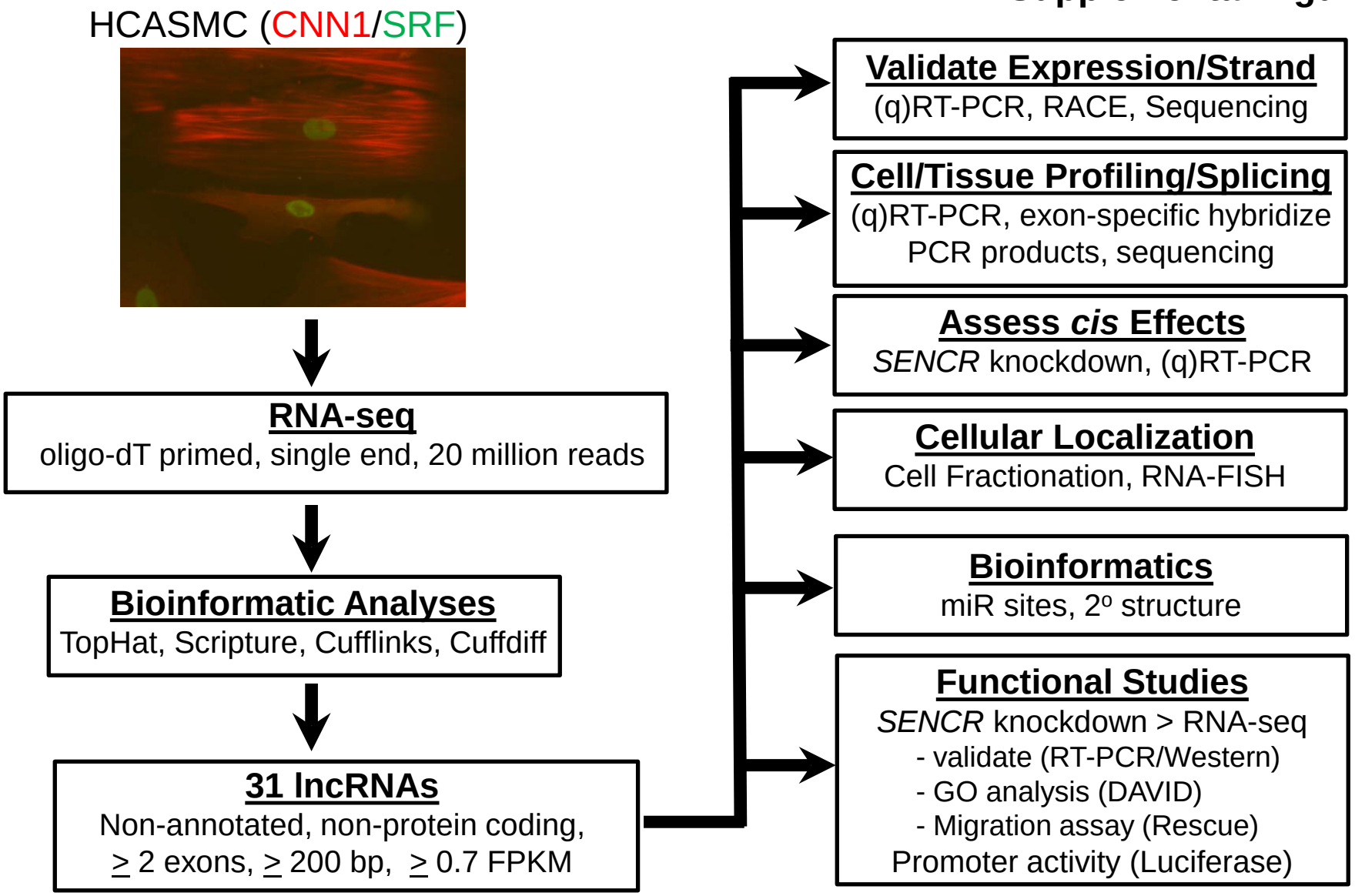
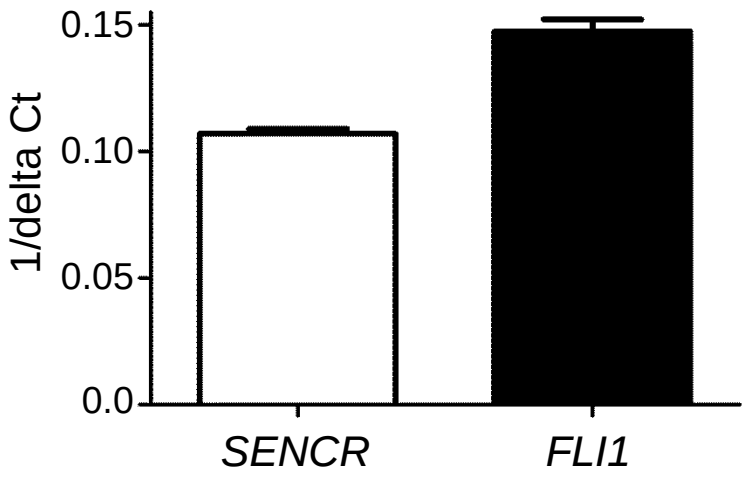
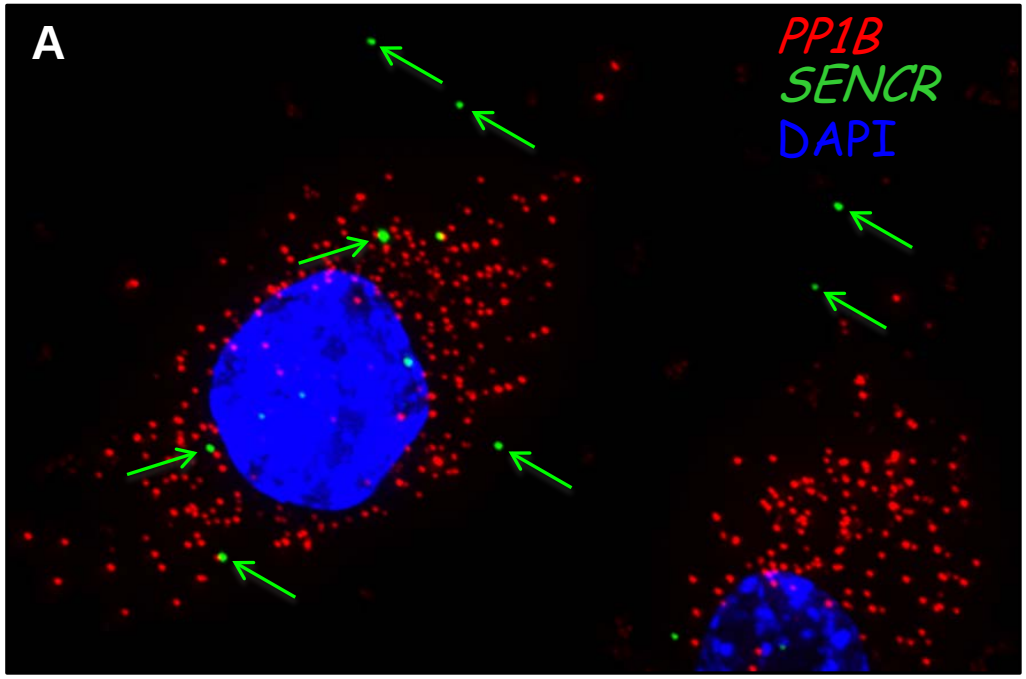
Supplemental Figure I

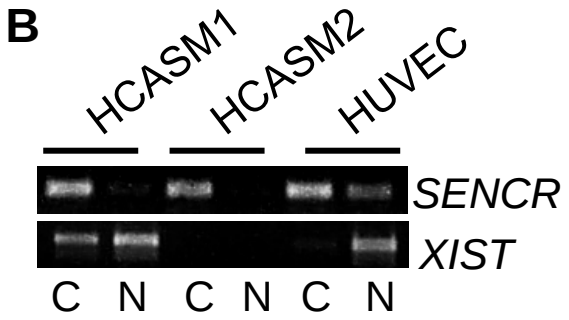


Supplemental Figure I. Summary of experimental workflow. We developed this workflow for the study of *SENCR* and other unannotated or uncharacterized lncRNAs. Primary cultures of HCASMC were chosen that express contractile proteins (such as CNN1 in red) as well as the SRF transcription factor (shown in green). See Materials and Methods and Results for further details.

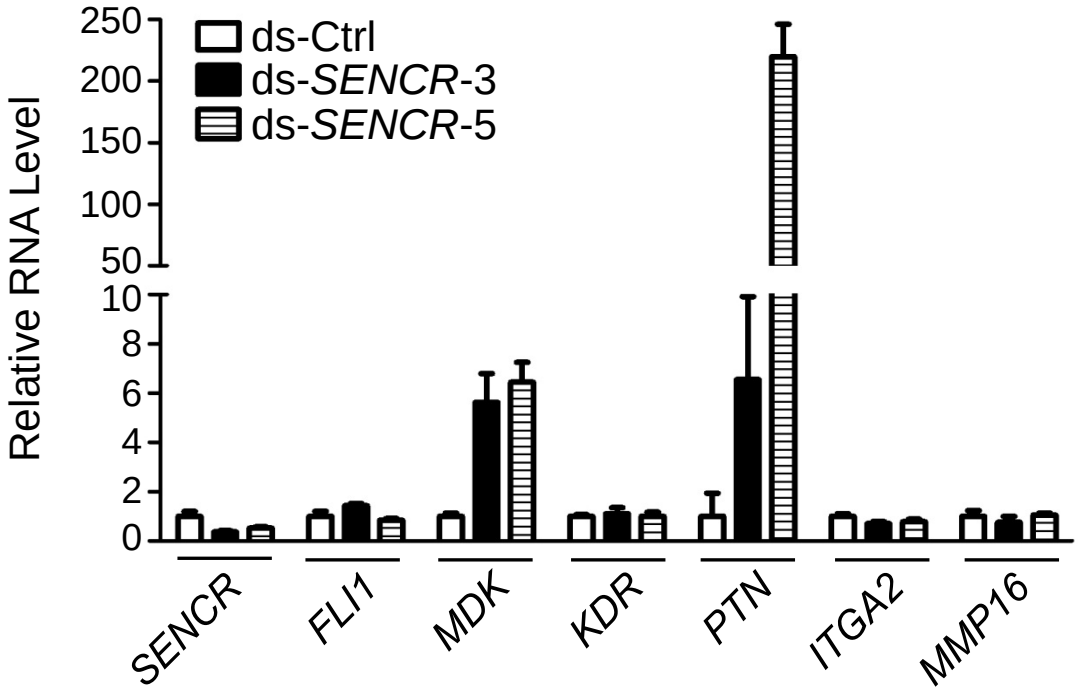


Supplemental Figure II. Relative level of *SENCR* versus *FLI1* in HCASMC. One divided by the delta Ct value for *SENCR* (n=9) and *FLI1* (n=9) RNA expression in HCASMC.

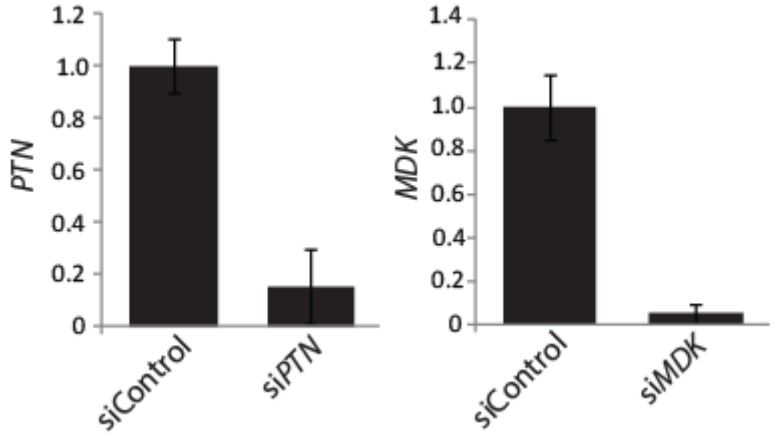




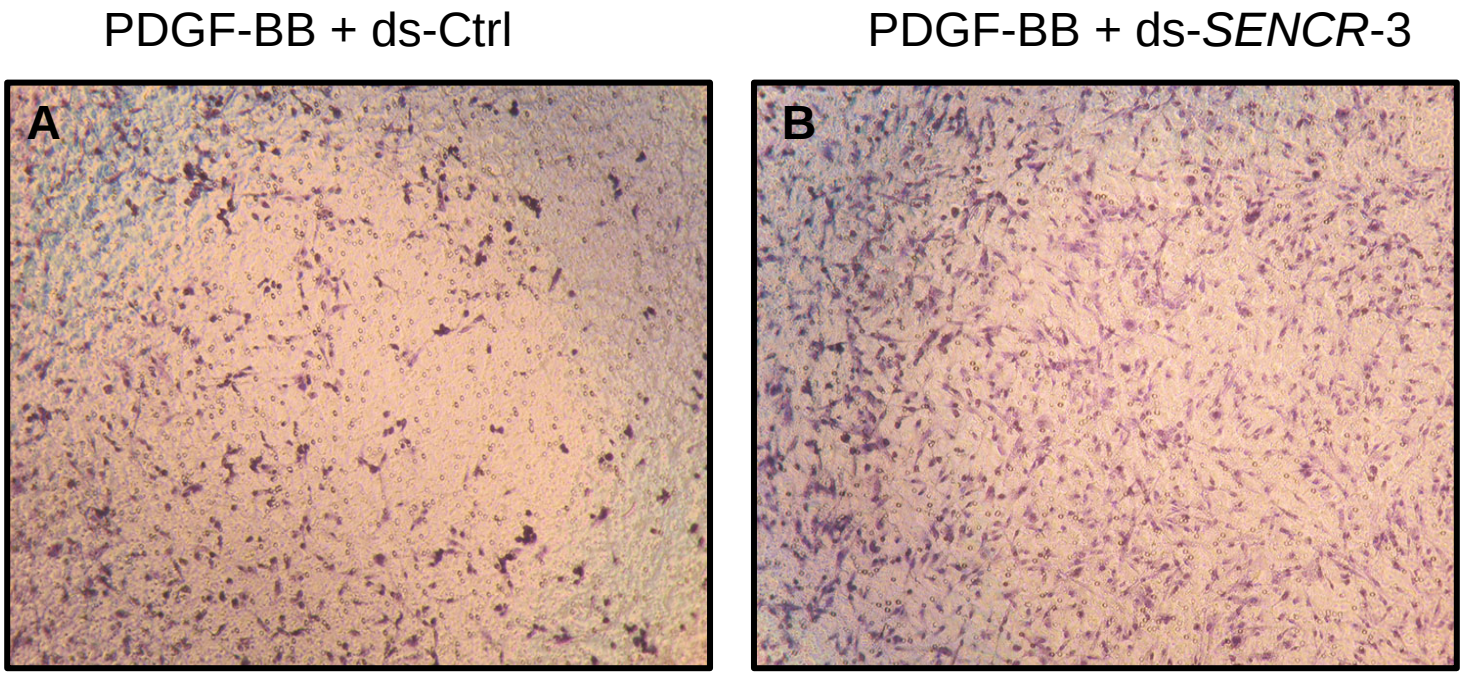
Supplemental Figure III. Localization of *SENCR*. (A) Higher magnification image of boxed region in Figure 4A. Arrows indicate *SENCR* transcripts localized to the cytoplasm of two HUVEC. Omission of labeled probes revealed no background fluorescence (not shown). (B) *SENCR* versus *XIST* RNA localization in cytoplasmic (C) or nuclear (N) fractions of the indicated cell types.



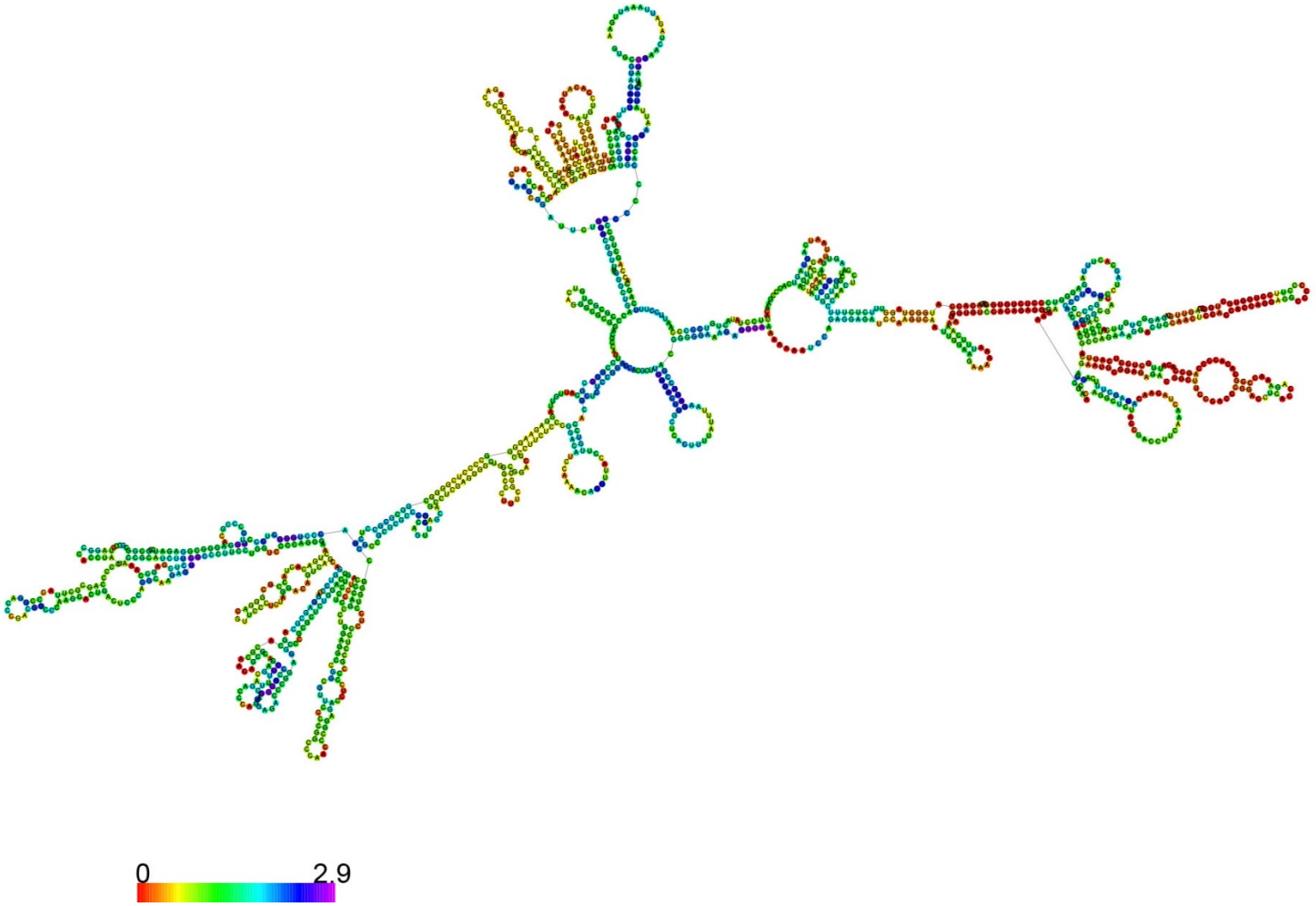
Supplemental Figure IV. Effect of *SENCR* knockdown on expression of pro-migratory genes in HUVEC. Quantitative RT-PCR of indicated genes following transfection with either control dicer substrate RNA or either of two dicer substrate RNAs that target different regions of *SENCR*. Note obvious reductions in *SENCR* upon its targeted knockdown with minimal effects on *FLI1*, but associated induction of *PTN* and *MDK*.



Supplemental Figure V. siRNA knockdown of *PTN* and *MDK*. Quantitative RT-PCR analysis of *PTN* (**left**) and *MDK* (**right**) mRNA levels after siRNA knockdown. The y-axis represents the normalized levels of each transcript with si-Controls set to 1.



Supplemental Figure VI. Effect of combined PDGF-BB treatment and *SENCR* knockdown on HCASMC migration. Boyden chamber assay with HCASMC transfected with either control (**A**) or *SENCR* (**B**) dicer substrate RNA followed by 6 hr stimulation with 25 ng/ml PDGF-BB. Note accentuated HCASMC migration with combined PDGF-BB/*SENCR* knockdown.



Supplemental Figure VII. Predicted secondary structure of *SENCR_V1*. This secondary structure was generated with the program RNAFold. See Discussion for more details.

Supplemental Table I: Oligonucleotides

Gene	Strand	Primer Sequence	Size (bp)	Application(s)
SENCR_V2	Forward Reverse	GTAGAGTTTAAGCAGTGTGGAG GGTGGTGGAGTTGGAGTC	259	RT-PCR, fractionation
SENCR_V2	Forward Reverse	TTACCTTGTCCACGCTCTCC CCGTCTCTCCGCATTCTCC	209	qPCR
FLI1	Forward Reverse	TGTCTCTTTCGCTCCGCTAC CTCCTTAATAGTCCCGTCCATTTG	211	qPCR
18S	Forward Reverse	ATGGGCGGCGGAAAATAGC TCTTGGTGAGGTCAATGTCTGC	100	qPCR
SENCR_V 1/V2	Forward Reverse	GTGCGTAGAGTTTAAGCAGTGTGGAGAT AGGGCAAGTCTTCAATTTAATCTAGTTCCATATTG	1288/600	RT-PCR, cloning
NEAT1	Forward Reverse	TTCCTTCTTCCCTTTAAGTTTCAC CTTACCATACAGAGCAACATACC	289	RT-PCR, fractionation
XIST	Forward Reverse	GAGATAGCTGCCTAGTGGAAATG CCTATCTGGGACCAGGAAAGTA	627	RT-PCR, fractionation
GAPD	Forward Reverse	CGCTCTCTGCTCCTCCTGTTC TTGACTCCGACCTTCACCTTCC	103	qPCR
ETS1	Forward Reverse	TGGACCAATCCAGCTATGGCAGTT AGGCCACGGCTCAGTTTCTCATAA	183	qPCR
KCNJ1	Forward Reverse	ATCAAAGGTGCAGGGACTTGCTCA AGTCCTCATGGATTGCTGGAGT	105	qPCR
MDK	Forward Reverse	ATTGCGGCGTGGGTTTC TCCTGGCACTGAGCATTGTA	202	qPCR
PTN	Forward Reverse	GAGCTGAGTGCAAGCAAAC CTTGGAGATGGTGACAGTCTT	200	qPCR
ITGA2	Forward Reverse	GTGGTTGTGTGTGATGAATCAAATAGT GTCTGGGATGTTGCTACAATCATTT	200	qPCR
MMP16	Forward Reverse	TGCAGAGACCATGCAGTC CTGTAAGTGATGTGCTTGTGC	210	qPCR
	Forward	GCGGCAGAGAAACCAGAC		

LMOD1	Reverse	CCACTTGCTTGCTTTCATCC	131	qPCR
CNN1	Forward Reverse	ATGTCCTCTGCTCACTTCAAC GCTGGTGGTCATACTTCTGG	95	qPCR
TAGLN	Forward Reverse	CATCCTGTCTGTCCGAACC CACTATGATCCACTCCACCAG	184	qPCR
MYOCD	Forward Reverse	TGCTGCTGTAAAGTCCAAATCC GCGTAGGCTGAGTCCATAGG	156	qPCR
lnc1	Forward Reverse	GGTGTCGAGCTTGAACGCTTTCTTAATTGG AAGAGCACACCCGTCTATGTAGCA	281	RT-PCR
lnc2	Forward Reverse	CTGGATTGCCACATGGCTCACATTG CTCCAGCAGCCTTCTTGTCCATTGCTTC	262	RT-PCR
lnc3	Forward Reverse	GCTTCCATTGGTGGGTCATTTT TATTGGCCAAGTGGAGACTGGTGT	222	RT-PCR
lnc4	Forward Reverse	GGCTACACCCTAGACCAAACCTACGC TAGGGTGGGGCGCATCCATATAGTC	302	RT-PCR
lnc5	Forward Reverse	ACTTTAGTGGCCTGTCCTGCTCA TGACGCCCACCCAGGTTAAGAATA	276	RT-PCR
lnc6	Forward Reverse	GGTGTGATGTTGGCTGTTGATGCTGTAA CTTCTCCATCAACGTCTTCAGCGA	415	RT-PCR
lnc7	Forward Reverse	TTCCACCTTCACCACCTGCTGTAT GCACATCTGACAGCATTGCACACT	412	RT-PCR
lnc8	Forward Reverse	GGTGTCGAGCTTGAACGCTTTCTT AAGAGCACACCCGTCTATGTAGCA	282	RT-PCR
lnc9 (SENCR)	Forward Reverse	CAGCCAGAAAGGACTCCAACTCC GGAGGCAGCTGGTGCTGAAAG	273	RT-PCR, V1+V2
lnc10	Forward Reverse	ACAGGTGGTGAAGCTCCTTATGGT AGCAACATGTCACCAGCGTACTCA	481	RT-PCR
lnc11	Forward Reverse	AGCCAAGGAAGGCATCGAGAAGAT CTGTGATGACACCCTTTCTTCCAACC	231	RT-PCR
lnc12	Forward Reverse	TACTGGTGGTGCAGTGTTTGGAGA AGGGCATCCGAACTCTGTCTTTCT	317	RT-PCR
	Forward	GCAGCTTCACGTTGATGCCATTTC		

lnc13	Reverse	CAAGCAAGAGTAGTCGCTGTTGGA	200	RT-PCR
lnc14	Forward Reverse	ATGTTCAACCTGTGTCCTGACCCT TCCAGTTCAGATACAACCAGGCCA	239	RT-PCR
lnc15	Forward Reverse	CCCATTTGAGTTTCTTCAGATAGATCC TCCTGCCTAAATTACATCCAGGACCC	206	RT-PCR
lnc16	Forward Reverse	ATGGTGGAAATTTCAGAGGAGCCC TAGCCACGATTGTTTCCTCGTCCT	238	RT-PCR
lnc17	Forward Reverse	TGGCCAGTACAGTGGTAGCAGTT TGGCAGTAGGGCTTACACCTAGTA	219	RT-PCR
lnc18	Forward Reverse	ACCTCACTGAAGCCAAGTCCACAA ATCTAGCAATTGGGAGGCAGCAGA	251	RT-PCR
lnc21	Forward Reverse	TAGAAGCATTACCTGCCAGCTCCA CAAAGCTGGAAAGGACAGTGGGAA	210	RT-PCR
lnc22	Forward Reverse	ACACTCGGGAGGTGTCTTGAGATT AACATTCCCTCCTTTGGCCCTACA	384	RT-PCR
lnc23	Forward Reverse	TTAGCCTTCTGAGCTTTCTGGGCA GAAATCTGGTGATGCTGCCATCGT	204	RT-PCR
lnc24	Forward Reverse	ACATGCACACACACGCATACACAC TCCTTGAACGTGAAGGACTGGGTT	527	RT-PCR
lnc26	Forward Reverse	TACCGGCAAGATCATCACCCTTGA TGTAGTCAGAAAGACTGCGGCCAT	383	RT-PCR
lnc27	Forward Reverse	TGGAGTGACGACTTCGGTTTGAGT CCCTTCCCAATTCCACAACGCAAT	212	RT-PCR
lnc29	Forward Reverse	AGAGAGGACATGGGTTTCTCTGC AAATGGTGGCAGACATGTGCAAGG	206	RT-PCR
lnc30	Forward Reverse	TGAAGGAGACTTGGAACGCACAGA ACCGATCTCTCAGCAAACTCAGCA	222	RT-PCR
ds-*SENCR*-1	Sense Anti-sense	GUGGCAGACACCAUGGCUAGGUUTC GAAACCUAGCCAUGGUCUCUGCCACAG	Knockdown exon 3	RT-PCR
ds-*SENCR*-2	Sense Anti-sense	GCAGUGGUGGAGAUAUUUCUUCACTT AAGUGAAGAAAUAUCUCCACACACUGCUU	Knockdown exon 1	RT-PCR

ds-*SENCR*-3	Sense Anti-sense	CAUUCAGCCAGAAAGGACUCCAACT AGUUGGAGUCCUUUCUGGCUGAAUGAG	Knockdown exon 3	RT-PCR RNA-FISH, Western
ds-*SENCR*-4	Sense Anti-sense	CUUCAAACUACAACAGAGCUUUCAG CUGAAAGCUCUGUUGUAGUUUGAAGGU	Knockdown exon 3	RT-PCR, RNA-FISH, Western
ds-*SENCR*-5	Sense Anti-sense	AGAGGAGAUCCAAGUCAAUUGGAAG CUUCCAAUUGACUUGGAUCUCCUCUGG	Knockdown exon 2	RT-PCR, RNA-FISH, Western
si-*PTN*	Sense Anti-sense	AAACCUCAAGCAGAAUCUAtt UAGAUUCUGCUUGAGGUUUgg	Knockdown exons 4-5	RT-PCR, Rescue migration
si-*MDK*	Sense Anti-sense	CGUUAGCUUUAAUCAAUCAtt UGAUUGAUUAAAGCUAACGag	Knockdown exon 5	RT-PCR, Rescue migration
si-*SRF*	Sense Anti-sense	UGAUGUACCCUAGCCCGCA UGCGGGCUAGGGUACAUCA	Knockdown exon 5	RT-PCR
SENCR promoter(1)	Forward Reverse	GATACGCTAGCTCACCAAGAGAGCAGAAGAATG GATACAAGCTTGATCCAGAAGGGTGGTAAGATG	555	Luciferase assay
SENCR promoter(2)	Forward Reverse	GATACGCTAGCCCATGTCTGTCTTCTCTGTCTC GATACAAGCTTGATCCAGAAGGGTGGTAAGATG	1390	Luciferase assay
SENCR promoter(3)	Forward Reverse	GATACGCTAGCCCATGTCTGTCTTCTCTGTCTC GATACAAGCTTAGCCTGGGTCTAGGTTGCAAAGTC	2145	Luciferase assay
SENCR promoter(4)	Forward Reverse	GATACAAGCTTCCATGTCTGTCTTCTCTGTCTC GATACGTCGACCTAGCCAACTCTCCCTCCATAC	3804	Luciferase assay
DLL4 promoter	Forward Reverse	GATACCTCGAGTGCTCAGCAAATGTGGGCAAAGCTC GATACAAGCTTCCCCTCGGGCGTCGCTCTCTCCAC	2673	Luciferase assay
FLI1 promoter	Forward Reverse	GATACGTCGACCTAGCCAACTCTCCCTCCATAC GATACGTCGACACACATTGACCCGGTTACAG	730	Luciferase assay

Supplemental Table II: HCASMC lncRNA Annotation

LncRNA	Chromosomal Coordinates	FPKM	Nearest Gene	Class of LncRNA	Gene (bp)	RNA (bp)	Exons
1	chr11:10529961-10530629	73.07686	*AMPD3*	Overlapping Antisense	670	434	3
2	chr12:44053658-44055300	25.7154	*PUS7L*	lincRNA	1644	1537	2
3	chr15:53229136-53230825	32.0959	*ONECUT1*	lincRNA	1691	1442	2
4	chr17:51183035-51183819	29.7556	*C17ORF112*	lincRNA	786	632	2
5	chr2:85568560-85568968	25.7651	*RETSAT*	lincRNA	410	316	2
6	chr12:8167668-8170528	10.44818	*FOXJ2*	lincRNA	2862	1763	3
7	chr1:186503185-186504791	2.49228	*PDC*	lincRNA	1608	188	2
8	chr11:10530055-10530570	10.6143	*AMPD3*	Overlapping Sense	517	256	2
9	chr11:128561579-128565159	0.817717	*FLI1*	Overlapping Antisense	4352	1324	3
10	chr11:3404694-3406064	1.05462	*ZNF195*	lincRNA	1372	ND	2
11	chr12:56905202-56906483	1.23896	*RBMS2*	lincRNA	1283	1019	3
12	chr12:102267056-102267421	6.90622	*DRAM1*	lincRNA	367	186	2
13	chr14:21189013-21190323	1.38877	*RNASE4*	lincRNA	1312	ND	2
14	chr14:35899242-35899465	7.58485	*NFKBIA*	lincRNA	225	168	2
15	chr14:43769419-43769826	18.2421	*FSCB*	lincRNA	409	279	2
16	chr14:45759231-45759672	0.76604	*MIS181*	lincRNA	443	390	2
17	chr14:44589064-44589961	2.76558	*FSCB*	lincRNA	899	205	2
18	chr15:23142469-23145926	16.8838	*LOC283683*	lincRNA	3459	ND	2
19	chr15:97094528-97095952	1.88622	*NR2F2*	lincRNA	1426	476	2
20	chr15:93277172-93277445	1.94676	*FAM174B*	Overlapping Antisense	275	196	2
21	chr16:15457519-15458790	1.76395	*NPIPA5*	Overlapping Sense	1273	479	2
22	chr16:27144448-27145052	14.9873	*C16orf82*	lincRNA	606	437	2
23	chr16:29223901-29232315	1.17883	*RRN3P2*	Intronic Antisense	8416	3751	3
24	chr17:58177984-58180097	0.785952	*APS12*	Overlapping Antisense	2115	769	2
25	chr17:21730708-21731863	9.14475	*UBC*	Overlapping Antisense	1157	1002	2
26	chr17:40684243-40686068	3.43368	*NAGLU*	lincRNA	1827	1180	2
27	chr18:12211342-12211882	1.34323	*C18ORF61*	Intronic Sense	542	449	2
28	chr18:51933119-51933506	10.7875	*C18ORF54*	lincRNA	389	333	2
29	chr19:42012005-42012823	11.747	*LOC100505495*	lincRNA	820	631	2
30	chr19:18141391-18144200	6.79831	*ARRDC2*	lincRNA	2811	2718	2
31	chr8:129347866-129355944	1.31767	*PVT1*	lincRNA	8080	5799	3
AVG		11.11386			1532.2	835.6	2.2

Supplemental Table III: Significantly Regulated Protein Coding Genes Upon *SENCR* Knockdown

Down-regulated genes (those highlighted in red are SMC contractile genes)

