Supplementary Figures.

Figure S1. Validation of EHF antibody for ChIP-seq. An antibody against EHF (Clone 5A.5, Thermo Scientific) was tested for specificity. Calu-3 cells were treated with either negative control (NC) or EHF targeted siRNA. Cell lysates were run on western blot and probed with the EHF antibody. A specific band was detected at 35kDa that decreased in intensity in the knockdown sample.

Figure S2. Principle Component Analysis (PCA) plot of individual samples based on gene expression FPKM values. Whole transcriptome expression values in FPKM at gene level were used to compare similarity among the samples through dimension reduction analysis of PCA. The top 3 Principle Components (PCs) that explain the largest variability of the data were plotted on a 3D plot, with different treatment groups represented by different colors (negative control samples in blue, EHF siRNA-treated samples in red). Samples from different treatment groups are segregated along PC#2, which explains 14.5% of all variability in the data.

Figure S3. Plot of the average distance between differentially expressed genes following EHF depletion and the nearest EHF ChIP-seq peak. The average distance between differentially expressed genes and the nearest EHF ChIP-seq peak is not significantly different between genes that decreased (2,930kb) and genes that increased (2,524kb) in expression.

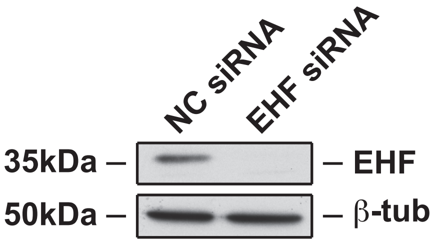


Figure 1

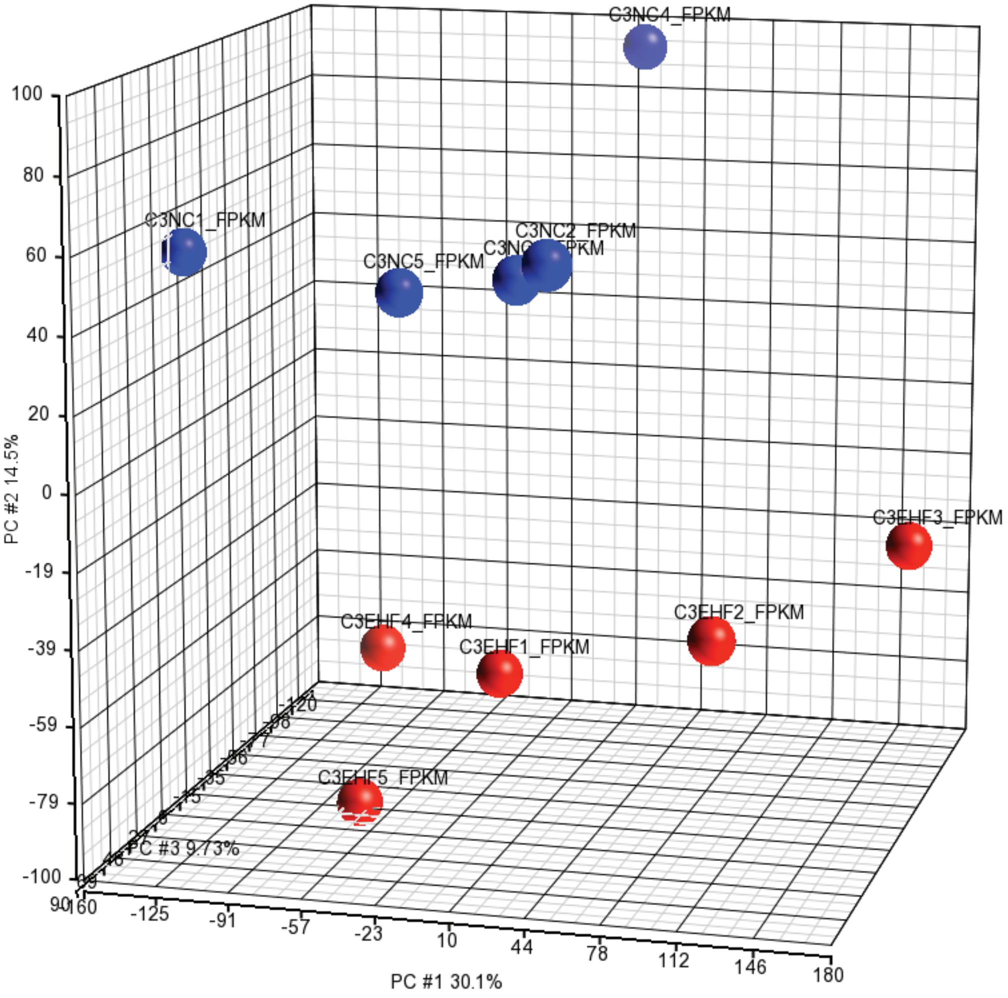
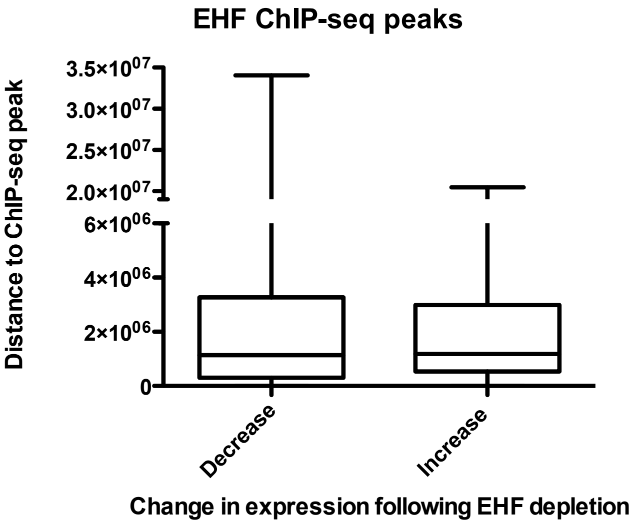

C3NC4_FPKM
C3NC1_FPKM
C3NC2_FPKM
C3NC5_FPKM
C3EHF3_FPKM
C3EHF4_FPKM
C3EHF2_FPKM
C3EHF1_FPKM
C3EHF5_FPKM
PC #2 14.5%
100
80
60
40
20
0
-19
-39
-59
-79
-100
PC #3 9.73%
-120
-98
-77
-56
-35
-15
6
27
48
69
90
PC #1 30.1%
-160
-125
-91
-57
-23
10
44
78
112
146
180

Figure 2



EHF ChIP-seq peaks
Distance to ChIP-seq peak
3.5×10^07
3.0×10^07
2.5×10^07
2.0×10^07
6×10^06
4×10^06
2×10^06
0
Decrease
Increase
Change in expression following EHF depletion

Figure 3

Table S1. Sequencing and alignment data for ChIP-seq experiments.

Experiment	Sequence Reads	Reads Aligned*	Percentage Reads Aligned
Calu-3 Input (Used for EHF ChIP-seq)	24147887	18849149	78.06
EHF ChIP-seq Replicate #1	14000252	10176290	72.69
EHF ChIP-seq Replicate #2	12203275	8418631	68.99
Calu-3 Input (Used for histone modification)	41720748	33082311	79.29
H3K4me1 ChIP-seq	15953914	12989646	81.41
H3K27ac ChIP-seq	25999778	21426939	82.41

*Sequence reads with >1 possible alignment were not aligned.

Table S2. Primer sequences.

	Sequence
qRT-PCR	
β-2 Microglobulin F	CTCTCTCTTTCTGGCCTGGAG
β-2 Microglobulin R	TCTGCTGGATGACGTGAGTA
DDAH1 F	TGCAACTTTAGATGGCGGAGA
DDAH1 R	GCCAAGATTTCAGCACCTCG
IL8 F	AGCTGGCCGTGGCTCTCT
IL8 R	CTGACATCTAAGTTCTTTAGCACTCCTT
CXCL1 F	CTTGCCTCAATCCTGCATC
CXCL1 R	CCTTCTGGTCAGTTGGATTTG
JDP2 F	TGGAGGTGAAACTGGGCAAG
JDP2 R	ACTTTGTTCTTCTCCCGGCG
TJP1 F	AGAGACAAGATGTCCGCCAG
TJP1 R	CAAATCCAAATCCAGGAGCCC
TJP2 F	GTGTCCGGAGGCAGAGACAA
TJP2 R	TGCCATTGACCATGACCACTC
ITGA2 F	TTGGAACGGGACTTTCGCAT
ITGA2 R	TCGGCTTTCTCATCAGGTTTCA
ChIP	
Promoter (ITGA2) F	GAAGTGTCCTGCCTCCCAAA
Promoter (ITGA2) R	AAGTCAGCCAGGTTTCAGGG
Promoter (OAS3) F	GGCTGGAAGCAAGGAGATGA
Promoter (OAS3) R	GACCTGACACCCACTTCCTG
Intron (TJP2) F	CCTGGTTTCTGCGTTACCCT
Intron (TJP2) R	AGCATGTGCATCCTCACCAA
Intron (AGAP1) F	CTGTTTGCTGAGGGTGGACT
Intron (AGAP1) R	GAGGGAATGACTGTGGCTCC
Intergenic (JDP2) F	CCAGCTTCCTTGTTGTTGGC
Intergenic (JDP2) R	CCACCCTAGCATGTTCCCAG
Intergenic (PLCH1) F	AGTAACTCACTGACGCTGGC
Intergenic (PLCH1) R	GCCTCTTCTCTCTGTGGCTG
Negative Control (EHF) F	TCCTTCCAGGTTTTGGCTCC
Negative Control (EHF) R	GCCCCAGATCAGGAGAGAGA

Table S3. List of EHF binding sites identified by ChIP-seq and present in both biological replicates.

Chromosome	Start	End	Peak Location Type
chr1	15417025	15417149	intron (NM_201628, intron 8 of 14)
chr1	17846600	17846724	Intergenic
chr1	21861388	21861512	intron (NM_001127501, intron 1 of 10)
chr1	23076848	23076972	intron (NM_017449, intron 1 of 15)
chr1	31449138	31449262	intron (NM_014676, intron 9 of 21)
chr1	31944644	31944768	Intergenic
chr1	32787504	32787628	intron (NM_004964, intron 3 of 13)
chr1	33446842	33446966	Intergenic
chr1	35667802	35667926	Intergenic
chr1	39864448	39864572	intron (NM_012090, intron 54 of 94)
chr1	43397556	43397680	intron (NM_006516, intron 2 of 9)
chr1	43637914	43638038	promoter-TSS (NM_001167965)
chr1	47789642	47789766	Intergenic
chr1	51086753	51086877	intron (NM_007051, intron 8 of 18)
chr1	52499386	52499510	promoter-TSS (NM_138417)
chr1	53480556	53480680	promoter-TSS (NM_001007100)
chr1	61038890	61039014	Intergenic
chr1	62190814	62190938	5' UTR (NM_032027, exon 1 of 7)
chr1	64386216	64386340	intron (NM_001083592, intron 1 of 6)
chr1	64637566	64637690	intron (NM_005012, intron 8 of 8)
chr1	65574145	65574269	Intergenic
chr1	65643175	65643299	intron (NM_203464, intron 2 of 5)
chr1	74059155	74059279	Intergenic
chr1	84609841	84609965	promoter-TSS (NM_182948)
chr1	94167319	94167443	intron (NM_001261408, intron 3 of 13)
chr1	95479610	95479734	intron (NM_144988, intron 3 of 3)
chr1	109189604	109189728	Intergenic
chr1	110778428	110778552	Intergenic
chr1	146987397	146987521	non-coding (NR_038423, exon 2 of 4)
chr1	147149057	147149181	Intergenic
chr1	156186486	156186610	intron (NM_001199664, intron 1 of 4)
chr1	156571220	156571344	promoter-TSS (NM_015590)
chr1	157652618	157652742	intron (NM_052939, intron 11 of 14)
chr1	157850562	157850686	Intergenic
chr1	160576993	160577117	Intergenic
chr1	162199994	162200118	intron (NM_014697, intron 2 of 9)
chr1	165738048	165738172	promoter-TSS (NM_019026)
chr1	169085463	169085587	intron (NM_001677, intron 2 of 5)
chr1	173683937	173684061	promoter-TSS (NM_014458)
chr1	173992859	173992983	Intergenic
chr1	182942192	182942316	Intergenic
chr1	183668898	183669022	intron (NM_015149, intron 1 of 18)

chr1	201521097	201521221	Intergenic
chr1	203595736	203595860	promoter-TSS (NM_001684)
chr1	204195582	204195706	intron (NM_014935, intron 21 of 22)
chr1	207126615	207126739	Intergenic
chr1	209822803	209822927	intron (NM_001017402, intron 2 of 21)
chr1	215287612	215287736	intron (NM_001017424, intron 2 of 6)
chr1	217202666	217202790	intron (NM_001243507, intron 1 of 7)
chr1	218847942	218848066	Intergenic
chr1	219121920	219122044	Intergenic
chr1	223895019	223895143	intron (NM_001146068, intron 1 of 20)
chr1	224253273	224253397	Intergenic
chr1	225632718	225632842	Intergenic
chr1	228353717	228353841	exon (NM_001010867, exon 1 of 3)
chr1	229076833	229076957	Intergenic
chr1	230707974	230708098	Intergenic
chr1	234908271	234908395	Intergenic
chr1	235099075	235099199	Intergenic
chr1	243894751	243894875	intron (NM_001206729, intron 2 of 13)
chr1	244466195	244466319	Intergenic
chr2	10631016	10631140	Intergenic
chr2	11893753	11893877	intron (NM_145693, intron 1 of 19)
chr2	20431518	20431642	Intergenic
chr2	26366954	26367078	Intergenic
chr2	38670199	38670323	Intergenic
chr2	43313694	43313818	Intergenic
chr2	45686407	45686531	intron (NM_018079, intron 16 of 20)
chr2	56185566	56185690	Intergenic
chr2	62805437	62805561	Intergenic
chr2	64343023	64343147	intron (NM_020651, intron 1 of 6)
chr2	84179993	84180117	Intergenic
chr2	85196747	85196871	Intergenic
chr2	96926246	96926370	intron (NM_017849, intron 2 of 3)
chr2	97093877	97094001	Intergenic
chr2	99374746	99374870	Intergenic
chr2	99485698	99485822	intron (NM_207362, intron 1 of 9)
chr2	109065498	109065622	promoter-TSS (NR_028063)
chr2	118870479	118870603	Intergenic
chr2	118880647	118880771	Intergenic
chr2	121886449	121886573	Intergenic
chr2	122118244	122118368	intron (NM_001207051, intron 35 of 37)
chr2	128848650	128848774	promoter-TSS (NR_027671)
chr2	138451239	138451363	Intergenic
chr2	142948614	142948738	Intergenic
chr2	144698453	144698577	Intergenic
chr2	150734632	150734756	Intergenic

chr2	153032465	153032589	promoter-TSS (NM_005843)
chr2	159456975	159457099	intron (NM_001005476, intron 3 of 20)
chr2	159980963	159981087	intron (NM_033394, intron 4 of 26)
chr2	160353835	160353959	intron (NM_013450, intron 2 of 36)
chr2	161826606	161826730	Intergenic
chr2	163589556	163589680	intron (NM_033272, intron 2 of 15)
chr2	165567550	165567674	intron (NM_014900, intron 6 of 13)
chr2	169659005	169659129	promoter-TSS (NM_001039724)
chr2	187454582	187454706	promoter-TSS (NM_002210)
chr2	188366914	188367038	intron (NM_001032281, intron 2 of 6)
chr2	188419143	188419267	promoter-TSS (NM_006287)
chr2	190387614	190387738	Intergenic
chr2	192242106	192242230	intron (NM_001161819, intron 13 of 30)
chr2	192545082	192545206	intron (NR_045623, intron 2 of 6)
chr2	204676364	204676488	Intergenic
chr2	206840122	206840246	Intergenic
chr2	208684638	208684762	Intergenic
chr2	213777282	213777406	Intergenic
chr2	214153753	214153877	intron (NR_047659, intron 2 of 17)
chr2	216545882	216546006	intron (NR_037195, intron 5 of 9)
chr2	216922399	216922523	intron (NM_018441, intron 4 of 7)
chr2	219051192	219051316	Intergenic
chr2	231191803	231191927	promoter-TSS (NM_138402)
chr2	235112132	235112256	Intergenic
chr2	236451560	236451684	intron (NM_001037131, intron 1 of 17)
chr2	241505284	241505408	Intergenic
chr2	242314095	242314219	intron (NM_014808, intron 2 of 26)
chr3	7546602	7546726	intron (NM_000844, intron 7 of 9)
chr3	13041109	13041233	intron (NM_001134382, intron 1 of 14)
chr3	15419747	15419871	Intergenic
chr3	19930896	19931020	intron (NM_144715, intron 9 of 12)
chr3	39166915	39167039	exon (NM_001105513, exon 10 of 28)
chr3	40841959	40842083	Intergenic
chr3	42694335	42694459	promoter-TSS (NM_145166)
chr3	45730549	45730673	promoter-TSS (NM_014016)
chr3	46249952	46250076	promoter-TSS (NM_001295)
chr3	49538588	49538712	intron (NM_001165928, intron 4 of 5)
chr3	57094486	57094610	promoter-TSS (NM_181727)
chr3	58633541	58633665	intron (NM_138805, intron 4 of 9)
chr3	65938026	65938150	intron (NM_015520, intron 1 of 24)
chr3	80745667	80745791	Intergenic
chr3	95986561	95986685	Intergenic
chr3	112518943	112519067	Intergenic
chr3	121638105	121638229	intron (NM_021082, intron 7 of 21)
chr3	127539443	127539567	intron (NM_001256585, intron 2 of 6)

chr3	129118468	129118592	promoter-TSS (NR_003111)
chr3	133662472	133662596	intron (NM_005630, intron 10 of 13)
chr3	133665390	133665514	intron (NM_005630, intron 9 of 13)
chr3	134346758	134346882	intron (NM_178554, intron 4 of 10)
chr3	135905217	135905341	intron (NM_018133, intron 1 of 1)
chr3	138048059	138048183	intron (NM_178130, intron 2 of 11)
chr3	141087062	141087186	intron (NM_001080412, intron 1 of 7)
chr3	141204953	141205077	promoter-TSS (NM_006506)
chr3	141659091	141659215	Intergenic
chr3	141934128	141934252	intron (NM_001039547, intron 2 of 15)
chr3	142316992	142317116	intron (NM_001145319, intron 1 of 15)
chr3	142679401	142679525	TTS (NM_198504)
chr3	143162710	143162834	intron (NM_173653, intron 12 of 15)
chr3	143184688	143184812	intron (NM_173653, intron 12 of 15)
chr3	146224581	146224705	Intergenic
chr3	148598556	148598680	intron (NM_001870, intron 6 of 10)
chr3	149119087	149119211	Intergenic
chr3	150264370	150264494	promoter-TSS (NM_014445)
chr3	151765417	151765541	Intergenic
chr3	152189828	152189952	Intergenic
chr3	152545997	152546121	Intergenic
chr3	152770034	152770158	Intergenic
chr3	152856515	152856639	Intergenic
chr3	153966113	153966237	intron (NM_015595, intron 12 of 14)
chr3	155455634	155455758	Intergenic
chr3	156399002	156399126	intron (NM_001184717, intron 2 of 5)
chr3	157827820	157827944	promoter-TSS (NM_001271838)
chr3	158489833	158489957	Intergenic
chr3	158887746	158887870	intron (NM_001197114, intron 1 of 9)
chr3	159136826	159136950	intron (NM_001197108, intron 1 of 6)
chr3	160984521	160984645	Intergenic
chr3	161033818	161033942	Intergenic
chr3	167883491	167883615	Intergenic
chr3	169102458	169102582	intron (NM_004991, intron 1 of 16)
chr3	170469278	170469402	Intergenic
chr3	170720020	170720144	intron (NM_000340, intron 8 of 10)
chr3	171046621	171046745	intron (NM_001161565, intron 2 of 30)
chr3	171562669	171562793	intron (NM_001164436, intron 1 of 4)
chr3	171685106	171685230	Intergenic
chr3	171805818	171805942	intron (NM_001135095, intron 1 of 25)
chr3	171860404	171860528	intron (NM_022763, intron 3 of 25)
chr3	172406456	172406580	intron (NM_001146276, intron 1 of 4)
chr3	172416084	172416208	intron (NM_001146276, intron 1 of 4)
chr3	172428968	172429092	promoter-TSS (NM_020792)
chr3	173246989	173247113	intron (NM_014932, intron 2 of 6)

chr3	173466058	173466182	intron (NM_014932, intron 3 of 6)
chr3	174580084	174580208	intron (NM_207015, intron 1 of 13)
chr3	175064848	175064972	intron (NM_207015, intron 5 of 13)
chr3	177063489	177063613	Intergenic
chr3	177246402	177246526	intron (NR_047568, intron 1 of 3)
chr3	177646036	177646160	Intergenic
chr3	180319897	180320021	promoter-TSS (NM_001042601)
chr3	182002806	182002930	Intergenic
chr3	182825778	182825902	Intergenic
chr3	183100287	183100411	intron (NM_015078, intron 2 of 29)
chr3	183853099	183853223	5' UTR (NM_003907, exon 1 of 16)
chr3	184089428	184089552	TTS (NM_001177597)
chr3	185069760	185069884	intron (NM_001242317, intron 2 of 12)
chr3	185255332	185255456	intron (NM_139248, intron 1 of 9)
chr3	186163390	186163514	Intergenic
chr3	186463965	186464089	Intergenic
chr3	187930050	187930174	promoter-TSS (NM_005578)
chr3	188156989	188157113	intron (NM_001167672, intron 2 of 9)
chr3	188906289	188906413	intron (NM_198485, intron 1 of 5)
chr3	189034249	189034373	intron (NM_198485, intron 5 of 5)
chr3	189042606	189042730	Intergenic
chr3	190284437	190284561	intron (NM_001167931, intron 3 of 11)
chr3	190604965	190605089	Intergenic
chr3	193500147	193500271	Intergenic
chr3	193561726	193561850	Intergenic
chr3	193723007	193723131	Intergenic
chr3	193807421	193807545	Intergenic
chr3	194248007	194248131	Intergenic
chr3	194304689	194304813	promoter-TSS (NR_047573)
chr3	195309979	195310103	intron (NM_001647, intron 1 of 4)
chr4	11634143	11634267	Intergenic
chr4	19741083	19741207	Intergenic
chr4	38689238	38689362	intron (NM_016531, intron 2 of 5)
chr4	54510979	54511103	Intergenic
chr4	74642025	74642149	Intergenic
chr4	77586506	77586630	intron (NM_020859, intron 2 of 10)
chr4	90349139	90349263	Intergenic
chr4	120715929	120716053	Intergenic
chr4	122383936	122384060	Intergenic
chr4	129349091	129349215	Intergenic
chr4	143471273	143471397	intron (NM_003866, intron 2 of 26)
chr4	147162749	147162873	Intergenic
chr4	147442131	147442255	intron (NM_001029998, intron 1 of 11)
chr4	174089300	174089424	promoter-TSS (NM_017423)
chr4	185276447	185276571	Intergenic

chr5	19041381	19041505	Intergenic
chr5	33440702	33440826	promoter-TSS (NM_152295)
chr5	40775685	40775809	intron (NM_206907, intron 2 of 9)
chr5	52283539	52283663	Intergenic
chr5	53997246	53997370	Intergenic
chr5	57531257	57531381	Intergenic
chr5	60704440	60704564	intron (NM_020928, intron 1 of 13)
chr5	67692706	67692830	Intergenic
chr5	71218887	71219011	Intergenic
chr5	72248013	72248137	Intergenic
chr5	73939228	73939352	Intergenic
chr5	75012908	75013032	intron (NM_001099271, intron 1 of 11)
chr5	78597293	78597417	intron (NM_152405, intron 6 of 10)
chr5	79477674	79477798	intron (NM_001174071, intron 2 of 12)
chr5	81147837	81147961	Intergenic
chr5	84589381	84589505	Intergenic
chr5	86371214	86371338	Intergenic
chr5	86410460	86410584	TTS (NR_036243)
chr5	90467245	90467369	Intergenic
chr5	90607693	90607817	Intergenic
chr5	93447365	93447489	promoter-TSS (NM_032042)
chr5	106724947	106725071	intron (NM_001962, intron 2 of 4)
chr5	106725534	106725658	intron (NM_001962, intron 2 of 4)
chr5	108416689	108416813	intron (NM_005246, intron 16 of 19)
chr5	114715689	114715813	Intergenic
chr5	114755664	114755788	Intergenic
chr5	118638753	118638877	intron (NM_001077654, intron 1 of 1)
chr5	123935466	123935590	Intergenic
chr5	124148526	124148650	Intergenic
chr5	126339956	126340080	intron (NM_178450, intron 1 of 4)
chr5	126539656	126539780	Intergenic
chr5	126656470	126656594	intron (NM_032446, intron 2 of 25)
chr5	129625429	129625553	Intergenic
chr5	130109586	130109710	Intergenic
chr5	130616884	130617008	intron (NM_001038702, intron 1 of 4)
chr5	130718179	130718303	intron (NM_001038702, intron 2 of 4)
chr5	131723410	131723534	intron (NM_003060, intron 5 of 9)
chr5	131765527	131765651	intron (NR_045116, intron 2 of 3)
chr5	133332464	133332588	intron (NM_003374, intron 1 of 8)
chr5	133772703	133772827	Intergenic
chr5	134896661	134896785	Intergenic
chr5	135347808	135347932	Intergenic
chr5	138861935	138862059	intron (NM_198282, intron 1 of 7)
chr5	139511583	139511707	Intergenic
chr5	140044225	140044349	promoter-TSS (NM_017706)

chr5	140383985	140384109	intron (NM_031849, intron 3 of 3)
chr5	145407447	145407571	intron (NM_152550, intron 5 of 9)
chr5	148352718	148352842	Intergenic
chr5	148724922	148725046	promoter-TSS (NM_152407)
chr5	151121319	151121443	Intergenic
chr5	154140737	154140861	intron (NM_015315, intron 1 of 18)
chr5	162834444	162834568	Intergenic
chr5	167751995	167752119	intron (NM_001161661, intron 1 of 22)
chr5	168078754	168078878	Intergenic
chr5	172234233	172234357	Intergenic
chr5	176250367	176250491	intron (NM_133369, intron 1 of 14)
chr5	176816839	176816963	3' UTR (NM_001167579, exon 9 of 9)
chr5	179512296	179512420	Intergenic
chr5	180288480	180288604	promoter-TSS (NM_001172638)
chr5	180618611	180618735	Intergenic
chr6	6811535	6811659	Intergenic
chr6	7042634	7042758	Intergenic
chr6	11632584	11632708	Intergenic
chr6	21742618	21742742	intron (NR_015410, intron 2 of 11)
chr6	25866430	25866554	intron (NM_001098486, intron 2 of 12)
chr6	26016980	26017104	TTS (NM_005325)
chr6	30484403	30484527	Intergenic
chr6	33330021	33330145	Intergenic
chr6	47012279	47012403	Intergenic
chr6	47428176	47428300	Intergenic
chr6	81348530	81348654	Intergenic
chr6	107639426	107639550	intron (NM_020381, intron 2 of 7)
chr6	109053986	109054110	Intergenic
chr6	109550850	109550974	Intergenic
chr6	112163169	112163293	intron (NM_002037, intron 2 of 13)
chr6	119468729	119468853	intron (NM_001100411, intron 1 of 16)
chr6	123005299	123005423	intron (NM_001270393, intron 6 of 7)
chr6	125320390	125320514	intron (NM_152553, intron 2 of 8)
chr6	126362080	126362204	Intergenic
chr6	136571378	136571502	promoter-TSS (NM_001099286)
chr6	158481537	158481661	intron (NM_001178088, intron 6 of 25)
chr6	163813140	163813264	Intergenic
chr6	167150150	167150274	intron (NM_001006932, intron 2 of 21)
chr6	168083625	168083749	Intergenic
chr7	988898	989022	intron (NM_006869, intron 1 of 10)
chr7	1495328	1495452	intron (NM_182924, intron 1 of 16)
chr7	2611740	2611864	intron (NM_152558, intron 4 of 21)
chr7	5436825	5436949	intron (NM_001080495, intron 2 of 29)
chr7	5601683	5601807	Intergenic
chr7	7455926	7456050	intron (NM_001037763, intron 27 of 34)

chr7	13889858	13889982	Intergenic
chr7	16468476	16468600	Intergenic
chr7	17170030	17170154	Intergenic
chr7	17409755	17409879	Intergenic
chr7	17484438	17484562	Intergenic
chr7	17572777	17572901	Intergenic
chr7	17712537	17712661	Intergenic
chr7	18053772	18053896	Intergenic
chr7	18707225	18707349	3' UTR (NM_001204146, exon 11 of 11)
chr7	20239173	20239297	intron (NM_182762, intron 1 of 6)
chr7	22143424	22143548	Intergenic
chr7	23510421	23510545	promoter-TSS (NM_006547)
chr7	25608594	25608718	Intergenic
chr7	26131786	26131910	Intergenic
chr7	27086623	27086747	Intergenic
chr7	27275040	27275164	Intergenic
chr7	27334932	27335056	Intergenic
chr7	28104149	28104273	intron (NM_175061, intron 1 of 4)
chr7	28966747	28966871	Intergenic
chr7	30027661	30027785	intron (NM_001145514, intron 1 of 7)
chr7	31533391	31533515	Intergenic
chr7	31915147	31915271	intron (NM_005020, intron 6 of 17)
chr7	37071541	37071665	intron (NM_001206480, intron 15 of 21)
chr7	37960161	37960285	promoter-TSS (NM_001242948)
chr7	38262239	38262363	intron (NM_032016, intron 7 of 8)
chr7	41229699	41229823	Intergenic
chr7	41264241	41264365	Intergenic
chr7	43687640	43687764	intron (NR_047701, intron 3 of 7)
chr7	44678882	44679006	intron (NM_001003941, intron 2 of 8)
chr7	46690873	46690997	Intergenic
chr7	47615722	47615846	intron (NM_022748, intron 1 of 30)
chr7	48031798	48031922	intron (NM_001030019, intron 8 of 9)
chr7	51410001	51410125	Intergenic
chr7	77111436	77111560	Intergenic
chr7	97601569	97601693	promoter-TSS (NR_002822)
chr7	98970248	98970372	Intergenic
chr7	100143208	100143332	intron (NM_006076, intron 1 of 11)
chr7	100143871	100143995	intron (NM_006076, intron 1 of 11)
chr7	105447127	105447251	intron (NM_020725, intron 2 of 11)
chr7	130572003	130572127	intron (NR_034120, intron 2 of 3)
chr7	130692375	130692499	intron (NR_024153, intron 1 of 2)
chr7	133538744	133538868	intron (NM_021807, intron 11 of 17)
chr7	138571394	138571518	intron (NM_001164665, intron 10 of 19)
chr7	141804702	141804826	intron (NM_004668, intron 47 of 47)
chr7	143065140	143065264	Intergenic

chr7	148842427	148842551	intron (NM_020781, intron 2 of 6)
chr7	151189074	151189198	intron (NM_005614, intron 1 of 7)
chr8	8153925	8154049	Intergenic
chr8	8170217	8170341	Intergenic
chr8	8414573	8414697	Intergenic
chr8	18067598	18067722	promoter-TSS (NM_001160172)
chr8	24151459	24151583	promoter-TSS (NM_014265)
chr8	27182927	27183051	promoter-TSS (NM_173176)
chr8	29999222	29999346	intron (NM_001100916, intron 1 of 2)
chr8	30112454	30112578	Intergenic
chr8	30295858	30295982	intron (NM_001008710, intron 1 of 8)
chr8	31691166	31691290	intron (NM_013962, intron 1 of 4)
chr8	32191946	32192070	intron (NM_013962, intron 1 of 4)
chr8	33411702	33411826	intron (NM_024787, intron 2 of 5)
chr8	37749531	37749655	intron (NM_001002814, intron 1 of 5)
chr8	38384864	38384988	intron (NM_207412, intron 1 of 2)
chr8	38895683	38895807	intron (NR_027638, intron 11 of 20)
chr8	39797573	39797697	intron (NM_194294, intron 1 of 10)
chr8	42114268	42114392	Intergenic
chr8	67579723	67579847	promoter-TSS (NM_001204173)
chr8	101881894	101882018	Intergenic
chr8	102171238	102171362	Intergenic
chr8	107218730	107218854	Intergenic
chr8	122824134	122824258	Intergenic
chr8	123476178	123476302	Intergenic
chr8	123807354	123807478	intron (NM_014943, intron 1 of 3)
chr8	123818268	123818392	intron (NM_014943, intron 1 of 3)
chr8	124549963	124550087	intron (NM_058229, intron 1 of 8)
chr8	124560643	124560767	Intergenic
chr8	124934556	124934680	intron (NM_001039112, intron 1 of 40)
chr8	125488559	125488683	intron (NM_007218, intron 1 of 1)
chr8	126181158	126181282	intron (NM_173685, intron 4 of 7)
chr8	126226619	126226743	intron (NM_173685, intron 5 of 7)
chr8	126304205	126304329	intron (NM_173685, intron 5 of 7)
chr8	128307073	128307197	Intergenic
chr8	128521844	128521968	Intergenic
chr8	129188949	129189073	Intergenic
chr8	129189373	129189497	Intergenic
chr8	130720022	130720146	Intergenic
chr8	131275017	131275141	intron (NM_018482, intron 3 of 29)
chr8	133333755	133333879	intron (NM_004519, intron 1 of 14)
chr8	133520056	133520180	Intergenic
chr8	134664324	134664448	Intergenic
chr8	135904986	135905110	Intergenic
chr8	140227437	140227561	Intergenic

chr8	141601618	141601742	intron (NM_001164623, intron 1 of 17)
chr8	143757594	143757718	intron (NR_033343, intron 1 of 2)
chr8	144655632	144655756	promoter-TSS (NM_001100878)
chr8	144980212	144980336	Intergenic
chr8	145547872	145547996	intron (NM_012079, intron 1 of 16)
chr9	4243203	4243327	intron (NM_001042413, intron 2 of 10)
chr9	4277814	4277938	intron (NM_001042413, intron 2 of 10)
chr9	8907998	8908122	intron (NM_002839, intron 11 of 45)
chr9	14212895	14213019	intron (NM_005596, intron 2 of 8)
chr9	19380170	19380294	promoter-TSS (NM_001010)
chr9	34186440	34186564	intron (NM_001171201, intron 1 of 5)
chr9	71795598	71795722	intron (NM_001170630, intron 1 of 18)
chr9	84352735	84352859	Intergenic
chr9	113515131	113515255	intron (NM_001166280, intron 8 of 12)
chr9	115086141	115086265	intron (NM_001163788, intron 1 of 13)
chr9	135424733	135424857	intron (NM_207417, intron 6 of 6)
chr9	140506809	140506933	intron (NM_152285, intron 1 of 7)
chr10	976636	976760	intron (NM_015155, intron 1 of 17)
chr10	1034335	1034459	promoter-TSS (NM_012341)
chr10	3088091	3088215	Intergenic
chr10	3514998	3515122	Intergenic
chr10	4746463	4746587	Intergenic
chr10	6317234	6317358	Intergenic
chr10	12085352	12085476	promoter-TSS (NM_080599)
chr10	14620705	14620829	intron (NM_031453, intron 2 of 4)
chr10	29173555	29173679	Intergenic
chr10	33227478	33227602	intron (NM_002211, intron 1 of 15)
chr10	33299008	33299132	Intergenic
chr10	33654773	33654897	Intergenic
chr10	35047416	35047540	intron (NM_001184790, intron 1 of 22)
chr10	35924539	35924663	Intergenic
chr10	43136554	43136678	Intergenic
chr10	56044432	56044556	intron (NM_001142773, intron 7 of 31)
chr10	60195951	60196075	Intergenic
chr10	60941527	60941651	intron (NM_001143774, intron 1 of 4)
chr10	61725170	61725294	Intergenic
chr10	62042690	62042814	intron (NM_001204403, intron 2 of 43)
chr10	63517427	63517551	intron (NM_173554, intron 4 of 6)
chr10	63771437	63771561	intron (NM_032199, intron 4 of 9)
chr10	65467193	65467317	Intergenic
chr10	70310639	70310763	Intergenic
chr10	70715800	70715924	promoter-TSS (NM_001256910)
chr10	73006776	73006900	intron (NM_170744, intron 1 of 16)
chr10	73103171	73103295	intron (NR_033414, intron 2 of 3)
chr10	73931025	73931149	intron (NR_045564, intron 5 of 9)

