007783-19577752	potassium voltage-gated channel subfamily H member 8	0.675	0.47
KCNJ16	chr17:68071320-68131746	potassium voltage-gated channel subfamily J member 16	0.138	0.005
KCNJ8	chr12:21917888-21928014	potassium voltage-gated channel subfamily J member 8	0.463	0.119
KCNK13	chr14:90527003-90652195	potassium two pore domain channel subfamily K member 13	2.128	3.934
KCNK5	chr6:39151668-39197259	potassium two pore domain channel subfamily K member 5	0.145	0.094
KCNMB4	chr12:70760061-70828072	potassium calcium-activated channel subfamily M regulatory beta subunit 4	0.504	0.356
KCNQ5	chr6:73331570-73908573	potassium voltage-gated channel subfamily Q member 5	2.746	3.433
KCTD14	chr11:77726760-77850699	potassium channel tetramerization domain containing 14	0.623	0.401
KCTD17	chr22:37447778-37505731	potassium channel tetramerization domain containing 17	1.93	2.386
KCTD3	chr1:215740507-215795151	potassium channel tetramerization domain containing 3	0.646	0.384
KCTD8	chr4:44175919-44450824	potassium channel tetramerization domain containing 8	1.517	2.275
KDELR3	chr22:38864082-38902373	KDEL endoplasmic reticulum protein retention receptor 3	0.574	0.37
KDM2B	chr12:121865890-122019034	lysine demethylase 2B	1.705	2.43
KDM8	chr16:27214806-27233118	lysine demethylase 8	0.449	0.271
KDR	chr4:55944425-55992383	kinase insert domain receptor	0.148	0.132
KGFLP1	chr9:46687556-46746820	fibroblast growth factor 7 pseudogene	1.452	2.158
KHDRBS3	chr8:136469658-136668646	KH domain containing, RNA binding, signal transduction associated 3	2.641	4.216
KHK	chr2:27309610-27341995	ketohexokinase	0.285	0.127
KIAA0040	chr1:175126122-175162229	KIAA0040	0.475	0.491
KIAA0146	chr8:48173488-48650726	scaffolding protein involved in DNA repair	1.425	2.221
KIAA0195	chr17:73452663-73511627	transmembrane protein 94	0.516	0.267
KIAA0226	chr3:197398258-197511317	RUN and cysteine rich domain containing beclin 1 interacting protein	1.976	2.792

KIAA0247	chr14:70078309-70181861	sushi domain containing 6	1.18	2.527
KIAA0355	chr19:34745455-34846471	KIAA0355	1.537	2.003
KIAA0391	chr14:35554303-35747687	KIAA0391	0.556	0.338
KIAA0513	chr16:85061409-85127834	KIAA0513	1.903	2.344
KIAA0556	chr16:27561407-27791692	KIAA0556	1.579	2.455
KIAA0930	chr22:45588122-45636650	KIAA0930	1.7	2.39
KIAA1147	chr7:141251077-141401953	KIAA1147	0.567	0.242
KIAA1199	chr15:81071711-81282227	cell migration inducing hyaluronan binding protein	0.986	2.361
KIAA1211L	chr2:99410308-99552684	KIAA1211-like	3.899	3.605
KIAA1407	chr3:113682983-113775460	coiled-coil domain containing 191	0.743	0.488
KIAA1456	chr8:12803182-12887507	KIAA1456	0.361	0.347
KIAA1468	chr18:59854500-59974428	KIAA1468	0.608	0.35
KIAA1522	chr1:33207404-33240833	KIAA1522	0.629	0.32
KIAA1524	chr3:108268391-108413693	KIAA1524	0.963	0.367
KIAA1683	chr19:18367905-18385319	KIAA1683	1.309	3.046
KIAA2018	chr3:113367232-113415493	upstream transcription factor family member 3	0.653	0.365
KIF18B	chr17:43002078-43025101	kinesin family member 18B	0.491	0.274
KIF20A	chr5:137475458-137549032	kinesin family member 20A	0.24	0.248
KIF21B	chr1:200938513-200992828	kinesin family member 21B	4.613	7.153
KIF23	chr15:69706596-69740764	kinesin family member 23	0.567	0.443
KIF2C	chr1:45205489-45233438	kinesin family member 2C	0.463	0.42
KIF4A	chrX:69509878-69640774	kinesin family member 4A	0.559	0.253
KIFC1	chr6:33359312-33377824	kinesin family member C1	0.614	0.413
KISS1	chr1:204159468-204165619	KiSS-1 metastasis-suppressor	0.146	0.021
KLC1	chr14:104095524-104181823	kinesin light chain 1	1.686	2.315
KLC2	chr11:66024764-66035332	kinesin light chain 2	2.362	3.525
KLC4	chr6:43027371-43042833	kinesin light chain 4	0.254	0.171
KLF11	chr2:10179239-10194963	Kruppel-like factor 11	1.732	2.537
KLF15	chr3:126061477-126076236	Kruppel-like factor 15	0.443	0.387
KLF16	chr19:1852397-1876193	Kruppel-like factor 16	2.524	5.409
KLF2	chr19:16435650-16438339	Kruppel-like factor 2	5.374	6.651
KLF4	chr9:110247132-110252462	Kruppel-like factor 4 (gut)	1.901	2.441
KLF5	chr13:73592920-73651676	Kruppel-like factor 5 (intestinal)	3.091	4.381
KLF6	chr10:3818187-3827473	Kruppel-like factor 6	2.103	2.657
KLHDC2	chr14:50233752-50319723	kelch domain containing 2	0.624	0.472
KLHDC7A	chr1:18807423-18812824	kelch domain containing 7A	0.32	0.061
KLHL29	chr2:23608297-23931483	kelch like family member 29	1.957	2.358
KLKB1	chr4:187135196-187179625	kallikrein B1	0.179	0.052
KNG1	chr3:186435097-186462199	kininogen 1	0.414	0.088
KNTC1	chr12:123011790-123111029	kinetochore associated 1	0.94	0.316
KPNA4	chr3:160212782-160287375	karyopherin subunit alpha 4	1.599	2.211
KRT5	chr12:52908283-52917348	keratin 5	0.1	0.077
KSR1	chr17:25783511-25953458	kinase suppressor of ras 1	1.567	2.362
KTI12	chr1:52485803-52521843	KTI12 chromatin associated homolog	1.582	2.484
KYNU	chr2:143635190-143799885	kynureninase	0.408	0.177
L3MBTL3	chr6:130339727-130462594	l(3)mbt-like 3 (Drosophila)	0.852	0.349
LACTB2	chr8:71520811-71581471	lactamase beta 2	0.613	0.405
LAD1	chr1:201349965-201369053	ladinin 1	0.342	0.039
LAGE3	chrX:153704800-153707627	L antigen family member 3	2.488	3.822
LAIR1	chr19:54865234-54876721	leukocyte associated immunoglobulin like receptor 1	0.171	0.104
LAMA1	chr18:6941742-7117813	laminin subunit alpha 1	3.493	8.019
LAMB1	chr7:107531573-107643804	laminin subunit beta 1	0.55	0.459
LAMB2P1	chr3:49190291-49191834	laminin subunit beta 2 pseudogene 1	1.398	2.238
LAMP3	chr3:182840002-182880667	lysosomal associated membrane protein 3	4.142	3.787
LAP3	chr4:17578926-17609590	leucine aminopeptidase 3	0.549	0.318
LAPTM4B	chr8:98787808-98864830	lysosomal protein transmembrane 4 beta	0.596	0.329
LARP6	chr15:71123888-71146498	La ribonucleoprotein domain family member 6	4.566	5.852
LBP	chr20:36974813-37005653	lipopolysaccharide binding protein	0.319	0.178
LCA5	chr6:80194707-80247147	Leber congenital amaurosis 5	1.72	2.537
LCA5L	chr21:40752212-40887433	Leber congenital amaurosis 5-like	1.703	2.231
LCP1	chr13:46700057-46756459	lymphocyte cytosolic protein 1	0.271	0.196
LDHA	chr11:18415935-18429765	lactate dehydrogenase A	0.545	0.468
LDHD	chr16:75032914-75150678	lactate dehydrogenase D	0.27	0.114
LDLRAD4	chr18:13217692-13652883	low density lipoprotein receptor class A domain containing 4	0.554	0.279
LEPREL1	chr3:189674516-189840226	prolyl 3-hydroxylase 2	1.512	2.027
LGALS3BP	chr17:76967334-76976061	lectin, galactoside binding soluble 3 binding protein	0.612	0.357
LGI4	chr19:35615416-35633954	leucine-rich repeat LGI family member 4	3.346	8.441
LGMN	chr14:93170151-93215047	legumain	1.515	2.11
LHFP	chr13:39917028-40177356	lipoma HMGIC fusion partner	2.343	3.596
LHFPL2	chr5:77781037-77944716	lipoma HMGIC fusion partner-like 2	4.276	7.711
LIMK1	chr7:73498106-73536855	LIM domain kinase 1	1.576	2.537
LIN7A	chr12:81172104-81331866	lin-7 homolog A, crumbs cell polarity complex component	0.625	0.067
LIPC	chr15:58702777-58861073	lipase C, hepatic type	0.351	0.162
LIPG	chr18:47086928-47119278	lipase G, endothelial type	0.123	0.171
LMBRD1	chr6:70385640-70535979	LMBR1 domain containing 1	0.566	0.39
LMCD1	chr3:8543504-8609806	LIM and cysteine rich domains 1	2.104	2.76
LMNB1	chr5:126112314-126172712	lamin B1	0.781	0.261
LMO4	chr1:87794150-87864430	LIM domain only 4	2.016	3.641
LONP2	chr16:48274602-48420559	lon peptidase 2, peroxisomal	0.669	0.483
LONRF2	chr2:100889752-100939195	LON peptidase N-terminal domain and ring finger 2	2.065	3.446
LPAL2	chr6:160887452-160941330	lipoprotein, Lp(a)-like 2, pseudogene	1.445	2.105
LPAR6	chr13:48877874-49056026	lysophosphatidic acid receptor 6	0.564	0.393
LPCAT3	chr12:7079943-7125842	lysophosphatidylcholine acyltransferase 3	0.482	0.364
LPIN1	chr2:11817704-11967603	lipin 1	0.543	0.488
LPIN3	chr20:39969412-39995498	lipin 3	0.29	0.199
LRBA	chr4:151185623-151936831	LPS responsive beige-like anchor protein	0.723	0.443
LRCH4	chr7:100136761-100205798	leucine-rich repeats and calponin homology (CH) domain containing 4	1.815	3.002
LRFN5	chr14:42076763-42373752	leucine rich repeat and fibronectin type III domain containing 5	0.381	0.106
LRIG3	chr12:59265936-59314319	leucine-rich repeats and immunoglobulin like domains 3	0.504	0.269
LRP11	chr6:150139893-150244214	LDL receptor related protein 11	1.639	2.397
LRP12	chr8:105497240-105601252	LDL receptor related protein 12	1.672	2.287
LRP5	chr11:68080090-68216743	LDL receptor related protein 5	0.604	0.399
LRP8	chr1:53692563-53794035	LDL receptor related protein 8	1.643	2.606
LRRC31	chr3:169555611-169587742	leucine rich repeat containing 31	0.514	0.024
LRRC37A3	chr17:62850283-62915585	leucine-rich repeat containing 37 member A3	1.655	2.353
LRRC45	chr17:79981053-79989413	leucine rich repeat containing 45	0.425	0.187
LRRC61	chr7:149944300-150035245	leucine rich repeat containing 61	0.565	0.284
LRRC73	chr6:43474702-43478081	leucine rich repeat containing 73	6.217	10.5
LRRC9	chr14:60385848-60530277	leucine rich repeat containing 9	1.669	3.271
LRRCC1	chr8:86019322-86058825	leucine rich repeat and coiled-coil centrosomal protein 1	0.758	0.457
LRRFIP1	chr2:238536219-238690290	leucine rich repeat (in FLII) interacting protein 1	1.751	2.405
LRRK2	chr12:40616913-40763086	leucine-rich repeat kinase 2	0.41	0.264
LRWD1	chr7:102105389-102119381	leucine-rich repeats and WD repeat domain containing 1	1.804	2.684

LTBP1	chr2:33172012-33624575	latent transforming growth factor beta binding protein 1	2.853	4.591
LUM	chr12:91497231-91505542	lumican	0.334	0.459
LY6E	chr8:144099901-144103827	lymphocyte antigen 6 complex, locus E	0.49	0.353
LYPD1	chr2:133174109-133429070	LY6/PLAUR domain containing 1	0.587	0.371
LYSMD4	chr15:100259027-100273626	LysM domain containing 4	1.964	2.169
MAD2L1	chr4:120980501-121087013	MAD2 mitotic arrest deficient-like 1 (yeast)	0.762	0.362
MADCAM1	chr19:489128-505507	mucosal vascular addressin cell adhesion molecule 1	1.597	2.317
MAF	chr16:79619798-79640625	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog	1.341	2.818
MAF1	chr8:145153535-145162515	MAF1 homolog, negative regulator of RNA polymerase III	1.493	2.4
MAFF	chr22:38597938-38612517	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F	7.352	13.59
MAFK	chr7:1570367-1596272	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog K	2.195	3.889
MAGED1	chrX:51546154-51645451	MAGE family member D1	0.505	0.311
MAL2	chr8:120220609-120257914	mal, T-cell differentiation protein 2 (gene/pseudogene)	1.603	2.265
MAML3	chr4:140586921-141075233	mastermind like transcriptional coactivator 3	0.717	0.442
MAN1A1	chr6:119498365-120326957	mannosidase alpha class 1A member 1	0.601	0.363
MAN1C1	chr1:25943314-26111258	mannosidase alpha class 1C member 1	1.862	2.544
MANEA	chr6:96004542-96206310	mannosidase endo-alpha	0.469	0.23
MANF	chr3:51422691-51426828	mesencephalic astrocyte derived neurotrophic factor	1.331	2.168
MAOA	chrX:43463486-43606071	monoamine oxidase A	0.391	0.181
MAOB	chrX:43625856-43741721	monoamine oxidase B	0.454	0.176
MAP1A	chr15:43663263-43956662	microtubule associated protein 1A	2.77	4.903
MAP1B	chr5:71391685-71505528	microtubule associated protein 1B	1.695	2.148
MAP1LC3A	chr20:33134687-33148149	microtubule associated protein 1 light chain 3 alpha	1.582	2.326
MAP1LC3B	chr16:87425800-87438380	microtubule associated protein 1 light chain 3 beta	3.142	6.471
MAP1LC3B2	chr12:116997185-117014425	microtubule associated protein 1 light chain 3 beta 2	2.528	4.64
MAP1S	chr19:17830302-17845324	microtubule associated protein 1S	1.649	2.323
MAP2	chr2:210288729-210598991	microtubule associated protein 2	2.097	2.688
MAP2K3	chr17:21187967-21218551	mitogen-activated protein kinase kinase 3	1.94	2.583
MAP2K6	chr17:67410837-67539093	mitogen-activated protein kinase kinase 6	0.23	0.048
MAP3K5	chr6:136878186-137114231	mitogen-activated protein kinase kinase kinase 5	0.431	0.315
MAP3K9	chr14:71189243-71276174	mitogen-activated protein kinase kinase kinase 9	1.574	2.203
MAP4	chr3:47892179-48130769	microtubule associated protein 4	1.868	2.702
MAPKAPK2	chr1:206858237-206907630	mitogen-activated protein kinase-activated protein kinase 2	1.538	2.693
MAPKBP1	chr15:42066113-42120120	mitogen-activated protein kinase binding protein 1	1.469	2.495
MARCH1	chr1:220959432-220988190	membrane associated ring-CH-type finger 1	0.757	0.377
MARCH2	chr1:220921486-220958285	membrane associated ring-CH-type finger 2	0.362	0.3
MARCH3	chr5:126203405-126366440	membrane associated ring-CH-type finger 3	2.165	6.846
MARCH5	chr10:93808396-94113721	membrane associated ring-CH-type finger 5	1.512	2.045
MARCKS	chr6:114178526-114184652	myristoylated alanine rich protein kinase C substrate	1.803	2.523
MARCKSL1	chr1:32799429-32801840	MARCKS-like 1	4.302	3.873
MARS	chr12:57881735-57914300	methionyl-tRNA synthetase	2.976	4.432
MARVELD3	chr16:71660055-71842990	MARVEL domain containing 3	0.416	0.443
MASP1	chr3:186933872-187009810	mannan binding lectin serine peptidase 1	0.297	0.048
MAST2	chr1:46269260-46501796	microtubule associated serine/threonine kinase 2	2.4	4.233
MAT1A	chr10:82031575-82049434	methionine adenosyltransferase 1A	0.135	0.017
MBNL3	chrX:131503342-131623996	muscleblind like splicing regulator 3	0.437	0.362
MCCC2	chr5:70882654-70954532	methylcrotonoyl-CoA carboxylase 2	0.527	0.259
MCEE	chr2:71336764-71357394	methylmalonyl-CoA epimerase	0.459	0.277
MCOLN3	chr1:85483462-85514273	mucolipin 3	1.898	2.455
MCPH1	chr8:6264112-6619021	microcephalin 1	2.707	7.769
MDGA1	chr6:37600108-37665932	MAM domain containing glycosylphosphatidylinositol anchor 1	1.847	2.476
MDH1	chr2:63348534-63834330	malate dehydrogenase 1	0.515	0.367
MECOM	chr3:168801286-169381563	MDS1 and EVI1 complex locus	0.731	0.428
MED26	chr19:16683381-16739015	mediator complex subunit 26	0.948	2.011
MEF2A	chr15:100105682-100257018	myocyte enhancer factor 2A	1.857	3.19
MEF2C	chr5:88014057-88200229	myocyte enhancer factor 2C	1.394	2.72
MERTK	chr2:112656043-112786945	MER proto-oncogene, tyrosine kinase	1.329	2.717
MESDC1	chr15:81293294-81296345	mesoderm development candidate 1	2.072	3.165
MEST	chr7:130126015-130371406	mesoderm specific transcript	0.738	0.444
METAP1D	chr2:172864803-172947273	methionyl aminopeptidase type 1D (mitochondrial)	0.456	0.247
METRNL	chr17:81037506-81058331	meteorin, glial cell differentiation regulator-like	2.116	4.587
METTL20	chr12:31800093-31822289	electron transfer flavoprotein beta subunit lysine methyltransferase	0.668	0.398
METTL22	chr16:8715526-8750298	methyltransferase like 22	1.335	2.02
METTL5	chr2:170655321-170681438	methyltransferase like 5	0.641	0.426
METTL7A	chr12:51318533-51326300	methyltransferase like 7A	0.369	0.148
MEX3B	chr15:82334118-82338551	mex-3 RNA binding family member B	2.579	3.584
MEX3C	chr18:48700919-48724051	mex-3 RNA binding family member C	1.697	2.543
MEX3D	chr19:1554667-1568057	mex-3 RNA binding family member D	2.241	3.024
MFHAS1	chr8:8640861-8751143	malignant fibrous histiocytoma amplified sequence 1	1.613	2.131
MFSD10	chr4:2932287-2936586	major facilitator superfamily domain containing 10	1.569	2.512
MFSD12	chr19:3506294-3557571	major facilitator superfamily domain containing 12	1.774	2.995
MFSD2A	chr1:40420783-40435810	major facilitator superfamily domain containing 2A	0.196	0.283
MGAT5	chr2:134877545-135212193	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	1.405	2.32
MGME1	chr20:17949564-17971766	mitochondrial genome maintenance exonuclease 1	0.759	0.388
MGMT	chr10:131265453-131565928	O-6-methylguanine-DNA methyltransferase	0.515	0.347
MGP	chr12:15034114-15038853	matrix Gla protein	0.317	0.206
MGST1	chr12:16500075-16530123	microsomal glutathione S-transferase 1	0.55	0.239
MGST2	chr4:140586921-141075233	microsomal glutathione S-transferase 2	0.353	0.179
MICA	chr6:31367560-31478901	MHC class I polypeptide-related sequence A	1.606	2.387
MICAL2	chr11:12132111-12285337	microtubule associated monooxygenase, calponin and LIM domain containing	1.481	2.346
MIDN	chr19:1248544-1259440	midnolin	2.242	2.496
MIPEPP3	chr13:21872263-22033508	mitochondrial intermediate peptidase pseudogene 3	2.114	3.939
MIR100HG	chr11:121959810-122073770	mir-100-let-7a-2 cluster host gene	1.747	2.573
MITF	chr3:69788585-70017836	microphthalmia-associated transcription factor	0.49	0.366
MKI67	chr10:129894924-129924468	marker of proliferation Ki-67	0.495	0.172
MKNK2	chr19:2037459-2051243	MAP kinase interacting serine/threonine kinase 2	2.768	4.719
MLIP	chr6:53875386-54131495	muscular LMNA-interacting protein	0.096	0.012
MLKL	chr16:74705752-74735077	mixed lineage kinase domain-like	0.328	0.257
MLX	chr17:40719077-40729849	MLX, MAX dimerization protein	0.48	0.261
MLXIP	chr12:122516651-122631893	MLX interacting protein	1.41	2.402
MMAB	chr12:109991520-110035071	methylmalonic aciduria (cobalamin deficiency) cblB type	0.383	0.195
MMACHC	chr1:45965855-45988562	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	0.261	0.103
MMD	chr17:53469973-53499341	monocyte to macrophage differentiation associated	1.822	2.834
MME	chr3:154652824-154901518	membrane metallo-endopeptidase	0.464	0.4
MMP10	chr11:102641232-102651359	matrix metallopeptidase 10	57.64	113.1
MMP16	chr8:89044316-89339800	matrix metallopeptidase 16	1.76	2.517
MMP19	chr12:56211805-56236767	matrix metallopeptidase 19	0.561	0.323
MMP3	chr11:102654406-102714342	matrix metallopeptidase 3	0.875	3.928
MMP7	chr11:102391238-102401478	matrix metallopeptidase 7	0.464	0.469
MOB3A	chr19:2071017-2096455	MOB kinase activator 3A	1.404	2.035
MOCS1	chr6:39760158-39902290	molybdenum cofactor synthesis 1	0.512	0.429
MOGAT1	chr2:223536281-223605238	monoacylglycerol O-acyltransferase 1	0.372	0.132
MON1A	chr3:49946301-50114685	MON1 homolog A, secretory trafficking associated	0.613	0.465