Gene Symbol	Chr Coordinates	Avg FPKM-*SI*	Avg FRKM-CT	Ratio	log2 fold	test_stat	p_value	q_value	Sig?
NPPB	1:11917520-11918992	1.67187	6.91744	0.241689	-2.04878	-7.56067	4.02E-14	6.36E-12	yes
AS3MT	10:104613966-104661656	0.1	0.43491	0.229933	-2.12072	1.79769e+	3.21E-11	3.00E-09	yes
KRT81	12:52679696-52685299	0.508238	1.58705	0.320241	-1.64277	-6.0158	1.79E-09	1.25E-07	yes
SAA2-SAA4	11:18252901-18270221	1.09508	3.28963	0.332889	-1.58689	-3.4807	0.0005	0.008951	yes
KRT83	12:52708084-52715182	0.320339	0.953714	0.335886	-1.57396	-4.50286	6.70E-06	0.000215	yes
INHBE	12:57849095-57851791	0.801588	2.26764	0.35349	-1.50026	-7.79683	6.44E-15	1.15E-12	yes
SAA3P	11:18134018-18137679	2.45141	6.87889	0.356367	-1.48856	-6.00159	1.95E-09	1.34E-07	yes
SAA1	11:18287807-18291524	5.78412	16.0323	0.360779	-1.47081	-7.22546	4.99E-13	6.48E-11	yes
SAA2	11:18252901-18270221	4.3833	11.931	0.367387	-1.44463	-6.36198	1.99E-10	1.63E-08	yes
KRT85	12:52753789-52761309	0.205943	0.558741	0.368584	-1.43993	-3.81788	0.000135	0.002998	yes
KRT86	12:52695648-52702947	0.318752	0.849578	0.375189	-1.41431	-4.22833	2.35E-05	0.000663	yes
LOC100506119	9:132099227-132109756	1.46674	3.79696	0.386293	-1.37223	-4.56135	5.08E-06	0.000166	yes
ACTBL2	5:56775842-56778636	7.85865	20.0093	0.39275	-1.34832	-17.8567	0	0	yes
ACTA2	10:90694830-90775542	86.5123	212.557	0.407008	-1.29687	-16.3592	0	0	yes
COL15A1	9:101706137-101833068	0.195063	0.476933	0.408995	-1.28985	-4.8835	1.04E-06	3.98E-05	yes
HAPLN1	5:82934016-83016896	1.83977	4.32533	0.425348	-1.23328	-12.8233	0	0	yes
TNFRSF11B	8:119935795-119964383	55.2971	129.003	0.42865	-1.22213	-16.0536	0	0	yes
HSPB7	1:16340522-16345285	3.14588	7.33526	0.428871	-1.22138	-12.7874	0	0	yes
CHAC1	15:41245635-41248717	1.70823	3.95139	0.432311	-1.20986	-6.95146	3.62E-12	4.07E-10	yes
RAB33A	X:129305772-129318844	1.00234	2.31748	0.432513	-1.20918	-4.35308	1.34E-05	0.0004	yes
LOC100131774	6:132266629-132272518	33.4117	77.1881	0.432861	-1.20803	-3.8935	9.88E-05	0.002297	yes
CCL20	2:228678557-228682280	1.85539	4.27492	0.434017	-1.20417	-4.86084	1.17E-06	4.43E-05	yes
ACTC1	15:35080296-35087927	19.2515	41.9828	0.458557	-1.12483	-15.4256	0	0	yes
TIMP3	22:32908538-33454377	46.4899	100.731	0.461525	-1.11552	-12.026	0	0	yes
KRT7	12:52626953-52642709	3.85443	8.32579	0.462951	-1.11107	-9.86012	0	0	yes
CXCR7	2:237478379-237490997	0.483021	1.03894	0.464917	-1.10495	-3.95532	7.64E-05	0.001845	yes
ENC1	5:73923233-73937249	6.00301	12.8552	0.466971	-1.09859	-15.277	0	0	yes
MYLK	3:123304402-123603149	18.5221	39.6366	0.467298	-1.09759	-11.9095	0	0	yes
NOV	8:120428551-120436678	0.787773	1.68063	0.468737	-1.09315	-5.60636	2.07E-08	1.11E-06	yes
KRT8P41	11:9115909-9117737	0.478481	1.00633	0.475471	-1.07257	-3.52188	0.000429	0.007865	yes
IGFBP3	7:45951843-45960871	191.608	402.169	0.476437	-1.06964	-11.7018	0	0	yes

CSF2RB	22:37309674-37336481	2.81491	5.89889	0.477193	-1.06735	-12.7188	0	0	yes
JPH2	20:42740336-42816218	0.69806	1.45422	0.480024	-1.05882	-6.21476	5.14E-10	3.94E-08	yes
LMOD1	1:201865583-201915716	2.65474	5.51853	0.481059	-1.05571	-11.5643	0	0	yes
ODZ2	5:166711842-167691162	1.06153	2.20623	0.481151	-1.05544	-11.5783	0	0	yes
C5orf46	5:147272270-147286101	22.2304	45.9869	0.483407	-1.04869	-10.3974	0	0	yes
ANKRD1	10:92671856-92681032	3.54056	7.31689	0.483889	-1.04725	-9.57888	0	0	yes
SYNPO2	4:119809995-119982402	1.81866	3.72613	0.488083	-1.0348	-12.0345	0	0	yes
GPR146	7:1036622-1177893	0.700562	1.43295	0.488895	-1.0324	-3.77002	0.000163	0.003542	yes
TAGLN3	3:111717585-111732735	34.9237	70.7745	0.49345	-1.01902	-14.1732	0	0	yes
MRVI1	11:10562786-10715535	0.347498	0.70418	0.493479	-1.01894	-4.08586	4.39E-05	0.001144	yes
RCAN1	21:35888781-35987382	29.2689	58.5358	0.500017	-0.99995	-11.0291	0	0	yes
TAGLN	11:117070039-117075508	368.996	735.728	0.501539	-0.99557	-8.84955	0	0	yes
LMCD1	3:8543510-8609806	3.44113	6.84249	0.502906	-0.99164	-8.36276	0	0	yes
CNN1	19:11649578-11661138	5.8471	11.5633	0.50566	-0.98376	-9.98346	0	0	yes
SH3D21	1:36771993-36786948	1.09867	2.12944	0.515943	-0.95472	-5.0487	4.45E-07	1.84E-05	yes
IL11	19:55875756-55881814	8.96239	17.3272	0.517244	-0.95108	-12.2345	0	0	yes
CTGF	6:132266629-132272518	64.4106	122.406	0.526205	-0.9263	-11.4823	0	0	yes
GADD45B	19:2476122-2478257	4.30825	8.15087	0.528563	-0.91985	-7.55741	4.11E-14	6.43E-12	yes
AMIGO2	12:47469489-47473734	30.6569	57.8879	0.529591	-0.91705	-12.1143	0	0	yes
MIR143HG	5:148786439-148812399	0.497345	0.933624	0.532704	-0.90859	-6.91726	4.60E-12	5.04E-10	yes
NEDD9	6:11183530-11382581	0.531277	0.98913	0.537115	-0.8967	-4.05812	4.95E-05	0.001266	yes
DDAH1	1:85784167-86044046	12.6296	23.4038	0.539639	-0.88993	-11.7766	0	0	yes
ACTG2	2:74120092-74146780	96.373	177.743	0.542204	-0.88309	-9.42404	0	0	yes
ASNS	7:97481428-97501854	8.13674	14.9365	0.544755	-0.87632	-8.1206	4.44E-16	8.89E-14	yes
ERRFI1	1:8071778-8086393	3.52708	6.37954	0.552874	-0.85498	-9.32079	0	0	yes
FGF11	17:7342688-7348251	2.56331	4.63438	0.553107	-0.85437	-7.787	6.88E-15	1.21E-12	yes
LOC100507632	8:57430876-57472382	1.87194	3.35846	0.55738	-0.84327	-6.36932	1.90E-10	1.57E-08	yes
PCSK7	11:117075787-117102811	8.66224	15.3665	0.563709	-0.82698	-11.3769	0	0	yes
ALDH1B1	9:38392701-38398658	4.15765	7.3168	0.568233	-0.81544	-9.26222	0	0	yes
MFAP5	12:8798539-8815433	12.1913	21.3741	0.570377	-0.81001	-11.2424	0	0	yes
LOC442028	2:95534429-95613087	1.45319	2.5378	0.572618	-0.80436	-6.16914	6.87E-10	5.18E-08	yes
IL6	7:22765013-22771621	229.219	399.805	0.573327	-0.80257	-9.80771	0	0	yes
C1orf198	1:230972864-231005335	8.83	15.4012	0.573332	-0.80256	-9.65789	0	0	yes
NRXN3	14:78870092-80330762	0.445496	0.773991	0.575583	-0.7969	-3.6789	0.000234	0.004794	yes

SFRP4	7:37945533-37956525	3.81677	6.58431	0.579677	-0.78668	-8.61986	0	0	yes
C7orf68	7:128095883-128098472	11.2654	19.4275	0.579869	-0.7862	-6.69588	2.14E-11	2.10E-09	yes
KRT5	12:52908358-52914243	0.777638	1.34052	0.580102	-0.78562	-3.61473	0.000301	0.005894	yes
GALNTL2	3:16216183-16271253	0.6391	1.1	0.581	-0.78339	-4.74781	2.06E-06	7.30E-05	yes
PIM1	6:37137921-37143204	1.66177	2.85703	0.581642	-0.7818	-5.7411	9.41E-09	5.53E-07	yes
ADM2	22:50920011-50924866	1.21708	2.08868	0.582703	-0.77917	-6.21668	5.08E-10	3.91E-08	yes
GRAMD3	5:125695787-125829853	3.53189	6.06045	0.582777	-0.77898	-4.96505	6.87E-07	2.73E-05	yes
PCK2	14:24563482-24573339	5.35134	9.15045	0.584817	-0.77394	-7.75219	9.10E-15	1.58E-12	yes
FHL1	X:135228860-135293518	3.81848	6.51074	0.586489	-0.76982	-4.71288	2.44E-06	8.52E-05	yes
NR4A1	12:52416615-52453291	2.71423	4.6032	0.58964	-0.76209	-4.197	2.70E-05	0.000755	yes
LBH	2:30454396-30482899	2.45928	4.1701	0.589741	-0.76185	-7.02591	2.13E-12	2.49E-10	yes
STK38L	12:27397077-27478892	5.33448	8.99421	0.593102	-0.75365	-10.2689	0	0	yes
POTEH	22:16256331-16287937	5.30341	8.92885	0.593963	-0.75155	-7.98588	1.33E-15	2.53E-13	yes
SORT1	1:109852186-109940563	1.4335	2.41072	0.594636	-0.74992	-7.31674	2.54E-13	3.42E-11	yes
COL4A3	2:228029280-228189936	0.291942	0.490896	0.594713	-0.74974	-4.0634	4.84E-05	0.001244	yes
LOC100128164	3:169661771-169684522	1.4763	2.48136	0.594956	-0.74915	-7.58895	3.22E-14	5.21E-12	yes
NUAK1	12:106457124-106533811	6.97374	11.6955	0.596275	-0.74595	-10.4316	0	0	yes
TGFBR1	9:101867411-101916474	4.26062	7.13381	0.597243	-0.74361	-9.47429	0	0	yes
SLC7A5	16:87863628-87903100	14.2379	23.7992	0.598251	-0.74118	-7.40368	1.33E-13	1.91E-11	yes
C8orf4	8:40010988-40012821	21.9927	36.7101	0.599091	-0.73915	-10.2989	0	0	yes
GPT2	16:46918307-46965201	2.81567	4.69091	0.60024	-0.73639	-6.70313	2.04E-11	2.01E-09	yes
CRISPLD2	16:84853586-84943116	1.07183	1.78392	0.600829	-0.73497	-5.69975	1.20E-08	6.81E-07	yes
USP54	10:75257295-75335433	0.849015	1.40984	0.602207	-0.73167	-5.88401	4.00E-09	2.55E-07	yes
SLC7A5P2	16:21529213-21531765	2.26612	3.75014	0.604276	-0.72672	-5.99186	2.07E-09	1.42E-07	yes
ACTA1	1:229566991-229569843	169.81	279.852	0.606785	-0.72074	-8.96577	0	0	yes
PDLIM3	4:186421813-186456712	5.74601	9.46597	0.607018	-0.72019	-8.15494	4.44E-16	8.89E-14	yes
NEGR1	1:71868624-72748277	3.99009	6.53264	0.610793	-0.71124	-9.44943	0	0	yes
SLC7A5P1	16:29624423-29625038	12.368	20.2202	0.611666	-0.70919	-5.71927	1.07E-08	6.17E-07	yes
MTHFD2	2:74425689-74442425	17.1286	27.9676	0.612444	-0.70735	-8.83224	0	0	yes
COL12A1	6:75794041-75915623	35.3785	57.7294	0.612833	-0.70643	-7.92224	2.44E-15	4.51E-13	yes
LOC284561	1:147751385-147763967	0.604675	0.983316	0.614935	-0.7015	-3.99698	6.42E-05	0.001594	yes
HAS1	19:52216364-52227221	1.04949	1.70604	0.615161	-0.70096	-3.51112	0.000446	0.008138	yes
CSRP2	12:77252495-77272799	7.05078	11.4299	0.616872	-0.69696	-5.50975	3.59E-08	1.83E-06	yes
ADM	11:10326641-10328923	28.3778	45.8628	0.618754	-0.69256	-9.65167	0	0	yes

C9orf3	9:97488950-97849500	2.28999	3.69514	0.61973	-0.69029	-5.53137	3.18E-08	1.64E-06	yes
F3	1:94994731-95007413	24.497	39.5184	0.619888	-0.68992	-9.62199	0	0	yes
VGLL3	3:86987122-87040257	1.95168	3.14827	0.619921	-0.68984	-8.98063	0	0	yes
KIAA1199	15:81071711-81243999	69.922	112.79	0.619931	-0.68982	-7.49181	6.79E-14	1.04E-11	yes
EDIL3	5:83238125-83680611	15.65	25.2432	0.619969	-0.68973	-9.64712	0	0	yes
ITGB3	17:45331207-45390077	3.19285	5.14619	0.62043	-0.68866	-8.33993	0	0	yes
ZNF503	10:77157601-77168740	2.94729	4.74955	0.620541	-0.6884	-6.91697	4.61E-12	5.04E-10	yes
KCTD11	17:7255207-7258263	5.16098	8.30621	0.62134	-0.68655	-8.28321	2.22E-16	4.64E-14	yes
BCYRN1	2:47562453-47562653	73.6527	118.024	0.624048	-0.68027	-3.61579	0.000299	0.005878	yes
C3orf58	3:143690639-143711210	3.01281	4.82682	0.624181	-0.67996	-4.65806	3.19E-06	0.000108	yes
PSAT1	9:80912058-80945009	12.79	20.4607	0.625101	-0.67784	-6.18064	6.38E-10	4.84E-08	yes
TUFT1	1:151512780-151556059	1.53846	2.45135	0.627597	-0.67209	-3.89303	9.90E-05	0.002297	yes
COL4A1	13:110801309-110959496	60.9007	96.567	0.630657	-0.66507	-7.56744	3.80E-14	6.08E-12	yes
BDNF	11:27528398-27743605	5.11372	8.07897	0.632967	-0.6598	-5.48087	4.23E-08	2.14E-06	yes
PCDH10	4:134070469-134112732	5.9721	9.41657	0.634212	-0.65696	-6.58229	4.63E-11	4.20E-09	yes
LOC100287562	17:38596273-38613982	138.386	218.199	0.634219	-0.65695	-4.3166	1.58E-05	0.000461	yes
CPE	4:166300096-166419482	2.44693	3.8548	0.634775	-0.65568	-5.41089	6.27E-08	3.00E-06	yes
FAM124A	13:51796469-51858377	0.615036	0.96612	0.636604	-0.65153	-3.54149	0.000398	0.007426	yes
PAWR	12:79985744-80084790	3.86918	6.07703	0.636689	-0.65134	-5.96291	2.48E-09	1.65E-07	yes
FNDC1	6:159590428-159693140	27.3832	42.8348	0.639275	-0.64549	-8.2997	0	0	yes
HAS3	16:69139466-69166493	1.92438	2.99925	0.64162	-0.64021	-3.6399	0.000273	0.00545	yes
KCTD16	5:143550436-143856944	0.798758	1.24328	0.64246	-0.63832	-4.49643	6.91E-06	0.000221	yes
ASS1	9:133320093-133376661	7.27298	11.3122	0.642932	-0.63726	-6.76087	1.37E-11	1.43E-09	yes
FILIP1L	3:99536677-99897476	8.09264	12.5776	0.643417	-0.63617	-8.37938	0	0	yes
MYOCD	17:12569206-12670651	3.96819	6.15508	0.644702	-0.6333	-6.64049	3.13E-11	2.94E-09	yes
KCTD20	6:36358327-36458319	10.1864	15.7901	0.645113	-0.63238	-8.84233	0	0	yes
FAM167A	8:11197145-11324276	2.35264	3.61814	0.650235	-0.62097	-6.27043	3.60E-10	2.83E-08	yes
CYR61	1:86046443-86049650	108.658	167.038	0.650499	-0.62038	-7.71783	1.18E-14	2.02E-12	yes
MAP3K8	10:30722865-30750761	1.27623	1.95935	0.651354	-0.61849	-4.18685	2.83E-05	0.000779	yes
PPP1R3C	10:93388198-93392858	9.49528	14.5764	0.651415	-0.61835	-8.23758	2.22E-16	4.64E-14	yes
NEXN	1:78347032-78409580	6.94943	10.6658	0.651562	-0.61803	-7.36445	1.78E-13	2.44E-11	yes
NUDT18	8:21964382-21966932	2.10553	3.22624	0.652627	-0.61567	-3.61344	0.000302	0.005915	yes
COL4A4	2:227867426-228029275	2.04299	3.12457	0.653847	-0.61298	-8.02856	8.88E-16	1.73E-13	yes
SNTB1	8:121547984-121824309	1.52126	2.32632	0.653934	-0.61278	-5.76539	8.15E-09	4.89E-07	yes

TPM1	15:63334837-63364114	421.155	643.819	0.654151	-0.6123	-5.36426	8.13E-08	3.77E-06	yes
INHBA	7:41728600-41818976	55.8217	84.9592	0.657041	-0.60594	-8.13955	4.44E-16	8.89E-14	yes
GABARAPL3	15:90889758-90892679	22.7483	34.5248	0.658897	-0.60187	-8.41196	0	0	yes
ELN	7:73442426-73484237	6.78584	10.2781	0.660223	-0.59897	-5.68141	1.34E-08	7.52E-07	yes
MYL3	3:46899356-46904973	4.30902	6.52644	0.66024	-0.59894	-3.7261	0.000194	0.004096	yes
FER1L4	20:34146506-34195484	1.25189	1.88939	0.66259	-0.59381	-5.79708	6.75E-09	4.12E-07	yes
HERPUD1	16:56965747-56977793	20.1093	30.3464	0.662659	-0.59366	-7.26201	3.81E-13	5.00E-11	yes
BNIP3	10:133781203-133795435	70.3039	105.556	0.666034	-0.58633	-7.99743	1.33E-15	2.53E-13	yes
FAM162A	3:122103022-122128961	24.7724	37.1675	0.666507	-0.58531	-7.14974	8.70E-13	1.08E-10	yes
DHRS3	1:12627938-12677820	7.30747	10.9315	0.668478	-0.58105	-6.48052	9.14E-11	8.08E-09	yes
INSIG2	2:118846049-118867597	6.83617	10.2132	0.669347	-0.57917	-7.13858	9.43E-13	1.16E-10	yes
NUPR1	16:28548661-28550495	28.6662	42.8156	0.669527	-0.57879	-4.88329	1.04E-06	3.98E-05	yes
PFKFB4	3:48555116-48594227	4.97112	7.42377	0.669622	-0.57858	-7.13003	1.00E-12	1.23E-10	yes
PLOD2	3:145787226-145879282	231.589	345.014	0.671245	-0.57509	-4.70867	2.49E-06	8.68E-05	yes
WDR69	2:228736326-228789026	3.49771	5.20606	0.671854	-0.57378	-4.55139	5.33E-06	0.000173	yes
FST	5:52776263-52782304	15.2873	22.7127	0.673073	-0.57117	-6.0322	1.62E-09	1.14E-07	yes
ALPK2	18:56148478-56296189	1.06674	1.58483	0.673094	-0.57112	-5.44792	5.10E-08	2.52E-06	yes
POSTN	13:38136718-38172981	299.681	443.557	0.675631	-0.56569	-5.26911	1.37E-07	6.13E-06	yes
MYL9	20:35169896-35178226	209.111	309.292	0.676096	-0.5647	-7.1265	1.03E-12	1.24E-10	yes
CALD1	7:134464163-134655480	116.282	171.794	0.676869	-0.56305	-4.94776	7.51E-07	2.98E-05	yes
VLDLR	9:2535651-2654485	4.82593	7.12623	0.677207	-0.56233	-4.85336	1.21E-06	4.57E-05	yes
MYL10	7:101256604-101272576	22.9946	33.9314	0.677679	-0.56133	-7.15403	8.43E-13	1.06E-10	yes
SIRPG	20:1609797-1638425	14.72	21.7044	0.678203	-0.56021	-7.43033	1.08E-13	1.59E-11	yes
CSRP1	1:201452657-201476387	53.8389	79.2873	0.679036	-0.55844	-7.51099	5.86E-14	9.08E-12	yes
ERMP1	9:5784571-5833081	0.877664	1.29236	0.679117	-0.55827	-4.14204	3.44E-05	0.000929	yes
POTEM	14:19983953-20020272	58.2372	85.7506	0.679146	-0.55821	-6.40466	1.51E-10	1.28E-08	yes
NUAK2	1:205271190-205290883	1.11567	1.64222	0.679367	-0.55774	-3.68097	0.000232	0.004762	yes
SIRPB1	20:1545028-1600689	23.1855	34.1212	0.679504	-0.55745	-6.36939	1.90E-10	1.57E-08	yes
CTPS	1:41445006-41478235	4.9542	7.27946	0.680572	-0.55518	-6.65621	2.81E-11	2.68E-09	yes
TES	7:115850546-115898837	4.71821	6.9194	0.681881	-0.55241	-4.34327	1.40E-05	0.000415	yes
CRIM1	2:36583369-36778278	32.3243	47.3953	0.682015	-0.55212	-7.12664	1.03E-12	1.24E-10	yes
POTEKP	2:132349267-132384999	234.709	343.773	0.682744	-0.55058	-5.75743	8.54E-09	5.11E-07	yes
FMOD	1:203309751-203320289	2.22705	3.26082	0.682972	-0.5501	-4.77878	1.76E-06	6.34E-05	yes
LOC644936	5:79594903-79596297	217.316	317.968	0.683452	-0.54909	-6.72286	1.78E-11	1.81E-09	yes

MYH10	17:8377529-8534036	19.95	29.1857	0.683554	-0.54887	-7.21753	5.29E-13	6.81E-11	yes
SLC6A9	1:44457279-44497134	1.64985	2.41318	0.683683	-0.5486	-4.13244	3.59E-05	0.000959	yes
GABARAPL1	12:10365488-10375727	24.6208	36.0053	0.68381	-0.54833	-7.67061	1.71E-14	2.86E-12	yes
PHGDH	1:120254418-120286849	9.43262	13.7941	0.683816	-0.54832	-6.83696	8.09E-12	8.57E-10	yes
LMO7	13:76194569-76434006	4.54695	6.64284	0.684489	-0.5469	-6.14449	8.02E-10	5.99E-08	yes
MXI1	10:111967362-112047123	8.93061	13.0451	0.684595	-0.54668	-5.06542	4.08E-07	1.70E-05	yes
IL8	4:74606222-74609433	1131.2	1651.84	0.684812	-0.54622	-4.83518	1.33E-06	4.97E-05	yes
TPM2	9:35681989-35690053	240.637	351.275	0.685039	-0.54574	-6.58908	4.43E-11	4.06E-09	yes
MTRNR2L1	17:22022436-22023991	315.626	460.427	0.685507	-0.54476	-6.12869	8.86E-10	6.58E-08	yes
MTRNR2L6	7:142374130-142375525	200.78	292.87	0.68556	-0.54464	-6.7508	1.47E-11	1.52E-09	yes
SLC1A5	19:47278139-47291842	20.6916	30.1766	0.685684	-0.54439	-4.80139	1.58E-06	5.75E-05	yes
MTRNR2L2	5:79922044-80172634	483.808	704.411	0.686826	-0.54198	-5.98369	2.18E-09	1.47E-07	yes
PDLIM5	4:95373037-95589377	13.4831	19.6296	0.686876	-0.54188	-7.00956	2.39E-12	2.76E-10	yes
MTRNR2L8	11:10529433-10530723	454.426	660.587	0.687912	-0.5397	-5.90661	3.49E-09	2.26E-07	yes
IL1A	2:113531491-113542971	25.3552	36.8025	0.688953	-0.53752	-7.44879	9.41E-14	1.40E-11	yes
SLC2A4	17:7185053-7191367	1.57212	2.28063	0.689336	-0.53672	-4.02422	5.72E-05	0.001437	yes
MXRA7	17:74671808-74707056	104.185	151.091	0.689551	-0.53627	-5.92806	3.07E-09	2.02E-07	yes
POTEG	14:19553364-19584942	11.3717	16.4879	0.6897	-0.53596	-6.89989	5.20E-12	5.63E-10	yes
GYS1	19:49471381-49496610	13.9779	20.2541	0.690127	-0.53507	-6.54893	5.80E-11	5.22E-09	yes
POTEJ	2:131369105-131415450	205.867	297.79	0.691316	-0.53258	-5.63815	1.72E-08	9.49E-07	yes
ADAM19	5:156904311-157002783	6.27006	9.06243	0.691874	-0.53142	-7.41765	1.19E-13	1.74E-11	yes
SLC39A8	4:103172197-103266655	6.31605	9.11168	0.693182	-0.52869	-5.60722	2.06E-08	1.11E-06	yes
MTRNR2L9	6:62284007-62284534	414.608	597.918	0.693419	-0.5282	-7.01141	2.36E-12	2.74E-10	yes
DDIT4	10:74033676-74035797	64.2195	92.5042	0.694233	-0.52651	-7.15316	8.48E-13	1.06E-10	yes
POTEI	2:131220388-131266808	211.813	305.072	0.694305	-0.52636	-5.51143	3.56E-08	1.82E-06	yes
CNN2	19:1026297-1039064	20.5256	29.5608	0.694352	-0.52626	-7.36487	1.77E-13	2.44E-11	yes
POTEF	2:130831107-130886795	185.661	267.319	0.69453	-0.52589	-5.34135	9.23E-08	4.21E-06	yes
KIAA0564	13:42140960-42535221	2.40492	3.46198	0.694666	-0.52561	-6.36628	1.94E-10	1.59E-08	yes
IGFBP4	17:38596273-38613982	96.2089	138.361	0.695347	-0.5242	-4.81513	1.47E-06	5.46E-05	yes
NDUFA4L2	12:57623355-57634545	11.5391	16.5827	0.695852	-0.52315	-3.61783	0.000297	0.00584	yes
PGK1	X:77359665-77382324	150.923	216.75	0.6963	-0.52222	-5.50928	3.60E-08	1.83E-06	yes
POTEE	2:131975923-132022416	228.934	328.605	0.696684	-0.52142	-5.32756	9.95E-08	4.48E-06	yes
AMY1B	1:104230040-104238889	30.9262	44.3715	0.696983	-0.5208	-7.28303	3.26E-13	4.31E-11	yes
DNAJB2	2:220144039-220151622	5.44206	7.80423	0.697322	-0.5201	-3.70536	0.000211	0.004408	yes

PGK2	6:49753363-49755053	163.641	234.233	0.698625	-0.51741	-6.39885	1.57E-10	1.31E-08	yes
SIRPA	20:1874812-1920540	23.8587	34.1101	0.699461	-0.51568	-6.91784	4.59E-12	5.04E-10	yes
LOC124685	17:69617121-69617577	694.493	992.871	0.69948	-0.51565	-6.64922	2.95E-11	2.79E-09	yes
RNF41	12:56596287-56615753	3.55152	5.07192	0.700232	-0.5141	-4.17103	3.03E-05	0.000829	yes
LOX	5:121398889-121414055	92.4893	132.054	0.70039	-0.51377	-5.56759	2.58E-08	1.36E-06	yes
CBS	21:44473300-44496472	5.7311	8.18095	0.700542	-0.51346	-5.87889	4.13E-09	2.62E-07	yes
MYL6	12:56552044-56555366	363.978	519.378	0.700796	-0.51293	-5.18794	2.13E-07	9.15E-06	yes
CTDSPL2	15:44719578-44819430	1.61778	2.30703	0.701239	-0.51202	-4.85538	1.20E-06	4.54E-05	yes
LOC648740	1:104068577-104122151	217.108	309.331	0.701863	-0.51074	-5.82979	5.55E-09	3.48E-07	yes
MYL1	2:211154867-211179895	43.5422	61.9576	0.702774	-0.50887	-6.9822	2.91E-12	3.30E-10	yes
STBD1	4:77227676-77232283	3.88109	5.51494	0.703741	-0.50688	-5.08306	3.71E-07	1.56E-05	yes
LOC644961	1:27648635-27662891	174.846	248.283	0.704221	-0.5059	-5.63569	1.74E-08	9.59E-07	yes
ACTG1	17:79476996-79479892	635.316	901.546	0.704696	-0.50493	-4.80225	1.57E-06	5.74E-05	yes
SLC1A4	2:65215578-65250999	1.77829	2.52281	0.704885	-0.50454	-4.29583	1.74E-05	0.000502	yes
LOC148709	1:202830881-202844369	18.1512	25.7339	0.705342	-0.50361	-7.03393	2.01E-12	2.37E-10	yes
AMY1C	1:104292440-104301310	33.8166	47.8485	0.706743	-0.50074	-6.98765	2.80E-12	3.20E-10	yes
INMT	7:30791750-30932002	6.11368	8.645	0.707193	-0.49982	-5.82419	5.74E-09	3.58E-07	yes
THBS4	5:79331169-79379110	2.14899	3.03703	0.707596	-0.499	-4.40494	1.06E-05	0.000325	yes
MTRNR2L10	X:55207823-55208944	65.1668	92.078	0.707735	-0.49872	-6.94671	3.74E-12	4.18E-10	yes
PPFIA4	1:203020310-203047864	2.18069	3.08083	0.707825	-0.49853	-5.32947	9.85E-08	4.45E-06	yes
PLIN2	9:19115758-19127604	102.091	144.135	0.708301	-0.49757	-6.2228	4.88E-10	3.78E-08	yes
MYL4	17:45286427-45301045	56.7508	79.9754	0.709603	-0.49492	-6.89904	5.24E-12	5.63E-10	yes
EPDR1	7:37960162-37991543	5.6807	7.99754	0.710306	-0.49349	-5.72924	1.01E-08	5.86E-07	yes
ITGA1	5:52083773-52249485	5.5866	7.85624	0.711104	-0.49187	-5.35478	8.57E-08	3.94E-06	yes
MTRNR2L7	10:37890365-37891859	17.7076	24.8957	0.711271	-0.49153	-6.52987	6.58E-11	5.89E-09	yes
STC2	5:172741725-172756506	49.1266	69.0484	0.711481	-0.4911	-6.04539	1.49E-09	1.06E-07	yes
ACTB	7:5566778-5573677	746.834	1049.64	0.711514	-0.49104	-4.3976	1.09E-05	0.000333	yes
FERMT2	14:53323988-53417815	16.783	23.5411	0.712923	-0.48818	-6.72367	1.77E-11	1.81E-09	yes
GAPDH	12:6643656-6647536	881.806	1236.83	0.712957	-0.48811	-4.76787	1.86E-06	6.64E-05	yes
AMY1A	1:104198140-104207173	29.5685	41.4382	0.713557	-0.4869	-6.70534	2.01E-11	2.00E-09	yes
WNT5A	3:55499742-55521331	9.90302	13.8681	0.714086	-0.48583	-6.77592	1.24E-11	1.30E-09	yes
LOC100130331	1:238025474-238091621	92.8914	130.056	0.714242	-0.48552	-5.91403	3.34E-09	2.18E-07	yes
CD55	1:207494816-207534311	6.16526	8.63012	0.714389	-0.48522	-4.70244	2.57E-06	8.93E-05	yes
ZNF281	1:200375419-200379166	7.09456	9.92682	0.714686	-0.48462	-6.46917	9.85E-11	8.61E-09	yes

FAM36A	1:244998638-245010243	4.52396	6.32551	0.715193	-0.4836	-3.84859	0.000119	0.002695	yes
RBM3	X:48432740-48439553	8.77194	12.253	0.715901	-0.48217	-6.72081	1.81E-11	1.82E-09	yes
CNN3	1:95362506-95392735	37.0523	51.7519	0.71596	-0.48205	-6.68105	2.37E-11	2.28E-09	yes
ADAMTS12	5:33527285-33892124	17.3835	24.2747	0.716116	-0.48173	-6.62665	3.43E-11	3.19E-09	yes
THBS1	15:39873279-39889668	713.254	995.572	0.716426	-0.48111	-3.66723	0.000245	0.004961	yes
WSB1	17:25621105-25640645	24.1835	33.7399	0.716763	-0.48043	-6.68282	2.34E-11	2.27E-09	yes
ITGBL1	13:102104965-102368794	15.908	22.1908	0.716874	-0.48021	-6.69122	2.21E-11	2.15E-09	yes
BAG2	6:57037103-57050013	6.95278	9.68296	0.718043	-0.47786	-5.44403	5.21E-08	2.57E-06	yes
MTRNR2L5	10:57358749-57360488	17.1633	23.8793	0.718752	-0.47643	-6.47177	9.69E-11	8.51E-09	yes
MTRNR2L4	16:3421052-3422283	17.9126	24.879	0.719989	-0.47395	-6.00409	1.92E-09	1.33E-07	yes
ENO2	12:7023613-7032859	58.5167	81.2349	0.720339	-0.47325	-6.30934	2.80E-10	2.24E-08	yes
SNTA1	20:31995762-32031698	2.32953	3.22926	0.721382	-0.47116	-3.6294	0.000284	0.00563	yes
LDHAL6B	15:59428562-59665071	57.4091	79.5247	0.721903	-0.47012	-5.74933	8.96E-09	5.31E-07	yes
DDX41	5:176938577-176943967	6.93934	9.60042	0.722816	-0.4683	-5.37245	7.77E-08	3.65E-06	yes
TST	22:37406905-37415491	6.81583	9.42903	0.722856	-0.46822	-4.05961	4.92E-05	0.00126	yes
RGNEF	5:72921982-73237818	1.1292	1.5598	0.723939	-0.46606	-4.20287	2.64E-05	0.000737	yes
MTRNR2L3	20:55926144-55953519	61.139	84.3901	0.724481	-0.46498	-6.18736	6.12E-10	4.66E-08	yes
C6orf145	6:3722835-3752246	10.1143	13.9584	0.724603	-0.46474	-6.01078	1.85E-09	1.28E-07	yes
LDHC	11:18433852-18472793	78.4234	108.204	0.724774	-0.4644	-6.39934	1.56E-10	1.31E-08	yes
BNIP3L	8:26240522-26270644	44.8552	61.8854	0.724811	-0.46432	-6.12013	9.35E-10	6.90E-08	yes
SCAND2	15:85174690-85185694	1.40308	1.93568	0.724851	-0.46424	-3.92852	8.55E-05	0.002032	yes
SIAH2	3:150458909-150481263	4.25221	5.86379	0.725164	-0.46362	-4.90023	9.57E-07	3.72E-05	yes
LDHA	11:18415935-18429765	332.797	458.864	0.725263	-0.46342	-4.79294	1.64E-06	5.96E-05	yes
OAS3	12:113376248-113411054	8.88438	12.2456	0.725516	-0.46292	-6.4492	1.12E-10	9.76E-09	yes
TMEM45A	3:100211462-100296285	26.4281	36.4189	0.72567	-0.46261	-6.44192	1.18E-10	1.02E-08	yes
MYL5	4:671710-682973	24.6617	33.9767	0.725842	-0.46227	-4.93479	8.02E-07	3.17E-05	yes
ATF4	22:39916568-39918691	99.2281	136.693	0.725919	-0.46212	-6.08205	1.19E-09	8.55E-08	yes
FOXD1	5:72742082-72744352	5.49426	7.54709	0.727997	-0.458	-5.00162	5.68E-07	2.30E-05	yes
RCOR1	14:103059232-103196913	2.44332	3.35459	0.728351	-0.45729	-5.21699	1.82E-07	7.94E-06	yes
ZNF395	8:28203101-28243977	6.28094	8.62316	0.72838	-0.45724	-6.26505	3.73E-10	2.92E-08	yes
IDH2	15:90627209-90645708	3.94547	5.41366	0.728799	-0.45641	-3.86399	0.000112	0.002543	yes
NDUFA4	7:10971579-10979813	13.2671	18.1849	0.729567	-0.45489	-6.10637	1.02E-09	7.45E-08	yes
LOXL3	2:74753774-74784678	19.3264	26.4687	0.730161	-0.45371	-5.24362	1.57E-07	6.98E-06	yes
ARID5B	10:63661012-63856707	6.10666	8.3583	0.73061	-0.45283	-6.33244	2.41E-10	1.95E-08	yes