chr10	74398679	74398803	Intergenic
chr10	75949986	75950110	intron (NM_001123, intron 1 of 10)
chr10	91043784	91043908	Intergenic
chr10	114787655	114787779	intron (NM_001146274, intron 4 of 13)
chr11	561483	561607	promoter-TSS (NM_003475)
chr11	7626887	7627011	promoter-TSS (NM_001256569)
chr11	9741519	9741643	intron (NM_015055, intron 3 of 11)
chr11	16023537	16023661	intron (NM_001145819, intron 13 of 15)
chr11	18343719	18343843	promoter-TSS (NM_007216)
chr11	28780983	28781107	Intergenic
chr11	33713804	33713928	Intergenic
chr11	34255718	34255842	intron (NM_145804, intron 1 of 16)
chr11	34400813	34400937	Intergenic
chr11	35030733	35030857	Intergenic
chr11	35099476	35099600	Intergenic
chr11	44976803	44976927	Intergenic
chr11	48131501	48131625	intron (NM_002843, intron 1 of 24)
chr11	56622844	56622968	Intergenic
chr11	58953710	58953834	intron (NM_015177, intron 2 of 8)
chr11	64863519	64863643	promoter-TSS (NM_013265)
chr11	65655932	65656056	promoter-TSS (NM_004214)
chr11	66462397	66462521	intron (NM_006946, intron 20 of 36)
chr11	67442229	67442353	promoter-TSS (NM_000695)
chr11	67858301	67858425	intron (NM_001277, intron 2 of 11)
chr11	67913641	67913765	Intergenic
chr11	68065570	68065694	Intergenic
chr11	73587960	73588084	promoter-TSS (NM_016565)
chr11	75400950	75401074	Intergenic
chr11	76695860	76695984	intron (NM_018367, intron 4 of 10)
chr11	104034801	104034925	5' UTR (NM_025208, exon 1 of 7)
chr11	109817073	109817197	Intergenic
chr11	110216675	110216799	Intergenic
chr11	114067275	114067399	intron (NM_006006, intron 4 of 6)
chr11	126686639	126686763	intron (NM_032531, intron 1 of 16)
chr12	498402	498526	promoter-TSS (NM_001130147)
chr12	647839	647963	intron (NM_173593, intron 3 of 19)
chr12	1457266	1457390	intron (NR_027948, intron 15 of 19)
chr12	6404504	6404628	Intergenic
chr12	11802018	11802142	promoter-TSS (NM_001987)
chr12	12957052	12957176	Intergenic
chr12	13158716	13158840	Intergenic
chr12	13530039	13530163	promoter-TSS (NR_036555)
chr12	14360929	14361053	Intergenic
chr12	15843025	15843149	intron (NM_004447, intron 1 of 20)
chr12	15853631	15853755	intron (NM_004447, intron 1 of 20)

chr12	18299454	18299578	Intergenic
chr12	29534073	29534197	promoter-TSS (NM_016570)
chr12	54762524	54762648	TTS (NM_015481)
chr12	63054652	63054776	intron (NM_020700, intron 9 of 9)
chr12	63124957	63125081	intron (NM_020700, intron 5 of 9)
chr12	65066746	65066870	intron (NR_040718, intron 1 of 3)
chr12	65927174	65927298	Intergenic
chr12	66042999	66043123	Intergenic
chr12	66539031	66539155	intron (NM_016056, intron 5 of 6)
chr12	76034935	76035059	Intergenic
chr12	76338435	76338559	Intergenic
chr12	76372228	76372352	Intergenic
chr12	79960270	79960394	Intergenic
chr12	82253417	82253541	Intergenic
chr12	82806114	82806238	intron (NM_032230, intron 5 of 11)
chr12	89132115	89132239	Intergenic
chr12	89466935	89467059	Intergenic
chr12	91751327	91751451	Intergenic
chr12	94071012	94071136	promoter-TSS (NM_003805)
chr12	95598267	95598391	intron (NM_018351, intron 2 of 20)
chr12	96591879	96592003	intron (NM_005230, intron 1 of 4)
chr12	107234178	107234302	intron (NM_018157, intron 4 of 8)
chr12	113376039	113376163	promoter-TSS (NM_006187)
chr12	120105684	120105808	promoter-TSS (NM_006253)
chr12	120111504	120111628	intron (NM_006253, intron 2 of 6)
chr12	120669200	120669324	intron (NM_001080855, intron 1 of 11)
chr13	24723038	24723162	Intergenic
chr13	34731182	34731306	Intergenic
chr13	35322329	35322453	Intergenic
chr13	40976683	40976807	intron (NR_024506, intron 5 of 5)
chr13	41848278	41848402	Intergenic
chr13	47558171	47558295	Intergenic
chr14	22384245	22384369	Intergenic
chr14	23299015	23299139	promoter-TSS (NM_181305)
chr14	23340304	23340428	promoter-TSS (NM_014045)
chr14	34513001	34513125	Intergenic
chr14	34844693	34844817	Intergenic
chr14	37220468	37220592	intron (NM_030631, intron 3 of 9)
chr14	45431177	45431301	promoter-TSS (NM_017658)
chr14	53167709	53167833	Intergenic
chr14	56269967	56270091	Intergenic
chr14	61905926	61906050	intron (NM_006255, intron 2 of 13)
chr14	62028775	62028899	Intergenic
chr14	62135204	62135328	Intergenic
chr14	65165831	65165955	Intergenic

chr14	65757685	65757809	Intergenic
chr14	69405584	69405708	intron (NM_001130005, intron 1 of 20)
chr14	75084807	75084931	Intergenic
chr14	75867110	75867234	Intergenic
chr14	77888608	77888732	intron (NM_001113475, intron 1 of 5)
chr14	92339036	92339160	intron (NM_006329, intron 10 of 10)
chr14	93412820	93412944	intron (NM_014216, intron 9 of 10)
chr14	101943449	101943573	Intergenic
chr14	102746009	102746133	intron (NM_014226, intron 2 of 11)
chr15	50716270	50716394	promoter-TSS (NM_005154)
chr15	53615557	53615681	Intergenic
chr15	57053214	57053338	Intergenic
chr15	58813884	58814008	intron (NM_000236, intron 1 of 8)
chr15	59158628	59158752	Intergenic
chr15	59566899	59567023	intron (NM_004998, intron 1 of 27)
chr15	59592687	59592811	intron (NM_004998, intron 1 of 27)
chr15	60700777	60700901	Intergenic
chr15	62411720	62411844	Intergenic
chr15	63182377	63182501	Intergenic
chr15	63188335	63188459	Intergenic
chr15	63797871	63797995	intron (NR_046342, intron 1 of 15)
chr15	64679778	64679902	promoter-TSS (NM_016213)
chr15	67224579	67224703	Intergenic
chr15	67440784	67440908	intron (NM_001145103, intron 1 of 8)
chr15	71075502	71075626	Intergenic
chr15	71428819	71428943	Intergenic
chr15	72448485	72448609	Intergenic
chr15	72519058	72519182	intron (NM_001206798, intron 1 of 10)
chr15	74092995	74093119	Intergenic
chr15	74281810	74281934	intron (NM_001256672, intron 2 of 6)
chr15	74908819	74908943	intron (NM_001130028, intron 1 of 12)
chr15	75160451	75160575	intron (NM_005697, intron 1 of 8)
chr15	75339503	75339627	intron (NM_021823, intron 4 of 5)
chr15	75468090	75468214	Intergenic
chr15	75918088	75918212	5' UTR (NM_001042581, exon 1 of 9)
chr15	76591492	76591616	intron (NM_000126, intron 1 of 11)
chr15	78667519	78667643	Intergenic
chr15	79296868	79296992	intron (NM_001145648, intron 14 of 26)
chr15	80729157	80729281	intron (NM_014862, intron 1 of 18)
chr15	90590198	90590322	intron (NM_198526, intron 1 of 4)
chr15	93340371	93340495	TTS (NR_033769)
chr15	101708435	101708559	Intergenic
chr16	88964	89088	Intergenic
chr16	1660624	1660748	5' UTR (NM_014714, exon 2 of 31)
chr16	2885757	2885881	Intergenic

chr16	4250323	4250447	intron (NM_001098814, intron 3 of 5)
chr16	8891608	8891732	promoter-TSS (NM_000303)
chr16	9217894	9218018	Intergenic
chr16	11706232	11706356	Intergenic
chr16	14091848	14091972	Intergenic
chr16	15684807	15684931	Intergenic
chr16	15993453	15993577	Intergenic
chr16	17489984	17490108	intron (NM_022166, intron 1 of 11)
chr16	19142143	19142267	Intergenic
chr16	19440629	19440753	intron (NM_001261841, intron 1 of 21)
chr16	19443842	19443966	intron (NM_001105248, intron 2 of 21)
chr16	20922154	20922278	intron (NM_001128301, intron 2 of 4)
chr16	21312059	21312183	promoter-TSS (NR_026675)
chr16	22199951	22200075	Intergenic
chr16	23710606	23710730	intron (NM_033266, intron 13 of 21)
chr16	24859538	24859662	intron (NM_001258413, intron 2 of 15)
chr16	25120995	25121119	Intergenic
chr16	28503371	28503495	promoter-TSS (NM_000086)
chr16	29827257	29827381	promoter-TSS (NM_024516)
chr16	30759394	30759518	promoter-TSS (NM_001172432)
chr16	48431291	48431415	Intergenic
chr16	51278081	51278205	Intergenic
chr16	58058498	58058622	promoter-TSS (NM_002428)
chr16	67970744	67970868	promoter-TSS (NM_002801)
chr16	68267992	68268116	intron (NM_024939, intron 2 of 14)
chr16	71549119	71549243	Intergenic
chr16	77225004	77225128	5' UTR (NM_014940, exon 1 of 6)
chr16	80574818	80574942	promoter-TSS (NM_130897)
chr16	81002678	81002802	Intergenic
chr16	81031295	81031419	intron (NM_020188, intron 1 of 3)
chr16	81327956	81328080	Intergenic
chr16	81614812	81614936	intron (NM_030629, intron 1 of 20)
chr16	84534810	84534934	intron (NM_020947, intron 1 of 7)
chr16	84652588	84652712	promoter-TSS (NM_021149)
chr16	89572013	89572137	Intergenic
chr16	89648661	89648785	intron (NM_014427, intron 3 of 16)
chr17	12634523	12634647	intron (NM_153604, intron 5 of 12)
chr17	28672040	28672164	Intergenic
chr17	32052836	32052960	intron (NM_001094, intron 1 of 9)
chr17	33047994	33048118	Intergenic
chr17	33048381	33048505	Intergenic
chr17	33846562	33846686	Intergenic
chr17	35969412	35969536	promoter-TSS (NM_001163547)
chr17	36106655	36106779	Intergenic
chr17	36906058	36906182	Intergenic

chr17	40086796	40086920	promoter-TSS (NM_031421)
chr17	40714105	40714229	promoter-TSS (NM_001042529)
chr17	42581003	42581127	promoter-TSS (NR_036474)
chr17	46679111	46679235	intron (NR_033202, intron 2 of 2)
chr17	46868444	46868568	intron (NM_001130918, intron 9 of 15)
chr17	48075775	48075899	Intergenic
chr17	48945021	48945145	non-coding (NR_038458, exon 2 of 2)
chr17	50383887	50384011	Intergenic
chr17	55977337	55977461	intron (NM_001271875, intron 1 of 10)
chr17	57925274	57925398	Intergenic
chr17	69325556	69325680	Intergenic
chr17	70455079	70455203	intron (NR_036488, intron 1 of 3)
chr17	73613472	73613596	intron (NR_003587, intron 39 of 60)
chr17	73693415	73693539	intron (NM_013260, intron 4 of 10)
chr17	74637792	74637916	intron (NM_018414, intron 1 of 8)
chr17	74641785	74641909	Intergenic
chr17	75084677	75084801	promoter-TSS (NR_003013)
chr17	75338543	75338667	intron (NM_006640, intron 1 of 10)
chr17	76954699	76954823	Intergenic
chr17	78228729	78228853	Intergenic
chr17	80817934	80818058	intron (NM_005993, intron 13 of 38)
chr18	2222927	2223051	Intergenic
chr18	2411585	2411709	Intergenic
chr18	3045533	3045657	Intergenic
chr18	9101894	9102018	promoter-TSS (NM_021074)
chr18	9825597	9825721	intron (NM_006868, intron 5 of 6)
chr18	12838178	12838302	intron (NM_001207013, intron 2 of 10)
chr18	20131906	20132030	Intergenic
chr18	21166715	21166839	promoter-TSS (NM_000271)
chr18	21408545	21408669	intron (NM_198129, intron 23 of 74)
chr18	29952658	29952782	intron (NM_022751, intron 2 of 5)
chr18	30696580	30696704	intron (NM_198995, intron 19 of 21)
chr18	30764297	30764421	intron (NM_198995, intron 19 of 21)
chr18	33077847	33077971	promoter-TSS (NM_001098817)
chr18	47624145	47624269	intron (NM_001080467, intron 1 of 39)
chr18	48362911	48363035	Intergenic
chr18	52443054	52443178	Intergenic
chr18	55297431	55297555	promoter-TSS (NM_001242804)
chr18	55396625	55396749	intron (NM_005603, intron 2 of 27)
chr18	55438572	55438696	intron (NM_005603, intron 1 of 27)
chr18	60088161	60088285	Intergenic
chr18	60384685	60384809	intron (NM_194449, intron 1 of 16)
chr18	60666884	60667008	Intergenic
chr18	61646809	61646933	intron (NM_001031848, intron 2 of 6)
chr18	74813386	74813510	intron (NM_001025101, intron 2 of 8)

chr18	74826904	74827028	intron (NM_001025101, intron 1 of 8)
chr19	13278300	13278424	Intergenic
chr19	17428319	17428443	intron (NM_024050, intron 4 of 4)
chr19	17586487	17586611	intron (NM_198580, intron 1 of 11)
chr19	33543374	33543498	intron (NM_033103, intron 1 of 14)
chr19	33667751	33667875	Intergenic
chr19	38423101	38423225	intron (NM_015073, intron 1 of 21)
chr19	39888459	39888583	3' UTR (NM_017592, exon 4 of 4)
chr19	40450049	40450173	Intergenic
chr19	42696168	42696292	Intergenic
chr19	42954697	42954821	intron (NR_073179, intron 1 of 1)
chr19	44669045	44669169	promoter-TSS (NM_001146220)
chr19	44711471	44711595	Intergenic
chr19	45004528	45004652	promoter-TSS (NM_013256)
chr19	45245341	45245465	Intergenic
chr19	45681686	45681810	promoter-TSS (NM_001270893)
chr19	47288111	47288235	promoter-TSS (NM_001145145)
chr19	50693952	50694076	Intergenic
chr19	55727940	55728064	Intergenic
chr19	56165183	56165307	promoter-TSS (NM_007279)
chr19	57702810	57702934	promoter-TSS (NM_003417)
chr19	57791235	57791359	promoter-TSS (NM_006635)
chr20	6104082	6104206	promoter-TSS (NM_017671)
chr20	9310939	9311063	intron (NM_182797, intron 2 of 35)
chr20	30292565	30292689	intron (NM_001191, intron 2 of 2)
chr20	30300625	30300749	intron (NM_001191, intron 2 of 2)
chr20	30865345	30865469	promoter-TSS (NM_004798)
chr20	31053451	31053575	intron (NM_001256798, intron 5 of 10)
chr20	32254222	32254346	promoter-TSS (NM_001024675)
chr20	32321761	32321885	intron (NM_032819, intron 1 of 14)
chr20	32377556	32377680	intron (NM_032819, intron 14 of 14)
chr20	34674808	34674932	Intergenic
chr20	36007730	36007854	intron (NM_005417, intron 2 of 13)
chr20	36772654	36772778	intron (NM_198951, intron 6 of 9)
chr20	36796497	36796621	Intergenic
chr20	37063940	37064064	promoter-TSS (NR_015366)
chr20	37101243	37101367	promoter-TSS (NM_020336)
chr20	39632352	39632476	Intergenic
chr20	41234324	41234448	intron (NM_133170, intron 7 of 31)
chr20	43991496	43991620	promoter-TSS (NM_033542)
chr20	44486072	44486196	promoter-TSS (NM_005469)
chr20	44834846	44834970	intron (NM_021248, intron 7 of 11)
chr20	45259931	45260055	intron (NM_001011554, intron 2 of 13)
chr20	46203807	46203931	intron (NM_006534, intron 1 of 22)
chr20	48061833	48061957	intron (NM_004975, intron 1 of 1)

chr20	48307573	48307697	intron (NM_004776, intron 1 of 8)
chr20	48381728	48381852	Intergenic
chr20	48410350	48410474	Intergenic
chr20	48854021	48854145	Intergenic
chr20	49040008	49040132	Intergenic
chr20	49345672	49345796	Intergenic
chr20	49378116	49378240	Intergenic
chr20	49575278	49575402	promoter-TSS (NM_014484)
chr20	50361245	50361369	intron (NM_006045, intron 1 of 27)
chr20	50847057	50847181	Intergenic
chr20	50848126	50848250	Intergenic
chr20	52237980	52238104	Intergenic
chr20	52732434	52732558	Intergenic
chr20	52750078	52750202	Intergenic
chr20	56273324	56273448	intron (NM_199171, intron 1 of 3)
chr20	56592816	56592940	Intergenic
chr20	58345621	58345745	intron (NM_080672, intron 5 of 12)
chr20	58406129	58406253	intron (NM_080672, intron 8 of 12)
chr20	61002690	61002814	promoter-TSS (NM_080833)
chr20	61863836	61863960	Intergenic
chr20	62528209	62528333	intron (NM_025219, intron 1 of 4)
chr21	43894416	43894540	intron (NM_080860, intron 8 of 8)
chr22	21132032	21132156	intron (NM_000185, intron 1 of 4)
chr22	21235608	21235732	intron (NM_004782, intron 3 of 4)
chr22	21983652	21983776	intron (NM_001017964, intron 2 of 4)
chr22	22751611	22751735	Intergenic
chr22	24798603	24798727	intron (NM_001254732, intron 13 of 14)
chr22	25290692	25290816	intron (NM_001098497, intron 17 of 24)
chr22	27561134	27561258	Intergenic
chr22	30195309	30195433	intron (NM_032204, intron 15 of 19)
chr22	30391138	30391262	intron (NM_153050, intron 7 of 19)
chr22	32072918	32073042	Intergenic
chr22	36727605	36727729	intron (NM_002473, intron 3 of 40)
chr22	36806135	36806259	Intergenic
chr22	37988569	37988693	Intergenic
chr22	41399136	41399260	Intergenic
chr22	42418606	42418730	intron (NM_152613, intron 5 of 5)
chr22	43336369	43336493	intron (NM_001184970, intron 1 of 10)
chr22	46035237	46035361	Intergenic
chr22	46084700	46084824	intron (NM_001167621, intron 1 of 10)
chr22	46692548	46692672	promoter-TSS (NR_024009)
chr22	46786857	46786981	intron (NM_014246, intron 16 of 34)
chr22	49895902	49896026	Intergenic
chrX	20534468	20534592	Intergenic
chrX	21992138	21992262	intron (NM_004595, intron 4 of 10)

chrX	64754806	64754930	promoter-TSS (NM_031206)
chrX	69353707	69353831	5' UTR (NM_001551, exon 2 of 7)
chrX	70585688	70585812	promoter-TSS (NM_004606)
chrX	96415344	96415468	intron (NM_006729, intron 22 of 26)
chrX	134220604	134220728	Intergenic
chrX	136007435	136007559	Intergenic

Table S4. List of enriched gene pathways from DAVID gene ontology analysis on nearest genes to EHF ChIP-seq peaks.

Term	P Value	Genes
GO:0016323~basolateral plasma membrane	1.05E-04	ATP1B1, LPP, FERMT1, ITGB4, ACTN1, ITGA2, RHOU, ITGB1, PXN, TNS3, SDC1, LAMA3, CD44, PTK2B, ANK3, SLC2A2, P2RY1, ADAM9
GO:0070161~anchoring junction	1.69E-04	PARD3, LPP, FERMT1, ITGA2, ACTN1, MYH9, RHOU, ITGB1, PXN, TNS3, SDC1, LAMA3, CD44, PTK2B, PKP4, TJP2
GO:0005912~adherens junction	1.92E-04	PARD3, LPP, FERMT1, ITGA2, ACTN1, MYH9, RHOU, ITGB1, PXN, TNS3, SDC1, LAMA3, CD44, PTK2B, TJP2
GO:0007155~cell adhesion	1.96E-04	PPFIA2, PARD3, NRP1, EPDR1, CCR1, ITGB4, FERMT1, KITLG, COL28A1, EDIL3, SOX9, ITGB1, CD2AP, MEGF10, SRC, PXN, PCDHAC2, LAMB3, LGALS3BP, CD44, ROBO1, PTK2B, ITGAV, TGFBI, ADAM9, LPP, COL22A1, NLGN1, ACTN1, ITGA2, PCDH15, PTPRT, CHST4, MYH9, CLDN23, HES1, CD84, LAMA3, CDH18, PKP4, FCGBP
GO:0022610~biological adhesion	1.96E-04	PPFIA2, PARD3, NRP1, EPDR1, CCR1, ITGB4, FERMT1, KITLG, COL28A1, EDIL3, SOX9, ITGB1, CD2AP, MEGF10, SRC, PXN, PCDHAC2, LAMB3, LGALS3BP, CD44, ROBO1, PTK2B, ITGAV, TGFBI, ADAM9, LPP, COL22A1, NLGN1, ACTN1, ITGA2, PCDH15, PTPRT, CHST4, MYH9, CLDN23, HES1, CD84, LAMA3, CDH18, PKP4, FCGBP
GO:0005925~focal adhesion	2.00E-04	TNS3, SDC1, LAMA3, CD44, LPP, PTK2B, FERMT1, ITGA2, ACTN1, RHOU, ITGB1, PXN
GO:0005924~cell-substrate adherens junction	2.81E-04	TNS3, SDC1, LAMA3, CD44, LPP, PTK2B, FERMT1, ITGA2, ACTN1, RHOU, ITGB1, PXN
GO:0030055~cell-substrate junction	4.53E-04	TNS3, SDC1, LAMA3, CD44, LPP, PTK2B, FERMT1, ITGA2, ACTN1, RHOU, ITGB1, PXN
GO:0007160~cell-matrix adhesion	4.76E-04	PPFIA2, EPDR1, CD44, PTK2B, ITGAV, ITGB4, ITGA2, ACTN1, ITGB1, PXN, ADAM9
GO:0001568~blood vessel development	7.66E-04	NRP1, IL8, MYO1E, TIPARP, ELK3, MYH9, TCF7L2, SLIT2, ANXA2, DLX3, CXCL17, HIF1A, MYOCD, CD44, ROBO1, PTK2B, ITGAV, TGM2, MKL2
GO:0001944~vasculature development	0.001012849	NRP1, IL8, MYO1E, TIPARP, ELK3, MYH9, TCF7L2, SLIT2, ANXA2, DLX3,

		CXCL17, HIF1A, MYOCD, CD44, ROBO1, PTK2B, ITGAV, TGM2, MKL2
GO:0031589~cell-substrate adhesion	0.001020184	PPFIA2, EPDR1, CD44, PTK2B, ITGAV, ITGB4, ITGA2, ACTN1, ITGB1, PXN, ADAM9
GO:0030155~regulation of cell adhesion	0.001299169	KNG1, GTPBP4, IL8, ITGA2, SMAD3, EDIL3, SRC, LAMA3, TGFBI, TGM2, NRG1, PIK3R1, ADAM9
GO:0042995~cell projection	0.001384726	PARD3, NRP1, ADORA2A, FERMT1, TTLL6, RDX, ITGB1, CD2AP, RHOU, PXN, MBP, SPAG16, ROBO1, ANK3, ATXN10, PTK2B, SLC2A2, SYNJ2, FGD6, CLN3, MAP1B, FSCN1, SLC34A1, ACTN1, ITGA2, PCDH15, MYH9, SDC1, HIF1A, TXNDC2, RASGRF1, GRM7, MYH14, LIPC, ATP6V0A4, HTR2A
GO:0032403~protein complex binding	0.001823318	YWHAZ, BCKDHB, MAP1B, ACTN1, ITGA2, EDIL3, CD2AP, ITGB1, LAMB3, PTK2B, SLC2A2, TGFBI, PTPN1, PIK3R1, ADAM9, HTR2A
GO:0005794~Golgi apparatus	0.001899271	SLC9A8, GALNT7, LITAF, HS3ST1, RHOU, ST3GAL1, TRAPPC6A, SERINC5, CD44, ANK3, XYLT1, MCCC1, B3GNT6, B4GALNT3, PDGFD, RAB27B, RNF122, FGD6, B4GALT5, SYS1, MGAT4A, CLN3, SYNRG, SCAMP2, GOLT1A, CTLA4, GOLIM4, CHST4, FZD5, ERGIC1, GCC2, ERGIC2, ST6GALNAC1, SACM1L, PJA2, NCOA3, CHSY3, CXCL14, CHSY1, MAP6, TMCO1, COG2
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	0.001973595	NRP1, FIBP, ADORA2A, PTPN2, MYO1E, TIPARP, PTPRT, SRC, PXN, MUSK, EPHA6, EPS8, PTK2B, ROR1, PTPN1, NRG1, PIK3R1
GO:0044459~plasma membrane part	0.002724782	SLC27A1, ATP1B1, KCNC4, SLC15A2, FERMT1, RHOU, MBP, SLC1A5, KCNQ3, ATP2B4, CD44, ANK3, ROBO1, SLC2A2, IL1RAP, ATP8B1, SYNJ2, NRG1, ADAM9, RAP2B, CLN3, PTPRH, SLC34A1, TANC1, ACTN1, PIGR, CD40, MMP15, MYH9, HLA-E, PJA2, CD84, TNS3, NPC1, SDC1, GRM7, ROR1, HAS2, EFNA5, TM4SF1, SLC40A1, SERP1, SNAP29, SNX18, PARD3, LITAF, ADORA2A, STAM2, CCR1, ITGB4, DAG1, NOSTRIN, RDX, BCL2L1, ITGB1, PXN, PCDHAC2, SRC, MUSK, PTK2B, ITGAV, P2RY1, IFT140, MICALL2, PARD6B, PTPRD, TM2D1, LPP, KCNB1,

		NLGN1, CTLA4, ITGA2, FZD5, KCNK2, CLDN23, EPHA6, LAMA3, SLC17A3, EPS8, PKP4, RHEB, SLC13A3, PTPN1, ATP6V0A4, TJP2, COG2, HTR2A
GO:0007167~enzyme linked receptor protein signaling pathway	0.002792907	PTPRD, NRP1, LTBP2, FIBP, ADORA2A, PTPN2, MYO1E, TIPARP, SMAD3, PTPRT, PXN, SRC, MUSK, EPHA6, EPS8, PTK2B, ROR1, PTPN1, NRG1, PIK3R1, ADAM9, TOB1
GO:0022604~regulation of cell morphogenesis	0.002846393	NRP1, ROBO1, FYN, CDC42SE2, MAP1B, SMAD3, MYH14, MYH9, FGD6, RHOU, SLIT2, MBP
GO:0040012~regulation of locomotion	0.003062075	PARD6B, GTPBP4, IL8, ADORA2A, SMAD3, ITGA2, SLIT2, TRIB1, HIF1A, LAMA3, PTK2B, HDAC9, IGFBP3, PIK3R1, ADAM9
GO:0030030~cell projection organization	0.003085777	PARD6B, PARD3, NRP1, ADORA2A, MAP1B, ITGB4, RDX, MYH9, LPIN1, CD2AP, SLIT2, SPAG16, HOXA1, CD44, ROBO1, ANK3, RASGRF1, UNC5A, PTK2B, ATXN10, EFNA5, SIAH1, FGD6
GO:0051270~regulation of cell motion	0.003209554	PARD6B, GTPBP4, PARD3, NRP1, SMAD3, ITGA2, ACTN1, TRIB1, HIF1A, LAMA3, PTK2B, HDAC9, IGFBP3, PIK3R1, ADAM9
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.003444251	TAF1, GLIS3, HNF1B, CEBPB, EVX1, ARNT2, SMAD3, SOX6, MECOM, SOX9, TCF7L2, AHR, ZBTB38, GTF2H1, HES1, HOXA1, HIF1A, PAX9, MYOCD, BCL3, MKL2, ARHGEF10L, NFIB
GO:0043534~blood vessel endothelial cell migration	0.004236743	ROBO1, PTK2B, MYH9, SLIT2
GO:0016202~regulation of striated muscle tissue development	0.004633076	MUSK, MYOCD, SMAD3, MKL2, NRG1, HDAC9, IGFBP3
GO:0014069~postsynaptic density	0.00475887	PJA2, YWHAZ, EPS8, ADORA2A, PTK2B, MAP1B, TANC1, NLGN1
GO:0048634~regulation of muscle development	0.005114568	MUSK, MYOCD, SMAD3, MKL2, NRG1, HDAC9, IGFBP3
GO:0048514~blood vessel morphogenesis	0.007078888	NRP1, IL8, MYO1E, TIPARP, ELK3, MYH9, SLIT2, ANXA2, CXCL17, HIF1A, MYOCD, PTK2B, ROBO1, TGM2, MKL2
GO:0045893~positive regulation of transcription, DNA-dependent	0.009089526	GLIS3, HNF1B, EVX1, ARNT2, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0044463~cell projection part	0.009440116	PARD3, ADORA2A, SLC34A1, ITGA2, TTLL6, ITGB1, SPAG16, MBP, TXNDC2,

		ROBO1, SLC2A2, GRM7, SYNJ2, ATP6V0A4, HTR2A
GO:0008305~integrin complex	0.009782397	ITGAV, ITGB4, ITGA2, MYH9, ITGB1
GO:0006897~endocytosis	0.009861124	MICALL2, CLN3, SYNRG, ADORA2A, LRP1B, NOSTRIN, MEGF10, ELMO1, NPC1, LRP10, CDC42SE2, PACSIN2, ITGAV, LRP3, LRP5
GO:0010324~membrane invagination	0.009861124	MICALL2, CLN3, SYNRG, ADORA2A, LRP1B, NOSTRIN, MEGF10, ELMO1, NPC1, LRP10, CDC42SE2, PACSIN2, ITGAV, LRP3, LRP5
GO:0001701~in utero embryonic development	0.009862249	HNF1B, CEBPB, MYO1E, ARNT2, BCL2L1, CAPN2, MECOM, MYH9, ITGB1, HES1, PCGF2, HIF1A, MKL2
GO:0005089~Rho guanyl-nucleotide exchange factor activity	0.009972872	MCF2L2, PLEKHG3, RASGRF1, PLEKHG6, FGD6, SPATA13, ARHGEF10L, FARP2
GO:0051254~positive regulation of RNA metabolic process	0.010143422	GLIS3, HNF1B, EVX1, ARNT2, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0045785~positive regulation of cell adhesion	0.011231173	TGM2, SMAD3, ITGA2, EDIL3, NRG1, SRC, ADAM9
GO:0008219~cell death	0.011657382	PHLPP1, SPG7, LITAF, ADORA2A, EGLN3, BCL2L1, STK17A, SYCP2, CRADD, TOP1, TMEM173, ATXN10, PTK2B, UNC5A, TGM2, DEDD2, PHLDA1, CLN3, TM2D1, PTPRH, BIRC7, SMAD3, CD5L, GAN, AHR, ELMO1, VDAC1, SLTM, RNF130, RASGRF1, TNFAIP8, ERN2, SIAH1, SLC5A11, HTR2A
GO:0009100~glycoprotein metabolic process	0.011686764	MGAT4A, CLN3, GALNT7, DCN, PMM2, ST6GALNAC1, ST3GAL1, HIF1A, B3GNT6, LIPC, UGGT1, SERP1, COG2, PHLDA1
GO:0031253~cell projection membrane	0.011947783	ADORA2A, ROBO1, SLC2A2, SLC34A1, SYNJ2, ATP6V0A4, ITGB1
GO:0040017~positive regulation of locomotion	0.012082288	HIF1A, IL8, PTK2B, SMAD3, ITGA2, HDAC9, SLIT2, PIK3R1, ADAM9
GO:0016265~death	0.012656501	PHLPP1, SPG7, LITAF, ADORA2A, EGLN3, BCL2L1, STK17A, SYCP2, CRADD, TOP1, TMEM173, ATXN10, PTK2B, UNC5A, TGM2, DEDD2, PHLDA1, CLN3, TM2D1, PTPRH, BIRC7, SMAD3, CD5L, GAN, AHR, ELMO1, VDAC1, SLTM, RNF130,

		RASGRF1, TNFAIP8, ERN2, SIAH1, SLC5A11, HTR2A
GO:0007172~signal complex assembly	0.012794399	MUSK, PTK2B, SRC, PXN
GO:0035023~regulation of Rho protein signal transduction	0.012795437	MCF2L2, PLEKHG3, PTK2B, RASGRF1, PLEKHG6, FGD6, SPATA13, ARHGEF10L, FARP2
GO:0008092~cytoskeletal protein binding	0.01327088	ADORA2A, RDX, PXN, PACSIN2, PLS1, MKL2, KLHL20, PHACTR3, MYO1B, MYO1E, ENC1, FSCN1, MAP1B, ACTN1, PTPRT, MYH9, CAPN2, COTL1, ANXA2, JMY, FARP2, ARPC1B, SDC1, EPB41L1, FYN, MYH14, MAP6
GO:0051056~regulation of small GTPase mediated signal transduction	0.013825188	AGFG2, RALGAPB, SIPA1L3, ADAP1, FARP2, MCF2L2, PLEKHG3, PTK2B, RASGRF1, PLEKHG6, AGAP1, SPATA13, FGD6, ARHGEF10L, IQSEC1, RASA2
GO:0006796~phosphate metabolic process	0.015000023	HUS1, STK17A, SRC, TRIB1, SGK223, TOP1, MUSK, UQCR10, CLK3, PTK2B, EEF2K, SYNJ2, GK5, PRKACB, PIK3R1, AKT3, ADAM9, TAF1, PTPRD, TNIK, NCEH1, PTPN2, PHKG2, PTPRH, BIRC7, PRKCH, PTPRT, PTPN12, SACM1L, RPS6KA3, EPHA6, PLK2, SLC17A3, FYN, RPS6KA2, RSRC1, NDUFV2, ROR1, ERN2, PTPN1, IKBKB, ATP6V0A4, MAP3K13, IGFBP3
GO:0006793~phosphorus metabolic process	0.015000023	HUS1, STK17A, SRC, TRIB1, SGK223, TOP1, MUSK, UQCR10, CLK3, PTK2B, EEF2K, SYNJ2, GK5, PRKACB, PIK3R1, AKT3, ADAM9, TAF1, PTPRD, TNIK, NCEH1, PTPN2, PHKG2, PTPRH, BIRC7, PRKCH, PTPRT, PTPN12, SACM1L, RPS6KA3, EPHA6, PLK2, SLC17A3, FYN, RPS6KA2, RSRC1, NDUFV2, ROR1, ERN2, PTPN1, IKBKB, ATP6V0A4, MAP3K13, IGFBP3
GO:0006928~cell motion	0.015386213	NRP1, KITLG, CD2AP, ITGB1, SRC, HOXA1, CD44, PTK2B, UNC5A, ANK3, ROBO1, IL8, BARHL1, ITGA2, CHST4, MYH9, SLIT2, ELMO1, TNS3, ARPC1B, HIF1A, FYN, SIAH1, EFNA5, LRP5
GO:0031175~neuron projection development	0.015705291	PARD6B, PARD3, NRP1, ADORA2A, MAP1B, SLIT2, HOXA1, CD44, UNC5A, PTK2B, ATXN10, RASGRF1, ANK3, ROBO1, EFNA5, SIAH1
GO:0051153~regulation of striated muscle cell differentiation	0.01736305	MUSK, MYOCD, NRG1, HDAC9, IGFBP3
GO:0042060~wound healing	0.017889119	KNG1, ADORA2A, ITGA2, SMAD3,