MORC4	chrX:106183834-106259004	MORC family CW-type zinc finger 4	1.685	2.352
MOSPD1	chrX:134015143-134049323	motile sperm domain containing 1	1.5	2.093
MOXD1	chr6:132617193-132722664	monooxygenase DBH like 1	1.478	2.021
MPC2	chr1:167885912-168045083	mitochondrial pyruvate carrier 2	0.498	0.353
MPDZ	chr9:13105672-13279620	multiple PDZ domain crumbs cell polarity complex component	0.529	0.276
MPI	chr15:75180870-75199593	mannose phosphate isomerase	0.591	0.357
MPP3	chr17:41878166-41910547	membrane palmitoylated protein 3	2.383	2.982
MPPE1	chr18:11689013-11908865	metallophosphoesterase 1	0.689	0.368
MPZ	chr1:161274524-161279762	myelin protein zero	0.45	0.104
MPZL1	chr1:167691086-167761156	myelin protein zero like 1	1.874	2.517
MPZL2	chr11:118124130-118135251	myelin protein zero like 2	0.638	0.109
MPZL3	chr11:118097414-118123161	myelin protein zero like 3	0.729	0.451
MRC2	chr17:60704761-60770962	mannose receptor C type 2	2.439	4.79
MREG	chr2:216807313-216946549	melanoregulin	0.437	0.201
MRO	chr18:48321489-48351754	maestro	0.281	0.153
MRPL1	chr4:78783320-78874072	mitochondrial ribosomal protein L1	0.555	0.317
MRPL11	chr11:66202549-66206310	mitochondrial ribosomal protein L11	0.606	0.417
MRPL13	chr8:121393353-121535875	mitochondrial ribosomal protein L13	0.584	0.392
MRPL15	chr8:55047712-55062105	mitochondrial ribosomal protein L15	0.541	0.498
MRPL16	chr11:59522435-59612974	mitochondrial ribosomal protein L16	0.522	0.29
MRPL19	chr2:75873658-75938455	mitochondrial ribosomal protein L19	0.567	0.244
MRPL23	chr11:1968501-2011150	mitochondrial ribosomal protein L23	0.558	0.349
MRPL24	chr1:156707093-156710995	mitochondrial ribosomal protein L24	0.587	0.307
MRPL27	chr17:48445227-48450562	mitochondrial ribosomal protein L27	0.636	0.442
MRPL35	chr2:86423940-86565206	mitochondrial ribosomal protein L35	0.625	0.469
MRPL39	chr21:26957967-26979801	mitochondrial ribosomal protein L39	0.696	0.421
MRPS12	chr19:39405903-39423659	mitochondrial ribosomal protein S12	0.511	0.328
MRPS27	chr5:71515235-71616085	mitochondrial ribosomal protein S27	0.723	0.455
MRPS30	chr5:44808646-44823149	mitochondrial ribosomal protein S30	0.598	0.434
MRPS35	chr12:27863705-27909237	mitochondrial ribosomal protein S35	0.717	0.49
MRPS36	chr5:68513572-68525985	mitochondrial ribosomal protein S36	0.503	0.43
MRPS5	chr2:95752951-95787754	mitochondrial ribosomal protein S5	0.535	0.405
MRPS9	chr2:105654482-105716418	mitochondrial ribosomal protein S9	0.632	0.472
MSC	chr8:72753776-72987819	musculin	3.808	6.042
MSI2	chr17:55333930-55762019	musashi RNA binding protein 2	0.492	0.297
MSMO1	chr4:166248817-166264314	methylsterol monooxygenase 1	0.282	0.152
MSR1	chr8:15965357-16512558	macrophage scavenger receptor 1	1.803	2.485
MSRB1	chr16:1985588-1993303	methionine sulfoxide reductase B1	0.392	0.276
MSRB2	chr10:23384426-23411641	methionine sulfoxide reductase B2	0.688	0.393
MST1	chr3:49721379-49726943	macrophage stimulating 1	0.839	0.344
MST1L	chr1:17080972-17090975	macrophage stimulating 1-like	0.754	0.401
MST1P2	chr1:16793788-16976915	macrophage stimulating 1 (hepatocyte growth factor-like) pseudogene 2	0.644	0.386
MSX1	chr4:4861391-4865660	msh homeobox 1	1.957	2.476
MT1F	chr16:56691854-56693215	metallothionein 1F	0.701	0.183
MTA3	chr2:42795670-42984055	metastasis associated 1 family member 3	0.633	0.328
MTCH2	chr11:47638857-47664206	mitochondrial carrier 2	0.624	0.427
MTHFD1	chr14:64854758-64926809	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetr	0.526	0.249
MTHFD1L	chr6:151186814-151423044	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	6.05	9.278
MTMR10	chr15:31195988-31283877	myotubularin related protein 10	0.637	0.424
MTMR3	chr22:30279111-30573062	myotubularin related protein 3	0.117	0.072
MTMR4	chr17:56566892-56595514	myotubularin related protein 4	0.468	0.417
MTMR9	chr8:11141999-11185654	myotubularin related protein 9	1.455	2.107
MTSS1L	chr16:70695106-70720110	metastasis suppressor 1-like	2.141	3.764
MTTP	chr4:100485239-100545154	microsomal triglyceride transfer protein	0.073	0.007
MTUS1	chr8:17501302-17658620	microtubule associated tumor suppressor 1	0.413	0.26
MUM1	chr19:1354950-1378430	melanoma associated antigen (mutated) 1	0.575	0.498
MUM1L1	chrX:105412297-105453017	melanoma associated antigen (mutated) 1-like 1	0.499	0.246
MUT	chr6:49398061-49431041	methylmalonyl-CoA mutase	0.388	0.22
MVK	chr12:109991520-110035071	mevalonate kinase	0.258	0.185
MXD1	chr2:70142172-70170076	MAX dimerization protein 1	2.518	4.911
MYADM	chr19:54369610-54379689	myeloid-associated differentiation marker	2.87	2.972
MYC	chr8:128748314-128753680	v-myc avian myelocytomatosis viral oncogene homolog	1.904	2.18
MYD88	chr3:38179291-38184513	myeloid differentiation primary response 88	0.505	0.309
MYH14	chr19:50706884-50813801	myosin, heavy chain 14, non-muscle	0.69	0.491
MYH9	chr22:36677320-36784063	myosin, heavy chain 9, non-muscle	3.069	5.511
MYL12B	chr18:3262110-3278282	myosin light chain 12B	0.628	0.386
MYL6B	chr12:56546203-56551771	myosin light chain 6B	0.458	0.358
MYLIP	chr6:16129316-16151258	myosin regulatory light chain interacting protein	1.387	2.142
MYLK	chr3:123304402-123603149	myosin light chain kinase	0.24	0.051
MYO15B	chr17:73584138-73663281	myosin XVB	0.321	0.13
MYO1D	chr17:30819627-31204123	myosin ID	1.936	3.069
MYO1E	chr15:59392743-59665083	myosin IE	1.765	3.017
MYO9B	chr19:17186590-17324104	myosin IXB	1.48	2.276
MYRF	chr11:61520088-61556188	myelin regulatory factor	0.944	0.403
NAALAD2	chr11:89867817-89926042	N-acetylated alpha-linked acidic dipeptidase 2	0.484	0.412
NABP1	chr2:192542707-192562133	nucleic acid binding protein 1	2.137	2.793
NANOS1	chr10:120789227-120794526	nanos homolog 1 (Drosophila)	2.035	2.96
NANS	chr9:100818958-100881488	N-acetylneuraminate synthase	1.717	2.699
NAT2	chr8:18244319-18258723	N-acetyltransferase 2 (arylamine N-acetyltransferase)	0.414	0.107
NAV1	chr1:201508360-201796102	neuron navigator 1	3.574	7.698
NAV2	chr11:19372270-20143147	neuron navigator 2	2.073	2.741
NBPF1	chr1:16793788-16976915	neuroblastoma breakpoint family member 15	2.26	3.357
NCALD	chr8:102698769-103137135	neurocalcin delta	0.524	0.233
NCAM1	chr11:112831968-113149158	neural cell adhesion molecule 1	5.652	11.79
NCAPD2	chr12:6601315-6641132	non-SMC condensin I complex subunit D2	0.531	0.412
NCAPG	chr4:17812435-18023483	non-SMC condensin I complex subunit G	0.707	0.182
NCAPG2	chr7:158423968-158497520	non-SMC condensin II complex subunit G2	0.797	0.33
NCDN	chr1:36023392-36032529	neurochondrin	1.347	2.157
NCF2	chr1:183524696-183560056	neutrophil cytosolic factor 2	4.615	3.955
NCK2	chr2:106361519-106510730	NCK adaptor protein 2	1.656	2.492
NCKAP5	chr2:133429371-134326069	NCK associated protein 5	0.605	0.069
NCOA2	chr8:71022002-71317651	nuclear receptor coactivator 2	0.625	0.468
NCOR1P1	chr20:26084051-26094677	nuclear receptor corepressor 1 pseudogene 1	1.499	2.158
NCS1	chr9:132934856-132999645	neuronal calcium sensor 1	2.233	3.313
NDC80	chr18:2571509-2616634	NDC80 kinetochore complex component	0.379	0.127
NDE1	chr16:15737123-15950887	nudE neurodevelopment protein 1	1.677	3.09
NDEL1	chr17:8339169-8371495	nudE neurodevelopment protein 1 like 1	1.797	2.751
NDRG1	chr8:134249413-134309547	N-myc downstream regulated 1	1.552	2.105
NDRG2	chr14:21484921-21493935	NDRG family member 2	0.313	0.125
NDUFA1	chrX:119004494-119010629	NADH:ubiquinone oxidoreductase subunit A1	0.515	0.368
NDUFA10	chr2:240896788-240964820	NADH:ubiquinone oxidoreductase subunit A10	0.637	0.42
NDUFA5	chr7:123181082-123197958	NADH:ubiquinone oxidoreductase subunit A5	0.638	0.445
NDUFA9	chr12:4758263-4796720	NADH:ubiquinone oxidoreductase subunit A9	0.535	0.276

NDUFB1	chr14:92582467-92588153	NADH:ubiquinone oxidoreductase subunit B1	0.547	0.402
NDUFB3	chr2:201838044-201950473	NADH:ubiquinone oxidoreductase subunit B3	0.559	0.422
NDUFB4	chr3:120315127-120321258	NADH:ubiquinone oxidoreductase subunit B4	0.602	0.451
NDUFB5	chr3:179322574-179342288	NADH:ubiquinone oxidoreductase subunit B5	0.492	0.363
NDUFS2	chr1:161169104-161184184	NADH:ubiquinone oxidoreductase core subunit S2	0.55	0.349
NDUFS3	chr11:47487488-47606116	NADH:ubiquinone oxidoreductase core subunit S3	0.534	0.371
NDUFV1	chr11:67374322-67380012	NADH:ubiquinone oxidoreductase core subunit V1	0.585	0.349
NDUFV2	chr18:9102627-9134343	NADH:ubiquinone oxidoreductase core subunit V2	0.613	0.436
NEAT1	chr11:65190268-65194003	nuclear paraspeckle assembly transcript 1 (non-protein coding)	1.502	2.25
NEBL	chr10:21068902-21463852	nebulette	4.568	7.193
NEIL3	chr4:178230990-178291191	nei like DNA glycosylase 3	0.73	0.212
NEK11	chr3:130745673-131100319	NIMA related kinase 11	1.529	2.341
NELFCD	chr20:57556262-57570188	negative elongation factor complex member C/D	0.656	0.36
NELL2	chr12:44902057-45342527	neural EGFL like 2	1.866	2.962
NET1	chr10:5454513-5501019	neuroepithelial cell transforming 1	0.41	0.21
NEU1	chr6:31826828-31830709	neuraminidase 1 (lysosomal sialidase)	1.829	2.768
NFE2L1	chr17:46125685-46139022	nuclear factor, erythroid 2 like 1	1.546	2.05
NFIA	chr1:61542945-61928460	nuclear factor I A	0.568	0.365
NFIL3	chr9:94171326-94187046	nuclear factor, interleukin 3 regulated	1.52	2.228
NFKB2	chr10:104153866-104162286	nuclear factor kappa B subunit 2	1.845	2.79
NFS1	chr20:34256609-34288902	NFS1 cysteine desulfurase	0.649	0.387
NGEF	chr2:233741396-233877976	neuronal guanine nucleotide exchange factor	0.175	0.14
NGFR	chr17:47572654-47592382	nerve growth factor receptor	10.29	35.37
NGFRAP1	chrX:102631267-102633002	brain expressed X-linked 3	0.55	0.354
NGRN	chr15:90808894-90815443	neugrin, neurite outgrowth associated	1.832	2.692
NHLRC3	chr13:39612447-39624564	NHL repeat containing 3	0.528	0.267
NHS	chrX:17393542-17754113	NHS actin remodeling regulator	1.524	2.895
NHSL1	chr6:138725335-139018519	NHS like 1	1.472	2.206
NIN	chr14:51186480-51298208	ninein	1.681	2.044
NIPSNAP1	chr22:29950797-29977326	nipsnap homolog 1 (C. elegans)	0.301	0.138
NIPSNAP3A	chr9:107509968-107522403	nipsnap homolog 3A	0.582	0.406
NIT2	chr3:99979660-100077124	nitrilase family member 2	0.606	0.371
NKD2	chr5:1009076-1038927	naked cuticle homolog 2	2.27	2.826
NKX3-1	chr8:23536205-23540450	NK3 homeobox 1	2.689	3.839
NNT	chr5:43571685-43705668	nicotinamide nucleotide transhydrogenase	0.581	0.296
NOS1AP	chr1:162039483-162356896	nitric oxide synthase 1 adaptor protein	0.343	0.238
NOTCH1	chr9:139388895-139440238	notch 1	1.13	2.427
NOXA1	chr9:140317833-140335901	NADPH oxidase activator 1	0.576	0.218
NOXO1	chr16:2021894-2037750	NADPH oxidase organizer 1	1.623	2.511
NPC1	chr18:21083433-21166937	Niemann-Pick disease, type C1	1.962	3.976
NPIP	chr16:15029230-15045931	nuclear pore complex interacting protein family member A1	1.748	2.714
NPR3	chr5:32710011-32791830	natriuretic peptide receptor 3	0.241	0.127
NPTX2	chr7:98246596-98259182	neuronal pentraxin 2	1.657	2.55
NPTXR	chr22:39214454-39240023	neuronal pentraxin receptor	3.017	5.879
NPY6R	chr5:137136881-137147602	neuropeptide Y receptor Y6 (pseudogene)	0.398	0.117
NQO1	chr16:69743303-69760533	NAD(P)H quinone dehydrogenase 1	0.139	0.077
NR1D2	chr3:23986750-24022109	nuclear receptor subfamily 1 group D member 2	1.613	2.497
NR1H4	chr12:100867550-100958177	nuclear receptor subfamily 1 group H member 4	0.285	0.039
NR1I2	chr3:119499330-119537651	nuclear receptor subfamily 1 group I member 2	0.184	0.029
NR1I3	chr1:161195562-161208000	nuclear receptor subfamily 1 group I member 3	0.136	0.033
NR2C1	chr12:95397609-95467452	nuclear receptor subfamily 2 group C member 1	0.669	0.414
NR2F6	chr19:17342693-17356348	nuclear receptor subfamily 2 group F member 6	0.537	0.413
NR4A1	chr12:52416615-52453291	nuclear receptor subfamily 4 group A member 1	3.26	4.587
NR5A2	chr1:199996729-200146550	nuclear receptor subfamily 5 group A member 2	0.373	0.199
NR6A1	chr9:127279363-127533577	nuclear receptor subfamily 6 group A member 1	1.472	2.074
NRF1	chr7:129251554-129396922	nuclear respiratory factor 1	4.22	4.893
NRG2	chr5:139124508-139423225	neuregulin 2	0.488	0.268
NRG4	chr15:76228317-76304789	neuregulin 4	0.309	0.171
NRP1	chr10:33466250-33624239	neuropilin 1	0.584	0.453
NRXN2	chr11:64373645-64490660	neurexin 2	0.132	0.044
NRXN3	chr14:78636715-80350650	neurexin 3	1.727	2.349
NSDHL	chrX:151995870-152037907	NAD(P) dependent steroid dehydrogenase-like	0.264	0.172
NSG1	chr4:4387982-4543775	neuron specific gene family member 1	0.279	0.199
NSMF	chr9:140339707-140353854	NMDA receptor synaptonuclear signaling and neuronal migration factor	1.779	2.52
NT5M	chr17:17206645-17250977	5',3'-nucleotidase, mitochondrial	1.927	2.405
NTHL1	chr16:2089815-2097867	nth-like DNA glycosylase 1	0.435	0.248
NTN1	chr17:8924858-9147317	netrin 1	1.749	4.046
NTN4	chr12:96043030-96189362	netrin 4	2.732	4.182
NTPCR	chr1:233086335-233114824	nucleoside-triphosphatase, cancer-related	0.531	0.31
NUBPL	chr14:32020110-32330429	nucleotide binding protein like	0.652	0.29
NUDT12	chr5:102877651-102898502	nudix hydrolase 12	0.736	0.379
NUDT13	chr10:74766979-74927853	nudix hydrolase 13	0.446	0.225
NUDT16	chr3:131100514-131107674	nudix hydrolase 16	0.301	0.186
NUDT4	chr12:93771700-93797024	nudix hydrolase 4	1.446	2.083
NUDT5	chr10:12171639-12292589	nudix hydrolase 5	0.652	0.433
NUDT7	chr16:77756388-77776180	nudix hydrolase 7	0.595	0.32
NUF2	chr1:163291722-163325553	NUF2, NDC80 kinetochore complex component	0.605	0.273
NUPL1	chr13:25875665-25916562	nucleoporin 58kDa	1.645	2.198
NXN	chr17:701510-883040	nucleoredoxin	1.654	2.507
OAF	chr11:120081472-120100651	out at first homolog	0.345	0.224
OAS2	chr12:113416203-113449528	2'-5'-oligoadenylate synthetase 2	0.41	0.195
OBSL1	chr2:220415333-220436952	obscurin-like 1	0.444	0.302
OCIAD2	chr4:48887395-48908940	OCIA domain containing 2	0.481	0.26
ODF2	chr9:131217433-131263636	outer dense fiber of sperm tails 2	2.011	3.148
OGDHL	chr10:50942600-50970425	oxoglutarate dehydrogenase-like	0.373	0.182
OGFRL1	chr6:71998377-72130579	opioid growth factor receptor-like 1	1.347	2.032
OGG1	chr3:9791627-9811668	8-oxoguanine DNA glycosylase	1.481	2.402
OLFM2	chr19:9964393-10047070	olfactomedin 2	0.665	0.317
OLFML3	chr1:114521659-114524875	olfactomedin like 3	0.102	0.029
OMA1	chr1:58946337-59012607	OMA1 zinc metallopeptidase	0.788	0.4
ONECUT1	chr15:53042094-53082353	one cut homeobox 1	0.159	0.051
OPLAH	chr8:145051319-145115633	5-oxoprolinase (ATP-hydrolysing)	0.65	0.417
ORAI1	chr12:122064454-122080980	ORAI calcium release-activated calcium modulator 1	2.311	4.627
OSBP2	chr22:31090108-31375380	oxysterol binding protein 2	2.098	4.14
OSBPL10	chr3:31702316-32033228	oxysterol binding protein like 10	2.591	2.382
OSBPL5	chr11:3105349-3186582	oxysterol binding protein like 5	0.346	0.277
OSGEPL1	chr2:190539171-190627924	O-sialoglycoprotein endopeptidase-like 1	0.689	0.336
OSMR	chr5:38845184-38935752	oncostatin M receptor	1.401	2.101
OTC	chrX:38208972-38282141	ornithine carbamoyltransferase	0.261	0.037
OTUD1	chr10:23728197-23731310	OTU deubiquitinase 1	1.897	3.368
OTUD3	chr1:20208887-20239440	OTU deubiquitinase 3	1.532	2.528
OTUD7A	chr15:31773191-31947542	OTU deubiquitinase 7A	1.843	3.485
OTX1	chr2:63277191-63284966	orthodenticle homeobox 1	0.715	0.47

OXA1L	chr14:23234798-23241638	oxidase (cytochrome c) assembly 1-like	0.674	0.482
OXNAD1	chr3:16306666-16555222	oxidoreductase NAD binding domain containing 1	0.535	0.425
P2RX5	chr17:3468739-3599698	purinergic receptor P2X 5	2.657	4.53
P2RX7	chr12:121570621-121625817	purinergic receptor P2X 7	1.967	3.013
P4HA2	chr5:131528259-131563556	prolyl 4-hydroxylase subunit alpha 2	2.263	2.928
PABPC4	chr1:40026483-40042555	poly(A) binding protein cytoplasmic 4	1.553	2.545
PACS1	chr11:65837823-66012218	phosphofurin acidic cluster sorting protein 1	1.718	2.552
PAFAH2	chr1:26282460-26335416	platelet activating factor acetylhydrolase 2	0.522	0.372
PAGE2B	chrX:55101488-55105336	PAGE family member 2	0.394	0.251
PAH	chr12:103232103-103311381	phenylalanine hydroxylase	0.304	0.027
PAK1	chr11:77032920-77185108	p21 protein (Cdc42/Rac)-activated kinase 1	0.617	0.295
PAK2	chr3:196433147-196559518	p21 protein (Cdc42/Rac)-activated kinase 2	1.699	2.122
PAMR1	chr11:35453375-35547176	peptidase domain containing associated with muscle regeneration 1	2.67	3.51
PANK1	chr10:91339253-91405329	pantothenate kinase 1	0.307	0.226
PAQR4	chr16:3019256-3030540	progestin and adipoQ receptor family member 4	2.701	2.946
PAQR5	chr15:69591238-69700405	progestin and adipoQ receptor family member 5	2.463	3.342
PARM1	chr4:75858284-75975325	prostate androgen-regulated mucin-like protein 1	1.607	2.309
PARP10	chr8:145051319-145115633	poly(ADP-ribose) polymerase family member 10	0.54	0.482
PARP14	chr3:122399671-122449687	poly(ADP-ribose) polymerase family member 14	0.646	0.359
PARP4	chr13:24995068-25086948	poly(ADP-ribose) polymerase family member 4	0.667	0.464
PARP9	chr3:122246759-122294049	poly(ADP-ribose) polymerase family member 9	0.592	0.314
PASK	chr2:242045468-242123064	PAS domain containing serine/threonine kinase	0.796	0.19
PAX8	chr2:113973549-114036498	paired box 8	2.024	4.524
PBK	chr8:27667137-27714062	PDZ binding kinase	0.487	0.148
PBX1	chr1:164528596-164821067	pre-B-cell leukemia homeobox 1	0.367	0.19
PBX2	chr6:32152509-32157963	pre-B-cell leukemia homeobox 2	0.536	0.325
PCBD1	chr10:72643266-72648541	pterin-4 alpha-carbinolamine dehydratase 1	0.712	0.455
PCCA	chr13:100740885-101241046	propionyl-CoA carboxylase alpha subunit	0.582	0.326
PCCB	chr3:135969166-136049013	propionyl-CoA carboxylase beta subunit	0.688	0.339
PCDH1	chr5:141230144-141258360	protocadherin 1	2.36	3.152
PCK1	chr20:56136136-56141513	phosphoenolpyruvate carboxykinase 1	0.016	0.002
PCSK6	chr15:101836893-102034233	proprotein convertase subtilisin/kexin type 6	0.531	0.246
PCSK9	chr1:55505148-55681039	proprotein convertase subtilisin/kexin type 9	0.192	0.168
PCYT2	chr17:79849593-79869371	phosphate cytidylyltransferase 2, ethanolamine	0.465	0.361
PDE10A	chr6:165740775-166078096	phosphodiesterase 10A	1.568	2.502
PDE11A	chr2:178487976-178973066	phosphodiesterase 11A	0.673	0.203
PDE1C	chr7:31790860-32338408	phosphodiesterase 1C	5.455	7.279
PDE5A	chr4:120375937-120549981	phosphodiesterase 5A	2.212	2.364
PDE7B	chr6:136172833-136516709	phosphodiesterase 7B	0.43	0.184
PDE8B	chr5:76476152-76788332	phosphodiesterase 8B	0.249	0.189
PDGFRB	chr5:149493401-149535422	platelet derived growth factor receptor beta	3.003	8.886
PDHX	chr11:34896795-35017675	pyruvate dehydrogenase complex component X	0.624	0.466
PDK2	chr17:48168199-48207246	pyruvate dehydrogenase kinase 2	0.436	0.268
PDK3	chrX:24483343-24568583	pyruvate dehydrogenase kinase 3	0.695	0.443
PDLIM2	chr8:22436253-22461662	PDZ and LIM domain 2	0.189	0.12
PDSS1	chr10:26986594-27150016	prenyl (decaprenyl) diphosphate synthase, subunit 1	0.557	0.269
PDZD3	chr11:119056163-119060932	PDZ domain containing 3	0.202	0.021
PDZK1	chr1:145726914-145764206	PDZ domain containing 1	0.188	0.028
PDZK1IP1	chr1:47649260-47655964	PDZK1 interacting protein 1	0.364	0.11
PEA15	chr1:160172204-160232394	phosphoprotein enriched in astrocytes 15	3.34	5.8
PEAK1	chr15:77400399-77712621	pseudopodium enriched atypical kinase 1	1.905	3.256
PEBP1	chr12:118573869-118583390	phosphatidylethanolamine binding protein 1	0.606	0.311
PEG10	chr7:94285636-94299008	paternally expressed 10	3.911	2.894
PEPD	chr19:33877854-34012799	peptidase D	0.51	0.387
PET112	chr4:152330326-152682179	glutamyl-tRNA(Gln) amidotransferase, subunit B	0.619	0.432
PEX11A	chr15:90224761-90234015	peroxisomal biogenesis factor 11 alpha	0.542	0.46
PEX3	chr6:143771917-143811751	peroxisomal biogenesis factor 3	0.607	0.383
PEX5	chr12:7341758-7371169	peroxisomal biogenesis factor 5	0.684	0.415
PEX7	chr6:137143701-137235072	peroxisomal biogenesis factor 7	0.685	0.398
PFKFB1	chrX:54946995-55026317	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	0.259	0.145
PFKM	chr12:48436407-48540441	phosphofructokinase, muscle	0.7	0.431
PGAP3	chr17:37827374-37884977	post-GPI attachment to proteins 3	0.598	0.363
PGBD5	chr1:230457391-230561674	piggyBac transposable element derived 5	2.14	3.266
PGC	chr6:41704448-41715139	progastricsin (pepsinogen C)	0.634	0.303
PGLYRP2	chr19:15579456-15591056	peptidoglycan recognition protein 2	0.28	0.089
PGM2L1	chr11:74041360-74109510	phosphoglucomutase 2-like 1	3.058	3.804
PGM3	chr6:83777372-83908586	phosphoglucomutase 3	1.522	2.424
PGM5	chr9:70970108-71145977	phosphoglucomutase 5	0.558	0.362
PHB	chr17:47481419-47492246	prohibitin	0.664	0.498
PHB2	chr12:7074514-7079916	prohibitin 2	0.584	0.451
PHF17	chr4:129730778-129796379	jade family PHD finger 1	0.554	0.465
PHGDH	chr1:120254418-120286849	phosphoglycerate dehydrogenase	3.226	4.733
PHKA2	chrX:18908413-19003085	phosphorylase kinase, alpha 2 (liver)	0.461	0.345
PHKB	chr16:47189273-47735440	phosphorylase kinase beta subunit	0.631	0.447
PHLDA1	chr12:76419226-76425556	pleckstrin homology like domain family A member 1	5.284	7.611
PHLDA2	chr11:2949502-2950650	pleckstrin homology like domain family A member 2	2.496	3.386
PHLDA3	chr1:201434606-201438299	pleckstrin homology like domain family A member 3	1.744	2.969
PHYHD1	chr9:131683173-131704320	phytanoyl-CoA dioxygenase domain containing 1	0.422	0.205
PI15	chr8:75729565-75767264	peptidase inhibitor 15	0.633	0.398
PI3	chr20:43803539-43805185	peptidase inhibitor 3	0.299	0.105
PIAS1	chr15:68346571-68522080	protein inhibitor of activated STAT 1	0.626	0.489
PICK1	chr22:38453261-38472114	protein interacting with PRKCA 1	0.679	0.445
PIEZO1	chr16:88762902-88851618	piezo type mechanosensitive ion channel component 1	2.45	4.252
PIEZO2	chr18:10670184-11149596	piezo type mechanosensitive ion channel component 2	0.631	0.329
PIGB	chr15:55609259-55800432	phosphatidylinositol glycan anchor biosynthesis class B	0.407	0.219
PIGK	chr1:77554666-77685132	phosphatidylinositol glycan anchor biosynthesis class K	0.653	0.377
PIGN	chr18:59711457-59854313	phosphatidylinositol glycan anchor biosynthesis class N	0.607	0.418
PIGR	chr1:207101866-207119811	polymeric immunoglobulin receptor	0.664	0.101
PIK3AP1	chr10:98353067-98480279	phosphoinositide-3-kinase adaptor protein 1	0.328	0.18
PIK3C2G	chr12:18395539-18890993	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma	0.194	0.004
PIK3IP1	chr22:31677419-31688520	phosphoinositide-3-kinase interacting protein 1	0.694	0.383
PIK3R2	chr19:18263987-18281343	phosphoinositide-3-kinase regulatory subunit 2	1.649	2.249
PIK3R3	chr1:46505811-46598984	phosphoinositide-3-kinase regulatory subunit 3	2.717	4.708
PIN4	chrX:71401199-71528334	peptidylprolyl cis/trans isomerase, NIMA-interacting 4	0.689	0.493
PIP4K2A	chr10:22823765-23003509	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha	1.551	2.546
PIPOX	chr17:27280400-27384367	pipecolic acid and sarcosine oxidase	0.159	0.029
PITPNA	chr17:1420212-1466110	phosphatidylinositol transfer protein alpha	1.564	2.029
PITPNC1	chr17:65373396-65693379	phosphatidylinositol transfer protein, cytoplasmic 1	2.47	4.098
PKD1	chr16:2097989-2185899	polycystin 1, transient receptor potential channel interacting	1.943	3.722
PKD1P1	chr16:16410664-16477549	polycystin 1, transient receptor potential channel interacting pseudogene 1	1.702	2.485
PKIA	chr8:79428335-79517827	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	2.04	2.752
PKLR	chr1:155247201-155271225	pyruvate kinase, liver and RBC	0.214	0.17
PKN3	chr9:131464801-131486408	protein kinase N3	0.679	0.231