GPR176	15:40092930-40213093	15.6113	21.3386	0.731599	-0.45087	-6.30487	2.88E-10	2.30E-08	yes
SCG5	15:32933869-32989298	9.18554	12.5503	0.731898	-0.45029	-4.58458	4.55E-06	0.00015	yes
STON1	2:48757063-49003656	1.12055	1.52974	0.73251	-0.44908	-3.57057	0.000356	0.006784	yes
PTTG1IP	21:46269499-46293818	39.5738	53.9889	0.732999	-0.44812	-6.08351	1.18E-09	8.51E-08	yes
FGF2	4:123747862-123844123	82.8179	112.895	0.733583	-0.44697	-4.81131	1.50E-06	5.51E-05	yes
DPYSL4	10:134000413-134019280	2.95641	4.02999	0.733602	-0.44693	-4.1811	2.90E-05	0.000796	yes
LIMS2	2:128395995-128439360	5.78178	7.8771	0.733999	-0.44615	-4.10525	4.04E-05	0.001062	yes
EIF4EBP1	8:37888019-37917883	17.2904	23.5477	0.734271	-0.44561	-4.86268	1.16E-06	4.40E-05	yes
HEG1	3:124684553-124774802	22.7278	30.9499	0.734342	-0.44548	-5.66773	1.45E-08	8.08E-07	yes
ATF5	19:50392910-50437193	17.0538	23.218	0.734508	-0.44515	-5.01891	5.20E-07	2.11E-05	yes
MYL6B	12:56546203-56551771	94.8446	128.983	0.735326	-0.44354	-6.10394	1.03E-09	7.53E-08	yes
TRIB3	20:361307-378203	6.46291	8.77332	0.736655	-0.44094	-5.20037	1.99E-07	8.61E-06	yes
BTG1	12:92534053-92539673	5.99009	8.13096	0.736701	-0.44085	-5.98638	2.15E-09	1.45E-07	yes
RAB23	6:57053580-57087078	10.1472	13.7442	0.73829	-0.43774	-4.40525	1.06E-05	0.000325	yes
SCD	10:102106771-102124588	22.6416	30.667	0.738305	-0.43771	-5.6824	1.33E-08	7.50E-07	yes
ANKZF1	2:220094478-220101391	3.99551	5.41105	0.738398	-0.43753	-3.5656	0.000363	0.006837	yes
PDLIM2	8:22436253-22455538	12.307	16.6427	0.739483	-0.43541	-3.75393	0.000174	0.003731	yes
ITGA4	2:182321618-182521834	3.08936	4.17742	0.739538	-0.4353	-5.36933	7.90E-08	3.69E-06	yes
BOK	2:242483798-242513553	15.0956	20.3868	0.74046	-0.43351	-6.0192	1.75E-09	1.23E-07	yes
HAS2	8:122625270-122657565	35.6404	48.1133	0.74076	-0.43292	-5.73513	9.74E-09	5.71E-07	yes
PKDCC	2:42275160-42285668	4.55051	6.14058	0.741055	-0.43235	-4.58378	4.57E-06	0.00015	yes
FSTL1	3:120113060-120169918	249.864	336.954	0.741537	-0.43141	-4.26344	2.01E-05	0.000575	yes
JMJD6	17:74708913-74722881	6.75535	9.10033	0.742319	-0.42989	-4.0358	5.44E-05	0.001378	yes
LDHAL6A	11:18477373-18501147	31.9483	43.0274	0.742511	-0.42952	-5.99032	2.09E-09	1.42E-07	yes
AVEN	15:34158427-34357287	5.07971	6.83911	0.742744	-0.42906	-3.82185	0.000132	0.002968	yes
SRGN	10:70847827-70864567	91.0891	122.631	0.74279	-0.42897	-5.84309	5.12E-09	3.22E-07	yes
ERO1L	14:53108604-53162419	21.9603	29.519	0.743938	-0.42675	-5.92141	3.19E-09	2.09E-07	yes
MEGF6	1:3404505-3528059	2.62333	3.52546	0.74411	-0.42641	-5.41309	6.19E-08	2.99E-06	yes
C12orf11	12:27058111-27091254	3.5294	4.73848	0.744838	-0.425	-4.4035	1.07E-05	0.000326	yes
ITGA11	15:68594041-68724492	26.5191	35.5967	0.744988	-0.42471	-5.67926	1.35E-08	7.58E-07	yes
LOC100335030	12:49760687-49921207	4.36356	5.85589	0.745157	-0.42438	-3.91869	8.90E-05	0.00211	yes
LOC653562	16:33778248-33786529	7.77623	10.4241	0.745986	-0.42278	-5.32968	9.84E-08	4.45E-06	yes
CEBPG	19:33864608-33873592	3.41538	4.5752	0.746499	-0.42179	-4.68325	2.82E-06	9.71E-05	yes
SERPINE1	7:100770378-100782547	784.353	1050.71	0.746498	-0.42179	-3.54691	0.00039	0.007293	yes

ENO3	17:4854383-4860426	81.2582	108.839	0.746591	-0.42161	-5.73228	9.91E-09	5.78E-07	yes
LIMA1	12:50569562-50677353	27.9841	37.4573	0.747093	-0.42064	-5.13241	2.86E-07	1.22E-05	yes
KCNK6	19:38810483-38819654	2.74194	3.66987	0.747149	-0.42053	-3.74078	0.000183	0.003887	yes
NMD3	3:160939098-160969795	6.41008	8.57699	0.747358	-0.42013	-5.11344	3.16E-07	1.34E-05	yes
FLNA	X:153576899-153603006	84.9516	113.64	0.74755	-0.41976	-4.32823	1.50E-05	0.000442	yes
CCDC80	3:112323406-112359977	52.8051	70.5544	0.748431	-0.41806	-5.23976	1.61E-07	7.11E-06	yes
SLC2A1	1:43391045-43449029	19.1205	25.5398	0.748655	-0.41763	-5.7937	6.89E-09	4.19E-07	yes
SLC6A10P	16:32888796-32896463	4.64381	6.19981	0.749025	-0.41692	-5.13103	2.88E-07	1.22E-05	yes
PYGL	14:51371934-51411248	7.45404	9.94779	0.749316	-0.41635	-5.20668	1.92E-07	8.34E-06	yes
TMEM47	X:34645180-34675405	12.3334	16.4443	0.750011	-0.41502	-5.80634	6.39E-09	3.91E-07	yes
SDC2	8:97505881-97624037	6.82852	9.09707	0.750628	-0.41383	-5.45892	4.79E-08	2.40E-06	yes
FNIP2	4:159690181-159956333	1.49575	1.99121	0.751176	-0.41278	-4.0015	6.29E-05	0.001572	yes
RIOK3	18:21032786-21063101	7.65195	10.1832	0.751429	-0.41229	-5.65793	1.53E-08	8.52E-07	yes
MTHFD1L	6:151186814-151473355	8.97544	11.9345	0.752058	-0.41108	-3.62358	0.000291	0.005727	yes
COL4A2	13:110959630-111165374	51.8889	68.9528	0.752528	-0.41018	-4.90194	9.49E-07	3.70E-05	yes
SNHG5	6:86386724-86388451	74.2457	98.647	0.75264	-0.40997	-5.41047	6.29E-08	3.00E-06	yes
ITGB8	7:20367923-20455382	2.72463	3.61584	0.753526	-0.40827	-5.42006	5.96E-08	2.89E-06	yes
PHF17	4:129730778-129796379	1.32689	1.75975	0.754022	-0.40732	-3.5293	0.000417	0.007696	yes
DUSP1	5:172195092-172198203	13.9021	18.4214	0.754671	-0.40608	-5.45833	4.81E-08	2.40E-06	yes
SLC38A1	12:46576837-46663208	7.62296	10.1009	0.754681	-0.40606	-4.22841	2.35E-05	0.000663	yes
DSTN	20:17550598-17588652	83.7018	110.852	0.755077	-0.4053	-5.4121	6.23E-08	2.99E-06	yes
DNAJB9	7:108210188-108215294	10.9017	14.4204	0.755992	-0.40356	-5.44266	5.25E-08	2.57E-06	yes
RORA	15:60780482-61521502	2.43902	3.22561	0.756142	-0.40327	-5.03713	4.73E-07	1.94E-05	yes
FTX	X:73164158-73513409	6.19788	8.194	0.756392	-0.40279	-3.69643	0.000219	0.004527	yes
ENAH	1:225674533-225840845	4.78026	6.31881	0.756513	-0.40256	-5.60554	2.08E-08	1.12E-06	yes
FAM57A	17:635846-646075	5.33553	7.04855	0.756968	-0.40169	-4.18701	2.83E-05	0.000779	yes
DSTNP2	12:6993845-6994950	78.1724	103.265	0.757008	-0.40162	-5.5688	2.57E-08	1.35E-06	yes
NNMT	11:114166534-114183238	41.8429	55.2189	0.757764	-0.40018	-5.57951	2.41E-08	1.28E-06	yes
LOC729454	3:39244497-39256163	124.703	164.428	0.758405	-0.39896	-5.57657	2.45E-08	1.30E-06	yes
RPSA	3:39448203-39454033	140.907	185.686	0.758846	-0.39812	-5.18888	2.12E-07	9.13E-06	yes
SLC6A8	X:152953751-152962048	8.78341	11.5654	0.759456	-0.39696	-4.38915	1.14E-05	0.000346	yes
EDARADD	1:236557679-236648008	203.46	267.796	0.759757	-0.39639	-4.32237	1.54E-05	0.000452	yes
RPL10L	14:47120215-47121028	212.622	279.811	0.759877	-0.39616	-5.29079	1.22E-07	5.47E-06	yes
TPI1P2	7:128695276-128697293	158.547	208.252	0.761323	-0.39342	-4.76894	1.85E-06	6.62E-05	yes

TPI1	12:6976583-6982521	213.361	280.081	0.761783	-0.39255	-4.85409	1.21E-06	4.56E-05	yes
CBLB	3:105377108-105587887	5.01342	6.57946	0.76198	-0.39217	-4.97291	6.60E-07	2.63E-05	yes
PPP1R3B	8:8993763-9009152	6.29082	8.25413	0.762142	-0.39187	-5.55802	2.73E-08	1.42E-06	yes
RPL10	X:153626570-153650065	74.4107	97.5549	0.762757	-0.3907	-4.89797	9.68E-07	3.74E-05	yes
ENO1	1:8921058-8939944	242.002	317.156	0.763038	-0.39017	-4.25296	2.11E-05	0.0006	yes
PDK1	2:173420778-173463862	2.85911	3.7465	0.763142	-0.38998	-4.37032	1.24E-05	0.000373	yes
TPI1P3	6:116262692-116381921	290.272	380.322	0.763227	-0.38982	-4.6936	2.68E-06	9.28E-05	yes
ANKRD13A	12:110437234-110477237	9.93568	13.0067	0.763889	-0.38856	-5.41347	6.18E-08	2.99E-06	yes
RPSAP58	19:23945815-24010937	150.47	196.744	0.764801	-0.38684	-5.00108	5.70E-07	2.30E-05	yes
RPSAP9	9:79013514-79014954	108.118	141.364	0.76482	-0.38681	-5.15545	2.53E-07	1.08E-05	yes
TNS1	2:218664511-218808796	17.0494	22.29	0.76489	-0.38668	-5.02855	4.94E-07	2.02E-05	yes
MME	3:154797435-154901518	64.0046	83.5975	0.765628	-0.38528	-4.00486	6.21E-05	0.001552	yes
AK4	1:65613231-65697828	7.52971	9.81661	0.767038	-0.38263	-4.55458	5.25E-06	0.000171	yes
PIK3IP1	22:31677578-31688520	3.8392	5.00506	0.767064	-0.38258	-3.76682	0.000165	0.003582	yes
MYL12A	18:3247527-3261845	220.754	287.779	0.767096	-0.38252	-4.74412	2.09E-06	7.41E-05	yes
KCNMB3	3:178957536-178984838	8.24445	10.7476	0.767097	-0.38252	-4.11035	3.95E-05	0.001043	yes
SMYD2	1:214454564-214510477	5.5927	7.28827	0.767356	-0.38203	-3.71416	0.000204	0.004288	yes
GARS	7:30634180-30673649	37.1564	48.3956	0.767764	-0.38127	-5.21508	1.84E-07	8.00E-06	yes
LOC283693	15:83394631-83408532	8.79271	11.4507	0.767875	-0.38106	-4.31084	1.63E-05	0.000471	yes
C4orf3	4:120217573-120225600	27.7163	36.0425	0.768989	-0.37896	-5.23786	1.62E-07	7.16E-06	yes
FLNB	3:57994126-58157982	24.0884	31.2704	0.770326	-0.37646	-3.79526	0.000147	0.003254	yes
HSPB6	19:36245469-36247930	8.47452	10.9939	0.770838	-0.3755	-3.98286	6.81E-05	0.00168	yes
HSP90B3P	1:92100567-92109335	192.945	250.121	0.771407	-0.37444	-4.71443	2.42E-06	8.48E-05	yes
PYCR1	17:79890266-79894968	11.2343	14.5327	0.773036	-0.37139	-4.81151	1.50E-06	5.51E-05	yes
GAS5	1:173832385-173837125	24.6607	31.9007	0.773046	-0.37137	-3.89007	0.0001	0.002321	yes
HSP90B1	12:104324188-104341703	173.276	224.133	0.773095	-0.37128	-4.17314	3.00E-05	0.000823	yes
SGK1	6:134490383-134639196	22.1743	28.6393	0.774261	-0.36911	-4.6979	2.63E-06	9.10E-05	yes
PAQR7	1:26187974-26197744	2.76596	3.57211	0.774321	-0.369	-3.49585	0.000473	0.008564	yes
COL5A2	2:189896640-190044605	89.3504	115.31	0.774871	-0.36797	-3.90128	9.57E-05	0.002238	yes
P4HA1	10:74766974-74856732	86.8348	112.057	0.774916	-0.36789	-4.54111	5.60E-06	0.000181	yes
ATP2A2	12:110719031-110788898	23.4274	30.2263	0.775067	-0.36761	-3.567	0.000361	0.006834	yes
PGRMC2	4:129179949-129209984	9.90028	12.7706	0.77524	-0.36729	-3.94684	7.92E-05	0.001895	yes
IGFBP5	2:217536827-217560272	36.7526	47.3996	0.775378	-0.36703	-4.62704	3.71E-06	0.000124	yes
MYL12B	18:3262110-3278282	304.183	392.277	0.775429	-0.36693	-4.6133	3.96E-06	0.000131	yes

RAB8B	15:63481727-63559975	7.7359	9.97227	0.775741	-0.36635	-5.09832	3.43E-07	1.44E-05	yes
B4GALT1	9:33110638-33167356	49.4304	63.7119	0.775843	-0.36616	-4.68916	2.74E-06	9.46E-05	yes
GBE1	3:81538849-81810950	49.3895	63.6351	0.776136	-0.36562	-4.84865	1.24E-06	4.65E-05	yes
MYADM	19:54369610-54379689	46.4151	59.7578	0.77672	-0.36453	-4.11889	3.81E-05	0.001012	yes
DDX50	10:70661033-70706603	5.61742	7.23203	0.776742	-0.36449	-4.14013	3.47E-05	0.000935	yes
SLC3A2	11:62623483-62656355	26.7448	34.4284	0.776824	-0.36434	-3.80498	0.000142	0.003134	yes
CD200	3:112051915-112085485	16.1955	20.8462	0.776904	-0.36419	-4.80079	1.58E-06	5.75E-05	yes
MYCT1	6:153019029-153045717	5.79749	7.45964	0.777181	-0.36368	-4.43116	9.37E-06	0.000292	yes
MIR22HG	17:1614797-1619566	12.4894	16.0686	0.777255	-0.36354	-3.7597	0.00017	0.003664	yes
TXNDC12	1:52485802-52521047	13.2778	17.0825	0.777275	-0.3635	-4.40677	1.05E-05	0.000324	yes
PLP2	X:49028183-49031469	22.0844	28.3946	0.777768	-0.36259	-4.57444	4.77E-06	0.000157	yes
AGPAT5	8:6565877-6619024	2.05714	2.64406	0.778023	-0.36211	-3.84148	0.000122	0.002757	yes
FLJ44635	X:71364033-71381600	242.731	311.943	0.778126	-0.36192	-3.99042	6.60E-05	0.001633	yes
UGCG	9:114659205-114695439	11.5	14.7705	0.778579	-0.36108	-4.39793	1.09E-05	0.000333	yes
DLC1	8:12940871-13372429	7.89025	10.13	0.778899	-0.36049	-3.48722	0.000488	0.008779	yes
MYO10	5:16662015-16936385	9.31505	11.9525	0.779339	-0.35968	-4.89356	9.90E-07	3.81E-05	yes
UAP1	1:162531295-162569633	23.8927	30.6577	0.779338	-0.35968	-5.02506	5.03E-07	2.05E-05	yes
RPL39L	3:186838740-186857263	40.8228	52.3384	0.779978	-0.35849	-4.62307	3.78E-06	0.000126	yes
PRKAB2	1:146626684-146644129	3.1892	4.08845	0.780051	-0.35836	-4.37922	1.19E-05	0.00036	yes
CD2AP	6:47445524-47594999	4.64713	5.95736	0.780065	-0.35833	-4.78397	1.72E-06	6.19E-05	yes
C18orf10	18:34376033-34805288	7.80032	9.98608	0.781119	-0.35639	-4.13726	3.51E-05	0.000945	yes
TPT1	13:45911000-45965618	677.672	867.042	0.781591	-0.35551	-3.66286	0.000249	0.005033	yes
SLC25A4	4:186064416-186071538	3.99791	5.11137	0.78216	-0.35446	-4.34518	1.39E-05	0.000413	yes
GPAM	10:113909621-113943525	2.96509	3.79044	0.782255	-0.35429	-4.4299	9.43E-06	0.000293	yes
CCNG2	4:78078356-78091213	4.204	5.36903	0.783009	-0.3529	-4.63216	3.62E-06	0.000122	yes
KIAA1191	5:175773064-175788809	22.945	29.2894	0.783389	-0.3522	-3.57526	0.00035	0.006704	yes
MYH11	16:15737123-15950887	21.7362	27.6784	0.785313	-0.34866	-4.55064	5.35E-06	0.000174	yes
RPS8	1:45241245-45244412	215.658	274.545	0.785511	-0.3483	-4.72015	2.36E-06	8.28E-05	yes
LMAN1	18:56995054-57026508	37.279	47.3272	0.787687	-0.34431	-4.48013	7.46E-06	0.000238	yes
CEBPD	8:48649475-48650726	15.3625	19.4888	0.788273	-0.34323	-4.14473	3.40E-05	0.000921	yes
FSTL3	19:676388-683392	20.6121	26.1444	0.788394	-0.34301	-4.79192	1.65E-06	5.98E-05	yes
FLNC	7:128470482-128499328	27.8336	35.2813	0.788905	-0.34208	-4.27874	1.88E-05	0.000539	yes
LOC391722	4:185220281-185238554	199.804	253.139	0.789305	-0.34134	-4.40326	1.07E-05	0.000326	yes
SLC16A1	1:113454468-113498975	19.8607	25.1344	0.79018	-0.33975	-4.47636	7.59E-06	0.000241	yes

MYADML	2:33951127-33953284	28.8406	36.4898	0.790374	-0.33939	-4.73593	2.18E-06	7.68E-05	yes
MYH9	22:36677322-36784063	80.761	102.149	0.79062	-0.33894	-3.63878	0.000274	0.005463	yes
GLS	2:191745546-191829776	6.9186	8.75069	0.790635	-0.33892	-4.62814	3.69E-06	0.000124	yes
WNK4	17:40932648-40949084	3.50668	4.43329	0.790988	-0.33827	-3.90847	9.29E-05	0.002183	yes
ALDH1L2	12:105413561-105478341	10.2204	12.9122	0.79153	-0.33728	-4.67032	3.01E-06	0.000103	yes
DSP	6:7540683-7586946	2.19096	2.76712	0.791784	-0.33682	-4.04663	5.20E-05	0.001327	yes
SEC61G	7:54819939-54826939	128.471	162.239	0.791863	-0.33668	-4.6646	3.09E-06	0.000105	yes
RARRES2	7:150035406-150038763	75.2888	95.0285	0.792276	-0.33592	-4.66404	3.10E-06	0.000105	yes
UGP2	2:64068097-64118696	22.5203	28.4205	0.792396	-0.33571	-4.41635	1.00E-05	0.000311	yes
PPP2R5B	11:64692142-64703360	4.16737	5.2591	0.792411	-0.33568	-3.50976	0.000449	0.008159	yes
PALLD	4:169418216-169849608	22.4636	28.348	0.792423	-0.33566	-3.90211	9.54E-05	0.002234	yes
PLEKHA2	8:38758752-38831431	2.66555	3.35867	0.793633	-0.33346	-3.89933	9.65E-05	0.002249	yes
AK2	1:33473540-33502512	11.1194	14.0102	0.793665	-0.3334	-4.1875	2.82E-05	0.000779	yes
IFRD1	7:112063198-112117258	5.03023	6.32838	0.794869	-0.33121	-3.68409	0.00023	0.004724	yes
PTGS2	1:186640943-186649559	37.0875	46.6396	0.795193	-0.33062	-4.3189	1.57E-05	0.000457	yes
EIF2S2	20:32676114-32700085	20.5928	25.8904	0.795384	-0.33028	-4.61668	3.90E-06	0.000129	yes
LOXL2	8:23154409-23261722	97.6083	122.715	0.795406	-0.33024	-3.87321	0.000107	0.002456	yes
GLIPR1	12:75874512-75905418	21.7385	27.326	0.795524	-0.33002	-4.16209	3.15E-05	0.000859	yes
FAM69A	1:93307720-93427079	4.71118	5.91977	0.795838	-0.32945	-3.5493	0.000386	0.007237	yes
MYH14	19:50706884-50813801	11.778	14.7885	0.79643	-0.32838	-4.54117	5.59E-06	0.000181	yes
RDH10	8:74207264-74237516	3.25137	4.08202	0.79651	-0.32824	-3.48457	0.000493	0.008856	yes
LRRFIP1	2:238536223-238690290	15.8295	19.8679	0.796737	-0.32782	-3.58561	0.000336	0.006478	yes
DACT1	14:59104756-59115039	25.8789	32.4573	0.797321	-0.32677	-3.44576	0.000569	0.009969	yes
OSMR	5:38845959-38935743	22.0667	27.646	0.798188	-0.3252	-4.09749	4.18E-05	0.001096	yes
HSPB1	7:75931874-75933614	74.9859	93.8373	0.799105	-0.32354	-4.52003	6.18E-06	0.000198	yes
RPS27A	2:55399682-55462989	125.882	157.417	0.799672	-0.32252	-4.36119	1.29E-05	0.000386	yes
IER3	6:30710975-30712327	168.786	210.826	0.800594	-0.32086	-4.1642	3.12E-05	0.000853	yes
RNF187	1:228675067-228683889	15.019	18.7379	0.801531	-0.31917	-4.46138	8.14E-06	0.000258	yes
CHSY1	15:101715927-101792137	9.47247	11.8147	0.801753	-0.31877	-4.44725	8.70E-06	0.000274	yes
TOMM7	7:22852250-22862421	34.2586	42.6866	0.802561	-0.31732	-3.95386	7.69E-05	0.001853	yes
RPL21	13:27825691-27830705	144.857	180.483	0.802607	-0.31723	-4.42899	9.47E-06	0.000294	yes
AMOTL2	3:134074189-134093406	8.33255	10.3756	0.803091	-0.31636	-4.41437	1.01E-05	0.000313	yes
EFEMP1	2:56093096-56151298	138.487	172.308	0.803718	-0.31524	-3.63536	0.000278	0.005517	yes
ZNF470	19:57078889-57094262	2.11272	2.62693	0.804254	-0.31428	-3.6819	0.000232	0.004751	yes

SYNE1	6:152442818-152958534	2.1712	2.69842	0.804619	-0.31362	-4.36094	1.30E-05	0.000386	yes
CLIC4	1:25071759-25170815	84.388	104.704	0.805967	-0.31121	-3.6609	0.000251	0.005065	yes
NPTN	15:73735498-73925753	31.0895	38.5592	0.80628	-0.31065	-4.3293	1.50E-05	0.000441	yes
RPLP0	12:120634502-120639014	193.405	239.72	0.806795	-0.30973	-3.63651	0.000276	0.0055	yes
GAS6	13:114523521-114567046	56.9231	70.5533	0.80681	-0.3097	-3.90023	9.61E-05	0.002244	yes
RPL7	8:74202873-74205869	175.601	217.566	0.807116	-0.30915	-4.18721	2.82E-05	0.000779	yes
ATP2A1	16:28889808-28936532	4.37921	5.42541	0.807167	-0.30906	-3.47349	0.000514	0.009178	yes
ZRANB1	10:126630691-126676005	4.65613	5.76597	0.807519	-0.30843	-4.03298	5.51E-05	0.00139	yes
MAP1LC3B	16:87425800-87438380	38.8774	48.1401	0.807589	-0.30831	-4.25346	2.10E-05	0.0006	yes
KLF9	9:72999512-73029573	3.21732	3.98219	0.807927	-0.3077	-3.70761	0.000209	0.004375	yes
WDR45L	17:80572437-80606411	13.1312	16.248	0.808173	-0.30726	-4.23024	2.33E-05	0.000659	yes
EIF3L	22:38245378-38284789	23.8815	29.5486	0.808211	-0.3072	-4.29479	1.75E-05	0.000503	yes
FIBIN	11:27015627-27018634	7.87506	9.74332	0.808252	-0.30712	-4.01297	6.00E-05	0.001502	yes
RPS23	5:81569138-81574235	32.1344	39.7497	0.808419	-0.30683	-4.18814	2.81E-05	0.000779	yes
SLC16A3	17:80186281-80197375	64.2668	79.4474	0.808923	-0.30593	-4.1516	3.30E-05	0.000896	yes
C7orf60	7:112459201-112579932	5.72388	7.06803	0.809827	-0.30431	-3.9531	7.71E-05	0.001856	yes
RPL21P28	1:212113740-212278187	312.177	385.284	0.810252	-0.30356	-3.98101	6.86E-05	0.001687	yes
PFKP	10:3109711-3178997	37.9049	46.7812	0.810259	-0.30354	-4.13321	3.58E-05	0.000958	yes
GFPT1	2:69546904-69614382	8.73715	10.7777	0.810669	-0.30281	-4.19655	2.71E-05	0.000755	yes
ISG15	1:948846-949920	149.468	184.28	0.811092	-0.30206	-4.18941	2.80E-05	0.000778	yes
RPLP0P2	11:61382507-61406921	74.6682	92.043	0.811232	-0.30181	-3.7565	0.000172	0.003705	yes
XBP1	22:29190547-29196560	25.9938	32.0378	0.811348	-0.30161	-4.21145	2.54E-05	0.000711	yes
TMSB10	2:85132762-85133799	994.528	1225.7	0.811396	-0.30152	-3.6892	0.000225	0.00465	yes
RPS15A	16:18794276-18801656	198.354	244.446	0.811443	-0.30144	-3.96127	7.46E-05	0.001805	yes
NEK7	1:198126107-198291550	31.9787	39.3873	0.811904	-0.30062	-4.03765	5.40E-05	0.00137	yes
RPL9	4:39455743-39460568	153.982	189.624	0.812039	-0.30038	-3.97871	6.93E-05	0.001701	yes
SARS	1:109756514-109780804	25.2561	31.0983	0.812138	-0.3002	-3.81439	0.000137	0.003031	yes
COX7C	5:85913783-85916583	120.502	148.281	0.81266	-0.29928	-3.9979	6.39E-05	0.00159	yes
PTPRF	1:43996546-44089343	12.6942	15.6072	0.813355	-0.29804	-4.0817	4.47E-05	0.001163	yes
PNRC1	6:89790428-89794879	10.5338	12.9503	0.813402	-0.29796	-3.82134	0.000133	0.002969	yes
SERTAD2	2:64858754-64881046	5.73076	7.04017	0.814009	-0.29688	-4.07484	4.60E-05	0.001193	yes
FOXN3	14:89622515-90085494	3.79509	4.66177	0.814088	-0.29674	-3.47051	0.000519	0.009246	yes
TBL2	7:72983273-72993013	5.74949	7.06032	0.814338	-0.2963	-3.58121	0.000342	0.00657	yes
HINT1	5:130494874-130501034	49.7761	61.0991	0.814678	-0.2957	-3.74474	0.000181	0.003833	yes

TRAM1L1	4:118004709-118006736	30.4018	37.3129	0.81478	-0.29552	-4.12609	3.69E-05	0.000984	yes
RPS3A	4:152020753-152025804	152.811	187.252	0.816071	-0.29323	-3.97486	7.04E-05	0.00172	yes
MYH7	14:23881946-23903496	2.58266	3.1636	0.816367	-0.29271	-3.44849	0.000564	0.009905	yes
TRAM1	8:71485452-71520694	51.8694	63.5356	0.816383	-0.29268	-3.86925	0.000109	0.002493	yes
PTRF	17:40554466-40575338	82.7658	101.325	0.816835	-0.29188	-3.56641	0.000362	0.006834	yes
LOC100652914	12:93397533-93771512	1048.45	1283.43	0.816912	-0.29175	-3.7016	0.000214	0.004461	yes
RAB3B	1:52373627-52456436	3.9699	4.85716	0.817329	-0.29101	-4.06798	4.74E-05	0.001225	yes
TMEM2	9:74298281-74383800	8.95897	10.9605	0.817387	-0.29091	-4.06003	4.91E-05	0.00126	yes
PACSIN2	22:43265771-43411184	7.39069	9.03392	0.818104	-0.28964	-3.67298	0.00024	0.004879	yes
LOC400590	17:29332139-29361715	799.506	976.836	0.818465	-0.28901	-3.57002	0.000357	0.006785	yes
RPL13AP3	14:56232962-56234435	84.9582	103.801	0.818472	-0.289	-3.9261	8.63E-05	0.002049	yes
CALM2	2:47387220-47403740	132.885	162.35	0.818509	-0.28893	-3.82925	0.000129	0.002885	yes
SLC7A2	8:17354596-17428077	3.94012	4.8114	0.818913	-0.28822	-3.62812	0.000285	0.005642	yes
RPS5	19:58898635-58906171	97.5307	119.083	0.819014	-0.28804	-4.0233	5.74E-05	0.001441	yes
RPL26	17:8280833-8286565	229.987	280.761	0.819156	-0.28779	-3.95672	7.60E-05	0.001837	yes
LOC100652998	7:137074384-137531609	1032.7	1260.58	0.819226	-0.28767	-3.56628	0.000362	0.006834	yes
VDAC2	10:76969911-76991206	29.5868	36.0931	0.819736	-0.28677	-3.52091	0.00043	0.007873	yes
RPS6	9:19376253-19380235	247.946	302.439	0.819822	-0.28662	-3.7761	0.000159	0.003472	yes
RPS12	6:133135707-133138703	185.78	226.546	0.820054	-0.28621	-3.98702	6.69E-05	0.001654	yes
SLC35E1	19:16660647-16683193	7.95875	9.6979	0.820667	-0.28513	-3.9748	7.04E-05	0.00172	yes
FKBP8	19:18642567-18654383	25	30.4625	0.820681	-0.28511	-3.97106	7.16E-05	0.001744	yes
RPL13A	19:49990864-49995565	151.797	184.955	0.820724	-0.28503	-3.78687	0.000153	0.003356	yes
WDR1	4:10075962-10118573	54.3199	66.178	0.820815	-0.28487	-3.74467	0.000181	0.003833	yes
SLC25A6	Y:1455044-1461039	44.7368	54.4796	0.821166	-0.28425	-3.5155	0.000439	0.008025	yes
DNAJB4	1:78470635-78482998	13.4347	16.356	0.821393	-0.28386	-3.84817	0.000119	0.002696	yes
LOC653075	15:30427989-30439395	5.18266	6.30821	0.821574	-0.28354	-3.45989	0.00054	0.009577	yes
RAP2A	13:98086474-98120252	4.04283	4.91931	0.821829	-0.28309	-3.44709	0.000567	0.009945	yes
NUCB2	11:17298285-17353070	29.6461	36.0633	0.822057	-0.28269	-3.94713	7.91E-05	0.001895	yes
RPL38	17:72199794-72206019	167.389	203.468	0.82268	-0.2816	-3.49439	0.000475	0.008589	yes
RPL3	22:39708886-39715670	182.881	222.231	0.822932	-0.28115	-3.6001	0.000318	0.006177	yes
ICAM1	19:10381516-10397291	21.146	25.6945	0.822978	-0.28107	-3.9093	9.26E-05	0.002179	yes
GLTP	12:110288747-110318293	8.98278	10.9049	0.823738	-0.27974	-3.53937	0.000401	0.007466	yes
GALNT10	5:153570294-153825382	9.26429	11.2338	0.82468	-0.27809	-3.83455	0.000126	0.002828	yes
IKBIP	12:99007181-99038589	30.3834	36.8388	0.824766	-0.27794	-3.70235	0.000214	0.004454	yes

TNFAIP2	14:103592663-103603776	5.79093	7.02022	0.824893	-0.27772	-3.64842	0.000264	0.005287	yes
C7orf74	7:106297210-106301634	5.58365	6.76744	0.825076	-0.2774	-3.66757	0.000245	0.004961	yes
HMOX1	22:35777059-35790207	79.5338	96.347	0.825493	-0.27667	-3.74033	0.000184	0.003888	yes
LOC100652902	20:21735848-21736174	1594.15	1930.6	0.825728	-0.27626	-3.53635	0.000406	0.007532	yes
OST4	2:27274490-27294567	135.775	164.166	0.827059	-0.27394	-3.59611	0.000323	0.006255	yes
RPL23P8	7:20866916-20867439	384.509	464.782	0.827289	-0.27354	-3.67799	0.000235	0.004804	yes
ARPC2	2:219081873-219119071	94.8255	114.614	0.827347	-0.27344	-3.65149	0.000261	0.005232	yes
PCYOX1	2:70485230-70508317	9.0546	10.9377	0.827834	-0.27259	-3.8123	0.000138	0.003047	yes
RPS29	14:50044038-50053094	302.526	365.248	0.828276	-0.27182	-3.48294	0.000496	0.008887	yes
CITED2	6:139693395-139695785	19.6832	23.7558	0.828564	-0.27132	-3.44972	0.000561	0.009884	yes
RPL31P11	1:161653484-161655042	57.9736	69.9551	0.828726	-0.27103	-3.74469	0.000181	0.003833	yes
EIF1	17:39845126-39847898	100.513	121.252	0.82896	-0.27063	-3.6669	0.000246	0.004961	yes
CNOT8	5:154238197-154256352	11.3161	13.6381	0.829742	-0.26927	-3.61799	0.000297	0.00584	yes
DHX40	17:57642885-57685713	6.08992	7.3383	0.829882	-0.26902	-3.47035	0.00052	0.009246	yes
RPS17	15:82821160-82824865	284.589	342.826	0.830127	-0.2686	-3.70891	0.000208	0.004359	yes
RPS17L	15:83205503-83209208	284.239	342.199	0.830625	-0.26773	-3.69703	0.000218	0.004527	yes
UBE2J1	6:90036343-90062619	7.89108	9.49676	0.830923	-0.26721	-3.6879	0.000226	0.004661	yes
HIVEP2	6:143072603-143266338	6.03976	7.26765	0.831047	-0.267	-3.72621	0.000194	0.004096	yes
RPL29P2	17:7623038-7737058	86.7852	104.387	0.831379	-0.26642	-3.67138	0.000241	0.004902	yes
MAP1LC3B2	12:116997185-117014425	57.9099	69.6388	0.831575	-0.26608	-3.69642	0.000219	0.004527	yes
SVEP1	9:113127527-113342160	5.41851	6.50278	0.833261	-0.26316	-3.65776	0.000254	0.005113	yes
HSPA13	21:15743435-15755509	13.2589	15.9098	0.833379	-0.26295	-3.67641	0.000237	0.00482	yes
PPIAL4B	1:144363461-144364246	57.0811	68.4821	0.833519	-0.26271	-3.62867	0.000285	0.005638	yes
RPL18A	19:17970730-17974124	191.655	229.878	0.833725	-0.26236	-3.62366	0.00029	0.005727	yes
RPS14	5:149823791-149829319	215.93	258.915	0.83398	-0.26191	-3.56249	0.000367	0.006901	yes
RPL23	17:37006320-37010053	268.432	321.715	0.834378	-0.26123	-3.56395	0.000365	0.006871	yes
DRAM1	12:102271104-102317401	37.1749	44.5512	0.834431	-0.26114	-3.51351	0.000442	0.008075	yes
PPAP2A	5:54603575-54830873	12.004	14.3826	0.83462	-0.26081	-3.60591	0.000311	0.006065	yes
RPL8	8:146015153-146017805	195.785	234.32	0.835545	-0.25921	-3.44578	0.000569	0.009969	yes
ACTR3	2:114588759-114716167	39.082	46.6986	0.836899	-0.25688	-3.51058	0.000447	0.008144	yes
RPS27	1:153963238-153964631	339.288	405.293	0.837143	-0.25645	-3.5822	0.000341	0.006554	yes
TEAD1	11:12695968-12966284	7.05372	8.42523	0.837214	-0.25633	-3.56608	0.000362	0.006834	yes
RPS16	19:39923846-39926618	146.61	175.062	0.837475	-0.25588	-3.56699	0.000361	0.006834	yes
RPL12	9:130209952-130213711	80.9397	96.5647	0.838191	-0.25465	-3.53368	0.00041	0.00759	yes