		CD40, ELK3, SDC1, HIF1A, CD44, P2RY1, TFPI, SERPIND1, NRG1
GO:0030334~regulation of cell migration	0.018059128	PARD6B, GTPBP4, HIF1A, LAMA3, PTK2B, SMAD3, ITGA2, HDAC9, IGFBP3, PIK3R1, ADAM9, TRIB1
GO:0046982~protein heterodimerization activity	0.018300342	HNF1B, JDP2, CEBPB, ADORA2A, ARNT2, ITGA2, SOX6, BCL2L1, SYCP2, ITGB1, PDSS2, HIF1A, ROBO1, IKBKB
GO:0012501~programmed cell death	0.018464029	PHLPP1, LITAF, ADORA2A, EGLN3, BCL2L1, STK17A, SYCP2, CRADD, TOP1, TMEM173, PTK2B, UNC5A, TGM2, DEDD2, PHLDA1, TM2D1, PTPRH, BIRC7, SMAD3, CD5L, AHR, ELMO1, VDAC1, SLTM, RNF130, RASGRF1, TNFAIP8, ERN2, SIAH1, SLC5A11
GO:0015937~coenzyme A biosynthetic process	0.018705343	COASY, PANK3, PPCDC
GO:0060260~regulation of transcription initiation from RNA polymerase II promoter	0.018705343	ATF7IP, TAF1, AHR
GO:0030054~cell junction	0.018931343	SNAP29, PARD3, FERMT1, RHOU, ITGB1, PXN, CD44, PTK2B, IFT140, MICALL2, PARD6B, LPP, TANC1, NLGN1, ACTN1, ITGA2, MYH9, CLDN23, PJA2, TNS3, SDC1, LAMA3, PKP4, SLC13A3, TJP2
GO:0030424~axon	0.019133871	NRP1, ADORA2A, ROBO1, PTK2B, ANK3, GRM7, MAP1B, SYNJ2, ITGA2, MYH14, MBP
GO:0031226~intrinsic to plasma membrane	0.021107558	KCNC4, ATP1B1, SLC15A2, SLC1A5, ATP2B4, KCNQ3, CD44, ROBO1, SLC2A2, IL1RAP, ATP8B1, ADAM9, PTPRH, SLC34A1, MMP15, CD40, PIGR, MYH9, CD84, SDC1, NPC1, GRM7, ROR1, HAS2, EFNA5, TM4SF1, SLC40A1, PARD3, ADORA2A, CCR1, DAG1, ITGB4, ITGB1, PCDHAC2, MUSK, ITGAV, P2RY1, PTPRD, TM2D1, KCNB1, CTLA4, NLGN1, ITGA2, FZD5, KCNK2, EPHA6, EPS8, SLC17A3, HTR2A
GO:0000139~Golgi membrane	0.021720628	SYS1, ST3GAL1, CLN3, SYNRG, SCAMP2, CHSY3, B4GALNT3, CHST4, CHSY1, PDGFD, ST6GALNAC1, COG2
GO:0000904~cell morphogenesis involved in differentiation	0.022648664	PARD6B, PARD3, NRP1, MAP1B, MYH9, SOX9, SLIT2, HES1, HOXA1, HIF1A, UNC5A, ANK3, ROBO1, EFNA5, SIAH1

GO:0019904~protein domain specific binding	0.022894596	RAP2B, YWHAZ, USP8, LITAF, ESRRG, CD2AP, CRADD, SRC, PTPN12, ELMO1, SH3BP5, WBP2NL, GRM7, TFDP2, TGM2, SYNJ2, ETV6, PMEPA1, ADAM9
GO:0005088~Ras guanyl-nucleotide exchange factor activity	0.0240104	MCF2L2, PLEKHG3, RASGRF1, PLEKHG6, FGD6, SPATA13, ARHGEF10L, FARP2
GO:0016601~Rac protein signal transduction	0.024426122	RHOU, ELMO1, FARP2
GO:0001666~response to hypoxia	0.025807195	ATP1B1, HIF1A, PTK2B, ARNT2, PDE5A, EGLN3, SMAD3, ITGA2, BCL2L1, CAPN2
GO:0016192~vesicle-mediated transport	0.025860359	SNAP29, YWHAZ, ATL2, ADORA2A, MARCKSL1, NOSTRIN, MEGF10, SRC, TRAPPC6A, PACSIN2, ITGAV, MICALL2, CLN3, SYNRG, SCAMP2, GOLT1A, LRP1B, NLGN1, SCRN1, ERGIC1, ERGIC2, ELMO1, NPC1, LRP10, CDC42SE2, LRP3, COG2, LRP5
GO:0005085~guanyl-nucleotide exchange factor activity	0.026281666	MCF2L2, PLEKHG3, RASGRF1, PLEKHG6, FGD6, SPATA13, ARHGEF10L, IQSEC1, FARP2, EIF2B5, BCAR3
GO:0008360~regulation of cell shape	0.027044274	FYN, CDC42SE2, MYH14, MYH9, FGD6, RHOU
GO:0032580~Golgi cisterna membrane	0.027095995	CHSY3, B4GALNT3, CHSY1
GO:0009101~glycoprotein biosynthetic process	0.027888166	ST3GAL1, MGAT4A, GALNT7, B3GNT6, LIPC, UGGT1, PMM2, ST6GALNAC1, PHLDA1, COG2, SERP1
GO:0005518~collagen binding	0.028324249	CD44, SMAD3, ITGA2, DCN, ADAM9
GO:0016337~cell-cell adhesion	0.028637306	PARD3, NLGN1, PTPRT, PCDH15, MYH9, SOX9, CD2AP, ITGB1, CLDN23, SRC, PCDHAC2, CD84, CD44, ROBO1, CDH18, ADAM9
GO:0016477~cell migration	0.028637306	NRP1, IL8, BARHL1, KITLG, MYH9, CD2AP, ITGB1, SRC, SLIT2, TNS3, HIF1A, CD44, PTK2B, FYN, ROBO1, LRP5
GO:0010551~regulation of specific transcription from RNA polymerase II promoter	0.028717249	HES1, TAF1, EVX1, MYOCD, SMAD3, HDAC9, TCF7L2, ARHGEF10L
GO:0031256~leading edge membrane	0.028912335	ADORA2A, ROBO1, SYNJ2, ITGB1
GO:0032101~regulation of response to external stimulus	0.028960609	KNG1, CLN3, NPC1, UACA, IL8, ADORA2A, TGM2, SMAD3, ITGA2, SLIT2, ANXA2
GO:0043542~endothelial cell migration	0.030623979	ROBO1, PTK2B, MYH9, SLIT2
GO:0015936~coenzyme A metabolic	0.030759116	COASY, PANK3, PPCDC

process		
GO:0001822~kidney development	0.031726705	ODC1, HNF1B, SDC1, CD44, MYO1E, SALL1, TIPARP, SLIT2
GO:0045202~synapse	0.032131543	SNAP29, CLN3, YWHAZ, ADORA2A, MAP1B, TANC1, NLGN1, PCDH15, MYH9, ITGB1, PJA2, MUSK, EPS8, PTK2B, ANK3, GRM7, SIAH1, SLC40A1
GO:0010552~positive regulation of specific transcription from RNA polymerase II promoter	0.033198228	HES1, TAF1, MYOCD, SMAD3, TCF7L2, ARHGEF10L
GO:0051147~regulation of muscle cell differentiation	0.033477256	MUSK, MYOCD, NRG1, HDAC9, IGFBP3
GO:0046578~regulation of Ras protein signal transduction	0.03411645	AGFG2, FARP2, ADAP1, MCF2L2, PLEKHG3, PTK2B, RASGRF1, PLEKHG6, AGAP1, FGD6, SPATA13, IQSEC1, ARHGEF10L
GO:0070482~response to oxygen levels	0.034264191	ATP1B1, HIF1A, PTK2B, ARNT2, PDE5A, EGLN3, SMAD3, ITGA2, BCL2L1, CAPN2
GO:0045727~positive regulation of translation	0.034416965	PTK2B, BCL3, ITGA2, EIF2B5
GO:0043228~non-membrane-bounded organelle	0.034910923	KIFC1, HNF1B, HINT1, FERMT1, TTLL6, RPL22L1, CD2AP, RHOU, GTSE1, SPAG16, EBNA1BP2, TOP1, RBM4B, PCGF2, ANK3, SYNJ2, DDX21, DEDD2, KLHL20, OXR1, MRPL52, KRR1, GTPBP4, HIST1H1A, BARHL1, ENC1, TANC1, ACTN1, LAS1L, GAN, MYH9, HMGA2, ELMO1, FARP2, PJA2, TNS3, ARPC1B, RFC3, EPB41L1, WBP2NL, HIF1A, IGBP1, MRO, DYNLRB2, SERP1, YWHAZ, PARD3, LITAF, ADORA2A, DAG1, KITLG, NOSTRIN, RDX, ELK3, SOX9, SYCP2, RPA4, PXN, TFAM, DDX47, WDR55, PTK2B, PLEKHG6, ETV6, FGD6, PHLDA1, NMD3, MICALL2, RPS10P7, CENPN, TAF1, KIF3B, TRIP4, EPPK1, MYO1B, MYO1E, MAP1B, FSCN1, NLGN1, KY, PCDH15, COTL1, RPS6, VDAC1, UACA, EPS8, CDC42SE2, RPS6KA2, SLC13A3, MYH14, MAP6, NFIB
GO:0043232~intracellular non-membrane-bounded organelle	0.034910923	KIFC1, HNF1B, HINT1, FERMT1, TTLL6, RPL22L1, CD2AP, RHOU, GTSE1, SPAG16, EBNA1BP2, TOP1, RBM4B, PCGF2, ANK3, SYNJ2, DDX21, DEDD2, KLHL20, OXR1, MRPL52, KRR1, GTPBP4, HIST1H1A, BARHL1,

		ENC1, TANC1, ACTN1, LAS1L, GAN, MYH9, HMGA2, ELMO1, FARP2, PJA2, TNS3, ARPC1B, RFC3, EPB41L1, WBP2NL, HIF1A, IGBP1, MRO, DYNLRB2, SERP1, YWHAZ, PARD3, LITAF, ADORA2A, DAG1, KITLG, NOSTRIN, RDX, ELK3, SOX9, SYCP2, RPA4, PXN, TFAM, DDX47, WDR55, PTK2B, PLEKHG6, ETV6, FGD6, PHLDA1, NMD3, MICALL2, RPS10P7, CENPN, TAF1, KIF3B, TRIP4, EPPK1, MYO1B, MYO1E, MAP1B, FSCN1, NLGN1, KY, PCDH15, COTL1, RPS6, VDAC1, UACA, EPS8, CDC42SE2, RPS6KA2, SLC13A3, MYH14, MAP6, NFIB
GO:0042692~muscle cell differentiation	0.037332331	SDC1, MUSK, MKL2, SOX6, MYH9, NRG1, CAPN2, ITGB1, TCF7L2
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.038140134	GLIS3, HNF1B, EVX1, ADORA2A, ARNT2, KITLG, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, CD40, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0005886~plasma membrane	0.039892056	QRFPR, ATP1B1, KCNC4, MEGF10, CD2AP, ATP2B4, CD44, ANK3, UNC5A, ROBO1, SLC2A2, DNAJC5, ADAM9, PTPRH, SLC34A1, TANC1, ACTN1, PTPRT, CD40, HLA-E, MYH9, TNS3, NPC1, OR4E2, RASGRF1, ROR1, TFPI, EFNA5, HAS2, PSCA, SLC40A1, LITAF, ADORA2A, STAM2, DAG1, ITGB4, NOSTRIN, BCL2L1, ITGB1, PXN, SRC, PCDHAC2, ADAP1, MUSK, ITGAV, P2RY1, IFT140, ADAM28, PARD6B, TM2D1, LPP, KCNB1, FSCN1, OR4B1, SMAD3, ITGA2, PCDH15, KCNK2, VDAC1, EPHA6, LAMA3, EPS8, CDC42SE2, PKP4, RHEB, SLC13A3, PTPN1, SLC27A1, GPR84, NRP1, SLC15A2, MARCKSL1, FERMT1, CXCR1, RHOU, MBP, FCRL3, SLC1A5, TMEM173, KCNQ3, IL1RAP, ATP8B1, SYNJ2, NRG1, RAP2B, CLN3, PRKCH, PIGR, MMP15, SLIT2, ELMO1, CD84, PJA2, SDC1, EPB41L1, GRM7, TM4SF1, PMEPA1, SERP1, SNAP29, ALPL, SNX18, PARD3, CCR1, KITLG, RDX, PTK2B, TGM2, SUCNR1, MICALL2,

		PTPRD, MAP1B, NLGN1, CTLA4, OR9G4, FZD5, CAPN2, CLDN23, ANXA2, SLC17A3, GPR110, FYN, PLSCR2, CDH18, ATP6V0A4, TJP2, COG2, HTR2A
GO:0010557~positive regulation of macromolecule biosynthetic process	0.039909575	GLIS3, HNF1B, EVX1, ARNT2, KITLG, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, PTK2B, BCL3, MKL2, ARHGEF10L, EIF2B5, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, ITGA2, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0048666~neuron development	0.040151834	PARD6B, PARD3, NRP1, ADORA2A, MAP1B, SLIT2, FARP2, HES1, HOXA1, CD44, ROBO1, UNC5A, PTK2B, ATXN10, RASGRF1, ANK3, EFNA5, SIAH1
GO:0006915~apoptosis	0.041031558	PHLPP1, LITAF, ADORA2A, EGLN3, STK17A, BCL2L1, SYCP2, CRADD, TMEM173, PTK2B, UNC5A, DEDD2, PHLDA1, TM2D1, PTPRH, BIRC7, SMAD3, CD5L, AHR, ELMO1, VDAC1, SLTM, RNF130, RASGRF1, TNFAIP8, ERN2, SIAH1, SLC5A11
GO:0005178~integrin binding	0.041951636	TGFBI, ITGA2, ACTN1, EDIL3, ITGB1, ADAM9
GO:0030029~actin filament-based process	0.04199523	MYO1E, FSCN1, ACTN1, MYH9, RHOU, LPIN1, ITGB1, ELMO1, EPB41L1, EPS8, PTK2B, PACSIN2, MYH14, FGD6
GO:0048742~regulation of skeletal muscle fiber development	0.042693491	MUSK, MYOCD, HDAC9, IGFBP3
GO:0031328~positive regulation of cellular biosynthetic process	0.042752064	GLIS3, HNF1B, EVX1, ADORA2A, ARNT2, KITLG, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, PTK2B, BCL3, MKL2, ARHGEF10L, EIF2B5, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, ITGA2, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0001525~angiogenesis	0.044462342	CXCL17, NRP1, HIF1A, IL8, ROBO1, PTK2B, ELK3, MYH9, SLIT2, ANXA2
GO:0033865~nucleoside bisphosphate metabolic process	0.045087736	COASY, PANK3, PPCDC
GO:0048471~perinuclear region of cytoplasm	0.045111291	GTPBP4, UPF2, RHPN2, MAP1B, CTLA4, ITGA2, CD2AP, ANXA2, NPC1, UACA, WBP2NL, PTK2B, ATXN10, SYNJ2, RASA2
GO:0005795~Golgi stack	0.045643457	CLN3, CHSY3, B4GALNT3, CHSY1, COG2
GO:0005887~integral to plasma	0.046046247	KCNC4, ATP1B1, ADORA2A, SLC15A2,

membrane		CCR1, ITGB4, DAG1, ITGB1, PCDHAC2, SLC1A5, MUSK, ATP2B4, KCNQ3, CD44, ROBO1, SLC2A2, ITGAV, IL1RAP, P2RY1, ATP8B1, PTPRD, TM2D1, KCNB1, PTPRH, NLGN1, CTLA4, SLC34A1, ITGA2, PIGR, MMP15, CD40, MYH9, FZD5, KCNK2, CD84, SDC1, NPC1, EPHA6, EPS8, SLC17A3, GRM7, ROR1, HAS2, TM4SF1, SLC40A1, HTR2A
GO:0001726~ruffle	0.046955774	SYNJ2, RDX, MYH9, FGD6, CD2AP, ITGB1
GO:0009611~response to wounding	0.047273582	YWHAZ, NRP1, ADORA2A, CCR1, CXCR1, ELK3, CD44, P2RY1, IL1RAP, MGLL, NRG1, KNG1, CEBPB, IL8, MAP1B, ITGA2, SMAD3, CHST4, CD40, MECOM, SDC1, HIF1A, TFPI, SERPIND1, HDAC9
GO:0042981~regulation of apoptosis	0.048266166	YWHAZ, ADORA2A, ARNT2, BCL2L1, STK17A, SOX9, TCF7L2, SRC, CRADD, PECR, PCGF2, CD44, TGM2, BCL3, DNAJC5, NRG1, DEDD2, ADAM9, PHLDA1, KNG1, CLN3, CEBPB, TM2D1, BARHL1, BIRC7, SMAD3, ACTN1, RPS6, JMY, UACA, RASGRF1, TNFAIP8, ERN2, IKBKB, IGFBP3
GO:0070085~glycosylation	0.049265362	ST3GAL1, MGAT4A, GALNT7, B3GNT6, UGGT1, PMM2, ST6GALNAC1, COG2, SERP1
GO:0043413~biopolymer glycosylation	0.049265362	ST3GAL1, MGAT4A, GALNT7, B3GNT6, UGGT1, PMM2, ST6GALNAC1, COG2, SERP1
GO:0006486~protein amino acid glycosylation	0.049265362	ST3GAL1, MGAT4A, GALNT7, B3GNT6, UGGT1, PMM2, ST6GALNAC1, COG2, SERP1
GO:0009891~positive regulation of biosynthetic process	0.049890836	GLIS3, HNF1B, EVX1, ADORA2A, ARNT2, KITLG, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, PTK2B, BCL3, MKL2, ARHGEF10L, EIF2B5, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, ITGA2, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0031252~cell leading edge	0.051060225	ADORA2A, ROBO1, SYNJ2, RDX, MYH9, FGD6, CD2AP, ITGB1, PXN
GO:0005856~cytoskeleton	0.051141504	KIFC1, HINT1, FERMT1, TTLL6, CD2AP, RHOU, GTSE1, SPAG16, ANK3, SYNJ2, KLHL20, ENC1, TANC1, ACTN1, GAN, MYH9, FARP2, ELMO1, PJA2, ARPC1B, WBP2NL, EPB41L1, IGBP1,

		DYNLRB2, PARD3, YWHAZ, LITAF, ADORA2A, DAG1, KITLG, RDX, NOSTRIN, PXN, PTK2B, PLEKHG6, FGD6, MICALL2, KIF3B, EPPK1, MYO1B, MYO1E, FSCN1, MAP1B, NLGN1, KY, COTL1, UACA, EPS8, CDC42SE2, SLC13A3, MAP6, MYH14
GO:0007411~axon guidance	0.05204112	HOXA1, NRP1, ROBO1, UNC5A, ANK3, SIAH1, EFNA5, SLIT2
GO:0006357~regulation of transcription from RNA polymerase II promoter	0.052651637	GLIS3, HNF1B, JDP2, EVX1, LITAF, TFCP2L1, ARNT2, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, PCGF2, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ZHX2, SMAD3, TLE1, MECOM, AHR, GTF2H1, JMY, HES1, HIF1A, HDAC9, NFIB
GO:0051098~regulation of binding	0.052877936	GTPBP4, NCOA3, SMAD3, BCL3, ITGA2, NRG1, IKBKB, MAP3K13, TRIB1, JMY
GO:0000768~syncytium formation by plasma membrane fusion	0.053001653	CD44, MYH9, CAPN2
GO:0014910~regulation of smooth muscle cell migration	0.053001653	ITGA2, IGFBP3, TRIB1
GO:0051173~positive regulation of nitrogen compound metabolic process	0.05332575	GLIS3, HNF1B, EVX1, ADORA2A, ARNT2, KITLG, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, CD40, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0043067~regulation of programmed cell death	0.053392226	YWHAZ, ADORA2A, ARNT2, BCL2L1, STK17A, SOX9, TCF7L2, SRC, CRADD, PECR, PCGF2, CD44, TGM2, BCL3, DNAJC5, NRG1, DEDD2, ADAM9, PHLDA1, KNG1, CLN3, CEBPB, TM2D1, BARHL1, BIRC7, SMAD3, ACTN1, RPS6, JMY, UACA, RASGRF1, TNFAIP8, ERN2, IKBKB, IGFBP3
GO:0045941~positive regulation of transcription	0.054079698	GLIS3, HNF1B, EVX1, ARNT2, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0050840~extracellular matrix binding	0.055709714	TGFBI, ITGA2, DCN, ADAM9
GO:0043193~positive regulation of gene-specific transcription	0.056372739	HES1, TAF1, HIF1A, MYOCD, SMAD3, TCF7L2, ARHGEF10L
GO:0010941~regulation of cell death	0.056579738	YWHAZ, ADORA2A, ARNT2, BCL2L1,

		STK17A, SOX9, TCF7L2, SRC, CRADD, PECR, PCGF2, CD44, TGM2, BCL3, DNAJC5, NRG1, DEDD2, ADAM9, PHLDA1, KNG1, CLN3, CEBPB, TM2D1, BARHL1, BIRC7, SMAD3, ACTN1, RPS6, JMY, UACA, RASGRF1, TNFAIP8, ERN2, IKBKB, IGFBP3
GO:0035051~cardiac cell differentiation	0.056784904	MYOCD, SOX6, NRG1, ITGB1
GO:0016044~membrane organization	0.057060628	MICALL2, SNAP29, CLN3, SYNRG, ADORA2A, LRP1B, NOSTRIN, BCL2L1, MEGF10, ELMO1, NPC1, LRP10, CDC42SE2, PACSIN2, PLSCR2, ITGAV, LRP3, SERP1, LRP5
GO:0000902~cell morphogenesis	0.058483758	PARD6B, PARD3, NRP1, ADORA2A, TFCP2L1, MAP1B, SOX6, MYH9, SOX9, SLIT2, HES1, HOXA1, HIF1A, ROBO1, UNC5A, ANK3, EFNA5, SIAH1
GO:0001655~urogenital system development	0.058733501	ODC1, HNF1B, SDC1, CD44, MYO1E, SALL1, TIPARP, SLIT2
GO:0060284~regulation of cell development	0.059674315	HES1, MUSK, NRP1, MYOCD, ROBO1, MAP1B, NLGN1, SMAD3, HDAC9, IGFBP3, SLIT2, MBP
GO:0032583~regulation of gene-specific transcription	0.061270002	HES1, TAF1, HIF1A, EVX1, MYOCD, SMAD3, HDAC9, TCF7L2, ARHGEF10L
GO:0030335~positive regulation of cell migration	0.061639726	HIF1A, PTK2B, SMAD3, ITGA2, HDAC9, PIK3R1, ADAM9
GO:0046128~purine ribonucleoside metabolic process	0.061912605	COASY, PANK3, ADK, PPCDC
GO:0048641~regulation of skeletal muscle tissue development	0.061912605	MUSK, MYOCD, HDAC9, IGFBP3
GO:0050921~positive regulation of chemotaxis	0.061912605	IL8, SMAD3, ITGA2, SLIT2
GO:0042278~purine nucleoside metabolic process	0.061912605	COASY, PANK3, ADK, PPCDC
GO:0033341~regulation of collagen binding	0.061991104	GTPBP4, ITGA2
GO:0010694~positive regulation of alkaline phosphatase activity	0.061991104	SMAD3, ITGA2
GO:0051674~localization of cell	0.06205127	NRP1, IL8, BARHL1, KITLG, MYH9, CD2AP, ITGB1, SRC, SLIT2, TNS3, HIF1A, CD44, PTK2B, FYN, ROBO1, LRP5
GO:0048870~cell motility	0.06205127	NRP1, IL8, BARHL1, KITLG, MYH9, CD2AP, ITGB1, SRC, SLIT2, TNS3, HIF1A, CD44, PTK2B, FYN, ROBO1, LRP5
GO:0016791~phosphatase activity	0.062950309	PHLPP1, ALPL, PTPRD, PTPN2, PTPRH, ACP6, PTPRT, LPIN2, LPIN1, PTPN12,

		SACM1L, SYNJ2, INPP4B, PTPN1
GO:0006909~phagocytosis	0.063722471	ADORA2A, CDC42SE2, ITGAV, MEGF10, ELMO1
GO:0005083~small GTPase regulator activity	0.063829196	TNIK, AGFG2, ADAP1, ANXA2, FARP2, MCF2L2, PLEKHG3, RASGRF1, PLEKHG6, AGAP1, FGD6, SPATA13, ARHGEF10L, IQSEC1, RASA2
GO:0008284~positive regulation of cell proliferation	0.064393384	ODC1, NRP1, MARCKSL1, ARNT2, ITGA2, KITLG, BCL2L1, CD40, ITGB1, HES1, TNS3, TNFRSF11A, HIF1A, MYOCD, PTK2B, TGM2, NRG1, THPO, LRP5, HTR2A
GO:0003779~actin binding	0.066339463	PHACTR3, MYO1B, MYO1E, ENC1, FSCN1, MAP1B, ACTN1, RDX, MYH9, COTL1, JMY, ARPC1B, EPB41L1, PLS1, MYH14, MKL2, KLHL20
GO:0016831~carboxy-lyase activity	0.066409837	ODC1, BCKDHB, PISD, PPCDC
GO:0048667~cell morphogenesis involved in neuron differentiation	0.066540676	HES1, HOXA1, PARD6B, PARD3, NRP1, ROBO1, UNC5A, ANK3, MAP1B, SIAH1, EFNA5, SLIT2
GO:0007229~integrin-mediated signaling pathway	0.069330945	ITGAV, ITGB4, ITGA2, MYH9, ITGB1, ADAM9
GO:0006949~syncytium formation	0.07013938	CD44, MYH9, CAPN2
GO:0010628~positive regulation of gene expression	0.070811693	GLIS3, HNF1B, EVX1, ARNT2, SOX6, SOX9, TCF7L2, ZBTB38, HOXA1, MYOCD, PAX9, BCL3, MKL2, ARHGEF10L, ATF7IP, TAF1, CEBPB, ESRRG, SMAD3, MECOM, AHR, GTF2H1, HES1, HIF1A, NCOA3, NFIB
GO:0050920~regulation of chemotaxis	0.072784442	IL8, SMAD3, ITGA2, SLIT2
GO:0033267~axon part	0.073930472	ADORA2A, ROBO1, SYNJ2, ITGA2, MBP
GO:0048812~neuron projection morphogenesis	0.074198788	HOXA1, PARD6B, PARD3, NRP1, ADORA2A, ROBO1, UNC5A, ANK3, MAP1B, SIAH1, EFNA5, SLIT2
GO:0043524~negative regulation of neuron apoptosis	0.076162881	CLN3, ADORA2A, BARHL1, DNAJC5, BCL2L1
GO:0050878~regulation of body fluid levels	0.07741169	KNG1, ADORA2A, P2RY1, TFPI, ITGA2, SERPIND1, CD40, PDSS2, ANXA2
GO:0008376~acetylgalactosaminyltransferase activity	0.077970576	CHSY3, GALNT7, B4GALNT3, CHSY1
GO:0032989~cellular component morphogenesis	0.078378089	PARD6B, PARD3, NRP1, ADORA2A, TFCP2L1, MAP1B, SOX6, MYH9, SOX9, ITGB1, SLIT2, HES1, HOXA1, HIF1A, ROBO1, UNC5A, ANK3, EFNA5, SIAH1
GO:0044087~regulation of cellular component biogenesis	0.079907227	ATF7IP, TAF1, ARPC1B, MUSK, MAP1B, SMAD3, RDX, AHR, ARHGEF10L
GO:0060589~nucleoside-triphosphatase regulator activity	0.080215671	GRPEL2, TNIK, AGFG2, RALGAPB, SIPA1L3, ADAP1, ANXA2, FARP2,

		MCF2L2, PLEKHG3, RASGRF1, PLEKHG6, AGAP1, SPATA13, FGD6, ARHGEF10L, IQSEC1, EIF2B5, RASA2, BCAR3
GO:0030705~cytoskeleton-dependent intracellular transport	0.080561692	SPG7, KIF3B, MYO1E, MYH14, MYH9
GO:0005768~endosome	0.082280983	KIFC1, CLN3, SCAMP2, STARD3NL, CHMP4B, STAM2, GOLIM4, ANXA2, NPC1, SLC29A3, FYN, SLC2A2, SIAH1, ATP6V0A4, RAB11FIP1
GO:0042127~regulation of cell proliferation	0.082523728	NRP1, ADORA2A, MARCKSL1, ARNT2, EGLN3, KITLG, BCL2L1, SOX9, ITGB1, TRIB1, TNFRSF11A, MYOCD, PTK2B, TGM2, NRG1, THPO, ODC1, TP53I11, GTPBP4, IL8, CTLA4, SMAD3, ITGA2, CD40, MECOM, HES1, TNS3, HIF1A, IGFBP3, NFIB, HTR2A, LRP5, TOB1
GO:0009898~internal side of plasma membrane	0.083709455	RAP2B, SNX18, LITAF, STAM2, FERMT1, NOSTRIN, RDX, BCL2L1, RHOU, MBP, RHEB, PTPN1, TJP2, SERP1, COG2
GO:0014033~neural crest cell differentiation	0.084441479	HIF1A, KITLG, SOX9, NRG1
GO:0014032~neural crest cell development	0.084441479	HIF1A, KITLG, SOX9, NRG1
GO:0007409~axonogenesis	0.0845304	HOXA1, PARD6B, PARD3, NRP1, ROBO1, UNC5A, ANK3, MAP1B, SIAH1, EFNA5, SLIT2
GO:0005516~calmodulin binding	0.085358134	ATP2B4, MARCKSL1, MYO1B, MYO1E, PHKG2, EEF2K, MYH14, MAP6, MYH9
GO:0043065~positive regulation of apoptosis	0.086342837	KNG1, CEBPB, TM2D1, ADORA2A, SMAD3, BCL2L1, STK17A, RPS6, CRADD, SRC, JMY, UACA, CD44, RASGRF1, TGM2, ERN2, BCL3, IGFBP3, DEDD2, PHLDA1
GO:0031532~actin cytoskeleton reorganization	0.088792903	EPS8, MYH9, LPIN1
GO:0051272~positive regulation of cell motion	0.088818772	HIF1A, PTK2B, SMAD3, ITGA2, HDAC9, PIK3R1, ADAM9
GO:0043068~positive regulation of programmed cell death	0.088838772	KNG1, CEBPB, TM2D1, ADORA2A, SMAD3, BCL2L1, STK17A, RPS6, CRADD, SRC, JMY, UACA, CD44, RASGRF1, TGM2, ERN2, BCL3, IGFBP3, DEDD2, PHLDA1
GO:0048520~positive regulation of behavior	0.090549788	IL8, SMAD3, ITGA2, SLIT2
GO:0042113~B cell activation	0.091225377	IGBP1, BCL3, CD40, HDAC9, ITGB1, PIK3R1
GO:0046856~phosphoinositide	0.091533599	SYNJ2, SACM1L

dephosphorylation		
GO:0010692~regulation of alkaline phosphatase activity	0.091533599	SMAD3, ITGA2
GO:0010507~negative regulation of autophagy	0.091533599	CLN3, NPC1
GO:0016075~rRNA catabolic process	0.091533599	ERN2, DEDD2
GO:0016242~negative regulation of macroautophagy	0.091533599	CLN3, NPC1
GO:0017124~SH3 domain binding	0.091587468	SH3BP5, USP8, SYNJ2, CD2AP, PTPN12, ADAM9, ELMO1
GO:0005667~transcription factor complex	0.091691545	ATF7IP, TAF1, HNF1B, HIF1A, ARNT2, TFDP2, SMAD3, TLE1, HDAC9, TCF7L2, GTF2H1
GO:0051015~actin filament binding	0.092357835	FSCN1, PLS1, ACTN1, MYH14, MYH9
GO:0015662~ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	0.092357835	ATP1B1, ATP2B4, ATP9A, ATP8B1, ATP6V0A4
GO:0043066~negative regulation of apoptosis	0.093827079	CLN3, YWHAZ, CEBPB, ADORA2A, BARHL1, ARNT2, BIRC7, SMAD3, BCL2L1, TCF7L2, PCGF2, TNFAIP8, TGM2, BCL3, DNAJC5, IKBKB, NRG1
GO:0010942~positive regulation of cell death	0.09395039	KNG1, CEBPB, TM2D1, ADORA2A, SMAD3, BCL2L1, STK17A, RPS6, CRADD, SRC, JMY, UACA, CD44, RASGRF1, TGM2, ERN2, BCL3, IGFBP3, DEDD2, PHLDA1
GO:0044431~Golgi apparatus part	0.094335965	SYS1, CLN3, SYNRG, SCAMP2, HS3ST1, GOLIM4, CHST4, ST6GALNAC1, ST3GAL1, CHSY3, B4GALNT3, CHSY1, PDGFD, COG2
GO:0010769~regulation of cell morphogenesis involved in differentiation	0.095184406	NRP1, ROBO1, MAP1B, SMAD3, SLIT2, MBP
GO:0009890~negative regulation of biosynthetic process	0.095502872	GLIS3, JDP2, TFCP2L1, HUS1, NOSTRIN, ELK3, IGF2BP3, SOX6, SOX9, PCGF2, ITGAV, ATP8B1, BCL3, NRG1, DEDD2, EIF2B5, ATF7IP, GTPBP4, ZHX2, SMAD3, TLE1, HES1, GRM7, ERN2, HDAC9
GO:0016310~phosphorylation	0.096006787	HUS1, STK17A, SRC, TRIB1, TOP1, SGK223, MUSK, UQCR10, CLK3, PTK2B, EEF2K, PRKACB, AKT3, PIK3R1, ADAM9, TAF1, TNIK, PHKG2, BIRC7, PRKCH, RPS6KA3, EPHA6, PLK2, FYN, RPS6KA2, RSRC1, NDUFV2, ROR1, ERN2, ATP6V0A4, IKBKB, MAP3K13, IGFBP3
GO:0009260~ribonucleotide biosynthetic process	0.09669166	ATP1B1, ATP2B4, ATP9A, ADK, ATP8B1, PRPS1L1, ATP6V0A4, CMPK1

GO:0010558~negative regulation of macromolecule biosynthetic process	0.098025328	ATF7IP, GLIS3, GTPBP4, JDP2, TFCP2L1, HUS1, ZHX2, SMAD3, TLE1, NOSTRIN, ELK3, SOX6, IGF2BP3, SOX9, HES1, PCGF2, ITGAV, ATP8B1, ERN2, BCL3, HDAC9, NRG1, DEDD2, EIF2B5
GO:0021700~developmental maturation	0.099124803	HES1, CD44, PTK2B, TFCP2L1, MAP1B, FZD5, FARP2
GO:0030182~neuron differentiation	0.099229699	PARD6B, PARD3, NRP1, CEBPB, EVX1, ADORA2A, MAP1B, SLIT2, FARP2, HES1, HOXA1, CD44, ROBO1, ANK3, UNC5A, PTK2B, ATXN10, RASGRF1, EFNA5, SIAH1

Table S5. List of transcripts differentially expressed by at least 1.5-fold in siRNA mediated EHF knockdown versus negative control Calu-3 cells.