PKP2	chr12:32943679-33049780	plakophilin 2	0.524	0.277
PLA1A	chr3:119316694-119348658	phospholipase A1 member A	0.661	0.158
PLA2G12B	chr10:74694325-74714673	phospholipase A2 group XIIB	0.059	0.009
PLA2G15	chr16:68278944-68294961	phospholipase A2 group XV	1.289	2.245
PLA2G16	chr11:63334381-63381990	phospholipase A2 group XVI	0.594	0.451
PLA2G1B	chr12:120759913-120765592	phospholipase A2 group IB	0.41	0.001
PLA2G2A	chr1:20301923-20306932	phospholipase A2 group IIA	0.854	0.346
PLA2G4A	chr1:186798031-186958113	phospholipase A2 group IVA	0.49	0.242
PLA2G4C	chr19:48551099-48614109	phospholipase A2 group IVC	1.708	2.136
PLAC8L1	chr5:145463875-145483946	PLAC8-like 1	1.296	3.425
PLCB1	chr20:8095207-8865547	phospholipase C beta 1	0.583	0.411
PLCD3	chr17:43189007-43229712	phospholipase C delta 3	1.486	2.478
PLCXD3	chr5:41307047-41510730	phosphatidylinositol specific phospholipase C X domain containing 3	0.81	0.466
PLD5	chr1:242251385-242687998	phospholipase D family member 5	3.677	8.174
PLD6	chr17:17104308-17109724	phospholipase D family member 6	1.323	2.538
PLEKHA6	chr1:204187978-204347655	pleckstrin homology domain containing A6	0.601	0.459
PLEKHA7	chr11:16798774-17036109	pleckstrin homology domain containing A7	0.519	0.309
PLEKHA8	chr7:30067976-30157961	pleckstrin homology domain containing A8	1.765	2.273
PLEKHG1	chr6:150920990-151164799	pleckstrin homology and RhoGEF domain containing G1	2.354	3.718
PLEKHG5	chr1:6484847-6580121	pleckstrin homology and RhoGEF domain containing G5	0.494	0.425
PLEKHH1	chr14:67999831-68067017	pleckstrin homology, MyTH4 and FERM domain containing H1	1.686	2.547
PLEKHH2	chr2:43864409-44001122	pleckstrin homology, MyTH4 and FERM domain containing H2	2.168	3.648
PLG	chr6:161123224-161175085	plasminogen	0.634	0.164
PLGLB2	chr2:88047605-88285309	plasminogen-like B2	0.133	0.063
PLIN2	chr9:19108423-19127604	perilipin 2	1.824	3.99
PLIN3	chr19:4838345-4867780	perilipin 3	0.561	0.452
PLK3	chr1:45266035-45452394	polo like kinase 3	1.714	2.674
PLS1	chr3:142315228-142432505	plastin 1	0.781	0.391
PLS3	chrX:114795176-114885179	plastin 3	0.69	0.403
PLVAP	chr19:17462263-17488694	plasmalemma vesicle associated protein	1.249	2.445
PLXNA1	chr3:126701928-126756235	plexin A1	3.064	4.92
PLXNA2	chr1:208195587-208417760	plexin A2	1.795	2.373
PLXNA3	chrX:153686505-153703594	plexin A3	3.483	5.808
PLXNB1	chr3:48444792-48471785	plexin B1	0.508	0.296
PLXNC1	chr12:94519704-94853764	plexin C1	0.632	0.347
PMAIP1	chr18:57567191-57571538	phorbol-12-myristate-13-acetate-induced protein 1	4.868	7.613
PMCHL2	chr5:70648324-70741726	pro-melanin concentrating hormone like 2 (pseudogene)	0.253	0.01
PMEPA1	chr20:56223447-56286592	prostate transmembrane protein, androgen induced 1	4.545	14.45
PNKD	chr2:219135114-219211516	paroxysmal nonkinesigenic dyskinesia	0.534	0.323
PNMA1	chr14:74178485-74181128	paraneoplastic Ma antigen 1	2.266	3.692
PNPLA3	chr22:44319614-44347393	patatin like phospholipase domain containing 3	0.352	0.205
PNPLA7	chr9:140354404-140445159	patatin like phospholipase domain containing 7	0.498	0.384
PNPO	chr17:46018888-46026674	pyridoxamine 5'-phosphate oxidase	0.563	0.425
PODXL	chr7:131185020-131241376	podocalyxin like	2.477	4.677
POLE2	chr14:50110269-50155098	polymerase (DNA) epsilon 2, accessory subunit	0.789	0.089
POLE4	chr2:75150546-75196859	polymerase (DNA) epsilon 4, accessory subunit	1.862	2.189
POLG	chr15:89787193-89878078	polymerase (DNA) gamma, catalytic subunit	1.632	2.099
PON1	chr7:94927668-94953884	paraoxonase 1	0.294	0.069
PON2	chr7:94989022-95064386	paraoxonase 2	0.496	0.223
PON3	chr7:94989022-95064386	paraoxonase 3	0.658	0.383
POP1	chr8:99129520-99197727	POP1 homolog, ribonuclease P/MRP subunit	0.498	0.202
POPDC2	chr3:119360907-119379404	popeye domain containing 2	2.846	5.346
POSTN	chr13:38136718-38172981	periostin, osteoblast specific factor	0.263	0.263
POU3F3	chr2:105421882-105475008	POU class 3 homeobox 3	0.614	0.387
POU5F1	chr6:31132113-31138451	POU class 5 homeobox 1	0.478	0.252
PPA2	chr4:106290233-106395267	pyrophosphatase (inorganic) 2	0.622	0.412
PPAP2B	chr1:56960418-57045257	phospholipid phosphatase 3	0.472	0.345
PPARD	chr6:35310329-35395968	peroxisome proliferator activated receptor delta	1.744	2.613
PPARG	chr3:12329348-12512396	peroxisome proliferator activated receptor gamma	1.65	2.048
PPARGC1A	chr4:23793622-23891700	PPARG coactivator 1 alpha	0.303	0.255
PPARGC1B	chr5:149109814-149234585	PPARG coactivator 1 beta	0.578	0.416
PPCS	chr1:42922172-42926086	phosphopantothenoylcysteine synthetase	0.647	0.448
PPDPF	chr20:62152121-62168882	pancreatic progenitor cell differentiation and proliferation factor	1.703	2.255
PPFIA1	chr11:70116805-70230607	PTPRF interacting protein alpha 1	1.685	2.874
PPIG	chr2:170440608-170497917	peptidylprolyl isomerase G	0.729	0.492
PPIL6	chr6:109711417-109777399	peptidylprolyl isomerase like 6	2.966	4.316
PPM1E	chr17:56833229-57184266	protein phosphatase, Mg2+/Mn2+ dependent 1E	4.244	6.885
PPM1J	chr1:113252227-113257950	protein phosphatase, Mg2+/Mn2+ dependent 1J	2.637	3.217
PPM1L	chr3:160470433-160797016	protein phosphatase, Mg2+/Mn2+ dependent 1L	1.497	2.537
PPP1R14C	chr6:150464187-150571528	protein phosphatase 1 regulatory inhibitor subunit 14C	2.757	3.146
PPP1R14D	chr15:41107642-41120907	protein phosphatase 1 regulatory inhibitor subunit 14D	0.172	0.018
PPP1R15A	chr19:49375648-49379319	protein phosphatase 1 regulatory subunit 15A	6.704	16.72
PPP1R16A	chr8:145703320-145728924	protein phosphatase 1 regulatory subunit 16A	0.403	0.317
PPP1R1A	chr12:54973023-54982443	protein phosphatase 1 regulatory inhibitor subunit 1A	0.41	0.448
PPP1R1C	chr2:182818967-182996109	protein phosphatase 1 regulatory inhibitor subunit 1C	0.344	0.169
PPP1R3B	chr8:8993763-9009152	protein phosphatase 1 regulatory subunit 3B	0.427	0.482
PPP1R3F	chrX:49126305-49144648	protein phosphatase 1 regulatory subunit 3F	1.381	2.051
PPP1R7	chr2:242045468-242123064	protein phosphatase 1 regulatory subunit 7	0.539	0.376
PPP2R4	chr9:131873227-131911404	protein phosphatase 2A regulatory subunit 4	0.61	0.458
PQLC2	chr1:19638739-19655856	PQ loop repeat containing 2	1.682	2.231
PRCD	chr17:74523429-74553748	progressive rod-cone degeneration	0.2	0.252
PRDM10	chr11:129769497-129875381	PR domain 10	0.753	0.438
PRDM16	chr1:2985576-3355185	PR domain 16	5.356	9.46
PRDM2	chr1:14026734-14151574	PR domain 2	1.579	2.461
PRDM4	chr12:108126642-108154980	PR domain 4	1.742	2.806
PRDX2	chr19:12907633-12912694	peroxiredoxin 2	0.76	0.41
PRDX3	chr10:120927214-120938345	peroxiredoxin 3	0.716	0.454
PREX2	chr8:68864602-69146468	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 2	0.517	0.268
PRG4	chr1:185703497-186446655	proteoglycan 4	0.689	0.165
PRICKLE1	chr12:42851031-42983572	prickle planar cell polarity protein 1	1.542	2.223
PRICKLE2	chr3:64053639-64253822	prickle planar cell polarity protein 2	0.565	0.45
PRKAG2	chr7:151253200-151576308	protein kinase AMP-activated non-catalytic subunit gamma 2	0.263	0.27
PRKAR2B	chr7:106685177-106802256	protein kinase cAMP-dependent type II regulatory subunit beta	0.146	0.095
PRKCA	chr17:64298734-64806862	protein kinase C alpha	1.997	3.37
PRLR	chr5:35048860-35231055	prolactin receptor	0.43	0.341
PRMT2	chr21:48055506-48085155	protein arginine methyltransferase 2	2.013	3.053
PRNP	chr20:4666796-4682234	prion protein	2.365	3.481
PRODH	chr22:18892275-18924066	proline dehydrogenase 1	0.228	0.221
PRODH2	chr19:36283214-36304201	proline dehydrogenase 2	0.303	0.058
PROS1	chr3:93591880-93692934	protein S (alpha)	0.577	0.445
PROSER1	chr13:39584001-39612213	proline and serine rich 1	1.581	2.167
PROX1	chr1:214161163-214214847	prospero homeobox 1	0.38	0.164
PRRC2B	chr9:134269379-134375802	proline rich coiled-coil 2B	1.61	2.406

PRRG4	chr11:32851350-32879669	proline rich and Gla domain 4	0.763	0.239
PRUNE2	chr9:79226291-79521056	prune homolog 2 (Drosophila)	1.419	2.095
PRX	chr19:40899670-40919271	periaxin	2.072	3.41
PSAT1	chr9:80912058-80945009	phosphoserine aminotransferase 1	10.07	17.65
PSCA	chr8:143738566-143764145	prostate stem cell antigen	0.591	0.32
PSD3	chr8:18384812-18871204	pleckstrin and Sec7 domain containing 3	2.144	3.748
PSD4	chr2:113915020-113962516	pleckstrin and Sec7 domain containing 4	0.651	0.347
PSMB1	chr6:170844203-170863248	proteasome subunit beta 1	0.663	0.487
PSMB10	chr16:67966395-67970780	proteasome subunit beta 10	0.553	0.345
PSORS1C3	chr6:31139415-31149542	psoriasis susceptibility 1 candidate 3 (non-protein coding)	0.458	0.2
PSPH	chr7:56077890-56119268	phosphoserine phosphatase	2.04	2.566
PSRC1	chr1:109822175-109825821	proline and serine rich coiled-coil 1	0.445	0.391
PSTPIP2	chr18:43563501-43652399	proline-serine-threonine phosphatase interacting protein 2	0.547	0.24
PTCD3	chr2:86333304-86369359	pentatricopeptide repeat domain 3	0.609	0.427
PTCHD3P1	chr10:29469247-29717029	patched domain containing 3 pseudogene 1	1.602	2.237
PTCHD4	chr6:47824556-48078994	patched domain containing 4	0.383	0.383
PTGR1	chr9:114287446-114362135	prostaglandin reductase 1	0.332	0.079
PTHLH	chr12:28111016-28124916	parathyroid hormone-like hormone	4.145	4.632
PTPLAD1	chr15:65822800-65870695	3-hydroxyacyl-CoA dehydratase 3	0.838	0.489
PTPN12	chr7:77166772-77269388	protein tyrosine phosphatase, non-receptor type 12	2.074	2.876
PTPN14	chr1:214522038-214725401	protein tyrosine phosphatase, non-receptor type 14	1.683	2.622
PTPN3	chr9:112137781-112260593	protein tyrosine phosphatase, non-receptor type 3	0.95	0.376
PTPN6	chr12:7055596-7070479	protein tyrosine phosphatase, non-receptor type 6	0.619	0.26
PTPRJ	chr11:48002109-48192394	protein tyrosine phosphatase, receptor type J	1.77	2.823
PTPRN2	chr7:157331748-158380482	protein tyrosine phosphatase, receptor type N2	0.537	0.288
PTPRQ	chr12:80837614-81073968	protein tyrosine phosphatase, receptor type Q	0.154	0.128
PTX3	chr3:156977531-157221415	pentraxin 3	3.279	7.633
PUS10	chr2:61108627-61365169	pseudouridylate synthase 10	0.26	0.175
PUS7	chr7:105096588-105162722	pseudouridylate synthase 7 (putative)	1.907	2.437
PVRL1	chr11:119508807-119599435	nectin cell adhesion molecule 1	2.574	4.456
PXK	chr3:58318611-58413032	PX domain containing serine/threonine kinase like	1.654	2.159
PXMP2	chr12:133264012-133281577	peroxisomal membrane protein 2	0.551	0.295
QDPR	chr4:17488015-17513857	quinoid dihydropteridine reductase	0.654	0.388
QPRT	chr16:29690237-29710022	quinolinate phosphoribosyltransferase	0.233	0.126
RAB17	chr2:238482962-238500223	RAB17, member RAS oncogene family	0.237	0.042
RAB20	chr13:111173300-111214125	RAB20, member RAS oncogene family	0.643	0.445
RAB23	chr6:56954807-57087083	RAB23, member RAS oncogene family	1.748	2.307
RAB37	chr17:72667255-72743474	RAB37, member RAS oncogene family	0.341	0.245
RAB3IL1	chr11:61664767-61687741	RAB3A interacting protein like 1	2.617	4.209
RAB8A	chr19:16222489-16244445	RAB8A, member RAS oncogene family	0.572	0.383
RABEPK	chr9:127962779-127996438	Rab9 effector protein with kelch motifs	0.494	0.435
RABL3	chr3:120405517-120461384	RAB, member of RAS oncogene family like 3	0.47	0.324
RAD51AP1	chr12:4647949-4669213	RAD51 associated protein 1	0.892	0.134
RALGPS1	chr9:129677052-129985445	Ral GEF with PH domain and SH3 binding motif 1	1.298	2.162
RALY	chr20:32581299-32700091	RALY heterogeneous nuclear ribonucleoprotein	1.57	2.39
RANBP1	chr22:20105023-20114877	RAN binding protein 1	0.749	0.39
RANGAP1	chr22:41641614-41682216	Ran GTPase activating protein 1	1.846	2.552
RAP1GAP2	chr17:2699731-2941036	RAP1 GTPase activating protein 2	2.797	4.047
RAP2A	chr13:98077191-98120252	RAP2A, member of RAS oncogene family	1.806	2.009
RAPGEF1	chr9:134431362-134615264	Rap guanine nucleotide exchange factor 1	2.057	2.972
RAPGEF4	chr2:173587917-173917620	Rap guanine nucleotide exchange factor 4	0.425	0.193
RAPH1	chr2:204298359-204400058	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	2.303	3.971
RARRES1	chr3:158414771-158450499	retinoic acid receptor responder 1	0.581	0.256
RARRES3	chr11:63014620-63330855	retinoic acid receptor responder 3	0.547	0.215
RASA4	chr7:102220092-102257205	RAS p21 protein activator 4	1.224	2.479
RASD1	chr17:17397752-17399709	ras related dexamethasone induced 1	10.77	12.52
RASD2	chr22:35937351-35950045	RASD family member 2	3.061	6.808
RASSF1	chr3:50367216-50378367	Ras association domain family member 1	1.651	2.757
RASSF4	chr10:45306471-45490173	Ras association domain family member 4	0.58	0.298
RASSF6	chr4:74437266-74486348	Ras association domain family member 6	0.874	0.196
RASSF7	chr11:532198-564025	Ras association domain family member 7	0.641	0.442
RASSF8	chr12:26097760-26232825	Ras association domain family member 8	1.447	2.211
RASSF9	chr12:86107052-86276770	Ras association domain family member 9	0.555	0.246
RBCK1	chr20:388683-412762	RANBP2-type and C3HC4-type zinc finger containing 1	1.735	2.484
RBKS	chr2:28004265-28561767	ribokinase	0.352	0.201
RBL2	chr16:53468350-53537170	retinoblastoma-like 2	0.555	0.371
RBM38	chr20:55904830-55998278	RNA binding motif protein 38	2.006	2.536
RBM45	chr2:178977159-179003552	RNA binding motif protein 45	0.662	0.403
RBM47	chr4:40425271-40632519	RNA binding motif protein 47	0.323	0.15
RBM6	chr3:49946301-50114685	RNA binding motif protein 6	1.4	2.03
RBMS3	chr3:29322679-30051886	RNA binding motif single stranded interacting protein 3	0.435	0.327
RBP1	chr3:139236275-139258671	retinol binding protein 1	0.949	0.291
RBP4	chr10:95351592-95360993	retinol binding protein 4	0.715	0.155
RBP5	chr12:7247145-7311530	retinol binding protein 5	0.172	0.056
RCAN2	chr6:46188466-46459804	regulator of calcineurin 2	2.303	2.84
RCC1	chr1:28832454-28870516	regulator of chromosome condensation 1	2.04	3.049
RCN1	chr11:32110308-32127272	reticulocalbin 1	1.675	2.261
RCN3	chr19:50030062-50046890	reticulocalbin 3	0.169	0.066
RCOR1	chr14:103058973-103196913	REST corepressor 1	1.662	2.429
RDH16	chr12:57345215-57351418	retinol dehydrogenase 16 (all-trans)	0.072	0.069
RELB	chr19:45504706-45541645	RELB proto-oncogene, NF-kB subunit	2.393	4.541
RELL2	chr5:141016511-141030986	RELT like 2	2.631	3.507
RELT	chr11:73087404-73108903	RELT tumor necrosis factor receptor	4.532	8.136
RFESD	chr5:94982456-95018714	Rieske Fe-S domain containing	1.856	2.587
RFK	chr9:79000432-79009456	riboflavin kinase	1.721	2.808
RFX2	chr19:5978413-6110664	regulatory factor X2	5.833	15.26
RFX3	chr9:3218379-3525989	regulatory factor X3	1.797	2.405
RFX5	chr1:151313114-151319769	regulatory factor X5	0.739	0.419
RGMB	chr5:98104998-98132198	repulsive guidance molecule family member b	1.848	3.033
RGN	chrX:46937595-46953067	regucalcin	0.225	0.039
RGPD1	chr2:88047605-88285309	RANBP2-like and GRIP domain containing 5	0.18	0.022
RGS14	chr5:176784654-176799599	regulator of G-protein signaling 14	0.496	0.405
RGS16	chr1:182567757-182573548	regulator of G-protein signaling 16	6.437	21.48
RGS3	chr9:116207008-116360023	regulator of G-protein signaling 3	0.577	0.302
RHBDD1	chr2:227700670-228179508	rhomboid domain containing 1	1.73	2.411
RHBDD2	chr7:75508316-75518244	rhomboid domain containing 2	1.942	2.666
RHCE	chr1:25664788-25747363	Rh blood group D antigen	2.231	3.452
RHEBL1	chr12:49458467-49463775	Ras homolog enriched in brain like 1	5.031	11.02
RHOBTB2	chr8:22844929-22941132	Rho related BTB domain containing 2	1.553	3.246
RIC3	chr11:8060179-8190590	RIC3 acetylcholine receptor chaperone	0.577	0.352
RILPL2	chr12:123894638-123921494	Rab interacting lysosomal protein like 2	0.621	0.49
RIMS3	chr1:41086351-41131324	regulating synaptic membrane exocytosis 3	1.624	2.333
RIN2	chr20:19780289-19983103	Ras and Rab interactor 2	0.443	0.361