SLC31A1	9:115983807-116026772	6.98466	8.3279	0.838706	-0.25376	-3.49206	0.000479	0.008643	yes
EGLN1	1:231499496-231560790	6.46792	7.71144	0.838743	-0.2537	-3.54488	0.000393	0.00734	yes

Up-regulated genes (those highlighted in red are associated with cell migration)

Gene Symbol	Chr Coordinates	Avg FPKM-*SI*	Avg FRKM-CI	Ratio	log2 fold	test_stat	p_value	q_value	Sig?
C10orf32-AS3MT	10:104613966-104661656	0.396633	0.06297	6.298761	2.655068	-1.79769e-	6.03E-09	3.71E-07	yes
CCDC102B	18:66382490-66722426	0.502518	0.130317	3.85612	1.94715	3.76098	0.000169	0.003654	yes
FAIM2	12:50260678-50297760	0.71242	0.190738	3.735071	1.901136	7.15878	8.14E-13	1.04E-10	yes
COLEC12	18:319354-500729	1.09535	0.3697	2.962808	1.566965	6.42172	1.35E-10	1.15E-08	yes
THBD	20:23026269-23030301	1.93042	0.698657	2.763044	1.466259	9.35384	0	0	yes
OLFML2B	1:161952981-161993644	0.505418	0.203372	2.48519	1.313356	3.91366	9.09E-05	0.002147	yes
KDR	4:55944425-55991762	0.764623	0.311649	2.453475	1.294827	6.70552	2.01E-11	2.00E-09	yes
VAT1L	16:77822482-78014001	1.78394	0.740952	2.407632	1.267615	7.87685	3.33E-15	6.07E-13	yes
C4B	6:31982571-32003195	0.422388	0.190638	2.215655	1.147733	4.32409	1.53E-05	0.000449	yes
ANK3	10:61786055-62493284	0.254212	0.115109	2.208446	1.143031	4.23612	2.27E-05	0.000644	yes
HECW2	2:197063976-197457335	5.89637	2.7008	2.183194	1.12644	14.3688	0	0	yes
C4A	6:31949833-31970457	0.419527	0.19364	2.166531	1.115387	4.2196	2.45E-05	0.000687	yes
COL22A1	8:139600477-139926236	0.659831	0.305568	2.159359	1.110603	5.72066	1.06E-08	6.14E-07	yes
AIM1	6:106959729-107018335	0.358271	0.168813	2.122295	1.085625	4.53353	5.80E-06	0.000187	yes
SYT14L	4:68918915-68995587	0.715295	0.350409	2.041315	1.029499	3.52487	0.000424	0.007796	yes
FER1L6	8:124953960-125132302	0.845457	0.422283	2.00211	1.001521	5.74983	8.93E-09	5.31E-07	yes
RAB27B	18:52495707-52562747	2.38977	1.20421	1.984513	0.988785	10.1118	0	0	yes
ASF1B	19:14230320-14247440	1.21721	0.620799	1.960715	0.97138	3.50169	0.000462	0.008389	yes
MID1	X:10413349-10851809	1.11223	0.56732	1.960498	0.971221	4.09503	4.22E-05	0.001104	yes
SYT14	1:210111537-210337636	0.640449	0.327976	1.952731	0.965493	3.97632	7.00E-05	0.001715	yes
KIFC1	6:33359312-33377701	0.802355	0.414097	1.937602	0.954272	3.58759	0.000334	0.006437	yes
SEMA3A	7:83587658-83824217	1.57747	0.817408	1.929844	0.948484	7.36954	1.71E-13	2.39E-11	yes
F2RL1	5:76114832-76131140	4.14153	2.1638	1.914008	0.936597	8.18572	2.22E-16	4.64E-14	yes
FRMD5	15:44165729-44487429	1.0916	0.585335	1.864915	0.89911	3.60217	0.000316	0.006136	yes
COL13A1	10:71561643-71718904	4.01725	2.16221	1.857937	0.893702	5.74318	9.29E-09	5.49E-07	yes
C6orf105	6:11713887-11779280	2.68042	1.44386	1.856427	0.892528	5.02237	5.10E-07	2.08E-05	yes
FOXRED2	22:36883232-36903148	1.2762	0.691523	1.845492	0.884005	3.52757	0.000419	0.007737	yes
TJP2	9:71736223-71870124	1.20231	0.657339	1.829056	0.871099	3.89299	9.90E-05	0.002297	yes
EFNA5	5:106712589-107006596	0.758232	0.41549	1.82491	0.867826	4.62443	3.76E-06	0.000126	yes

MDK	11:46402617-46405375	23.6992	13.0124	1.821278	0.864951	7.70934	1.27E-14	2.15E-12	yes
PPAP2B	1:56960418-57045257	10.3843	5.72659	1.813348	0.858656	10.9651	0	0	yes
LOC154822	7:158801044-158818929	0.822098	0.45516	1.806174	0.852937	4.0957	4.21E-05	0.001103	yes
ALDH1A3	15:101420008-101610317	16.5924	9.19227	1.805038	0.85203	10.5189	0	0	yes
DIO2	14:80663867-80921810	1.11387	0.619964	1.796669	0.845325	5.81927	5.91E-09	3.65E-07	yes
CALCRL	2:188207845-188313021	0.496976	0.277136	1.793257	0.842582	3.53732	0.000404	0.007515	yes
PLAU	10:75669726-75682535	2.84444	1.58908	1.789992	0.839953	5.36797	7.96E-08	3.70E-06	yes
DUSP10	1:221874763-221915516	3.34895	1.87493	1.786173	0.836872	5.04441	4.55E-07	1.87E-05	yes
PTN	7:136912087-137028546	6.42444	3.60595	1.781622	0.833191	5.9099	3.42E-09	2.22E-07	yes
E2F7	12:77415025-77459360	2.19282	1.24021	1.768104	0.822203	7.66326	1.82E-14	3.02E-12	yes
MCM5	22:35796115-35820495	1.48353	0.842836	1.760164	0.81571	4.16076	3.17E-05	0.000862	yes
MSX1	4:4861391-4865663	1.90864	1.08963	1.75164	0.808707	4.03539	5.45E-05	0.001378	yes
DOCK4	7:111366163-111846462	0.556459	0.318998	1.744397	0.802728	4.67971	2.87E-06	9.86E-05	yes
AKR1C4	10:5238797-5260910	27.7957	15.9399	1.743781	0.802219	9.97906	0	0	yes
AKR1C1	10:5005453-5020158	30.5206	17.7637	1.718144	0.780851	10.2397	0	0	yes
HSD11B1	1:209859524-209908295	9.74382	5.69075	1.712221	0.775869	7.30581	2.76E-13	3.68E-11	yes
SLC6A15	12:85253266-85306606	2.92193	1.70712	1.711614	0.775357	6.11961	9.38E-10	6.90E-08	yes
AKR1C3	10:5136567-5149878	32.4446	18.9717	1.710158	0.774129	10.0245	0	0	yes
PODXL	7:131185020-131241376	0.994479	0.582804	1.70637	0.77093	5.05233	4.36E-07	1.81E-05	yes
AKR1C2	10:5031964-5060207	28.611	16.7682	1.706265	0.770842	9.64899	0	0	yes
TAKR	10:4913858-4958465	2.22318	1.30417	1.70467	0.769493	3.46603	0.000528	0.009384	yes
NPTXR	22:39214455-39240017	0.669527	0.393393	1.701929	0.767171	4.11065	3.95E-05	0.001043	yes
ABCA9	17:66970772-67057136	3.50095	2.0574	1.701638	0.766924	8.97017	0	0	yes
GEM	8:95261480-95274547	4.65609	2.7541	1.690603	0.757538	3.68342	0.00023	0.00473	yes
PREX1	20:47240792-47444420	1.01226	0.600197	1.686546	0.754072	5.33281	9.67E-08	4.40E-06	yes
FAM65C	20:49202644-49253426	0.739215	0.438899	1.684249	0.752105	3.57153	0.000355	0.006773	yes
RRM2	2:10262694-10271546	3.02627	1.80452	1.67705	0.745926	5.78029	7.46E-09	4.51E-07	yes
GRB14	2:165349322-165478360	1.53209	0.914768	1.67484	0.744023	3.78192	0.000156	0.003407	yes
AKR1CL1	10:5196654-5227150	2.26676	1.3566	1.670913	0.740636	4.30137	1.70E-05	0.000491	yes
MELK	9:36572904-36677679	1.44043	0.87027	1.655153	0.726965	3.63858	0.000274	0.005463	yes
TNXB	6:32006092-32077151	0.291891	0.176461	1.654139	0.72608	3.45011	0.00056	0.009882	yes
CLSPN	1:36197712-36235551	0.400198	0.242857	1.647875	0.720607	3.59111	0.000329	0.006368	yes
STEAP3	2:119981383-120023228	3.584	2.19077	1.635954	0.710133	4.81348	1.48E-06	5.48E-05	yes
TMEM119	12:108983621-108991894	4.03039	2.46684	1.633827	0.708255	6.22395	4.85E-10	3.78E-08	yes

LRP4	11:46867961-46940173	0.704852	0.432339	1.630323	0.705157	4.64279	3.44E-06	0.000116	yes
SHCBP1	16:46614465-46655311	1.29329	0.793813	1.629212	0.704175	3.9067	9.36E-05	0.002196	yes
DCBLD2	3:98514813-98620533	43.3509	26.7977	1.61771	0.693953	8.86138	0	0	yes
MMP16	8:89049459-89339717	4.33342	2.68206	1.615706	0.692165	8.65347	0	0	yes
APCDD1L	20:57034425-57089949	2.24462	1.39306	1.611287	0.688214	4.94462	7.63E-07	3.02E-05	yes
NAV2	11:19372270-20143147	3.10926	1.9427	1.600484	0.678508	5.70235	1.18E-08	6.73E-07	yes
CDH6	5:31193761-31329253	1.43108	0.89755	1.594429	0.67304	6.42839	1.29E-10	1.11E-08	yes
ITGA2	5:52285155-52390609	43.0837	27.06	1.592154	0.67098	8.2837	2.22E-16	4.64E-14	yes
MCM3	6:52128811-52149582	3.30652	2.07677	1.592145	0.670972	5.82126	5.84E-09	3.63E-07	yes
TMEM132B	12:125811161-126143589	5.63993	3.55953	1.584459	0.66399	8.93753	0	0	yes
LOC643723	1:219254314-219347130	3.22156	2.04194	1.577696	0.657819	3.9911	6.58E-05	0.001631	yes
SERPINB2	18:61554938-61571124	6.20319	3.94279	1.5733	0.653793	5.86546	4.48E-09	2.83E-07	yes
AKAP1	17:55162552-55198710	1.01019	0.64255	1.572158	0.652746	3.60527	0.000312	0.006071	yes
DSEL	18:65173818-65566856	9.57568	6.10176	1.569331	0.65015	8.96105	0	0	yes
LOC100130009	2:74645221-74645569	92.5258	59.0825	1.566044	0.647125	6.5834	4.60E-11	4.19E-09	yes
TNFRSF1B	1:12227059-12269277	1.36189	0.874141	1.557975	0.639672	3.93882	8.19E-05	0.001953	yes
NCAPG	4:17812524-18023483	1.19116	0.764637	1.557811	0.63952	3.88682	0.000102	0.002345	yes
C2orf81	2:74641302-74644844	6.32247	4.05999	1.557262	0.639012	6.33092	2.44E-10	1.96E-08	yes
C12orf35	12:32112352-32146041	2.36312	1.51766	1.557081	0.638844	6.62466	3.48E-11	3.21E-09	yes
EVC	4:5712923-5816031	32.0223	20.5835	1.555727	0.637589	8.34466	0	0	yes
PLA2G4A	1:186798031-186958113	3.40606	2.19423	1.55228	0.634389	5.45832	4.81E-08	2.40E-06	yes
BDKRB1	14:96722558-96731100	24.1233	15.5423	1.552106	0.634227	7.95661	1.78E-15	3.32E-13	yes
SCG2	2:224461657-224467217	2.67058	1.75643	1.520459	0.604507	4.35086	1.36E-05	0.000403	yes
SDC1	2:20400557-20427748	5.73657	3.7805	1.51741	0.601611	6.72421	1.77E-11	1.81E-09	yes
DRP2	X:100474932-100519485	1.49607	0.988982	1.512737	0.597162	3.81534	0.000136	0.003024	yes
HMGA1	6:34204576-34214008	37.7608	25.0092	1.509876	0.59443	5.48735	4.08E-08	2.07E-06	yes
CFB	6:31913720-31919861	17.1619	11.3757	1.508646	0.593254	8.03028	8.88E-16	1.73E-13	yes
CHAF1A	19:4402659-4443394	1.34371	0.893419	1.504009	0.588813	3.47175	0.000517	0.00922	yes
UHRF1	19:4909509-4962165	1.38534	0.921921	1.502667	0.587525	3.91518	9.03E-05	0.002137	yes
ARL4C	2:235401684-235405693	2.96582	1.9744	1.502137	0.587017	5.55861	2.72E-08	1.42E-06	yes
NAV3	12:78225068-78606790	2.79497	1.86879	1.495604	0.580728	7.33883	2.15E-13	2.93E-11	yes
MCM2	3:127317252-127341279	1.36272	0.912179	1.493917	0.5791	3.49543	0.000473	0.008567	yes
OAF	11:120081746-120100650	17.7937	11.9132	1.493612	0.578806	7.4852	7.15E-14	1.08E-11	yes
TIMELESS	12:56810156-56843200	0.878326	0.58858	1.49228	0.577518	3.45893	0.000542	0.009599	yes

LAMA5	20:60884120-60942368	0.952993	0.63885	1.491732	0.576988	5.34145	9.22E-08	4.21E-06	yes
NES	1:156638554-156647189	3.27173	2.19478	1.490687	0.575977	6.49636	8.23E-11	7.32E-09	yes
HMGA1P7	6:134435099-134438818	14.1505	9.49992	1.489539	0.574866	7.37479	1.65E-13	2.32E-11	yes
ODZ4	11:78364327-79151695	0.833253	0.559504	1.489271	0.574606	5.37664	7.59E-08	3.57E-06	yes
F2R	5:76011867-76031595	14.7738	9.94247	1.485929	0.571365	7.87228	3.55E-15	6.40E-13	yes
CDC25B	20:3776400-3786762	3.27509	2.20756	1.483579	0.569082	3.78493	0.000154	0.003377	yes
C6orf174	6:127759550-127840500	0.663155	0.447288	1.482613	0.568142	4.33798	1.44E-05	0.000425	yes
GPR125	4:22388998-22517672	2.94599	1.98843	1.481566	0.567123	5.70225	1.18E-08	6.73E-07	yes
KIF11	10:94352824-94415152	0.939755	0.63486	1.480255	0.565846	3.4925	0.000479	0.00864	yes
RGMB	5:98104998-98132198	18.0053	12.1865	1.477479	0.563138	7.62034	2.53E-14	4.14E-12	yes
CNIH3	1:224804178-224928249	5.80379	3.95259	1.468351	0.554197	5.53961	3.03E-08	1.57E-06	yes
KITLG	12:88886569-88974250	2.47579	1.68822	1.466509	0.552386	3.78156	0.000156	0.003407	yes
MCM4	8:48872762-48890720	3.33618	2.27779	1.464657	0.550562	4.62354	3.77E-06	0.000126	yes
TMTC1	12:29653745-29937692	2.21551	1.51367	1.463668	0.549588	6.27988	3.39E-10	2.68E-08	yes
LAMB3	1:209788214-209825820	2.4877	1.70424	1.459712	0.545684	4.81901	1.44E-06	5.37E-05	yes
ANGPTL2	9:129677052-129985445	17.9466	12.3234	1.456303	0.54231	7.47669	7.62E-14	1.14E-11	yes
FGF5	4:81187741-81212171	3.1439	2.16959	1.449076	0.535133	5.58374	2.35E-08	1.26E-06	yes
TPX2	20:30326903-30389603	1.89584	1.3093	1.44798	0.534042	3.96954	7.20E-05	0.00175	yes
CXCR4	2:136871918-136875725	3.96526	2.73851	1.447963	0.534024	3.57411	0.000351	0.006715	yes
KCTD12	13:77454303-77460540	12.2348	8.45459	1.447119	0.533184	7.38484	1.53E-13	2.18E-11	yes
HYAL2	3:50355220-50360281	5.19444	3.59377	1.445401	0.53147	4.18636	2.83E-05	0.000779	yes
DUSP6	12:89741836-89746296	8.43159	5.83446	1.445136	0.531206	5.98316	2.19E-09	1.47E-07	yes
PHF15	5:133861797-133918918	2.65792	1.84245	1.442601	0.528672	5.89705	3.70E-09	2.38E-07	yes
SCFD2	4:53739148-54232242	2.13589	1.48291	1.440337	0.526406	3.84869	0.000119	0.002695	yes
SERINC5	5:79407049-79551898	2.64792	1.84639	1.434107	0.520152	3.50484	0.000457	0.008301	yes
TGFBR3	1:92145899-92371559	1.61721	1.128	1.433697	0.51974	4.38797	1.14E-05	0.000347	yes
B7H6	11:17373308-17398868	1.11171	0.776557	1.431588	0.517617	3.95031	7.81E-05	0.001874	yes
CDC42EP4	17:71279762-71308143	2.09076	1.46263	1.429452	0.515463	3.6969	0.000218	0.004527	yes
CD68	17:7482804-7485429	29.8699	20.9017	1.429066	0.515072	7.07817	1.46E-12	1.74E-10	yes
SPATA18	4:52917592-52963458	1.96569	1.37592	1.428637	0.514639	4.25305	2.11E-05	0.0006	yes
RGL1	1:183605207-183897666	4.32307	3.03149	1.426055	0.512029	6.16437	7.08E-10	5.31E-08	yes
CAD	2:27440257-27466654	1.64073	1.15096	1.425532	0.5115	4.92319	8.51E-07	3.34E-05	yes
CAMK2N1	1:20808883-20812728	4.89981	3.45261	1.419161	0.505038	4.71474	2.42E-06	8.48E-05	yes
IGF2BP3	7:23349827-23509995	3.74646	2.64134	1.418394	0.504258	5.42195	5.90E-08	2.87E-06	yes

PIK3R1	5:67511583-67597649	3.30526	2.33433	1.415935	0.501755	5.45088	5.01E-08	2.49E-06	yes
NCAPD3	11:134022336-134094426	1.23084	0.871173	1.412854	0.498612	3.75368	0.000174	0.003731	yes
MKI67	10:129894922-129924468	3.15522	2.24307	1.406652	0.492266	6.86397	6.70E-12	7.15E-10	yes
SLC43A3	11:57174426-57195053	11.2311	8.00665	1.402721	0.488229	5.95268	2.64E-09	1.75E-07	yes
CTSS	1:150702671-150738433	3.39805	2.42563	1.400894	0.486348	4.97935	6.38E-07	2.55E-05	yes
IFI30	19:18284578-18288927	19.3064	13.7846	1.400577	0.486022	5.38693	7.17E-08	3.40E-06	yes
CARD6	5:40841409-40855456	4.61878	3.29834	1.400335	0.485772	5.58706	2.31E-08	1.24E-06	yes
PTX3	3:156977530-157221415	126.339	90.3325	1.3986	0.483983	5.71444	1.10E-08	6.32E-07	yes
GPR68	14:91698875-91720224	7.91961	5.68157	1.393912	0.47914	5.7767	7.62E-09	4.59E-07	yes
TNFRSF21	6:47199267-47277680	8.04996	5.80796	1.386022	0.47095	6.06388	1.33E-09	9.50E-08	yes
TFPI2	7:93515744-93520065	384.439	277.916	1.383292	0.468106	5.61542	1.96E-08	1.07E-06	yes
ABCA6	17:67074846-67138015	3.58598	2.59597	1.381364	0.466094	5.36915	7.91E-08	3.69E-06	yes
CTSL1P8	9:90459659-90462339	110.044	79.6738	1.381182	0.465903	6.35044	2.15E-10	1.75E-08	yes
SEMA3D	7:84624868-84751247	1.48283	1.07784	1.375742	0.46021	4.03914	5.36E-05	0.001368	yes
SNX8	7:2291404-2354099	3.36755	2.45218	1.373288	0.457634	5.00036	5.72E-07	2.30E-05	yes
EGFR	7:55086724-55275031	9.09437	6.62297	1.373156	0.457495	5.06002	4.19E-07	1.75E-05	yes
ANPEP	15:90328125-90358072	58.0081	42.2954	1.371499	0.455754	5.94086	2.84E-09	1.87E-07	yes
XPC	3:14186646-14220172	5.04751	3.69663	1.365436	0.449361	5.12651	2.95E-07	1.25E-05	yes
FUT8	14:65877309-66210839	10.2275	7.49059	1.36538	0.449302	5.60637	2.07E-08	1.11E-06	yes
CAPN5	11:76777991-76837201	2.42523	1.7803	1.362259	0.446001	4.1427	3.43E-05	0.000928	yes
RFWD3	16:74655296-74700779	1.66752	1.22576	1.360397	0.444028	3.68847	0.000226	0.004657	yes
BTN3A2	6:26365397-26378548	12.1514	8.93236	1.36038	0.444009	4.55611	5.21E-06	0.00017	yes
TUBGCP6	22:50656117-50683400	3.29498	2.42375	1.359455	0.443029	5.21866	1.80E-07	7.89E-06	yes
MMP15	16:58059281-58080805	5.65405	4.16121	1.358751	0.442282	5.54115	3.00E-08	1.56E-06	yes
PNP	14:20937537-20946165	5.21239	3.84582	1.355339	0.438654	4.32016	1.56E-05	0.000456	yes
CD82	11:44587140-44641339	8.05202	5.94261	1.354964	0.438254	3.87619	0.000106	0.002438	yes
CORO2B	15:68871307-69020145	3.31479	2.44761	1.354297	0.437544	3.75591	0.000173	0.003709	yes
FMNL2	2:153191750-153506348	13.5812	10.0309	1.353936	0.43716	6.06348	1.33E-09	9.50E-08	yes
SLC5A3	21:35445822-35515334	1.3567	1.00293	1.352736	0.435881	4.53007	5.90E-06	0.00019	yes
STMN1	1:26210676-26233368	10.2749	7.59622	1.352633	0.435771	3.60981	0.000306	0.005991	yes
BTN3A3	6:26440699-26453643	12.6288	9.34225	1.351794	0.434876	4.09424	4.24E-05	0.001106	yes
CTSL2	9:99791958-99801925	10.3538	7.66216	1.35129	0.434337	5.88949	3.87E-09	2.48E-07	yes
SLC20A1	2:113403433-113421402	18.0317	13.3448	1.351215	0.434258	6.01583	1.79E-09	1.25E-07	yes
DNMT1	19:10244021-10305755	2.92311	2.16612	1.349468	0.432391	4.44441	8.81E-06	0.000277	yes

CENPF	1:214776531-214837914	1.00746	0.747651	1.3475	0.430286	3.57913	0.000345	0.006614	yes
MTHFD1	14:64854758-64926725	3.21928	2.39232	1.345673	0.428328	4.03791	5.39E-05	0.00137	yes
BTN3A1	6:26402464-26415444	10.1491	7.55559	1.343257	0.425735	3.9997	6.34E-05	0.001581	yes
CTSL1	9:90340973-90346384	78.6862	58.5892	1.343015	0.425476	4.46654	7.95E-06	0.000252	yes
KCNC4	1:110753335-110776674	2.14062	1.5941	1.342839	0.425287	3.75086	0.000176	0.003767	yes
NRP1	10:33466418-33623833	83.1694	61.9658	1.342182	0.424581	4.67028	3.01E-06	0.000103	yes
ARHGAP22	10:49654078-49813138	5.076	3.78339	1.341654	0.424013	4.38636	1.15E-05	0.000349	yes
BIVM	13:103436630-103528351	2.6184	1.95199	1.3414	0.42374	5.24432	1.57E-07	6.98E-06	yes
C11orf41	11:33563876-33695648	1.57889	1.17827	1.340007	0.42224	4.8925	9.96E-07	3.83E-05	yes
ITPR3	6:33589155-33664351	2.97258	2.219	1.339603	0.421806	5.35305	8.65E-08	3.97E-06	yes
CSF1	1:110453232-110472355	5.98236	4.468	1.338935	0.421086	4.11235	3.92E-05	0.001037	yes
RHOJ	14:63671144-63758559	9.98096	7.45709	1.338452	0.420566	4.78849	1.68E-06	6.07E-05	yes
TXNIP	1:145430993-145442635	48.0338	35.9145	1.337449	0.419484	5.5136	3.52E-08	1.81E-06	yes
DNMBP	10:101635333-101769676	3.82265	2.86011	1.33654	0.418502	5.22372	1.75E-07	7.70E-06	yes
CTSL1P2	10:48155942-48158691	31.6799	23.7239	1.335358	0.417227	5.44173	5.28E-08	2.58E-06	yes
CNDP2	18:72163499-72190689	4.01754	3.01345	1.333203	0.414896	4.81345	1.48E-06	5.48E-05	yes
LOC100506912	9:90479080-90481209	64.4061	48.4213	1.330119	0.411556	4.63883	3.50E-06	0.000118	yes
ODC1	2:10580507-10588453	10.314	7.75668	1.329693	0.411093	4.84993	1.24E-06	4.63E-05	yes
LHFPL2	5:77781037-77944648	16.5727	12.4929	1.326569	0.4077	5.64213	1.68E-08	9.31E-07	yes
HSPH1	13:31710761-31736117	15.178	11.4557	1.32493	0.405916	5.62441	1.86E-08	1.02E-06	yes
AHNAK2	14:105403590-105444694	17.7289	13.385	1.324535	0.405486	4.98238	6.28E-07	2.52E-05	yes
MAN1A1	6:119280994-119670926	32.808	24.8009	1.322855	0.403655	5.44258	5.25E-08	2.57E-06	yes
BDKRB2	14:96671134-96710666	30.3346	22.9479	1.32189	0.402602	5.45273	4.96E-08	2.47E-06	yes
DOCK10	2:225629806-225907330	2.67228	2.02458	1.319918	0.400449	4.74337	2.10E-06	7.42E-05	yes
TLE4	9:82186877-82341656	4.78013	3.62394	1.319042	0.399491	4.90279	9.45E-07	3.69E-05	yes
FOSL1	11:65659691-65667997	13.8079	10.4683	1.31902	0.399467	4.80703	1.53E-06	5.62E-05	yes
MMP14	14:23305792-23316803	174.287	132.137	1.318987	0.39943	4.45598	8.35E-06	0.000264	yes
RNF168	3:196195653-196230639	4.84445	3.67529	1.318114	0.398475	5.05674	4.26E-07	1.77E-05	yes
CTSL3	9:90387829-90401799	48.389	36.7283	1.317485	0.397787	4.89884	9.64E-07	3.73E-05	yes
ARMCX1	X:100805513-100809683	7.86784	5.97904	1.315904	0.396054	4.36137	1.29E-05	0.000386	yes
SYT11	1:155829259-155854990	7.88228	5.99929	1.313869	0.393821	5.38306	7.32E-08	3.46E-06	yes
BMP2	20:6748744-6760910	33.3766	25.404	1.313832	0.393781	5.40781	6.38E-08	3.03E-06	yes
SLC44A1	9:108006928-108153682	16.6341	12.7252	1.307178	0.386455	5.36235	8.21E-08	3.79E-06	yes
PPFIBP1	12:27677044-27848497	6.27699	4.80421	1.30656	0.385774	4.31115	1.62E-05	0.000471	yes

STK36	2:219528586-219567440	2.37542	1.8252	1.301457	0.380128	3.52648	0.000421	0.007759	yes
TGFB1	19:41836811-41859831	13.7635	10.5802	1.300873	0.37948	4.93055	8.20E-07	3.23E-05	yes
FAM198B	4:159045731-159094202	8.32673	6.40212	1.300621	0.3792	4.12052	3.78E-05	0.001007	yes
RAB31	18:9708227-9862553	14.3482	11.0347	1.30028	0.378822	5.25493	1.48E-07	6.61E-06	yes
AK5	1:77747661-78025654	3.34999	2.58265	1.297113	0.375305	3.55332	0.00038	0.007136	yes
CD276	15:73976621-74006859	27.0966	20.9013	1.296407	0.374519	5.17585	2.27E-07	9.73E-06	yes
HMGA2	12:66151799-66360071	11.2547	8.68281	1.296205	0.374294	4.60563	4.11E-06	0.000136	yes
PCNA	20:5095598-5107268	17.3892	13.4326	1.294552	0.372453	4.43169	9.35E-06	0.000292	yes
IL1R1	2:102770401-102796334	25.2119	19.4754	1.294551	0.372452	5.07243	3.93E-07	1.65E-05	yes
RHBDF1	16:108057-122629	6.24751	4.83337	1.292578	0.370252	4.27383	1.92E-05	0.00055	yes
MMP24	20:33814538-33864804	6.81119	5.2873	1.288217	0.365376	4.77569	1.79E-06	6.42E-05	yes
B4GALT5	20:48249481-48330421	7.40624	5.75065	1.287896	0.365016	4.90552	9.32E-07	3.65E-05	yes
VPS18	15:41186627-41196173	3.71234	2.88347	1.287456	0.364523	3.88758	0.000101	0.002342	yes
ESF1	20:13694968-13765532	3.59044	2.78914	1.287293	0.36434	3.53511	0.000408	0.007558	yes
HCP5	6:31430956-31433586	5.80976	4.53818	1.280196	0.356365	3.79118	0.00015	0.003303	yes
CDK4	12:58138783-58146164	23.7341	18.5493	1.279515	0.355597	4.10984	3.96E-05	0.001043	yes
LPHN2	1:82266081-82458107	8.81604	6.90112	1.27748	0.3533	4.88928	1.01E-06	3.88E-05	yes
CTSC	11:88026759-88070941	34.496	27.0363	1.275914	0.351531	4.29897	1.72E-05	0.000495	yes
FZD8	10:35927176-35930362	8.47194	6.66194	1.271693	0.34675	4.43276	9.30E-06	0.000291	yes
FLG	1:152274650-152297679	0.929484	0.731606	1.270471	0.345363	3.45658	0.000547	0.00966	yes
GFPT2	5:179727699-179780315	17.5497	13.8326	1.26872	0.343374	4.75383	2.00E-06	7.10E-05	yes
POLR1A	2:86253450-86333278	1.99701	1.57601	1.26713	0.341565	3.57042	0.000356	0.006784	yes
KIAA0930	22:45588122-45636650	2.99167	2.36786	1.263449	0.337367	3.92867	8.54E-05	0.002032	yes
S1PR3	9:91605777-91619925	4.43468	3.51194	1.262744	0.336562	3.87376	0.000107	0.002455	yes
LRRC15	3:194075975-194090472	8.1559	6.47126	1.260326	0.333797	4.45536	8.38E-06	0.000264	yes
FASN	17:80036213-80056106	2.74411	2.18397	1.256478	0.329385	4.11683	3.84E-05	0.001019	yes
ARHGEF40	14:21538526-21558036	5.68627	4.52586	1.256395	0.329291	4.36188	1.29E-05	0.000386	yes
RIN2	20:19867164-19983103	4.06033	3.23459	1.255284	0.328014	3.73448	0.000188	0.003974	yes
CPT1A	11:68522087-68609399	6.66341	5.3339	1.249257	0.32107	3.87613	0.000106	0.002438	yes
MARVELD1	10:99473464-99493298	13.5913	10.9025	1.246622	0.318024	4.02772	5.63E-05	0.001419	yes
USP5	12:6961284-6975796	6.20465	4.98262	1.245259	0.316445	3.67738	0.000236	0.004809	yes
CTHRC1	8:104383785-104395217	71.3557	57.34	1.244431	0.315487	4.37789	1.20E-05	0.000361	yes
GNPDA1	5:141380233-141392620	9.51457	7.66915	1.240629	0.311072	3.76231	0.000168	0.003642	yes
PHLDA1	12:76419226-76425556	19.7046	15.8846	1.240484	0.310904	4.24504	2.19E-05	0.00062	yes