Gene ID	Gene Name	FPKM		Log2 (fold change)	Fold Change	P value
		Negative Control siRNA	EHF siRNA			
ENSG00000237550	RPL9P9	16.7	0.0	NA	0.0	0.0043
ENSG00000230937	MIR205HG	47.4	0.1	8.3	0.0	0.00065
ENSG00000230903	RPL9P8	19.4	0.1	7.4	0.0	0.00335
ENSG00000121552	CSTA	5.6	0.3	4.1	0.1	0.0013
ENSG00000186081	KRT5	37.3	2.8	3.8	0.1	5.00E-05
ENSG00000205420	KRT6A	17.2	1.3	3.7	0.1	5.00E-05
ENSG00000143546	S100A8	7.6	0.9	3.2	0.1	5.00E-05
ENSG00000065618	COL17A1	1.8	0.2	3.0	0.1	5.00E-05
ENSG00000170477	KRT4	2.5	0.4	2.8	0.1	5.00E-05
ENSG00000131746	TNS4	0.5	0.1	2.6	0.2	5.00E-05
ENSG00000163220	S100A9	13.1	2.2	2.6	0.2	5.00E-05
ENSG00000168878	SFTPB	0.7	0.1	2.6	0.2	0.0001
ENSG00000185303	SFTPA2	0.5	0.1	2.4	0.2	5.00E-05
ENSG00000189001	SBSN	0.6	0.1	2.4	0.2	0.00025
ENSG00000169469	SPRR1B	8.9	1.9	2.2	0.2	5.00E-05
ENSG00000138294	MSMB	4.6	1.2	1.9	0.3	5.00E-05
ENSG00000149021	SCGB1A1	6.5	1.8	1.8	0.3	5.00E-05
ENSG00000081277	PKP1	0.6	0.2	1.8	0.3	5.00E-05
ENSG00000168484	SFTPC	0.7	0.2	1.7	0.3	0.0015
ENSG00000108602	ALDH3A1	2.3	0.7	1.7	0.3	5.00E-05
ENSG00000088726	TMEM40	0.7	0.2	1.6	0.3	0.00085
ENSG00000176884	GRIN1	0.5	0.2	1.5	0.3	0.00185
ENSG00000132386	SERPINF1	1.5	0.5	1.5	0.4	5.00E-05
ENSG00000169474	SPRR1A	4.5	1.6	1.5	0.4	5.00E-05
ENSG00000227217	RP11-367J7.3	1.4	0.5	1.5	0.4	0.0026
ENSG00000140519	RHCG	1.0	0.4	1.4	0.4	5.00E-05
ENSG00000264462	MIR3648	1438.2	544.3	1.4	0.4	5.00E-05
ENSG00000156869	FRRS1	3.5	1.3	1.4	0.4	5.00E-05
ENSG00000135373	EHF	11.9	4.8	1.3	0.4	5.00E-05
ENSG00000247844	CCAT1	2.6	1.2	1.2	0.5	5.00E-05
ENSG00000187994	RINL	1.2	0.6	1.1	0.5	0.00035
ENSG00000169752	NRG4	1.4	0.7	1.1	0.5	0.00045
ENSG00000231298	LINC00704	2.4	1.1	1.1	0.5	5.00E-05
ENSG00000198643	FAM3D	0.9	0.4	1.0	0.5	0.00245
ENSG00000124664	SPDEF	7.4	3.6	1.0	0.5	5.00E-05
ENSG00000171033	PKIA	1.5	0.7	1.0	0.5	0.0001
ENSG00000198855	FICD	7.0	3.5	1.0	0.5	0.0005

ENSG00000140199	SLC12A6	0.6	0.3	1.0	0.5	0.00065
ENSG00000180535	BHLHA15	2.3	1.2	1.0	0.5	0.0007
ENSG00000147689	FAM83A	0.8	0.4	1.0	0.5	0.00135
ENSG00000139117	CPNE8	3.4	1.7	1.0	0.5	5.00E-05
ENSG00000250606	PRSS3P2	1.7	0.9	1.0	0.5	0.00125
ENSG00000171928	TVP23B	10.0	5.1	1.0	0.5	5.00E-05
ENSG00000196611	MMP1	1.9	1.0	1.0	0.5	5.00E-05
ENSG00000196754	S100A2	57.9	30.3	0.9	0.5	5.00E-05
ENSG00000186847	KRT14	25.2	13.3	0.9	0.5	5.00E-05
ENSG00000124762	CDKN1A	53.5	28.5	0.9	0.5	5.00E-05
ENSG00000169359	SLC33A1	22.7	12.1	0.9	0.5	5.00E-05
ENSG00000163904	SENP2	15.1	8.1	0.9	0.5	5.00E-05
ENSG00000183723	CMTM4	22.4	12.1	0.9	0.5	5.00E-05
ENSG00000125999	BPIFB1	2.5	1.4	0.9	0.6	5.00E-05
ENSG00000166128	RAB8B	2.2	1.2	0.8	0.6	5.00E-05
ENSG00000004961	HCCS	36.3	20.4	0.8	0.6	5.00E-05
ENSG00000188505	NCCRP1	1.6	0.9	0.8	0.6	0.00045
ENSG00000260912	RP11-363E7.4	3.7	2.1	0.8	0.6	5.00E-05
ENSG00000086619	ERO1LB	2.8	1.6	0.8	0.6	5.00E-05
ENSG00000047634	SCML1	4.1	2.4	0.8	0.6	5.00E-05
ENSG00000143398	PIP5K1A	12.0	6.9	0.8	0.6	5.00E-05
ENSG00000117461	PIK3R3	3.9	2.2	0.8	0.6	0.00405
ENSG00000033867	SLC4A7	3.0	1.7	0.8	0.6	5.00E-05
ENSG00000116161	CACYBP	183.1	106.3	0.8	0.6	5.00E-05
ENSG00000068793	CYFIP1	15.0	8.8	0.8	0.6	0.00035
ENSG00000269378	ITGB1P1	22.2	13.2	0.8	0.6	5.00E-05
ENSG00000149212	SESN3	0.9	0.6	0.8	0.6	0.0005
ENSG00000142583	SLC2A5	1.7	1.0	0.8	0.6	0.00155
ENSG00000187800	PEAR1	0.9	0.6	0.8	0.6	0.00065
ENSG00000267473	AC005789.11	1.2	0.7	0.7	0.6	0.00325
ENSG00000176697	BDNF	3.3	2.0	0.7	0.6	5.00E-05
ENSG00000165023	DIRAS2	0.7	0.4	0.7	0.6	0.00065
ENSG00000169184	MN1	1.0	0.6	0.7	0.6	0.00115
ENSG00000134755	DSC2	6.0	3.6	0.7	0.6	5.00E-05
ENSG00000150961	SEC24D	8.1	4.9	0.7	0.6	5.00E-05
ENSG00000132541	HRSP12	27.6	16.8	0.7	0.6	5.00E-05
ENSG00000064787	BCAS1	5.9	3.6	0.7	0.6	5.00E-05
ENSG00000186832	KRT16	36.1	22.1	0.7	0.6	5.00E-05
ENSG00000018610	CXorf56	12.2	7.5	0.7	0.6	5.00E-05
ENSG00000100934	SEC23A	5.9	3.7	0.7	0.6	5.00E-05
ENSG00000180730	SHISA2	1.2	0.7	0.7	0.6	0.00085

ENSG00000196950	SLC39A10	8.0	5.0	0.7	0.6	5.00E-05
ENSG00000139973	SYT16	0.7	0.4	0.7	0.6	0.004
ENSG00000110422	HIPK3	3.6	2.2	0.7	0.6	5.00E-05
ENSG00000213654	GPSM3	3.8	2.4	0.7	0.6	0.0007
ENSG00000164171	ITGA2	15.3	9.6	0.7	0.6	5.00E-05
ENSG00000140835	CHST4	3.6	2.3	0.7	0.6	0.0017
ENSG00000122861	PLAU	634.7	400.2	0.7	0.6	5.00E-05
ENSG00000106351	AGFG2	35.7	22.6	0.7	0.6	5.00E-05
ENSG00000164300	SERINC5	1.5	1.0	0.7	0.6	0.0043
ENSG00000144908	ALDH1L1	5.2	3.3	0.7	0.6	5.00E-05
ENSG00000109321	AREG	45.2	28.8	0.7	0.6	5.00E-05
ENSG00000204983	PRSS1	9.5	6.0	0.7	0.6	5.00E-05
ENSG00000163735	CXCL5	207.3	132.3	0.6	0.6	5.00E-05
ENSG00000114353	GNAI2	77.3	49.5	0.6	0.6	5.00E-05
ENSG00000106541	AGR2	243.2	156.1	0.6	0.6	5.00E-05
ENSG00000165272	AQP3	5.6	3.6	0.6	0.6	5.00E-05
ENSG00000167130	DOLPP1	12.5	8.0	0.6	0.6	5.00E-05
ENSG00000166575	TMEM135	3.6	2.3	0.6	0.6	0.00105
ENSG00000115520	COQ10B	11.6	7.5	0.6	0.6	5.00E-05
ENSG00000165997	ARL5B	3.8	2.5	0.6	0.6	5.00E-05
ENSG00000137094	DNAJB5	3.7	2.4	0.6	0.7	5.00E-05
ENSG00000148082	SHC3	6.0	3.9	0.6	0.7	0.0006
ENSG00000151117	TMEM86A	6.6	4.3	0.6	0.7	5.00E-05
ENSG00000115339	GALNT3	27.1	17.8	0.6	0.7	5.00E-05
ENSG00000173227	SYT12	1.1	0.7	0.6	0.7	0.00355
ENSG00000102359	SRPX2	9.3	6.1	0.6	0.7	5.00E-05
ENSG00000175040	CHST2	0.9	0.6	0.6	0.7	0.00375
ENSG00000137699	TRIM29	2.9	2.0	0.6	0.7	0.0017
ENSG00000127955	GNAI1	3.9	2.6	0.6	0.7	0.00105
ENSG00000138623	SEMA7A	64.8	43.2	0.6	0.7	5.00E-05
ENSG00000139496	NUPL1	5.1	3.4	0.6	0.7	5.00E-05
ENSG00000105656	ELL	3.0	2.0	0.6	0.7	0.0001
ENSG00000134668	SPOCD1	2.5	1.6	0.6	0.7	0.0005
ENSG00000019186	CYP24A1	112.1	74.9	0.6	0.7	0.00015
ENSG00000144959	NCEH1	34.0	22.8	0.6	0.7	5.00E-05
ENSG00000124875	CXCL6	13.1	8.8	0.6	0.7	5.00E-05
ENSG00000221926	TRIM16	22.1	14.9	0.6	0.7	5.00E-05
ENSG00000170412	GPRC5C	23.0	15.5	0.6	0.7	5.00E-05
ENSG00000113742	CPEB4	3.2	2.1	0.6	0.7	0.00015
ENSG00000203666	EFCAB2	5.6	3.7	0.6	0.7	0.00195
ENSG00000198833	UBE2J1	8.6	5.8	0.6	0.7	5.00E-05

ENSG00000074416	MGLL	21.1	14.3	0.6	0.7	5.00E-05
ENSG00000163605	PPP4R2	10.2	6.9	0.6	0.7	5.00E-05
ENSG00000100479	POLE2	7.4	11.2	-0.6	1.5	0.0016
ENSG00000196533	C1orf186	17.6	26.6	-0.6	1.5	5.00E-05
ENSG00000111331	OAS3	4.2	6.4	-0.6	1.5	0.00325
ENSG00000160446	ZDHHC12	55.1	83.7	-0.6	1.5	5.00E-05
ENSG00000132031	MATN3	2.4	3.6	-0.6	1.5	5.00E-05
ENSG00000143549	TPM3	138.6	210.7	-0.6	1.5	5.00E-05
ENSG00000170745	KCNS3	1.2	1.8	-0.6	1.5	0.00165
ENSG00000161243	FBXO27	19.0	29.0	-0.6	1.5	5.00E-05
ENSG00000137959	IFI44L	1.6	2.5	-0.6	1.5	0.0037
ENSG00000138750	NUP54	9.0	13.8	-0.6	1.5	5.00E-05
ENSG00000072401	UBE2D1	9.7	14.9	-0.6	1.5	5.00E-05
ENSG00000163739	CXCL1	67.2	102.9	-0.6	1.5	5.00E-05
ENSG00000134574	DDB2	10.3	15.9	-0.6	1.5	5.00E-05
ENSG00000159166	LAD1	90.4	138.8	-0.6	1.5	5.00E-05
ENSG00000103355	PRSS33	4.7	7.3	-0.6	1.5	5.00E-05
ENSG00000119946	CNNM1	0.5	0.8	-0.6	1.5	0.00165
ENSG00000118507	AKAP7	1.1	1.7	-0.6	1.5	0.0032
ENSG00000023445	BIRC3	4.9	7.6	-0.6	1.5	5.00E-05
ENSG00000143147	GPR161	1.3	2.0	-0.6	1.5	0.00015
ENSG00000135314	KHDC1	3.0	4.6	-0.6	1.5	0.0014
ENSG00000269215	AC008964.1	6.4	9.9	-0.6	1.5	5.00E-05
ENSG00000106366	SERPINE1	1.0	1.6	-0.6	1.6	0.0004
ENSG00000065320	NTN1	0.6	0.9	-0.6	1.6	0.00035
ENSG00000196715	VKORC1L1	6.0	9.4	-0.6	1.6	5.00E-05
ENSG00000140511	HAPLN3	3.7	5.7	-0.6	1.6	5.00E-05
ENSG00000040608	RTN4R	7.8	12.2	-0.6	1.6	5.00E-05
ENSG00000244509	APOBEC3C	10.1	15.7	-0.6	1.6	5.00E-05
ENSG00000137767	SQRDL	17.8	27.8	-0.6	1.6	5.00E-05
ENSG00000107566	ERLIN1	4.9	7.6	-0.6	1.6	5.00E-05
ENSG00000163993	S100P	441.4	695.2	-0.7	1.6	5.00E-05
ENSG00000135378	PRRG4	3.1	4.8	-0.7	1.6	5.00E-05
ENSG00000008282	SYPL1	31.0	48.9	-0.7	1.6	5.00E-05
ENSG00000160862	AZGP1	8.3	13.1	-0.7	1.6	5.00E-05
ENSG00000138061	CYP1B1	1.1	1.7	-0.7	1.6	0.0002
ENSG00000089157	RPLP0	2305.7	3668.2	-0.7	1.6	0.00135
ENSG00000134323	MYCN	3.4	5.4	-0.7	1.6	5.00E-05
ENSG00000160223	ICOSLG	0.6	1.0	-0.7	1.6	0.0017
ENSG00000203817	FAM72C	1.5	2.4	-0.7	1.6	0.00335
ENSG00000204516	MICB	20.9	33.6	-0.7	1.6	5.00E-05

ENSG00000132563	REEP2	1.8	2.9	-0.7	1.6	0.0001
ENSG00000197632	SERPINB2	8.8	14.3	-0.7	1.6	5.00E-05
ENSG00000165905	GYLTL1B	14.1	22.7	-0.7	1.6	0.0029
ENSG00000178980	SEPW1	203.4	330.1	-0.7	1.6	5.00E-05
ENSG00000134762	DSC3	0.5	0.8	-0.7	1.6	0.0002
ENSG00000153012	LGI2	0.4	0.6	-0.7	1.6	0.0011
ENSG00000157240	FZD1	0.9	1.5	-0.7	1.6	5.00E-05
ENSG00000146281	PM20D2	2.7	4.4	-0.7	1.6	5.00E-05
ENSG00000184979	USP18	3.0	4.9	-0.7	1.6	5.00E-05
ENSG00000157601	MX1	8.2	13.6	-0.7	1.6	5.00E-05
ENSG00000105717	PBX4	3.1	5.1	-0.7	1.7	0.00035
ENSG00000176153	GPX2	62.1	102.9	-0.7	1.7	0.00025
ENSG00000229119	CTB-63M22.1	233.9	388.2	-0.7	1.7	5.00E-05
ENSG00000177706	FAM20C	7.7	12.7	-0.7	1.7	5.00E-05
ENSG00000012124	CD22	0.4	0.6	-0.7	1.7	0.0012
ENSG00000159231	CBR3	1.8	3.0	-0.7	1.7	0.0018
ENSG00000213886	UBD	11.4	18.9	-0.7	1.7	5.00E-05
ENSG00000150556	LYPD6B	2.4	4.0	-0.7	1.7	0.0001
ENSG00000127528	KLF2	5.4	9.1	-0.7	1.7	5.00E-05
ENSG00000236824	BCYRN1	0.5	0.8	-0.7	1.7	5.00E-05
ENSG00000101489	CELF4	1.7	2.9	-0.7	1.7	0.0002
ENSG00000060138	YBX3	148.5	249.1	-0.7	1.7	5.00E-05
ENSG00000153310	FAM49B	45.4	76.3	-0.7	1.7	5.00E-05
ENSG00000182934	SRPR	15.7	26.7	-0.8	1.7	5.00E-05
ENSG00000065268	WDR18	41.9	71.3	-0.8	1.7	5.00E-05
ENSG00000163009	C2orf48	0.9	1.5	-0.8	1.7	0.001
ENSG00000168350	DEGS2	1.4	2.3	-0.8	1.7	0.00445
ENSG00000131094	C1QL1	1.3	2.2	-0.8	1.7	0.0009
ENSG00000101096	NFATC2	0.7	1.3	-0.8	1.7	5.00E-05
ENSG00000138614	VWA9	9.7	16.7	-0.8	1.7	5.00E-05
ENSG00000255198	SNHG9	19.0	32.7	-0.8	1.7	5.00E-05
ENSG00000148400	NOTCH1	0.8	1.3	-0.8	1.7	0.0001
ENSG00000128408	RIBC2	1.1	2.0	-0.8	1.7	0.0032
ENSG00000105559	PLEKHA4	12.5	21.6	-0.8	1.7	5.00E-05
ENSG00000162444	RBP7	3.0	5.2	-0.8	1.7	0.00055
ENSG00000183876	ARSI	0.5	0.9	-0.8	1.7	0.0024
ENSG00000117318	ID3	18.6	32.2	-0.8	1.7	5.00E-05
ENSG00000197587	DMBX1	1.2	2.1	-0.8	1.7	5.00E-05
ENSG00000168453	HR	6.6	11.5	-0.8	1.7	5.00E-05
ENSG00000171564	FGB	1.5	2.7	-0.8	1.8	5.00E-05
ENSG00000181617	FDCSP	342.0	599.0	-0.8	1.8	5.00E-05

ENSG00000007968	E2F2	0.6	1.1	-0.8	1.8	5.00E-05
ENSG00000169862	CTNND2	1.0	1.7	-0.8	1.8	5.00E-05
ENSG00000152076	CCDC74B	1.0	1.8	-0.8	1.8	0.001
ENSG00000182240	BACE2	13.9	24.5	-0.8	1.8	5.00E-05
ENSG00000122691	TWIST1	1.1	1.9	-0.8	1.8	0.0025
ENSG00000134827	TCN1	26.7	47.5	-0.8	1.8	5.00E-05
ENSG00000166682	TMPRSS5	1.1	2.0	-0.8	1.8	5.00E-05
ENSG00000100867	DHRS2	1.2	2.2	-0.8	1.8	5.00E-05
ENSG00000106211	HSPB1	238.0	429.2	-0.9	1.8	5.00E-05
ENSG00000122641	INHBA	2.1	3.8	-0.9	1.8	5.00E-05
ENSG00000132530	XAF1	0.5	0.9	-0.9	1.8	0.00305
ENSG00000111199	TRPV4	2.4	4.3	-0.9	1.8	5.00E-05
ENSG00000140044	JDP2	8.5	15.5	-0.9	1.8	5.00E-05
ENSG00000230453	ANKRD18B	8.4	15.3	-0.9	1.8	5.00E-05
ENSG00000104067	TJP1	6.3	11.6	-0.9	1.8	0.00035
ENSG00000272010	CTD-3025N20.3	1.3	2.5	-0.9	1.8	0.0038
ENSG00000171119	NRTN	4.0	7.4	-0.9	1.8	5.00E-05
ENSG00000164362	TERT	0.4	0.7	-0.9	1.9	0.00425
ENSG00000185621	LMLN	0.8	1.4	-0.9	1.9	0.00135
ENSG00000268313	AC119673.1	34.2	63.6	-0.9	1.9	5.00E-05
ENSG00000153993	SEMA3D	0.3	0.6	-0.9	1.9	0.00025
ENSG00000153904	DDAH1	19.1	35.9	-0.9	1.9	5.00E-05
ENSG00000138101	DTNB	11.3	21.4	-0.9	1.9	5.00E-05
ENSG00000187193	MT1X	27.5	52.5	-0.9	1.9	5.00E-05
ENSG00000122694	GLIPR2	0.4	0.8	-0.9	1.9	0.0014
ENSG00000121207	LRAT	2.5	4.8	-0.9	1.9	5.00E-05
ENSG00000260923	AC137934.1	6.8	13.0	-0.9	1.9	0.0015
ENSG00000224940	PRRT4	1.0	2.0	-1.0	2.0	5.00E-05
ENSG00000156113	KCNMA1	0.6	1.2	-1.0	2.0	0.003
ENSG00000111335	OAS2	1.3	2.7	-1.0	2.0	0.004
ENSG00000005513	SOX8	0.4	0.9	-1.0	2.0	0.0002
ENSG00000156535	CD109	0.3	0.5	-1.0	2.0	0.0017
ENSG00000133030	MPRIP	76.9	153.5	-1.0	2.0	5.00E-05
ENSG00000004399	PLXND1	35.5	71.1	-1.0	2.0	5.00E-05
ENSG00000021762	OSBPL5	0.5	1.0	-1.0	2.0	0.0027
ENSG00000269430	LRRC3DN	0.2	0.4	-1.0	2.0	0.0016
ENSG00000127863	TNFRSF19	1.8	3.6	-1.0	2.0	5.00E-05
ENSG00000178162	AC140481.1	0.2	0.4	-1.1	2.1	0.0029
ENSG00000125148	MT2A	15.1	32.7	-1.1	2.2	5.00E-05
ENSG00000271824	AC009014.3	1.0	2.1	-1.1	2.2	5.00E-05
ENSG00000197406	DIO3	2.3	5.1	-1.1	2.2	5.00E-05

ENSG00000064300	NGFR	0.3	0.6	-1.1	2.2	0.0002
ENSG00000198183	BPIFA1	1.6	3.6	-1.2	2.2	5.00E-05
ENSG00000157765	SLC34A2	0.6	1.3	-1.2	2.2	5.00E-05
ENSG00000249242	TMEM150C	0.2	0.5	-1.2	2.3	0.00135
ENSG00000092758	COL9A3	1.4	3.3	-1.2	2.3	0.00165
ENSG00000197903	HIST1H2BK	52.4	122.1	-1.2	2.3	5.00E-05
ENSG00000109099	PMP22	0.4	0.9	-1.2	2.4	0.00025
ENSG00000161570	CCL5	0.3	0.6	-1.3	2.5	0.0012
ENSG00000263934	SNORD3A	348.7	897.8	-1.4	2.6	5.00E-05
ENSG00000154027	AK5	0.3	0.8	-1.5	2.8	0.0009
ENSG00000241549	GUSBP2	1.6	4.9	-1.7	3.2	0.0016
ENSG00000178776	C5orf46	0.3	0.9	-1.7	3.3	0.00205
ENSG00000198417	MT1F	7.2	26.3	-1.9	3.6	5.00E-05
ENSG00000177359	RP11-551L14.1	0.6	4.0	-2.6	6.2	5.00E-05
ENSG00000169429	IL8*	19.1	26.7	-0.5	1.4	5.00E-05
ENSG00000119139	TJP2*	18.4	12.7	0.5	0.7	5.00E-05

*Genes referred to in the text that showed a significant but less than 1.5-fold change in expression in siRNA mediated EHF knockdown versus negative control Calu-3 cells.

Table S6. List of enriched gene pathways from DAVID gene ontology analysis of significantly differentially expressed genes with >1.5-fold change in expression following EHF depletion.

Term	PValue	Genes
GO:0030855~epithelial cell differentiation	6.85E-05	RHCG, KRT5, SPRR1A, SPRR1B, KRT14, FZD1, EHF, CSTA, ID3, KRT4
GO:0045682~regulation of epidermis development	1.61E-04	INHBA, NOTCH1, TRIM16, NGFR, AQP3
GO:0005576~extracellular region	6.17E-04	CXCL1, NRTN, NRG4, CXCL5, FAM3D, MSMB, ARSI, FAM20C, CD109, PRSS1, CXCL6, CCL5, SCGB1A1, MMP1, AZGP1, GLIPR2, C5ORF46, COL17A1, BDNF, PRRG4, COL9A3, FGB, SBSN, SERPINE1, SEMA3D, SFTPC, LGI2, PRSS33, SFTPB, MATN3, HAPLN3, LAD1, TCN1, NTN1, INHBA, SERPINF1, SRPX2, SFTPA2, C1QL1, SERPINB2, AREG, CMTM4, AGR2, PLAU
GO:0060429~epithelium development	7.13E-04	RHCG, KRT5, SPRR1A, SPRR1B, KRT14, FZD1, EHF, CSTA, ID3, KRT4, TWIST1
GO:0007398~ectoderm development	0.001089007	KRT6A, COL17A1, NOTCH1, KRT5, KRT16, SPRR1A, SPRR1B, KRT14, CSTA, NGFR
GO:0008544~epidermis development	0.002608863	COL17A1, NOTCH1, KRT5, KRT16, SPRR1A, SPRR1B, KRT14, CSTA, NGFR
GO:0007626~locomotory behavior	0.002899408	KCNMA1, CXCL1, DMBX1, CXCL5, GRIN1, S100A9, C1QL1, CXCL6, CMTM4, CCL5, PLAU
GO:0007610~behavior	0.00296785	CXCL1, KCNMA1, DMBX1, S100P, CXCL5, S100A9, GRIN1, CTNND2, CXCL6, CCL5, BDNF, C1QL1, CMTM4, SHC3, PLAU
GO:0009611~response to wounding	0.003509121	CXCL1, S100A8, S100A9, CHST2, ITGA2, CHST4, CXCL6, CCL5, NOTCH1, FGB, SERPINE1, SERPINB2, MGLL, ID3, NGFR, PLAU
GO:0032101~regulation of response to external stimulus	0.004469944	GPX2, SERPINF1, GRIN1, SERPINE1, ITGA2, CCL5, SCGB1A1, PLAU
GO:0051241~negative regulation of multicellular organismal process	0.005288313	KCNMA1, INHBA, NOTCH1, GNAI2, SERPINE1, NGFR, SCGB1A1, PLAU
GO:0042127~regulation of cell proliferation	0.006057187	CXCL1, KRT6A, GNAI2, CXCL5, ITGA2, NTN1, SCGB1A1, MYCN, AZGP1, DHRS2, NOTCH1, BDNF, CDKN1A, KRT5, SERPINE1, NGFR, KRT4, PMP22, ICOSLG, PLAU
GO:0044421~extracellular region part	0.007417859	CXCL1, MATN3, HAPLN3, LAD1, CXCL5, MSMB, PRSS1, CD109, CXCL6, CCL5, NTN1, MMP1, INHBA, COL17A1, COL9A3, SERPINF1, FGB, SFTPA2, SERPINB2, SFTPC, AREG, CMTM4, SFTPB
GO:0006970~response to osmotic stress	0.007888697	KCNMA1, TRPV4, ITGA2, ICOSLG
GO:0045616~regulation of keratinocyte differentiation	0.008382668	NOTCH1, TRIM16, AQP3
GO:0006928~cell motion	0.008431952	NRTN, S100P, S100A9, ITGA2, CHST4, CCL5, NTN1, TPM3, BDNF, HSPB1, NGFR, PLAU, S100A2, TWIST1

GO:0033273~response to vitamin	0.010261122	CYP24A1, MICB, ITGA2, TRIM16, AQP3
GO:0007267~cell-cell signaling	0.010616919	KCNMA1, CXCL5, S100A9, GRIN1, FZD1, CHST4, CXCL6, CCL5, INHBA, BDNF, SYPL1, BHLHA15, TRPV4, AREG, PMP22, SHC3
GO:0005125~cytokine activity	0.011541164	CXCL1, INHBA, FAM3D, CXCL5, CXCL6, AREG, CMTM4, CCL5
GO:0006884~cell volume homeostasis	0.013523298	SLC12A6, KCNMA1, TRPV4
GO:0045604~regulation of epidermal cell differentiation	0.013523298	NOTCH1, TRIM16, AQP3
GO:0043066~negative regulation of apoptosis	0.016285402	DHRS2, CDKN1A, BDNF, NOTCH1, HIPK3, GRIN1, SERPINB2, HSPB1, NGFR, BIRC3, TERT
GO:0050727~regulation of inflammatory response	0.016554541	GPX2, SERPINF1, ITGA2, CCL5, SCGB1A1
GO:0042592~homeostatic process	0.016693547	SLC12A6, KCNMA1, SEPW1, GRIN1, ITGA2, CCL5, SLC34A2, GPX2, INHBA, SERINC5, GYLTL1B, RHCG, BHLHA15, MT2A, SERPINE1, TRPV4, PMP22, TERT
GO:0006935~chemotaxis	0.017284984	CXCL1, CXCL5, S100A9, CXCL6, CMTM4, CCL5, PLAU
GO:0042330~taxis	0.017284984	CXCL1, CXCL5, S100A9, CXCL6, CMTM4, CCL5, PLAU
GO:0043069~negative regulation of programmed cell death	0.017780392	DHRS2, CDKN1A, BDNF, NOTCH1, HIPK3, GRIN1, SERPINB2, HSPB1, NGFR, BIRC3, TERT
GO:0060548~negative regulation of cell death	0.018091186	DHRS2, CDKN1A, BDNF, NOTCH1, HIPK3, GRIN1, SERPINB2, HSPB1, NGFR, BIRC3, TERT
GO:0008009~chemokine activity	0.019881564	CXCL1, CXCL5, CXCL6, CCL5
GO:0050768~negative regulation of neurogenesis	0.019992178	BDNF, RTN4R, NGFR, NTN1
GO:0050767~regulation of neurogenesis	0.020331091	BDNF, NOTCH1, SERPINF1, GRIN1, RTN4R, NGFR, NTN1
GO:0004857~enzyme inhibitor activity	0.020679989	CDKN1A, SERPINF1, SERPINE1, SERPINB2, CD109, CSTA, SCGB1A1, PKIA, TWIST1
GO:0009628~response to abiotic stimulus	0.020723889	KCNMA1, MICB, CDKN1A, GRIN1, KRT14, DDB2, HSPB1, TRPV4, ITGA2, NGFR, ICOSLG
GO:0005509~calcium ion binding	0.021655328	GALNT3, KCNMA1, S100P, S100A8, ARSI, GRIN1, FAM20C, S100A9, PRSS1, ITGA2, MMP1, NOTCH1, PRRG4, SFTPA2, DSC3, DTNB, EFCAB2, DSC2, TRPV4, S100A2
GO:0042379~chemokine receptor binding	0.023484341	CXCL1, CXCL5, CXCL6, CCL5
GO:0010721~negative regulation of cell development	0.023699431	BDNF, RTN4R, NGFR, NTN1
GO:0051799~negative regulation of hair follicle development	0.025559926	INHBA, NGFR
GO:0006971~hypotonic response	0.025559926	TRPV4, ITGA2
GO:0048589~developmental growth	0.025788477	DMBX1, NOTCH1, SERPINE1, CYFIP1, PLAU
GO:0017171~serine hydrolase activity	0.026024769	NCEH1, SERPINE1, PRSS1, SERPINB2, PRSS33, TMPRSS5, PLAU

GO:0070161~anchoring junction	0.026058385	TNS4, TJP1, PKP1, CTNND2, DSC3, ITGA2, DSC2
GO:0051094~positive regulation of developmental process	0.027412635	INHBA, BDNF, NOTCH1, SERPINF1, TRIM16, NGFR, CCL5, DDAH1, NTN1
GO:0031344~regulation of cell projection organization	0.027740919	GRIN1, RTN4R, ITGA2, NGFR, NTN1
GO:0030057~desmosome	0.027940525	PKP1, DSC3, DSC2
GO:0045664~regulation of neuron differentiation	0.028630228	BDNF, NOTCH1, GRIN1, RTN4R, NGFR, NTN1
GO:0045597~positive regulation of cell differentiation	0.028688082	INHBA, BDNF, NOTCH1, SERPINF1, TRIM16, NGFR, CCL5, NTN1
GO:0044092~negative regulation of molecular function	0.028839339	CDKN1A, FICD, GNAI2, GNAI1, HIPK3, HR, CSTA, ID3, UBE2D1, PKIA
GO:0001533~cornified envelope	0.033395385	SPRR1A, SPRR1B, CSTA
GO:0007584~response to nutrient	0.034614604	CYP24A1, MICB, GNAI2, ITGA2, TRIM16, AQP3
GO:0050878~regulation of body fluid levels	0.035528104	KCNMA1, FGB, SERPINE1, ITGA2, AGR2, PLAU
GO:0005615~extracellular space	0.036188885	CXCL1, CXCL5, MSMB, PRSS1, CD109, CXCL6, CCL5, INHBA, SERPINF1, FGB, SFTPA2, SERPINB2, SFTPC, AREG, CMTM4, SFTPB
GO:0050770~regulation of axonogenesis	0.036894035	GRIN1, RTN4R, NGFR, NTN1
GO:0051960~regulation of nervous system development	0.037868918	BDNF, NOTCH1, SERPINF1, GRIN1, RTN4R, NGFR, NTN1
GO:0019725~cellular homeostasis	0.038481239	SLC12A6, KCNMA1, SEPW1, SERINC5, GYLTL1B, RHCG, MT2A, GRIN1, TRPV4, PMP22, CCL5, SLC34A2
GO:0050769~positive regulation of neurogenesis	0.040243057	NOTCH1, SERPINF1, NGFR, NTN1
GO:0021675~nerve development	0.040663649	BDNF, NRTN, NGFR
GO:0050771~negative regulation of axonogenesis	0.040663649	RTN4R, NGFR, NTN1
GO:0021700~developmental maturation	0.041276904	KCNMA1, NOTCH1, BHLHA15, GRIN1, SOX8
GO:0051969~regulation of transmission of nerve impulse	0.041321632	BDNF, S100P, GNAI2, GRIN1, CTNND2, ITGA2
GO:0043296~apical junction complex	0.041438171	TJP1, PKP1, DSC3, DSC2, PMP22
GO:0018149~peptide cross-linking	0.043687732	SPRR1A, SPRR1B, CSTA
GO:0004252~serine-type endopeptidase activity	0.04471012	SERPINE1, PRSS1, SERPINB2, PRSS33, TMPRSS5, PLAU
GO:0010817~regulation of hormone levels	0.045329742	DHRS2, LRAT, CYP1B1, DIO3, BACE2, TRPV4
GO:0016327~apicolateral plasma membrane	0.045410206	TJP1, PKP1, DSC3, DSC2, PMP22
GO:0044057~regulation of system process	0.046470503	KCNMA1, INHBA, BDNF, S100P, GNAI2, GRIN1, CTNND2, ITGA2, TPM3
GO:0031644~regulation of neurological system process	0.047473756	BDNF, S100P, GNAI2, GRIN1, CTNND2, ITGA2
GO:0042445~hormone metabolic	0.047846491	DHRS2, LRAT, CYP1B1, DIO3, BACE2

process		
GO:0048167~regulation of synaptic plasticity	0.049261832	BDNF, S100P, GRIN1, CTNND2
GO:0060284~regulation of cell development	0.049269588	BDNF, NOTCH1, SERPINF1, GRIN1, RTN4R, NGFR, NTN1
GO:0010035~response to inorganic substance	0.049269588	KCNMA1, CDKN1A, FGB, SERPINE1, KRT14, AQP3, MT1X
GO:0004090~carbonyl reductase (NADPH) activity	0.049287246	DHRS2, CBR3
GO:0031345~negative regulation of cell projection organization	0.049976041	RTN4R, NGFR, NTN1
GO:0006916~anti-apoptosis	0.050954825	BDNF, HIPK3, SERPINB2, HSPB1, NGFR, BIRC3, TERT
GO:0016323~basolateral plasma membrane	0.051012745	TNS4, SLC12A6, COL17A1, TJP1, RHCG, ITGA2, AQP3
GO:0012505~endomembrane system	0.052066229	SEC23A, CYP1B1, SLC33A1, CHST2, ERLIN1, CHST4, PIP5K1A, NUPL1, SENP2, DHRS2, ERO1LB, SRPR, CACYBP, NUP54, DOLPP1, SEC24D, DEGS2
GO:0008083~growth factor activity	0.052302717	CXCL1, INHBA, BDNF, NRTN, NRG4, AREG
GO:0006873~cellular ion homeostasis	0.052669053	SLC12A6, KCNMA1, SERINC5, RHCG, MT2A, GRIN1, TRPV4, PMP22, CCL5, SLC34A2
GO:0030856~regulation of epithelial cell differentiation	0.053235208	NOTCH1, TRIM16, AQP3
GO:0007611~learning or memory	0.054961999	BDNF, S100P, GRIN1, CTNND2, SHC3
GO:0055082~cellular chemical homeostasis	0.057107494	SLC12A6, KCNMA1, SERINC5, RHCG, MT2A, GRIN1, TRPV4, PMP22, CCL5, SLC34A2
GO:0015296~anion:cation symporter activity	0.057456812	SLC12A6, SLC4A7, SLC34A2
GO:0010720~positive regulation of cell development	0.059178398	NOTCH1, SERPINF1, NGFR, NTN1
GO:0031099~regeneration	0.059178398	CDKN1A, NOTCH1, SERPINE1, PLAU
GO:0045596~negative regulation of cell differentiation	0.06047139	INHBA, BDNF, NOTCH1, RTN4R, NGFR, NTN1, TWIST1
GO:0008430~selenium binding	0.060795385	GPX2, SEPW1, DIO3
GO:0001517~N-acetylglucosamine 6-O-sulfotransferase activity	0.061227009	CHST2, CHST4
GO:0010975~regulation of neuron projection development	0.06126625	GRIN1, RTN4R, NGFR, NTN1
GO:0045606~positive regulation of epidermal cell differentiation	0.062686866	NOTCH1, TRIM16
GO:0045618~positive regulation of keratinocyte differentiation	0.062686866	NOTCH1, TRIM16
GO:0045683~negative regulation of epidermis development	0.062686866	INHBA, NGFR
GO:0042246~tissue regeneration	0.063443479	NOTCH1, SERPINE1, PLAU
GO:0005789~endoplasmic reticulum membrane	0.064716573	ERO1LB, CYP1B1, SLC33A1, SRPR, ERLIN1, DOLPP1, SEC24D, DEGS2

GO:0009991~response to extracellular stimulus	0.065556044	CYP24A1, MICB, CDKN1A, GNAI2, ITGA2, TRIM16, AQP3
GO:0016477~cell migration	0.065945622	NRTN, S100P, S100A9, CCL5, NTN1, PLAU, S100A2, TWIST1
GO:0005200~structural constituent of cytoskeleton	0.066043876	KRT6A, KRT5, KRT16, KRT14
GO:0048878~chemical homeostasis	0.066615003	SLC12A6, KCNMA1, SERINC5, RHCG, BHLHA15, MT2A, GRIN1, SERPINE1, TRPV4, PMP22, CCL5, SLC34A2
GO:0043086~negative regulation of catalytic activity	0.066940416	CDKN1A, FICD, GNAI2, GNAI1, HIPK3, CSTA, UBE2D1, PKIA
GO:0032526~response to retinoic acid	0.06698198	MICB, TRIM16, AQP3
GO:0001763~morphogenesis of a branching structure	0.069955223	NOTCH1, CTNND2, PLXND1, MYCN
GO:0016779~nucleotidyltransferase activity	0.072501207	FICD, POLE2, OAS3, OAS2, TERT
GO:0008236~serine-type peptidase activity	0.074012513	SERPINE1, PRSS1, SERPINB2, PRSS33, TMPRSS5, PLAU
GO:0042634~regulation of hair cycle	0.074747243	INHBA, NGFR
GO:0051797~regulation of hair follicle development	0.074747243	INHBA, NGFR
GO:0010769~regulation of cell morphogenesis involved in differentiation	0.076816494	GRIN1, RTN4R, NGFR, NTN1
GO:0031348~negative regulation of defense response	0.077973096	GPX2, MICB, SERPINF1
GO:0007585~respiratory gaseous exchange	0.077973096	SFTPA2, SFTPC, SFTPB
GO:0030054~cell junction	0.079814762	TNS4, COL17A1, TJP1, PKP1, GRIN1, SYT12, CTNND2, DSC3, CYFIP1, ITGA2, DSC2, PMP22
GO:0005783~endoplasmic reticulum	0.080125101	SEC23A, NCEH1, CYP1B1, SLC33A1, UBE2J1, RTN4R, ERLIN1, OAS2, ALDH3A1, ERO1LB, SERINC5, LRAT, SHISA2, SRPR, BACE2, DOLPP1, AGR2, SEC24D, DEGS2
GO:0042175~nuclear envelope-endoplasmic reticulum network	0.08108359	ERO1LB, CYP1B1, SLC33A1, SRPR, ERLIN1, DOLPP1, SEC24D, DEGS2
GO:0050801~ion homeostasis	0.081931268	SLC12A6, KCNMA1, SERINC5, RHCG, MT2A, GRIN1, TRPV4, PMP22, CCL5, SLC34A2
GO:0010038~response to metal ion	0.084988099	KCNMA1, FGB, KRT14, AQP3, MT1X
GO:0070011~peptidase activity, acting on L-amino acid peptides	0.085207207	SENP2, USP18, BACE2, PM20D2, SERPINE1, PRSS1, SERPINB2, PRSS33, LMLN, TMPRSS5, MMP1, PLAU
GO:0008284~positive regulation of cell proliferation	0.086783827	CDKN1A, KRT6A, NOTCH1, GNAI2, CXCL5, ITGA2, NGFR, NTN1, ICOSLG, MYCN
GO:0040007~growth	0.087500967	DMBX1, INHBA, NOTCH1, SERPINE1, CYFIP1, PLAU
GO:0022604~regulation of cell morphogenesis	0.088735293	GRIN1, RTN4R, CYFIP1, NGFR, NTN1
GO:0002683~negative regulation of	0.091380877	GPX2, INHBA, MICB, SCGB1A1

immune system process		
GO:0005882~intermediate filament	0.093508939	KRT6A, PKP1, KRT5, KRT16, KRT14, KRT4
GO:0042981~regulation of apoptosis	0.094410082	KCNMA1, GRIN1, BIRC3, INHBA, DHRS2, NOTCH1, BDNF, CDKN1A, HIPK3, SERPINB2, HSPB1, TNFRSF19, ID3, NGFR, MX1, TERT
GO:0008285~negative regulation of cell proliferation	0.09465443	CXCL1, AZGP1, DHRS2, CDKN1A, BDNF, KRT5, KRT4, PMP22, SCGB1A1
GO:0050804~regulation of synaptic transmission	0.098445286	BDNF, S100P, GNAI2, GRIN1, CTNND2
GO:0042060~wound healing	0.099997985	NOTCH1, FGB, SERPINE1, SERPINB2, ITGA2, PLAU

Table S7. List of transcripts differentially expressed by at least 1.5-fold in EHF-overexpressing versus pcDNA control A549 clones.