RMDN2	chr2:38152332-38294285	regulator of microtubule dynamics 2	0.501	0.364
RND1	chr12:49250915-49259653	Rho family GTPase 1	1.087	0.409
RND3	chr2:151324706-151344209	Rho family GTPase 3	2.805	3.616
RNF122	chr8:33405272-33424643	ring finger protein 122	2.159	4.324
RNF125	chr18:29598440-29653154	ring finger protein 125, E3 ubiquitin protein ligase	0.585	0.386
RNF128	chrX:105937067-106040246	ring finger protein 128, E3 ubiquitin protein ligase	0.766	0.45
RNF165	chr18:43914186-44043090	ring finger protein 165	1.371	2.403
RNF187	chr1:228674580-228686224	ring finger protein 187	2.201	3.018
RNF19B	chr1:33399716-33430491	ring finger protein 19B	2.127	3.133
RNF24	chr20:3827445-3996294	ring finger protein 24	3.128	5.382
RNF43	chr17:56378587-56494931	ring finger protein 43	0.312	0.109
RNF5	chr6:32146161-32148570	ring finger protein 5	0.431	0.218
RNPS1	chr16:2303086-2318451	RNA binding protein with serine rich domain 1	1.545	2.235
ROBO1	chr3:78646251-79817059	roundabout guidance receptor 1	2.017	3.156
ROBO2	chr3:77089293-77699114	roundabout guidance receptor 2	1.993	3.444
ROGDI	chr16:4846962-4852951	rogdi homolog	1.676	2.157
ROR2	chr9:94484821-94712444	receptor tyrosine kinase like orphan receptor 2	1.401	2.173
RORC	chr1:151778546-151826173	RAR related orphan receptor C	0.178	0.073
ROS1	chr6:117608513-117747520	ROS proto-oncogene 1, receptor tyrosine kinase	0.535	0.317
RP9P	chr7:32956042-32983010	retinitis pigmentosa 9 pseudogene	2.198	3.213
RPH3AL	chr17:54477-236030	rabphilin 3A-like (without C2 domains)	0.625	0.268
RPL23AP64	chr11:118868851-118889057	ribosomal protein L23a pseudogene 64	0.607	0.398
RPL28	chr19:55895922-55919325	ribosomal protein L28	1.449	2.169
RPL36	chr19:5690271-5691678	ribosomal protein L36	1.543	2.341
RPP25	chr15:75247442-75249775	ribonuclease P/MRP subunit p25	1.608	2.247
RPS6KA2	chr6:166822853-167275771	ribosomal protein S6 kinase A2	2.15	3.92
RRAD	chr16:66955581-66959439	Ras-related associated with diabetes	3.807	3.933
RRM1	chr11:4115923-4160106	ribonucleotide reductase catalytic subunit M1	0.74	0.266
RRM2	chr2:10260965-10271546	ribonucleotide reductase regulatory subunit M2	0.566	0.023
RRP7A	chr22:42896584-42915829	ribosomal RNA processing 7 homolog A	1.75	3.081
RSPH3	chr6:159309618-159421848	radial spoke 3 homolog	1.468	2.291
RTEL1	chr20:62289162-62370906	regulator of telomere elongation helicase 1	0.865	0.437
RTN2	chr19:45988144-46030240	reticulon 2	2.935	4.88
RTN3	chr11:63448921-63527363	reticulon 3	1.632	2.029
RTN4	chr2:55199321-55277734	reticulon 4	1.605	2.322
RTN4IP1	chr6:106959632-107077374	reticulon 4 interacting protein 1	0.474	0.238
RTN4R	chr22:20228937-20255816	reticulon 4 receptor	2.39	5.367
RTP4	chr3:187086167-187089369	receptor (chemosensory) transporter protein 4	0.198	0.048
RUNDC3A	chr17:42367721-42396038	RUN domain containing 3A	1.545	2.759
RUNX1	chr21:36160097-36421595	runt related transcription factor 1	2.383	3.969
RUNX2	chr6:44776944-45518819	runt related transcription factor 2	1.851	2.415
RUSC2	chr9:35489318-35563896	RUN and SH3 domain containing 2	2.288	3.276
RXRA	chr9:137218315-137332571	retinoid X receptor alpha	0.586	0.431
RYBP	chr3:72423743-72495774	RING1 and YY1 binding protein	2.279	4.598
S100A11	chr1:152004981-152009511	S100 calcium binding protein A11	1.99	3.071
S100A2	chr1:153533584-153538306	S100 calcium binding protein A2	0.314	0.243
S100A3	chr1:153519808-153521734	S100 calcium binding protein A3	0.35	0.115
S100A4	chr1:153516094-153518282	S100 calcium binding protein A4	0.698	0.468
S100A8	chr1:153362507-153363664	S100 calcium binding protein A8	0.385	0.316
SAA1	chr11:18287807-18291523	serum amyloid A1	0.478	0.155
SAA2	chr11:18252901-18270221	serum amyloid A2	0.431	0.192
SACS	chr13:23902876-24007841	sacsin molecular chaperone	2.543	3.396
SALL1	chr16:51169885-51186152	spalt-like transcription factor 1	0.603	0.46
SAMD4A	chr14:55032697-55260033	sterile alpha motif domain containing 4A	1.878	2.356
SAMD4B	chr19:39833107-39891204	sterile alpha motif domain containing 4B	1.55	2.816
SAMM50	chr22:44351260-44392412	SAMM50 sorting and assembly machinery component	0.407	0.239
SARDH	chr9:136526468-136605077	sarcosine dehydrogenase	0.096	0.035
SARS	chr1:109756514-109780804	seryl-tRNA synthetase	1.856	2.222
SARS2	chr19:39405903-39423659	seryl-tRNA synthetase 2, mitochondrial	0.663	0.304
SASS6	chr1:100549101-100598511	SAS-6 centriolar assembly protein	1.063	0.494
SAT1	chrX:23801274-23804327	spermidine/spermine N1-acetyltransferase 1	2.089	2.906
SCFD2	chr4:53656160-54232242	sec1 family domain containing 2	0.494	0.196
SCG5	chr15:32933869-32989298	secretogranin V	1.906	2.617
SCGB1D2	chr11:62009723-62012280	secretoglobin, family 1D member 2	0.447	0.139
SCGN	chr6:25652428-25702011	secretagogin, EF-hand calcium binding protein	0.281	0.033
SCN3B	chr11:123499894-123525315	sodium voltage-gated channel beta subunit 3	4.288	9.694
SCN9A	chr2:167051696-167232497	sodium voltage-gated channel alpha subunit 9	1.627	2.108
SCNN1A	chr12:6454433-6500737	sodium channel epithelial 1 alpha subunit	0.432	0.301
SCP2	chr1:53392900-53517289	sterol carrier protein 2	0.332	0.142
SCRN3	chr2:175212877-175295175	secernin 3	0.597	0.421
SCTR	chr2:120189407-120282028	secretin receptor	0.242	0.072
SDC1	chr2:20400553-20425194	syndecan 1	0.536	0.38
SDCCAG3	chr9:139296373-139305054	serologically defined colon cancer antigen 3	1.545	2.473
SDHA	chr5:218355-256814	succinate dehydrogenase complex flavoprotein subunit A	0.75	0.395
SDHB	chr1:17345224-17380665	succinate dehydrogenase complex iron sulfur subunit B	0.609	0.414
SDHC	chr1:161284165-161340702	succinate dehydrogenase complex subunit C	0.652	0.413
SDHD	chr11:111957570-111966518	succinate dehydrogenase complex subunit D	0.574	0.43
SDK1	chr7:3341079-4308631	sidekick cell adhesion molecule 1	0.144	0.011
SDPR	chr2:192699031-192712006	serum deprivation response	0.352	0.086
SDS	chr12:113830250-113841738	serine dehydratase	0.403	0.072
SDSL	chr12:113860039-113876096	serine dehydratase like	0.81	0.452
SEC16B	chr1:177897800-177942446	SEC16 homolog B, endoplasmic reticulum export factor	0.295	0.073
SEC23A	chr14:39501122-39572538	Sec23 homolog A, coat complex II component	0.491	0.324
SEC61A1	chr3:127771211-127790526	Sec61 translocon alpha 1 subunit	1.611	2.457
SELENBP1	chr1:151336776-151345210	selenium binding protein 1	0.258	0.094
SELL	chr1:169659805-169681113	selectin L	0.308	0.092
SELPLG	chr12:109015679-109030486	selectin P ligand	5.462	15.41
SELRC1	chr1:53150053-53174145	cytochrome c oxidase assembly factor 7 (putative)	0.601	0.379
SEMA3C	chr7:80371853-80548667	semaphorin 3C	1.396	2.584
SEMA3E	chr7:82992353-83278479	semaphorin 3E	0.535	0.414
SEMA3F	chr3:50192509-50235129	semaphorin 3F	0.076	2.791
SEMA4B	chr15:90727951-90772892	semaphorin 4B	0.466	0.327
SEMA4C	chr2:97525472-97535735	semaphorin 4C	0.561	0.421
SEMA4G	chr10:102729256-102747272	semaphorin 4G	0.237	0.122
SENP7	chr3:101043117-101232251	SUMO1/sentrin specific peptidase 7	0.591	0.335
SEPP1	chr5:42756919-42812024	selenoprotein P, plasma, 1	0.372	0.189
SEPSECS	chr4:25121626-25162266	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.633	0.443
SEPT4	chr17:56597610-56618179	septin 4	0.294	0.245
SEPT6	chrX:118749687-118827333	septin 6	0.501	0.388
SERAC1	chr6:158530477-158589312	serine active site containing 1	1.784	2.263
SERP1	chr3:150259779-150321006	stress-associated endoplasmic reticulum protein 1	1.624	2.591
SERPINA1	chr14:94843083-94857029	serpin family A member 1	0.715	0.186
SERPINA10	chr14:94640633-94763483	serpin family A member 10	0.089	0.016

SERPINA3	chr14:95078643-95090395	serpin family A member 3	0.472	0.104
SERPINA4	chr14:95027771-95036243	serpin family A member 4	0.442	0.075
SERPINA5	chr14:95047705-95065282	serpin family A member 5	0.363	0.236
SERPINA6	chr14:94770584-94789693	serpin family A member 6	0.382	0.056
SERPINA7	chrX:105259681-105282739	serpin family A member 7	0.232	0.047
SERPINB8	chr18:61637262-61656608	serpin family B member 8	1.678	2.275
SERPINC1	chr1:173872941-173886516	serpin family C member 1	0.682	0.148
SERPIND1	chr22:21061976-21245501	serpin family D member 1	0.413	0.096
SERPINE1	chr7:100770369-100782547	serpin family E member 1	11.05	30.46
SERPINE2	chr2:224839764-224904036	serpin family E member 2	4.966	6.533
SERPINF1	chr17:1665258-1681250	serpin family F member 1	0.651	0.216
SERPINF2	chr17:1646129-1658559	serpin family F member 2	0.237	0.047
SERPING1	chr11:57365026-57382326	serpin family G member 1	0.853	0.417
SERPINI1	chr3:167453165-167543357	serpin family I member 1	2.176	3.507
SERTAD1	chr19:40928408-40931932	SERTA domain containing 1	2.262	3.505
SESN2	chr1:28585962-28609002	sestrin 2	5.359	10.89
SETMAR	chr3:4344891-4359268	SET domain and mariner transposase fusion gene	0.553	0.296
SFI1	chr22:31891964-32058351	SFI1 centrin binding protein	1.604	2.063
SFN	chr1:27189632-27190947	stratifin	0.77	0.275
SFTPD	chr10:81697495-81708861	surfactant protein D	0.448	0.417
SFXN3	chr10:102790995-102801232	sideroflexin 3	0.435	0.264
SFXN4	chr10:120900378-120925584	sideroflexin 4	0.532	0.386
SGIP1	chr1:66999824-67210768	SH3-domain GRB2-like (endophilin) interacting protein 1	0.85	0.229
SGK2	chr20:42187634-42215583	SGK2, serine/threonine kinase 2	0.216	0.053
SGK223	chr8:8175021-8243951	homolog of rat pragma of Rnd2	2.061	3.46
SGPL1	chr10:72575681-72640932	sphingosine-1-phosphate lyase 1	1.837	2.525
SGTB	chr5:64920557-65125230	small glutamine rich tetratricopeptide repeat containing beta	2.561	3.824
SH2B2	chr7:101928404-101962178	SH2B adaptor protein 2	2.967	6.826
SH2B3	chr12:111842666-111889427	SH2B adaptor protein 3	2.495	4.052
SH2D3A	chr19:6752172-6767523	SH2 domain containing 3A	0.693	0.373
SH3BGRL	chrX:80369199-80554046	SH3 domain binding glutamate rich protein like	0.492	0.337
SH3BGRL2	chr6:80340986-80413374	SH3 domain binding glutamate rich protein like 2	0.761	0.295
SH3BP2	chr4:2794749-2842823	SH3 domain binding protein 2	1.684	3.065
SH3BP4	chr2:235860627-235964358	SH3 domain binding protein 4	1.973	2.518
SH3BP5	chr3:15247732-15382901	SH3 domain binding protein 5	1.83	2.238
SH3GL1	chr19:4343523-4400565	SH3 domain containing GRB2 like 1	1.684	2.823
SH3GLB1	chr1:87169081-87213867	SH3 domain containing GRB2 like endophilin B1	1.478	2.029
SH3KBP1	chrX:19552082-19905744	SH3 domain containing kinase binding protein 1	2.398	3.783
SH3PXD2B	chr5:171760502-171881527	SH3 and PX domains 2B	2.654	4.955
SH3RF1	chr4:170015399-170192249	SH3 domain containing ring finger 1	1.56	2.607
SH3RF2	chr5:145316125-145461416	SH3 domain containing ring finger 2	0.286	0.195
SH3RF3	chr2:109743783-110262207	SH3 domain containing ring finger 3	2.393	3.633
SHANK2	chr11:70313960-70963724	SH3 and multiple ankyrin repeat domains 2	0.401	0.137
SHB	chr9:37910525-38069234	SH2 domain containing adaptor protein B	1.785	2.134
SHC2	chr19:416393-461840	SHC (Src homology 2 domain containing) transforming protein 2	0.935	0.476
SHH	chr7:155593019-155604967	sonic hedgehog	0.531	0.133
SHMT1	chr17:18218593-18266856	serine hydroxymethyltransferase 1	0.383	0.126
SIGIRR	chr11:405715-417397	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	0.533	0.342
SIK1	chr21:44834397-44847002	salt inducible kinase 1	2.431	5.217
SIPA1L2	chr1:232533683-232766227	signal induced proliferation associated 1 like 2	2.927	5.482
SIRT1	chr10:69644420-69678147	sirtuin 1	1.546	2.152
SKA3	chr13:21727733-21753220	spindle and kinetochore associated complex subunit 3	0.899	0.235
SKI	chr1:2160133-2241654	SKI proto-oncogene	2.221	4.531
SKIDA1	chr10:21776208-21814611	SKI/DACH domain containing 1	0.546	0.239
SKIL	chr3:170075419-170114637	SKI-like proto-oncogene	1.432	2.132
SLC10A1	chr14:70242551-70264793	solute carrier family 10 member 1	0.181	0.026
SLC10A3	chrX:153715649-153719012	solute carrier family 10 member 3	2.092	3.162
SLC12A8	chr3:124801479-124931609	solute carrier family 12 member 8	0.851	0.452
SLC13A4	chr7:135347128-135412933	solute carrier family 13 member 4	1.675	2.272
SLC15A1	chr13:99336054-99404929	solute carrier family 15 member 1	0.14	0.013
SLC15A3	chr11:60691912-60719257	solute carrier family 15 member 3	0.357	0.079
SLC15A4	chr12:129277738-129308541	solute carrier family 15 member 4	1.638	2.017
SLC16A1	chr1:113454469-113498975	solute carrier family 16 member 1	1.991	2.597
SLC16A13	chr17:6939393-6943440	solute carrier family 16 member 13	0.801	0.432
SLC16A3	chr17:80175782-80197789	solute carrier family 16 member 3	0.624	0.332
SLC16A7	chr12:59989820-60183635	solute carrier family 16 member 7	0.465	0.247
SLC17A4	chr6:25754926-25781403	solute carrier family 17 member 4	0.246	0.055
SLC17A9	chr20:61583998-61600265	solute carrier family 17 member 9	0.363	0.217
SLC18B1	chr6:133090506-133119770	solute carrier family 18 member B1	0.479	0.383
SLC19A1	chr21:46825096-46962385	solute carrier family 19 member 1	0.784	0.438
SLC19A3	chr2:228549810-228582745	solute carrier family 19 member 3	0.705	0.475
SLC1A3	chr5:36606456-36688436	solute carrier family 1 member 3	0.348	0.312
SLC1A4	chr2:65215578-65251000	solute carrier family 1 member 4	6.882	12.79
SLC1A5	chr19:47278136-47291842	solute carrier family 1 member 5	4.224	6.902
SLC22A1	chr6:160542862-160579750	solute carrier family 22 member 1	0.726	0.213
SLC22A17	chr14:23815522-23822116	solute carrier family 22 member 17	0.669	0.474
SLC22A18	chr11:2909326-2946476	solute carrier family 22 member 18	0.504	0.176
SLC22A18AS	chr11:2909326-2946476	solute carrier family 22 member 18 antisense	0.311	0.066
SLC22A4	chr5:131630144-131731306	solute carrier family 22 member 4	2.821	6.699
SLC22A7	chr6:43265713-43276530	solute carrier family 22 member 7	0.085	0.03
SLC23A1	chr5:138669157-138719039	solute carrier family 23 member 1	0.163	0.113
SLC24A1	chr15:65871095-66084735	solute carrier family 24 member 1	0.709	0.333
SLC25A18	chr22:18043182-18074562	solute carrier family 25 member 18	0.544	0.11
SLC25A19	chr17:73267344-73285530	solute carrier family 25 member 19	1.493	2.265
SLC25A20	chr3:48894355-48936426	solute carrier family 25 member 20	0.351	0.191
SLC25A29	chr14:100704493-100772860	solute carrier family 25 member 29	2.255	3.355
SLC25A30	chr13:45967339-45992516	solute carrier family 25 member 30	1.262	2.232
SLC25A42	chr19:19174802-19223841	solute carrier family 25 member 42	0.461	0.317
SLC26A1	chr4:972862-1003433	solute carrier family 26 member 1	0.591	0.356
SLC26A2	chr5:149340299-149366963	solute carrier family 26 member 2	1.801	2.262
SLC26A4	chr7:107296960-107358252	solute carrier family 26 member 4	3.113	6.422
SLC27A2	chr15:50474392-50528596	solute carrier family 27 member 2	0.49	0.129
SLC27A4	chr9:131102838-131127870	solute carrier family 27 member 4	1.554	2.2
SLC27A5	chr19:59009569-59023594	solute carrier family 27 member 5	0.216	0.14
SLC28A1	chr15:85427784-85489200	solute carrier family 28 member 1	0.244	0.047
SLC28A2	chr15:45543493-45571436	solute carrier family 28 member 2	2.847	4.186
SLC29A2	chr11:66129449-66139291	solute carrier family 29 member 2	0.618	0.287
SLC2A12	chr6:134308718-134373789	solute carrier family 2 member 12	0.398	0.28
SLC2A13	chr12:40148822-40499881	solute carrier family 2 member 13	1.613	2.135
SLC2A14	chr12:7965832-8130438	solute carrier family 2 member 14	0.099	0.018
SLC2A2	chr3:170711973-170744768	solute carrier family 2 member 2	0.068	0.003
SLC30A10	chr1:220046618-220321383	solute carrier family 30 member 10	0.757	0.123
SLC35D1	chr1:67464886-67520345	solute carrier family 35 member D1	0.5	0.283

SLC35E4	chr22:31031680-31043862	solute carrier family 35 member E4	2.334	5.035
SLC35F6	chr2:26987092-27004922	solute carrier family 35 member F6	2.354	3.456
SLC35G1	chr10:95653727-95663523	solute carrier family 35 member G1	0.635	0.25
SLC36A1	chr5:150827162-150875931	solute carrier family 36 member 1	1.813	2.264
SLC37A4	chr11:118895023-118901616	solute carrier family 37 member 4	0.356	0.113
SLC38A1	chr12:46576840-46663208	solute carrier family 38 member 1	2.311	3.842
SLC38A3	chr3:50242691-50258494	solute carrier family 38 member 3	0.162	0.078
SLC38A4	chr12:47158543-47219780	solute carrier family 38 member 4	0.392	0.429
SLC38A6	chr14:61447831-61550451	solute carrier family 38 member 6	0.71	0.463
SLC39A10	chr2:196521531-196602426	solute carrier family 39 member 10	1.632	2.134
SLC39A11	chr17:70642084-71111934	solute carrier family 39 member 11	0.743	0.442
SLC39A5	chr12:56623819-56654263	solute carrier family 39 member 5	0.434	0.213
SLC39A6	chr18:33688493-33709357	solute carrier family 39 member 6	1.709	2.422
SLC3A2	chr11:62623483-62656355	solute carrier family 3 member 2	3.65	5.973
SLC40A1	chr2:190425315-190445537	solute carrier family 40 member 1	0.813	0.317
SLC43A2	chr17:1473923-1532930	solute carrier family 43 member 2	0.639	0.377
SLC44A3	chr1:95285897-95360878	solute carrier family 44 member 3	0.503	0.16
SLC44A5	chr1:75667815-76076799	solute carrier family 44 member 5	0.389	0.276
SLC45A1	chr1:8382458-8404227	solute carrier family 45 member 1	0.634	0.214
SLC46A3	chr13:29274217-29293150	solute carrier family 46 member 3	0.754	0.371
SLC47A1	chr17:19437166-19482628	solute carrier family 47 member 1	0.546	0.229
SLC47A2	chr17:19581293-19620043	solute carrier family 47 member 2	0.119	0.064
SLC4A4	chr4:72053002-72437804	solute carrier family 4 member 4	0.569	0.4
SLC4A7	chr3:27414061-27525911	solute carrier family 4 member 7	2.505	4.334
SLC52A2	chr8:145575912-145585217	solute carrier family 52 member 2	1.78	3.293
SLC5A6	chr2:27422453-27440046	solute carrier family 5 member 6	1.383	2.25
SLC5A9	chr1:48688331-48714511	solute carrier family 5 member 9	0.14	0.027
SLC6A17	chr1:110693131-110744823	solute carrier family 6 member 17	7.985	15.86
SLC6A6	chr3:14444088-14583588	solute carrier family 6 member 6	1.6	2.638
SLC6A8	chrX:152953751-152962048	solute carrier family 6 member 8	1.814	2.893
SLC6A9	chr1:44457279-44506190	solute carrier family 6 member 9	5.109	9.985
SLC7A11	chr4:138948576-139163503	solute carrier family 7 member 11	20.34	38.91
SLC7A5	chr16:87863628-87903100	solute carrier family 7 member 5	14.15	22.59
SLC7A7	chr14:23242397-23289020	solute carrier family 7 member 7	0.652	0.319
SLC9A1	chr1:27425298-27481869	solute carrier family 9 member A1	5.382	13.79
SLC9A7	chrX:46458483-46618607	solute carrier family 9 member A7	1.757	2.321
SLC9A9	chr3:142984063-143567373	solute carrier family 9 member A9	0.653	0.46
SLCO1B1	chr12:21279103-21548371	solute carrier organic anion transporter family member 1B1	0.354	0.069
SLCO2B1	chr11:74862031-74917445	solute carrier organic anion transporter family member 2B1	0.107	0.03
SLCO3A1	chr15:92396937-92715665	solute carrier organic anion transporter family member 3A1	1.787	2.427
SLCO5A1	chr8:70581844-70747299	solute carrier organic anion transporter family member 5A1	9.167	19.65
SLFN5	chr17:33559381-33600676	schlafen family member 5	2.897	4.432
SLIT2	chr4:20253545-20622661	slit guidance ligand 2	2.005	3.556
SLMO1	chr18:12407894-12433004	PRELI domain containing 3A	2.466	4.827
SMARCA1	chrX:128313820-128657511	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, s	0.449	0.244
SMARCC2	chr12:56555635-56583351	SWI/SNF related, matrix associated, actin dependent regulator of chromatin su	0.625	0.461
SMC2	chr9:106854695-106903723	structural maintenance of chromosomes 2	0.679	0.247
SMCR8	chr17:18218593-18266856	Smith-Magenis syndrome chromosome region, candidate 8	1.438	2.157
SMG1	chr16:18816096-18938045	SMG1 phosphatidylinositol 3-kinase-related kinase	1.428	2.075
SMLR1	chr6:131148439-131384462	small leucine-rich protein 1	0.151	0.018
SMOC1	chr14:70346113-70655787	SPARC related modular calcium binding 1	0.476	0.14
SMPDL3A	chr6:123108220-123130864	sphingomyelin phosphodiesterase acid like 3A	0.484	0.222
SMPX	chrX:21724089-21788953	small muscle protein, X-linked	0.244	0.055
SMTNL1	chr11:57295935-57318587	smoothelin-like 1	1.835	2.746
SMURF1	chr7:98476112-98741743	SMAD specific E3 ubiquitin protein ligase 1	1.498	2.08
SMURF2	chr17:62538398-62658466	SMAD specific E3 ubiquitin protein ligase 2	1.476	2.01
SNAI2	chr8:49830238-49834501	snail family zinc finger 2	1.993	2.863
SNAPC2	chr19:7985193-7988136	small nuclear RNA activating complex polypeptide 2	1.736	2.866
SNHG15	chr7:45022626-45026311	small nucleolar RNA host gene 15	1.707	2.566
SNHG5	chr6:86386724-86388451	small nucleolar RNA host gene 5	1.562	2.306
SNPH	chr20:1246959-1289971	syntaphilin	1.774	2.441
SNRNP35	chr12:123942650-123950941	small nuclear ribonucleoprotein U11/U12 subunit 35	0.603	0.292
SNUPN	chr15:75890257-75918719	snurportin 1	0.572	0.369
SNX29	chr16:12070600-12668146	sorting nexin 29	1.482	2.157
SNX4	chr3:125134053-125239058	sorting nexin 4	0.668	0.359
SOCS1	chr16:11343556-11350047	suppressor of cytokine signaling 1	2.201	3.12
SOCS7	chr17:36507757-36561848	suppressor of cytokine signaling 7	1.469	2.51
SOD1	chr21:33031934-33041243	superoxide dismutase 1, soluble	0.676	0.455
SOD2	chr6:160100122-160177352	superoxide dismutase 2, mitochondrial	0.527	0.311
SOGA2	chr18:8706002-8832775	microtubule crosslinking factor 1	2.432	3.658
SORBS2	chr4:186506597-186877870	sorbin and SH3 domain containing 2	0.221	0.051
SORBS3	chr8:22409250-22433010	sorbin and SH3 domain containing 3	0.52	0.369
SORD	chr15:45315301-45367287	sorbitol dehydrogenase	0.246	0.122
SORL1	chr11:121322911-121504471	sortilin-related receptor, L(DLR class) A repeats containing	0.406	0.318
SOWAHA	chr5:132149032-132152489	sosondowah ankyrin repeat domain family member A	0.771	0.11
SOWAHC	chr2:110371910-110376564	sosondowah ankyrin repeat domain family member C	2.25	3.874
SOX4	chr6:21593971-21598849	SRY-box 4	3.342	2.362
SOX6	chr11:15987994-16629286	SRY-box 6	0.436	0.25
SP100	chr2:231276514-231410317	SP100 nuclear antigen	0.594	0.416
SPAG5	chr17:26904582-26926102	sperm associated antigen 5	0.427	0.323
SPARC	chr5:151040656-151066809	secreted protein acidic and cysteine rich	0.258	0.299
SPATA2L	chr16:89749863-89769135	spermatogenesis associated 2 like	1.636	2.208
SPC24	chr19:11256178-11266639	SPC24, NDC80 kinetochore complex component	0.582	0.064
SPC25	chr2:169727400-169747130	SPC25, NDC80 kinetochore complex component	0.585	0.39
SPECC1	chr17:19912648-20220533	sperm antigen with calponin homology and coiled-coil domains 1	1.641	2.509
SPHK1	chr17:74305440-74383941	sphingosine kinase 1	4.21	11.48
SPINK1	chr5:147204142-147211260	serine peptidase inhibitor, Kazal type 1	0.491	0.07
SPINK5	chr5:147443534-147516925	serine peptidase inhibitor, Kazal type 5	0.337	0.194
SPINT3	chr20:44141100-44144264	serine peptidase inhibitor, Kunitz type, 3	0.273	0.001
SPIRE1	chr18:12446503-12657912	spire type actin nucleation factor 1	2.073	3.577
SPIRE2	chr16:89883245-89938205	spire type actin nucleation factor 2	1.744	2.349
SPOCK2	chr10:73818791-73848790	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	2.452	5.136
SPON2	chr4:1160720-1202750	spondin 2	0.37	0.361
SPP1	chr4:88896455-88904563	secreted phosphoprotein 1	0.134	0.044
SPRED1	chr15:38544286-38649450	sprouty related EVH1 domain containing 1	1.543	2.564
SPRED2	chr2:65537947-65662000	sprouty related EVH1 domain containing 2	1.886	2.921
SPRED3	chr19:38880677-38891435	sprouty related EVH1 domain containing 3	1.587	2.419
SPRY2	chr13:80910111-80915086	sprouty RTK signaling antagonist 2	1.459	2.52
SPRY4	chr5:141689991-141704620	sprouty RTK signaling antagonist 4	3.257	6.334
SPRYD4	chr12:56862300-56882181	SPRY domain containing 4	0.562	0.313
SPRYD7	chr13:50486841-50510625	SPRY domain containing 7	0.68	0.402
SPTBN5	chr15:42120282-42186275	spectrin beta, non-erythrocytic 5	4.112	5.906
SPTLC3	chr20:12989620-13149751	serine palmitoyltransferase long chain base subunit 3	0.366	0.156