CCND1	11:69455872-69469242	77.6181	62.5755	1.240391	0.310795	3.8179	0.000135	0.002998	yes
PRNP	20:4666796-4682234	119.637	96.5328	1.23934	0.309573	3.60868	0.000308	0.006008	yes
SCAP	3:47455183-47517445	4.19896	3.38844	1.239202	0.309411	3.56874	0.000359	0.006809	yes
SLC22A23	6:3228158-3456793	6.19312	5.00332	1.237802	0.307781	4.13457	3.56E-05	0.000954	yes
NBN	8:90945563-90996899	4.39676	3.55722	1.23601	0.305691	3.66959	0.000243	0.00493	yes
CHPF	2:220403668-220408487	25.0437	20.2999	1.233686	0.302975	3.94442	8.00E-05	0.001911	yes
TMEM132A	11:60691912-60719257	34.854	28.2808	1.232426	0.301501	3.96427	7.36E-05	0.001786	yes
RAC2	22:37621309-37640305	27.109	21.998	1.232339	0.3014	4.07818	4.54E-05	0.001178	yes
EMP3	19:48828628-48833810	37.6514	30.5589	1.232093	0.301111	3.81286	0.000137	0.003045	yes
NBPF10	1:145293370-145368684	40.4249	32.8172	1.231821	0.300792	3.52205	0.000428	0.007865	yes
SH2B3	12:111843751-111889427	6.7173	5.45715	1.230917	0.299734	4.06509	4.80E-05	0.001238	yes
ZMAT3	3:178735010-178789656	4.24759	3.46118	1.227209	0.295381	4.06977	4.71E-05	0.001217	yes
TTYH3	7:2671602-2704436	21.8028	17.7818	1.22613	0.294112	4.03849	5.38E-05	0.001369	yes
IFNAR1	21:34697213-34732129	4.98744	4.06935	1.225611	0.293501	3.88554	0.000102	0.002354	yes
PRRX1	1:170633312-170708541	31.6513	25.8403	1.224881	0.292642	3.46383	0.000533	0.009449	yes
LMNB2	19:2428163-2456958	6.31382	5.15633	1.224479	0.292169	3.83865	0.000124	0.002785	yes
MAN2A1	5:109025155-109203429	7.269	5.93815	1.224119	0.291743	3.96963	7.20E-05	0.00175	yes
CD47	3:107761940-107809935	6.78989	5.55849	1.221535	0.288695	3.91238	9.14E-05	0.002155	yes
CSGALNACT2	10:43633933-43680750	12.1603	9.95507	1.221518	0.288675	3.9825	6.82E-05	0.00168	yes
C5orf30	5:102594441-102614361	7.16369	5.87183	1.22001	0.286893	3.48867	0.000485	0.008743	yes
PYHIN1	1:158901341-158946844	12.9657	10.6363	1.219005	0.285704	3.44916	0.000562	0.009893	yes
ARRDC4	15:98503932-98517068	7.16271	5.87612	1.218952	0.285642	3.7465	0.000179	0.003822	yes
TTL	13:40921268-41055143	4.65106	3.81608	1.218806	0.285468	3.59895	0.00032	0.006196	yes
LOC100652752	16:32164129-32191996	9.59284	7.87423	1.218258	0.284819	3.71053	0.000207	0.004344	yes
NBPF8	1:144146786-144224264	3.54834	2.91269	1.218235	0.284792	3.846	0.00012	0.002716	yes
LENG8	19:54960064-54974894	7.5477	6.21099	1.215217	0.281214	3.64392	0.000269	0.005373	yes
DST	6:56322784-56507694	8.6748	7.13858	1.2152	0.281193	3.70924	0.000208	0.004359	yes
ELTD1	1:79355448-79472495	13.0699	10.7604	1.21463	0.280516	3.87585	0.000106	0.002438	yes
DIAPH1	5:140894587-140998622	4.41122	3.63206	1.214523	0.28039	3.5744	0.000351	0.006715	yes
LOC100288142	1:148250248-148278218	24.6713	20.3199	1.214145	0.27994	3.78211	0.000156	0.003407	yes
DDX23	12:49223538-49245957	7.602	6.26794	1.212839	0.278388	3.52132	0.000429	0.007871	yes
HERC2P3	15:20613648-20711433	8.53303	7.03593	1.212779	0.278317	3.77799	0.000158	0.003451	yes
SH3PXD2B	5:171760502-171881527	7.30642	6.02982	1.211714	0.27705	3.85254	0.000117	0.002661	yes
EDEM3	1:184659624-184724041	7.77074	6.41459	1.211416	0.276695	3.84268	0.000122	0.002748	yes

IGFBP6	12:53491435-53496128	49.7276	41.0794	1.210524	0.275632	3.77124	0.000162	0.00353	yes
TMEM181	6:158957467-159056467	9.63327	7.96162	1.209964	0.274964	3.81823	0.000134	0.002998	yes
MDM2	12:69201970-69239212	10.9419	9.05958	1.207771	0.272347	3.77328	0.000161	0.003507	yes
ZC3H7B	22:41697566-41756151	8.0625	6.67911	1.207122	0.271571	3.76071	0.000169	0.003654	yes
NBPF16	1:148739441-148758311	32.3159	26.8228	1.204792	0.268784	3.65917	0.000253	0.005092	yes
GTF3C1	16:27471933-27561251	4.93515	4.09896	1.204001	0.267836	3.62945	0.000284	0.00563	yes
SF3B3	16:70557690-70611571	3.41951	2.85181	1.199067	0.261912	3.52959	0.000416	0.007696	yes
CPXM2	10:125505151-125651500	15.2215	12.7264	1.196057	0.258286	3.59022	0.00033	0.006381	yes
TNS3	7:47314751-47621742	13.211	11.0509	1.195468	0.257576	3.53983	0.0004	0.007463	yes
NBPF11	1:146032541-146082633	23.9644	20.0635	1.194428	0.25632	3.47332	0.000514	0.009178	yes
NBPF14	1:148003641-148025848	27.9643	23.49	1.190477	0.25154	3.45859	0.000543	0.0096	yes
AMOTL1	11:94501507-94609918	5.35174	4.49667	1.190156	0.251151	3.48304	0.000496	0.008887	yes

Supplemental Table IV: GO Terms for Genes Downregulated with *SENCR* Knockdown

Biological Process (BP)

Term	Count	%	p value	Fold Enri	Bonferro	Benjamir	FDR
GO:0006414~translational elongation	27	0.435835	2.35E-18	9.529253	5.43E-15	5.43E-15	4.11E-15
GO:0006412~translation	36	0.581114	1.25E-11	3.876957	2.88E-08	1.44E-08	2.18E-08
GO:0030029~actin filament-based process	29	0.468119	1.72E-10	4.289409	3.97E-07	1.32E-07	3.01E-07
GO:0019318~hexose metabolic process	25	0.403551	8.06E-10	4.641467	1.86E-06	4.65E-07	1.41E-06
GO:0006006~glucose metabolic process	22	0.355125	1.70E-09	5.125635	3.92E-06	7.84E-07	2.97E-06
GO:0005996~monosaccharide metabolic process	26	0.419693	3.22E-09	4.174811	7.44E-06	1.24E-06	5.63E-06
GO:0006096~glycolysis	13	0.209847	4.21E-09	9.85966	9.72E-06	1.39E-06	7.36E-06
GO:0065008~regulation of biological quality	78	1.25908	3.45E-08	1.892733	7.97E-05	9.96E-06	6.03E-05
GO:0031032~actomyosin structure organization	10	0.161421	4.14E-08	12.73088	9.56E-05	1.06E-05	7.24E-05
GO:0006007~glucose catabolic process	13	0.209847	5.44E-08	7.989725	1.26E-04	1.26E-05	9.51E-05
GO:0030036~actin cytoskeleton organization	24	0.387409	9.27E-08	3.785465	2.14E-04	1.95E-05	1.62E-04
GO:0030048~actin filament-based movement	9	0.145278	1.19E-07	13.94862	2.74E-04	2.29E-05	2.08E-04
GO:0019320~hexose catabolic process	13	0.209847	4.07E-07	6.716001	9.40E-04	7.23E-05	7.12E-04
GO:0007517~muscle organ development	22	0.355125	4.91E-07	3.716693	0.001134	8.11E-05	8.59E-04
GO:0046365~monosaccharide catabolic process	13	0.209847	5.62E-07	6.526817	0.001298	8.66E-05	9.83E-04
GO:0044275~cellular carbohydrate catabolic process	14	0.225989	6.30E-07	5.871182	0.001454	9.09E-05	0.001102
GO:0022603~regulation of anatomical structure morphogenesi	22	0.355125	9.07E-07	3.580923	0.002093	1.23E-04	0.001586
GO:0003012~muscle system process	19	0.306699	1.12E-06	4.031445	0.002572	1.43E-04	0.00195
GO:0045765~regulation of angiogenesis	12	0.193705	1.19E-06	6.789803	0.002753	1.45E-04	0.002087
GO:0006936~muscle contraction	18	0.290557	1.33E-06	4.193702	0.003076	1.54E-04	0.002333
GO:0046164~alcohol catabolic process	13	0.209847	2.41E-06	5.721038	0.00556	2.65E-04	0.004221
GO:0006928~cell motion	33	0.532688	4.17E-06	2.476491	0.009573	4.37E-04	0.007283
GO:0005975~carbohydrate metabolic process	35	0.564972	5.93E-06	2.354012	0.013592	5.95E-04	0.01036
GO:0030198~extracellular matrix organization	14	0.225989	6.45E-06	4.798563	0.014789	6.21E-04	0.011279
GO:0016052~carbohydrate catabolic process	14	0.225989	1.09E-05	4.578445	0.024786	0.001003	0.019
GO:0044262~cellular carbohydrate metabolic process	28	0.451977	1.26E-05	2.579072	0.028659	0.001118	0.022012
GO:0006091~generation of precursor metabolites and energy	24	0.387409	2.47E-05	2.733275	0.055489	0.002112	0.043212
GO:0016051~carbohydrate biosynthetic process	13	0.209847	4.40E-05	4.330879	0.096616	0.003622	0.076898
GO:0006082~organic acid metabolic process	34	0.54883	4.56E-05	2.16425	0.099838	0.00362	0.079601
GO:0010941~regulation of cell death	44	0.71025	4.56E-05	1.924472	0.100034	0.003507	0.079766

GO:0043062~extracellular structure organization	16	0.258273	5.36E-05	3.499039	0.116407	0.003984	0.093655
GO:0048731~system development	96	1.549637	6.09E-05	1.468696	0.131252	0.004387	0.10647
GO:0030049~muscle filament sliding	5	0.08071	6.81E-05	19.80359	0.14543	0.004751	0.118914
GO:0033275~actin-myosin filament sliding	5	0.08071	6.81E-05	19.80359	0.14543	0.004751	0.118914
GO:0070252~actin-mediated cell contraction	5	0.08071	6.81E-05	19.80359	0.14543	0.004751	0.118914
GO:0006066~alcohol metabolic process	28	0.451977	7.64E-05	2.326576	0.161813	0.005178	0.133551
GO:0043067~regulation of programmed cell death	43	0.694108	8.75E-05	1.887682	0.183021	0.005759	0.152926
GO:0030705~cytoskeleton-dependent intracellular transport	9	0.145278	8.96E-05	6.16958	0.186983	0.005734	0.156601
GO:0043436~oxoacid metabolic process	33	0.532688	9.19E-05	2.115707	0.191187	0.005718	0.160519
GO:0019752~carboxylic acid metabolic process	33	0.532688	9.19E-05	2.115707	0.191187	0.005718	0.160519
GO:0042060~wound healing	17	0.274415	9.44E-05	3.172722	0.195915	0.005722	0.164951
GO:0048519~negative regulation of biological process	78	1.25908	9.71E-05	1.53445	0.200791	0.005731	0.169548
GO:0016477~cell migration	21	0.338983	1.01E-04	2.712231	0.207645	0.005802	0.176058
GO:0007507~heart development	18	0.290557	1.17E-04	2.984355	0.236052	0.006546	0.203648
GO:0034637~cellular carbohydrate biosynthetic process	10	0.161421	1.23E-04	5.166154	0.247773	0.006756	0.215329
GO:0014706~striated muscle tissue development	13	0.209847	1.25E-04	3.894152	0.250139	0.006672	0.217709
GO:0042180~cellular ketone metabolic process	33	0.532688	1.33E-04	2.074662	0.264695	0.006964	0.232516
GO:0042981~regulation of apoptosis	42	0.677966	1.45E-04	1.862129	0.283939	0.007395	0.252546
GO:0042692~muscle cell differentiation	13	0.209847	1.46E-04	3.829785	0.286603	0.007315	0.255361
GO:0007155~cell adhesion	38	0.613398	1.51E-04	1.935094	0.294349	0.00739	0.263605
GO:0022610~biological adhesion	38	0.613398	1.56E-04	1.932333	0.301735	0.007455	0.27155
GO:0030336~negative regulation of cell migration	9	0.145278	1.74E-04	5.628389	0.331302	0.008179	0.304213
GO:0048856~anatomical structure development	100	1.614205	1.89E-04	1.410624	0.3532	0.008677	0.329341
GO:0060537~muscle tissue development	13	0.209847	1.99E-04	3.707232	0.368642	0.008977	0.347574
GO:0008285~negative regulation of cell proliferation	24	0.387409	2.16E-04	2.369848	0.392348	0.009534	0.376444
GO:0048513~organ development	74	1.194512	2.21E-04	1.517744	0.400028	0.009593	0.386037
GO:0006916~anti-apoptosis	17	0.274415	2.26E-04	2.941699	0.406192	0.009605	0.393826
GO:0032879~regulation of localization	34	0.54883	2.33E-04	1.986852	0.415766	0.009724	0.406083
GO:0015804~neutral amino acid transport	6	0.096852	2.35E-04	10.1847	0.418835	0.009645	0.410054
GO:0030239~myofibril assembly	6	0.096852	2.35E-04	10.1847	0.418835	0.009645	0.410054
GO:0044267~cellular protein metabolic process	94	1.517353	2.39E-04	1.422831	0.423655	0.009621	0.416334
GO:0007010~cytoskeleton organization	27	0.435835	2.45E-04	2.207465	0.432721	0.009727	0.428287
GO:0045785~positive regulation of cell adhesion	9	0.145278	2.51E-04	5.34697	0.439698	0.00977	0.437615
GO:0040013~negative regulation of locomotion	9	0.145278	2.82E-04	5.259314	0.478326	0.010787	0.491446

GO:0051270~regulation of cell motion	16	0.258273	3.49E-04	2.955147	0.553789	0.013142	0.609094
GO:0051271~negative regulation of cell motion	9	0.145278	3.53E-04	5.092352	0.557455	0.013063	0.615302
GO:0032502~developmental process	118	1.904762	3.61E-04	1.336176	0.565373	0.013139	0.628885
GO:0001558~regulation of cell growth	16	0.258273	3.69E-04	2.939915	0.573063	0.013211	0.642315
GO:0006915~apoptosis	33	0.532688	3.89E-04	1.954042	0.592487	0.013716	0.677335
GO:0048870~cell motility	21	0.338983	4.12E-04	2.438358	0.614227	0.014328	0.718555
GO:0051674~localization of cell	21	0.338983	4.12E-04	2.438358	0.614227	0.014328	0.718555
GO:0009987~cellular process	324	5.230024	4.30E-04	1.09567	0.629188	0.014698	0.748282
GO:0044057~regulation of system process	21	0.338983	4.48E-04	2.422575	0.644578	0.015097	0.780129
GO:0012501~programmed cell death	33	0.532688	5.04E-04	1.925259	0.687845	0.016732	0.87759
GO:0042221~response to chemical stimulus	57	0.920097	5.08E-04	1.586142	0.690481	0.016614	0.883956
GO:0009888~tissue development	35	0.564972	5.17E-04	1.87613	0.696727	0.016664	0.899251
GO:0051240~positive regulation of multicellular organismal prc	18	0.290557	5.19E-04	2.629657	0.698328	0.016507	0.903222
GO:0008219~cell death	37	0.597256	5.19E-04	1.83438	0.698687	0.016299	0.904116
GO:0060548~negative regulation of cell death	23	0.371267	5.23E-04	2.277413	0.700848	0.016176	0.909516
GO:0009064~glutamine family amino acid metabolic process	8	0.129136	5.75E-04	5.484071	0.735105	0.017556	1.000714
GO:0055002~striated muscle cell development	8	0.129136	5.75E-04	5.484071	0.735105	0.017556	1.000714
GO:0016265~death	37	0.597256	5.92E-04	1.821712	0.745133	0.017826	1.029635
GO:0007275~multicellular organismal development	108	1.743341	6.03E-04	1.343741	0.751731	0.017931	1.049289
GO:0060341~regulation of cellular localization	18	0.290557	6.24E-04	2.587243	0.763515	0.018316	1.08571
GO:0040008~regulation of growth	22	0.355125	6.25E-04	2.299772	0.763982	0.018111	1.087192
GO:0032535~regulation of cellular component size	19	0.306699	6.31E-04	2.499199	0.766955	0.018042	1.096686
GO:0045766~positive regulation of angiogenesis	6	0.096852	6.77E-04	8.226107	0.790689	0.019123	1.177079
GO:0007229~integrin-mediated signaling pathway	9	0.145278	7.26E-04	4.583117	0.813071	0.020244	1.261659
GO:0003013~circulatory system process	15	0.242131	7.54E-04	2.874715	0.82473	0.020762	1.309791
GO:0008015~blood circulation	15	0.242131	7.54E-04	2.874715	0.82473	0.020762	1.309791
GO:0051146~striated muscle cell differentiation	10	0.161421	7.80E-04	4.050735	0.834959	0.021219	1.354711
GO:0046942~carboxylic acid transport	13	0.209847	8.74E-04	3.152408	0.867348	0.023485	1.51774
GO:0007015~actin filament organization	9	0.145278	8.77E-04	4.455808	0.868114	0.023281	1.522056
GO:0055001~muscle cell development	8	0.129136	9.06E-04	5.092352	0.87668	0.02377	1.572111
GO:0006865~amino acid transport	10	0.161421	9.18E-04	3.960718	0.880059	0.023811	1.592815
GO:0015849~organic acid transport	13	0.209847	9.28E-04	3.131108	0.882837	0.023804	1.610274
GO:0030334~regulation of cell migration	14	0.225989	9.43E-04	2.952962	0.88684	0.02392	1.636163
GO:0043066~negative regulation of apoptosis	22	0.355125	0.001008	2.215317	0.902618	0.02527	1.747928

GO:0050900~leukocyte migration	8	0.129136	0.001008	5.003013	0.902679	0.025005	1.748398
GO:0040012~regulation of locomotion	15	0.242131	0.001021	2.78488	0.905505	0.025049	1.770314
GO:0006090~pyruvate metabolic process	7	0.112994	0.001033	5.941077	0.908114	0.025076	1.791132
GO:0043069~negative regulation of programmed cell death	22	0.355125	0.001202	2.184463	0.937726	0.0288	2.079953
GO:0048523~negative regulation of cellular process	68	1.097659	0.001214	1.460217	0.939443	0.028788	2.10068
GO:0051049~regulation of transport	25	0.403551	0.001254	2.048647	0.944877	0.029436	2.170341
GO:0050793~regulation of developmental process	34	0.54883	0.001295	1.79819	0.949828	0.030072	2.240013
GO:0051051~negative regulation of transport	12	0.193705	0.00144	3.168575	0.964137	0.033058	2.488211
GO:0019538~protein metabolic process	104	1.678773	0.001558	1.318361	0.9727	0.035368	2.689403
GO:0051239~regulation of multicellular organismal process	43	0.694108	0.001661	1.635857	0.978451	0.037281	2.863524
GO:0060048~cardiac muscle contraction	5	0.08071	0.001677	9.380649	0.979232	0.037272	2.890693
GO:0006541~glutamine metabolic process	5	0.08071	0.001677	9.380649	0.979232	0.037272	2.890693
GO:0006950~response to stress	68	1.097659	0.001774	1.438552	0.983408	0.039013	3.055578
GO:0009605~response to external stimulus	42	0.677966	0.001883	1.638021	0.987123	0.040986	3.241466
GO:0043065~positive regulation of apoptosis	24	0.387409	0.002317	1.98957	0.995285	0.04974	3.974685
GO:0040011~locomotion	24	0.387409	0.002391	1.984954	0.996026	0.050815	4.098944
GO:0060538~skeletal muscle organ development	8	0.129136	0.002397	4.320784	0.996076	0.050464	4.108132
GO:0007519~skeletal muscle tissue development	8	0.129136	0.002397	4.320784	0.996076	0.050464	4.108132
GO:0043068~positive regulation of programmed cell death	24	0.387409	0.002586	1.975786	0.997466	0.053848	4.425123
GO:0010942~positive regulation of cell death	24	0.387409	0.002709	1.966701	0.998097	0.05585	4.631974
GO:0042274~ribosomal small subunit biogenesis	4	0.064568	0.003035	12.96235	0.999105	0.061809	5.174812
GO:0006929~substrate-bound cell migration	4	0.064568	0.003035	12.96235	0.999105	0.061809	5.174812
GO:0010927~cellular component assembly involved in morpho	6	0.096852	0.003086	5.941077	0.999205	0.062271	5.25986
GO:0046364~monosaccharide biosynthetic process	6	0.096852	0.003488	5.780508	0.999686	0.069497	5.92502
GO:0060047~heart contraction	5	0.08071	0.003507	7.749231	0.9997	0.069262	5.955995
GO:0003015~heart process	5	0.08071	0.003507	7.749231	0.9997	0.069262	5.955995
GO:0001568~blood vessel development	16	0.258273	0.003811	2.327932	0.999852	0.074414	6.456329
GO:0006937~regulation of muscle contraction	8	0.129136	0.003931	3.960718	0.999888	0.076036	6.653762
GO:0009611~response to wounding	27	0.435835	0.004028	1.815952	0.99991	0.077194	6.812333
GO:0046394~carboxylic acid biosynthetic process	12	0.193705	0.004245	2.759726	0.999946	0.080523	7.166642
GO:0016053~organic acid biosynthetic process	12	0.193705	0.004245	2.759726	0.999946	0.080523	7.166642
GO:0051147~regulation of muscle cell differentiation	6	0.096852	0.004402	5.484071	0.999962	0.082699	7.421768
GO:0001666~response to hypoxia	11	0.177563	0.004414	2.926202	0.999963	0.082247	7.441204
GO:0051046~regulation of secretion	14	0.225989	0.0045	2.470547	0.99997	0.083127	7.581925

GO:0006520~cellular amino acid metabolic process	15	0.242131	0.004595	2.365916	0.999976	0.084131	7.735325
GO:0001944~vasculature development	16	0.258273	0.004751	2.272285	0.999983	0.086197	7.9888
GO:0048742~regulation of skeletal muscle fiber development	5	0.08071	0.004794	7.129293	0.999985	0.086256	8.057085
GO:0032787~monocarboxylic acid metabolic process	18	0.290557	0.004842	2.131682	0.999986	0.08641	8.134365
GO:0051128~regulation of cellular component organization	24	0.387409	0.005031	1.867937	0.999991	0.088967	8.440412
GO:0030155~regulation of cell adhesion	11	0.177563	0.005157	2.862125	0.999993	0.090403	8.642602
GO:0015837~amine transport	10	0.161421	0.005878	3.020887	0.999999	0.101643	9.79307
GO:0002526~acute inflammatory response	9	0.145278	0.006162	3.273655	0.999999	0.105507	10.24192
GO:0070482~response to oxygen levels	11	0.177563	0.006298	2.78093	1	0.106924	10.45648
GO:0048514~blood vessel morphogenesis	14	0.225989	0.006492	2.365168	1	0.109241	10.76149
GO:0044087~regulation of cellular component biogenesis	11	0.177563	0.006612	2.761346	1	0.110346	10.94933
GO:0006112~energy reserve metabolic process	6	0.096852	0.006719	4.973925	1	0.111243	11.11775
GO:0006930~substrate-bound cell migration, cell extension	3	0.048426	0.007385	21.38788	1	0.120749	12.15346
GO:0046165~alcohol biosynthetic process	6	0.096852	0.00741	4.860882	1	0.120295	12.19304
GO:0048545~response to steroid hormone stimulus	13	0.209847	0.00782	2.413563	1	0.125659	12.82493
GO:0006413~translational initiation	6	0.096852	0.00815	4.752862	1	0.129716	13.32949
GO:0048641~regulation of skeletal muscle tissue development	5	0.08071	0.008244	6.145942	1	0.130229	13.47356
GO:0030199~collagen fibril organization	5	0.08071	0.008244	6.145942	1	0.130229	13.47356
GO:0009266~response to temperature stimulus	8	0.129136	0.008539	3.435804	1	0.133673	13.92246
GO:0051235~maintenance of location	7	0.112994	0.008836	3.898832	1	0.137078	14.3716
GO:0006941~striated muscle contraction	6	0.096852	0.008939	4.649539	1	0.137648	14.52694
GO:0043462~regulation of ATPase activity	4	0.064568	0.009285	8.911616	1	0.141663	15.04703
GO:0048646~anatomical structure formation involved in morpl	19	0.306699	0.01033	1.924099	1	0.155356	16.59969
GO:0014866~skeletal myofibril assembly	3	0.048426	0.010873	17.82323	1	0.161825	17.39672
GO:0034101~erythrocyte homeostasis	6	0.096852	0.011619	4.364873	1	0.170889	18.47912
GO:0051153~regulation of striated muscle cell differentiation	5	0.08071	0.01169	5.56976	1	0.170763	18.58111
GO:0007160~cell-matrix adhesion	8	0.129136	0.012302	3.204177	1	0.177798	19.45859
GO:0032956~regulation of actin cytoskeleton organization	8	0.129136	0.012302	3.204177	1	0.177798	19.45859
GO:0016202~regulation of striated muscle tissue development	6	0.096852	0.012622	4.277576	1	0.180876	19.91285
GO:0010035~response to inorganic substance	13	0.209847	0.012742	2.260508	1	0.181326	20.0829
GO:0030593~neutrophil chemotaxis	4	0.064568	0.012982	7.921437	1	0.18331	20.42201
GO:0006939~smooth muscle contraction	5	0.08071	0.013015	5.400979	1	0.182632	20.46899
GO:0008361~regulation of cell size	13	0.209847	0.013195	2.249534	1	0.183819	20.72214
GO:0048634~regulation of muscle development	6	0.096852	0.013682	4.193702	1	0.188823	21.40219

GO:0008652~cellular amino acid biosynthetic process	6	0.096852	0.013682	4.193702	1	0.188823	21.40219
GO:0040007~growth	12	0.193705	0.014035	2.337473	1	0.192095	21.89321
GO:0032970~regulation of actin filament-based process	8	0.129136	0.014576	3.099693	1	0.197608	22.63929
GO:0046653~tetrahydrofolate metabolic process	3	0.048426	0.014942	15.27706	1	0.200904	23.14035
GO:0005977~glycogen metabolic process	5	0.08071	0.015944	5.092352	1	0.211718	24.49555
GO:0030154~cell differentiation	61	0.984665	0.017035	1.328304	1	0.223289	25.94463
GO:0051241~negative regulation of multicellular organismal pr	11	0.177563	0.017087	2.390921	1	0.222647	26.01309
GO:0002685~regulation of leukocyte migration	4	0.064568	0.017405	7.129293	1	0.22507	26.43111
GO:0044042~glucan metabolic process	5	0.08071	0.017552	4.950898	1	0.225503	26.62267
GO:0006073~cellular glucan metabolic process	5	0.08071	0.017552	4.950898	1	0.225503	26.62267
GO:0051592~response to calcium ion	6	0.096852	0.018516	3.888705	1	0.235119	27.87136
GO:0030595~leukocyte chemotaxis	5	0.08071	0.019256	4.81709	1	0.242051	28.81692
GO:0006563~L-serine metabolic process	3	0.048426	0.019558	13.36742	1	0.24406	29.19837
GO:0051017~actin filament bundle formation	4	0.064568	0.019893	6.789803	1	0.246408	29.62059
GO:0031589~cell-substrate adhesion	8	0.129136	0.019996	2.909915	1	0.246224	29.74969
GO:0009991~response to extracellular stimulus	13	0.209847	0.021015	2.106382	1	0.255781	31.01504
GO:0048738~cardiac muscle tissue development	6	0.096852	0.021307	3.752259	1	0.257534	31.37418
GO:0060326~cell chemotaxis	5	0.08071	0.022964	4.57006	1	0.27334	33.37728
GO:0001525~angiogenesis	10	0.161421	0.023375	2.408545	1	0.276143	33.86598
GO:0007596~blood coagulation	8	0.129136	0.024307	2.795801	1	0.284111	34.96088
GO:0050817~coagulation	8	0.129136	0.024307	2.795801	1	0.284111	34.96088
GO:0014829~vascular smooth muscle contraction	3	0.048426	0.024685	11.88215	1	0.286454	35.40003
GO:0032781~positive regulation of ATPase activity	3	0.048426	0.024685	11.88215	1	0.286454	35.40003
GO:0051094~positive regulation of developmental process	15	0.242131	0.024783	1.92337	1	0.286015	35.51319
GO:0006953~acute-phase response	5	0.08071	0.024969	4.455808	1	0.286439	35.72754
GO:0016525~negative regulation of angiogenesis	4	0.064568	0.025426	6.199385	1	0.289485	36.25175
GO:0015807~L-amino acid transport	4	0.064568	0.025426	6.199385	1	0.289485	36.25175
GO:0009653~anatomical structure morphogenesis	46	0.742534	0.025438	1.369872	1	0.288214	36.26582
GO:0008064~regulation of actin polymerization or depolymeriz	6	0.096852	0.027678	3.50621	1	0.308044	38.77851
GO:0043627~response to estrogen stimulus	8	0.129136	0.027932	2.715921	1	0.308968	39.05824
GO:0050873~brown fat cell differentiation	4	0.064568	0.02847	5.941077	1	0.312482	39.6446
GO:0060284~regulation of cell development	12	0.193705	0.029358	2.086622	1	0.319119	40.60154
GO:0051789~response to protein stimulus	8	0.129136	0.030543	2.665156	1	0.328275	41.85688
GO:0030832~regulation of actin filament length	6	0.096852	0.031271	3.394901	1	0.33322	42.61577

GO:0010033~response to organic substance	30	0.484262	0.031583	1.483209	1	0.334456	42.93764	
GO:0006094~gluconeogenesis	4	0.064568	0.031698	5.703434	1	0.333977	43.05652	
GO:0007599~hemostasis	8	0.129136	0.031908	2.640479	1	0.334312	43.27133	
GO:0032501~multicellular organismal process	138	2.227603	0.032682	1.149349	1	0.339476	44.05926	
GO:0042127~regulation of cell proliferation	32	0.516546	0.034094	1.449412	1	0.349901	45.47005	
GO:0008544~epidermis development	11	0.177563	0.034356	2.131039	1	0.350577	45.72754	
GO:0001501~skeletal system development	16	0.258273	0.034851	1.78791	1	0.35317	46.21191	
GO:0048869~cellular developmental process	61	0.984665	0.035007	1.274581	1	0.35296	46.36408	
GO:0006917~induction of apoptosis	16	0.258273	0.035334	1.782323	1	0.354139	46.68069	
GO:0055114~oxidation reduction	27	0.435835	0.035787	1.506189	1	0.356321	47.11624	
GO:0009070~serine family amino acid biosynthetic process	3	0.048426	0.036351	9.721763	1	0.359368	47.65468	
GO:0045661~regulation of myoblast differentiation	3	0.048426	0.036351	9.721763	1	0.359368	47.65468	
GO:0005978~glycogen biosynthetic process	3	0.048426	0.036351	9.721763	1	0.359368	47.65468	
GO:0009250~glucan biosynthetic process	3	0.048426	0.036351	9.721763	1	0.359368	47.65468	
GO:0043433~negative regulation of transcription factor activity	5	0.08071	0.036545	3.960718	1	0.359436	47.83889	
GO:0012502~induction of programmed cell death	16	0.258273	0.036587	1.776771	1	0.358297	47.87875	
GO:0051493~regulation of cytoskeleton organization	9	0.145278	0.037332	2.358957	1	0.362701	48.579	
GO:0060415~muscle tissue morphogenesis	4	0.064568	0.038703	5.280958	1	0.371869	49.84416	
GO:0055008~cardiac muscle tissue morphogenesis	4	0.064568	0.038703	5.280958	1	0.371869	49.84416	
GO:0006519~cellular amino acid and derivative metabolic proc	17	0.274415	0.039148	1.721562	1	0.373792	50.24852	
GO:0051222~positive regulation of protein transport	6	0.096852	0.039301	3.192221	1	0.373474	50.38676	
GO:0051223~regulation of protein transport	8	0.129136	0.040955	2.501506	1	0.384433	51.8592	
GO:0010811~positive regulation of cell-substrate adhesion	4	0.064568	0.042476	5.092352	1	0.394139	53.17615	
GO:0031099~regeneration	6	0.096852	0.043745	3.099693	1	0.401812	54.24955	
GO:0030308~negative regulation of cell growth	7	0.112994	0.044155	2.712231	1	0.403222	54.59133	
GO:0050878~regulation of body fluid levels	9	0.145278	0.044639	2.275306	1	0.405135	54.99113	
GO:0045185~maintenance of protein location	5	0.08071	0.044748	3.713173	1	0.404393	55.08132	
GO:0051179~localization	99	1.598063	0.044894	1.179085	1	0.403911	55.20105	
GO:0050921~positive regulation of chemotaxis	4	0.064568	0.046426	4.916754	1	0.413065	56.44033	
GO:0044106~cellular amine metabolic process	15	0.242131	0.047803	1.753105	1	0.420963	57.52711	
GO:0006986~response to unfolded protein	6	0.096852	0.048479	3.012377	1	0.423999	58.05125	

Cellular Component (CC)

Term	Count	%	PValue	Fold Enri	Bonferro	Benjamir	FDR

GO:0022626~cytosolic ribosome	25	0.403551	6.79E-19	11.36545	2.34E-16	2.34E-16	9.26E-16
GO:0044445~cytosolic part	30	0.484262	7.20E-17	7.267909	3.82E-14	1.91E-14	1.55E-13
GO:0015629~actin cytoskeleton	38	0.613398	2.67E-16	5.201914	7.64E-14	2.54E-14	3.00E-13
GO:0033279~ribosomal subunit	27	0.435835	7.12E-16	7.767578	2.29E-13	5.73E-14	9.10E-13
GO:0044449~contractile fiber part	25	0.403551	3.12E-15	8.146919	1.07E-12	2.14E-13	4.24E-12
GO:0043292~contractile fiber	25	0.403551	1.56E-14	7.60828	5.39E-12	8.98E-13	2.13E-11
GO:0005840~ribosome	30	0.484262	9.42E-13	5.138243	3.24E-10	4.63E-11	1.28E-09
GO:0022627~cytosolic small ribosomal subunit	14	0.225989	2.19E-11	12.88843	7.54E-09	9.42E-10	2.99E-08
GO:0030017~sarcomere	19	0.306699	1.22E-10	7.139361	4.20E-08	4.67E-09	1.67E-07
GO:0016459~myosin complex	16	0.258273	1.47E-10	9.064387	5.05E-08	5.05E-09	2.00E-07
GO:0030016~myofibril	19	0.306699	1.02E-09	6.30322	3.52E-07	3.20E-08	1.40E-06
GO:0005737~cytoplasm	261	4.213075	1.03E-09	1.313169	3.56E-07	2.97E-08	1.41E-06
GO:0015935~small ribosomal subunit	14	0.225989	1.08E-08	8.183128	3.72E-06	2.86E-07	1.48E-05
GO:0005829~cytosol	72	1.162228	2.13E-08	1.993484	7.32E-06	5.23E-07	2.90E-05
GO:0005856~cytoskeleton	73	1.17837	4.35E-08	1.94653	1.50E-05	9.98E-07	5.94E-05
GO:0022625~cytosolic large ribosomal subunit	11	0.177563	4.60E-08	10.6596	1.58E-05	9.90E-07	6.28E-05
GO:0043232~intracellular non-membrane-bounded organelle	114	1.840194	8.08E-08	1.617082	2.78E-05	1.63E-06	1.10E-04
GO:0043228~non-membrane-bounded organelle	114	1.840194	8.08E-08	1.617082	2.78E-05	1.63E-06	1.10E-04
GO:0044444~cytoplasmic part	184	2.970137	1.37E-07	1.384194	4.71E-05	2.62E-06	1.87E-04
GO:0015934~large ribosomal subunit	13	0.209847	2.09E-07	7.14497	7.19E-05	3.78E-06	2.85E-04
GO:0042641~actomyosin	9	0.145278	3.84E-07	12.27469	1.32E-04	6.61E-06	5.24E-04
GO:0005859~muscle myosin complex	8	0.129136	5.83E-07	14.72963	2.01E-04	9.55E-06	7.95E-04
GO:0016460~myosin II complex	8	0.129136	1.22E-06	13.39057	4.21E-04	1.91E-05	0.00167
GO:0044421~extracellular region part	53	0.855529	1.37E-06	2.032996	4.70E-04	2.04E-05	0.001862
GO:0001725~stress fiber	8	0.129136	2.37E-06	12.27469	8.15E-04	3.40E-05	0.003233
GO:0032432~actin filament bundle	8	0.129136	4.30E-06	11.33048	0.001477	5.91E-05	0.005862
GO:0031674~I band	10	0.161421	1.52E-05	6.695286	0.005227	2.02E-04	0.020779
GO:0005576~extracellular region	86	1.388216	1.62E-05	1.575557	0.005547	2.06E-04	0.022056
GO:0031012~extracellular matrix	25	0.403551	2.48E-05	2.668411	0.008503	3.05E-04	0.033856
GO:0030529~ribonucleoprotein complex	32	0.516546	2.99E-05	2.288098	0.010221	3.54E-04	0.040733
GO:0005581~collagen	8	0.129136	3.56E-05	8.416931	0.012166	4.08E-04	0.04853
GO:0000267~cell fraction	53	0.855529	3.99E-05	1.802102	0.013648	4.43E-04	0.05448
GO:0032991~macromolecular complex	120	1.937046	4.94E-05	1.400599	0.016854	5.31E-04	0.067382
GO:0030485~smooth muscle contractile fiber	4	0.064568	7.74E-05	36.82407	0.026281	8.07E-04	0.105559