Gene ID	Gene Name	FPKM		Log2 (fold change)	Fold Change	P value
		pcDNA clones	EHF clones			
ENSG00000250846	RP11-807H7.1	3.8	0.1	6.2	0.0	5.00E-05
ENSG00000198542	ITGBL1	1.2	0.0	6.0	0.0	5.00E-05
ENSG00000140538	NTRK3	21.4	1.2	4.1	0.1	5.00E-05
ENSG00000162624	LHX8	9.1	0.6	3.9	0.1	5.00E-05
ENSG00000135744	AGT	5.7	0.4	3.7	0.1	5.00E-05
ENSG00000196757	ZNF700	0.6	0.0	3.6	0.1	5.00E-05
ENSG00000261717	RP11-77K12.1	2.9	0.2	3.6	0.1	0.00175
ENSG00000169439	SDC2	3.9	0.4	3.4	0.1	5.00E-05
ENSG00000265404	AC099796.1	77.8	7.5	3.4	0.1	0.00555
ENSG00000101134	DOK5	1.2	0.1	3.3	0.1	0.00025
ENSG00000144476	ACKR3	2.2	0.2	3.2	0.1	5.00E-05
ENSG00000156298	TSPAN7	14.9	1.6	3.2	0.1	5.00E-05
ENSG00000066032	CTNNA2	1.5	0.2	3.1	0.1	5.00E-05
ENSG00000228439	TSTD3	11.9	1.5	3.0	0.1	0.0051
ENSG00000239389	PCDHA13	0.8	0.1	3.0	0.1	0.0023
ENSG00000151892	GFRA1	1.2	0.2	3.0	0.1	5.00E-05
ENSG00000188916	FAM196A	0.8	0.1	3.0	0.1	0.00035
ENSG00000099998	GGT5	1.1	0.2	2.8	0.1	5.00E-05
ENSG00000160471	COX6B2	1.1	0.2	2.8	0.1	5.00E-05
ENSG00000164741	DLC1	0.8	0.1	2.8	0.1	5.00E-05
ENSG00000052850	ALX4	1.4	0.2	2.7	0.2	5.00E-05
ENSG00000119283	TRIM67	1.0	0.1	2.7	0.2	5.00E-05
ENSG00000021826	CPS1	41.4	6.6	2.6	0.2	5.00E-05
ENSG00000198203	SULT1C2	8.7	1.5	2.6	0.2	5.00E-05
ENSG00000109819	PPARGC1A	2.7	0.5	2.5	0.2	5.00E-05
ENSG00000224149	RP11-510C10.3	1.4	0.3	2.4	0.2	0.0001
ENSG00000116774	OLFML3	12.6	2.4	2.4	0.2	5.00E-05
ENSG00000123243	ITIH5	1.0	0.2	2.4	0.2	5.00E-05
ENSG00000150594	ADRA2A	0.7	0.2	2.3	0.2	5.00E-05
ENSG00000180767	CHST13	1.5	0.3	2.3	0.2	5.00E-05
ENSG00000151388	ADAMTS12	1.4	0.3	2.3	0.2	5.00E-05
ENSG00000250305	KIAA1456	0.4	0.1	2.2	0.2	5.00E-05
ENSG00000261115	TMEM178B	1.0	0.2	2.1	0.2	5.00E-05
ENSG00000151490	PTPRO	0.5	0.1	2.1	0.2	5.00E-05
ENSG00000143473	KCNH1	1.1	0.3	2.1	0.2	5.00E-05
ENSG00000102032	RENBP	1.7	0.4	2.1	0.2	5.00E-05
ENSG00000110169	HPX	1.8	0.4	2.0	0.2	5.00E-05
ENSG00000169918	OTUD7A	0.4	0.1	2.0	0.2	5.00E-05
ENSG00000165023	DIRAS2	0.4	0.1	2.0	0.3	5.00E-05
ENSG00000101197	BIRC7	4.3	1.1	2.0	0.3	5.00E-05
ENSG00000134769	DTNA	1.1	0.3	2.0	0.3	5.00E-05

ENSG00000246877	DNM1P35	0.6	0.1	2.0	0.3	5.00E-05
ENSG00000144908	ALDH1L1	0.5	0.1	1.9	0.3	5.00E-05
ENSG00000133636	NTS	104.6	27.2	1.9	0.3	5.00E-05
ENSG00000104081	BMF	1.8	0.5	1.9	0.3	5.00E-05
ENSG00000064205	WISP2	4.6	1.2	1.9	0.3	5.00E-05
ENSG00000180066	C10orf91	12.3	3.3	1.9	0.3	5.00E-05
ENSG00000089250	NOS1	0.3	0.1	1.9	0.3	5.00E-05
ENSG00000224596	ZMIZ1-AS1	0.6	0.2	1.8	0.3	5.00E-05
ENSG00000196368	NUDT11	1.0	0.3	1.8	0.3	5.00E-05
ENSG00000101198	NKAIN4	1.8	0.5	1.8	0.3	5.00E-05
ENSG00000250799	PRODH2	1.1	0.3	1.8	0.3	0.00045
ENSG00000166073	GPR176	1.8	0.5	1.7	0.3	5.00E-05
ENSG00000223749	MIR503HG	7.0	2.1	1.7	0.3	5.00E-05
ENSG00000135253	KCP	1.9	0.6	1.7	0.3	0.0019
ENSG00000197106	SLC6A17	0.3	0.1	1.7	0.3	5.00E-05
ENSG00000095383	TBC1D2	14.0	4.3	1.7	0.3	5.00E-05
ENSG00000149571	KIRREL3	2.0	0.6	1.7	0.3	5.00E-05
ENSG00000130222	GADD45G	1.8	0.6	1.7	0.3	5.00E-05
ENSG00000108924	HLF	0.7	0.2	1.7	0.3	5.00E-05
ENSG00000068831	RASGRP2	0.4	0.1	1.7	0.3	0.00045
ENSG00000196668	LINC00173	2.8	0.9	1.7	0.3	0.0001
ENSG00000167693	NXN	11.7	3.7	1.7	0.3	5.00E-05
ENSG00000170965	PLAC1	1.7	0.5	1.6	0.3	5.00E-05
ENSG00000182870	GALNT9	1.4	0.5	1.6	0.3	5.00E-05
ENSG00000133019	CHRM3	1.4	0.5	1.6	0.3	0.00045
ENSG00000146592	CREB5	1.0	0.3	1.6	0.3	5.00E-05
ENSG00000136881	BAAT	23.2	7.7	1.6	0.3	5.00E-05
ENSG00000109846	CRYAB	42.4	14.1	1.6	0.3	5.00E-05
ENSG00000187634	SAMD11	8.7	2.9	1.6	0.3	0.0086
ENSG00000147697	GSDMC	0.5	0.2	1.5	0.3	0.002
ENSG00000095066	HOOK2	22.5	7.8	1.5	0.3	5.00E-05
ENSG00000095752	IL11	7.6	2.6	1.5	0.3	5.00E-05
ENSG00000185345	PARK2	0.4	0.2	1.5	0.3	0.00125
ENSG00000231107	RP11-389K14.3	1.4	0.5	1.5	0.4	0.0001
ENSG00000249196	RP11-669N7.2	1.9	0.7	1.5	0.4	0.00835
ENSG00000107518	ATRNL1	0.9	0.3	1.5	0.4	5.00E-05
ENSG00000166106	ADAMTS15	0.7	0.2	1.5	0.4	5.00E-05
ENSG00000099994	SUSD2	4.7	1.7	1.5	0.4	5.00E-05
ENSG00000165507	C10orf10	1.7	0.6	1.5	0.4	0.00285
ENSG00000026751	SLAMF7	3.9	1.4	1.5	0.4	5.00E-05
ENSG00000196605	ZNF846	1.7	0.6	1.5	0.4	0.0001
ENSG00000020181	GPR124	1.0	0.4	1.5	0.4	0.0073
ENSG00000143502	SUSD4	3.2	1.2	1.5	0.4	5.00E-05
ENSG00000262454	RP11-65J21.3	3.9	1.4	1.5	0.4	0.0002
ENSG00000169255	B3GALNT1	0.5	0.2	1.5	0.4	0.00065

ENSG00000110076	NRXN2	0.4	0.1	1.5	0.4	5.00E-05
ENSG00000250303	RP11-356J5.12	6.1	2.2	1.5	0.4	5.00E-05
ENSG00000066468	FGFR2	0.5	0.2	1.4	0.4	5.00E-05
ENSG00000088538	DOCK3	1.9	0.7	1.4	0.4	5.00E-05
ENSG00000077092	RARB	2.2	0.8	1.4	0.4	5.00E-05
ENSG00000104324	CPQ	3.3	1.2	1.4	0.4	5.00E-05
ENSG00000091513	TF	9.9	3.7	1.4	0.4	5.00E-05
ENSG00000136244	IL6	2.1	0.8	1.4	0.4	5.00E-05
ENSG00000182256	GABRG3	0.4	0.1	1.4	0.4	0.0003
ENSG00000184845	DRD1	0.6	0.2	1.4	0.4	0.00075
ENSG00000115353	TACR1	1.0	0.4	1.4	0.4	0.00405
ENSG00000198125	MB	3.3	1.2	1.4	0.4	5.00E-05
ENSG00000221955	SLC12A8	0.6	0.2	1.4	0.4	0.00045
ENSG00000225138	CTD-2228K2.7	28.8	11.2	1.4	0.4	5.00E-05
ENSG00000119865	CNRIP1	1.3	0.5	1.4	0.4	0.00655
ENSG00000114948	ADAM23	4.5	1.8	1.4	0.4	0.0001
ENSG00000235169	SMIM1	0.8	0.3	1.4	0.4	0.0015
ENSG00000128564	VGF	3.0	1.2	1.3	0.4	5.00E-05
ENSG00000234311	RP11-432J24.3	4.4	1.7	1.3	0.4	5.00E-05
ENSG00000147614	ATP6V0D2	0.7	0.3	1.3	0.4	5.00E-05
ENSG00000151136	BTBD11	9.1	3.6	1.3	0.4	5.00E-05
ENSG00000171119	NRTN	2.0	0.8	1.3	0.4	5.00E-05
ENSG00000156113	KCNMA1	4.9	1.9	1.3	0.4	0.0001
ENSG00000137731	FXYD2	94.9	38.0	1.3	0.4	5.00E-05
ENSG00000124564	SLC17A3	7.5	3.0	1.3	0.4	5.00E-05
ENSG00000132718	SYT11	0.8	0.3	1.3	0.4	0.00025
ENSG00000134207	SYT6	1.8	0.7	1.3	0.4	0.002
ENSG00000176928	GCNT4	1.0	0.4	1.3	0.4	0.00225
ENSG00000258654	RP11-509A17.3	0.6	0.2	1.3	0.4	0.00195
ENSG00000003989	SLC7A2	30.6	12.5	1.3	0.4	5.00E-05
ENSG00000147872	PLIN2	195.0	80.3	1.3	0.4	5.00E-05
ENSG00000078018	MAP2	7.7	3.2	1.3	0.4	5.00E-05
ENSG00000153294	GPR115	8.4	3.5	1.3	0.4	5.00E-05
ENSG00000129910	CDH15	0.5	0.2	1.3	0.4	0.00225
ENSG00000124813	RUNX2	0.5	0.2	1.3	0.4	0.00245
ENSG00000256258	RP11-495K9.9	0.6	0.2	1.3	0.4	0.0074
ENSG00000113083	LOX	3.0	1.2	1.3	0.4	0.0086
ENSG00000152377	SPOCK1	0.8	0.3	1.3	0.4	0.00245
ENSG00000164379	FOXQ1	9.7	4.0	1.3	0.4	5.00E-05
ENSG00000166923	GREM1	29.0	12.1	1.3	0.4	5.00E-05
ENSG00000125869	LAMP5	1.0	0.4	1.3	0.4	0.0001
ENSG00000015413	DPEP1	1.1	0.5	1.2	0.4	0.00135
ENSG00000135917	SLC19A3	5.1	2.2	1.2	0.4	5.00E-05
ENSG00000117016	RIMS3	0.8	0.3	1.2	0.4	5.00E-05
ENSG00000136630	HLX	1.9	0.8	1.2	0.4	0.00035

ENSG00000182600	C2orf82	24.7	10.5	1.2	0.4	0.00015
ENSG00000188897	CTD-3088G3.8	0.7	0.3	1.2	0.4	0.0006
ENSG00000108387	SEPT4	1.4	0.6	1.2	0.4	5.00E-05
ENSG00000105605	CACNG7	1.3	0.6	1.2	0.4	5.00E-05
ENSG00000132563	REEP2	1.9	0.8	1.2	0.4	5.00E-05
ENSG00000115363	EVA1A	4.1	1.7	1.2	0.4	0.0001
ENSG00000174899	C3orf55	3.5	1.5	1.2	0.4	0.00255
ENSG00000185070	FLRT2	1.4	0.6	1.2	0.4	0.00025
ENSG00000115380	EFEMP1	19.2	8.4	1.2	0.4	5.00E-05
ENSG00000181495	AC026703.1	5.6	2.5	1.2	0.4	0.0005
ENSG00000130208	APOC1	18.6	8.2	1.2	0.4	5.00E-05
ENSG00000187867	PALM3	0.4	0.2	1.2	0.4	0.009
ENSG00000133069	TMCC2	1.4	0.6	1.2	0.4	5.00E-05
ENSG00000197766	CFD	67.1	30.0	1.2	0.4	5.00E-05
ENSG00000150347	ARID5B	2.7	1.2	1.2	0.4	5.00E-05
ENSG00000171791	BCL2	1.7	0.7	1.2	0.4	0.0021
ENSG00000178821	TMEM52	0.6	0.3	1.2	0.4	0.00145
ENSG00000079931	MOXD1	1.4	0.6	1.1	0.5	0.0001
ENSG00000183570	PCBP3	0.8	0.4	1.1	0.5	0.00025
ENSG00000115596	WNT6	0.8	0.3	1.1	0.5	0.0021
ENSG00000100342	APOL1	13.0	5.9	1.1	0.5	5.00E-05
ENSG00000259974	LINC00261	3.5	1.6	1.1	0.5	5.00E-05
ENSG00000124568	SLC17A1	1.0	0.5	1.1	0.5	0.00045
ENSG00000185760	KCNQ5	0.5	0.2	1.1	0.5	0.003
ENSG00000259343	RP11-761I4.3	4.2	1.9	1.1	0.5	0.0086
ENSG00000227619	RP11-492E3.2	0.6	0.3	1.1	0.5	0.0013
ENSG00000134533	RERG	2.0	0.9	1.1	0.5	0.0001
ENSG00000129946	SHC2	4.4	2.1	1.1	0.5	5.00E-05
ENSG00000151117	TMEM86A	0.8	0.4	1.1	0.5	0.00075
ENSG00000144681	STAC	5.1	2.4	1.1	0.5	5.00E-05
ENSG00000180739	S1PR5	0.5	0.2	1.1	0.5	0.00985
ENSG00000077420	APBB1IP	1.2	0.6	1.1	0.5	0.0031
ENSG00000267279	RP11-879F14.2	1.2	0.6	1.1	0.5	0.0085
ENSG00000149380	P4HA3	11.1	5.2	1.1	0.5	0.00545
ENSG00000146374	RSPO3	27.2	12.8	1.1	0.5	5.00E-05
ENSG00000166473	PKD1L2	9.3	4.4	1.1	0.5	5.00E-05
ENSG00000183098	GPC6	3.7	1.7	1.1	0.5	5.00E-05
ENSG00000090661	CERS4	6.3	3.0	1.1	0.5	5.00E-05
ENSG00000115226	FNDC4	0.8	0.4	1.1	0.5	0.00245
ENSG00000219755	RP1-199J3.5	0.7	0.3	1.1	0.5	0.00785
ENSG00000154134	ROBO3	2.9	1.4	1.1	0.5	5.00E-05
ENSG00000126353	CCR7	0.8	0.4	1.1	0.5	0.0027
ENSG00000104888	SLC17A7	0.5	0.2	1.1	0.5	0.00125
ENSG00000103485	QPRT	0.8	0.4	1.1	0.5	0.00855
ENSG00000114923	SLC4A3	0.8	0.4	1.1	0.5	0.0005

ENSG00000171368	TPPP	1.0	0.5	1.0	0.5	0.00245
ENSG00000092096	SLC22A17	6.0	2.9	1.0	0.5	5.00E-05
ENSG00000218336	TENM3	1.1	0.5	1.0	0.5	0.0018
ENSG00000019144	PHLDB1	2.5	1.2	1.0	0.5	5.00E-05
ENSG00000155816	FMN2	1.3	0.6	1.0	0.5	0.002
ENSG00000153208	MERTK	1.7	0.8	1.0	0.5	0.00015
ENSG00000186642	PDE2A	1.3	0.6	1.0	0.5	5.00E-05
ENSG00000161249	DMKN	24.0	11.7	1.0	0.5	5.00E-05
ENSG00000164733	CTSB	558.4	274.2	1.0	0.5	5.00E-05
ENSG00000213694	S1PR3	17.2	8.5	1.0	0.5	5.00E-05
ENSG00000072163	LIMS2	0.9	0.5	1.0	0.5	0.001
ENSG00000139269	INHBE	3.2	1.6	1.0	0.5	5.00E-05
ENSG00000101210	EEF1A2	157.7	77.8	1.0	0.5	5.00E-05
ENSG00000223764	RP11-54O7.3	0.9	0.4	1.0	0.5	0.0002
ENSG00000062282	DGAT2	1.6	0.8	1.0	0.5	0.00435
ENSG00000173210	ABLIM3	21.7	10.8	1.0	0.5	5.00E-05
ENSG00000100307	CBX7	3.3	1.6	1.0	0.5	5.00E-05
ENSG00000237950	RP11-7O11.3	1.2	0.6	1.0	0.5	0.00755
ENSG00000130147	SH3BP4	20.9	10.5	1.0	0.5	5.00E-05
ENSG00000175866	BAIAP2	14.7	7.4	1.0	0.5	5.00E-05
ENSG00000144583	MARCH4	0.6	0.3	1.0	0.5	0.00095
ENSG00000226674	TEX41	12.9	6.5	1.0	0.5	0.00135
ENSG00000169220	RGS14	6.7	3.4	1.0	0.5	0.0016
ENSG00000169856	ONECUT1	0.7	0.3	1.0	0.5	0.00455
ENSG00000183722	LHFP	3.1	1.6	1.0	0.5	0.00045
ENSG00000127561	SYNGR3	10.4	5.2	1.0	0.5	0.0001
ENSG00000135549	PKIB	28.0	14.1	1.0	0.5	5.00E-05
ENSG00000025708	TYMP	15.2	7.7	1.0	0.5	0.0001
ENSG00000073670	ADAM11	0.5	0.3	1.0	0.5	0.00125
ENSG00000197857	ZNF44	0.8	0.4	1.0	0.5	0.0032
ENSG00000182771	GRID1	1.1	0.6	1.0	0.5	0.0008
ENSG00000130720	FIBCD1	7.9	4.0	1.0	0.5	0.0065
ENSG00000118257	NRP2	27.0	13.9	1.0	0.5	5.00E-05
ENSG00000102271	KLHL4	2.8	1.4	1.0	0.5	0.00015
ENSG00000168398	BDKRB2	12.5	6.4	1.0	0.5	5.00E-05
ENSG00000131409	LRRC4B	1.0	0.5	1.0	0.5	0.00125
ENSG00000186648	LRRC16B	0.5	0.3	1.0	0.5	0.0029
ENSG00000230176	RP4-779E11.3	2.3	1.2	0.9	0.5	0.0048
ENSG00000224189	HOXD-AS1	1.5	0.8	0.9	0.5	0.00685
ENSG00000186897	C1QL4	1.5	0.8	0.9	0.5	0.00065
ENSG00000105255	FSD1	2.6	1.4	0.9	0.5	0.00035
ENSG00000070182	SPTB	0.9	0.5	0.9	0.5	0.00885
ENSG00000247746	USP51	0.9	0.5	0.9	0.5	0.0005
ENSG00000205795	CYS1	0.5	0.3	0.9	0.5	0.00595
ENSG00000147100	SLC16A2	5.6	2.9	0.9	0.5	5.00E-05

ENSG00000198729	PPP1R14C	1.6	0.9	0.9	0.5	0.0033
ENSG00000012124	CD22	6.8	3.6	0.9	0.5	5.00E-05
ENSG00000170469	SPATA24	4.6	2.4	0.9	0.5	0.0017
ENSG00000174951	FUT1	1.9	1.0	0.9	0.5	5.00E-05
ENSG00000232176	RP11-146N23.1	8.8	4.6	0.9	0.5	0.0021
ENSG00000127948	POR	187.6	99.1	0.9	0.5	5.00E-05
ENSG00000167680	SEMA6B	4.8	2.6	0.9	0.5	5.00E-05
ENSG00000177932	ZNF354C	0.9	0.5	0.9	0.5	0.0013
ENSG00000146678	IGFBP1	405.5	215.9	0.9	0.5	5.00E-05
ENSG00000115828	QPCT	67.8	36.1	0.9	0.5	5.00E-05
ENSG00000137273	FOXF2	5.4	2.9	0.9	0.5	5.00E-05
ENSG00000261578	RP11-21L23.2	14.0	7.5	0.9	0.5	5.00E-05
ENSG00000170425	ADORA2B	10.5	5.6	0.9	0.5	5.00E-05
ENSG00000154678	PDE1C	4.3	2.3	0.9	0.5	5.00E-05
ENSG00000133805	AMPD3	4.9	2.6	0.9	0.5	5.00E-05
ENSG00000115257	PCSK4	1.2	0.7	0.9	0.5	0.00355
ENSG00000154027	AK5	7.2	3.9	0.9	0.5	0.0018
ENSG00000100292	HMOX1	171.5	93.4	0.9	0.5	5.00E-05
ENSG00000173698	GPR64	4.9	2.7	0.9	0.5	5.00E-05
ENSG00000221890	NPTXR	16.0	8.7	0.9	0.5	5.00E-05
ENSG00000112183	RBM24	9.4	5.1	0.9	0.5	5.00E-05
ENSG00000164690	SHH	3.6	2.0	0.9	0.5	0.00015
ENSG00000011028	MRC2	15.1	8.3	0.9	0.5	5.00E-05
ENSG00000113389	NPR3	9.7	5.3	0.9	0.5	0.0001
ENSG00000184524	CEND1	1.0	0.5	0.9	0.5	0.00555
ENSG00000004660	CAMKK1	8.1	4.4	0.9	0.5	5.00E-05
ENSG00000169031	COL4A3	5.0	2.7	0.9	0.5	0.00955
ENSG00000176720	BOK	2.7	1.5	0.9	0.6	5.00E-05
ENSG00000116833	NR5A2	20.1	11.1	0.9	0.6	5.00E-05
ENSG00000240184	PCDHGC3	2.1	1.2	0.9	0.6	0.00775
ENSG00000223573	TINCR	1.8	1.0	0.9	0.6	0.0003
ENSG00000056487	PHF21B	0.5	0.3	0.9	0.6	0.0031
ENSG00000260604	RP1-140K8.5	0.4	0.2	0.9	0.6	0.00415
ENSG00000178860	MSC	53.2	29.5	0.9	0.6	5.00E-05
ENSG00000115194	SLC30A3	1.2	0.7	0.9	0.6	0.00195
ENSG00000144730	IL17RD	0.5	0.3	0.8	0.6	0.00315
ENSG00000142871	CYR61	14.5	8.0	0.8	0.6	5.00E-05
ENSG00000187094	CCK	2.2	1.2	0.8	0.6	0.00295
ENSG00000108840	HDAC5	13.3	7.4	0.8	0.6	5.00E-05
ENSG00000117114	LPHN2	7.8	4.4	0.8	0.6	5.00E-05
ENSG00000006071	ABCC8	1.0	0.6	0.8	0.6	0.00085
ENSG00000118596	SLC16A7	5.8	3.2	0.8	0.6	0.003
ENSG00000204869	IGFL4	4.3	2.4	0.8	0.6	0.0004
ENSG00000171873	ADRA1D	2.6	1.5	0.8	0.6	0.0008
ENSG00000103145	HCFC1R1	71.5	40.1	0.8	0.6	5.00E-05

ENSG00000124613	ZNF391	0.4	0.2	0.8	0.6	0.0081
ENSG00000226328	CTA-217C2.1	7.3	4.1	0.8	0.6	0.00275
ENSG00000114270	COL7A1	47.9	26.9	0.8	0.6	5.00E-05
ENSG00000057593	F7	8.4	4.7	0.8	0.6	5.00E-05
ENSG00000134030	CTIF	11.0	6.2	0.8	0.6	5.00E-05
ENSG00000165029	ABCA1	3.5	2.0	0.8	0.6	0.0001
ENSG00000231767	MIR4426	47.7	26.9	0.8	0.6	5.00E-05
ENSG00000178947	LINC00086	0.9	0.5	0.8	0.6	0.0015
ENSG00000149150	SLC43A1	11.9	6.7	0.8	0.6	5.00E-05
ENSG00000138207	RBP4	25.1	14.1	0.8	0.6	5.00E-05
ENSG00000189058	APOD	3.3	1.9	0.8	0.6	0.0008
ENSG00000153233	PTPRR	1.9	1.1	0.8	0.6	0.00325
ENSG00000110328	GALNT18	5.0	2.8	0.8	0.6	0.0032
ENSG00000087076	HSD17B14	40.4	22.9	0.8	0.6	5.00E-05
ENSG00000105971	CAV2	108.0	61.4	0.8	0.6	0.00215
ENSG00000176046	NUPR1	79.2	45.1	0.8	0.6	5.00E-05
ENSG00000187955	COL14A1	0.4	0.2	0.8	0.6	0.0059
ENSG00000143369	ECM1	2.1	1.2	0.8	0.6	0.00115
ENSG00000124615	MOCS1	0.8	0.5	0.8	0.6	0.0028
ENSG00000221968	FADS3	30.5	17.5	0.8	0.6	5.00E-05
ENSG00000183087	GAS6	5.3	3.0	0.8	0.6	5.00E-05
ENSG00000134013	LOXL2	46.7	26.9	0.8	0.6	0.00015
ENSG00000119547	ONECUT2	1.2	0.7	0.8	0.6	5.00E-05
ENSG00000155265	GOLGA7B	4.9	2.8	0.8	0.6	0.0001
ENSG00000122870	BICC1	21.4	12.3	0.8	0.6	5.00E-05
ENSG00000259803	SLC22A31	5.1	2.9	0.8	0.6	0.0052
ENSG00000122694	GLIPR2	2.1	1.2	0.8	0.6	0.0062
ENSG00000169554	ZEB2	3.0	1.8	0.8	0.6	5.00E-05
ENSG00000156587	UBE2L6	14.1	8.2	0.8	0.6	5.00E-05
ENSG00000130203	APOE	6.2	3.6	0.8	0.6	0.0006
ENSG00000116729	WLS	19.2	11.2	0.8	0.6	0.00965
ENSG00000106617	PRKAG2	31.2	18.3	0.8	0.6	5.00E-05
ENSG00000138769	CDKL2	1.6	0.9	0.8	0.6	0.0039
ENSG00000114771	AADAC	14.5	8.5	0.8	0.6	0.0007
ENSG00000026508	CD44	230.1	135.0	0.8	0.6	5.00E-05
ENSG00000113739	STC2	81.6	48.0	0.8	0.6	5.00E-05
ENSG00000250479	CHCHD10	146.4	86.2	0.8	0.6	5.00E-05
ENSG00000111799	COL12A1	3.7	2.2	0.8	0.6	0.0008
ENSG00000184489	PTP4A3	7.9	4.7	0.8	0.6	0.00015
ENSG00000135116	HRK	0.9	0.5	0.8	0.6	0.00515
ENSG00000182704	TSKU	298.0	176.3	0.8	0.6	5.00E-05
ENSG00000197043	ANXA6	29.4	17.4	0.8	0.6	5.00E-05
ENSG00000173706	HEG1	14.4	8.6	0.7	0.6	0.00015
ENSG00000085662	AKR1B1	992.2	592.9	0.7	0.6	5.00E-05
ENSG00000133816	MICAL2	20.5	12.3	0.7	0.6	5.00E-05

ENSG00000235034	C19orf81	12.2	7.3	0.7	0.6	0.0055
ENSG00000100167	SEPT3	1.0	0.6	0.7	0.6	0.0032
ENSG00000026559	KCNG1	11.2	6.7	0.7	0.6	0.0002
ENSG00000198853	RUSC2	27.8	16.9	0.7	0.6	5.00E-05
ENSG00000173221	GLRX	434.2	263.7	0.7	0.6	5.00E-05
ENSG00000123685	BATF3	9.0	5.5	0.7	0.6	0.0033
ENSG00000053747	LAMA3	7.1	4.3	0.7	0.6	5.00E-05
ENSG00000105835	NAMPT	306.9	187.7	0.7	0.6	5.00E-05
ENSG00000175344	CHRNA7	0.7	0.4	0.7	0.6	0.0037
ENSG00000117984	CTSD	729.3	446.6	0.7	0.6	5.00E-05
ENSG00000227051	C14orf132	5.4	3.3	0.7	0.6	0.00065
ENSG00000138166	DUSP5	64.2	39.5	0.7	0.6	5.00E-05
ENSG00000164951	PDP1	9.4	5.8	0.7	0.6	5.00E-05
ENSG00000184986	TMEM121	1.9	1.2	0.7	0.6	0.0088
ENSG00000146233	CYP39A1	7.4	4.6	0.7	0.6	0.0036
ENSG00000203867	RBM20	0.9	0.5	0.7	0.6	0.00895
ENSG00000118402	ELOVL4	2.8	1.8	0.7	0.6	0.00205
ENSG00000104725	NEFL	2.1	1.3	0.7	0.6	0.0032
ENSG00000152270	PDE3B	3.7	2.3	0.7	0.6	0.0001
ENSG00000106366	SERPINE1	53.7	33.5	0.7	0.6	5.00E-05
ENSG00000213362	FTH1P12	40.2	25.1	0.7	0.6	5.00E-05
ENSG00000141542	RAB40B	17.8	11.1	0.7	0.6	0.00065
ENSG00000111962	UST	10.5	6.6	0.7	0.6	0.0003
ENSG00000150764	DIXDC1	3.4	2.2	0.7	0.6	0.00015
ENSG00000104870	FCGRT	21.4	13.4	0.7	0.6	5.00E-05
ENSG00000145730	PAM	29.6	18.6	0.7	0.6	5.00E-05
ENSG00000187601	MAGEH1	6.6	4.1	0.7	0.6	0.0007
ENSG00000163083	INHBB	38.8	24.4	0.7	0.6	5.00E-05
ENSG00000143512	HHIPL2	19.1	12.0	0.7	0.6	0.0001
ENSG00000186806	VSIG10L	4.6	2.9	0.7	0.6	0.00085
ENSG00000229644	NAMPTL	94.4	59.7	0.7	0.6	0.0001
ENSG00000099822	HCN2	17.9	11.3	0.7	0.6	5.00E-05
ENSG00000183688	FAM101B	3.5	2.2	0.7	0.6	0.00065
ENSG00000131196	NFATC1	1.9	1.2	0.7	0.6	0.0061
ENSG00000159263	SIM2	4.1	2.6	0.7	0.6	0.00025
ENSG00000148926	ADM	36.5	23.2	0.7	0.6	5.00E-05
ENSG00000178773	CPNE7	25.1	16.0	0.6	0.6	0.00185
ENSG00000177707	PVRL3	24.6	15.7	0.6	0.6	5.00E-05
ENSG00000105928	DFNA5	28.1	17.9	0.6	0.6	5.00E-05
ENSG00000069424	KCNAB2	21.7	13.9	0.6	0.6	5.00E-05
ENSG00000182379	NXPH4	2.7	1.7	0.6	0.6	0.0058
ENSG00000153395	LPCAT1	35.4	22.7	0.6	0.6	5.00E-05
ENSG00000025434	NR1H3	17.0	10.9	0.6	0.6	0.0038
ENSG00000123700	KCNJ2	1.6	1.0	0.6	0.6	0.00525
ENSG00000151726	ACSL1	19.5	12.5	0.6	0.6	5.00E-05