SQLE	chr8:126010719-126034525	squalene epoxidase	0.461	0.398
SQSTM1	chr5:179224597-179285840	sequestosome 1	1.921	2.138
SRBD1	chr2:45615818-45838433	S1 RNA binding domain 1	0.76	0.405
SREBF1	chr17:17584786-17740325	sterol regulatory element binding transcription factor 1	0.406	0.408
SREBF2	chr22:42229082-42303312	sterol regulatory element binding transcription factor 2	0.59	0.495
SRGAP1	chr12:64237839-64542203	SLIT-ROBO Rho GTPase activating protein 1	1.876	2.361
SRGAP2	chr1:206511462-206637842	SLIT-ROBO Rho GTPase activating protein 2	1.626	2.799
SRGAP2D	chr1:121107151-121204419	SLIT-ROBO Rho GTPase activating protein 2D (pseudogene)	1.667	2.897
SRPX2	chrX:99899162-99926424	sushi repeat containing protein, X-linked 2	0.687	0.377
SRXN1	chr20:627256-634014	sulfiredoxin 1	3.557	5.057
SSH1	chr12:109176465-109251397	slingshot protein phosphatase 1	2.024	2.649
SSH3	chr11:67070918-67080272	slingshot protein phosphatase 3	0.534	0.362
SSPO	chr7:149461300-149531063	SCO-spondin	0.317	0.182
SSTR5	chr16:1114081-1131454	somatostatin receptor 5	0.184	0.046
ST3GAL5	chr2:86066270-86116157	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.781	0.475
ST3GAL6	chr3:98433176-98620543	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	0.411	0.212
ST6GAL1	chr3:186648314-186796459	ST6 beta-galactoside alpha-2,6-sialyltransferase 1	0.363	0.038
STAC	chr3:36421968-36589496	SH3 and cysteine rich domain	3.592	5.593
STAC2	chr17:37366788-37382040	SH3 and cysteine rich domain 2	0.116	0.061
STAP2	chr19:4324039-4338914	signal transducing adaptor family member 2	0.394	0.178
STARD10	chr11:72465773-72504750	StAR related lipid transfer domain containing 10	0.402	0.123
STARD9	chr15:42867856-43029417	StAR related lipid transfer domain containing 9	1.493	2.569
STAT6	chr12:57482676-57505452	signal transducer and activator of transcription 6	0.312	0.192
STC1	chr8:23699433-23712320	stanniocalcin 1	2.776	5.174
STEAP3	chr2:119981383-120023227	STEAP3 metalloreductase	0.417	0.449
STIM1	chr11:3876862-4114440	stromal interaction molecule 1	1.714	2.331
STK10	chr5:171469073-171615346	serine/threonine kinase 10	1.872	2.556
STK24	chr13:99102454-99229547	serine/threonine kinase 24	2.662	5.877
STK32A	chr5:146614570-146767607	serine/threonine kinase 32A	2.903	3.678
STK35	chr20:2082527-2129202	serine/threonine kinase 35	1.498	2.454
STOM	chr9:124101265-124132582	stomatin	0.506	0.413
STON2	chr14:81726885-81902794	stonin 2	2.58	4.732
STPG1	chr1:24645811-24800136	sperm tail PG-rich repeat containing 1	1.849	2.633
STX11	chr6:144471653-144513076	syntaxin 11	1.92	3.035
STX1A	chr7:73113515-73134039	syntaxin 1A	1.816	2.817
STX6	chr1:180882312-180992172	syntaxin 6	1.469	2.197
STXBP1	chr9:130374485-130455968	syntaxin binding protein 1	1.892	3.194
SUCLG1	chr2:84650646-85046713	succinate-CoA ligase alpha subunit	0.543	0.375
SUCLG2	chr3:67410883-67705038	succinate-CoA ligase GDP-forming beta subunit	0.564	0.179
SUCO	chr1:172501856-172581077	SUN domain containing ossification factor	1.602	2.141
SULT1A1	chr16:28616907-28634907	sulfotransferase family 1A member 1	0.253	0.072
SULT1A2	chr16:28603263-28608391	sulfotransferase family 1A member 2	0.354	0.094
SULT1B1	chr4:70591804-70626430	sulfotransferase family 1B member 1	0.067	0.003
SULT1C2	chr2:108905094-108926371	sulfotransferase family 1C member 2	0.238	0.059
SULT2A1	chr19:48373722-48389654	sulfotransferase family 2A member 1	0.038	0.002
SUOX	chr12:56391042-56399340	sulfite oxidase	0.504	0.327
SURF2	chr9:136223420-136228213	surfeit 2	1.753	2.728
SUSD3	chr9:95820985-95847555	sushi domain containing 3	0.207	0.058
SUV39H1	chrX:48555130-48567406	suppressor of variegation 3-9 homolog 1	0.737	0.335
SVIL	chr10:29746111-30025908	supervillin	1.689	2.448
SYDE1	chr19:15218213-15236584	synapse defective Rho GTPase homolog 1	0.664	0.33
SYNGR1	chr22:39745953-39781593	synaptogyrin 1	0.698	0.407
SYNJ2	chr6:158402887-158520435	synaptojanin 2	2.258	2.306
SYP	chrX:49044264-49056661	synaptophysin	6.129	12.57
SYT1	chr12:79257772-80084858	synaptotagmin 1	0.549	0.266
SYT17	chr16:19179637-19279605	synaptotagmin 17	0.24	0.103
SYTL1	chr1:27668482-27680423	synaptotagmin like 1	0.448	0.338
SZRD1	chr1:16693524-16724643	SUZ RNA binding domain containing 1	1.899	3.144
TACC1	chr8:38585691-38710546	transforming acidic coiled-coil containing protein 1	0.39	0.267
TACC2	chr10:123748630-124014059	transforming acidic coiled-coil containing protein 2	1.435	2.279
TANC2	chr17:60778674-61505236	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	1.929	2.698
TANGO2	chr22:20008601-20055454	transport and golgi organization 2 homolog	2.053	3.436
TANGO6	chr16:68877461-69119202	transport and golgi organization 6 homolog	0.716	0.427
TAOK3	chr12:118587605-118810750	TAO kinase 3	1.464	2.127
TAP2	chr6:32789609-32806547	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	2.065	2.78
TAPBPL	chr12:6561176-6579843	TAP binding protein like	0.522	0.434
TAPT1	chr4:16162127-16228161	transmembrane anterior posterior transformation 1	0.67	0.433
TAS2R5	chr7:141487183-141494377	taste 2 receptor member 5	1.852	2.132
TAT	chr16:71481500-71645739	tyrosine aminotransferase	0.104	0.031
TBC1D15	chr12:72233486-72320629	TBC1 domain family member 15	1.64	2.132
TBC1D20	chr20:415994-443203	TBC1 domain family member 20	1.718	2.621
TBC1D8	chr2:101618690-101767909	TBC1 domain family member 8	1.38	2.132
TBC1D8B	chrX:106045918-106119377	TBC1 domain family member 8B	0.563	0.351
TBL1X	chrX:9431334-9687782	transducin (beta)-like 1X-linked	3.34	5.334
TBX20	chr7:35237606-35293711	T-box 20	1.532	2.268
TBX3	chr12:115108058-115122150	T-box 3	1.604	2.105
TCAIM	chr3:44379462-44450944	T-cell activation inhibitor, mitochondrial	0.647	0.478
TCEAL1	chrX:102883604-102885883	transcription elongation factor A like 1	0.533	0.341
TCEAL8	chrX:102507919-102510121	transcription elongation factor A like 8	0.572	0.3
TCEANC2	chr1:54519233-54576766	transcription elongation factor A N-terminal and central domain containing 2	0.678	0.434
TCTEX1D4	chr1:45266035-45452394	Tctex1 domain containing 4	1.814	2.72
TDRKH	chr1:151732118-151763010	tudor and KH domain containing	1.805	2.276
TEC	chr4:48065969-48271866	tec protein tyrosine kinase	1.486	2.449
TENC1	chr12:53436972-53473204	tensin 2	0.217	0.083
TENM1	chrX:123509750-124319525	teneurin transmembrane protein 1	0.672	0.335
TENM3	chr4:182128476-183724310	teneurin transmembrane protein 3	1.613	2.334
TES	chr7:115850546-115898837	testin LIM domain protein	2.177	3.049
TESK1	chr9:35603231-35618424	testis-specific kinase 1	1.938	3.568
TEX11	chrX:69664704-70128567	testis expressed 11	0.36	0.148
TF	chr3:133464976-133497850	transferrin	0.505	0.105
TFAP2A	chr6:10396915-10419797	transcription factor AP-2 alpha	1.934	2.983
TFAP2E	chr1:36033239-36107451	transcription factor AP-2 epsilon	2.076	4.225
TFB2M	chr1:246703862-246831884	transcription factor B2, mitochondrial	0.525	0.343
TFPI	chr2:188328957-188419406	tissue factor pathway inhibitor	0.398	0.283
TFPI2	chr7:93486139-93520303	tissue factor pathway inhibitor 2	5.252	7.415
TGFA	chr2:70674411-70781278	transforming growth factor alpha	1.817	2.359
TGFB1	chr19:41768390-41859860	transforming growth factor beta 1	2.537	3.851
TGFB2	chr1:218517537-218617961	transforming growth factor beta 2	3.355	3.858
TGIF1	chr18:3412071-3458406	TGFB induced factor homeobox 1	2.204	3.858
TGM2	chr20:36756859-36793700	transglutaminase 2	2.658	5.549
THBS1	chr15:39873169-39889668	thrombospondin 1	3.371	2.261
THOC3	chr5:175386533-175395545	THO complex 3	0.83	0.322
THOC6	chr16:3072625-3077756	THO complex 6	2.285	3.076

THPO	chr3:184089772-184097640	thrombopoietin	0.254	0.036
THRSP	chr11:77726760-77850699	thyroid hormone responsive	0.422	0.152
THSD1	chr13:52951302-52980629	thrombospondin type 1 domain containing 1	1.91	2.416
THYN1	chr11:134118172-134123260	thymocyte nuclear protein 1	0.598	0.391
TJP3	chr19:3708334-3761673	tight junction protein 3	0.346	0.071
TLE4	chr9:82186866-82341893	transducin like enhancer of split 4	1.65	2.738
TLN2	chr15:62682531-63136830	talin 2	1.942	3.422
TLR2	chr4:154605147-154681387	toll like receptor 2	1.757	2.437
TLR3	chr4:186989940-187007794	toll like receptor 3	0.345	0.177
TM4SF1	chr3:149086804-149096876	transmembrane 4 L six family member 1	0.529	0.205
TM4SF4	chr3:149192361-149221181	transmembrane 4 L six family member 4	0.139	0.012
TM7SF2	chr11:64863464-64887176	transmembrane 7 superfamily member 2	0.828	0.452
TM7SF3	chr12:27091304-27167339	transmembrane 7 superfamily member 3	0.584	0.458
TM9SF2	chr13:100153518-100216302	transmembrane 9 superfamily member 2	0.714	0.467
TMBIM4	chr12:66524586-66563821	transmembrane BAX inhibitor motif containing 4	0.631	0.41
TMED5	chr1:93615298-93811378	transmembrane p24 trafficking protein 5	1.362	2.082
TMEM102	chr17:7338623-7341751	transmembrane protein 102	0.683	0.326
TMEM132A	chr11:60691912-60719257	transmembrane protein 132A	1.612	2.579
TMEM144	chr4:159131400-159176439	transmembrane protein 144	0.446	0.191
TMEM14A	chr6:52535883-52551385	transmembrane protein 14A	0.511	0.265
TMEM158	chr3:45265955-45267814	transmembrane protein 158 (gene/pseudogene)	2.058	3.027
TMEM160	chr19:47549166-47551882	transmembrane protein 160	0.758	0.318
TMEM173	chr5:138855112-138862353	transmembrane protein 173	0.432	0.36
TMEM176A	chr7:150488375-150502208	transmembrane protein 176A	0.374	0.099
TMEM176B	chr7:150488375-150502208	transmembrane protein 176B	0.477	0.109
TMEM178B	chr7:140704723-141180179	transmembrane protein 178B	2.223	3.511
TMEM180	chr10:104220584-104236992	major facilitator superfamily domain containing 13A	2.39	3.642
TMEM184B	chr22:38615297-38669040	transmembrane protein 184B	2.633	4.346
TMEM191A	chr22:21055401-21059292	transmembrane protein 191A (pseudogene)	1.621	2.604
TMEM192	chr4:165995657-166034024	transmembrane protein 192	0.668	0.441
TMEM198B	chr12:56211805-56236767	transmembrane protein 198B (pseudogene)	0.636	0.456
TMEM201	chr1:9648824-9674960	transmembrane protein 201	1.618	2.679
TMEM217	chr6:37179953-37300746	transmembrane protein 217	4.01	2.831
TMEM229B	chr14:67936982-67982021	transmembrane protein 229B	0.297	0.158
TMEM231	chr16:75572014-75590184	transmembrane protein 231	2.089	3.292
TMEM238	chr19:55890611-55895627	transmembrane protein 238	0.698	0.225
TMEM26	chr10:63166400-63213356	transmembrane protein 26	0.399	0.295
TMEM30B	chr14:61744088-62017698	transmembrane protein 30B	0.397	0.175
TMEM37	chr2:120189407-120282028	transmembrane protein 37	0.469	0.106
TMEM47	chrX:34645180-34675458	transmembrane protein 47	2.062	3.696
TMEM48	chr1:54224043-54304225	NDC1 transmembrane nucleoporin	0.753	0.322
TMEM74B	chr20:1160968-1166087	transmembrane protein 74B	0.555	0.409
TMEM79	chr1:156182778-156262234	transmembrane protein 79	1.593	2.345
TMEM87A	chr15:42502725-42704515	transmembrane protein 87A	1.24	2.035
TMEM97	chr17:26646120-26662515	transmembrane protein 97	0.308	0.113
TMPO	chr12:98906750-98944157	thymopoietin	0.794	0.449
TMPRSS2	chr21:42836477-42880085	transmembrane protease, serine 2	0.807	0.193
TMPRSS6	chr22:37447778-37505731	transmembrane protease, serine 6	0.73	0.249
TMSB10	chr2:85116659-85133799	thymosin beta 10	2.072	2.434
TMTC2	chr12:83080793-83528600	transmembrane and tetratricopeptide repeat containing 2	2.068	3.048
TMTC4	chr13:101255977-101327103	transmembrane and tetratricopeptide repeat containing 4	0.658	0.372
TMUB1	chr7:150778169-150780620	transmembrane and ubiquitin like domain containing 1	0.609	0.364
TNC	chr9:117781853-117888638	tenascin C	2.805	6.508
TNFAIP8L1	chr19:4639526-4655580	TNF alpha induced protein 8 like 1	0.372	0.261
TNFRSF10B	chr8:22844929-22941132	tumor necrosis factor receptor superfamily member 10b	1.486	2.359
TNFRSF10C	chr8:22941867-22979485	tumor necrosis factor receptor superfamily member 10c	0.366	0.235
TNFRSF11A	chr18:59992519-60058405	tumor necrosis factor receptor superfamily member 11a	2.87	4.704
TNFRSF11B	chr8:119935795-119964410	tumor necrosis factor receptor superfamily member 11b	0.304	0.169
TNFRSF12A	chr16:3070312-3072383	tumor necrosis factor receptor superfamily member 12A	4.105	6.524
TNFRSF14	chr1:2487207-2495346	tumor necrosis factor receptor superfamily member 14	0.311	0.175
TNFRSF1A	chr12:6437922-6451283	tumor necrosis factor receptor superfamily member 1A	0.699	0.479
TNFRSF21	chr6:47199267-47277680	tumor necrosis factor receptor superfamily member 21	2.614	2.792
TNFRSF9	chr1:7975930-8003225	tumor necrosis factor receptor superfamily member 9	20.11	27.5
TNFSF10	chr3:172223297-172241306	tumor necrosis factor superfamily member 10	0.239	0.082
TNFSF14	chr19:6663147-6670599	tumor necrosis factor superfamily member 14	0.458	0.35
TNFSF9	chr19:6531009-6535939	tumor necrosis factor superfamily member 9	2.476	3.42
TNIP3	chr4:122050891-122226112	TNFAIP3 interacting protein 3	0.257	0.193
TNNI2	chr11:1860232-1862910	troponin I2, fast skeletal type	0.111	0.307
TNNI3	chr19:55663132-55669276	troponin I3, cardiac type	3.06	7.209
TNPO1	chr5:72112417-72210215	transportin 1	1.4	2.018
TNRC18	chr7:5346092-5463210	trinucleotide repeat containing 18	1.46	2.125
TNRC6C	chr17:75955237-76107880	trinucleotide repeat containing 6C	1.546	2.365
TNS1	chr2:218664298-218808827	tensin 1	0.363	0.288
TNXA	chr6:31971726-31981050	tenascin XA (pseudogene)	0.122	0.056
TNXB	chr6:32006092-32077151	tenascin XB	0.302	0.393
TOMM34	chr20:43570770-43589114	translocase of outer mitochondrial membrane 34	2.353	3.637
TOMM40L	chr1:161195562-161208000	translocase of outer mitochondrial membrane 40 like	0.495	0.167
TOP2A	chr17:38544772-38574202	topoisomerase (DNA) II alpha	0.329	0.205
TOPBP1	chr3:133319413-133380813	topoisomerase (DNA) II binding protein 1	0.94	0.461
TP53I11	chr11:44785975-44972857	tumor protein p53 inducible protein 11	1.689	2.269
TPBG	chr6:83072922-83080390	trophoblast glycoprotein	1.655	2.899
TPM4	chr19:16178316-16213813	tropomyosin 4	2.612	2.644
TPPP	chr5:659976-693510	tubulin polymerization promoting protein	2.772	4.58
TPRXL	chr3:13978806-14107481	tetra-peptide repeat homeobox-like	1.995	24.81
TPST2	chr22:26917876-26986114	tyrosylprotein sulfotransferase 2	1.246	2.188
TPX2	chr20:30326776-30389603	TPX2, microtubule nucleation factor	0.475	0.365
TRAF3	chr14:103243815-103377837	TNF receptor associated factor 3	1.798	2.63
TRIB1	chr8:126442562-126450644	tribbles pseudokinase 1	2.3	2.82
TRIB3	chr20:361307-378203	tribbles pseudokinase 3	12.08	20.94
TRIM10	chr6:30119718-30140473	tripartite motif containing 10	0.569	0.193
TRIM14	chr9:100818958-100881488	tripartite motif containing 14	0.455	0.271
TRIM15	chr6:30119718-30140473	tripartite motif containing 15	0.641	0.218
TRIM22	chr11:5710816-5732093	tripartite motif containing 22	0.43	0.325
TRIM25	chr17:54965269-54991409	tripartite motif containing 25	1.473	2.401
TRIM31	chr6:30070573-30080867	tripartite motif containing 31	0.345	0.133
TRIM34	chr11:5617330-5665633	tripartite motif containing 34	0.489	0.145
TRIM47	chr17:73870244-73874656	tripartite motif containing 47	1.636	2.176
TRIM56	chr7:100728578-100741267	tripartite motif containing 56	1.388	2.286
TRIM62	chr1:33593830-33766320	tripartite motif containing 62	1.483	2.08
TRIM9	chr14:51441980-51562627	tripartite motif containing 9	2.801	3.052
TRIML1	chr4:189054658-189098156	tripartite motif family like 1	1.912	2.483
TRIO	chr5:14143828-14510279	trio Rho guanine nucleotide exchange factor	1.937	2.539
TRNP1	chr1:27320191-27327377	TMF1-regulated nuclear protein 1	2.448	2.945