GO:0005884~actin filament	8	0.129136	1.03E-04	7.185185	0.034949	0.001046	0.140975
GO:0008305~integrin complex	7	0.112994	1.07E-04	8.88857	0.036092	0.00105	0.145666
GO:0000015~phosphopyruvate hydratase complex	4	0.064568	1.90E-04	29.45926	0.063161	0.001811	0.258396
GO:0030055~cell-substrate junction	12	0.193705	2.29E-04	3.945437	0.075656	0.002124	0.31149
GO:0070161~anchoring junction	15	0.242131	2.51E-04	3.211402	0.08272	0.00227	0.341813
GO:0005912~adherens junction	14	0.225989	3.10E-04	3.326045	0.101015	0.002727	0.421399
GO:0005587~collagen type IV	4	0.064568	3.72E-04	24.54938	0.120035	0.003192	0.505808
GO:0016323~basolateral plasma membrane	16	0.258273	4.34E-04	2.90239	0.138836	0.003639	0.590986
GO:0005578~proteinaceous extracellular matrix	21	0.338983	4.77E-04	2.41658	0.151327	0.003899	0.648568
GO:0005924~cell-substrate adherens junction	11	0.177563	6.02E-04	3.821366	0.187208	0.004809	0.818617
GO:0030935~sheet-forming collagen	4	0.064568	6.37E-04	21.04233	0.196926	0.004972	0.865917
GO:0044430~cytoskeletal part	44	0.71025	6.93E-04	1.701953	0.212123	0.005284	0.940992
GO:0005625~soluble fraction	20	0.322841	9.31E-04	2.352976	0.274081	0.006939	1.262209
GO:0043235~receptor complex	11	0.177563	0.001215	3.491938	0.341723	0.008857	1.644459
GO:0044420~extracellular matrix part	11	0.177563	0.001297	3.462092	0.360102	0.009258	1.754841
GO:0005925~focal adhesion	10	0.161421	0.001794	3.610203	0.460727	0.012524	2.41914
GO:0005792~microsome	16	0.258273	0.002086	2.486013	0.512459	0.014265	2.808604
GO:0005626~insoluble fraction	38	0.613398	0.002462	1.667836	0.571697	0.016489	3.306617
GO:0042598~vesicular fraction	16	0.258273	0.002759	2.414693	0.613352	0.018108	3.698147
GO:0005615~extracellular space	32	0.516546	0.003722	1.720249	0.722712	0.023911	4.959447
GO:0005624~membrane fraction	36	0.581114	0.004352	1.638649	0.776926	0.0274	5.775857
GO:0044446~intracellular organelle part	139	2.243745	0.006096	1.21149	0.87798	0.037525	8.003445
GO:0005938~cell cortex	11	0.177563	0.00646	2.774417	0.892396	0.039027	8.460976
GO:0044422~organelle part	139	2.243745	0.007611	1.204081	0.927791	0.045062	9.89757
GO:0030018~Z disc	6	0.096852	0.007846	4.80314	0.933444	0.045645	10.1884
GO:0031672~A band	4	0.064568	0.008505	9.206019	0.947034	0.048579	10.99814
GO:0044459~plasma membrane part	77	1.242938	0.014712	1.287087	0.993894	0.081464	18.30541
GO:0005604~basement membrane	7	0.112994	0.019063	3.304725	0.998668	0.102856	23.09168
GO:0044424~intracellular part	309	4.987893	0.019807	1.071032	0.998974	0.105061	23.88399
GO:0030054~cell junction	23	0.371267	0.025379	1.635046	0.999856	0.130961	29.57931
GO:0005886~plasma membrane	120	1.937046	0.033297	1.169947	0.999991	0.166415	36.99539
GO:0043234~protein complex	85	1.372074	0.040469	1.209446	0.999999	0.196381	43.08145
GO:0030863~cortical cytoskeleton	5	0.08071	0.043257	3.757559	1	0.205849	45.29615
GO:0031410~cytoplasmic vesicle	26	0.419693	0.045466	1.491318	1	0.212514	46.99423

GO:0042175~nuclear envelope-endoplasmic reticulum network	14	0.225989	0.045947	1.815271	1	0.211756	47.35767

Molecular Function (MF)

Term	Count	%	PValue	Fold Enri	Bonferro	Benjamir	FDR
GO:0005198~structural molecule activity	66	1.065375	1.87E-20	3.753335	1.18E-17	1.18E-17	2.78E-17
GO:0003735~structural constituent of ribosome	30	0.484262	2.16E-15	6.43835	1.34E-12	6.68E-13	3.14E-12
GO:0003779~actin binding	37	0.597256	1.34E-12	4.092105	8.45E-10	2.82E-10	1.99E-09
GO:0008092~cytoskeletal protein binding	46	0.742534	3.64E-12	3.290712	2.30E-09	5.75E-10	5.41E-09
GO:0005515~protein binding	291	4.697337	5.66E-11	1.286723	3.58E-08	7.16E-09	8.42E-08
GO:0008307~structural constituent of muscle	12	0.193705	1.26E-08	10.30136	7.99E-06	1.33E-06	1.88E-05
GO:0005488~binding	380	6.133979	4.30E-06	1.093353	0.002716	3.88E-04	0.006392
GO:0019838~growth factor binding	13	0.209847	3.29E-05	4.463923	0.020595	0.002598	0.048898
GO:0030898~actin-dependent ATPase activity	5	0.08071	3.70E-05	22.53423	0.023169	0.002601	0.055079
GO:0003774~motor activity	15	0.242131	3.97E-05	3.808602	0.024832	0.002511	0.059082
GO:0005520~insulin-like growth factor binding	7	0.112994	4.90E-05	10.09533	0.030569	0.002818	0.07294
GO:0004634~phosphopyruvate hydratase activity	4	0.064568	2.02E-04	28.84381	0.119924	0.010589	0.299794
GO:0004459~L-lactate dehydrogenase activity	4	0.064568	2.02E-04	28.84381	0.119924	0.010589	0.299794
GO:0015175~neutral amino acid transmembrane transporter a	6	0.096852	2.23E-04	10.30136	0.131859	0.010818	0.331786
GO:0004457~lactate dehydrogenase activity	4	0.064568	3.95E-04	24.03651	0.221407	0.017717	0.586477
GO:0005201~extracellular matrix structural constituent	10	0.161421	6.10E-04	4.192414	0.320579	0.025438	0.904314
GO:0046943~carboxylic acid transmembrane transporter activi	10	0.161421	9.97E-04	3.918996	0.468251	0.038705	1.473452
GO:0005342~organic acid transmembrane transporter activity	10	0.161421	0.001078	3.876856	0.494683	0.039356	1.59145
GO:0015171~amino acid transmembrane transporter activity	8	0.129136	0.001165	4.888781	0.521886	0.040166	1.719354
GO:0005516~calmodulin binding	12	0.193705	0.001773	3.090408	0.674723	0.057396	2.605044
GO:0050501~hyaluronan synthase activity	3	0.048426	0.002249	36.05476	0.759607	0.068793	3.294811
GO:0017022~myosin binding	5	0.08071	0.002846	8.194264	0.835327	0.082309	4.150858
GO:0051015~actin filament binding	7	0.112994	0.003312	4.76195	0.877545	0.091041	4.815843
GO:0005200~structural constituent of cytoskeleton	8	0.129136	0.004317	3.897812	0.935319	0.112242	6.233079
GO:0005275~amine transmembrane transporter activity	8	0.129136	0.004317	3.897812	0.935319	0.112242	6.233079
GO:0005509~calcium ion binding	40	0.645682	0.005279	1.569304	0.964933	0.130297	7.572616
GO:0005178~integrin binding	7	0.112994	0.00566	4.277684	0.972486	0.133872	8.098041
GO:0022804~active transmembrane transporter activity	20	0.322841	0.006058	1.986488	0.97864	0.137511	8.643315
GO:0008201~heparin binding	9	0.145278	0.007759	3.150416	0.992777	0.166908	10.94199
GO:0000146~microfilament motor activity	4	0.064568	0.010716	8.483473	0.998908	0.216168	14.80983

GO:0008194~UDP-glycosyltransferase activity	9	0.145278	0.011925	2.923359	0.999497	0.230381	16.34599
GO:0015370~solute:sodium symporter activity	6	0.096852	0.01417	4.160165	0.999881	0.26001	19.12908
GO:0001968~fibronectin binding	3	0.048426	0.014627	15.45204	0.999911	0.259836	19.68568
GO:0005539~glycosaminoglycan binding	10	0.161421	0.015884	2.57534	0.99996	0.271466	21.19589
GO:0003785~actin monomer binding	3	0.048426	0.019149	13.52054	0.999995	0.309869	24.99762
GO:0030246~carbohydrate binding	18	0.290557	0.019852	1.833293	0.999997	0.31155	25.79331
GO:0032403~protein complex binding	12	0.193705	0.020635	2.207434	0.999998	0.314161	26.67107
GO:0016758~transferase activity, transferring hexosyl groups	11	0.177563	0.023077	2.279324	1	0.336699	29.3442
GO:0030247~polysaccharide binding	10	0.161421	0.027527	2.341218	1	0.379692	33.98409
GO:0001871~pattern binding	10	0.161421	0.027527	2.341218	1	0.379692	33.98409
GO:0046983~protein dimerization activity	24	0.387409	0.028306	1.596521	1	0.380174	34.76615
GO:0015291~secondary active transmembrane transporter act	12	0.193705	0.029312	2.090131	1	0.382989	35.76398
GO:0042805~actinin binding	3	0.048426	0.029672	10.81643	1	0.379151	36.11758
GO:0005343~organic acid:sodium symporter activity	4	0.064568	0.03081	5.768762	1	0.383172	37.22357
GO:0016836~hydro-lyase activity	5	0.08071	0.032857	4.097132	1	0.395599	39.16695
GO:0015293~symporter activity	9	0.145278	0.036675	2.368561	1	0.42307	42.64339
GO:0016706~oxidoreductase activity, acting on paired donors,	4	0.064568	0.041313	5.15068	1	0.454997	46.61728
GO:0005524~ATP binding	53	0.855529	0.041368	1.293773	1	0.448048	46.66344
GO:0016491~oxidoreductase activity	28	0.451977	0.044153	1.465215	1	0.462808	48.92219
GO:0015294~solute:cation symporter activity	7	0.112994	0.04811	2.656667	1	0.485244	51.97995
GO:0003714~transcription corepressor activity	9	0.145278	0.048503	2.237882	1	0.480905	52.27385
GO:0005523~tropomyosin binding	3	0.048426	0.048707	8.32033	1	0.475369	52.42604

Supplemental Table V: GO Terms for Genes Upregulated with *SENCR* Knockdown

Biological Process (BP)

Term	Count	%	p value	Fold Enri	Bonferro	Benjamir	FDR
GO:0042127~regulation of cell proliferation	38	1.398087	6.41E-10	3.170166	1.23E-06	1.23E-06	1.10E-06
GO:0008284~positive regulation of cell proliferation	26	0.956586	3.94E-09	4.123312	7.55E-06	3.78E-06	6.74E-06
GO:0009611~response to wounding	24	0.883002	5.76E-06	2.973093	0.010988	0.003676	0.00986
GO:0051270~regulation of cell motion	14	0.515085	7.73E-06	4.762598	0.014707	0.003697	0.013222
GO:0006950~response to stress	49	1.802796	9.93E-06	1.909279	0.018861	0.003801	0.016992
GO:0001763~morphogenesis of a branching structure	9	0.331126	1.56E-05	7.985167	0.029522	0.004982	0.02674
GO:0040017~positive regulation of locomotion	10	0.367918	1.75E-05	6.699573	0.033005	0.004783	0.029947
GO:0009605~response to external stimulus	32	1.177336	2.01E-05	2.298672	0.037715	0.004794	0.034304
GO:0040012~regulation of locomotion	13	0.478293	3.65E-05	4.445446	0.06766	0.007754	0.062503
GO:0032502~developmental process	74	2.72259	4.53E-05	1.54337	0.083109	0.008639	0.077404
GO:0030334~regulation of cell migration	12	0.441501	5.35E-05	4.661951	0.097526	0.009285	0.091536
GO:0030335~positive regulation of cell migration	9	0.331126	6.03E-05	6.639352	0.109195	0.00959	0.103139
GO:0016477~cell migration	15	0.551876	8.25E-05	3.568251	0.146343	0.012097	0.141108
GO:0051272~positive regulation of cell motion	9	0.331126	1.20E-04	6.029616	0.204945	0.016248	0.204467
GO:0007049~cell cycle	27	0.993377	1.21E-04	2.284416	0.207406	0.015377	0.207228
GO:0032101~regulation of response to external stimulus	11	0.404709	1.56E-04	4.542226	0.257862	0.018466	0.265791
GO:0007275~multicellular organismal development	67	2.465048	1.57E-04	1.535406	0.259241	0.017497	0.267445
GO:0048731~system development	57	2.09713	2.03E-04	1.606172	0.321881	0.021348	0.346053
GO:0042221~response to chemical stimulus	37	1.361295	2.08E-04	1.896382	0.329205	0.020796	0.35571
GO:0048870~cell motility	15	0.551876	2.50E-04	3.207939	0.380915	0.02369	0.427023
GO:0051674~localization of cell	15	0.551876	2.50E-04	3.207939	0.380915	0.02369	0.427023
GO:0048856~anatomical structure development	60	2.207506	2.84E-04	1.558903	0.42025	0.025626	0.485341
GO:0040011~locomotion	18	0.662252	3.11E-04	2.742006	0.44917	0.026742	0.530776
GO:0006928~cell motion	19	0.699043	3.40E-04	2.626233	0.479017	0.027951	0.580215
GO:0048754~branching morphogenesis of a tube	7	0.257542	4.44E-04	7.070626	0.573001	0.034836	0.756569
GO:0009628~response to abiotic stimulus	16	0.588668	4.99E-04	2.854601	0.616235	0.037585	0.851072
GO:0048518~positive regulation of biological process	50	1.839588	5.37E-04	1.614752	0.642657	0.038806	0.91417
GO:0048522~positive regulation of cellular process	46	1.692421	7.62E-04	1.635175	0.767964	0.052668	1.295275
GO:0050921~positive regulation of chemotaxis	5	0.183959	9.06E-04	11.31997	0.824047	0.060169	1.538689
GO:0008283~cell proliferation	17	0.62546	0.001018	2.559974	0.858101	0.065116	1.727523

GO:0050920~regulation of chemotaxis	5	0.183959	0.001172	10.58965	0.894423	0.072205	1.986498
GO:0060541~respiratory system development	8	0.294334	0.001276	4.863394	0.913439	0.075898	2.160046
GO:0001568~blood vessel development	12	0.441501	0.001301	3.215795	0.917512	0.07501	2.202127
GO:0006954~inflammatory response	14	0.515085	0.001387	2.82825	0.930095	0.07746	2.346483
GO:0048513~organ development	43	1.582046	0.001387	1.624396	0.930162	0.075296	2.347318
GO:0051592~response to calcium ion	6	0.220751	0.001436	7.162452	0.936396	0.075698	2.42877
GO:0001944~vasculature development	12	0.441501	0.001584	3.138923	0.952093	0.080939	2.675242
GO:0022403~cell cycle phase	16	0.588668	0.001651	2.537423	0.957901	0.082052	2.787428
GO:0006270~DNA replication initiation	4	0.147167	0.001663	16.41395	0.958851	0.080534	2.807222
GO:0048520~positive regulation of behavior	5	0.183959	0.001667	9.655267	0.959202	0.078755	2.814661
GO:0051128~regulation of cellular component organization	17	0.62546	0.001681	2.437006	0.960232	0.077453	2.836834
GO:0001525~angiogenesis	9	0.331126	0.001881	3.992583	0.972917	0.084258	3.169385
GO:0007167~enzyme linked receptor protein signaling pathwa	14	0.515085	0.002194	2.687665	0.985166	0.095395	3.688163
GO:0030501~positive regulation of bone mineralization	4	0.147167	0.00237	14.59018	0.989412	0.100366	3.977565
GO:0007242~intracellular signaling cascade	33	1.214128	0.00246	1.725033	0.991106	0.101769	4.126911
GO:0006260~DNA replication	10	0.367918	0.002476	3.455569	0.991364	0.100212	4.152047
GO:0042060~wound healing	10	0.367918	0.002558	3.437477	0.992632	0.101252	4.28779
GO:0001894~tissue homeostasis	6	0.220751	0.002632	6.252935	0.993603	0.101912	4.408423
GO:0030154~cell differentiation	40	1.47167	0.002722	1.604296	0.994616	0.103125	4.555342
GO:0050927~positive regulation of positive chemotaxis	4	0.147167	0.002783	13.82228	0.995213	0.103287	4.655528
GO:0070169~positive regulation of biomineral formation	4	0.147167	0.002783	13.82228	0.995213	0.103287	4.655528
GO:0050926~regulation of positive chemotaxis	4	0.147167	0.002783	13.82228	0.995213	0.103287	4.655528
GO:0032103~positive regulation of response to external stimul	6	0.220751	0.00282	6.155233	0.995547	0.102627	4.716986
GO:0032501~multicellular organismal process	85	3.127299	0.003115	1.303912	0.997471	0.110639	5.196752
GO:0010033~response to organic substance	22	0.809419	0.003161	2.003367	0.997688	0.110173	5.272888
GO:0022604~regulation of cell morphogenesis	8	0.294334	0.003815	4.009515	0.999343	0.129132	6.330575
GO:0030324~lung development	7	0.257542	0.003937	4.64233	0.999481	0.13069	6.526775
GO:0051239~regulation of multicellular organismal process	26	0.956586	0.004159	1.821826	0.999661	0.135214	6.882338
GO:0009653~anatomical structure morphogenesis	31	1.140545	0.004289	1.700359	0.999736	0.13682	7.089314
GO:0000278~mitotic cell cycle	14	0.515085	0.004292	2.484274	0.999738	0.134678	7.094208
GO:0030323~respiratory tube development	7	0.257542	0.004559	4.505791	0.999843	0.140162	7.518884
GO:0030155~regulation of cell adhesion	8	0.294334	0.004875	3.833916	0.999915	0.146807	8.019936
GO:0048583~regulation of response to stimulus	16	0.588668	0.004898	2.259125	0.999918	0.145181	8.056521
GO:0048514~blood vessel morphogenesis	10	0.367918	0.004931	3.11165	0.999923	0.143878	8.108957

GO:0050795~regulation of behavior	5	0.183959	0.005094	7.136502	0.999944	0.146071	8.366423
GO:0016043~cellular component organization	54	1.986755	0.005449	1.419301	0.999972	0.153165	8.923657
GO:0060249~anatomical structure homeostasis	7	0.257542	0.005495	4.335761	0.999974	0.152153	8.99658
GO:0045778~positive regulation of ossification	4	0.147167	0.005498	10.94264	0.999974	0.150061	9.000577
GO:0048869~cellular developmental process	40	1.47167	0.00553	1.539409	0.999976	0.148753	9.05016
GO:0022402~cell cycle process	18	0.662252	0.005623	2.09169	0.99998	0.148996	9.196296
GO:0042493~response to drug	10	0.367918	0.005725	3.039621	0.999983	0.149446	9.356061
GO:0051789~response to protein stimulus	7	0.257542	0.00575	4.29524	0.999984	0.148035	9.39446
GO:0051129~negative regulation of cellular component organi	8	0.294334	0.005915	3.698919	0.999988	0.149955	9.65132
GO:0006996~organelle organization	33	1.214128	0.005971	1.626608	0.99999	0.149307	9.738685
GO:0032967~positive regulation of collagen biosynthetic proce	3	0.110375	0.006031	24.62093	0.999991	0.148768	9.832155
GO:0010714~positive regulation of collagen metabolic process	3	0.110375	0.006031	24.62093	0.999991	0.148768	9.832155
GO:0035295~tube development	10	0.367918	0.006445	2.984355	0.999996	0.156173	10.47273
GO:0007204~elevation of cytosolic calcium ion concentration	7	0.257542	0.006566	4.178097	0.999997	0.156883	10.65795
GO:0007010~cytoskeleton organization	15	0.551876	0.006797	2.258801	0.999998	0.159977	11.01318
GO:0048762~mesenchymal cell differentiation	5	0.183959	0.007357	6.436845	0.999999	0.169936	11.86731
GO:0014031~mesenchymal cell development	5	0.183959	0.007357	6.436845	0.999999	0.169936	11.86731
GO:0060485~mesenchyme development	5	0.183959	0.007877	6.313059	1	0.178716	12.65432
GO:0055074~calcium ion homeostasis	9	0.331126	0.007971	3.143097	1	0.178543	12.79483
GO:0042476~odontogenesis	5	0.183959	0.008989	6.079242	1	0.196768	14.31398
GO:0002376~immune system process	26	0.956586	0.009077	1.710472	1	0.196278	14.44408
GO:0008285~negative regulation of cell proliferation	13	0.478293	0.00909	2.364337	1	0.194354	14.46303
GO:0051480~cytosolic calcium ion homeostasis	7	0.257542	0.009149	3.894836	1	0.193351	14.55008
GO:0048871~multicellular organismal homeostasis	6	0.220751	0.009404	4.634528	1	0.196063	14.92625
GO:0048584~positive regulation of response to stimulus	10	0.367918	0.009977	2.782026	1	0.204544	15.76417
GO:0042542~response to hydrogen peroxide	5	0.183959	0.010199	5.862126	1	0.206411	16.08574
GO:0009612~response to mechanical stimulus	5	0.183959	0.010199	5.862126	1	0.206411	16.08574
GO:0030500~regulation of bone mineralization	4	0.147167	0.010319	8.754109	1	0.206424	16.25978
GO:0006259~DNA metabolic process	16	0.588668	0.010364	2.076073	1	0.205111	16.32507
GO:0002684~positive regulation of immune system process	10	0.367918	0.010489	2.758648	1	0.205237	16.50666
GO:0055066~di-, tri-valent inorganic cation homeostasis	10	0.367918	0.010777	2.747105	1	0.208149	16.92023
GO:0051347~positive regulation of transferase activity	10	0.367918	0.011053	2.735659	1	0.210801	17.31621
GO:0032965~regulation of collagen biosynthetic process	3	0.110375	0.011498	17.90613	1	0.216213	17.95047
GO:0006261~DNA-dependent DNA replication	5	0.183959	0.011509	5.659984	1	0.214317	17.96616

GO:0032879~regulation of localization	18	0.662252	0.011592	1.937385	1	0.213633	18.08337
GO:0000279~M phase	12	0.441501	0.011737	2.394741	1	0.213979	18.28907
GO:0022414~reproductive process	21	0.772627	0.011925	1.809412	1	0.215002	18.55446
GO:0000904~cell morphogenesis involved in differentiation	10	0.367918	0.01222	2.690812	1	0.217698	18.96933
GO:0070167~regulation of biomineral formation	4	0.147167	0.012331	8.206977	1	0.217454	19.12492
GO:0006952~defense response	18	0.662252	0.012486	1.921634	1	0.217902	19.34204
GO:0006979~response to oxidative stress	8	0.294334	0.01255	3.202723	1	0.216941	19.43141
GO:0009888~tissue development	19	0.699043	0.012551	1.87588	1	0.215047	19.43356
GO:0000003~reproduction	21	0.772627	0.012736	1.797617	1	0.215955	19.6913
GO:0035239~tube morphogenesis	7	0.257542	0.012843	3.618824	1	0.215683	19.84018
GO:0055065~metal ion homeostasis	9	0.331126	0.012984	2.88245	1	0.215917	20.03571
GO:0010035~response to inorganic substance	9	0.331126	0.012984	2.88245	1	0.215917	20.03571
GO:0048511~rhythmic process	7	0.257542	0.01331	3.590552	1	0.218847	20.48589
GO:0010712~regulation of collagen metabolic process	3	0.110375	0.013661	16.41395	1	0.222077	20.96839
GO:0007431~salivary gland development	3	0.110375	0.013661	16.41395	1	0.222077	20.96839
GO:0008354~germ cell migration	3	0.110375	0.013661	16.41395	1	0.222077	20.96839
GO:0060389~pathway-restricted SMAD protein phosphorylatio	3	0.110375	0.013661	16.41395	1	0.222077	20.96839
GO:0010038~response to metal ion	7	0.257542	0.013788	3.562719	1	0.22205	21.14276
GO:0050793~regulation of developmental process	19	0.699043	0.01423	1.850832	1	0.226464	21.74561
GO:0009607~response to biotic stimulus	13	0.478293	0.014293	2.222723	1	0.225497	21.83066
GO:0051301~cell division	11	0.404709	0.014662	2.448183	1	0.228768	22.32921
GO:0044253~positive regulation of multicellular organismal me	3	0.110375	0.015985	15.15134	1	0.244839	24.09454
GO:0033273~response to vitamin	5	0.183959	0.017812	4.973925	1	0.266842	26.47025
GO:0050896~response to stimulus	68	2.50184	0.017947	1.27487	1	0.266531	26.64248
GO:0006268~DNA unwinding during replication	3	0.110375	0.018465	14.0691	1	0.27107	27.30169
GO:0022603~regulation of anatomical structure morphogenesi	9	0.331126	0.018619	2.698184	1	0.270977	27.49717
GO:0042698~ovulation cycle	5	0.183959	0.018724	4.899688	1	0.270275	27.62993
GO:0007067~mitosis	9	0.331126	0.019112	2.68592	1	0.273047	28.11689
GO:0000280~nuclear division	9	0.331126	0.019112	2.68592	1	0.273047	28.11689
GO:0050817~coagulation	6	0.220751	0.019459	3.862107	1	0.275284	28.55148
GO:0007596~blood coagulation	6	0.220751	0.019459	3.862107	1	0.275284	28.55148
GO:0007178~transmembrane receptor protein serine/threonin	6	0.220751	0.020208	3.824611	1	0.282268	29.47935
GO:0045860~positive regulation of protein kinase activity	9	0.331126	0.020541	2.649786	1	0.284193	29.88794
GO:0051781~positive regulation of cell division	4	0.147167	0.021034	6.73393	1	0.28795	30.4897

GO:0002687~positive regulation of leukocyte migration	3	0.110375	0.021095	13.13116	1	0.286655	30.56394
GO:0000087~M phase of mitotic cell cycle	9	0.331126	0.021149	2.637957	1	0.285289	30.6286
GO:0006874~cellular calcium ion homeostasis	8	0.294334	0.021428	2.8702	1	0.286514	30.96637
GO:0007229~integrin-mediated signaling pathway	5	0.183959	0.021633	4.689701	1	0.286883	31.21344
GO:0030005~cellular di-, tri-valent inorganic cation homeostasi	9	0.331126	0.022466	2.603094	1	0.294227	32.2081
GO:0065008~regulation of biological quality	33	1.214128	0.022633	1.474909	1	0.294112	32.4062
GO:0048285~organelle fission	9	0.331126	0.023576	2.58036	1	0.302409	33.51296
GO:0050764~regulation of phagocytosis	3	0.110375	0.023871	12.31047	1	0.303613	33.85689
GO:0007599~hemostasis	6	0.220751	0.024235	3.647545	1	0.305515	34.27743
GO:0033674~positive regulation of kinase activity	9	0.331126	0.024706	2.558019	1	0.3085	34.81755
GO:0032270~positive regulation of cellular protein metabolic p	9	0.331126	0.026038	2.536061	1	0.320286	36.32442
GO:0031575~G1/S transition checkpoint	3	0.110375	0.026788	11.58632	1	0.325877	37.15784
GO:0044246~regulation of multicellular organismal metabolic p	3	0.110375	0.026788	11.58632	1	0.325877	37.15784
GO:0000302~response to reactive oxygen species	5	0.183959	0.027065	4.377054	1	0.326641	37.46287
GO:0007165~signal transduction	56	2.060338	0.027112	1.294622	1	0.325121	37.51492
GO:0007093~mitotic cell cycle checkpoint	4	0.147167	0.027185	6.107518	1	0.323875	37.59527
GO:0007162~negative regulation of cell adhesion	4	0.147167	0.027185	6.107518	1	0.323875	37.59527
GO:0008406~gonad development	6	0.220751	0.027805	3.517276	1	0.327987	38.27168
GO:0050727~regulation of inflammatory response	5	0.183959	0.02824	4.319461	1	0.330246	38.74297
GO:0032268~regulation of cellular protein metabolic process	14	0.515085	0.028739	1.939201	1	0.33307	39.27852
GO:0030509~BMP signaling pathway	4	0.147167	0.028857	5.96871	1	0.332245	39.40476
GO:0010769~regulation of cell morphogenesis involved in diffe	5	0.183959	0.029446	4.263365	1	0.335853	40.03009
GO:0006508~proteolysis	25	0.919794	0.029589	1.557301	1	0.335254	40.18081
GO:0051726~regulation of cell cycle	11	0.404709	0.029649	2.181915	1	0.3339	40.24459
GO:0033993~response to lipid	3	0.110375	0.02984	10.94264	1	0.333769	40.44589
GO:0032392~DNA geometric change	3	0.110375	0.02984	10.94264	1	0.333769	40.44589
GO:0032508~DNA duplex unwinding	3	0.110375	0.02984	10.94264	1	0.333769	40.44589
GO:0001837~epithelial to mesenchymal transition	3	0.110375	0.02984	10.94264	1	0.333769	40.44589
GO:0006875~cellular metal ion homeostasis	8	0.294334	0.029943	2.679829	1	0.332828	40.55369
GO:0055080~cation homeostasis	10	0.367918	0.030675	2.295658	1	0.33761	41.31683
GO:0030278~regulation of ossification	5	0.183959	0.030681	4.208706	1	0.335792	41.32291
GO:0001503~ossification	6	0.220751	0.03069	3.425521	1	0.334021	41.33216
GO:0001775~cell activation	10	0.367918	0.031088	2.287659	1	0.335729	41.74256
GO:0051247~positive regulation of protein metabolic process	9	0.331126	0.032128	2.431697	1	0.343047	42.80368

GO:0051240~positive regulation of multicellular organismal prc	9	0.331126	0.032725	2.421731	1	0.346372	43.40347
GO:0002682~regulation of immune system process	12	0.441501	0.033022	2.046415	1	0.347084	43.7006
GO:0035272~exocrine system development	3	0.110375	0.033024	10.36671	1	0.345263	43.70203
GO:0051302~regulation of cell division	4	0.147167	0.034192	5.587729	1	0.353315	44.85412
GO:0048519~negative regulation of biological process	38	1.398087	0.035326	1.376888	1	0.360901	45.95194
GO:0010721~negative regulation of cell development	4	0.147167	0.036076	5.471318	1	0.365184	46.66576
GO:0002685~regulation of leukocyte migration	3	0.110375	0.036333	9.848372	1	0.36542	46.90919
GO:0030516~regulation of axon extension	3	0.110375	0.036333	9.848372	1	0.36542	46.90919
GO:0032570~response to progesterone stimulus	3	0.110375	0.036333	9.848372	1	0.36542	46.90919
GO:0008361~regulation of cell size	8	0.294334	0.037671	2.54974	1	0.374282	48.15596
GO:0060348~bone development	6	0.220751	0.03928	3.202723	1	0.385035	49.61901
GO:0030003~cellular cation homeostasis	9	0.331126	0.040028	2.326387	1	0.38892	50.28623
GO:0007399~nervous system development	25	0.919794	0.040598	1.508635	1	0.391383	50.78887
GO:0048646~anatomical structure formation involved in morpl	11	0.404709	0.042483	2.051744	1	0.403631	52.41691
GO:0048608~reproductive structure development	6	0.220751	0.042842	3.126467	1	0.404378	52.72167
GO:0048286~lung alveolus development	3	0.110375	0.043313	8.953066	1	0.40593	53.11799
GO:0045137~development of primary sexual characteristics	6	0.220751	0.044072	3.101849	1	0.409541	53.74995
GO:0000902~cell morphogenesis	11	0.404709	0.044297	2.028691	1	0.409268	53.93552
GO:0002248~connective tissue replacement during inflammatc	2	0.073584	0.044797	43.77054	1	0.410968	54.34679
GO:0070141~response to UV-A	2	0.073584	0.044797	43.77054	1	0.410968	54.34679
GO:0060317~cardiac epithelial to mesenchymal transition	2	0.073584	0.044797	43.77054	1	0.410968	54.34679
GO:0001889~liver development	4	0.147167	0.046275	4.955156	1	0.419504	55.53983
GO:0031344~regulation of cell projection organization	5	0.183959	0.046278	3.688529	1	0.417643	55.54222
GO:0003006~reproductive developmental process	9	0.331126	0.046457	2.255352	1	0.417023	55.68511
GO:0001932~regulation of protein amino acid phosphorylation	7	0.257542	0.048269	2.656594	1	0.427581	57.1041
GO:0000075~cell cycle checkpoint	5	0.183959	0.04951	3.607462	1	0.434044	58.05043

Cellular Component (CC)

Term	Count	%	p value	Fold Enri	Bonferro	Benjamir	FDR
GO:0044421~extracellular region part	30	1.103753	3.02E-04	2.054236	0.083669	0.083669	0.400917
GO:0016020~membrane	136	5.003679	7.48E-04	1.230393	0.19437	0.102431	0.988747
GO:0005578~proteinaceous extracellular matrix	14	0.515085	0.00121	2.87593	0.29533	0.110126	1.596375
GO:0031226~intrinsic to plasma membrane	33	1.214128	0.001524	1.78541	0.356468	0.104341	2.006121
GO:0031012~extracellular matrix	14	0.515085	0.002378	2.667529	0.497446	0.128562	3.113836

GO:0044459~plasma membrane part	50	1.839588	0.003325	1.491955	0.618095	0.148223	4.329016
GO:0005794~Golgi apparatus	25	0.919794	0.003465	1.88462	0.633249	0.133502	4.50694
GO:0005887~integral to plasma membrane	31	1.140545	0.003991	1.715321	0.685163	0.134513	5.174683
GO:0032580~Golgi cisterna membrane	3	0.110375	0.007671	21.91185	0.891973	0.219065	9.72523
GO:0031224~intrinsic to membrane	102	3.752759	0.009393	1.222429	0.934619	0.238719	11.78551
GO:0000307~cyclin-dependent protein kinase holoenzyme com	3	0.110375	0.011488	17.92787	0.964532	0.261813	14.23146
GO:0005576~extracellular region	44	1.618837	0.01179	1.438987	0.967531	0.248453	14.57902
GO:0044425~membrane part	118	4.341428	0.013586	1.179202	0.980811	0.262219	16.61982
GO:0000922~spindle pole	4	0.147167	0.01454	7.733593	0.985491	0.260924	17.68457
GO:0005764~lysosome	9	0.331126	0.01521	2.803885	0.98808	0.255694	18.42519
GO:0000323~lytic vacuole	9	0.331126	0.01521	2.803885	0.98808	0.255694	18.42519
GO:0005886~plasma membrane	73	2.685798	0.016346	1.270504	0.991461	0.257474	19.66684
GO:0016021~integral to membrane	97	3.568801	0.018824	1.203766	0.995881	0.276074	22.31456
GO:0005694~chromosome	14	0.515085	0.023314	2.000647	0.998906	0.315289	26.90749
GO:0044428~nuclear part	39	1.434879	0.025512	1.407072	0.999429	0.325034	29.06306
GO:0005615~extracellular space	18	0.662252	0.031741	1.727357	0.999911	0.372551	34.85636
GO:0005795~Golgi stack	4	0.147167	0.032332	5.716134	0.999925	0.36384	35.38305
GO:0044427~chromosomal part	12	0.441501	0.033524	2.043592	0.999947	0.361055	36.43258
GO:0005773~vacuole	9	0.331126	0.038531	2.347698	0.999988	0.389651	40.67154
GO:0031985~Golgi cisterna	3	0.110375	0.043273	8.963937	0.999997	0.412978	44.444
GO:0009897~external side of plasma membrane	7	0.257542	0.044958	2.706757	0.999998	0.412431	45.73001
GO:0005654~nucleoplasm	21	0.772627	0.046995	1.565132	0.999999	0.414351	47.24751