ENSG00000165996	PTPLA	53.1	34.2	0.6	0.6	5.00E-05
ENSG00000198053	SIRPA	11.9	7.7	0.6	0.6	5.00E-05
ENSG00000223361	FTH1P10	41.6	26.8	0.6	0.6	0.0015
ENSG00000120708	TGFBI	129.2	83.3	0.6	0.6	5.00E-05
ENSG00000074370	ATP2A3	3.8	2.4	0.6	0.6	0.00015
ENSG00000158825	CDA	19.0	12.3	0.6	0.6	0.0006
ENSG00000245060	LINC00847	13.2	8.6	0.6	0.6	0.00025
ENSG00000089486	CDIP1	6.4	4.1	0.6	0.6	0.0006
ENSG00000140519	RHCG	9.4	6.1	0.6	0.7	0.00025
ENSG00000125148	MT2A	91.7	59.6	0.6	0.7	5.00E-05
ENSG00000107968	MAP3K8	13.7	8.9	0.6	0.7	0.00255
ENSG00000153815	CMIP	36.9	24.1	0.6	0.7	0.0005
ENSG00000130635	COL5A1	4.8	3.1	0.6	0.7	5.00E-05
ENSG00000141753	IGFBP4	742.7	485.5	0.6	0.7	5.00E-05
ENSG00000222009	BTBD19	5.4	3.5	0.6	0.7	0.0033
ENSG00000154511	FAM69A	9.5	6.2	0.6	0.7	0.0004
ENSG00000102409	BEX4	10.8	7.1	0.6	0.7	0.00625
ENSG00000167994	RAB3IL1	15.4	10.1	0.6	0.7	5.00E-05
ENSG00000111252	SH2B3	3.4	2.3	0.6	0.7	0.0003
ENSG00000146038	DCDC2	15.2	10.0	0.6	0.7	5.00E-05
ENSG00000204175	GPRIN2	20.4	13.4	0.6	0.7	0.0001
ENSG00000160867	FGFR4	31.3	20.6	0.6	0.7	5.00E-05
ENSG00000197355	UAP1L1	15.5	10.2	0.6	0.7	5.00E-05
ENSG00000241839	PLEKHO2	3.3	2.2	0.6	0.7	0.0071
ENSG00000101928	MOSPD1	35.2	23.2	0.6	0.7	0.0001
ENSG00000164742	ADCY1	3.6	2.3	0.6	0.7	0.00535
ENSG00000075643	MOCOS	14.2	9.4	0.6	0.7	0.00065
ENSG00000165124	SVEP1	1.6	1.1	0.6	0.7	0.0077
ENSG00000103260	METRN	43.6	28.8	0.6	0.7	0.00435
ENSG00000128335	APOL2	14.9	9.9	0.6	0.7	0.0001
ENSG00000174080	CTSF	34.1	22.6	0.6	0.7	5.00E-05
ENSG00000105639	JAK3	0.8	0.5	0.6	0.7	0.00875
ENSG00000197943	PLCG2	4.9	3.3	0.6	0.7	0.00045
ENSG00000196923	PDLIM7	9.1	6.1	0.6	0.7	0.00275
ENSG00000219507	FTH1P8	56.6	37.6	0.6	0.7	0.00015
ENSG00000179546	HTR1D	33.2	22.1	0.6	0.7	5.00E-05
ENSG00000135525	MAP7	32.9	49.4	-0.6	1.5	5.00E-05
ENSG00000186204	CYP4F12	4.4	6.6	-0.6	1.5	0.00615
ENSG00000173905	GOLIM4	8.9	13.4	-0.6	1.5	5.00E-05
ENSG00000101076	HNF4A	4.3	6.5	-0.6	1.5	0.00065
ENSG00000101811	CSTF2	9.9	14.9	-0.6	1.5	5.00E-05
ENSG00000151491	EPS8	48.0	72.3	-0.6	1.5	5.00E-05
ENSG00000168404	MLKL	10.1	15.2	-0.6	1.5	0.0001
ENSG00000168497	SDPR	1.5	2.2	-0.6	1.5	0.00785
ENSG00000211445	GPX3	3.7	5.5	-0.6	1.5	0.0058

ENSG00000130816	DNMT1	9.3	14.0	-0.6	1.5	0.0001
ENSG00000130309	COLGALT1	29.9	45.2	-0.6	1.5	5.00E-05
ENSG00000156026	MCU	30.4	45.9	-0.6	1.5	5.00E-05
ENSG00000139190	VAMP1	3.2	4.9	-0.6	1.5	0.00555
ENSG00000196498	NCOR2	37.5	56.6	-0.6	1.5	0.00025
ENSG00000163362	C1orf106	14.6	22.0	-0.6	1.5	5.00E-05
ENSG00000107960	OBFC1	11.9	18.0	-0.6	1.5	0.0001
ENSG00000164104	HMGB2	16.4	24.8	-0.6	1.5	5.00E-05
ENSG00000080839	RBL1	2.1	3.2	-0.6	1.5	0.00115
ENSG00000154822	PLCL2	1.9	2.9	-0.6	1.5	0.00245
ENSG00000164136	IL15	10.8	16.4	-0.6	1.5	0.00185
ENSG00000186529	CYP4F3	13.1	19.9	-0.6	1.5	0.0001
ENSG00000128567	PODXL	4.9	7.4	-0.6	1.5	5.00E-05
ENSG00000182952	HMGN4	29.1	44.2	-0.6	1.5	5.00E-05
ENSG00000076604	TRAF4	34.6	52.5	-0.6	1.5	5.00E-05
ENSG00000143466	IKBKE	3.2	4.9	-0.6	1.5	0.0012
ENSG00000104783	KCNN4	7.7	11.8	-0.6	1.5	5.00E-05
ENSG00000116406	EDEM3	14.7	22.5	-0.6	1.5	5.00E-05
ENSG00000158769	F11R	13.9	21.2	-0.6	1.5	5.00E-05
ENSG00000175793	SFN	27.0	41.3	-0.6	1.5	5.00E-05
ENSG00000014914	MTMR11	4.9	7.5	-0.6	1.5	0.0033
ENSG00000185900	POMK	3.7	5.7	-0.6	1.5	0.00175
ENSG00000135476	ESPL1	2.1	3.2	-0.6	1.5	0.00455
ENSG00000273297	RP11-38M8.1	7.1	10.9	-0.6	1.5	0.0065
ENSG00000176485	PLA2G16	72.0	110.7	-0.6	1.5	5.00E-05
ENSG00000154642	C21orf91	1.4	2.2	-0.6	1.5	0.0026
ENSG00000106804	C5	54.2	83.4	-0.6	1.5	5.00E-05
ENSG00000147027	TMEM47	2.0	3.0	-0.6	1.5	0.00315
ENSG00000137142	IGFBPL1	3.5	5.4	-0.6	1.5	0.00615
ENSG00000023445	BIRC3	8.7	13.4	-0.6	1.5	5.00E-05
ENSG00000197077	KIAA1671	5.3	8.3	-0.6	1.5	5.00E-05
ENSG00000175548	ALG10B	2.5	3.8	-0.6	1.5	0.00395
ENSG00000076067	RBMS2	9.0	13.9	-0.6	1.5	5.00E-05
ENSG00000138160	KIF11	4.7	7.2	-0.6	1.5	5.00E-05
ENSG00000138182	KIF20B	2.0	3.0	-0.6	1.5	0.001
ENSG00000185480	PARPBP	4.2	6.4	-0.6	1.5	0.0049
ENSG00000058272	PPP1R12A	13.4	20.7	-0.6	1.5	0.00055
ENSG00000175920	DOK7	6.1	9.5	-0.6	1.5	0.00295
ENSG00000146670	CDCA5	4.7	7.3	-0.6	1.6	0.00035
ENSG00000167325	RRM1	13.0	20.3	-0.6	1.6	5.00E-05
ENSG00000123219	CENPK	7.6	11.8	-0.6	1.6	0.00315
ENSG00000057294	PKP2	2.9	4.5	-0.6	1.6	0.0001
ENSG00000167703	SLC43A2	2.2	3.4	-0.6	1.6	0.004
ENSG00000163624	CDS1	1.1	1.7	-0.6	1.6	0.0027
ENSG00000140577	CRTC3	14.0	21.9	-0.6	1.6	5.00E-05

ENSG00000136111	TBC1D4	5.2	8.2	-0.6	1.6	5.00E-05
ENSG00000150687	PRSS23	65.1	101.8	-0.6	1.6	0.0001
ENSG00000126561	STAT5A	1.7	2.7	-0.6	1.6	0.00135
ENSG00000004700	RECQL	17.1	26.7	-0.6	1.6	5.00E-05
ENSG00000140332	TLE3	3.4	5.3	-0.6	1.6	0.004
ENSG00000030419	IKZF2	0.3	0.4	-0.6	1.6	0.00915
ENSG00000132297	HHLA1	1.3	2.0	-0.6	1.6	0.0046
ENSG00000127334	DYRK2	5.8	9.0	-0.6	1.6	5.00E-05
ENSG00000065357	DGKA	5.4	8.5	-0.6	1.6	0.00045
ENSG00000211459	MT-RNR1	1286.2	2018.0	-0.6	1.6	5.00E-05
ENSG00000115616	SLC9A2	3.2	5.0	-0.7	1.6	5.00E-05
ENSG00000108582	CPD	62.6	98.3	-0.7	1.6	5.00E-05
ENSG00000120519	SLC10A7	3.1	4.8	-0.7	1.6	0.0066
ENSG00000104760	FGL1	55.1	86.6	-0.7	1.6	5.00E-05
ENSG00000110881	ASIC1	1.9	2.9	-0.7	1.6	0.0008
ENSG00000139734	DIAPH3	1.2	1.9	-0.7	1.6	0.00335
ENSG00000142627	EPHA2	30.4	47.8	-0.7	1.6	5.00E-05
ENSG00000136603	SKIL	11.7	18.5	-0.7	1.6	0.0001
ENSG00000080503	SMARCA2	10.7	16.7	-0.7	1.6	0.0002
ENSG00000153904	DDAH1	5.7	8.9	-0.7	1.6	0.0006
ENSG00000129317	PUS7L	5.2	8.2	-0.7	1.6	0.0001
ENSG00000179104	TMTC2	5.2	8.2	-0.7	1.6	5.00E-05
ENSG00000138386	NAB1	9.4	14.9	-0.7	1.6	5.00E-05
ENSG00000046604	DSG2	31.9	50.4	-0.7	1.6	5.00E-05
ENSG00000124766	SOX4	12.9	20.4	-0.7	1.6	5.00E-05
ENSG00000109586	GALNT7	37.5	59.4	-0.7	1.6	5.00E-05
ENSG00000069702	TGFBR3	1.6	2.6	-0.7	1.6	0.0001
ENSG00000133466	C1QTNF6	7.3	11.5	-0.7	1.6	5.00E-05
ENSG00000146247	PHIP	4.2	6.7	-0.7	1.6	5.00E-05
ENSG00000151150	ANK3	2.4	3.7	-0.7	1.6	0.00305
ENSG00000124429	POF1B	6.8	10.8	-0.7	1.6	5.00E-05
ENSG00000170624	SGCD	5.2	8.3	-0.7	1.6	0.00355
ENSG00000175274	TP53I11	26.8	42.7	-0.7	1.6	5.00E-05
ENSG00000119938	PPP1R3C	9.3	14.8	-0.7	1.6	5.00E-05
ENSG00000148344	PTGES	20.9	33.3	-0.7	1.6	5.00E-05
ENSG00000108639	SYNGR2	125.0	199.5	-0.7	1.6	5.00E-05
ENSG00000184384	MAML2	0.7	1.1	-0.7	1.6	0.0028
ENSG00000127329	PTPRB	1.3	2.0	-0.7	1.6	0.00035
ENSG00000114812	VIPR1	0.6	0.9	-0.7	1.6	0.00485
ENSG00000176788	BASP1	122.3	195.7	-0.7	1.6	5.00E-05
ENSG00000145012	LPP	14.5	23.3	-0.7	1.6	5.00E-05
ENSG00000106003	LFNG	2.2	3.5	-0.7	1.6	0.00385
ENSG00000099860	GADD45B	4.2	6.8	-0.7	1.6	0.0011
ENSG00000171723	GPHN	7.6	12.2	-0.7	1.6	0.00095
ENSG00000089057	SLC23A2	46.4	74.4	-0.7	1.6	5.00E-05

ENSG00000129493	HEATR5A	24.4	39.2	-0.7	1.6	5.00E-05
ENSG00000109321	AREG	3.7	6.0	-0.7	1.6	0.00605
ENSG00000047365	ARAP2	0.8	1.2	-0.7	1.6	0.00735
ENSG00000114805	PLCH1	2.4	3.8	-0.7	1.6	5.00E-05
ENSG00000160191	PDE9A	3.9	6.3	-0.7	1.6	0.00195
ENSG00000160588	MPZL3	0.7	1.2	-0.7	1.6	0.0073
ENSG00000185950	IRS2	18.2	29.4	-0.7	1.6	5.00E-05
ENSG00000125657	TNFSF9	12.3	19.8	-0.7	1.6	5.00E-05
ENSG00000133424	LARGE	2.4	3.9	-0.7	1.6	0.0009
ENSG00000133321	RARRES3	6.8	10.9	-0.7	1.6	0.00165
ENSG00000188660	LINC00319	1.2	2.0	-0.7	1.6	0.00185
ENSG00000148773	MKI67	5.4	8.8	-0.7	1.6	5.00E-05
ENSG00000111816	FRK	4.7	7.6	-0.7	1.6	5.00E-05
ENSG00000144891	AGTR1	2.9	4.7	-0.7	1.6	0.0019
ENSG00000120211	INSL4	14.6	23.8	-0.7	1.6	5.00E-05
ENSG00000196639	HRH1	1.4	2.3	-0.7	1.6	0.00135
ENSG00000151746	BICD1	7.0	11.4	-0.7	1.6	0.00115
ENSG00000110841	PPFIBP1	12.6	20.5	-0.7	1.6	5.00E-05
ENSG00000166147	FBN1	3.3	5.3	-0.7	1.6	0.0001
ENSG00000269028	MTRNR2L12	10.4	17.0	-0.7	1.6	0.0003
ENSG00000166165	CKB	17.3	28.2	-0.7	1.6	0.00065
ENSG00000088325	TPX2	10.1	16.4	-0.7	1.6	5.00E-05
ENSG00000159184	HOXB13	1.7	2.8	-0.7	1.6	0.0004
ENSG00000123416	TUBA1B	116.6	189.9	-0.7	1.6	5.00E-05
ENSG00000163558	PRKCI	12.7	20.7	-0.7	1.6	5.00E-05
ENSG00000163507	KIAA1524	3.2	5.3	-0.7	1.6	0.0004
ENSG00000136824	SMC2	4.1	6.8	-0.7	1.6	5.00E-05
ENSG00000143344	RGL1	4.1	6.8	-0.7	1.6	5.00E-05
ENSG00000139318	DUSP6	12.7	20.8	-0.7	1.6	5.00E-05
ENSG00000110723	EXPH5	0.5	0.8	-0.7	1.6	0.00075
ENSG00000168079	SCARA5	5.7	9.3	-0.7	1.6	5.00E-05
ENSG00000134755	DSC2	1.2	1.9	-0.7	1.6	0.00105
ENSG00000088367	EPB41L1	27.9	45.8	-0.7	1.6	0.0026
ENSG00000130818	ZNF426	0.8	1.3	-0.7	1.6	0.00835
ENSG00000005108	THSD7A	6.8	11.2	-0.7	1.6	5.00E-05
ENSG00000197119	SLC25A29	23.1	37.9	-0.7	1.6	0.0016
ENSG00000139132	FGD4	2.2	3.6	-0.7	1.6	0.0001
ENSG00000148498	PARD3	29.9	49.0	-0.7	1.6	5.00E-05
ENSG00000176532	PRR15	20.6	33.8	-0.7	1.6	5.00E-05
ENSG00000118777	ABCG2	8.6	14.1	-0.7	1.6	0.0002
ENSG00000177409	SAMD9L	0.3	0.5	-0.7	1.6	0.0078
ENSG00000143036	SLC44A3	1.7	2.8	-0.7	1.6	0.00545
ENSG00000109339	MAPK10	0.6	1.0	-0.7	1.6	0.00355
ENSG00000142207	URB1	4.7	7.8	-0.7	1.6	5.00E-05
ENSG00000184205	TSPYL2	8.7	14.3	-0.7	1.6	5.00E-05

ENSG00000100558	PLEK2	2.1	3.5	-0.7	1.6	0.0062
ENSG00000175130	MARCKSL1	33.7	55.5	-0.7	1.6	5.00E-05
ENSG00000132646	PCNA	67.2	110.8	-0.7	1.6	5.00E-05
ENSG00000139083	ETV6	4.2	6.9	-0.7	1.6	5.00E-05
ENSG00000149636	DSN1	4.5	7.4	-0.7	1.7	0.0004
ENSG00000266714	MYO15B	81.7	135.0	-0.7	1.7	0.0048
ENSG00000198682	PAPSS2	40.3	66.6	-0.7	1.7	5.00E-05
ENSG00000105738	SIPA1L3	19.6	32.4	-0.7	1.7	5.00E-05
ENSG00000042317	SPATA7	8.4	14.0	-0.7	1.7	0.0023
ENSG00000102218	RP2	6.6	10.9	-0.7	1.7	5.00E-05
ENSG00000213145	CRIP1	111.2	184.5	-0.7	1.7	5.00E-05
ENSG00000159640	ACE	0.2	0.3	-0.7	1.7	0.00795
ENSG00000006611	USH1C	1.4	2.3	-0.7	1.7	0.00585
ENSG00000065809	FAM107B	74.1	123.2	-0.7	1.7	5.00E-05
ENSG00000153113	CAST	83.2	138.5	-0.7	1.7	5.00E-05
ENSG00000138061	CYP1B1	16.1	26.8	-0.7	1.7	5.00E-05
ENSG00000162545	CAMK2N1	28.5	47.5	-0.7	1.7	5.00E-05
ENSG00000171241	SHCBP1	6.2	10.3	-0.7	1.7	5.00E-05
ENSG00000224081	LINC01057	2.7	4.5	-0.7	1.7	0.00055
ENSG00000106258	CYP3A5	3.0	5.0	-0.7	1.7	0.0023
ENSG00000139323	POC1B	11.3	18.8	-0.7	1.7	0.00015
ENSG00000181744	C3orf58	8.2	13.7	-0.7	1.7	5.00E-05
ENSG00000188641	DPYD	3.1	5.2	-0.7	1.7	0.0004
ENSG00000197747	S100A10	221.0	370.1	-0.7	1.7	5.00E-05
ENSG00000176697	BDNF	4.7	7.9	-0.7	1.7	5.00E-05
ENSG00000197892	KIF13B	6.0	10.0	-0.7	1.7	5.00E-05
ENSG00000101333	PLCB4	5.3	8.9	-0.7	1.7	0.0001
ENSG00000081026	MAGI3	2.8	4.7	-0.8	1.7	5.00E-05
ENSG00000211455	STK38L	7.2	12.2	-0.8	1.7	5.00E-05
ENSG00000111490	TBC1D30	1.9	3.1	-0.8	1.7	0.0013
ENSG00000139116	KIF21A	18.3	30.8	-0.8	1.7	5.00E-05
ENSG00000141449	GREB1L	0.4	0.6	-0.8	1.7	0.00905
ENSG00000176208	ATAD5	0.7	1.2	-0.8	1.7	0.001
ENSG00000113368	LMNB1	5.5	9.3	-0.8	1.7	0.0002
ENSG00000247844	CCAT1	6.4	10.8	-0.8	1.7	5.00E-05
ENSG00000135750	KCNK1	17.0	28.8	-0.8	1.7	5.00E-05
ENSG00000151229	SLC2A13	6.9	11.8	-0.8	1.7	5.00E-05
ENSG00000120802	TMPO	22.8	38.7	-0.8	1.7	5.00E-05
ENSG00000198554	WDHD1	2.3	3.9	-0.8	1.7	5.00E-05
ENSG00000255414	LINC01059	1.2	2.0	-0.8	1.7	0.0039
ENSG00000171631	P2RY6	4.5	7.6	-0.8	1.7	0.00095
ENSG00000158470	B4GALT5	21.4	36.4	-0.8	1.7	5.00E-05
ENSG00000177084	POLE	4.4	7.5	-0.8	1.7	5.00E-05
ENSG00000188643	S100A16	105.4	179.4	-0.8	1.7	5.00E-05
ENSG00000180535	BHLHA15	3.9	6.6	-0.8	1.7	0.00315

ENSG00000092470	WDR76	1.3	2.2	-0.8	1.7	0.00315
ENSG00000107821	KAZALD1	4.8	8.1	-0.8	1.7	0.0008
ENSG00000114790	ARHGEF26	1.5	2.5	-0.8	1.7	0.00125
ENSG00000257027	RP11-705C15.3	1.4	2.3	-0.8	1.7	0.00175
ENSG00000139725	RHOF	26.6	45.5	-0.8	1.7	5.00E-05
ENSG00000170004	CHD3	31.8	54.3	-0.8	1.7	5.00E-05
ENSG00000118640	VAMP8	14.8	25.3	-0.8	1.7	5.00E-05
ENSG00000122966	CIT	2.3	4.0	-0.8	1.7	0.00175
ENSG00000214391	RP11-121L10.3	2.2	3.7	-0.8	1.7	0.0008
ENSG00000171951	SCG2	2.1	3.6	-0.8	1.7	0.00085
ENSG00000108691	CCL2	3.8	6.5	-0.8	1.7	0.00265
ENSG00000136044	APPL2	20.3	34.8	-0.8	1.7	5.00E-05
ENSG00000182168	UNC5C	0.2	0.4	-0.8	1.7	0.00135
ENSG00000197933	ZNF823	0.6	1.0	-0.8	1.7	0.0032
ENSG00000138696	BMPR1B	7.9	13.6	-0.8	1.7	5.00E-05
ENSG00000123473	STIL	2.0	3.4	-0.8	1.7	0.00025
ENSG00000155130	MARCKS	33.8	58.2	-0.8	1.7	5.00E-05
ENSG00000135318	NT5E	23.4	40.4	-0.8	1.7	5.00E-05
ENSG00000187546	AGMO	0.8	1.4	-0.8	1.7	0.00565
ENSG00000153956	CACNA2D1	6.3	10.9	-0.8	1.7	5.00E-05
ENSG00000144645	OSBPL10	12.6	21.8	-0.8	1.7	0.0003
ENSG00000178162	AC140481.1	0.7	1.3	-0.8	1.7	0.00275
ENSG00000173237	C11orf86	1.5	2.5	-0.8	1.7	0.00685
ENSG00000170647	TMEM133	3.9	6.8	-0.8	1.7	0.0005
ENSG00000125885	MCM8	5.4	9.4	-0.8	1.7	5.00E-05
ENSG00000118515	SGK1	3.8	6.6	-0.8	1.7	5.00E-05
ENSG00000112837	TBX18	15.2	26.4	-0.8	1.7	5.00E-05
ENSG00000235162	C12orf75	112.6	196.0	-0.8	1.7	5.00E-05
ENSG00000132470	ITGB4	38.4	67.0	-0.8	1.7	0.0001
ENSG00000132437	DDC	3.6	6.3	-0.8	1.7	5.00E-05
ENSG00000267056	AC005336.4	9.2	16.0	-0.8	1.7	5.00E-05
ENSG00000104738	MCM4	7.3	12.7	-0.8	1.7	5.00E-05
ENSG00000197329	PELI1	2.3	4.0	-0.8	1.8	5.00E-05
ENSG00000184445	KNTC1	4.4	7.7	-0.8	1.8	0.00035
ENSG00000164683	HEY1	1.3	2.2	-0.8	1.8	0.0014
ENSG00000071073	MGAT4A	1.1	1.9	-0.8	1.8	0.0019
ENSG00000112699	GMDS	23.2	40.8	-0.8	1.8	5.00E-05
ENSG00000100297	MCM5	3.3	5.9	-0.8	1.8	0.00035
ENSG00000250221	KRT8P32	0.6	1.1	-0.8	1.8	0.0054
ENSG00000168453	HR	5.4	9.5	-0.8	1.8	5.00E-05
ENSG00000166426	CRABP1	5.8	10.4	-0.8	1.8	0.0002
ENSG00000182809	CRIP2	4.2	7.4	-0.8	1.8	0.0008
ENSG00000109881	CCDC34	8.7	15.5	-0.8	1.8	5.00E-05
ENSG00000021300	PLEKHB1	0.6	1.0	-0.8	1.8	0.0002
ENSG00000105825	TFPI2	37.8	67.2	-0.8	1.8	5.00E-05

ENSG00000272761	RP11-572C15.6	0.3	0.5	-0.8	1.8	0.0051
ENSG00000166532	RIMKLB	41.5	73.8	-0.8	1.8	5.00E-05
ENSG00000123094	RASSF8	2.9	5.2	-0.8	1.8	5.00E-05
ENSG00000187193	MT1X	51.8	92.3	-0.8	1.8	5.00E-05
ENSG00000198018	ENTPD7	4.5	8.0	-0.8	1.8	0.00685
ENSG00000150630	VEGFC	3.8	6.8	-0.8	1.8	5.00E-05
ENSG00000155465	SLC7A7	57.0	101.9	-0.8	1.8	5.00E-05
ENSG00000256579	AC135776.1	6.6	11.7	-0.8	1.8	0.00635
ENSG00000186193	SAPCD2	2.2	4.0	-0.8	1.8	5.00E-05
ENSG00000156869	FRRS1	1.8	3.3	-0.8	1.8	0.0069
ENSG00000128833	MYO5C	8.2	14.8	-0.8	1.8	5.00E-05
ENSG00000158555	GDPD5	2.0	3.5	-0.8	1.8	0.00025
ENSG00000119969	HELLS	4.0	7.3	-0.8	1.8	5.00E-05
ENSG00000214114	MYCBP	4.5	8.1	-0.8	1.8	0.003
ENSG00000170456	DENND5B	7.1	12.9	-0.9	1.8	5.00E-05
ENSG00000118418	HMGN3	16.6	30.0	-0.9	1.8	5.00E-05
ENSG00000101003	GINS1	4.7	8.4	-0.9	1.8	5.00E-05
ENSG00000196154	S100A4	456.6	829.1	-0.9	1.8	5.00E-05
ENSG00000165895	ARHGAP42	6.3	11.4	-0.9	1.8	5.00E-05
ENSG00000184992	BRI3BP	7.8	14.2	-0.9	1.8	5.00E-05
ENSG00000076003	MCM6	3.1	5.6	-0.9	1.8	5.00E-05
ENSG00000116962	NID1	0.4	0.6	-0.9	1.8	0.00285
ENSG00000198650	TAT	0.3	0.5	-0.9	1.8	0.0026
ENSG00000153246	PLA2R1	0.6	1.2	-0.9	1.8	0.00035
ENSG00000184564	SLITRK6	8.5	15.6	-0.9	1.8	5.00E-05
ENSG00000091428	RAPGEF4	0.4	0.7	-0.9	1.8	0.00495
ENSG00000166741	NNMT	75.6	138.4	-0.9	1.8	5.00E-05
ENSG00000156802	ATAD2	2.9	5.3	-0.9	1.8	5.00E-05
ENSG00000157890	MEGF11	0.3	0.6	-0.9	1.8	0.00645
ENSG00000214381	LINC00488	0.5	0.9	-0.9	1.8	0.0023
ENSG00000184226	PCDH9	4.5	8.2	-0.9	1.8	5.00E-05
ENSG00000135063	FAM189A2	1.1	2.1	-0.9	1.8	0.0009
ENSG00000176907	C8orf4	48.6	89.2	-0.9	1.8	5.00E-05
ENSG00000187244	BCAM	7.3	13.4	-0.9	1.8	5.00E-05
ENSG00000198223	CSF2RA	11.6	21.4	-0.9	1.8	5.00E-05
ENSG00000143631	FLG	0.2	0.3	-0.9	1.8	0.0034
ENSG00000189143	CLDN4	1.9	3.4	-0.9	1.8	0.00025
ENSG00000052126	PLEKHA5	6.0	11.1	-0.9	1.8	5.00E-05
ENSG00000113319	RASGRF2	2.5	4.6	-0.9	1.9	0.0005
ENSG00000119508	NR4A3	1.2	2.3	-0.9	1.9	0.0001
ENSG00000183580	FBXL7	0.4	0.7	-0.9	1.9	0.0018
ENSG00000126217	MCF2L	0.9	1.8	-0.9	1.9	5.00E-05
ENSG00000224520	KRT8P45	2.8	5.2	-0.9	1.9	5.00E-05
ENSG00000179403	VWA1	5.0	9.3	-0.9	1.9	5.00E-05
ENSG00000163611	SPICE1	3.2	5.9	-0.9	1.9	5.00E-05

ENSG00000128655	PDE11A	0.2	0.4	-0.9	1.9	0.00185
ENSG00000122952	ZWINT	6.9	12.9	-0.9	1.9	5.00E-05
ENSG00000123684	LPGAT1	35.7	66.6	-0.9	1.9	5.00E-05
ENSG00000041353	RAB27B	22.0	41.1	-0.9	1.9	5.00E-05
ENSG00000237682	RP3-514P16.1	0.2	0.4	-0.9	1.9	0.0089
ENSG00000206530	WDR52	2.5	4.7	-0.9	1.9	0.00025
ENSG00000134830	C5AR2	0.3	0.5	-0.9	1.9	0.0025
ENSG00000161955	TNFSF13	2.9	5.4	-0.9	1.9	0.00265
ENSG00000155158	TTC39B	3.5	6.7	-0.9	1.9	5.00E-05
ENSG00000188906	LRRK2	3.9	7.3	-0.9	1.9	5.00E-05
ENSG00000170312	CDK1	12.3	23.1	-0.9	1.9	5.00E-05
ENSG00000112419	PHACTR2	2.3	4.4	-0.9	1.9	0.0001
ENSG00000164045	CDC25A	0.7	1.3	-0.9	1.9	0.00035
ENSG00000125398	SOX9	4.6	8.7	-0.9	1.9	5.00E-05
ENSG00000162174	ASRGL1	3.0	5.6	-0.9	1.9	0.0042
ENSG00000115590	IL1R2	1.2	2.2	-0.9	1.9	0.0012
ENSG00000123080	CDKN2C	4.9	9.4	-0.9	1.9	5.00E-05
ENSG00000157064	NMNAT2	2.6	4.9	-0.9	1.9	5.00E-05
ENSG00000106686	SPATA6L	2.7	5.1	-0.9	1.9	0.004
ENSG00000249119	MTND6P4	97.0	184.3	-0.9	1.9	0.0045
ENSG00000114541	FRMD4B	1.5	2.9	-0.9	1.9	5.00E-05
ENSG00000102934	PLLP	1.6	3.1	-0.9	1.9	0.00025
ENSG00000157557	ETS2	13.0	24.8	-0.9	1.9	5.00E-05
ENSG00000178445	GLDC	2.2	4.1	-0.9	1.9	5.00E-05
ENSG00000108821	COL1A1	0.9	1.8	-0.9	1.9	0.0031
ENSG00000081913	PHLPP1	1.3	2.5	-0.9	1.9	5.00E-05
ENSG00000125462	C1orf61	1.3	2.5	-0.9	1.9	0.0001
ENSG00000121690	DEPDC7	1.2	2.3	-0.9	1.9	0.0006
ENSG00000137486	ARRB1	4.6	8.8	-0.9	1.9	5.00E-05
ENSG00000167900	TK1	10.5	20.0	-0.9	1.9	5.00E-05
ENSG00000138347	MYPN	0.5	0.9	-0.9	1.9	0.0021
ENSG00000106789	CORO2A	2.1	4.1	-0.9	1.9	5.00E-05
ENSG00000059804	SLC2A3	30.3	58.6	-1.0	1.9	5.00E-05
ENSG00000169435	RASSF6	3.5	6.8	-1.0	1.9	5.00E-05
ENSG00000167711	SERPINF2	0.9	1.7	-1.0	1.9	0.0001
ENSG00000085840	ORC1	0.6	1.2	-1.0	1.9	0.00035
ENSG00000120756	PLS1	25.3	49.2	-1.0	1.9	5.00E-05
ENSG00000172296	SPTLC3	2.0	3.9	-1.0	1.9	0.0094
ENSG00000094755	GABRP	2.2	4.2	-1.0	1.9	0.00715
ENSG00000117461	PIK3R3	0.8	1.5	-1.0	1.9	0.00075
ENSG00000125726	CD70	21.7	42.2	-1.0	1.9	5.00E-05
ENSG00000023171	GRAMD1B	15.8	30.8	-1.0	1.9	5.00E-05
ENSG00000075240	GRAMD4	6.3	12.2	-1.0	2.0	5.00E-05
ENSG00000165272	AQP3	10.7	20.9	-1.0	2.0	5.00E-05
ENSG00000163735	CXCL5	359.6	705.5	-1.0	2.0	5.00E-05

ENSG00000111665	CDCA3	4.4	8.7	-1.0	2.0	0.0009
ENSG00000170439	METTL7B	4.3	8.4	-1.0	2.0	0.00545
ENSG00000171766	GATM	4.8	9.4	-1.0	2.0	5.00E-05
ENSG00000214012	KRT18P38	1.9	3.8	-1.0	2.0	0.0001
ENSG00000128917	DLL4	0.3	0.6	-1.0	2.0	0.0012
ENSG00000258474	RP11-187E13.1	2.0	4.0	-1.0	2.0	0.0019
ENSG00000267573	KRT8P5	1.4	2.8	-1.0	2.0	5.00E-05
ENSG00000167772	ANGPTL4	9.8	19.4	-1.0	2.0	0.0066
ENSG00000012171	SEMA3B	12.6	25.0	-1.0	2.0	5.00E-05
ENSG00000137310	TCF19	1.0	1.9	-1.0	2.0	0.00445
ENSG00000196878	LAMB3	9.6	19.1	-1.0	2.0	5.00E-05
ENSG00000141429	GALNT1	40.0	79.6	-1.0	2.0	5.00E-05
ENSG00000138771	SHROOM3	2.1	4.1	-1.0	2.0	5.00E-05
ENSG00000112576	CCND3	40.5	80.6	-1.0	2.0	5.00E-05
ENSG00000006283	CACNA1G	0.8	1.5	-1.0	2.0	5.00E-05
ENSG00000174371	EXO1	1.8	3.6	-1.0	2.0	0.0006
ENSG00000260963	RP11-297L17.2	1.9	3.7	-1.0	2.0	0.0051
ENSG00000164265	SCGB3A2	1.6	3.1	-1.0	2.0	0.00585
ENSG00000121858	TNFSF10	0.6	1.2	-1.0	2.0	0.0053
ENSG00000104267	CA2	6.3	12.6	-1.0	2.0	5.00E-05
ENSG00000162552	WNT4	1.2	2.4	-1.0	2.0	0.0029
ENSG00000117143	UAP1	17.0	33.9	-1.0	2.0	5.00E-05
ENSG00000132031	MATN3	3.0	6.0	-1.0	2.0	5.00E-05
ENSG00000250910	AC097467.2	0.2	0.4	-1.0	2.0	0.0002
ENSG00000233461	RP11-295G20.2	18.7	37.5	-1.0	2.0	5.00E-05
ENSG00000100479	POLE2	1.4	2.8	-1.0	2.0	0.0011
ENSG00000170786	SDR16C5	1.6	3.3	-1.0	2.0	0.00015
ENSG00000126947	ARMCX1	0.5	1.1	-1.0	2.0	0.00825
ENSG00000137642	SORL1	2.6	5.2	-1.0	2.0	5.00E-05
ENSG00000125730	C3	29.0	58.6	-1.0	2.0	5.00E-05
ENSG00000181449	SOX2	4.1	8.2	-1.0	2.0	0.0009
ENSG00000213943	KRT18P17	0.5	1.0	-1.0	2.0	0.0014
ENSG00000167157	PRRX2	0.4	0.9	-1.0	2.0	0.0056
ENSG00000185186	LINC00313	5.4	10.9	-1.0	2.0	0.0006
ENSG00000181690	PLAG1	0.2	0.4	-1.0	2.0	0.0013
ENSG00000123843	C4BPB	0.3	0.6	-1.0	2.0	0.0049
ENSG00000134369	NAV1	2.5	5.1	-1.0	2.0	0.0021
ENSG00000114698	PLSCR4	6.7	13.7	-1.0	2.0	5.00E-05
ENSG00000164078	MST1R	4.6	9.4	-1.0	2.0	5.00E-05
ENSG00000120054	CPN1	0.4	0.7	-1.0	2.0	0.00075
ENSG00000178999	AURKB	6.6	13.4	-1.0	2.1	5.00E-05
ENSG00000143476	DTL	1.3	2.7	-1.0	2.1	0.0001
ENSG00000050405	LIMA1	1.2	2.5	-1.0	2.1	5.00E-05
ENSG00000173227	SYT12	0.4	0.9	-1.0	2.1	5.00E-05
ENSG00000164684	ZNF704	2.4	4.9	-1.0	2.1	0.0014