TRPM3	chr9:73149965-73736514	transient receptor potential cation channel subfamily M member 3	0.544	0.4
TSC22D2	chr3:150125875-150184207	TSC22 domain family member 2	2.047	3.628
TSEN2	chr3:12525868-12575010	tRNA splicing endonuclease subunit 2	0.852	0.449
TSFM	chr12:58176527-58213433	Ts translation elongation factor, mitochondrial	0.697	0.499
TSGA10	chr2:99613723-99779752	testis specific 10	2.645	4.589
TSKU	chr11:76493356-76509198	tsukushi, small leucine rich proteoglycan	0.389	0.136
TSLP	chr5:110405777-110413722	thymic stromal lymphopoietin	2.543	3.486
TSNAXIP1	chr16:67841009-67861971	translin associated factor X interacting protein 1	0.647	0.314
TSPAN5	chr4:99391517-99579812	tetraspanin 5	1.884	2.619
TSPAN6	chrX:99883695-99891857	tetraspanin 6	0.783	0.396
TSPEAR	chr21:45905219-46131495	thrombospondin-type laminin G domain and EAR repeats	3.302	4.719
TST	chr22:37406899-37425863	thiosulfate sulfurtransferase	0.482	0.284
TTC22	chr1:55245382-55267221	tetratricopeptide repeat domain 22	0.41	0.243
TTC23L	chr5:34837830-34899564	tetratricopeptide repeat domain 23 like	0.687	3.656
TTC27	chr2:32847067-33046118	tetratricopeptide repeat domain 27	0.619	0.323
TTC30A	chr2:178477798-178483706	tetratricopeptide repeat domain 30A	0.63	0.275
TTC30B	chr2:178413632-178418029	tetratricopeptide repeat domain 30B	0.488	0.203
TTC38	chr22:46663860-46690451	tetratricopeptide repeat domain 38	0.503	0.24
TTC39B	chr9:15163638-15307358	tetratricopeptide repeat domain 39B	1.723	2.584
TTC39C	chr18:21572736-21715977	tetratricopeptide repeat domain 39C	0.511	0.271
TTC7B	chr14:91006931-91282761	tetratricopeptide repeat domain 7B	1.76	2.098
TTK	chr6:80714321-80752244	TTK protein kinase	0.476	0.248
TTL	chr2:113239717-113290236	tubulin tyrosine ligase	1.993	2.754
TTLL11	chr9:124577984-124855885	tubulin tyrosine ligase like 11	1.527	2.052
TTPA	chr8:63971799-63998645	tocopherol (alpha) transfer protein	0.194	0.036
TTR	chr18:29171729-29178986	transthyretin	0.098	0.016
TUBA3D	chr2:132202795-132360468	tubulin alpha 3c	0.48	0.373
TUBB	chr6:30688156-30693195	tubulin beta class I	1.828	2.019
TUBB4B	chr9:140135710-140177093	tubulin beta 4B class IVb	3.109	3.924
TUBE1	chr6:112391859-112575917	tubulin epsilon 1	1.663	2.216
TUFT1	chr1:151512780-151556059	tuftelin 1	5.384	8.115
TULP4	chr6:158653226-158932984	tubby like protein 4	1.524	2.369
TUSC3	chr8:15274713-15744806	tumor suppressor candidate 3	1.689	2.821
TWF2	chr3:52262625-52273194	twinfilin actin binding protein 2	0.624	0.469
TXNDC15	chr5:134209459-134240226	thioredoxin domain containing 15	0.468	0.264
TXNIP	chr1:145438461-145442628	thioredoxin interacting protein	0.655	0.36
TXNRD2	chr22:19863039-20004309	thioredoxin reductase 2	0.558	0.362
TYRO3	chr15:41850419-41876259	TYRO3 protein tyrosine kinase	1.94	3.104
TYW3	chr1:75171073-75232360	tRNA-yW synthesizing protein 3 homolog	0.686	0.461
U2AF1	chr21:44513065-44527697	U2 small nuclear RNA auxiliary factor 1	0.692	0.491
UAP1	chr1:162531267-162569633	UDP-N-acetylglucosamine pyrophosphorylase 1	1.466	2.115
UBASH3B	chr11:122526397-122685187	ubiquitin associated and SH3 domain containing B	6.496	11.52
UBD	chr6:29520359-29527702	ubiquitin D	0.639	0.088
UBE2A	chrX:118708498-118718379	ubiquitin conjugating enzyme E2 A	1.507	2.05
UBE2L6	chr11:57319127-57335803	ubiquitin conjugating enzyme E2 L6	0.678	0.423
UBE2S	chr19:55895922-55919325	ubiquitin conjugating enzyme E2 S	1.982	3.037
UBE3D	chr6:83602185-83775545	ubiquitin protein ligase E3D	0.843	0.433
UBN1	chr16:4897911-4932363	ubinuclein 1	1.541	2.419
UBXN11	chr1:26608278-26647014	UBX domain protein 11	0.547	0.314
UBXN8	chr8:30601533-30624520	UBX domain protein 8	0.502	0.241
UFC1	chr1:161070345-161128646	ubiquitin-fold modifier conjugating enzyme 1	0.587	0.404
UFSP2	chr4:186317069-186347264	UFM1-specific peptidase 2	0.62	0.363
UGDH	chr4:39500374-39529218	UDP-glucose 6-dehydrogenase	0.532	0.197
UGP2	chr2:64068097-64246490	UDP-glucose pyrophosphorylase 2	0.571	0.405
UGT1A1	chr2:234526290-234681951	UDP glucuronosyltransferase family 1 member A1	0.452	0.08
UGT2A3	chr4:69794176-69817509	UDP glucuronosyltransferase family 2 member A3	0.247	0.035
UGT2B15	chr4:69382873-69536494	UDP glucuronosyltransferase family 2 member B15	0.23	0.033
UGT2B4	chr4:70345882-70361626	UDP glucuronosyltransferase family 2 member B4	0.183	0.044
UGT2B7	chr4:69962192-70267587	UDP glucuronosyltransferase family 2 member B7	0.351	0.069
UGT3A1	chr5:35953190-36001130	UDP glycosyltransferase family 3 member A1	0.452	0.185
UHRF1BP1	chr6:34759793-34845308	UHRF1 binding protein 1	1.741	2.37
ULK1	chr12:132379160-132407819	unc-51 like autophagy activating kinase 1	1.736	2.602
UNC5A	chr5:176237559-176326333	unc-5 netrin receptor A	0.837	0.304
UNC5B	chr10:72972291-73062635	unc-5 netrin receptor B	25.96	72.69
UPB1	chr22:24891250-24922582	ureidopropionase, beta	0.234	0.12
UPP1	chr7:48128007-48148330	uridine phosphorylase 1	5.027	16.78
UPP2	chr2:158733116-158992666	uridine phosphorylase 2	1.437	10.27
UQCRC2	chr16:21964608-21994668	ubiquinol-cytochrome c reductase core protein II	0.586	0.412
UQCRHL	chr1:16133656-16134194	ubiquinol-cytochrome c reductase hinge protein like	2.429	4.618
UROD	chr1:45477614-45481341	uroporphyrinogen decarboxylase	0.486	0.337
USF1	chr1:161009040-161015769	upstream transcription factor 1	0.732	0.462
USP18	chr22:18632717-18660162	ubiquitin specific peptidase 18	0.412	0.247
USP25	chr21:17102269-17252377	ubiquitin specific peptidase 25	1.669	2.086
USP30	chr12:109489845-109525831	ubiquitin specific peptidase 30	0.551	0.371
USP31	chr16:23072674-23160643	ubiquitin specific peptidase 31	1.687	2.116
USP32P2	chr17:18414386-18430935	ubiquitin specific peptidase 32 pseudogene 2	1.688	3.632
USP35	chr11:77899857-78128868	ubiquitin specific peptidase 35	0.711	0.387
USP43	chr17:9547665-9633138	ubiquitin specific peptidase 43	0.36	0.164
UST	chr6:149068093-149398148	uronyl 2-sulfotransferase	1.582	2.719
UTP20	chr12:101673904-101801653	UTP20, small subunit processome component	0.789	0.415
UXS1	chr2:106709758-106810795	UDP-glucuronate decarboxylase 1	2.518	3.96
VAMP5	chr2:85811530-85820519	vesicle associated membrane protein 5	0.797	0.485
VAMP8	chr2:85804613-85809156	vesicle associated membrane protein 8	0.381	0.147
VARS	chr6:31745296-31763742	valyl-tRNA synthetase	0.778	0.485
VASN	chr16:4390251-4470502	vasorin	1.611	2.842
VAT1	chr17:41166621-41174459	vesicle amine transport 1	2.156	2.731
VCAN	chr5:82767403-82878122	versican	2.512	4.187
VDR	chr12:48235026-48298814	vitamin D (1,25- dihydroxyvitamin D3) receptor	2.2	3.408
VEGFA	chr6:43737945-43754223	vascular endothelial growth factor A	1.379	2.082
VEPH1	chr3:156977531-157221415	ventricular zone expressed PH domain containing 1	0.344	0.148
VGF	chr7:100805789-100810472	VGF nerve growth factor inducible	3.288	5.534
VGLL4	chr3:11314009-11762220	vestigial like family member 4	1.546	2.563
VIL1	chr2:219283837-219461158	villin 1	0.427	0.057
VIMP	chr15:101811213-101817700	VCP interacting membrane selenoprotein	1.692	2.684
VNN1	chr6:133001996-133041070	vanin 1	0.238	0.052
VNN2	chr6:133065008-133084651	vanin 2	0.462	0.163
VNN3	chr6:133043925-133055904	vanin 3	0.091	0.007
VPS52	chr6:33217312-33239662	VPS52, GARP complex subunit	0.566	0.331
VSNL1	chr2:17721806-17837706	visinin like 1	0.482	0.145
VTN	chr17:26694298-26697373	vitronectin	0.701	0.163
VWA1	chr1:1370638-1432486	von Willebrand factor A domain containing 1	0.635	0.322
VWA5A	chr11:123986110-124017618	von Willebrand factor A domain containing 5A	0.68	0.399
VWA5B2	chr3:183948316-183967313	von Willebrand factor A domain containing 5B2	5.062	4.237

WARS	chr14:100800124-100842680	tryptophanyl-tRNA synthetase	3.235	3.687
WARS2	chr1:119573838-119727028	tryptophanyl tRNA synthetase 2, mitochondrial	1.694	2.136
WAS	chrX:48535015-48549817	Wiskott-Aldrich syndrome	0.642	0.306
WASL	chr7:123321996-123389116	Wiskott-Aldrich syndrome like	1.718	3.376
WBSCR22	chr7:73097894-73112551	Williams-Beuren syndrome chromosome region 22	1.718	3.371
WDR18	chr19:984112-994741	WD repeat domain 18	0.638	0.425
WDR25	chr14:100842754-100996640	WD repeat domain 25	1.635	2.394
WDR92	chr2:68356961-68384692	WD repeat domain 92	0.722	0.464
WFS1	chr4:6271576-6304992	wolframin ER transmembrane glycoprotein	1.696	2.75
WISP2	chr20:43342918-43356656	WNT1 inducible signaling pathway protein 2	0.266	0.343
WNK1	chr12:861713-1605099	WNK lysine deficient protein kinase 1	1.422	2.089
WNK4	chr17:40932626-40949130	WNK lysine deficient protein kinase 4	1.724	3.123
WNT4	chr1:22443797-22469564	Wnt family member 4	3.163	6.763
WNT6	chr2:219724545-219738954	Wnt family member 6	0.33	0.37
WNT7B	chr22:46316247-46373008	Wnt family member 7B	3.557	2.971
WSB1	chr17:25621102-25643328	WD repeat and SOCS box containing 1	1.792	2.589
WWC3	chrX:9982749-10112518	WWC family member 3	2.425	4.335
XDH	chr2:31557187-31637611	xanthine dehydrogenase	0.441	0.188
XKRX	chrX:100143678-100184344	XK related, X-linked	0.66	0.452
XPOT	chr12:64797937-64845063	exportin for tRNA	2.653	3.812
XRCC4	chr5:82373316-82649579	X-ray repair complementing defective repair in Chinese hamster cells 4	0.524	0.295
XYLB	chr3:38388250-38469000	xylulokinase homolog (H. influenzae)	0.558	0.317
YARS	chr1:33240839-33324480	tyrosyl-tRNA synthetase	2.98	4.543
YKT6	chr7:44240577-44253893	YKT6 v-SNARE homolog (S. cerevisiae)	1.913	2.807
YPEL1	chr22:22020272-22090071	yippee like 1	1.566	2.564
YPEL3	chr16:30103634-30107584	yippee like 3	0.531	0.314
ZBTB7B	chr1:154974646-154991001	zinc finger and BTB domain containing 7B	0.419	0.137
ZC2HC1A	chr8:79578281-79631997	zinc finger C2HC-type containing 1A	2.143	2.995
ZC3H12C	chr11:109963707-110042566	zinc finger CCCH-type containing 12C	1.428	2.219
ZC3H13	chr13:46528610-46626896	zinc finger CCCH-type containing 13	0.573	0.485
ZCCHC14	chr16:87439851-87525869	zinc finger CCHC-type containing 14	1.381	2.543
ZEB2	chr2:145141941-145278465	zinc finger E-box binding homeobox 2	2.102	2.134
ZFAND3	chr6:37787248-38122399	zinc finger AN1-type containing 3	1.73	2.722
ZFP36L1	chr14:69254371-69262960	ZFP36 ring finger protein-like 1	1.614	2.273
ZFPM1	chr16:88520013-88601574	zinc finger protein, FOG family member 1	1.772	4.859
ZFYVE1	chr14:73436158-73493920	zinc finger FYVE-type containing 1	1.332	2.078
ZIC4	chr3:147103834-147134506	Zic family member 4	0.524	0.248
ZIC5	chr13:100615274-100624178	Zic family member 5	0.472	0.457
ZMIZ1	chr10:80828538-81076285	zinc finger MIZ-type containing 1	1.572	2.506
ZMYM3	chrX:70430034-70948962	zinc finger MYM-type containing 3	0.404	0.188
ZMYND15	chr17:4643309-4649414	zinc finger MYND-type containing 15	1.968	2.59
ZMYND19	chr9:140474737-140484937	zinc finger MYND-type containing 19	2.045	2.372
ZNF124	chr1:247285276-247335531	zinc finger protein 124	1.823	2.353
ZNF143	chr11:9482398-9550071	zinc finger protein 143	1.87	2.147
ZNF189	chr9:104161162-104175491	zinc finger protein 189	0.587	0.474
ZNF204P	chr6:27325601-27343153	zinc finger protein 204, pseudogene	0.679	0.33
ZNF213	chr16:3185056-3193170	zinc finger protein 213	1.643	3.004
ZNF219	chr14:21538476-21572863	zinc finger protein 219	0.325	0.233
ZNF222	chr19:44529493-44537262	zinc finger protein 222	1.401	2.165
ZNF277	chr7:111846642-111996501	zinc finger protein 277	0.684	0.458
ZNF280C	chrX:129336672-129402922	zinc finger protein 280C	1.592	2.071
ZNF320	chr19:53379424-53400900	zinc finger protein 320	0.802	0.394
ZNF333	chr19:14800869-14834101	zinc finger protein 333	1.995	3.593
ZNF385B	chr2:180306710-180726232	zinc finger protein 385B	0.476	0.411
ZNF385D	chr3:21461996-21792885	zinc finger protein 385D	0.593	0.384
ZNF395	chr8:28203101-28243977	zinc finger protein 395	0.417	0.284
ZNF425	chr7:148799877-148823438	zinc finger protein 425	2.045	3.391
ZNF432	chr19:52534477-52599027	zinc finger protein 432	1.548	2.164
ZNF433	chr19:12098439-12188626	zinc finger protein 433	1.57	4.591
ZNF444	chr19:56652381-56676006	zinc finger protein 444	0.409	0.185
ZNF449	chrX:134478673-134497555	zinc finger protein 449	1.629	2.301
ZNF467	chr7:149461300-149531063	zinc finger protein 467	0.238	0.175
ZNF512B	chr20:62571181-62601223	zinc finger protein 512B	0.642	0.318
ZNF518A	chr10:97889150-98031357	zinc finger protein 518A	0.628	0.433
ZNF552	chr19:58258163-58427978	zinc finger protein 552	0.627	0.373
ZNF573	chr19:38228982-38271190	zinc finger protein 573	0.598	0.471
ZNF598	chr16:2047540-2059822	zinc finger protein 598	1.473	2.103
ZNF608	chr5:123972609-124084487	zinc finger protein 608	0.634	0.369
ZNF618	chr9:116638561-116818875	zinc finger protein 618	0.341	0.214
ZNF674	chrX:46356911-46457838	zinc finger protein 674	1.641	2.287
ZNF697	chr1:120161082-120190925	zinc finger protein 697	2.713	4.593
ZNF70	chr22:24083047-24093279	zinc finger protein 70	1.901	2.563
ZNF703	chr8:37553300-37557527	zinc finger protein 703	2.623	5.081
ZNF76	chr6:35227307-35264199	zinc finger protein 76	0.82	0.492
ZNF883	chr9:115759399-115774472	zinc finger protein 883	0.649	0.239
ZNHIT1	chr7:100849257-100867473	zinc finger HIT-type containing 1	0.512	0.418
ZNRF2P2	chr7:29685537-29791473	zinc and ring finger 2 pseudogene 2	1.678	2.462
ZRANB3	chr2:135957252-136288806	zinc finger RANBP2-type containing 3	0.763	0.473
ZSWIM3	chr20:44486219-44507769	zinc finger SWIM-type containing 3	0.428	0.368
ZSWIM4	chr19:13906273-13943176	zinc finger SWIM-type containing 4	2.245	5.177
ZSWIM6	chr5:60628099-60842127	zinc finger SWIM-type containing 6	2.354	3.475
ZWINT	chr10:58117122-58121034	ZW10 interacting kinetochore protein	0.878	0.157

Supplementary Table 2 **Deregulated genes in HepaRG cells exposed to APAP (Fold change>10)**

Gene Symbol*	Gene Locus	Fold change (5mM APAP)	Fold change (10 mM APAP)
A1CF	chr10:52559047-52645435	0.271	0.031
AADAC	chr3:151347319-151546276	0.322	0.036
ABCA6	chr17:67074817-67138015	0.212	0.04
ABCB4	chr7:87031171-87461646	0.164	0.032
ABCC2	chr10:101542178-101613520	0.33	0.027
ABCC6P1	chr16:18582506-18609629	0.26	0.068
ABCC6P2	chr16:14908173-14918610	0.239	0.096
ABCG5	chr2:44039610-44110328	0.057	0.001
ABCG8	chr2:44039610-44110328	0.033	0.001
ACMSD	chr2:135595889-135716915	0.173	0.02
ACOT12	chr5:80256507-81047072	0.144	0.057
ACOX2	chr3:58490862-58522929	0.12	0.051
ACSM2A	chr16:20462738-20498991	0.199	0.026
ACSM2B	chr16:20529072-20593323	0.209	0.036
ACSM3	chr16:20775311-20860990	0.255	0.043
ACSM5	chr16:20420855-20452618	0.267	0.048
ACSS1	chr20:24986865-25038818	0.056	0.013
ACY3	chr11:67410025-67418190	0.237	0.032
ADH4	chr4:100010007-100273917	0.038	0.008
ADH6	chr4:100010007-100273917	0.115	0.007
AFM	chr4:74347405-74395600	0.177	0.021
AGMAT	chr1:15853351-15911605	0.303	0.057
AGMO	chr7:15198958-15601645	0.304	0.023
AGXT	chr2:241797144-241818536	0.186	0.061
AGXT2	chr5:34997071-35048240	0.12	0.015
AHSG	chr3:186330849-186339107	0.302	0.082
AKR1B10	chr7:134212253-134226166	0.406	0.033
AKR1C4	chr10:5005453-5326522	0.177	0.018
AKR1C6P	chr10:4913858-4958540	0.062	0.008
AKR1D1	chr7:137749922-137803050	0.092	0.023
ALB	chr4:74269971-74287129	0.527	0.099
ALDH1A1	chr9:75515577-75568233	0.294	0.061
ALDH3A1	chr17:19641280-19651750	0.173	0.048
ALDOB	chr9:104182697-104211853	0.209	0.047
ALOXE3	chr17:7999217-8022234	13.02	24.91
ALPL	chr1:21835857-21904905	0.078	0.022
ANG	chr14:21151120-21168758	0.162	0.091
ANGPTL3	chr1:62920396-63154039	0.172	0.035
ANKS4B	chr16:21245015-21263750	0.211	0.03
ANXA10	chr4:169013687-169246998	0.116	0.008
ANXA13	chr8:124693033-124749647	0.071	0.001
ANXA8L2	chr10:47746875-47769716	0.205	0.037
AOX1	chr2:201450730-201537620	0.418	0.097
AP1M2	chr19:10683346-10697991	0.296	0.057
APCS	chr1:159557615-159558661	0.325	0.03
APOA2	chr1:161192082-161193418	0.487	0.041
APOB	chr2:21224129-21266962	0.459	0.075
APOBEC3H	chr22:39493228-39500072	0.133	0.089
AQP7	chr9:33384384-33402517	0.498	0.096
AQP9	chr15:58430407-58478110	0.267	0.072
ARG1	chr6:131894343-131949379	0.075	0.014
ARHGEF16	chr1:3371146-3397677	0.264	0.055
ARHGEF2	chr1:155916540-155953675	8.114	10.63
ARL4C	chr2:235401517-235405751	5.636	11.52
ART4	chr12:14939411-14996548	0.358	0.043
ASGR1	chr17:7076750-7082883	0.194	0.044
ASNS	chr7:97481428-97501854	12.93	28.77
ASPA	chr17:3377403-3403781	0.128	0.069
ATF3	chr1:212738675-212794119	11.82	14.48
B3GNT3	chr19:17905624-17924417	0.225	0.033
BAAT	chr9:104117616-104147287	0.071	0.009
BBOX1	chr11:27062508-27149354	0.238	0.033
BDH1	chr3:197236653-197300194	0.035	0.024
BLNK	chr10:97889150-98031357	0.15	0.022
BTNL8	chr5:180326076-180378350	0.255	0.022
C14orf105	chr14:57936054-57960609	0.535	0.052
C2orf54	chr2:241825388-241836249	0.009	0.001

C4BPB	chr1:207262211-207273337	0.195	0.043
C5orf4	chr5:154197942-154256352	0.262	0.076
C6	chr5:41142247-41261540	0.243	0.045
C8A	chr1:57320442-57383894	0.338	0.07
CA9	chr9:35673914-35681154	0.038	0.065
CASP14	chr19:15160212-15169109	0.081	0.024
CCDC170	chr6:151815174-151942328	0.189	0.036
CCDC85B	chr11:65657289-65667997	4.946	12.03
CCL14	chr17:34310691-34329170	0.199	0.048
CCL15	chr17:34310691-34329170	0.199	0.048
CCL2	chr17:32582295-32584220	0.285	0.086
CD200	chr3:112051408-112081658	5.178	10.75
CDH1	chr16:68771194-68869444	0.252	0.054
CEACAM1	chr19:42901299-43156507	0.528	0.075
CES5A	chr16:55880065-55989943	0.582	0.082
CFHR2	chr1:196912933-196928356	0.13	0.027
CHAC1	chr15:41245545-41254871	17.53	35.5
CHST4	chr16:71481500-71645739	0.382	0.062
CHST8	chr19:34112860-34264414	3.956	10.42
CIDEC	chr3:9906149-10149915	0.235	0.035
CLDN14	chr21:37832919-37948867	0.026	0.05
CLRN3	chr10:129676113-129691211	0.085	0.004
CPA4	chr7:129932973-129964020	10.63	28.01
CPB2	chr13:46626982-46679211	0.39	0.061
CREB3L3	chr19:4153597-4173051	0.075	0.014
CRP	chr1:159682077-159726405	0.221	0.071
CST7	chr20:24922507-24942898	0.071	0.044
CTSS	chr1:150702671-150738433	0.508	0.096
CXCL1	chr4:74735108-74737019	0.359	0.043
CXCL10	chr4:76932332-77033955	0.315	0.038
CXCL2	chr4:74962750-74964999	0.274	0.052
CYP1A1	chr15:75011882-75017979	0.318	0.086
CYP21A1P	chr6:31971726-31981050	0.15	0.048
CYP21A2	chr6:32006092-32077151	0.151	0.042
CYP2B6	chr19:41430169-41524301	0.167	0.057
CYP2B7P1	chr19:41430169-41524301	0.167	0.057
CYP2C18	chr10:96442636-96495947	0.238	0.041
CYP2C19	chr10:96522462-96612671	0.253	0.049
CYP2C8	chr10:96796528-96829254	0.215	0.07
CYP2C9	chr10:96698384-96749148	0.178	0.052
CYP2E1	chr10:135238569-135392077	0.267	0.094
CYP3A4	chr7:99354582-99381904	0.207	0.044
CYP3A7	chr7:99282301-99332819	0.129	0.013
CYP4X1	chr1:47489239-47516423	0.098	0.019
CYP8B1	chr3:42913683-42917633	0.09	0.005
DAO	chr12:109270653-109294797	0.189	0.011
DBH	chr9:136501484-136525168	0.061	0.029
DCLK1	chr13:35516377-36705967	6.652	10.59
DDC	chr7:50526128-50633154	0.18	0.019
DIO1	chr1:54359860-54376759	0.291	0.076
DPYS	chr8:105391651-105482804	0.229	0.067
DUSP5	chr10:112257624-112271302	14.32	24.98
DUSP9	chrX:152890864-152916781	0.109	0.038
E2F8	chr11:19245609-19263202	0.778	0.044
ECM2	chr9:95059196-95432547	0.219	0.033
EDN2	chr1:41944445-41950344	0.071	0.018
EHHADH	chr3:184880688-184971886	0.263	0.065
EPS8L3	chr1:110292701-110306644	0.436	0.086
ESCO2	chr8:27590832-27662424	0.624	0.057
ESPN	chr1:6484847-6580121	0.15	0.07
ETNK2	chr1:204100176-204121307	0.168	0.069
F11	chr4:187181417-187422212	0.271	0.041
F13B	chr1:197007888-197036397	0.226	0.045
F5	chr1:169481191-169555840	0.362	0.048
FABP1	chr2:88422507-88427650	0.056	0.031
FAM222A	chr12:110151812-110211292	4.68	10.48
FAM65B	chr6:24804512-25004893	0.067	0.015
FETUB	chr3:186358148-186370797	0.254	0.074
FGA	chr4:155499904-155511897	0.234	0.038