Molecular Function (MF)

Term	Count	%	p value	Fold Enri	Bonferro	Benjamir	FDR
GO:0005515~protein binding	151	5.555556	9.10E-06	1.268896	0.004693	0.004693	0.013164
GO:0033764~steroid dehydrogenase activity, acting on the CH-	5	0.183959	5.85E-04	12.68896	0.261114	0.140415	0.843273
GO:0032403~protein complex binding	11	0.404709	5.97E-04	3.845531	0.265517	0.097749	0.859856
GO:0016229~steroid dehydrogenase activity	5	0.183959	0.001003	11.05167	0.404624	0.121589	1.440702
GO:0004033~aldo-keto reductase activity	4	0.147167	0.00121	18.2721	0.465158	0.117641	1.735992
GO:0047115~trans-1,2-dihydrobenzene-1,2-diol dehydrogenas	3	0.110375	0.001237	51.39027	0.472575	0.101137	1.774388
GO:0017048~Rho GTPase binding	5	0.183959	0.002173	9.015837	0.67517	0.148398	3.097759
GO:0016628~oxidoreductase activity, acting on the CH-CH grou	4	0.147167	0.002468	14.42534	0.721306	0.147605	3.512282
GO:0004197~cysteine-type endopeptidase activity	6	0.220751	0.00393	5.71003	0.869436	0.202449	5.538121

GO:0016616~oxidoreductase activity, acting on the CH-OH grou	7	0.257542	0.004089	4.611947	0.879759	0.190895	5.755615
GO:0008233~peptidase activity	18	0.662252	0.004331	2.148722	0.893958	0.184532	6.086445
GO:0005102~receptor binding	24	0.883002	0.00501	1.856082	0.925492	0.19459	7.009417
GO:0070011~peptidase activity, acting on L-amino acid peptide	17	0.62546	0.006487	2.12176	0.965432	0.228047	8.986607
GO:0016614~oxidoreductase activity, acting on CH-OH group o	7	0.257542	0.006932	4.134849	0.972577	0.226541	9.574431
GO:0016787~hydrolase activity	48	1.766004	0.007481	1.440638	0.979393	0.228028	10.29466
GO:0015924~mannosyl-oligosaccharide mannosidase activity	3	0.110375	0.008756	20.55611	0.989399	0.247367	11.94797
GO:0004175~endopeptidase activity	13	0.478293	0.008829	2.375373	0.989795	0.236391	12.04165
GO:0030234~enzyme regulator activity	22	0.809419	0.010695	1.79672	0.996148	0.265707	14.40761
GO:0030246~carbohydrate binding	12	0.441501	0.014624	2.322724	0.999508	0.330258	19.19593
GO:0008234~cysteine-type peptidase activity	7	0.257542	0.017031	3.40172	0.999861	0.358558	22.00497
GO:0008201~heparin binding	6	0.220751	0.01717	3.991477	0.999871	0.347128	22.16441
GO:0015923~mannosidase activity	3	0.110375	0.01948	13.70407	0.999962	0.370167	24.77011
GO:0019899~enzyme binding	15	0.551876	0.020753	1.965211	0.99998	0.375874	26.17093
GO:0001871~pattern binding	7	0.257542	0.02504	3.114562	0.999998	0.420899	30.71205
GO:0030247~polysaccharide binding	7	0.257542	0.02504	3.114562	0.999998	0.420899	30.71205
GO:0047042~3-alpha-hydroxysteroid dehydrogenase (B-specifi	2	0.073584	0.028846	68.52036	1	0.454096	34.52407
GO:0047026~3-alpha-hydroxysteroid dehydrogenase (A-specifi	2	0.073584	0.028846	68.52036	1	0.454096	34.52407
GO:0047718~indanol dehydrogenase activity	2	0.073584	0.028846	68.52036	1	0.454096	34.52407
GO:0042277~peptide binding	8	0.294334	0.029175	2.70031	1	0.444986	34.8439
GO:0008083~growth factor activity	7	0.257542	0.030346	2.979146	1	0.445715	35.97233
GO:0003824~catalytic activity	90	3.311258	0.032772	1.186386	1	0.459498	38.2514
GO:0005088~Ras guanyl-nucleotide exchange factor activity	5	0.183959	0.039275	3.893202	1	0.510468	43.99334
GO:0016627~oxidoreductase activity, acting on the CH-CH grou	4	0.147167	0.039725	5.270797	1	0.502702	44.37155
GO:0005488~binding	193	7.100809	0.040924	1.055337	1	0.501856	45.36795
GO:0004947~bradykinin receptor activity	2	0.073584	0.042957	45.68024	1	0.508048	47.01984
GO:0003680~AT DNA binding	2	0.073584	0.042957	45.68024	1	0.508048	47.01984
GO:0017016~Ras GTPase binding	5	0.183959	0.043553	3.764855	1	0.50224	47.49514
GO:0005509~calcium ion binding	21	0.772627	0.046254	1.565754	1	0.513305	49.59991
GO:0042802~identical protein binding	16	0.588668	0.04687	1.713009	1	0.507909	50.06916

Supplemental Table VI: UCSC Genome Browser Antisense LncRNAs

Gene Symbol/Chromsome Coordinates	Type
A1BG-AS1 at chr19:58863336-58866549 - (ENST00000595302)	NAT
A2M-AS1 at chr12:9217773-9220651 - (ENST00000499762)	NAT
A2ML1-AS1 at chr12:8928815-8983543 - (ENST00000537288)	5' overlapping
AATK-AS1 at chr17:79139316-79155778 - (ENST00000571031)	5' overlapping
ABCA9-AS1 at chr17:67000855-67014464 - (ENST00000458677)	Completely overlapping
ABCC5-AS1 at chr3:183724126-183729207 - (ENST00000422946	Intronic
ACTA2-AS1 at chr10:90699232-90700368 - (ENST00000596007)	NAT
ACTN1-AS1 at chr14:69446758-69448270 - (ENST00000553944)	Divergent
ACVR2B-AS1 at chr3:38492518-38496311 - (ENST00000441531)	5' overlapping
ADAMTS19-AS1 at chr5:128795252-128796382 - (ENST0000050	NAT
ADAMTS9-AS1 at chr3:64568827-64572897 - (ENST0000046622	Intronic
ADARB2-AS1 at chr10:1568958-1577868 - (ENST00000381301)	Intronic
ADIPOQ-AS1 at chr3:186569675-186573912 - (ENST0000042271	NAT
ADORA2A-AS1 at chr22:24856465-24890763 - (ENST000004127	NAT
ADPGK-AS1 at chr15:73077353-73085304 - (ENST00000566745)	NAT
AGAP2-AS1 at chr12:58120054-58122139 - (ENST00000542466)	NAT
AGBL1-AS1 at chr15:86848282-86860404 - (ENST00000563472)	Intronic
AGBL5-AS1 at chr2:27272551-27273132 - (ENST00000444217)	Divergent
AIRN at chr6:160424323-160428696	Intronic
ALDH1L1-AS1 at chr3:125822483-125826912 - (ENST000005123	NAT
ALG13-AS1 at chrX:110949877-110954329 - (ENST00000430794	Completely overlapping
ALKBH3-AS1 at chr11:43933997-43942444 - (ENST00000527960	Completely overlapping
ANKRD33B-AS1 at chr5:10627372-10628337 - (ENST000005063(	NAT
ANO1-AS1 at chr11:70033894-70034615 - (ENST00000524987)	NAT
RASSF1-AS1 at chr3:50,374,942-50,375,727	Completely overlapping
AP4B1-AS1 at chr1:114399257-114443859 - (ENST00000419536	NAT
APCDD1L-AS1 at chr20:57098216-57148880 - (ENST000004242(	Divergent
APOBEC3B-AS1 at chr22:39387564-39394214 - (ENST00000513	NAT
AQP4-AS1 at chr18:24445272-24515910 - (ENST00000568797)	5' overlapping
ARAP1-AS1 at chr11:72396120-72404853 - (ENST00000542022)	NAT
ARHGAP26-AS1 at chr5:142239169-142248487 - (ENST0000043	Intronic
ARHGAP31-AS1 at chr3:119033140-119041607 - (ENST0000046(	Intronic
ARHGAP5-AS1 at chr14:32544625-32545999 - (ENST000005535(	Divergent
ARHGEF19-AS1 at chr1:16524349-16524852 - (ENST000004578(	NAT
ARHGEF26-AS1 at chr3:153744333-153748153 - (ENST00000597	NAT
ARHGEF3-AS1 at chr3:56974104-56975076 - (ENST0000049593(	Completely overlapping
ARHGEF7-AS1 at chr13:111796652-111797080 - (ENST0000043(	Intronic
ARL5B-AS1 at chr10:18943793-18948167 - (ENST00000414939)	Divergent
ARMC2-AS1 at chr6:109244179-109245306 - (ENST0000042673	Completely overlapping
ARMCX3-AS1 at chrX:100877973-100879154 - (ENST000004542	NAT
ARPP21-AS1 at chr3:35691689-35693453 - (ENST00000415706)	Intronic
ARRDC3-AS1 at chr5:90676164-90716532	5' overlapping
ARSD-AS1 at chrX:2822945-2824122 - (ENST00000414053)	NAT

ASB16-AS1 at chr17:42255065-42264085 - (ENST00000592897)	NAT
ASH1L-AS1 at chr1:155531864-155533735 - (ENST00000452809	NAT
ASMTL-AS1 at chrX:1522403-1532917 - (ENST00000602357)	NAT
ATG10-AS1 at chr5:81368874-81369521 - (ENST00000504846)	Intronic
ATP11A-AS1 at chr13:113399763-113409007 - (ENST000004464	Intronic
ATP13A5-AS1 at chr3:193025033-193032151 - (ENST000004146	3' overlapping
ATP1B3-AS1 at chr3:141637094-141637863 - (ENST0000049272	Intronic
ATP6V0E2-AS1 at chr7:149567387-149577699 - (ENST00000464	NAT
B4GALT4-AS1 at chr3:118945333-119009513 - (ENST000004707	NAT
BACH1-AS1 at chr21:30742340-30743547 - (ENST00000449923)	NAT
BAIAP2-AS1 at chr17:79003502-79008501 - (ENST00000573167	Divergent
BCDIN3D-AS1 at chr12:50222506-50233987 - (ENST0000054912	NAT
BDNF-AS at chr11:27528399-27719718	NAT
BHLHE40-AS1 at chr3:4940364-5021622 - (ENST00000441386)	Divergent
BIRC6-AS1 at chr2:32602699-32604667 - (ENST00000455572)	NAT
BOK-AS1 at chr2:242483818-242498392 - (ENST00000434306)	NAT
BOLA3-AS1 at chr2:74375172-74377115 - (ENST00000533563)	NAT
BRWD1-AS1 at chr21:40687633-40695144 - (ENST00000423274	Divergent
BSN-AS1 at chr3:49677916-49679202 - (ENST00000442384)	Intronic
BTBD9-AS1 at chr6:38449468-38450307 - (ENST00000412822)	Intronic
BVES-AS1 at chr6:105585698-105606912 - (ENST00000369120)	Divergent
BZRAP1-AS1 at chr17:56414719-56430648 - (ENST00000579859	Divergent
C10orf71-AS1 at chr10:50504495-50507063 - (ENST000004427(	Divergent
C17orf76-AS1 at chr17:16344540-16344612 - (ENST0000039107	Divergent
C1QTNF1-AS1 at chr17:77015674-77023737 - (ENST0000057752	5' overlapping
C1QTNF9-AS1 at chr13:24889863-24895736 - (ENST000004496[	NAT
C1QTNF9B-AS1 at chr13:24465598-24471402 - (ENST00000417(	NAT
C1RL-AS1 at chr12:7273154-7275097 - (ENST00000535078)	NAT
C20orf166-AS1 at chr20:61144021-61148718 - (ENST000004361	5' overlapping
C4A-AS1 at chr6_ssto_hap7:3333217-3336746 - (ENST00000428	NAT
C4B-AS1 at chr6_ssto_hap7:3234936-3242210 - (ENST00000429	NAT
C6orf47-AS1 at chr6_ssto_hap7:2956904-2959294 - (ENST0000(	NAT
C9orf135-AS1 at chr9:72434743-72435599 - (ENST00000526458	Divergent
CACNA1C-AS1 at chr12:2799064-2800323 - (ENST00000541673)	NAT
CACNA1G-AS1 at chr17:48634535-48636771 - (ENST000005089[	5' overlapping
CACNA2D3-AS1 at chr3:54908632-54935282 - (ENST000004712(	NAT
CACTIN-AS1 at chr19:3607245-3613928 - (ENST00000592274)	NAT
CADM2-AS1 at chr3:86041333-86077157 - (ENST00000476021)	Intronic
CALML3-AS1 at chr10:5559332-5568204 - (ENST00000545372)	NAT
CAPN10-AS1 at chr2:241522117-241526116 - (ENST0000056781	Divergent
CARS-AS1 at chr11:3050624-3062490 - (ENST00000499962)	NAT
CASK-AS1 at chrX:41379289-41381589 - (ENST00000451126)	NAT
CBR3-AS1 at chr21:37513705-37523008 - (ENST00000432988)	NAT
CCDC13-AS1 at chr3:42774069-42788260 - (ENST00000418161)	NAT
CCDC147-AS1 at chr10:106111349-106113333 - (ENST00000435	Divergent
CCDC148-AS1 at chr2:159023162-159092681 - (ENST000004127	3' overlapping
CCDC39-AS1 at chr3:180397872-180418237 - (ENST0000049535	Intronic

CCDC74B-AS1 at chr2:130893551-130895332 - (ENST000004247	NAT
CD27-AS1 at chr12:6559577-6560615 - (ENST00000538616)	NAT
CDH23-AS1 at chr10:73267910-73271630 - (ENST00000428918)	Completely overlapping
CDIPT-AS1 at chr16:29875155-29879368 - (ENST00000398859)	Divergent
CDKN2B-AS1 at chr9:22113677-22121096 - (ENST00000422420)	NAT
CEBPA-AS1 at chr19:33793976-33795656 - (ENST00000320232)	Divergent
CECR5-AS1 at chr22:17640289-17646335 - (ENST00000431923)	NAT
CELF2-AS1 at chr10:11358797-11361847 - (ENST00000379256)	Intronic
CERS6-AS1 at chr2:169639649-169642939 - (ENST00000594898	NAT
CFLAR-AS1 at chr2:202015884-202018341 - (ENST00000601974	NAT
CHKB-AS1 at chr22:51021455-51022306 - (ENST00000380711)	Divergent
CHL1-AS1 at chr3:405053-427478 - (ENST00000417612)	NAT
CHODL-AS1 at chr21:19207333-19257925 - (ENST00000447175)	Divergent
CHRM3-AS1 at chr1:240061316-240063172 - (ENST0000044472	Intronic
CIRBP-AS1 at chr19:1269822-1270139 - (ENST00000600215)	5' overlapping
CLDN10-AS1 at chr13:96131698-96186164 - (ENST00000416909	Intronic
CLRN1-AS1 at chr3:150690465-150797617 - (ENST00000465576	NAT
CLYBL-AS1 at chr13:100378501-100379745 - (ENST0000041600	Intronic
CNOT10-AS1 at chr3:32772127-32778946 - (ENST00000475395)	Completely overlapping
CNTN4-AS1 at chr3:3080717-3102829 - (ENST00000442749)	NAT
COL18A1-AS1 at chr21:46839631-46844985 - (ENST000004852(	Intronic
COL4A2-AS1 at chr13:111154922-111160526 - (ENST000004179	NAT
COL5A1-AS1 at chr9:137541231-137544689 - (ENST0000037181	Intronic
COX10-AS1 at chr17:13937168-13972796 - (ENST00000602539)	NAT
CPB2-AS1 at chr13:46627037-46687467 - (ENST00000415033)	Completely overlapping
CRYM-AS1 at chr16:21314568-21329912 - (ENST00000444326)	5' overlapping
CSNK1G2-AS1 at chr19:1952588-1954585 - (ENST00000586395)	Intronic
CSTF3-AS1 at chr11:33183234-33213144 - (ENST00000500025)	Divergent
CTBP1-AS1 at chr4:1243088-1244234	Divergent
CYP17A1-AS1 at chr10:104592478-104594273 - (ENST00000369	NAT
CYP1B1-AS1 at chr2:38358247-38408997 - (ENST00000413828)	Divergent
CYP4A22-AS1 at chr1:47562325-47644943 - (ENST00000444042	Completely overlapping
DACT3-AS1 at chr19:47165242-47176893 - (ENST00000525352)	NAT
DAOA-AS1 at chr13:106111404-106158030 - (ENST0000044840	Completely overlapping
DBH-AS1 at chr9:136519708-136522435 - (ENST00000425189)	NAT
DCTN1-AS1 at chr2:74612845-74621009 - (ENST00000437991)	NAT
DDR1-AS1 at chr6_qbl_hap6:2127752-2136685 - (ENST0000043	Divergent
DDX11-AS1 at chr12:31203850-31213684 - (ENST00000535870)	NAT
DDX26B-AS1 at chrX:134654008-134654599 - (ENST000004308	NAT
DDX39B-AS1 at chr6_ssto_hap7:2840955-2841720 - (ENST0000(	NAT
DENND5B-AS1 at chr12:31744246-31768600 - (ENST000005373	5' overlapping
DGUOK-AS1 at chr2:74185097-74208560 - (ENST00000439192)	NAT
DHRS4-AS1 at chr14:24422199-24423061 - (ENST00000554036)	NAT
DIAPH2-AS1 at chrX:96857829-96897588 - (ENST00000542084)	NAT
DIAPH3-AS2 at chr13:60587440-60618491 - (ENST00000432995	Intronic
DIAPH3-AS1 at chr13:60587440-60618491 - (ENST00000432995	Completely overlapping
DICER1-AS1 at chr14:95643820-95646262 - (ENST00000439999	NAT

DIO2-AS1 at chr14:80677762-80921812 - (ENST00000553979)	NAT
DLEU7-AS1 at chr13:51381992-51423190 - (ENST00000413510)	Completely overlapping
DLG1-AS1 at chr3:197025123-197030618 - (ENST00000430666)	NAT
DLG3-AS1 at chrX:69672812-69675844 - (ENST00000431103)	Completely overlapping
DLG5-AS1 at chr10:79687130-79689582 - (ENST00000449852)	Divergent
DLGAP1-AS1 at chr18:3594453-3597226 - (ENST00000573355)	Intronic
DLX6-AS1 at chr7:96608393-96641194 - (ENST00000437541)	Completely overlapping
DMD-AS1 at chrX:31115794-31187673 - (ENST00000481143)	NAT
DNAH17-AS1 at chr17:76494911-76499138 - (ENST0000059837	NAT
DNAJB8-AS1 at chr3:128182437-128191160 - (ENST0000047162	NAT
DNAJC27-AS1 at chr2:25195052-25195699 - (ENST00000421842	Divergent
DNAJC3-AS1 at chr13:96325089-96329179 - (ENST00000499499	Divergent
DNAJC9-AS1 at chr10:75008141-75009116 - (ENST00000513954	NAT
DNMBP-AS1 at chr10:101686966-101718138 - (ENST000004344	NAT
DOCK9-AS1 at chr13:99484338-99486883 - (ENST00000439367)	Intronic
DPH6-AS1 at chr15:36148678-36150503 - (ENST00000560866)	Divergent
DPYD-AS1 at chr1:97561479-97788511 - (ENST00000422980)	NAT
DSCAM-AS1 at chr21:41755010-41757285 - (ENST00000455354	Intronic
DYNLL1-AS1 at chr12:120928131-120933743 - (ENST000005007	Intronic
EAF1-AS1 at chr3:15481397-15484963 - (ENST00000599742)	NAT
EFCAB14-AS1 at chr1:47139800-47157769 - (ENST00000418985	Completely overlapping
EFCAB6-AS1 at chr22:43912134-43932747 - (ENST00000431327	NAT
EGFLAM-AS1 at chr5:38425138-38427478 - (ENST00000508986)	NAT
EGFR-AS1 at chr7:55247443-55256627 - (ENST00000442411)	NAT
EHHADH-AS1 at chr3:184880689-184909743 - (ENST000004177	NAT
EHMT2-AS1 at chr6:31851538-31851831 - (ENST00000434689)	NAT
EIF1AX-AS1 at chrX:20158086-20158562 - (ENST00000424026)	Intronic
EIF2B5-AS1 at chr3:184264502-184274706 - (ENST00000421870	Intronic
EIF3J-AS1 at chr15:44827450-44829098 - (ENST00000560049)	Divergent
ELMO1-AS1 at chr7:37037401-37053235 - (ENST00000419535)	NAT
ELOVL2-AS1 at chr6:11044926-11078459 - (ENST00000456616)	Intronic
ENO1-AS1 at chr1:8938894-8939953 - (ENST00000442636)	NAT
ENOX1-AS1 at chr13:44118054-44122192 - (ENST00000444442)	Intronic
ENTPD1-AS1 at chr10:97848666-97849956 - (ENST0000044375	NAT
ENTPD3-AS1 at chr3:40487834-40494820 - (ENST00000420850)	NAT
EPB41L4A-AS1 at chr5:111496631-111498008 - (ENST00000508	Intronic
EPHA1-AS1 at chr7:143104926-143112923 - (ENST00000421648	5' overlapping
EPN2-AS1 at chr17:19199909-19209574 - (ENST00000451099)	Intronic
ERICH1-AS1 at chr8:833328-1055066 - (ENST00000578889)	Completely overlapping
ETV5-AS1 at chr3:185796959-185798736 - (ENST00000453370)	Completely overlapping
EVX1-AS1 at chr7:27281048-27286848	NAT
EXTL3-AS1 at chr8:28557642-28558770 - (ENST00000519870)	NAT
EZR-AS1 at chr6:159239043-159241625 - (ENST00000451712)	NAT
F10-AS1 at chr13:113782469-113783194 - (ENST00000424635)	Intronic
FAM13A-AS1 at chr4:89642866-89649837 - (ENST00000511543	NAT
FAM170B-AS1 at chr10:50345540-50359195 - (ENST000004400	Completely overlapping
FAM181A-AS1 at chr14:94391579-94393412 - (ENST000005557	5' overlapping

FAM222A-AS1 at chr12:110172217-110173762 - (ENST0000053	3' overlapping
FAM83C-AS1 at chr20:33873054-33873559 - (ENST0000042916	NAT
FAM83H-AS1 at chr8:144823268-144828506 - (ENST000004350	Divergent
FANK1-AS1 at chr10:127660757-127661695 - (ENST0000044545	Intronic
FARP1-AS1 at chr13:99087659-99088094 - (ENST00000432229)	NAT
FBXL19-AS1 at chr16:30930640-30934590 - (ENST00000563777	NAT
FENDRR at chr16:86521271-86542466	Divergent
FER1L6-AS1 at chr8:124996378-125053023 - (ENST0000051856	Completely overlapping
FEZF1-AS1 at chr7:121946935-121948611 - (ENST00000424404)	NAT
FGD5-AS1 at chr3:14986531-14989012 - (ENST00000440079)	3' overlapping
FGF12-AS1 at chr3:191956419-192000886 - (ENST00000414920	Intronic
FGF13-AS1 at chrX:137794269-137798779 - (ENST00000438238	Intronic
FGF14-AS1 at chr13:103019914-103026016 - (ENST0000045163	Intronic
FLG-AS1 at chr1:152309544-152339163 - (ENST00000445097)	NAT
FLNB-AS1 at chr3:58149700-58151041 - (ENST00000472922)	NAT
FLVCR1-AS1 at chr1:213029946-213031430 - (ENST0000042616	Divergent
FMR1-AS1 at chrX:146990949-146993335 - (ENST00000601841)	NAT
FOXD2-AS1 at chr1:47897805-47900313 - (ENST00000445551)	Divergent
FOXN3-AS1 at chr14:89883698-89886137 - (ENST00000555562)	Intronic
FOXP1-AS1 at chr3:71338920-71355004 - (ENST00000465742)	Completely overlapping
FREM2-AS1 at chr13:39395935-39401707 - (ENST00000448887)	NAT
FRMPD4-AS1 at chrX:12391286-12393252 - (ENST00000425057	Intronic
FRY-AS1 at chr13:32599451-32605776 - (ENST00000428419)	NAT
FTCD-AS1 at chr21:47571528-47572561 - (ENST00000446649)	NAT
FZD10-AS1 at chr12:130640279-130646801 - (ENST0000053709	Divergent
GABPB1-AS1 at chr15:50648668-50659636 - (ENST0000055859	NAT
GAS5-AS1 at chr1:173832386-173833079 - (ENST00000602767)	NAT
GAS6-AS1 at chr13:114518603-114542321 - (ENST00000458001	NAT
GATA3-AS1 at chr10:8092439-8094458 - (ENST00000438755)	Intronic
GATA6-AS1 at chr18:19747631-19748331 - (ENST00000584201)	Divergent
GCSAML-AS1 at chr1:247687981-247690054 - (ENST000004204	Completely overlapping
GDNF-AS1 at chr5:37873527-37875901 - (ENST00000510986)	Divergent
GFOD1-AS1 at chr6:13486526-13487084 - (ENST00000446001)	NAT
GK-AS1 at chrX:30718115-30742291 - (ENST00000464659)	Completely overlapping
GLIS3-AS1 at chr9:3898642-3901248 - (ENST00000451340)	NAT
GLYCTK-AS1 at chr3:52330673-52332930 - (ENST00000472761)	Intronic
GNAS-AS1 at chr20:57414837-57415899 - (ENST00000443966)	5' overlapping
GNG12-AS1 at chr1:68604040-68607471 - (ENST00000434072)	5' overlapping
GPC5-AS1 at chr13:93353642-93373867 - (ENST00000419288)	Intronic
GPC6-AS1 at chr13:94806447-94840245 - (ENST00000436329)	Intronic
GPR158-AS1 at chr10:25447001-25465205 - (ENST00000449643	NAT
GPR50-AS1 at chrX:150343664-150346308 - (ENST00000454196	NAT
GRIK1-AS2 at chr21:31132713-31136321 - (ENST00000413131)	3' overlapping
GRIK1-AS1 at chr21:31132713-31136321 - (ENST00000413131)	Intronic
GRM5-AS1 at chr11:88244916-88245529 - (ENST00000531994)	NAT
GRM7-AS1 at chr3:7561428-7576971 - (ENST00000420230)	Intronic
GRTP1-AS1 at chr13:114006131-114016183 - (ENST0000042324	NAT

GSN-AS1 at chr9:124043046-124047808 - (ENST00000414544)	NAT
GYG2-AS1 at chrX:2770781-2771801 - (ENST00000445107)	Intronic
H1FX-AS1 at chr3:129037079-129043412 - (ENST00000502789)	NAT
HAND2-AS1 at chr4:174452696-174458510 - (ENST0000050442	Divergent
HAS2-AS1 at chr8:122653676-122656933 - (ENST00000520043)	NAT
HCFC1-AS1 at chrX:153234776-153235538 - (ENST00000438219	Intronic
HDAC11-AS1 at chr3:13518482-13521553 - (ENST00000424112)	NAT
HEXA-AS1 at chr15:72668454-72671129 - (ENST00000567598)	NAT
HHATL-AS1 at chr3:42744203-42748154 - (ENST00000600839)	NAT
HHIP-AS1 at chr4:145564524-145582509 - (ENST00000512359)	NAT
HIF1A-AS1 at chr14:62147759-62162541 - (ENST00000557544)	NAT
HLA-AS1 at chr1:221006105-221053482 - (ENST00000552026)	NAT
HLA-DQB1-AS1 at chr6_ssto_hap7:4056409-4057258 - (ENST00(	NAT
HLA-F-AS1 at chr6_ssto_hap7:1047268-1054496 - (ENST000005(	NAT
HLTF-AS1 at chr3:148804119-148820610 - (ENST00000492461)	NAT
HM13-AS1 at chr20:30155510-30161066 - (ENST00000412178)	3' overlapping
HNF1A-AS1 at chr12:121412188-121418768 - (ENST000005353(	5' overlapping
HNRNPU-AS1 at chr1:245008554-245017805 - (ENST000004897	Divergent
HOTTIP at chr7:27240040-27246130	Divergent
HOXA11-AS at chr7:27225027-27228912	NAT
HOXB-AS1 at chr17:46624054-46628610 - (ENST00000502764)	NAT
HOXC-AS1 at chr12:54392806-54393794 - (ENST00000505700)	Intronic
HOXD-AS1 at chr2:177041252-177053259 - (ENST00000452365)	NAT
HPN-AS1 at chr19:35549963-35597208 - (ENST00000392227)	Divergent
HS6ST2-AS1 at chrX:131801670-131803916 - (ENST0000045526	Completely overlapping
HTR2A-AS1 at chr13:47426287-47430434 - (ENST00000430913)	Intronic
HTR3E-AS1 at chr3:183812906-183822966 - (ENST00000431427	NAT
HTT-AS1 at chr4:3065198-3076241 - (ENST00000503893)	Divergent
HYI-AS1 at chr1:43919598-43922666 - (ENST00000444386)	NAT
IDH1-AS1 at chr2:209120124-209120892 - (ENST00000448588)	Divergent
IDI2-AS1 at chr10:1068614-1081861 - (ENST00000434470)	NAT
IFNG-AS1 at chr12:68383309-68628466 - (ENST00000536914)	Divergent
IGBP1-AS1 at chrX:69383692-69385056 - (ENST00000366397)	Intronic
IGSF11-AS1 at chr3:118661920-118667088 - (ENST0000047700	Intronic
IL10RB-AS1 at chr21:34636178-34638565 - (ENST00000411998)	NAT
IL20RB-AS1 at chr3:136677967-136701038 - (ENST0000046217(	Completely overlapping
IL21-AS1 at chr4:123540138-123610311 - (ENST00000417927)	NAT
IL21R-AS1 at chr16:27458990-27464714 - (ENST00000563191)	NAT
ILF3-AS1 at chr19:10762538-10764520 - (ENST00000591501)	Divergent
INHBA-AS1 at chr7:41733546-41752792 - (ENST00000420821)	3' overlapping
INTS6-AS1 at chr13:52028304-52036761 - (ENST00000601034)	NAT
IPO9-AS1 at chr1:201789583-201798213 - (ENST00000421159)	NAT
IQCF5-AS1 at chr3:51907612-51909783 - (ENST00000440723)	NAT
IQCH-AS1 at chr15:67812344-67813400 - (ENST00000559702)	3' overlapping
IQCJ-SCHIP1-AS1 at chr3:159486106-159486401 - (ENST000004	Intronic
ISM1-AS1 at chr20:13218448-13220321 - (ENST00000431407)	Intronic

ITCH-AS1 at chr20:33029397-33029830 - (ENST00000454205)	Intronic
ITGB2-AS1 at chr21:46341241-46347943 - (ENST00000429132)	NAT
ITGB5-AS1 at chr3:124500002-124506604 - (ENST00000495917)	NAT
ITIH4-AS1 at chr3:52857951-52859330 - (ENST00000478366)	NAT
ITPK1-AS1 at chr14:93533797-93538497 - (ENST00000553639)	Intronic
ITPKB-AS1 at chr1:226856598-226864046 - (ENST00000453525)	Intronic
ITPR1-AS1 at chr3:4532575-4534847 - (ENST00000412804)	Divergent
JARID2-AS1 at chr6:15248046-15248865 - (ENST00000441978)	Intronic
JAZF1-AS1 at chr7:28279503-28283536 - (ENST00000444500)	NAT
JPX at chrX:73164159-73290217	5' overlapping
JRKL-AS1 at chr11:96180296-96239990 - (ENST00000511243)	Intronic
KANSL1-AS1 at chr17:44273424-44274089 - (ENST00000572634	Intronic
KCNAB1-AS1 at chr3:156158946-156164694 - (ENST000004677	Intronic
KCNC4-AS1 at chr1:110751456-110752609 - (ENST00000455967	Divergent
KCND3-AS1 at chr1:112452307-112453552 - (ENST00000419258	Intronic
KCNIP2-AS1 at chr10:103578835-103588536 - (ENST000004123	NAT
KCNJ2-AS1 at chr17:68163102-68165543 - (ENST00000590966)	NAT
KCNQ1-AS1 at chr11:2861365-2882798 - (ENST00000440887)	NAT
KCNQ5-AS1 at chr6:73844526-73853237 - (ENST00000429832)	Intronic
KCTD21-AS1 at chr11:77884821-77886369 - (ENST00000600795	NAT
KDM4A-AS1 at chr1:44169985-44173001 - (ENST00000418149)	NAT
KIAA0196-AS1 at chr8:126052926-126057231 - (ENST00000519	NAT
KIAA1984-AS1 at chr9:139698379-139703300 - (ENST00000414	NAT
KIF25-AS1 at chr6:168394852-168397757 - (ENST00000414364)	Divergent
KIF9-AS1 at chr3:47205987-47288091 - (ENST00000429315)	NAT
KIRREL3-AS1 at chr11:126413842-126480843 - (ENST000005482	Intronic
KLHL6-AS1 at chr3:183266523-183270114 - (ENST00000491676	Intronic
KLHL7-AS1 at chr7:23140847-23145322 - (ENST00000419813)	Divergent
KRBOX1-AS1 at chr3:42975744-42978277 - (ENST00000447834)	NAT
KRTAP5-AS1 at chr11:1594879-1618671 - (ENST00000534077)	Completely overlapping
KTN1-AS1 at chr14:56042905-56046814 - (ENST00000535211)	Divergent
LAMTOR5-AS1 at chr1:110968593-110969392 - (ENST00000597	NAT
LARGE-AS1 at chr22:34140116-34146670 - (ENST00000416275)	Intronic
LARS2-AS1 at chr3:45525466-45551037 - (ENST00000442534)	Completely overlapping
LATS2-AS1 at chr13:21579296-21592261 - (ENST00000422510)	Intronic
LBX1-AS1 at chr10:102997760-102998616 - (ENST00000456391	NAT
LBX2-AS1 at chr2:74729722-74731805 - (ENST00000548978)	NAT
LDLRAD4-AS1 at chr18:13419420-13427479 - (ENST0000058867	Intronic
LEF1-AS1 at chr4:109097444-109177992 - (ENST00000512129)	NAT
LEMD1-AS1 at chr1:205342380-205356568 - (ENST0000044783	3' overlapping
LENG8-AS1 at chr19:54959343-54960223 - (ENST00000448978)	NAT
LEPREL1-AS1 at chr3:189838753-189862635 - (ENST000004122	5' overlapping
LGALS8-AS1 at chr1:236686371-236687800 - (ENST0000049381	NAT
LHFPL3-AS1 at chr7:104439840-104443986 - (ENST0000045089	Intronic
LIFR-AS1 at chr5:38559044-38579696 - (ENST00000514291)	5' overlapping
LIMD1-AS1 at chr3:45720535-45730374 - (ENST00000427644)	NAT
LIPE-AS1 at chr19:42965000-42989625 - (ENST00000596116)	NAT