ENSG00000011422	PLAUR	19.5	40.2	-1.0	2.1	5.00E-05
ENSG00000260461	RP11-541N10.3	0.7	1.4	-1.0	2.1	5.00E-05
ENSG00000135378	PRRG4	0.2	0.5	-1.0	2.1	0.00045
ENSG00000165891	E2F7	0.7	1.5	-1.0	2.1	5.00E-05
ENSG00000214207	KRT18P10	1.3	2.7	-1.0	2.1	0.0015
ENSG00000136492	BRIP1	0.8	1.6	-1.0	2.1	0.00035
ENSG00000231131	RP11-346D6.6	1.1	2.3	-1.0	2.1	0.0004
ENSG00000165474	GJB2	0.4	0.9	-1.0	2.1	0.00295
ENSG00000111261	MANSC1	8.1	16.8	-1.0	2.1	5.00E-05
ENSG00000114374	USP9Y	2.9	6.0	-1.1	2.1	0.0015
ENSG00000112541	PDE10A	4.3	9.0	-1.1	2.1	0.00035
ENSG00000117115	PADI2	0.2	0.5	-1.1	2.1	0.00055
ENSG00000103089	FA2H	29.2	61.1	-1.1	2.1	5.00E-05
ENSG00000135766	EGLN1	28.1	59.1	-1.1	2.1	5.00E-05
ENSG00000143416	SELENBP1	12.8	26.9	-1.1	2.1	5.00E-05
ENSG00000270145	CTD-2267D19.6	0.5	1.1	-1.1	2.1	0.0029
ENSG00000236824	BCYRN1	0.9	2.0	-1.1	2.1	5.00E-05
ENSG00000116785	CFHR3	1.7	3.7	-1.1	2.1	0.0002
ENSG00000257594	GALNT4	5.4	11.5	-1.1	2.1	5.00E-05
ENSG00000065361	ERBB3	2.5	5.3	-1.1	2.1	0.0081
ENSG00000124107	SLPI	77.3	164.2	-1.1	2.1	5.00E-05
ENSG00000167232	ZNF91	0.2	0.4	-1.1	2.1	0.0017
ENSG00000103460	TOX3	5.7	12.1	-1.1	2.1	5.00E-05
ENSG00000164176	EDIL3	0.5	1.1	-1.1	2.1	0.0032
ENSG00000111331	OAS3	4.5	9.6	-1.1	2.1	5.00E-05
ENSG00000152217	SETBP1	1.2	2.6	-1.1	2.1	5.00E-05
ENSG00000171303	KCNK3	0.5	1.0	-1.1	2.1	5.00E-05
ENSG00000185101	ANO9	0.5	1.0	-1.1	2.1	0.0023
ENSG00000135362	PRR5L	1.1	2.3	-1.1	2.1	5.00E-05
ENSG00000018236	CNTN1	110.0	235.8	-1.1	2.1	5.00E-05
ENSG00000203635	AC144450.2	0.2	0.3	-1.1	2.1	0.0044
ENSG00000144063	MALL	22.6	48.4	-1.1	2.1	5.00E-05
ENSG00000132326	PER2	5.7	12.2	-1.1	2.1	5.00E-05
ENSG00000233493	TMEM238	3.4	7.2	-1.1	2.1	5.00E-05
ENSG00000196353	CPNE4	1.9	4.0	-1.1	2.2	5.00E-05
ENSG00000178726	THBD	7.4	15.9	-1.1	2.2	5.00E-05
ENSG00000106537	TSPAN13	30.7	66.3	-1.1	2.2	5.00E-05
ENSG00000106546	AHR	18.6	40.1	-1.1	2.2	5.00E-05
ENSG00000093009	CDC45	1.8	3.9	-1.1	2.2	0.00125
ENSG00000198879	SFMBT2	1.3	2.8	-1.1	2.2	5.00E-05
ENSG00000225485	ARHGAP23	3.8	8.2	-1.1	2.2	5.00E-05
ENSG00000159713	TPPP3	1.0	2.2	-1.1	2.2	0.0003
ENSG00000111247	RAD51AP1	3.6	7.8	-1.1	2.2	5.00E-05
ENSG00000182179	UBA7	0.2	0.4	-1.1	2.2	0.0029
ENSG00000152056	AP1S3	12.9	28.3	-1.1	2.2	5.00E-05

ENSG00000149798	CDC42EP2	6.4	14.0	-1.1	2.2	5.00E-05
ENSG00000248590	GLDCP1	0.1	0.3	-1.1	2.2	0.00305
ENSG00000104140	RHOV	4.5	9.8	-1.1	2.2	5.00E-05
ENSG00000165244	ZNF367	0.4	1.0	-1.1	2.2	0.0038
ENSG00000173848	NET1	20.8	46.1	-1.1	2.2	5.00E-05
ENSG00000169116	PARM1	8.6	19.1	-1.1	2.2	5.00E-05
ENSG00000225783	MIAT	0.2	0.4	-1.2	2.2	5.00E-05
ENSG00000138193	PLCE1	1.1	2.5	-1.2	2.2	0.0004
ENSG00000171219	CDC42BPG	0.2	0.5	-1.2	2.2	0.00355
ENSG00000042493	CAPG	15.9	35.9	-1.2	2.3	5.00E-05
ENSG00000142089	IFITM3	17.0	38.4	-1.2	2.3	5.00E-05
ENSG00000166510	CCDC68	9.5	21.4	-1.2	2.3	5.00E-05
ENSG00000204616	TRIM31	0.4	1.0	-1.2	2.3	0.0001
ENSG00000094804	CDC6	7.8	17.6	-1.2	2.3	5.00E-05
ENSG00000168743	NPNT	0.2	0.5	-1.2	2.3	0.00955
ENSG00000113532	ST8SIA4	3.3	7.6	-1.2	2.3	5.00E-05
ENSG00000261829	RP11-223I10.1	0.3	0.6	-1.2	2.3	0.00845
ENSG00000079385	CEACAM1	7.6	17.4	-1.2	2.3	0.00025
ENSG00000163734	CXCL3	11.7	26.9	-1.2	2.3	5.00E-05
ENSG00000080493	SLC4A4	1.3	2.9	-1.2	2.3	5.00E-05
ENSG00000175040	CHST2	0.7	1.7	-1.2	2.3	5.00E-05
ENSG00000163110	PDLIM5	42.2	97.4	-1.2	2.3	5.00E-05
ENSG00000204262	COL5A2	16.5	38.1	-1.2	2.3	5.00E-05
ENSG00000105289	TJP3	3.4	7.9	-1.2	2.3	5.00E-05
ENSG00000054598	FOXC1	4.4	10.2	-1.2	2.3	5.00E-05
ENSG00000239887	C1orf226	0.5	1.2	-1.2	2.3	0.0001
ENSG00000082458	DLG3	3.1	7.1	-1.2	2.3	5.00E-05
ENSG00000143842	SOX13	5.6	13.0	-1.2	2.3	5.00E-05
ENSG00000198208	RPS6KL1	0.3	0.6	-1.2	2.3	0.0002
ENSG00000235750	KIAA0040	0.4	0.9	-1.2	2.3	5.00E-05
ENSG00000198157	HMGN5	1.5	3.6	-1.2	2.3	0.0005
ENSG00000163082	SGPP2	2.8	6.5	-1.2	2.3	5.00E-05
ENSG00000150722	PPP1R1C	0.7	1.7	-1.2	2.3	0.0009
ENSG00000171564	FGB	80.2	188.4	-1.2	2.3	5.00E-05
ENSG00000168306	ACOX2	1.8	4.3	-1.2	2.4	5.00E-05
ENSG00000172602	RND1	5.2	12.3	-1.2	2.4	5.00E-05
ENSG00000186526	CYP4F8	0.2	0.5	-1.2	2.4	0.0069
ENSG00000076356	PLXNA2	2.3	5.3	-1.2	2.4	5.00E-05
ENSG00000180210	F2	0.5	1.3	-1.2	2.4	5.00E-05
ENSG00000000971	CFH	35.8	84.7	-1.2	2.4	5.00E-05
ENSG00000104537	ANXA13	18.9	44.8	-1.2	2.4	5.00E-05
ENSG00000005981	ASB4	0.5	1.3	-1.3	2.4	0.0007
ENSG00000106025	TSPAN12	0.9	2.2	-1.3	2.4	0.00025
ENSG00000227502	RP1-249H1.4	0.2	0.5	-1.3	2.4	0.0005
ENSG00000172159	FRMD3	2.1	4.9	-1.3	2.4	5.00E-05

ENSG00000179913	B3GNT3	3.9	9.5	-1.3	2.4	5.00E-05
ENSG00000185149	NPY2R	0.2	0.4	-1.3	2.4	0.0051
ENSG00000101144	BMP7	0.3	0.6	-1.3	2.4	0.0003
ENSG00000099725	PRKY	0.5	1.2	-1.3	2.4	0.00035
ENSG00000226958	CTD-2328D6.1	3166.3	7678.9	-1.3	2.4	5.00E-05
ENSG00000218052	RP11-561C5.5	0.3	0.6	-1.3	2.4	0.00775
ENSG00000198692	EIF1AY	10.4	25.3	-1.3	2.4	5.00E-05
ENSG00000170703	TTLL6	0.8	1.9	-1.3	2.4	5.00E-05
ENSG00000157227	MMP14	0.9	2.3	-1.3	2.5	5.00E-05
ENSG00000114200	BCHE	1.0	2.4	-1.3	2.5	5.00E-05
ENSG00000012817	KDM5D	2.7	6.7	-1.3	2.5	0.00185
ENSG00000171431	KRT20	1.0	2.6	-1.3	2.5	0.00015
ENSG00000034063	UHRF1	1.0	2.4	-1.3	2.5	5.00E-05
ENSG00000130600	H19	0.3	0.6	-1.3	2.5	0.0091
ENSG00000170476	MZB1	0.4	1.0	-1.3	2.5	0.00125
ENSG00000172137	CALB2	0.3	0.8	-1.3	2.5	5.00E-05
ENSG00000172403	SYNPO2	1.2	3.1	-1.3	2.5	5.00E-05
ENSG00000169894	MUC3A	0.2	0.5	-1.3	2.5	0.0015
ENSG00000168237	GLYCTK	4.4	11.1	-1.3	2.5	0.00925
ENSG00000101842	VSIG1	0.1	0.4	-1.3	2.5	0.00105
ENSG00000174607	UGT8	0.3	0.7	-1.3	2.5	0.0004
ENSG00000150471	LPHN3	0.2	0.6	-1.3	2.5	0.0007
ENSG00000165061	ZMAT4	0.5	1.3	-1.3	2.5	0.0003
ENSG00000257660	RP11-579D7.4	0.7	1.9	-1.3	2.5	0.00045
ENSG00000132821	VSTM2L	1.5	3.8	-1.3	2.5	5.00E-05
ENSG00000170373	CST1	1.4	3.4	-1.4	2.6	0.00015
ENSG00000058085	LAMC2	3.2	8.3	-1.4	2.6	5.00E-05
ENSG00000168772	CXXC4	0.6	1.6	-1.4	2.6	5.00E-05
ENSG00000167766	ZNF83	0.5	1.3	-1.4	2.6	5.00E-05
ENSG00000242147	RP13-463N16.6	0.2	0.6	-1.4	2.6	0.009
ENSG00000004948	CALCR	0.2	0.4	-1.4	2.6	0.00045
ENSG00000235269	AL162759.1	3.0	7.7	-1.4	2.6	5.00E-05
ENSG00000115252	PDE1A	0.3	0.9	-1.4	2.6	0.00975
ENSG00000117472	TSPAN1	1.9	5.0	-1.4	2.6	0.0031
ENSG00000164976	KIAA1161	3.2	8.2	-1.4	2.6	5.00E-05
ENSG00000250722	SEPP1	0.8	2.1	-1.4	2.6	5.00E-05
ENSG00000168077	SCARA3	2.5	6.7	-1.4	2.6	5.00E-05
ENSG00000147394	ZNF185	2.3	5.9	-1.4	2.6	5.00E-05
ENSG00000095539	SEMA4G	9.6	25.3	-1.4	2.6	5.00E-05
ENSG00000092853	CLSPN	0.6	1.5	-1.4	2.6	0.0011
ENSG00000197959	DNM3	0.3	0.9	-1.4	2.6	0.0074
ENSG00000235978	AC018816.3	0.4	1.2	-1.4	2.6	0.0046
ENSG00000162777	DENND2D	0.8	2.2	-1.4	2.7	5.00E-05
ENSG00000128849	CGNL1	0.2	0.6	-1.4	2.7	5.00E-05
ENSG00000138792	ENPEP	0.2	0.5	-1.4	2.7	0.0006

ENSG00000125735	TNFSF14	0.3	0.8	-1.4	2.7	0.00035
ENSG00000170959	DCDC1	1.4	3.7	-1.4	2.7	5.00E-05
ENSG00000086730	LAT2	1.3	3.4	-1.4	2.7	5.00E-05
ENSG00000171557	FGG	83.2	222.7	-1.4	2.7	5.00E-05
ENSG00000205809	KLRC2	1.5	3.9	-1.4	2.7	0.00025
ENSG00000184779	RPS17	61.5	165.0	-1.4	2.7	5.00E-05
ENSG00000007968	E2F2	0.2	0.6	-1.4	2.7	5.00E-05
ENSG00000198478	SH3BGRL2	1.7	4.6	-1.4	2.7	5.00E-05
ENSG00000249867	RP11-115J23.1	0.3	0.8	-1.4	2.7	0.00375
ENSG00000117226	GBP3	1.1	3.0	-1.4	2.7	5.00E-05
ENSG00000168298	HIST1H1E	0.2	0.4	-1.4	2.7	0.00585
ENSG00000154734	ADAMTS1	0.2	0.4	-1.4	2.7	0.00065
ENSG00000198691	ABCA4	0.1	0.4	-1.4	2.7	0.0031
ENSG00000129824	RPS4Y1	60.3	163.8	-1.4	2.7	5.00E-05
ENSG00000006747	SCIN	0.3	0.7	-1.4	2.7	5.00E-05
ENSG00000169213	RAB3B	2.1	5.8	-1.4	2.7	5.00E-05
ENSG00000167244	IGF2	0.3	0.7	-1.5	2.7	5.00E-05
ENSG00000119888	EPCAM	1.8	5.0	-1.5	2.7	5.00E-05
ENSG00000105011	ASF1B	1.5	4.1	-1.5	2.7	5.00E-05
ENSG00000198959	TGM2	44.7	123.1	-1.5	2.8	5.00E-05
ENSG00000164142	FAM160A1	0.2	0.4	-1.5	2.8	0.00025
ENSG00000182489	XKRX	0.3	0.8	-1.5	2.8	5.00E-05
ENSG00000196628	TCF4	1.7	4.7	-1.5	2.8	5.00E-05
ENSG00000125999	BPIFB1	1.2	3.5	-1.5	2.8	5.00E-05
ENSG00000102554	KLF5	23.0	64.1	-1.5	2.8	5.00E-05
ENSG00000144847	IGSF11	0.7	2.0	-1.5	2.8	5.00E-05
ENSG00000231483	RP11-336A10.5	0.2	0.6	-1.5	2.8	0.00685
ENSG00000177570	SAMD12	0.5	1.3	-1.5	2.8	5.00E-05
ENSG00000133328	HRASLS2	0.3	1.0	-1.5	2.8	0.0003
ENSG00000104490	NCALD	2.2	6.2	-1.5	2.8	5.00E-05
ENSG00000169862	CTNND2	0.1	0.4	-1.5	2.8	0.00735
ENSG00000065328	MCM10	0.6	1.7	-1.5	2.8	5.00E-05
ENSG00000138798	EGF	0.5	1.3	-1.5	2.8	5.00E-05
ENSG00000101412	E2F1	1.8	5.1	-1.5	2.8	5.00E-05
ENSG00000166145	SPINT1	0.6	1.6	-1.5	2.8	5.00E-05
ENSG00000151164	RAD9B	0.1	0.4	-1.5	2.8	0.00705
ENSG00000130508	PXDN	10.6	30.5	-1.5	2.9	5.00E-05
ENSG00000129173	E2F8	0.2	0.7	-1.5	2.9	5.00E-05
ENSG00000165929	TC2N	15.5	44.5	-1.5	2.9	5.00E-05
ENSG00000164626	KCNK5	1.8	5.0	-1.5	2.9	5.00E-05
ENSG00000248771	RP11-294O2.2	2.9	8.3	-1.5	2.9	0.0001
ENSG00000163053	SLC16A14	0.2	0.7	-1.5	2.9	5.00E-05
ENSG00000140092	FBLN5	1.9	5.5	-1.5	2.9	5.00E-05
ENSG00000127324	TSPAN8	0.2	0.7	-1.5	2.9	0.0034
ENSG00000165246	NLGN4Y	1.1	3.2	-1.5	2.9	0.0055

ENSG00000108602	ALDH3A1	238.0	697.2	-1.6	2.9	5.00E-05
ENSG00000102854	MSLN	0.5	1.6	-1.6	2.9	0.00015
ENSG00000176153	GPX2	304.9	894.6	-1.6	2.9	5.00E-05
ENSG00000147689	FAM83A	0.8	2.4	-1.6	2.9	5.00E-05
ENSG00000232721	RP11-403I13.5	0.3	0.8	-1.6	2.9	0.0022
ENSG00000184530	C6orf58	0.2	0.7	-1.6	3.0	0.00695
ENSG00000160183	TMPRSS3	0.1	0.4	-1.6	3.0	5.00E-05
ENSG00000154146	NRGN	0.3	0.8	-1.6	3.0	0.005
ENSG00000133067	LGR6	0.9	2.9	-1.6	3.0	5.00E-05
ENSG00000102760	RGCC	2.4	7.4	-1.6	3.0	5.00E-05
ENSG00000079112	CDH17	13.2	40.3	-1.6	3.0	5.00E-05
ENSG00000085276	MECOM	0.5	1.6	-1.6	3.0	0.0001
ENSG00000120217	CD274	0.5	1.5	-1.6	3.1	5.00E-05
ENSG00000183878	UTY	1.1	3.3	-1.6	3.1	0.00025
ENSG00000115008	IL1A	0.1	0.3	-1.6	3.1	0.00115
ENSG00000019186	CYP24A1	50.1	155.7	-1.6	3.1	5.00E-05
ENSG00000129270	MMP28	0.4	1.2	-1.6	3.1	0.00375
ENSG00000164736	SOX17	0.4	1.3	-1.6	3.1	5.00E-05
ENSG00000106078	COBL	1.6	4.9	-1.6	3.1	5.00E-05
ENSG00000134531	EMP1	1.6	5.2	-1.6	3.1	5.00E-05
ENSG00000189057	FAM111B	0.4	1.2	-1.6	3.1	5.00E-05
ENSG00000159708	LRRC36	0.2	0.8	-1.7	3.2	5.00E-05
ENSG00000233725	LINC00284	0.2	0.7	-1.7	3.2	0.00185
ENSG00000101057	MYBL2	2.7	8.5	-1.7	3.2	5.00E-05
ENSG00000168421	RHOH	0.1	0.3	-1.7	3.2	5.00E-05
ENSG00000125968	ID1	23.7	76.9	-1.7	3.2	5.00E-05
ENSG00000013588	GPRC5A	36.1	117.7	-1.7	3.3	5.00E-05
ENSG00000226652	PSMD10P2	0.2	0.8	-1.7	3.3	0.0012
ENSG00000162078	ZG16B	1.3	4.2	-1.7	3.3	5.00E-05
ENSG00000204128	C2orf72	3.0	9.7	-1.7	3.3	5.00E-05
ENSG00000133962	CATSPERB	0.7	2.4	-1.7	3.3	0.00025
ENSG00000166863	TAC3	0.1	0.5	-1.7	3.3	0.0044
ENSG00000123838	C4BPA	6.6	21.8	-1.7	3.3	5.00E-05
ENSG00000135324	MRAP2	0.4	1.3	-1.7	3.3	5.00E-05
ENSG00000225431	AP001626.1	0.2	0.6	-1.7	3.3	0.00015
ENSG00000124102	PI3	1.1	3.7	-1.7	3.3	5.00E-05
ENSG00000156966	B3GNT7	0.3	0.8	-1.7	3.4	5.00E-05
ENSG00000165591	FAAH2	1.0	3.2	-1.7	3.4	5.00E-05
ENSG00000134827	TCN1	2.8	9.4	-1.8	3.4	5.00E-05
ENSG00000067646	ZFY	0.8	2.9	-1.8	3.4	5.00E-05
ENSG00000005001	PRSS22	0.6	2.1	-1.8	3.4	5.00E-05
ENSG00000150540	HNMT	1.1	3.6	-1.8	3.4	5.00E-05
ENSG00000232306	AC012485.2	0.9	3.0	-1.8	3.4	5.00E-05
ENSG00000079257	LXN	6.2	21.2	-1.8	3.4	0.0048
ENSG00000133135	RNF128	0.5	1.7	-1.8	3.4	0.0003

ENSG00000154620	TMSB4Y	0.2	0.5	-1.8	3.5	0.00015
ENSG00000149212	SESN3	1.4	4.9	-1.8	3.5	5.00E-05
ENSG00000010438	PRSS3	2.9	10.1	-1.8	3.5	0.0059
ENSG00000171345	KRT19	40.5	143.5	-1.8	3.5	5.00E-05
ENSG00000239776	AC079949.1	36882.2	130895.0	-1.8	3.5	0.00335
ENSG00000070526	ST6GALNAC1	1.0	3.6	-1.8	3.6	0.00015
ENSG00000171848	RRM2	5.3	18.9	-1.8	3.6	5.00E-05
ENSG00000255717	SNHG1	95.6	343.3	-1.8	3.6	5.00E-05
ENSG00000182511	FES	0.4	1.3	-1.8	3.6	5.00E-05
ENSG00000004799	PDK4	10.4	37.5	-1.9	3.6	5.00E-05
ENSG00000105855	ITGB8	0.4	1.6	-1.9	3.6	5.00E-05
ENSG00000170298	LGALS9B	0.2	0.6	-1.9	3.6	0.0017
ENSG00000171246	NPTX1	0.2	0.8	-1.9	3.7	5.00E-05
ENSG00000257335	MGAM	0.7	2.5	-1.9	3.7	5.00E-05
ENSG00000121797	CCRL2	0.2	0.6	-1.9	3.7	0.00245
ENSG00000131002	TXLNG2P	6.7	24.6	-1.9	3.7	5.00E-05
ENSG00000136542	GALNT5	1.5	5.6	-1.9	3.7	5.00E-05
ENSG00000141338	ABCA8	0.2	0.8	-1.9	3.7	5.00E-05
ENSG00000161132	XXbac-B444P24.10	0.3	1.1	-1.9	3.8	5.00E-05
ENSG00000064651	SLC12A2	19.5	73.3	-1.9	3.8	5.00E-05
ENSG00000268358	EPB41L4A-AS2	0.3	1.1	-1.9	3.8	5.00E-05
ENSG00000244128	RP11-85M11.2	0.7	2.7	-1.9	3.8	5.00E-05
ENSG00000125266	EFNB2	0.3	1.0	-1.9	3.9	5.00E-05
ENSG00000137440	FGFBP1	0.8	3.3	-2.0	3.9	5.00E-05
ENSG00000171916	LGALS9C	0.3	1.2	-2.0	3.9	0.00415
ENSG00000203697	CAPN8	0.5	2.0	-2.0	3.9	5.00E-05
ENSG00000124664	SPDEF	6.9	27.0	-2.0	3.9	5.00E-05
ENSG00000116106	EPHA4	0.2	0.6	-2.0	3.9	5.00E-05
ENSG00000157542	KCNJ6	0.2	0.8	-2.0	3.9	0.0071
ENSG00000263424	CTD-2541J13.2	0.1	0.5	-2.0	4.0	0.00455
ENSG00000196074	SYCP2	0.6	2.5	-2.0	4.0	5.00E-05
ENSG00000137809	ITGA11	0.3	1.3	-2.0	4.0	5.00E-05
ENSG00000211448	DIO2	0.9	3.4	-2.0	4.0	5.00E-05
ENSG00000165757	KIAA1462	0.2	0.8	-2.0	4.0	5.00E-05
ENSG00000040731	CDH10	0.3	1.0	-2.0	4.0	0.00015
ENSG00000214814	FER1L6	0.3	1.2	-2.0	4.0	5.00E-05
ENSG00000130038	EFCAB4B	0.3	1.3	-2.0	4.0	5.00E-05
ENSG00000144057	ST6GAL2	3.3	13.7	-2.0	4.1	5.00E-05
ENSG00000100033	PRODH	8.9	37.0	-2.1	4.2	5.00E-05
ENSG00000067048	DDX3Y	5.5	23.0	-2.1	4.2	5.00E-05
ENSG00000198734	F5	0.3	1.1	-2.1	4.2	5.00E-05
ENSG00000170369	CST2	0.1	0.4	-2.1	4.2	0.00055
ENSG00000174502	SLC26A9	0.2	0.8	-2.1	4.2	5.00E-05
ENSG00000154188	ANGPT1	0.5	2.0	-2.1	4.3	5.00E-05
ENSG00000243955	GSTA1	0.3	1.3	-2.1	4.3	0.0001

ENSG00000129595	EPB41L4A	1.6	6.9	-2.1	4.3	5.00E-05
ENSG00000105523	FAM83E	0.2	0.7	-2.1	4.3	5.00E-05
ENSG00000119139	TJP2	1.0	4.2	-2.1	4.3	5.00E-05
ENSG00000181634	TNFSF15	1.6	7.0	-2.1	4.4	5.00E-05
ENSG00000042980	ADAM28	1.4	6.3	-2.1	4.4	5.00E-05
ENSG00000169562	GJB1	0.1	0.5	-2.1	4.4	0.00015
ENSG00000054179	ENTPD2	1.0	4.2	-2.1	4.4	5.00E-05
ENSG00000185432	METTL7A	0.1	0.6	-2.1	4.4	5.00E-05
ENSG00000172572	PDE3A	2.6	11.4	-2.2	4.5	5.00E-05
ENSG00000175161	CADM2	0.1	0.6	-2.2	4.5	0.005
ENSG00000170477	KRT4	0.6	2.9	-2.2	4.5	5.00E-05
ENSG00000050438	SLC4A8	0.3	1.4	-2.2	4.5	5.00E-05
ENSG00000111348	ARHGDIB	0.2	0.8	-2.2	4.6	0.0004
ENSG00000127863	TNFRSF19	0.4	1.9	-2.2	4.6	5.00E-05
ENSG00000166866	MYO1A	0.2	0.8	-2.2	4.6	5.00E-05
ENSG00000264462	MIR3648	11.4	52.0	-2.2	4.6	5.00E-05
ENSG00000184574	LPAR5	0.1	0.4	-2.2	4.6	5.00E-05
ENSG00000261183	RP11-532F12.5	0.1	0.4	-2.2	4.6	0.0003
ENSG00000101276	SLC52A3	0.4	1.9	-2.2	4.6	5.00E-05
ENSG00000169903	TM4SF4	6.7	31.2	-2.2	4.6	5.00E-05
ENSG00000185499	MUC1	7.4	34.9	-2.2	4.7	5.00E-05
ENSG00000164488	DACT2	0.1	0.6	-2.3	4.8	0.00015
ENSG00000171346	KRT15	0.5	2.4	-2.3	4.9	5.00E-05
ENSG00000006042	TMEM98	2.5	12.5	-2.3	4.9	5.00E-05
ENSG00000089127	OAS1	8.5	41.9	-2.3	4.9	5.00E-05
ENSG00000198758	EPS8L3	0.9	4.6	-2.3	5.0	5.00E-05
ENSG00000133519	ZDHHC8P1	0.9	4.6	-2.3	5.0	5.00E-05
ENSG00000170775	GPR37	2.1	10.5	-2.3	5.0	5.00E-05
ENSG00000179766	ATP8B5P	0.4	1.8	-2.4	5.1	5.00E-05
ENSG00000137672	TRPC6	2.6	13.2	-2.4	5.1	5.00E-05
ENSG00000225840	AC010970.2	37.2	193.6	-2.4	5.2	5.00E-05
ENSG00000182795	C1orf116	0.6	3.2	-2.4	5.2	5.00E-05
ENSG00000131746	TNS4	3.7	19.5	-2.4	5.3	5.00E-05
ENSG00000166143	PPP1R14D	0.3	1.5	-2.4	5.3	0.0004
ENSG00000133687	TMTC1	0.1	0.6	-2.4	5.4	5.00E-05
ENSG00000261069	SNORD116-20	1.5	8.4	-2.4	5.4	0.00335
ENSG00000248605	CTD-2306M5.1	0.4	2.2	-2.4	5.4	5.00E-05
ENSG00000270066	SCARNA2	0.3	1.4	-2.4	5.5	5.00E-05
ENSG00000148700	ADD3	2.3	12.5	-2.5	5.5	5.00E-05
ENSG00000198848	CES1	9.8	54.5	-2.5	5.5	5.00E-05
ENSG00000145335	SNCA	1.6	8.6	-2.5	5.6	5.00E-05
ENSG00000206159	GYG2P1	0.3	1.4	-2.5	5.6	0.0002
ENSG00000234928	AP000344.3	0.1	0.6	-2.5	5.7	0.00935
ENSG00000100079	LGALS2	0.3	1.5	-2.5	5.7	5.00E-05
ENSG00000081138	CDH7	0.2	1.2	-2.5	5.7	5.00E-05

ENSG00000147676	MAL2	2.2	12.9	-2.5	5.8	5.00E-05
ENSG00000175311	ANKS4B	0.3	1.9	-2.6	5.9	5.00E-05
ENSG00000128573	FOXP2	0.1	0.9	-2.6	5.9	5.00E-05
ENSG00000137699	TRIM29	0.8	4.7	-2.6	6.0	5.00E-05
ENSG00000137393	RNF144B	0.7	4.4	-2.6	6.1	5.00E-05
ENSG00000154175	ABI3BP	0.2	1.0	-2.6	6.1	5.00E-05
ENSG00000184305	CCSER1	0.1	0.5	-2.6	6.1	5.00E-05
ENSG00000215182	MUC5AC	5.6	34.5	-2.6	6.2	5.00E-05
ENSG00000077264	PAK3	0.2	1.5	-2.6	6.2	5.00E-05
ENSG00000251705	RNA5-8SP6	105.9	665.7	-2.7	6.3	5.00E-05
ENSG00000160180	TFF3	0.3	1.8	-2.7	6.3	0.00055
ENSG00000169851	PCDH7	0.5	3.4	-2.7	6.5	5.00E-05
ENSG00000072858	SIDT1	0.6	4.0	-2.7	6.5	5.00E-05
ENSG00000157613	CREB3L1	0.5	3.2	-2.7	6.5	5.00E-05
ENSG00000176658	MYO1D	1.2	7.7	-2.7	6.7	5.00E-05
ENSG00000151715	TMEM45B	0.3	1.7	-2.7	6.7	5.00E-05
ENSG00000110195	FOLR1	0.1	0.5	-2.8	6.8	5.00E-05
ENSG00000188959	C9orf152	0.7	4.9	-2.8	6.8	5.00E-05
ENSG00000085117	CD82	0.7	4.5	-2.8	6.8	5.00E-05
ENSG00000227640	SOX21-AS1	0.6	3.8	-2.8	6.8	5.00E-05
ENSG00000073282	TP63	0.5	3.3	-2.8	6.8	5.00E-05
ENSG00000134258	VTCN1	0.6	4.1	-2.8	7.1	5.00E-05
ENSG00000202198	RN7SK	21.4	152.3	-2.8	7.1	5.00E-05
ENSG00000148513	ANKRD30A	0.2	1.2	-2.8	7.2	5.00E-05
ENSG00000177335	C8orf31	0.0	0.4	-2.9	7.7	0.00085
ENSG00000119125	GDA	0.5	4.2	-2.9	7.7	5.00E-05
ENSG00000121005	CRISPLD1	0.1	0.9	-3.0	7.7	0.00035
ENSG00000180178	AC018865.8	0.1	0.8	-3.0	7.9	5.00E-05
ENSG00000226377	AC084809.2	0.1	1.1	-3.0	8.3	0.00665
ENSG00000111885	MAN1A1	0.1	0.4	-3.1	8.6	5.00E-05
ENSG00000135373	EHF	3.6	31.4	-3.1	8.6	5.00E-05
ENSG00000163736	PPBP	0.1	0.6	-3.2	9.0	0.00015
ENSG00000180861	C12orf36	0.1	0.6	-3.2	9.0	5.00E-05
ENSG00000200434	RNA5-8SP2	8.3	75.4	-3.2	9.0	5.00E-05
ENSG00000215808	RP11-371I1.2	0.1	1.3	-3.2	9.2	0.003
ENSG00000235687	LINC00993	0.4	3.4	-3.2	9.3	0.0007
ENSG00000007952	NOX1	0.2	1.7	-3.2	9.4	5.00E-05
ENSG00000012779	ALOX5	0.6	6.1	-3.3	9.7	5.00E-05
ENSG00000064787	BCAS1	0.2	1.9	-3.3	9.8	5.00E-05
ENSG00000110934	BIN2	0.1	0.5	-3.3	9.9	5.00E-05
ENSG00000197614	MFAP5	0.1	1.1	-3.3	10.0	5.00E-05
ENSG00000125285	SOX21	0.4	3.7	-3.3	10.2	5.00E-05
ENSG00000255774	AP000439.3	0.2	1.6	-3.4	10.2	5.00E-05
ENSG00000269900	RMRP	17.2	184.9	-3.4	10.7	5.00E-05
ENSG00000090920	FCGBP	2.5	27.7	-3.4	10.9	5.00E-05

ENSG00000196620	UGT2B15	0.1	1.1	-3.6	11.9	5.00E-05
ENSG00000196741	CXorf24	1.2	15.2	-3.7	13.1	5.00E-05
ENSG00000114638	UPK1B	1.0	13.5	-3.8	13.7	5.00E-05
ENSG00000114378	HYAL1	0.2	3.0	-3.8	14.2	5.00E-05
ENSG00000136155	SCEL	0.1	1.6	-3.8	14.3	5.00E-05
ENSG00000248434	RP11-553P9.2	0.1	2.1	-3.8	14.4	5.00E-05
ENSG00000259001	RPPH1	6.4	93.6	-3.9	14.7	0.00795
ENSG00000006210	CX3CL1	0.6	9.5	-3.9	15.2	5.00E-05
ENSG00000173702	MUC13	7.1	109.2	-3.9	15.3	5.00E-05
ENSG00000007216	SLC13A2	0.0	0.4	-4.0	16.1	0.0003
ENSG00000257588	RP11-469H8.6	0.0	0.5	-4.1	17.6	5.00E-05
ENSG00000044012	GUCA2B	0.0	0.8	-4.1	17.7	0.0048
ENSG00000160182	TFF1	1.2	22.2	-4.2	17.9	5.00E-05
ENSG00000230937	MIR205HG	0.3	5.8	-4.2	18.7	5.00E-05
ENSG00000159763	PIP	0.2	4.7	-4.3	19.3	5.00E-05
ENSG00000150667	FSIP1	0.5	10.2	-4.5	21.9	5.00E-05
ENSG00000250775	RP11-12K22.1	0.0	0.8	-4.6	23.5	0.00035
ENSG00000167165	UGT1A6	0.3	6.4	-4.6	23.6	5.00E-05
ENSG00000224259	RP11-48O20.4	0.2	3.9	-4.6	24.1	0.00075
ENSG00000257512	RP11-486A14.1	0.2	5.9	-4.6	24.3	5.00E-05
ENSG00000164418	GRIK2	0.1	3.5	-4.6	24.9	5.00E-05
ENSG00000087916	SLC6A14	0.1	2.1	-4.7	25.2	5.00E-05
ENSG00000105388	CEACAM5	0.2	5.4	-4.8	28.0	0.0004
ENSG00000127831	VIL1	0.2	7.4	-4.9	30.7	5.00E-05
ENSG00000138650	PCDH10	0.1	2.0	-5.0	31.7	5.00E-05
ENSG00000244474	UGT1A4	0.0	0.3	-5.3	40.6	0.0001
ENSG00000260908	CTB-134H23.3	0.2	7.9	-5.6	48.7	5.00E-05
ENSG00000135333	EPHA7	0.0	3.6	-6.3	77.5	0.0065
ENSG00000261043	MIR4313	0.0	3.3	-6.4	84.1	0.00015
ENSG00000086548	CEACAM6	2.4	266.8	-6.8	109.9	5.00E-05
ENSG00000241635	UGT1A1	1.0	121.6	-6.9	118.7	5.00E-05
ENSG00000265506	AC004656.1	0.0	90.3	NA	NA	0.00355

Table S8. List of enriched gene pathways from DAVID gene ontology analysis of significantly differentially expressed genes with ≥1.5-fold change in expression following EHF overexpression.