FGB	chr4:155484128-155493915	0.205	0.03
FGG	chr4:155525285-155533918	0.253	0.051
FMO3	chr1:171060010-171086959	0.242	0.055
FMO5	chr1:146626681-146767447	0.154	0.014
FOSL1	chr11:65657289-65667997	11.84	18.99
FRK	chr6:116252829-116567088	0.295	0.091
FYN	chr6:111981534-112194655	0.107	0.001
G6PC	chr17:41052813-41066450	0.109	0.034
GALNT15	chr3:16216047-16273367	0.124	0.05
GALNT5	chr2:158114073-158169951	0.206	0.075
GAS2	chr11:22649821-22834547	0.218	0.078
GBA3	chr4:22694547-22821192	0.241	0.011
GDF15	chr19:18496967-18499986	8.279	16.48
GGT8P	chr2:91963332-91978189	0.185	0.095
GJB1	chrX:70430034-70948962	0.131	0.011
GJB5	chr1:35220647-35224113	13.31	81.92
GLYAT	chr11:58466955-58499480	0.036	0.004
GLYATL1	chr11:58695101-58825925	0.027	0.005
GNMT	chr6:42928499-42981719	0.165	0.092
GPR1	chr2:207040041-207082771	10.85	11.96
GPX2	chr14:65381078-65569413	0.107	0.01
GRAMD3	chr5:125695787-125830209	0.374	0.084
GYG2	chrX:2746793-2801206	0.141	0.01
GYS2	chr12:21689122-21757865	0.118	0.041
HABP2	chr10:115310589-115423829	0.285	0.044
HAL	chr12:96366439-96390143	0.262	0.091
HAMP	chr19:35773409-35776045	0.669	0.075
HAO1	chr20:7826328-7921179	0.116	0.01
HAO2	chr1:119904920-119936755	0.026	0.008
HAP1	chr17:39873997-39890898	5.634	16.73
HCN4	chr15:73612199-73661605	13.02	20.23
HFE	chr6:26086547-26098258	6.392	14.11
HFE2	chr1:145413122-145417545	0.09	0.006
HGD	chr3:120347014-120401418	0.41	0.047
HMGCS2	chr1:120290618-120311555	0.106	0.014
HNF1A	chr12:121415244-121454300	0.298	0.07
HNF4A	chr20:42984440-43061485	0.146	0.02
HNMT	chr2:138721807-138773934	0.224	0.059
HOXA3	chr7:27145808-27170399	0.26	0.05
HPD	chr12:122277432-122326517	0.278	0.066
HPGD	chr4:175411122-175444086	0.621	0.093
HSD17B2	chr16:82068857-82132139	0.118	0.012
HSPB2	chr11:111783459-111797595	0.397	0.036
HULC	chr6:8435855-8789203	0.077	0.032
ICOSLG	chr21:45642608-45660888	3.632	13.42
IFITM2	chr11:309531-311834	0.353	0.081
IGFBP3	chr7:45951843-45960871	5.6	12.48
IKBKE	chr1:206643585-206670223	0.163	0.046
IL1R2	chr2:102608305-102644884	0.163	0.051
IL22RA1	chr1:24446190-24469775	0.381	0.065
IQGAP2	chr5:75699105-76003957	0.275	0.027
IRF6	chr1:209958856-209979520	0.175	0.064
ITGAM	chr16:31265166-31344213	0.311	0.087
ITIH2	chr10:7745197-7791483	0.533	0.092
IYD	chr6:150690027-150725765	0.306	0.06
KCNJ16	chr17:68071320-68131746	0.138	0.005
KCNK5	chr6:39151668-39197259	0.145	0.094
KISS1	chr1:204159468-204165619	0.146	0.021
KLHDC7A	chr1:18807423-18812824	0.32	0.061
KLKB1	chr4:187135196-187179625	0.179	0.052
KNG1	chr3:186435097-186462199	0.414	0.088
KRT5	chr12:52908283-52917348	0.1	0.077
LAD1	chr1:201349965-201369053	0.342	0.039
LIN7A	chr12:81172104-81331866	0.625	0.067
LRRC31	chr3:169555611-169587742	0.514	0.024
LRRC73	chr6:43474702-43478081	6.217	10.5
MAFF	chr22:38597938-38612517	7.352	13.59
MAP2K6	chr17:67410837-67539093	0.23	0.048
MASP1	chr3:186933872-187009810	0.297	0.048

MAT1A	chr10:82031575-82049434	0.135	0.017
MLIP	chr6:53875386-54131495	0.096	0.012
MMP10	chr11:102641232-102651359	57.64	113.1
MTMR3	chr22:30279111-30573062	0.117	0.072
MTTP	chr4:100485239-100545154	0.073	0.007
MYLK	chr3:123304402-123603149	0.24	0.051
NCAM1	chr11:112831968-113149158	5.652	11.79
NCKAP5	chr2:133429371-134326069	0.605	0.069
NGFR	chr17:47572654-47592382	10.29	35.37
NQO1	chr16:69743303-69760533	0.139	0.077
NR1H4	chr12:100867550-100958177	0.285	0.039
NR1I2	chr3:119499330-119537651	0.184	0.029
NR1I3	chr1:161195562-161208000	0.136	0.033
NRXN2	chr11:64373645-64490660	0.132	0.044
OLFML3	chr1:114521659-114524875	0.102	0.029
ONECUT1	chr15:53042094-53082353	0.159	0.051
OTC	chrX:38208972-38282141	0.261	0.037
PAH	chr12:103232103-103311381	0.304	0.027
PCK1	chr20:56136136-56141513	0.016	0.002
PDZD3	chr11:119056163-119060932	0.202	0.021
PDZK1	chr1:145726914-145764206	0.188	0.028
PGLYRP2	chr19:15579456-15591056	0.28	0.089
PIK3C2G	chr12:18395539-18890993	0.194	0.004
PIPOX	chr17:27280400-27384367	0.159	0.029
PLA2G12B	chr10:74694325-74714673	0.059	0.009
PLA2G1B	chr12:120759913-120765592	0.41	0.001
PLGLB2	chr2:88047605-88285309	0.133	0.063
PMCHL2	chr5:70648324-70741726	0.253	0.01
PMEPA1	chr20:56223447-56286592	4.545	14.45
POLE2	chr14:50110269-50155098	0.789	0.089
PON1	chr7:94927668-94953884	0.294	0.069
PPP1R14D	chr15:41107642-41120907	0.172	0.018
PPP1R15A	chr19:49375648-49379319	6.704	16.72
PRKAR2B	chr7:106685177-106802256	0.146	0.095
PRODH2	chr19:36283214-36304201	0.303	0.058
PSAT1	chr9:80912058-80945009	10.07	17.65
PTGR1	chr9:114287446-114362135	0.332	0.079
RAB17	chr2:238482962-238500223	0.237	0.042
RASD1	chr17:17397752-17399709	10.77	12.52
RBP5	chr12:7247145-7311530	0.172	0.056
RCN3	chr19:50030062-50046890	0.169	0.066
RDH16	chr12:57345215-57351418	0.072	0.069
RFX2	chr19:5978413-6110664	5.833	15.26
RGN	chrX:46937595-46953067	0.225	0.039
RGPD1	chr2:88047605-88285309	0.18	0.022
RGS16	chr1:182567757-182573548	6.437	21.48
RHEBL1	chr12:49458467-49463775	5.031	11.02
RORC	chr1:151778546-151826173	0.178	0.073
RRM2	chr2:10260965-10271546	0.566	0.023
RTP4	chr3:187086167-187089369	0.198	0.048
SARDH	chr9:136526468-136605077	0.096	0.035
SCGN	chr6:25652428-25702011	0.281	0.033
SCTR	chr2:120189407-120282028	0.242	0.072
SDK1	chr7:3341079-4308631	0.144	0.011
SDPR	chr2:192699031-192712006	0.352	0.086
SDS	chr12:113830250-113841738	0.403	0.072
SEC16B	chr1:177897800-177942446	0.295	0.073
SELENBP1	chr1:151336776-151345210	0.258	0.094
SELL	chr1:169659805-169681113	0.308	0.092
SELPLG	chr12:109015679-109030486	5.462	15.41
SERPINA10	chr14:94640633-94763483	0.089	0.016
SERPINA4	chr14:95027771-95036243	0.442	0.075
SERPINA6	chr14:94770584-94789693	0.382	0.056
SERPINA7	chrX:105259681-105282739	0.232	0.047
SERPIND1	chr22:21061976-21245501	0.413	0.096
SERPINE1	chr7:100770369-100782547	11.05	30.46
SERPINF2	chr17:1646129-1658559	0.237	0.047
SESN2	chr1:28585962-28609002	5.359	10.89
SGK2	chr20:42187634-42215583	0.216	0.053

SLC10A1	chr14:70242551-70264793	0.181	0.026
SLC15A1	chr13:99336054-99404929	0.14	0.013
SLC15A3	chr11:60691912-60719257	0.357	0.079
SLC17A4	chr6:25754926-25781403	0.246	0.055
SLC1A4	chr2:65215578-65251000	6.882	12.79
SLC22A18AS	chr11:2909326-2946476	0.311	0.066
SLC22A7	chr6:43265713-43276530	0.085	0.03
SLC28A1	chr15:85427784-85489200	0.244	0.047
SLC2A14	chr12:7965832-8130438	0.099	0.018
SLC2A2	chr3:170711973-170744768	0.068	0.003
SLC38A3	chr3:50242691-50258494	0.162	0.078
SLC47A2	chr17:19581293-19620043	0.119	0.064
SLC5A9	chr1:48688331-48714511	0.14	0.027
SLC6A17	chr1:110693131-110744823	7.985	15.86
SLC6A9	chr1:44457279-44506190	24.2	41.11
SLC7A11	chr4:138948576-139163503	20.34	38.91
SLC7A5	chr16:87863628-87903100	14.15	22.59
SLC9A1	chr1:27425298-27481869	5.382	13.79
SLCO1B1	chr12:21279103-21548371	0.354	0.069
SLCO2B1	chr11:74862031-74917445	0.107	0.03
SLCO5A1	chr8:70581844-70747299	9.167	19.65
SMLR1	chr6:131148439-131384462	0.151	0.018
SMPX	chrX:21724089-21788953	0.244	0.055
SORBS2	chr4:186506597-186877870	0.221	0.051
SPC24	chr19:11256178-11266639	0.582	0.064
SPHK1	chr17:74305440-74383941	4.21	11.48
SPINK1	chr5:147204142-147211260	0.491	0.07
SPINT3	chr20:44141100-44144264	0.273	0.001
SPP1	chr4:88896455-88904563	0.134	0.044
SSTR5	chr16:1114081-1131454	0.184	0.046
ST6GAL1	chr3:186648314-186796459	0.363	0.038
STAC2	chr17:37366788-37382040	0.116	0.061
SULT1A1	chr16:28616907-28634907	0.253	0.072
SULT1A2	chr16:28603263-28608391	0.354	0.094
SULT1B1	chr4:70591804-70626430	0.067	0.003
SULT1C2	chr2:108905094-108926371	0.238	0.059
SULT2A1	chr19:48373722-48389654	0.038	0.002
SUSD3	chr9:95820985-95847555	0.207	0.058
SYP	chrX:49044264-49056661	6.129	12.57
TAT	chr16:71481500-71645739	0.104	0.031
TENC1	chr12:53436972-53473204	0.217	0.083
THPO	chr3:184089772-184097640	0.254	0.036
TJP3	chr19:3708334-3761673	0.346	0.071
TM4SF4	chr3:149192361-149221181	0.139	0.012
TMEM176A	chr7:150488375-150502208	0.374	0.099
TNFRSF9	chr1:7975930-8003225	20.11	27.5
TNFSF10	chr3:172223297-172241306	0.239	0.082
TNXA	chr6:31971726-31981050	0.122	0.056
TPRXL	chr3:13978806-14107481	1.995	24.81
TRIB3	chr20:361307-378203	12.08	20.94
TTPA	chr8:63971799-63998645	0.194	0.036
TTR	chr18:29171729-29178986	0.098	0.016
UBASH3B	chr11:122526397-122685187	6.496	11.52
UBD	chr6:29520359-29527702	0.639	0.088
UGT1A1-9	chr2:234526290-234681951	0.452	0.08
UGT2A3	chr4:69794176-69817509	0.247	0.035
UGT2B15	chr4:69382873-69536494	0.23	0.033
UGT2B4	chr4:70345882-70361626	0.183	0.044
UGT2B7	chr4:69962192-70267587	0.351	0.069
UNC5B	chr10:72972291-73062635	25.96	72.69
UPP1	chr7:48128007-48148330	5.027	16.78
UPP2	chr2:158733116-158992666	1.437	10.27
VIL1	chr2:219283837-219461158	0.427	0.057
VNN1	chr6:133001996-133041070	0.238	0.052
VNN3	chr6:133043925-133055904	0.091	0.007

Supplementary Table 3 Top 10 significant canonical pathways identified by Ingenuity Pathways Analysis using 339 deregulated genes

Ingenuity Canonical Pathways	-log(B-H p-value)	Ratio	Downregulated	No change	Upregulated	No overlap with dataset	Molecules
FXR/RXR Activation	19.2	1.96E-01	27/138 (20%)	0/138 (0%)	0/138 (0%)	111/138 (80%)	KNG1,ABCG8,ABCG5,SLC10A1,APOB,NR1H4,APOA2,ABCC2,SLC22A7,HNF1A,CYP8B1,MTTP,PON1,NR1I2,HNF4A,BAAT,TTR,UGT2B4,AHSG,FETUB,SERPINF2,SULT2A1,ALB,ABCB4,G6PC,SLCO1B1,FGA
Nicotine Degradation II	15.7	2.60E-01	19/73 (26%)	0/73 (0%)	0/73 (0%)	54/73 (74%)	CYP3A7,FMO3,CYP1A1,UGT2B4,UGT2B7,CYP2C18,CYP2C9,FMO5,UGT1A1,CYP2C19,UGT2B15,CYP3A4,UGT2A3,CYP2E1,NADP,CYP4X1,CYP2B6,AOX1,CYP2C8
Melatonin Degradation I	15.2	2.65E-01	18/68 (26%)	0/68 (0%)	0/68 (0%)	50/68 (74%)	CYP3A7,CYP1A1,UGT2B4,UGT2B7,CYP2C18,CYP2C9,UGT1A1,CYP2C19,UGT2B15,SULT1A2,UGT2A3,CYP3A4,CYP2E1,SULT1A1,CYP4X1,CYP2B6,SULT1B1,CYP2C8
LPS/IL-1 Mediated Inhibition of R	15.2	1.25E-01	27/224 (12%)	0/224 (0%)	1/224 (0%)	196/224 (88%)	ABCG8,CYP3A7,ABCG5,CHST4,SLC10A1,NR1H4,ABCC2,CYP2C9,FMO5,HMGCS2,SULT1A2,CYP2C19,IL1R2,ALDH1A1,NR1I2,NGFR,NR1I3,FABP1,ALDH3A1,FMO3,SULT1C2,ACOX2,SULT2A1,CYP3A4,SULT1A1,CYP2B6,SULT1B1,CYP2C8
Xenobiotic Metabolism Signaling	13.9	1.06E-01	29/274 (11%)	0/274 (0%)	0/274 (0%)	245/274 (89%)	MAP2K6,CYP3A7,CYP1A1,FMO3,CHST4,UGT2B4,SULT1C2,UGT2B7,ABCC2,NQO1,PIK3C2G,CYP2C9,FMO5,UGT1A1,SULT2A1,CYP2C19,UGT2B15,SULT1A2,ALDH1A1,CYP3A4,NR1I2,SULT1A1,NR1I3,CES5A,CYP2B6,SLCO1B1,ALDH3A1,SULT1B1,CYP2C8
Superpathway of Melatonin Degr	13.8	2.20E-01	18/82 (22%)	0/82 (0%)	0/82 (0%)	64/82 (78%)	CYP3A7,CYP1A1,UGT2B4,UGT2B7,CYP2C18,CYP2C9,UGT1A1,CYP2C19,UGT2B15,SULT1A2,UGT2A3,CYP3A4,CYP2E1,SULT1A1,CYP4X1,CYP2B6,SULT1B1,CYP2C8
Nicotine Degradation III	13.8	2.71E-01	16/59 (27%)	0/59 (0%)	0/59 (0%)	43/59 (73%)	CYP3A7,CYP1A1,UGT2B4,UGT2B7,CYP2C18,CYP2C9,UGT1A1,CYP2C19,UGT2B15,UGT2A3,CYP3A4,CYP2E1,CYP4X1,CYP2B6,AOX1,CYP2C8
PXR/RXR Activation	12.4	2.22E-01	16/72 (22%)	0/72 (0%)	0/72 (0%)	56/72 (78%)	CYP3A7,ABCC2,CYP2C9,HMGCS2,UGT1A1,SULT2A1,CYP2C19,ALDH1A1,PRKAR2B,CYP3A4,NR1I2,NR1I3,G6PC,CYP2B6,HNF4A,CYP2C8
Estrogen Biosynthesis	11.2	2.77E-01	13/47 (28%)	0/47 (0%)	0/47 (0%)	34/47 (72%)	CYP3A7,CYP1A1,CYP2C18,CYP2C9,CYP2C19,CYP3A4,CYP2E1,NADP,CYP4X1,CYP2B6,AKR1C4,HSD17B2,CYP2C8
Acute Phase Response Signalin	11.2	1.23E-01	19/171 (11%)	0/171 (0%)	2/171 (1%)	150/171 (88%)	MAP2K6,HAMP,TTR,C4BPB,APOA2,AHSG,IKBKE,HNF1A,SERPINF2,FGG,SERPIND1,KLKB1,ALB,ITIH2,APCS,NGFR,CRP,FGB,FGA,SERPINE1,RBP5

Supplementary Table 4 **Deregulated miRNAs in HepaRG cells exposed to APAP (Fold changes>2)**

miRNAs*	Fold change (5mM APAP)	Fold change (10 mM APAP)
hsa-miR-7974	0.352	0.101
hsa-miR-216b-5p	0.731	0.164
hsa-miR-122-5p	0.685	0.201
hsa-miR-194-5p	0.776	0.293
hsa-miR-194-3p	0.679	0.297
hsa-miR-210-5p	0.474	0.316
hsa-miR-30b-3p	0.622	0.32
hsa-miR-130b-5p	0.675	0.335
hsa-miR-122-3p	0.938	0.348
hsa-miR-33b-3p	0.435	0.358
hsa-miR-29b-1-5p	0.54	0.396
hsa-miR-185-5p	0.65	0.421
hsa-miR-192-3p	0.571	0.448
hsa-miR-1268a	0.769	0.458
hsa-miR-3605-3p	0.593	0.462
hsa-miR-1268b	0.773	0.464
hsa-miR-192-5p	0.863	0.465
hsa-miR-128-1-5p	0.658	0.469
hsa-miR-92b-3p	0.604	0.482
hsa-miR-181d-5p	1.366	2.049
hsa-miR-221-5p	1.38	2.08
hsa-miR-4792	1.775	2.098
hsa-miR-199a-3p	1.76	2.103
hsa-miR-877-5p	1.84	2.12
hsa-miR-129-5p	0.875	2.156
hsa-miR-143-3p	1.748	2.234
hsa-miR-10b-5p	1.78	2.306
hsa-miR-3613-3p	1.783	2.351
hsa-miR-7705	2.6	2.44
hsa-miR-320a	1.688	2.481
hsa-miR-1290	2.633	2.52
hsa-miR-887-3p	1.641	2.538
hsa-miR-449a	1.379	2.586
hsa-miR-7704	1.611	2.703
hsa-miR-4454	1.833	2.75
hsa-miR-3144-3p	2.166	2.933
hsa-miR-3614-5p	3.68	3.12
hsa-miR-139-5p	2.366	3.133
hsa-miR-19b-3p	2.097	3.236
hsa-miR-3065-5p	2.312	3.564
hsa-miR-224-5p	2.121	3.737
hsa-miR-19a-3p	2.745	4.187
hsa-miR-1246	6.382	5.994
hsa-miR-320b	3.001	6.75
hsa-miR-320c	2.967	7.557
hsa-miR-4485-3p	9.741	8.451
hsa-miR-320d	3.5	10.65

Supplementary Table 5 ***In Silico*** **analysis to identify the miRNA-targeting genes using miRTar.Human database**

miRNA name*	Target genes#	Target transcript†	Target positions‡
hsa-miR-10b-5p	*ALPL*	NM_001127501	2013–34
hsa-miR-10b-5p	*ANXA13*	NM_001003954	1158–77
hsa-miR-10b-5p	*BDH1*	NM_203315	1390–411
hsa-miR-10b-5p	*CHST4*	NM_005769	1892–913
hsa-miR-10b-5p	*ECM2*	BC036806	1301–19
hsa-miR-10b-5p	*ETNK2*	AB073608	1167–87
hsa-miR-10b-5p	*IYD*	NM_203395	1853–71
hsa-miR-10b-5p	*MTMR3*	NM_021090	5334–53;5590–611
hsa-miR-10b-5p	*SDPR*	NM_004657	2855–73
hsa-miR-10b-5p	*SLC10A1*	BC069799	1275–96
hsa-miR-10b-5p	*VNN1*	AJ132099	2058–78
hsa-miR-122-5p	*GPR1*	NM_005279	2071–89
hsa-miR-122-5p	*MAFF*	NM_012323	2197–215
hsa-miR-122-5p	*NCAM1*	NM_181351	3179–200
hsa-miR-122-5p	*RGS16*	NM_002928	1309–29
hsa-miR-122-5p	*SESN2*	NM_031459	2181–202
hsa-miR-122-5p	*SLC7A11*	NM_014331	6525–43
hsa-miR-122-5p	*SLC7A5*	NM_003486	4105–26
hsa-miR-122-5p	*SLC9A1*	NM_003047	3557–78;3803–24;3902–23;4293–314
hsa-miR-122-5p	*SLCO5A1*	AK022760	3524–45
hsa-miR-1246	*HMGCS2*	NM_005518	1580–98
hsa-miR-1268a	*MAFF*	NM_012323	763–80
hsa-miR-1268a	*SLC6A9*	NM_001024845	2229–46
hsa-miR-1268a	*UNC5B*	AB096256	3664–81
hsa-miR-128-1-5p	*CPA4*	NM_016352	1696–717
hsa-miR-128-1-5p	*DCLK1*	BC152456	3460–82
hsa-miR-128-1-5p	*HFE*	NM_000410	1216–32
hsa-miR-128-1-5p	*ICOSLG*	NM_015259	1372–88;2986–3007
hsa-miR-128-1-5p	*NCAM1*	NM_181351	4438–58
hsa-miR-128-1-5p	*NGFR*	NM_002507	1826–45
hsa-miR-128-1-5p	*SLC1A4*	BC026216	2378–99
hsa-miR-128-1-5p	*SLC6A17*	NM_001010898	6017–37
hsa-miR-128-1-5p	*SLC7A11*	NM_014331	9028–46
hsa-miR-128-1-5p	*SLC7A5*	NM_003486	4358–78
hsa-miR-128-1-5p	*TPRXL*	AK092426	1452–71;1109–26
hsa-miR-128-1-5p	*ASNS*	M15798	1774–94
hsa-miR-1290	*HNMT*	AK301462	814–32
hsa-miR-1290	*MTMR3*	NM_021090	4867–85
hsa-miR-1290	*PLGLB2*	NM_002665	552–73
hsa-miR-129-5p	*ABCA6*	BC070125	809–29
hsa-miR-129-5p	*MTTP*	NM_000253	3615–36
hsa-miR-129-5p	*PIPOX*	NM_016518	2140–161
hsa-miR-130b-5p	*MAFF*	NM_012323	1164–85
hsa-miR-130b-5p	*SESN2*	NM_031459	1957–78
hsa-miR-130b-5p	*SLC7A11*	NM_014331	6520–41
hsa-miR-130b-5p	*UPP2*	AY225131	1476–97
hsa-miR-139-5p	*ALDH1A1*	BC001505	1898–919
hsa-miR-139-5p	*CDH1*	NM_004360	4660–79
hsa-miR-139-5p	*HNMT*	NM_006895	2138–59
hsa-miR-139-5p	*MYLK*	NM_053025	7764–85
hsa-miR-139-5p	*SERPIND1*	NM_000185	1774–95
hsa-miR-139-5p	*ST6GAL1*	NM_173217	2411–32
hsa-miR-139-5p	*TNFSF10*	AK296085	1599–619
hsa-miR-143-3p	*MASP1*	NM_001031849	1528–49
hsa-miR-181d-5p	*ACSS1*	NM_032501	3661–82
hsa-miR-181d-5p	*AQP9*	NM_020980	2352–72
hsa-miR-181d-5p	*IYD*	NM_203395	3683–705
hsa-miR-181d-5p	*KCNK5*	NM_003740	3156–76
hsa-miR-181d-5p	*SLC5A9*	AK131200	2335–56
hsa-miR-185-5p	*CPA4*	NM_016352	1825–46
hsa-miR-185-5p	*HCN4*	AJ132429	4198–219;4907–26;4955–76
hsa-miR-185-5p	*HFE*	NM_000410	2003–24