LMCD1-AS1 at chr3:8651124-8653586 - (ENST00000458666)	Intronic
LMLN-AS1 at chr3:197765192-197766105 - (ENST00000423460)	NAT
LNX1-AS1 at chr4:54368058-54405515 - (ENST00000514364)	Completely overlapping
LOXL1-AS1 at chr15:74211544-74220036 - (ENST00000564963)	NAT
LPP-AS1 at chr3:188280026-188286454 - (ENST00000434996)	Intronic
LRP4-AS1 at chr11:46867978-46895947 - (ENST00000502049)	NAT
LRRC3-AS1 at chr21:45870869-45875167 - (ENST00000426578)	Divergent
LSAMP-AS1 at chr3:116078871-116088937 - (ENST0000049035	Intronic
LY86-AS1 at chr6:6621197-6622930 - (ENST00000606044)	5' overlapping
LYST-AS1 at chr1:236002783-236003482 - (ENST00000412098)	Intronic
LZTS1-AS1 at chr8:20147685-20147800 - (ENST00000363023)	Intronic
MACC1-AS1 at chr7:20181539-20193154 - (ENST00000439285)	Intronic
MACROD2-AS1 at chr20:14885587-14910161 - (ENST000004394	Intronic
MAFG-AS1 at chr17:79886277-79888393 - (ENST00000583492)	Divergent
MAGEA8-AS1 at chrX:149007636-149009870 - (ENST000004276	Completely overlapping
MAGI1-AS1 at chr3:65879491-65910972 - (ENST00000472514)	Intronic
MAGI2-AS1 at chr7:78569166-78570211 - (ENST00000428298)	Intronic
MAMDC2-AS1 at chr9:72786915-72787683 - (ENST0000042057	Completely overlapping
MANEA-AS1 at chr6:96023059-96025326 - (ENST00000564541)	NAT
MAP3K14-AS1 at chr17:43339558-43345630 - (ENST000005853	NAT
MAPKAPK5-AS1 at chr12:112277581-112279514 - (ENST000005	NAT
MAPT-AS1 at chr17:43921352-43922123 - (ENST00000581125)	5' overlapping
MAST4-AS1 at chr5:66297211-66299781 - (ENST00000451496)	Intronic
MATN1-AS1 at chr1:31198567-31199211 - (ENST00000443076)	NAT
MCCC1-AS1 at chr3:182734043-182735596 - (ENST0000047173	NAT
MCF2L-AS1 at chr13:113621798-113623138 - (ENST000004467	NAT
MCM3AP-AS1 at chr21:47649438-47655367 - (ENST000004200	NAT
MDC1-AS1 at chr6_ssto_hap7:2003151-2013267 - (ENST000004	NAT
MED14-AS1 at chrX:40594652-40597950 - (ENST00000456333)	NAT
MED4-AS1 at chr13:48651273-48654127 - (ENST00000422483)	NAT
MEF2C-AS1 at chr5:88714624-88762215 - (ENST00000508742)	5' overlapping
MEIS1-AS1 at chr2:66666575-66668968 - (ENST00000454595)	NAT
MFI2-AS1 at chr3:196730621-196731611 - (ENST00000414354)	NAT
MID1IP1-AS1 at chrX:38660821-38663136 - (ENST00000436893	NAT
MIS18A-AS1 at chr21:33650174-33653299 - (ENST00000453549	5' overlapping
MKNK1-AS1 at chr1:47004368-47035927 - (ENST00000602433)	NAT
MLIP-AS1 at chr6:53911899-53944524 - (ENST00000589041)	Intronic
MLK7-AS1 at chr2:174062440-174146764 - (ENST00000423106)	NAT
MLLT4-AS1 at chr6:168226371-168227135 - (ENST00000414943	Divergent
MME-AS1 at chr3:154876530-154901074 - (ENST00000484721)	NAT
MMP24-AS1 at chr20:33865145-33865932 - (ENST0000045679(	NAT
MORC1-AS1 at chr3:108820303-108829189 - (ENST0000048082	Completely overlapping
MORC2-AS1 at chr22:31318436-31328436 - (ENST00000441558	NAT
MORF4L2-AS1 at chrX:102942212-102946700 - (ENST00000435	NAT
MPRIP-AS1 at chr17:16979352-16981066 - (ENST00000428367)	Intronic
MRGPRG-AS1 at chr11:3242905-3243597 - (ENST00000541883)	NAT
MRPL23-AS1 at chr11:2004467-2011150 - (ENST00000419080)	NAT

MRVI1-AS1 at chr11:10614744-10621453 - (ENST00000525578)	3' overlapping
MTOR-AS1 at chr1:11204481-11209594 - (ENST00000420480)	NAT
MTUS2-AS1 at chr13:30056257-30061654 - (ENST00000587588	Completely overlapping
MYB-AS1 at chr6:135516221-135517133 - (ENST00000455534)	NAT
MYCBP2-AS2 at chr13:77649673-77651737 - (ENST0000059634	Intronic
MYCBP2-AS1 at chr13:77649673-77651737 - (ENST0000059634	NAT
MYLK-AS1 at chr3:123304403-123349668 - (ENST00000470449)	NAT
MYO16-AS1 at chr13:109816250-109853831 - (ENST000004392	Completely overlapping
NAALADL2-AS1 at chr3:175490933-175494121 - (ENST0000042(	Intronic
NADK2-AS1 at chr5:36221157-36222004 - (ENST00000501794)	Intronic
NALCN-AS1 at chr13:101360579-101711638 - (ENST000004578	NAT
NAPA-AS1 at chr19:47987565-48004854 - (ENST00000594367)	NAT
NAV2-AS1 at chr11:20141230-20142178 - (ENST00000526642)	NAT
NCAM1-AS1 at chr11:113140441-113144623 - (ENST000005262	NAT
NCBP2-AS1 at chr3:196666748-196669405 - (ENST00000447775	NAT
NCOA7-AS1 at chr6:126119002-126140004 - (ENST0000042900	NAT
NDFIP2-AS1 at chr13:80051499-80055366 - (ENST00000457171	NAT
NDP-AS1 at chrX:43808978-43828866 - (ENST00000435093)	Completely overlapping
NDUFA6-AS1 at chr22:42519739-42521033 - (ENST000004514	Divergent
NDUFB2-AS1 at chr7:140395136-140396877 - (ENST000004654(	NAT
NEBL-AS1 at chr10:21463283-21463852 - (ENST00000417845)	NAT
NEXN-AS1 at chr1:78347044-78353374 - (ENST00000597757)	NAT
NHS-AS1 at chrX:17570470-17575508 - (ENST00000452788)	Intronic
NICN1-AS1 at chr3:49460379-49461864 - (ENST00000424915)	NAT
NKX2-1-AS1 at chr14:36988483-36992221 - (ENST00000521292	NAT
NKX2-2-AS1 at chr20:21492085-21492947 - (ENST00000549659	NAT
NLGN1-AS1 at chr3:173628426-173638448 - (ENST000004571(	Intronic
LGN4Y-AS1 at chrY:16905522-16915913 - (ENST00000434164)	Intronic
NOP14-AS1 at chr4:2939378-2942168 - (ENST00000512802)	NAT
NOVA1-AS1 at chr14:27251374-27275673 - (ENST00000552101	Divergent
NPHP3-AS1 at chr3:132441186-132593067 - (ENST000005044(	NAT
NPPA-AS1 at chr1:11903918-11908136 - (ENST00000400892)	NAT
NPSR1-AS1 at chr7:34758474-34873941 - (ENST00000442669)	5' overlapping
NR2F1-AS1 at chr5:92889467-92921354 - (ENST00000513055)	3' overlapping
NR2F2-AS1 at chr15:96833674-96870556 - (ENST00000560010)	5' overlapping
NREP-AS1 at chr5:111305149-111353006 - (ENST00000503242)	5' overlapping
NRG3-AS1 at chr10:83992006-83992676 - (ENST00000505481)	Intronic
NRON at chr9:129170054-129172783	Intronic
NTRK3-AS1 at chr15:88795961-88814297 - (ENST00000569588)	5' overlapping
NUCB1-AS1 at chr19:49414187-49422148 - (ENST00000416432)	NAT
NUTM2A-AS1 at chr10:89093797-89096586 - (ENST000003664	Divergent
OCIAD1-AS1 at chr4:48854025-48862220 - (ENST00000513576)	Completely overlapping
OGFR-AS1 at chr20:61431979-61436939 - (ENST00000431361)	5' overlapping
OIP5-AS1 at chr15:41576230-41601901 - (ENST00000501665)	Divergent
OOEP-AS1 at chr6:74079427-74097440 - (ENST00000445350)	NAT
OPA1-AS1 at chr3:193336398-193345126 - (ENST00000444085)	NAT
OSBPL10-AS1 at chr3:31758483-31763069 - (ENST00000444503	Intronic

OSER1-AS1 at chr20:42839892-42853618 - (ENST00000435163) Divergent
OSGEPL1-AS1 at chr2:190627565-190630053 - (ENST000005238 NAT
OSTM1-AS1 at chr6:108444837-108480596 - (ENST0000044118 Intronic
OSTN-AS1 at chr3:190931080-190952394 - (ENST00000430375) NAT
OTX2-AS1 at chr14:57280009-57395757 - (ENST00000554358) Intronic
OVCH1-AS1 at chr12:29578858-29640421 - (ENST00000549411) Divergent
OXCT1-AS1 at chr5:41870222-41870818 - (ENST00000510509) NAT
P4HA2-AS1 at chr5:131520569-131528501 - (ENST00000417667 NAT
PABPC5-AS1 at chrX:90669877-90689998 - (ENST00000456187) 5' overlapping
PAN3-AS1 at chr13:28710980-28712330 - (ENST00000563843) NAT
PAPPA-AS1 at chr9:119160439-119162885 - (ENST00000445861 NAT
PARD3-AS1 at chr10:35104695-35105314 - (ENST00000446211) Divergent
PAXBP1-AS1 at chr21:34102663-34109784 - (ENST00000455170 3' overlapping
PCBP1-AS1 at chr2:70310712-70313313 - (ENST00000437019) Divergent
PCCA-AS1 at chr13:101131813-101133411 - (ENST00000414553 Intronic
PCDH9-AS1 at chr13:66878003-66897693 - (ENST00000430861) NAT
PCED1B-AS1 at chr12:47602203-47610218 - (ENST00000500365 NAT
PCOLCE-AS1 at chr7:100200537-100201829 - (ENST0000044602 NAT
PCYT1B-AS1 at chrX:24668190-24676354 - (ENST00000432626) Intronic
PDCD4-AS1 at chr10:112629626-112631991 - (ENST000004203(Divergent
PDX1-AS1 at chr13:28407581-28495541 - (ENST00000499662) 5' overlapping
PDZRN3-AS1 at chr3:73672719-73674658 - (ENST00000478988) 5' overlapping
PEX5L-AS1 at chr3:179593164-179599397 - (ENST00000466064 NAT
PGM5-AS1 at chr9:70970105-70972768 - (ENST00000417887) 5' overlapping
PHEX-AS1 at chrX:22180850-22191100 - (ENST00000424650) Completely overlapping
PHKA1-AS1 at chrX:71908800-71932190 - (ENST00000420998) Completely overlapping
PHKA2-AS1 at chrX:18910862-18912615 - (ENST00000439295) NAT
PITPNA-AS1 at chr17:1420225-1421390 - (ENST00000425081) NAT
PITRM1-AS1 at chr10:3185241-3190814 - (ENST00000430356) NAT
PLCB2-AS1 at chr15:40592871-40594021 - (ENST00000559520) NAT
PLCE1-AS1 at chr10:96042918-96046828 - (ENST00000440198) NAT
PLCH1-AS1 at chr3:155166973-155175542 - (ENST00000475196 Intronic
PLCL2-AS1 at chr3:17084234-17085684 - (ENST00000414844) NAT
PLCXD2-AS1 at chr3:111395583-111396280 - (ENST0000049313 Intronic
PLS1-AS1 at chr3:142373626-142375587 - (ENST00000485338) Intronic
PLSCR5-AS1 at chr3:146307389-146308112 - (ENST0000047381 NAT
POTEH-AS1 at chr22:16274560-16278602 - (ENST00000422014) NAT
POU6F2-AS1 at chr7:39444197-39445945 - (ENST00000433519) Intronic
PPEF1-AS1 at chrX:18706762-18709723 - (ENST00000430641) 5' overlapping
PPP1R26-AS1 at chr9:138372161-138372584 - (ENST000006038 Divergent
PRC1-AS1 at chr15:91509602-91531854 - (ENST00000554388) NAT
PRICKLE2-AS1 at chr3:64085454-64086790 - (ENST00000460946 NAT
PRKAG2-AS1 at chr7:151574550-151576299 - (ENST000004674 NAT
PRKAR2A-AS1 at chr3:48885390-48889414 - (ENST00000416209 Divergent
PRKCQ-AS1 at chr10:6625641-6626260 - (ENST00000449648) Divergent
PRKG1-AS1 at chr10:54060563-54073888 - (ENST00000420193) NAT
PRKX-AS1 at chrX:3577528-3586233 - (ENST00000414074) Intronic

PRMT5-AS1 at chr14:23390250-23396105 - (ENST00000590290)	NAT
PROSER2-AS1 at chr10:11899288-11916794 - (ENST0000045324	3' overlapping
PROX1-AS1 at chr1:214139475-214160973 - (ENST00000598091	Divergent
PRR7-AS1 at chr5:176872980-176874699 - (ENST00000506465)	5' overlapping
PRRT3-AS1 at chr3:9989088-9996471 - (ENST00000431558)	NAT
PSMD5-AS1 at chr9:123609011-123613557 - (ENST0000058791(	Divergent
PSMG3-AS1 at chr7:1609870-1615607 - (ENST00000524978)	Divergent
PTCSC3 at chr14:36604916-36645857	Non-overlapping 3'utr
PTENP1-AS at chr9:33677266-33688008	NAT
PTOV1-AS1 at chr19:50342484-50354314 - (ENST00000600742)	NAT
PTPRG-AS1 at chr3:62279948-62304307 - (ENST00000479588)	NAT
PVRL3-AS1 at chr3:110765749-110788237 - (ENST00000463025	Divergent
PXN-AS1 at chr12:120639174-120650941 - (ENST00000535200)	NAT
RAB11B-AS1 at chr19:8439305-8442711 - (ENST00000597407)	NAT
RAB30-AS1 at chr11:82783397-82785010 - (ENST00000530270)	Divergent
RAD21-AS1 at chr8:117886663-117889107 - (ENST00000521487	NAT
RAD51-AS1 at chr15:40985939-40987305 - (ENST00000499988)	NAT
RAI1-AS1 at chr17:17662468-17674135 - (ENST00000443696)	Intronic
RAMP2-AS1 at chr17:40910313-40913029 - (ENST00000592195	NAT
RAPGEF4-AS1 at chr2:173587914-173600934 - (ENST000004353	5' overlapping
RASAL2-AS1 at chr1:178062285-178062707 - (ENST0000045286	NAT
RASSF8-AS1 at chr12:26107968-26111998 - (ENST00000537801	Divergent
RBM12B-AS1 at chr8:94752349-94753001 - (ENST00000391680	Intronic
RBM26-AS1 at chr13:79980499-79992001 - (ENST00000607864	Intronic
RBMS3-AS1 at chr3:29968302-29975647 - (ENST00000414547)	Intronic
RBPMS-AS1 at chr8:30239640-30242809 - (ENST00000519753)	NAT
RERG-AS1 at chr12:15304857-15308217 - (ENST00000541243)	Intronic
RGMB-AS1 at chr5:98106784-98108482 - (ENST00000515003)	NAT
RGPD4-AS1 at chr2:108439520-108442583	Divergent
RHPN1-AS1 at chr8:144450336-144450515 - (ENST0000059659	Divergent
RMDN2-AS1 at chr2:38263031-38294184 - (ENST00000601029)	3' overlapping
RNASEH2B-AS1 at chr13:51456745-51484730 - (ENST000005942	5' overlapping
RNF144A-AS1 at chr2:7057163-7058810 - (ENST00000437589)	5' overlapping
RNF157-AS1 at chr17:74150181-74150731 - (ENST00000592748	NAT
RNF185-AS1 at chr22:31601250-31601602 - (ENST00000526089	NAT
RNF219-AS1 at chr13:79152611-79191463 - (ENST00000560584	NAT
ROPN1L-AS1 at chr5:10441402-10441904 - (ENST00000513037)	Divergent
RPL34-AS1 at chr4:109511519-109541616 - (ENST00000510212	Divergent
RPS6KA2-AS1 at chr6:167317186-167318323 - (ENST000004553	Intronic
RRM1-AS1 at chr11:4158346-4159487 - (ENST00000529323)	NAT
RSBN1L-AS1 at chr7:77314102-77325570 - (ENST00000447009)	NAT
RUSC1-AS1 at chr1:155289950-155293967 - (ENST00000450199	NAT
RUVBL1-AS1 at chr3:127794653-127797899 - (ENST0000048521	Intronic
SACS-AS1 at chr13:23993110-24002818 - (ENST00000443092)	Intronic
SAMSN1-AS1 at chr21:15954523-15970624 - (ENST0000044921(	NAT
SAP30L-AS1 at chr5:153822557-153825382 - (ENST0000052231	3' overlapping
SAPCD1-AS1 at chr6_mcf_hap5:3111784-3113062 - (ENST00000	NAT

SATB2-AS1 at chr2:200334619-200341658 - (ENST00000416200	NAT
SBF2-AS1 at chr11:9806698-9812784 - (ENST00000526617)	NAT
SCEL-AS1 at chr13:78173932-78180651 - (ENST00000456280)	NAT
SDCBP2-AS1 at chr20:1306065-1358827 - (ENST00000446423)	3' overlapping
SEC24B-AS1 at chr4:110351119-110354973 - (ENST0000049935	NAT
SEC62-AS1 at chr3:169696324-169703503 - (ENST00000479626	Completely overlapping
SENCR at chr11:128561575-128565918 - (ENST00000526269)	5' overlapping
SERTAD4-AS1 at chr1:210404801-210407392 - (ENST000004800	5' overlapping
SETD5-AS1 at chr3:9435634-9438752 - (ENST00000383834)	Divergent
SGOL1-AS1 at chr3:20215778-20227607 - (ENST00000441442)	NAT
SH3BP5-AS1 at chr3:15298962-15300563 - (ENST00000436602)	NAT
SH3RF3-AS1 at chr2:109743783-109745386 - (ENST0000056749	NAT
SHANK2-AS1 at chr11:70477199-70481595 - (ENST00000429561	Intronic
SIAH2-AS1 at chr3:150479724-150480325 - (ENST00000461943	NAT
SIDT1-AS1 at chr3:113307595-113309036 - (ENST00000462180)	Intronic
SIX3-AS1 at chr2:45167723-45168633 - (ENST00000456467)	Divergent
SLC25A21-AS1 at chr14:37641093-37643016 - (ENST000005566	NAT
SLC25A30-AS1 at chr13:45992297-45994506 - (ENST000005066	NAT
SLC25A5-AS1 at chrX:118600387-118603061 - (ENST000004457	NAT
SLC26A4-AS1 at chr7:107301746-107302596 - (ENST000004497	NAT
SLC2A1-AS1 at chr1:43424775-43442099 - (ENST00000416689)	NAT
SLC39A12-AS1 at chr10:18292033-18296199 - (ENST000004452	NAT
SLC6A1-AS1 at chr3:11047784-11060910 - (ENST00000414969)	5' overlapping
SLC7A11-AS1 at chr4:139092784-139095924 - (ENST000005125	NAT
SLC8A1-AS1 at chr2:40478563-40481686 - (ENST00000417875)	3' overlapping
SLC9A9-AS1 at chr3:143061088-143065913 - (ENST0000047903	Intronic
SMAD5-AS1 at chr5:135465196-135470579 - (ENST0000029716	NAT
SMAD9-AS1 at chr13:37423503-37424183 - (ENST00000437983	Intronic
SMARCA5-AS1 at chr4:144434625-144435788 - (ENST00000500	NAT
SMC5-AS1 at chr9:72808913-72873782 - (ENST00000594708)	Divergent
SMG7-AS1 at chr1:183430881-183440864 - (ENST00000432837	Divergent
SMIM2-AS1 at chr13:44717729-44813010 - (ENST00000437867	NAT
SNAI3-AS1 at chr16:88751542-88753587 - (ENST00000596908)	Completely overlapping
SNAP25-AS1 at chr20:10085033-10200172 - (ENST00000605592	5' overlapping
SNAP47-AS1 at chr1:227931532-227934892 - (ENST0000041334	Intronic
SNRK-AS1 at chr3:43391136-43393454 - (ENST00000422681)	NAT
SOCS2-AS1 at chr12:93959360-93965174 - (ENST00000551626)	5' overlapping
SORCS3-AS1 at chr10:106424366-106425958 - (ENST000004498	Intronic
SOX21-AS1 at chr13:95364970-95368500 - (ENST00000438290)	Divergent
SPAG5-AS1 at chr17:26942702-26944390 - (ENST00000584675)	Divergent
SPATA13-AS1 at chr13:24826887-24828577 - (ENST0000043073	Intronic
SPATA8-AS1 at chr15:97315237-97326542 - (ENST00000558722	Divergent
SPIN4-AS1 at chrX:62569525-62572057 - (ENST00000451979)	NAT
SPTY2D1-AS1 at chr11:18624534-18625440 - (ENST0000054217	NAT
SRD5A3-AS1 at chr4:56230138-56249563 - (ENST00000433175)	3' overlapping
SRGAP2-AS1 at chr1:206552219-206554954 - (ENST0000045087	Completely overlapping

SRGAP3-AS1 at chr3:9055807-9057663 - (ENST00000414633)	NAT
SRP14-AS1 at chr15:40356588-40357906 - (ENST00000559012)	Divergent
SRRM2-AS1 at chr16:2799787-2802519 - (ENST00000570677)	NAT
SSSCA1-AS1 at chr11:65337131-65337744 - (ENST00000567594	Divergent
SSTR5-AS1 at chr16:1116494-1128707 - (ENST00000566499)	5' overlapping
ST3GAL6-AS1 at chr3:98434149-98451495 - (ENST00000461931	NAT
ST7-AS1 at chr7:116592500-116594388 - (ENST00000456775)	NAT
ST8SIA6-AS1 at chr10:17450026-17455502 - (ENST0000045119(	Completely overlapping
STARD4-AS1 at chr5:111066086-111067878 - (ENST0000051322	NAT
STAU2-AS1 at chr8:74332309-74353761 - (ENST00000517604)	3' overlapping
STEAP2-AS1 at chr7:89838584-89840949 - (ENST00000433534)	Completely overlapping
STEAP3-AS1 at chr2:120001998-120006647 - (ENST0000045426	NAT
STK24-AS1 at chr13:99229498-99231084 - (ENST00000434547)	Divergent
STK4-AS1 at chr20:43592441-43594258 - (ENST00000445571)	Divergent
STPG2-AS1 at chr4:98288077-98411315 - (ENST00000508933)	Divergent
STT3A-AS1 at chr11:125443352-125462473 - (ENST0000053271	Divergent
STX18-AS1 at chr4:4544145-4546787 - (ENST00000514763)	Divergent
STXBP5-AS1 at chr6:147440553-147523603 - (ENST0000041750	NAT
SUCLA2-AS1 at chr13:48575525-48576688 - (ENST00000423869	Intronic
SYNE1-AS1 at chr6:152701681-152702699 - (ENST00000412161	NAT
SYNPR-AS1 at chr3:63409272-63535727 - (ENST00000488201)	Completely overlapping
SYP-AS1 at chrX:49055425-49058913 - (ENST00000433499)	NAT
SZT2-AS1 at chr1:43913447-43914315 - (ENST00000396885)	NAT
TAB3-AS1 at chrX:30852740-30853417 - (ENST00000428263)	Intronic
TAPT1-AS1 at chr4:16228668-16259810 - (ENST00000570786)	Divergent
TBC1D4-AS1 at chr13:75949647-75951430 - (ENST00000440094	Intronic
TBL1XR1-AS1 at chr3:176762649-176765711 - (ENST000004547	Completely overlapping
TBX5-AS1 at chr12:114849094-114849329 - (ENST00000595315	NAT
TCEAL3-AS1 at chrX:102881004-102881420 - (ENST0000042488	Intronic
TET2-AS1 at chr4:106092511-106099220 - (ENST00000515414)	Intronic
TEX26-AS1 at chr13:31505924-31507568 - (ENST00000591300)	Divergent
THAP7-AS1 at chr22:21356497-21364631 - (ENST00000452284)	NAT
THAP9-AS1 at chr4:83820976-83821722 - (ENST00000503704)	NAT
THOC7-AS1 at chr3:63846321-63847495 - (ENST00000468961)	Intronic
THRB-AS1 at chr3:24540116-24541109 - (ENST00000594183)	5' overlapping
TIE1-AS1	NAT
TIPARP-AS1 at chr3:156389711-156390659 - (ENST0000046344	NAT
TLR8-AS1 at chrX:12920936-12926452 - (ENST00000451564)	Completely overlapping
TM4SF19-AS1 at chr3:196045277-196051059 - (ENST000004445	NAT
TM4SF1-AS1 at chr3:149096006-149104368 - (ENST0000048404	Divergent
TMEM161B-AS1 at chr5:87722512-87732183 - (ENST000005136	Divergent
TMEM212-AS1 at chr3:171594142-171618530 - (ENST00000449	Intronic
TMEM220-AS1 at chr17:10633113-10718481 - (ENST000005808	NAT
TMEM254-AS1 at chr10:81806616-81838651 - (ENST000004122	NAT
TMEM44-AS1 at chr3:194304740-194310989 - (ENST000004536	3' overlapping
TMEM51-AS1 at chr1:15442448-15478898 - (ENST00000404665	Divergent
TMEM5-AS1 at chr12:64202625-64215936 - (ENST00000546214	NAT

TMEM72-AS1 at chr10:45306472-45455137 - (ENST0000045028	Completely overlapping
TMEM9B-AS1 at chr11:8986222-8997830 - (ENST00000525484)	NAT
TMLHE-AS1 at chrX:154695631-154697321 - (ENST0000054115	3' overlapping
TMPO-AS1 at chr12:98906751-98910200 - (ENST00000548760)	NAT
TMPRSS4-AS1 at chr11:117886487-117957508 - (ENST0000052	5' overlapping
TNKS2-AS1 at chr10:93542596-93558048 - (ENST00000432938)	Divergent
TNRC6C-AS1 at chr17:76103479-76106416 - (ENST0000059293	NAT
TOB1-AS1 at chr17:48944040-48945668 - (ENST00000416263)	NAT
TOLLIP-AS1 at chr11:1330999-1331937 - (ENST00000530897)	Divergent
TOPORS-AS1 at chr9:32551142-32553002 - (ENST00000453396)	NAT
TP73-AS1 at chr1:3652548-3663340 - (ENST00000418088)	NAT
TPRG1-AS2 at chr3:188659504-188665428 - (ENST00000444488	NAT
TPRG1-AS1 at chr3:188659504-188665428 - (ENST00000444488	Divergent
TPT1-AS1 at chr13:45915480-45965618 - (ENST00000517509)	Divergent
TRAF3IP2-AS1 at chr6:111804714-111814206 - (ENST0000053	NAT
TRAM2-AS1 at chr6:52442105-52448783 - (ENST00000606714)	Divergent
TRAPPC12-AS1 at chr2:3485013-3486180 - (ENST00000453806)	Intronic
TRHDE-AS1 at chr12:72647288-72652020 - (ENST00000549957)	NAT
TRIM31-AS1 at chr6:30073017-30082501 - (ENST00000440874)	NAT
TRMT2B-AS1 at chrX:100297573-100298694 - (ENST000004438	Intronic
TRPC7-AS1 at chr5:135549736-135557847 - (ENST00000514459	NAT
TSIX at chrX:73012040-73049066	NAT
TSPEAR-AS1 at chr21:45926690-45935738 - (ENST00000451035	NAT
TTC28-AS1 at chr22:28315364-28389280 - (ENST00000430853)	NAT
TTC3-AS1 at chr21:38559967-38566227 - (ENST00000424733)	NAT
TTLL10-AS1 at chr1:1108436-1114935 - (ENST00000379317)	NAT
TTN-AS1 at chr2:179385910-179396305 - (ENST00000585625)	NAT
TUG1 at chr22:31365634-31375380	Divergent
UBAC2-AS1 at chr13:99848631-99852964 - (ENST00000426037)	NAT
UBE2E1-AS1 at chr3:23845515-23848396 - (ENST00000426702)	5' overlapping
UBE2Q1-AS1 at chr1:154526085-154527493 - (ENST000004416	NAT
UBL7-AS1 at chr15:74753606-74771563 - (ENST00000564137)	Divergent
UBOX5-AS1 at chr20:3087559-3131513 - (ENST00000446537)	NAT
UBXN7-AS1 at chr3:196158235-196160242 - (ENST0000059888	NAT
UCHL1-AS1 at chr4:41222091-41258744 - (ENST00000507190)	NAT
UFL1-AS1 at chr6:96806250-96969545 - (ENST00000430796)	Divergent
UGDH-AS1 at chr4:39529639-39596327 - (ENST00000504032)	Divergent
UNC5B-AS1 at chr10:72976981-72977582 - (ENST00000449737)	Intronic
UPK1A-AS1 at chr19:36158850-36164193 - (ENST00000443196)	Divergent
USP12-AS2 at chr13:27736992-27743272 - (ENST00000440657)	Intronic
USP12-AS1 at chr13:27736992-27743272 - (ENST00000440657)	Intronic
USP27X-AS1 at chrX:49641892-49643844 - (ENST00000437322)	Divergent
USP2-AS1 at chr11:119252488-119280472 - (ENST00000577297	Divergent
USP30-AS1 at chr12:109490155-109491757 - (ENST0000047880	NAT
USP3-AS1 at chr15:63836446-63881253 - (ENST00000560350)	NAT
USP46-AS1 at chr4:53525573-53527835 - (ENST00000503051)	Divergent
UXT-AS1 at chrX:47518232-47519510	NAT

VAC14-AS1 at chr16:70789001-70807154 - (ENST00000562507) NAT
VAV3-AS1 at chr1:108507065-108537229 - (ENST00000438318) 5' overlapping
VCAN-AS1 at chr5:82827171-82858133 - (ENST00000512090) Completely overlapping
VIM-AS1 at chr10:17256238-17268897 - (ENST00000437232) NAT
VIPR1-AS1 at chr3:42548016-42573554 - (ENST00000600342) Completely overlapping
VPS13A-AS1 at chr9:79791672-79792910 - (ENST00000415172) NAT
VPS9D1-AS1 at chr16:89778264-89784573 - (ENST00000562866 NAT
WAC-AS1 at chr10:28811581-28821672 - (ENST00000527986) Divergent
WASF3-AS1 at chr13:27180681-27215501 - (ENST00000586418) Completely overlapping
WASF3-AS1 at chr13:27214658-27215501 - (ENST00000585599) NAT
WDFY3-AS2 at chr4:85724411-85731544 - (ENST00000510449) NAT
WDFY3-AS1 at chr4:85724411-85731544 - (ENST00000510449) NAT
WDR11-AS1 at chr10:122521324-122536396 - (ENST000004561 NAT
WDR52-AS1 at chr3:113122838-113145893 - (ENST0000047332 NAT
WDR86-AS1 at chr7:151106247-151110440 - (ENST0000048963 5' overlapping
WEE2-AS1 at chr7:141404138-141438030 - (ENST00000488785) NAT
WNT5A-AS1 at chr3:55521727-55522336 - (ENST00000469484) Divergent
WWC2-AS2 at chr4:184154781-184161787 - (ENST0000051184(Divergent
WWC2-AS1 at chr4:184154781-184161787 - (ENST0000051184(Intronic
WWC3-AS1 at chrX:9992882-10006694 - (ENST00000430057) Intronic
WWTR1-AS1 at chr3:149374807-149376098 - (ENST000004950(Intronic
XIAP-AS1 at chrX:123006476-123007782 - (ENST00000458331) Intronic
XIRP2-AS1 at chr2:167980414-167997465 - (ENST00000525330) Completely overlapping
XXYLT1-AS1 at chr3:194815317-194816786 - (ENST0000045853 Intronic
YEATS2-AS1 at chr3:183524245-183526729 - (ENST0000042500 NAT
YTHDF3-AS1 at chr8:64080284-64081001 - (ENST00000603538) Divergent
ZBED3-AS1 at chr5:76382565-76443781 - (ENST00000503969) 5' overlapping
ZBED5-AS1 at chr11:10879806-10900823 - (ENST00000501079) Divergent
ZBTB11-AS1 at chr3:101395274-101396431 - (ENST0000053686 NAT
ZBTB20-AS1 at chr3:114070658-114085891 - (ENST0000049621 Completely overlapping
ZEB1-AS1 at chr10:31495207-31608620 - (ENST00000605946) NAT
ZEB2-AS1 at chr2:145278173-145279044 - (ENST00000595449) NAT
ZFAT-AS1 at chr8:135610314-135612932 - (ENST00000505776) NAT
ZFHX4-AS1 at chr8:77403435-77595391 - (ENST00000522961) 5' overlapping
ZFX-AS1 at chrX:24164342-24167771 - (ENST00000427551) NAT
ZFY-AS1 at chrY:2834885-2870667 - (ENST00000417305) NAT
ZIC4-AS1 at chr3:147104754-147105240 - (ENST00000462168) NAT
ZMIZ1-AS1 at chr10:80703085-80827652 - (ENST00000456353) Divergent
ZMYM4-AS1 at chr1:35824423-35831678 - (ENST00000432683) NAT
ZMYND10-AS1 at chr3:50378537-50383128 - (ENST0000044001 NAT
ZNF197-AS1 at chr3:44658620-44666289 - (ENST00000447691) Divergent
ZNF205-AS1 at chr16:3160461-3165599 - (ENST00000572691) NAT
ZNF252P-AS1 at chr8:146228197-146231432 - (ENST000005270 NAT
ZNF32-AS2 at chr10:44139320-44140495 - (ENST00000453284) NAT
ZNF32-AS1 at chr10:44139320-44140495 - (ENST00000453284) 3' overlapping
ZNF385D-AS1 at chr3:21584308-21621451 - (ENST00000412369 Completely overlapping
ZNF503-AS1 at chr10:77029577-77118465 - (ENST00000524517 Divergent

ZNF571-AS1 at chr19:38039816-38076660 - (ENST00000591430 NAT
ZNF582-AS1 at chr19:56905025-56909521 - (ENST00000591172 Divergent
ZNF630-AS1 at chrX:47915699-47925971 - (ENST00000436124) 3' overlapping
ZNF667-AS1 at chr19:56989559-57005688 - (ENST00000591797 Divergent
ZNF674-AS1 at chrX:46404928-46407671 - (ENST00000421685) Divergent
ZNRD1-AS1 at chr6:29968788-30028705 - (ENST00000425604) NAT
ZNRF3-AS1 at chr22:29420987-29427464 - (ENST00000325660) Intronic
ZRANB2-AS1 at chr1:71514538-71532867 - (ENST00000450461) NAT

NAT = 332/707 = 47.0%
Intronic = 133/707 = 18.8%
Divergent = 116/707 = 16.4%
Completely overlapping = 52/707 = 7.4%
5' overlapping = 50/707 = 7.1%
3' overlapping = 24/707 = 3.4%