hsa-miR-185-5p	*NCAM1*	NM_181351	5316–37
hsa-miR-185-5p	*RGS16*	NM_002928	917–38
hsa-miR-185-5p	*SESN2*	NM_031459	2202–23
hsa-miR-185-5p	*SLCO5A1*	AK022760	3383–402
hsa-miR-185-5p	*SYP*	NM_003179	1321–41
hsa-miR-192-3p	*DUSP5*	NM_004419	2045–66
hsa-miR-192-3p	*ICOSLG*	NM_015259	2624–45
hsa-miR-192-5p	*ARL4C*	BC089043	1846–66
hsa-miR-192-5p	*ATF3*	NM_001030287	1480–501
hsa-miR-192-5p	*NGFR*	NM_002507	1980–2001
hsa-miR-192-5p	*PSAT1*	NM_021154	1466–85
hsa-miR-194-3p	*ARHGEF2*	NM_004723	3002–23
hsa-miR-194-3p	*ARL4C*	AJ579850	2580–601
hsa-miR-194-3p	*FOSL1*	NM_005438	1172–92;1417–38
hsa-miR-194-3p	*HAP1*	NM_177977	3381–401
hsa-miR-194-3p	*ICOSLG*	NM_015259	1365–86;1625–46
hsa-miR-194-3p	*MAFF*	NM_012323	1772–93
hsa-miR-194-3p	*NCAM1*	NM_001076682	3479–98
hsa-miR-194-3p	*NGFR*	NM_002507	2188–209
hsa-miR-194-3p	*RFX2*	AK024288	2161–82
hsa-miR-194-3p	*SERPINE1*	BC010860	1656–77
hsa-miR-194-3p	*SLC1A4*	BC026216	4499–520
hsa-miR-194-3p	*SLC6A17*	NM_001010898	5426–47;5565–86;6014–35
hsa-miR-194-3p	*SLC7A5*	NM_003486	3575–600
hsa-miR-199a-3p	*PLGLB2*	NM_002665	2333–54
hsa-miR-199a-3p	*SGK2*	NM_016276	1511–29
hsa-miR-210-5p	*HCN4*	AJ132429	4791–812
hsa-miR-210-5p	*IGFBP3*	X64875	1400–21
hsa-miR-210-5p	*NCAM1*	NM_181351	2992–3013
hsa-miR-210-5p	*NGFR*	NM_002507	2440–61
hsa-miR-224-5p	*CDH1*	NM_004360	3988–09
hsa-miR-224-5p	*CYP3A4*	NM_017460	2214–33
hsa-miR-224-5p	*DIO1*	NM_000792	1776–95
hsa-miR-224-5p	*IFITM2*	NM_006435	710–29
hsa-miR-224-5p	*KLHDC7A*	NM_152375	2887–905
hsa-miR-224-5p	*MTMR3*	NM_021090	5091–112
hsa-miR-224-5p	*OLFML3*	NM_020190	1658–79
hsa-miR-224-5p	*SDS*	BC020750	1002–19
hsa-miR-224-5p	*SLC47A2*	NM_001099646	2077–98
hsa-miR-3065-5p	*DDC*	NM_000790	1759–80
hsa-miR-3065-5p	*ECM2*	BC036806	1081–102
hsa-miR-30b-3p	*ARL4C*	BC089043	1360–81
hsa-miR-30b-3p	*CPA4*	NM_016352	2096–117
hsa-miR-30b-3p	*HAP1*	NM_177977	2275–96
hsa-miR-30b-3p	*MAFF*	NM_012323	1102–23
hsa-miR-30b-3p	*NGFR*	NM_002507	1705–26
hsa-miR-30b-3p	*SLC7A5*	NM_003486	1709–28
hsa-miR-30b-3p	*SYP*	NM_003179	1334–55
hsa-miR-30b-3p	*TNFRSF9*	NM_001561	1296–317
hsa-miR-30b-3p	*UNC5B*	AB096256	3324–45
hsa-miR-3144-3p	*SORBS2*	AK056758	2038–59
hsa-miR-3144-3p	*UGT2A3*	NM_024743	2838–59
hsa-miR-320a	*C6*	J05024	3259–80
hsa-miR-320a	*CYP8B1*	NM_004391	3632–53
hsa-miR-320a	*DDC*	NM_000790	1734–55
hsa-miR-320a	*EDN2*	BC034393	990–1007
hsa-miR-320a	*FYN*	NM_002037	2236–56
hsa-miR-320a	*HNF1A*	NM_000545	2605–26
hsa-miR-320a	*HOXA3*	NM_030661	2266–87
hsa-miR-320a	*MAP2K6*	BX641121	1148–69
hsa-miR-320a	*MTMR3*	NM_021090	8898–916
hsa-miR-320a	*NQO1*	NM_000903	1538–58
hsa-miR-320a	*RCN3*	AF183423	1279–98
hsa-miR-320a	*RORC*	NM_005060	1872–93

hsa-miR-320a	*SELL*	NM_000655	1524–45
hsa-miR-320a	*SLC17A4*	AB020527	2139–60
hsa-miR-320a	*SORBS2*	NM_003603	4120–41
hsa-miR-320a	*TM4SF4*	NM_004617	971–92
hsa-miR-320b	*C6*	J05024	3259–80
hsa-miR-320b	*CYP8B1*	NM_004391	3632–53
hsa-miR-320b	*DDC*	NM_000790	1734–55
hsa-miR-320b	*EDN2*	BC034393	990–1007
hsa-miR-320b	*FYN*	NM_002037	2236–56
hsa-miR-320b	*HNF1A*	NM_000545	2605–26
hsa-miR-320b	*HOXA3*	NM_030661	2266–87
hsa-miR-320b	*MAP2K6*	BX641121	1148–69
hsa-miR-320b	*MTMR3*	NM_021090	8898–916
hsa-miR-320b	*NQO1*	NM_000903	1538–58
hsa-miR-320b	*RCN3*	AF183423	1279–98
hsa-miR-320b	*RORC*	NM_005060	1872–93
hsa-miR-320b	*SELL*	NM_000655	1524–45
hsa-miR-320b	*SLC17A4*	AB020527	2139–60
hsa-miR-320b	*TM4SF4*	NM_004617	971–92
hsa-miR-320c	*C6*	J05024	3259–80
hsa-miR-320c	*CYP8B1*	NM_004391	3632–53
hsa-miR-320c	*DDC*	NM_000790	1734–55
hsa-miR-320c	*EDN2*	BC034393	990–1007
hsa-miR-320c	*FYN*	NM_002037	2236–56
hsa-miR-320c	*HNF1A*	NM_000545	2605–26
hsa-miR-320c	*HOXA3*	NM_030661	2266–87
hsa-miR-320c	*MAP2K6*	BX641121	1148–69
hsa-miR-320c	*NQO1*	NM_000903	1538–58
hsa-miR-320c	*RCN3*	AF183423	1279–98
hsa-miR-320c	*RORC*	NM_005060	1872–93
hsa-miR-320c	*SELL*	NM_000655	1524–45
hsa-miR-320c	*SLC17A4*	AB020527	2139–60
hsa-miR-320c	*TM4SF4*	NM_004617	971–92
hsa-miR-320d	*C6*	J05024	3259–80
hsa-miR-320d	*CYP8B1*	NM_004391	3632–53
hsa-miR-320d	*EDN2*	BC034393	990–1007
hsa-miR-320d	*HOXA3*	NM_030661	2266–87
hsa-miR-320d	*MAP2K6*	BX641121	1148–69
hsa-miR-320d	*NQO1*	NM_000903	1538–58
hsa-miR-320d	*RCN3*	AF183423	1279–98
hsa-miR-320d	*RORC*	NM_005060	1872–93
hsa-miR-320d	*SELL*	NM_000655	1524–45
hsa-miR-320d	*TM4SF4*	NM_004617	971–92
hsa-miR-33b-3p	*ARL4C*	AJ579850	2000–21
hsa-miR-33b-3p	*SLC6A17*	NM_001010898	5920–41
hsa-miR-33b-3p	*UPP2*	AY225131	1338–58
hsa-miR-449a	*CEACAM1*	NM_001712	1835–56
hsa-miR-449a	*ESPN*	NM_031475	3384–405
hsa-miR-449a	*FETUB*	NM_014375	1436–57
hsa-miR-449a	*GBA3*	NM_020973	1917–38
hsa-miR-449a	*HNF4A*	NM_000457	1664–85;1755–75
hsa-miR-449a	*IYD*	NM_203395	1904–23
hsa-miR-449a	*KRT5*	NM_000424	1939–59
hsa-miR-449a	*MASP1*	NM_001879	4147–65
hsa-miR-449a	*NQO1*	NM_000903	2280–301
hsa-miR-449a	*NRXN2*	NM_138734	2519–38
hsa-miR-449a	*TM4SF4*	NM_004617	1146–65
hsa-miR-877-5p	*AQP9*	NM_020980	2373–91
hsa-miR-877-5p	*CYP1A1*	AM233518	835–55
hsa-miR-877-5p	*G6PC*	NM_000151	2054–74
hsa-miR-877-5p	*MASP1*	NM_139125	2994–3015
hsa-miR-877-5p	*MAT1A*	NM_000429	3229–48
hsa-miR-877-5p	*NR1I2*	NM_003889	3675–93
hsa-miR-877-5p	*OLFML3*	NM_020190	1425–46

hsa-miR-92b-3p	*SLC9A1*	NM_003047	4334–54

*Deregulated miRNAs in HepaRG cells treated by 10 mM acetaminophen (Fold changes>2 or <0.5)
#Deregulated genes in HepaRG cells treated by 10 mM acetaminophen (Fold changes>10 or <0.1)
† The representative transcript.
‡ Counting from the transcription start site.

Supplementary Table 6 **Target molecules by transcription factors HNF1A, HNF4A and NR1I2**

TFs	**Genes***
HNF4A	*ABCA6*
HNF4A	*ALDH1A1*
NR1I2	*ALDH1A1*
HNF1A	*AQP9*
HNF4A	*AQP9*
HNF4A	*BDH1*
HNF4A	*CDH1*
HNF4A	*CEACAM1*
HNF4A	*CYP1A1*
NR1I2	*CYP1A1*
HNF4A	*CYP3A4*
NR1I2	*CYP3A4*
HNF4A	*CYP8B1*
HNF1A	*DDC*
HNF4A	*ETNK2*
HNF4A	*FETUB*
HNF1A	*G6PC*
HNF4A	*G6PC*
NR1I2	*HMGCS2*
HNF1A	*HNF1A*
HNF4A	*HNF1A*
HNF1A	*HNF4A*
HNF4A	*HNF4A*
NR1I2	*HNF4A*
HNF1A	*HNMT*
HNF4A	*IFITM2*
HNF1A	*MTTP*
HNF4A	*MTTP*
NR1I2	*MTTP*
HNF4A	*NR1I2*
NR1I2	*NR1I2*
NR1I2	*PIPOX*
HNF4A	*RORC*
NR1I2	*SERPIND1*
HNF1A	*SGK2*
HNF4A	*SGK2*
HNF1A	*SLC10A1*
HNF4A	*SLC10A1*
HNF1A	*TM4SF4*
HNF4A	*TM4SF4*
HNF1A	*UGT1A1*
HNF4A	*UGT1A1*
NR1I2	*UGT1A1*
HNF1A	*UGT2A3*
HNF4A	*UGT2A3*
HNF1A	*A1CF*
HNF1A	*AADAC*
HNF1A	*ABCC2*
HNF1A	*ADH4*

HNF1A	*ADH6*
HNF1A	*AHSG*
HNF1A	*AKR1C4*
HNF1A	*ALB*
HNF1A	*ALDOB*
HNF1A	*ANGPTL3*
HNF1A	*ANKS4B*
HNF1A	*APCS*
HNF1A	*APOA2*
HNF1A	*APOB*
HNF1A	*ASGR1*
HNF1A	*C14orf105*
HNF1A	*C8A*
HNF1A	*CPB2*
HNF1A	*CRP*
HNF1A	*CYP2E1*
HNF1A	*F11*
HNF1A	*FABP1*
HNF1A	*FGA*
HNF1A	*FGB*
HNF1A	*FRK*
HNF1A	*GJB1*
HNF1A	*GPX2*
HNF1A	*HABP2*
HNF1A	*HAL*
HNF1A	*HAO1*
HNF1A	*HGD*
HNF1A	*HSD17B2*
HNF1A	*KNG1*
HNF1A	*LRRC31*
HNF1A	*NR1H4*
HNF1A	*ONECUT1*
HNF1A	*PAH*
HNF1A	*PCK1*
HNF1A	*RBP5*
HNF1A	*SERPINA10*
HNF1A	*SERPINA7*
HNF1A	*SLC2A2*
HNF1A	*SLCO1B1*
HNF1A	*SULT1C2*
HNF1A	*TAT*
HNF1A	*TTR*
HNF1A	*UGT2B15*
HNF1A	*UGT2B7*
HNF1A	*VIL1*
HNF1A	*VNN3*
HNF4A	*A1CF*
HNF4A	*ABCC2*
HNF4A	*ABCG5*
HNF4A	*ABCG8*
HNF4A	*ACMSD*

HNF4A	*ACOX2*
HNF4A	*ACY3*
HNF4A	*ADH6*
HNF4A	*AGXT2*
HNF4A	*AHSG*
HNF4A	*AKR1C4*
HNF4A	*ALDH3A1*
HNF4A	*ALDOB*
HNF4A	*ANG*
HNF4A	*APCS*
HNF4A	*APOA2*
HNF4A	*APOB*
HNF4A	*ASGR1*
HNF4A	*BAAT*
HNF4A	*CCDC170*
HNF4A	*CCL14*
HNF4A	*CCL15*
HNF4A	*CIDEC*
HNF4A	*CPB2*
HNF4A	*CYP2B6*
HNF4A	*CYP2C8*
HNF4A	*CYP2C9*
HNF4A	*CYP2E1*
HNF4A	*CYP3A7*
HNF4A	*EPS8L3*
HNF4A	*F11*
HNF4A	*F13B*
HNF4A	*FABP1*
HNF4A	*FGA*
HNF4A	*FGB*
HNF4A	*FRK*
HNF4A	*GDF15*
HNF4A	*GJB1*
HNF4A	*GLYAT*
HNF4A	*GPX2*
HNF4A	*GYS2*
HNF4A	*HAL*
HNF4A	*HAO1*
HNF4A	*HGD*
HNF4A	*HPD*
HNF4A	*HSD17B2*
HNF4A	*IL22RA1*
HNF4A	*IRF6*
HNF4A	*KNG1*
HNF4A	*LAD1*
HNF4A	*NR1H4*
HNF4A	*NR1I3*
HNF4A	*ONECUT1*
HNF4A	*OTC*
HNF4A	*PCK1*
HNF4A	*PDZK1*

HNF4A	*PLA2G12B*
HNF4A	*PON1*
HNF4A	*PPP1R14D*
HNF4A	*PRODH2*
HNF4A	*RBP5*
HNF4A	*SERPINA10*
HNF4A	*SERPINA4*
HNF4A	*SLC22A18AS*
HNF4A	*SLC2A2*
HNF4A	*SPP1*
HNF4A	*SULT1A1*
HNF4A	*SULT1C2*
HNF4A	*SULT2A1*
HNF4A	*TAT*
HNF4A	*THPO*
HNF4A	*TMEM176A*
HNF4A	*TTR*
HNF4A	*UGT2B15*
NR1I2	*ABCC2*
NR1I2	*ANG*
NR1I2	*CYP2B6*
NR1I2	*CYP2C19*
NR1I2	*CYP2C8*
NR1I2	*CYP2C9*
NR1I2	*CYP3A7*
NR1I2	*FMO5*
NR1I2	*NR1H4*
NR1I2	*NR1I3*
NR1I2	*SLC22A7*
NR1I2	*SLCO1B1*
NR1I2	*SULT2A1*

*Data obtained from IPA software

Supplementary Table 7 Primers or Oligos used in this study

No.	Name	Sequence (5'--3')	Purpose
1	miR-122-5p-RT-F	UGGAGTGTGACAATGGTGTTTG	qRT-PCR
2	miR-194-5p-RT-F	TGTAACAGCAACTCCATGTGGA	qRT-PCR
3	miR-224-5p-RT-F	CAAGTCACTAGTGGTTCCGTT	qRT-PCR
4	miR-449a-RT-F	TGGCAGTGTATTGTTAGCTGGT	qRT-PCR
5	miR-320a-RT-F	AAAAGCTGGGTTGAGAGGGCGA	qRT-PCR
6	miR-877-5p-RT-F	GTAGAGGAGATGGCGCAGGG	qRT-PCR
7	U6-RT-F	CTCGCTTCGGCAGCACA	qRT-PCR
8	U6-RT-R	AACGCTTCACGAATTTGCGT	qRT-PCR
9	CYP2A6-RT-F	CCCTCATGAAGATCAGTGAGC	qRT-PCR
10	CYP2A6-RT-R	GCGCTCCCCGTTGCTGAATA	qRT-PCR
11	GSTT1-RT-F	AGAGTTGGATGTGACCCTGCA	qRT-PCR
12	GSTT1-RT-R	TCAGCTAAGGAGATGTGAGGACC	qRT-PCR
13	GSTM1-RT-F	CTATGATGTCCTTGACCTCCACCGTATA	qRT-PCR
14	GSTM1-RT-R	ATGTTCACGAAGGATAGTGGGTAGCTGA	qRT-PCR
15	SULT1A4-RT-F	GCCGCACCCACCCTGTTCTC	qRT-PCR
16	SULT1A4-RT-R	TGAGCTCCTGGGGGACGGTG	qRT-PCR
17	UGT1A1-2RT-F	CATGCTGGGAAGATACTGTTGAT	qRT-PCR
18	UGT1A1-2RT-R	GCCCGAGACTAACAAAAGACTCT	qRT-PCR
19	UGT1A6-RT-F	ACTTTGGGGCATGGTTGTAG	qRT-PCR
20	UGT1A6-RT-R	TGGTCATACGGCACTGGATA	qRT-PCR
21	UGT1A9-RT-F	CCCCCTTCCTCTATGTGTGTG	qRT-PCR
22	UGT1A9-RT-R	TCATACTCCGTAACAGGTGTTTG	qRT-PCR
23	SULT2A1-RT-F	TGAGTTCGTGATAAGGGATGAA	qRT-PCR
24	SULT2A1-RT-R	CAGATGGGCACAGATTGGAT	qRT-PCR
25	UGT2B15-RT-F	GAAAATTCTCGATAGATGGATATATGGTG	qRT-PCR
26	UGT2B15-RT-R	AACTGCATCTTTACAGAGCTTGTTACTG	qRT-PCR
27	UGT1A1-RT-F	GCTTTTGTCTGGCTGTTCCCACT	qRT-PCR
28	UGT1A1-RT-R	TCGAAGGTCATGTGATCTGAATGAGA	qRT-PCR
29	CYP2E1-RT-F	ACGGTATCACCGTGACTGTGG	qRT-PCR
30	CYP2E1-RT-R	GCATCTCTTGCCTATCCTTGA	qRT-PCR
31	SULT1A1-RT-F	AGGAGTTCATGGACCACAGC	qRT-PCR
32	SULT1A1-RT-R	TGAAGGTGGTCTTCCAGTCC	qRT-PCR
33	HNF1A-RT-F	AGTGAGTCCGGGCTTCACAC	qRT-PCR
34	HNF1A-RT-R	TGAAGGTCTCGATGACGCTG	qRT-PCR
35	HNF4A-RT-F	GTACTCCTGCAGATTTAGCC	qRT-PCR
36	HNF4A-RT-R	CTGTCCTCATAGCTTGACCT	qRT-PCR
37	CYP3A4-RT-F	TGTGCCTGAGAACACCAGAG	qRT-PCR
38	CYP3A4-RT-R	GTGGTGGAAATAGTCCCGTG	qRT-PCR
39	NR1I2-RT-F	TGCGAGATCACCCGGAAGAC	qRT-PCR
40	NR1I2-RT-R	ATGGGAGAAGGTAGTGTCAAAGG	qRT-PCR
41	GAPDH-RT-F	GAAATCCCATCACCATCTTCCAGG	qRT-PCR
42	GAPDH-RT-R	GAGCCCCAGCCTTCTCCATG	qRT-PCR
43	CYP3A4-long-F	GGGAAAGUTTCCTAAGGACTTCTGCTTTGC	Reporter gene assays
44	CYP3A4-long-R	GGAGACAUGCGAGTCCACCATGCCTAGC	Reporter gene assays
45	CYP3A4-M-F	GAAAGTTAATCCACTGTCTATTTGCCCATTGTTTAGAAAG	Reporter gene assays
46	CYP3A4-M-R	CTTTCTAAACAATGGGCAAATAGACAGTGGATTAACTTTC	Reporter gene assays
47	HNF1A-long-F	GGGAAAGUTGGAGAGCTAGGAGCAAAGC	Reporter gene assays
48	HNF1A-long-R	GGAGACAUAGGGTAGACGCGGTACACTG	Reporter gene assays
49	HNF1A-M-F	CTCTCCCAGGCCCCATGAAATCGTCGTTTCCTGTATTTGTTCC	Reporter gene assays
50	HNF1A-M-R	GGAACAAATACAGGAAACGACGATTTCATGGGGCCTGGGAGAG	Reporter gene assays
51	HNF4A-long-F	GGGAAAGUCCATCACCAAGCAGGAAGTT	Reporter gene assays
52	HNF4A-long-R	GGAGACAUGAGAAGACGGGATGGCTGAG	Reporter gene assays
53	NR1I2-M-F	GAGTATCTGTGGGAGTAAAATAGAGAGATGAGAAG	Reporter gene assays
54	NR1I2-M-R	CTTCTCATCTCTCTATTTTACTCCCACAGATACTC	Reporter gene assays
55	NR1I2-long-F	GGGAAAGUTGGGTGACACCTCCGAGA	Reporter gene assays
56	NR1I2-long-R	GGAGACAUAACTCTGTGAGCTCAGGATC	Reporter gene assays
57	HNF4A-M1685-F	CTAAGGGCCACATCCCACAAACACCCTTGACGCCCTGC	Reporter gene assays
58	HNF4A-M1685-R	GCAGGGCGTCAAGGGTGTTTGTGGGATGTGGCCCTTAG	Reporter gene assays
59	HNF4A-M1775-F	TTCTCATGTTGAAGCCACAAACTTCACCTTCACCTTCATC	Reporter gene assays
60	HNF4A-M1775-R	GATGAAGGTGAAGGTGAAGTTTGTGGCTTCAACATGAGAA	Reporter gene assays
61	Dye-CYP3A4-224-TAR	/5Cy55/ mAmGmUmUmAmAmUmCmCmAmCmUmGmUmGmAmCmUmUmU	RNA EMSAs
62	Dye-HNF1A-320-TAR	/5Cy55/mGmGmCmCmCmCmAmUmGmAmCmCmUmCmCmAmGmCmUmU	RNA EMSAs
63	Dye-HNF4A-449-TAR-1664	/5Cy55/ mUmAmAmGmGmGmCmCmAmCmAmUmCmCmCmAmCmUmGmC	RNA EMSAs
64	Dye-HNF4A-449-TAR-1775	/5Cy55/ mCmUmCmAmUmGmUmUmGmAmAmGmCmCmAmCmUmGmCmC	RNA EMSAs
65	Dye-NR1I2-877-TAR	/5Cy55/mAmUmCmUmGmUmGmGmGmAmGmUmCmCmUmCmUmAmG	RNA EMSAs
66	Dye-hsa-miR-224-5p	/5IRD800CWN/ rCrArArGrUrCrArCrUrArGrUrGrGrUrUrCrCrGrUrU	RNA EMSAs
67	Dye-hsa-miR-320a	/5IRD800CWN/ rArArArArGrCrUrGrGrGrUrUrGrArGrArGrGrGrCrGrA	RNA EMSAs
68	Dye-hsa-miR-449a	/5IRD800CWN/ rUrGrGrCrArGrUrGrUrArUrUrGrUrUrArGrCrUrGrGrU	RNA EMSAs
69	Dye-hsa-miR-877-5p	/5IRD800CWN/ rGrUrArGrArGrGrArGrArUrGrGrCrGrCrArGrGrG	RNA EMSAs
70	Cold-hsa-miR-224-5p	rCrArArGrUrCrArCrUrArGrUrGrGrUrUrCrCrGrUrU	RNA EMSAs
71	Cold-hsa-miR-320a	rArArArArGrCrUrGrGrGrUrUrGrArGrArGrGrGrCrGrA	RNA EMSAs
72	Cold-hsa-miR-449a	rUrGrGrCrArGrUrGrUrArUrUrGrUrUrArGrCrUrGrGrU	RNA EMSAs

73	Cold-hsa-miR-877-5p	rGrUrArGrArGrGrArGrArUrGrGrCrGrCrArGrGrG	RNA EMSAs
74	Cold-NC	rUrCrArCrArArCrCrUrCrCrUrArGrArArArGrArGrUrArGrA	RNA EMSAs
75	Bio-miR-224-Duplex-F	rCrArArGrUrCrArCrUrArGrUrGrGrUrUrCrCrGrUrU/3Bio/	Capture by biotinylated miRNA duplexes
76	Bio-miR-224-Duplex-R	rCrGrGrArArCrGrArCrUrArGrUrGrArCrUrArGrArG	Capture by biotinylated miRNA duplexes
77	Bio-miR-320-Duplex-F	rArArArArGrCrUrGrGrGrUrUrGrArGrArGrGrGrCrGrA/3Bio/	Capture by biotinylated miRNA duplexes
78	Bio-miR-320-Duplex-R	rGrCrCrCrUrCrArCrArArCrCrCrArGrCrUrUrArUrArG	Capture by biotinylated miRNA duplexes
79	Bio-miR-449-Duplex-F	rUrGrGrCrArGrUrGrUrArUrUrGrUrUrArGrCrUrGrGrU/3Bio/	Capture by biotinylated miRNA duplexes
80	Bio-miR-449-Duplex-R	rCrArGrCrUrArUrCrArArUrArCrArCrUrGrCrGrArArG	Capture by biotinylated miRNA duplexes
81	Bio-miR-877-Duplex-F	rGrUrArGrArGrGrArGrArUrGrGrCrGrCrArGrGrG/3Bio/	Capture by biotinylated miRNA duplexes
82	Bio-miR-877-Duplex-R	rCrUrGrCrGrCrGrArUrCrUrCrCrUrCrUrUrCrArG	Capture by biotinylated miRNA duplexes
83	Bio-miR-NC-Duplex-F	rUrCrArCrArArCrCrUrCrCrUrArGrArArArGrArGrUrArGrA/3Bio/	Capture by biotinylated miRNA duplexes
84	Bio-miR-NC-Duplex-R	rUrArCrUrCrUrCrUrCrUrArGrGrArGrGrUrUrGrUrCrArArG	Capture by biotinylated miRNA duplexes