Term	P Value	Genes
GO:0044421~extracellular region part	2.37E-13	TNFSF15, TNFSF14, TNFSF13, IL15, SHH, IL11, WNT4, APOD, CD44, APOE, TGFBI, CFH, COL12A1, LOX, WNT6, CFD, TFPI2, IL1A, MATN3, FIBCD1, VEGFC, THBD, PPBP, F5, SERPINF2, F2, ADAMTS1, LAMC2, COL1A1, MFAP5, RBP4, CCL2, ERBB3, APOC1, CD70, CX3CL1, GREM1, LAMB3, FGG, ACE, BCHE, FGB, TFF3, FGL1, TFF1, EGF, ENTPD2, ANGPTL4, EFEMP1, ECM1, TNFSF10, APOL1, COL14A1, LAMA3, PI3, TGFBR3, MUC5AC, AREG, BMP7, INSL4, NPNT, SORL1, MMP28, VGF, CFHR3, METRN, DMKN, HMOX1, GPC6, GPX3, ANGPT1, SEPP1, VWA1, LOXL2, HYAL1, MMP14, NPTXR, ADM, KCP, CA2, TF, CCK, CXCL5, C3, CXCL3, C5, ADAMTS15, SPOCK1, SFN, TAC3, CPN1, COL7A1, AGT, PRSS3, ADAMTS12, PLA2R1, FGFBP1, SCG2, COL4A3, FLRT2, IL6, FBN1, NID1, IGF2, TNFSF9, COL5A2, COL5A1, HPX, FBLN5, KAZALD1, AKR1B1, IGFBP1, IGFBP4
GO:0005576~extracellular region	6.97E-11	NRTN, C6ORF58, C2ORF72, TNFSF15, TNFSF14, TNFSF13, EDIL3, IL15, SHH, IL11, OLFML3, WNT4, BDNF, CD44, APOD, APOE, TGFBI, SERPINE1, CFH, COL12A1, LOX, CFD, WNT6, GUCA2B, TFPI2, MUC13, IL1A, HHIPL2, MATN3, STC2, CST2, CST1, FIBCD1, F7, TCN1, PLAUR, VEGFC, THBD, PPBP, F5, SERPINF2, F2, ADAMTS1, LAMC2, COL1A1, MFAP5, FGFR2, PAM, RBP4, CCL2, IGFBPL1, ERBB3, APOC1, CD70, CX3CL1, GREM1, ITGBL1, LAMB3, ACE, FGG, BCHE, FOLR1, FGB, MSLN, PIP, HEG1, TFF3, CDA, FGL1, TFF1, EGF, PCDHA13, ENTPD2, LFNG, ANGPTL4, MUC1, ADAM28, MGAT4A, IGFL4, ADAM23, EFEMP1, ECM1, GAS6, APOL2, TNFSF10, LAMA3, COL14A1, APOL1, PI3, TGFBR3, MUC5AC, AREG, FCGBP, BMP7, PXDN, INSL4, NXPH4, NPNT, SORL1, MMP28, VGF, METRN, CFHR3, WISP2, RSPO3, HMOX1, GPC6, DMKN, GPX3, ITIH5, SEMA3B, ANGPT1, SEPP1, LOXL2, VWA1, TSKU, CEACAM1, CSF2RA, KIRREL3, CYR61, HYAL1, SPINT1, MMP14, INHBB, MUC3A, NPTXR, ADM, INHBE, KCP, CTSD, SLPI, SCGB3A2, CA2, CTSB, C1QL4, TF, GALNT1, CCK, CXCL5, C3, CXCL3, C5, ADAMTS15, SPOCK1, SFN, CPN1, TAC3, ZG16B, GLIPR2, C1QTNF6, PRRG4, PLIN2, COL7A1, CRISPLD1, AGT, PRSS3, ADAMTS12, PLA2R1, FGFBP1, SCG2, FLRT2, COL4A3, IL6, SVEP1, PLAC1, FBN1, IGF2, NID1, C4BPB, C4BPA, TNFSF9, COL5A2, COL5A1, NTS, C3ORF58, HPX, KAZALD1, FBLN5, AKR1B1, IGFBP1, PRSS23, PRSS22, IGFBP4
GO:0044459~plasma membrane part	4.74E-10	DLC1, KLRC2, RP2, SYT6, AQP3, S1PR3, AGTR1, DIRAS2, CD44, APOE, KCNK5, CHRNA7, HTR1D, GRID1, F11R, MAGI3, EFNB2, PTPRO, CTNNA2,

		CCR7, RND1, RHCG, LAMC2, MST1R, ADD3, ERBB3, ITGA11, CD70, FCGRT, BDKRB2, KCNJ2, RAB40B, ITGBL1, RIMS3, ACE, PVRL3, KCNK1, KCNK3, EPHA2, CAMK2N1, SYNGR3, NTRK3, EPHA4, EPHA7, KCNJ6, LAMA3, EPS8, PKP2, TGFBR3, MAP7, KCNH1, LIMA1, MCF2L, AP1S3, SLC23A2, CEACAM6, CEACAM5, ATP6V0D2, KCNG1, CEACAM1, KCNMA1, GPR176, CACNG7, MMP14, DOK7, SLC26A9, SGCD, TF, RAB3B, PARD3, SHROOM3, LIMS2, NPY2R, C5, GPR64, APBB1IP, GPHN, CD22, FUT1, DTNA, FLRT2, IL6, GJB1, GJB2, SLC16A2, SLC16A7, CDH17, TJP3, TJP2, GRIK2, TNFSF15, TSPAN7, TNFSF13, IL15, ENPEP, VIPR1, CALB2, SLC7A7, ANK3, SLC4A4, SLC4A3, TNS4, THBD, ARRB1, VAMP1, SPTB, CGNL1, FXYD2, CAV2, DRD1, FGFR4, ADORA2B, ITGB4, ABCA1, ABCA4, FGG, P2RY6, FGB, FOLR1, ITGB8, ADRA2A, B3GNT3, SLC30A3, PCDHA13, GABRP, MUC1, HCN2, DIXDC1, MYO1A, CACNA2D1, ADAM23, LPP, SYT11, PODXL, SYT12, SLC6A14, SLC6A17, TNFSF10, DSG2, GPR37, SLC7A2, CD274, CACNA1G, SLC13A2, MERTK, SCARA5, ADRA1D, CLDN4, TACR1, SORL1, BCAM, RHOV, SYNGR2, SDC2, EPCAM, CCRL2, KCNQ5, GPC6, HMOX1, SDPR, RHOF, SLC43A1, CSF2RA, RHOH, GABRG3, PRKCI, PCDH7, UGT1A1, MUC3A, CHRM3, CD82, CNTN1, CTSB, CA2, TM4SF4, CALCR, CTNND2, GPRC5A, ANXA6, UGT1A6, HRH1, RASGRP2, UGT1A4, PLA2R1, PTPRB, SLC12A2, NOX1, TSPAN13, SLC17A7, KCNN4, TMEM47, SLC17A3, SLC17A1, DSC2, BMPR1B
GO:0005615~extracellular space	2.01E-09	INSL4, SORL1, TNFSF15, TNFSF14, TNFSF13, IL15, VGF, SHH, IL11, CFHR3, METRN, APOD, APOE, DMKN, GPC6, HMOX1, GPX3, TGFBI, CFH, ANGPT1, SEPP1, LOX, LOXL2, CFD, IL1A, HYAL1, FIBCD1, VEGFC, NPTXR, THBD, PPBP, F5, ADM, SERPINF2, F2, KCP, LAMC2, CA2, TF, RBP4, CCL2, CCK, CXCL5, ERBB3, C3, CXCL3, C5, APOC1, CD70, CX3CL1, SFN, GREM1, TAC3, CPN1, FGG, ACE, BCHE, FGB, AGT, PRSS3, FGL1, TFF1, PLA2R1, EGF, FGFBP1, ANGPTL4, SCG2, IL6, FBN1, IGF2, TNFSF9, TNFSF10, APOL1, HPX, AKR1B1, TGFBR3, IGFBP1, AREG, BMP7, IGFBP4
GO:0005886~plasma membrane	1.65E-08	DLC1, KLRC2, ADCY1, VTCN1, GPR124, RP2, SNCA, SYT6, MEGF11, SHH, AQP3, LPHN2, AGTR1, LPHN3, S1PR3, DIRAS2, MALL, CD44, APOE, KCNK5, SERPINE1, S1PR5, CHRNA7, HTR1D, MUC13, GRID1, F11R, MAGI3, CRYAB, EFNB2, PTPRR, F7, PTPRO, SIRPA, PLAUR, CTNNA2, CCR7, KRT19, RND1, F5, LPAR5, RHCG, F2, MGAM, LAMC2, MST1R, ADD3, SLC2A13, ERBB3, ITGA11, FCGRT, CD70, BDKRB2, KCNJ2, RAB40B, RIMS3, ITGBL1, ACE, CDC42EP2, PVRL3, TRPC6, PCDH10, PPFIBP1, KCNK1, SYNGR3, EPHA2, KCNK3,

		CAMK2N1, ABCG2, NTRK3, EPHA4, GGT5, EPHA7, LAMA3, KCNJ6, EPS8, PKP2, TGFBR3, MAP7, NRP2, KCNH1, SLC16A14, LIMA1, MARCKSL1, SUSD2, MCF2L, AP1S3, SLC23A2, CEACAM6, CEACAM5, ATP6V0D2, NT5E, CEACAM1, DPEP1, KCNG1, KCNMA1, ADAM11, GPR176, CACNG7, MMP14, EPB41L1, ALG10B, SLC26A9, DOK7, NAB1, SGCD, TF, RAB3B, PARD3, SHROOM3, LIMS2, PLEK2, NPY2R, GPR64, C5, XKRX, APBB1IP, DGKA, IGSF11, GPHN, ACSL1, PLIN2, CD22, FUT1, DTNA, FLRT2, PLA2G16, IL6, NOS1, MAPK10, GJB1, GJB2, SLC16A2, CDH15, SLC16A7, PTP4A3, CDH17, GFRA1, TJP3, TJP2, ABCC8, CDH10, GRIK2, PLXNA2, TNFSF15, TNFSF14, TSPAN7, TNFSF13, IL15, ENPEP, VIPR1, IL17RD, CALB2, SLC7A7, ANK3, SLC2A3, SLC4A4, SLC4A3, IRS2, BAIAP2, BASP1, TNS4, LAT2, PLCE1, THBD, RASGRF2, ARRB1, COL1A1, LRRK2, VAMP1, EMP1, SPTB, ABCA8, FGFR2, CAV2, FXYD2, CGNL1, FGFR4, DRD1, ADORA2B, IFITM3, ITGB4, NKAIN4, ANKS4B, ABCA1, CX3CL1, ABCA4, FGG, P2RY6, FGB, FOLR1, ITGB8, MSLN, DDX3Y, ADRA2A, B3GNT3, SLC30A3, PCDHA13, EGF, BMF, GABRP, ADAM28, MUC1, DIXDC1, HCN2, CACNA2D1, MYO1A, ADAM23, LPP, PODXL, SYT11, SYT12, SLC6A14, SLC6A17, TNFSF10, GPR37, DIO2, DSG2, SLC7A2, CD274, PLCG2, CACNA1G, SLC13A2, MERTK, SCARA5, ADRA1D, CLDN4, TACR1, SORL1, BCAM, RHOV, LGR6, SYNGR2, SDC2, CCRL2, EPCAM, KCNQ5, WISP2, HMOX1, GPC6, SDPR, RHOF, SLC43A1, CSF2RA, SLC43A2, KIRREL3, RHOH, SGK1, GABRG3, PRKCI, PCDH9, PCDH7, UGT1A1, MUC3A, NPTXR, CHRM3, CD82, CNTN1, CA2, CTSB, TM4SF4, CALCR, MAL2, CTNND2, PCDHGC3, GPRC5A, ANXA6, UGT1A6, CDH7, HRH1, UGT1A4, RASGRP2, TGM2, PALM3, PLA2R1, FGFBP1, PTPRB, SLC12A2, NOX1, TSPAN13, SLC17A7, KCNN4, TMEM47, SLC17A3, SLC17A1, DSC2, ANXA13, ALOX5, BMPR1B, GPR115
GO:0031226~intrinsic to plasma membrane	2.60E-08	KLRC2, GRIK2, TNFSF15, TSPAN7, TNFSF13, ENPEP, IL15, VIPR1, SLC7A7, S1PR3, AGTR1, CD44, KCNK5, CHRNA7, SLC4A4, HTR1D, SLC4A3, EFNB2, PTPRO, CCR7, THBD, RHCG, MST1R, VAMP1, SPTB, CAV2, FXYD2, FGFR4, DRD1, ADORA2B, ERBB3, ITGA11, ITGB4, CD70, BDKRB2, ABCA1, KCNJ2, ABCA4, ITGBL1, P2RY6, ITGB8, FOLR1, ADRA2A, B3GNT3, SLC30A3, PCDHA13, MUC1, HCN2, ADAM23, PODXL, SYT11, SLC6A14, SLC6A17, KCNK1, KCNK3, EPHA2, SYNGR3, NTRK3, EPHA4, EPHA7, TNFSF10, KCNJ6, GPR37, EPS8, SLC7A2, SLC13A2, TGFBR3, MERTK, SCARA5, ADRA1D, KCNH1, CLDN4, TACR1, SORL1, BCAM, SYNGR2, SDC2, CCRL2, KCNQ5, SLC23A2,

		GPC6, CEACAM6, CEACAM5, SLC43A1, CEACAM1, KCNG1, CSF2RA, KCNMA1, GPR176, PCDH7, MMP14, UGT1A1, CHRM3, CD82, TM4SF4, CALCR, PARD3, NPY2R, GPR64, C5, GPRC5A, UGT1A6, HRH1, UGT1A4, CD22, FUT1, PLA2R1, PTPRB, FLRT2, IL6, SLC12A2, NOX1, TSPAN13, KCNN4, SLC16A2, SLC17A3, SLC16A7, SLC17A1, BMPR1B
GO:0005887~integral to plasma membrane	2.66E-08	KLRC2, GRIK2, TNFSF15, TSPAN7, TNFSF13, ENPEP, IL15, VIPR1, SLC7A7, S1PR3, AGTR1, CD44, KCNK5, CHRNA7, SLC4A4, HTR1D, SLC4A3, EFNB2, PTPRO, CCR7, THBD, RHCG, MST1R, VAMP1, CAV2, FXYD2, FGFR4, DRD1, ADORA2B, ERBB3, ITGA11, ITGB4, CD70, BDKRB2, ABCA1, KCNJ2, ABCA4, ITGBL1, P2RY6, ITGB8, FOLR1, ADRA2A, B3GNT3, SLC30A3, PCDHA13, MUC1, HCN2, ADAM23, PODXL, SYT11, SLC6A14, SLC6A17, KCNK1, KCNK3, EPHA2, SYNGR3, NTRK3, EPHA4, EPHA7, TNFSF10, KCNJ6, GPR37, EPS8, SLC7A2, SLC13A2, TGFBR3, MERTK, SCARA5, ADRA1D, KCNH1, CLDN4, TACR1, SORL1, BCAM, SYNGR2, SDC2, CCRL2, KCNQ5, SLC23A2, GPC6, CEACAM6, CEACAM5, SLC43A1, CEACAM1, KCNG1, CSF2RA, KCNMA1, GPR176, PCDH7, MMP14, UGT1A1, CHRM3, CD82, TM4SF4, CALCR, NPY2R, GPR64, C5, GPRC5A, UGT1A6, HRH1, UGT1A4, CD22, FUT1, PLA2R1, PTPRB, FLRT2, IL6, SLC12A2, NOX1, TSPAN13, KCNN4, SLC16A2, SLC17A3, SLC16A7, SLC17A1, BMPR1B
GO:0042127~regulation of cell proliferation	1.38E-07	DLC1, NAMPT, RARRES3, MARCKSL1, STAT5A, E2F7, TACR1, TNFSF15, TP63, TNFSF13, PRRX2, IL15, VIPR1, SHH, IL11, AGTR1, S1PR3, WISP2, BDNF, PTGES, CDKN2C, APOE, HLX, HMOX1, SERPINE1, DLG3, CHRNA7, RARB, IL1A, CDC6, HYAL1, IRS2, MECOM, VEGFC, HNF4A, ADM, SCIN, ADAMTS1, MST1R, TBX18, SMARCA2, TM4SF4, FGFR2, CAV2, FRK, RBP4, FGFR4, CCL2, CXCL5, ERBB3, SOX2, SOX4, SFN, BDKRB2, SOX9, AGT, BCL2, ADRA2A, TGM2, KRT4, EGF, RUNX2, FGFBP1, SCG2, KLF5, COL4A3, IL6, TP53I11, CRIP2, NOX1, IGF2, FOXP2, RERG, NUPR1, CD274, TGFBR3, MUC5AC, NR5A2, BMP7, ADRA1D
GO:0009725~response to hormone stimulus	1.58E-07	ADCY1, TACR1, STAT5A, PDE3B, VGF, SHH, HMOX1, ANGPT1, LOX, MB, KCNMA1, IRS2, GATM, CRYAB, BAIAP2, PRKCI, MMP14, UGT1A1, TAT, KRT19, ADM, COL1A1, CA2, CALCR, RBP4, CAV2, DRD1, HMGB2, CCL2, ERBB3, CPN1, PHIP, UGT1A6, BCHE, BCL2, UGT1A4, TFF3, TFF1, PIK3R3, NEFL, IL6, IGF2, NR4A3, CPS1, HDAC5, RERG, TGFBR3, IGFBP1, BMP7
GO:0009611~response to wounding	1.97E-07	TACR1, IL15, SHH, IL11, S1PR3, CD44, HMOX1, SERPINE1, CFH, LOX, CFD, TFPI2, IL1A, F11R, GATM, CHST2, F7, MECOM, PLAUR, CCR7, THBD, ADM, F5, HNF4A, SERPINF2, F2, PLLP, CTSB, TM4SF4, TF, CCL2, ERBB3, C3, CXCL3, C5,

		HOXB13, BDKRB2, HRH1, FGG, FGB, BCL2, NEFL, ENTPD2, PAPSS2, SCG2, IL6, NOX1, C4BPB, IGF2, C4BPA, COL5A1, HDAC5, APOL2, PLSCR4, NUPR1, FBLN5, IGFBP1, ALOX5, BMPR1B, IGFBP4
GO:0005509~calcium ion binding	7.31E-07	S100A4, PDP1, PXDN, STAT5A, NPNT, SNCA, SYT6, ENPEP, EDIL3, MMP28, CALB2, PLCB4, PLS1, ANO9, KCNMA1, NRXN2, NCALD, CACNG7, VIL1, PADI2, PCDH9, PCDH7, F7, MAN1A1, MMP14, PLCE1, NPTXR, THBD, F5, RASGRF2, DLL4, SCIN, F2, GALNT9, GALNT1, GALNT7, GALNT5, GALNT4, ITGA11, SPOCK1, PCDHGC3, EDEM3, EFCAB4B, PKD1L2, PLCL2, ANXA6, DGKA, CDH7, FGG, NPTX1, PRRG4, LPCAT1, ENTPD7, RASGRP2, PLCH1, PRSS3, TGM2, HEG1, EGF, PCDHA13, ENTPD2, DTNA, SCG2, CACNA2D1, SVEP1, S100A16, TRPC6, CAPN8, SYT11, MRC2, FBN1, EFEMP1, PCDH10, S100A10, NID1, GAS6, CDH15, DSG2, PLSCR4, CDH17, ATP2A3, FLG, FBLN5, PLCG2, CACNA1G, DSC2, ANXA13, ALOX5, CDH10
GO:0008283~cell proliferation	1.68E-06	E2F1, STIL, INSL4, E2F8, TP63, TNFSF14, ZEB2, IL15, ENPEP, FES, SHH, HMOX1, TGFBI, IL1A, CYR61, IRS2, TPX2, MMP14, VEGFC, PLCE1, UHRF1, CCND3, CHRM3, FOXC1, EMP1, RBP4, SPOCK1, EHF, CD70, SFN, ACE, BCL2, AGT, HELLS, GINS1, COL4A3, CRIP1, MKI67, TNFSF9, APPL2, GAS6, CDC25A, EPS8, CD274, PCNA, TGFBR3, TCF19, AREG, ADRA1D, IGFBP4
GO:0001655~urogenital system development	2.18E-06	RBP4, ARID5B, FBN1, TP63, HOXB13, NID1, GREM1, SHH, AGTR1, PLCE1, BDNF, ACE, CD44, AGT, BCL2, FOXC1, ADAMTS1, RARB, CA2, BMP7, HELLS
GO:0009719~response to endogenous stimulus	2.60E-06	ADCY1, TACR1, STAT5A, PDE3B, VGF, SHH, HMOX1, ANGPT1, LOX, MB, KCNMA1, IRS2, GATM, CRYAB, BAIAP2, PRKCI, MMP14, UGT1A1, TAT, KRT19, ADM, COL1A1, CA2, CALCR, RBP4, CAV2, DRD1, HMGB2, CCL2, ERBB3, CPN1, PHIP, UGT1A6, BCHE, BCL2, UGT1A4, TFF3, TFF1, PIK3R3, NEFL, IL6, IGF2, NR4A3, CPS1, HDAC5, RERG, TGFBR3, IGFBP1, BMP7
GO:0043434~response to peptide hormone stimulus	3.81E-06	RBP4, CAV2, DRD1, ERBB3, STAT5A, PDE3B, VGF, PHIP, BCL2, TFF3, TFF1, PIK3R3, NEFL, IRS2, GATM, BAIAP2, PRKCI, IGF2, NR4A3, CPS1, HDAC5, ADM, COL1A1, IGFBP1, BMP7
GO:0007155~cell adhesion	6.77E-06	DLC1, NRP2, MPZL3, CLDN4, NPNT, BCAM, EDIL3, WISP2, CD44, TGFBI, COL12A1, LOXL2, CEACAM1, CYR61, F11R, NRXN2, PCDH9, PCDH7, SIRPA, CTNNA2, F5, CNTN1, LAMC2, PARD3, CCL2, ITGB4, ITGA11, CTNND2, SPOCK1, PCDHGC3, CX3CL1, SOX9, ITGBL1, IGSF11, CDH7, LAMB3, COL7A1, ITGB8, PVRL3, BCL2, AGT, MSLN, CD22, PCDHA13, COL4A3, FLRT2, SVEP1, GMDS, LPP, ADAM23, PCDH10, PPFIBP1, NID1, SLAMF7, COL5A1, CDH15, COL14A1, LAMA3, DSG2, NLGN4Y, CDH17, PKP2, FBLN5, DSC2, FCGBP,

		MUC5AC, BMPR1B, CDH10
GO:0022610~biological adhesion	7.13E-06	DLC1, NRP2, MPZL3, CLDN4, NPNT, BCAM, EDIL3, WISP2, CD44, TGFBI, COL12A1, LOXL2, CEACAM1, CYR61, F11R, NRXN2, PCDH9, PCDH7, SIRPA, CTNNA2, F5, CNTN1, LAMC2, PARD3, CCL2, ITGB4, ITGA11, CTNND2, SPOCK1, PCDHGC3, CX3CL1, SOX9, ITGBL1, IGSF11, CDH7, LAMB3, COL7A1, ITGB8, PVRL3, BCL2, AGT, MSLN, CD22, PCDHA13, COL4A3, FLRT2, SVEP1, GMDS, LPP, ADAM23, PCDH10, PPFIBP1, NID1, SLAMF7, COL5A1, CDH15, COL14A1, LAMA3, DSG2, NLGN4Y, CDH17, PKP2, FBLN5, DSC2, FCGBP, MUC5AC, BMPR1B, CDH10
GO:0008285~negative regulation of cell proliferation	9.18E-06	DLC1, CAV2, RARRES3, RBP4, FRK, E2F7, TNFSF15, IL15, BDKRB2, SFN, SHH, WISP2, BDNF, PTGES, APOE, CDKN2C, HMOX1, BCL2, AGT, DLG3, KRT4, RARB, FGFBP1, IL1A, SCG2, CDC6, HYAL1, COL4A3, TP53I11, IL6, RERG, NUPR1, HNF4A, ADM, CD274, SCIN, TGFBR3, ADAMTS1, MUC5AC, BMP7, SMARCA2, TM4SF4
GO:0000267~cell fraction	1.23E-05	CYP3A5, GRIK2, PDLIM5, SNCA, PDE3B, IL15, STAC, ANK3, SERPINE1, RAPGEF4, SLC4A3, CRYAB, FA2H, POR, AADAC, PLCE1, VAMP8, ARRB1, F2, LAMC2, CPD, VAMP1, LRRK2, EMP1, CAV2, DRD1, CYP1B1, OAS3, CD70, OAS1, ABCA1, ABCA4, PPP1R3C, ACE, FGB, FOLR1, BCHE, PLCH1, SLC30A3, PCDHA13, EGF, CAMK2N1, DOCK3, TNFSF10, EPS8, SLC7A2, PLCG2, MAP2, SLC13A2, MERTK, NRP2, INSL4, TP63, TSPAN12, WISP2, CYP39A1, PTGES, SLC23A2, HMOX1, GPX3, NT5E, CEACAM1, SPINT1, MAN1A1, UGT1A1, DGAT2, ADM, TPPP, CNTN1, CTSB, UGT2B15, TM4SF4, PCDHGC3, TAC3, UGT1A6, ACSL1, BCL2, AGT, RASGRP2, UGT1A4, FUT1, DTNA, SLC12A2, FADS3, TSPAN13, PDE3A, NPR3, CYP4F12, SLC17A7, SLC16A2, CYP4F8, SLC16A7, SLC17A3, NTS, SLC17A1, FBLN5, CYP4F3, ALOX5, DUSP6
GO:0008081~phosphoric diester hydrolase activity	1.73E-05	PDE11A, PDE3B, GDPD5, PDE3A, PDE10A, BDKRB2, PLCL2, PLCE1, PLCB4, CHRM3, PDE2A, PDE1C, HMOX1, PLCH1, PDE1A, PLCG2, PDE9A
GO:0005578~proteinaceous extracellular matrix	1.86E-05	TF, NPNT, ADAMTS15, SPOCK1, MMP28, LAMB3, WNT4, COL7A1, GPC6, TGFBI, TFF3, COL12A1, ADAMTS12, LOX, WNT6, VWA1, TFPI2, ENTPD2, ANGPTL4, FLRT2, COL4A3, MATN3, FBN1, EFEMP1, NID1, MMP14, ECM1, COL5A2, COL5A1, LAMA3, COL14A1, FBLN5, KAZALD1, PI3, ADAMTS1, LAMC2, MUC5AC, COL1A1, MFAP5
GO:0042060~wound healing	1.88E-05	ERBB3, SHH, IL11, FGG, CD44, FGB, HMOX1, SERPINE1, LOX, TFPI2, PAPSS2, ENTPD2, IL6, GATM, C4BPB, IGF2, F7, COL5A1, PLAUR, THBD, F5, HNF4A, PLSCR4, FBLN5, F2, IGFBP1, TM4SF4
GO:0031012~extracellular matrix	1.98E-05	TF, NPNT, ADAMTS15, SPOCK1, MMP28, LAMB3, WNT4, CD44, COL7A1, GPC6, TGFBI, TFF3, COL12A1, ADAMTS12, LOX, WNT6, VWA1, TFPI2,

		ENTPD2, ANGPTL4, FLRT2, COL4A3, MATN3, FBN1, EFEMP1, NID1, MMP14, COL5A2, ECM1, COL5A1, LAMA3, COL14A1, FBLN5, KAZALD1, PI3, ADAMTS1, LAMC2, MUC5AC, COL1A1, BMP7, MFAP5
GO:0046545~development of primary female sexual characteristics	2.00E-05	RBP4, STAT5A, TP63, VGF, MMP14, INHBB, WNT4, BCL2, AGT, ANGPT1, FOXC1, ADAMTS1, LHX8, BMPR1B, LFNG
GO:0046660~female sex differentiation	2.00E-05	RBP4, STAT5A, TP63, VGF, MMP14, INHBB, WNT4, BCL2, AGT, ANGPT1, FOXC1, ADAMTS1, LHX8, BMPR1B, LFNG
GO:0045137~development of primary sexual characteristics	2.06E-05	RBP4, HMGB2, STAT5A, SOX2, TP63, VGF, MMP14, SOX9, SYCP2, SHH, GJB2, INHBB, WNT4, AGT, BCL2, ADAMTS1, ANGPT1, FOXC1, BMPR1B, LHX8, LFNG
GO:0032101~regulation of response to external stimulus	2.11E-05	DRD1, IL6, CCK, ADORA2B, C3, STAT5A, IGF2, TSPAN8, CX3CL1, F7, GREM1, CTNNA2, NTRK3, GPX2, AGTR1, APOE, SERPINF2, AGT, F2, SERPINE1, TGM2, CHRNA7, NT5E, SCG2
GO:0001944~vasculature development	2.25E-05	NRP2, TNFSF13, PRRX2, ENPEP, SHH, TYMP, ACE, CD44, HEY1, APOE, HMOX1, AGT, TGM2, ANGPT1, LOX, SOX17, EGF, CEACAM1, SCG2, CYR61, ANGPTL4, KLF5, EFNB2, NOX1, MMP14, COL5A1, VEGFC, ID1, DLL4, TGFBR3, FOXC1, COL1A1
GO:0010033~response to organic substance	3.32E-05	ADCY1, STAT5A, TACR1, SNCA, PDE3B, VGF, SHH, CD44, APOE, HMOX1, CREB3L1, ANGPT1, CHRNA7, LOX, MB, CYR61, KCNMA1, IRS2, GATM, CRYAB, BAIAP2, PRKCI, MMP14, TAT, UGT1A1, KRT19, THBD, ADM, HNF4A, SERPINF2, COL1A1, CA2, CALCR, CAV2, TF, RBP4, DRD1, HMGB2, CYP1B1, CCL2, ERBB3, EDEM3, CPN1, PHIP, UGT1A6, ACSL1, PLIN2, BCHE, BCL2, UGT1A4, TFF3, TFF1, PIK3R3, NEFL, COL4A3, IL6, PDE3A, IGF2, NR4A3, CPS1, RERG, HDAC5, EPS8, ID1, PLCG2, TGFBR3, IGFBP1, BMP7, TJP2
GO:0001568~blood vessel development	3.57E-05	NRP2, TNFSF13, PRRX2, ENPEP, SHH, TYMP, ACE, CD44, HEY1, APOE, HMOX1, AGT, TGM2, ANGPT1, LOX, SOX17, EGF, CEACAM1, SCG2, CYR61, ANGPTL4, KLF5, NOX1, MMP14, COL5A1, VEGFC, ID1, DLL4, TGFBR3, FOXC1, COL1A1
GO:0044420~extracellular matrix part	3.89E-05	COL4A3, TF, FBN1, NID1, COL5A2, COL5A1, LAMB3, LAMA3, COL14A1, COL7A1, COL12A1, TFF3, LAMC2, ADAMTS1, MUC5AC, COL1A1, LOX, VWA1, MFAP5, ENTPD2
GO:0007596~blood coagulation	4.04E-05	IL6, C4BPB, F7, SHH, IL11, PLAUR, FGG, THBD, PLSCR4, HNF4A, F5, FGB, FBLN5, SERPINE1, F2, TFPI2, ENTPD2, PAPSS2
GO:0050817~coagulation	4.04E-05	IL6, C4BPB, F7, SHH, IL11, PLAUR, FGG, THBD, PLSCR4, HNF4A, F5, FGB, FBLN5, SERPINE1, F2, TFPI2, ENTPD2, PAPSS2
GO:0005624~membrane fraction	4.87E-05	NRP2, CYP3A5, GRIK2, PDLIM5, SNCA, PDE3B, TP63, IL15, TSPAN12, CYP39A1, PTGES, ANK3, SLC23A2, HMOX1, RAPGEF4, SLC4A3, NT5E, CEACAM1, FA2H, SPINT1, MAN1A1, UGT1A1, POR,

		AADAC, PLCE1, DGAT2, ARRB1, VAMP8, CNTN1, LAMC2, CPD, UGT2B15, LRRK2, VAMP1, TM4SF4, EMP1, CAV2, DRD1, CYP1B1, OAS3, OAS1, CD70, PCDHGC3, ABCA1, ABCA4, UGT1A6, ACE, PPP1R3C, ACSL1, BCHE, FOLR1, BCL2, UGT1A4, RASGRP2, PLCH1, FUT1, SLC30A3, PCDHA13, DTNA, SLC12A2, FADS3, TSPAN13, CYP4F12, NPR3, CAMK2N1, SLC17A7, CYP4F8, SLC16A2, SLC16A7, SLC17A3, EPS8, SLC7A2, SLC17A1, MAP2, PLCG2, SLC13A2, CYP4F3
GO:0005626~insoluble fraction	5.35E-05	NRP2, CYP3A5, GRIK2, PDLIM5, SNCA, PDE3B, TP63, IL15, TSPAN12, CYP39A1, PTGES, ANK3, SLC23A2, HMOX1, RAPGEF4, SLC4A3, NT5E, CEACAM1, CRYAB, FA2H, SPINT1, MAN1A1, UGT1A1, POR, AADAC, PLCE1, DGAT2, ARRB1, VAMP8, CNTN1, LAMC2, CPD, UGT2B15, LRRK2, VAMP1, TM4SF4, EMP1, CAV2, DRD1, CYP1B1, OAS3, OAS1, CD70, PCDHGC3, ABCA1, ABCA4, UGT1A6, ACE, PPP1R3C, ACSL1, BCHE, FOLR1, BCL2, UGT1A4, RASGRP2, PLCH1, FUT1, SLC30A3, PCDHA13, DTNA, SLC12A2, FADS3, TSPAN13, PDE3A, CYP4F12, NPR3, CAMK2N1, SLC17A7, CYP4F8, SLC16A2, SLC16A7, SLC17A3, EPS8, SLC7A2, SLC17A1, MAP2, PLCG2, SLC13A2, CYP4F3
GO:0048878~chemical homeostasis	6.31E-05	GRIK2, TACR1, SNCA, SLC9A2, PDE3B, VGF, CKB, AGTR1, S1PR3, MALL, APOE, BHLHA15, HMOX1, SERPINE1, CHRNA7, KCNMA1, IRS2, PPARGC1A, PLCE1, CCR7, ADM, HNF4A, RHCG, F2, NAB1, SLC26A9, PLLP, CALCR, TF, RBP4, DRD1, CCK, CCL2, EGLN1, ABCA1, BDKRB2, AGT, BCL2, TGM2, HCN2, TRPC6, NOX1, IGF2, CPS1, TMPRSS3, HPX, PLCG2, MT2A, CACNA1G, NR5A2, SCARA5
GO:0042312~regulation of vasodilation	6.32E-05	KCNMA1, AGTR1, ACE, NOS1, ADM, HMOX1, IGF2, CPS1
GO:0042592~homeostatic process	6.44E-05	GRIK2, STAT5A, TACR1, SLC9A2, SNCA, TNFSF14, PDE3B, VGF, CKB, GPX2, AGTR1, S1PR3, MALL, APOE, BHLHA15, HMOX1, SERPINE1, CHRNA7, IL1A, MB, KCNMA1, IRS2, MECOM, PPARGC1A, MUC3A, PLCE1, CCR7, ADM, HNF4A, RHCG, RPS17, F2, NAB1, SLC26A9, PLLP, CALCR, TF, RBP4, DRD1, PARD3, CCL2, CCK, EGLN1, ABCA1, BDKRB2, AGT, BCL2, TGM2, TFF1, GLRX, HCN2, IL6, SLC12A2, TRPC6, NOX1, IGF2, CPS1, TMPRSS3, KCNN4, LARGE, NXN, HPX, MT2A, PLCG2, CACNA1G, TGFBR3, NR5A2, SCARA5
GO:0001822~kidney development	6.76E-05	ARID5B, FBN1, NID1, GREM1, SHH, AGTR1, PLCE1, BDNF, ACE, CD44, BCL2, AGT, FOXC1, ADAMTS1, RARB, CA2, BMP7
GO:0016324~apical plasma membrane	7.57E-05	KCNMA1, MUC1, CAV2, PARD3, MYO1A, SHROOM3, SLC12A2, ERBB3, GPR64, PRKCI, ENPEP, EPCAM, ANXA6, P2RY6, MUC3A, RHCG, CD44, SLC23A2, SLC26A9, CTSB, ATP6V0D2
GO:0007599~hemostasis	8.50E-05	IL6, C4BPB, F7, SHH, IL11, PLAUR, FGG, THBD,

		PLSCR4, HNF4A, F5, FGB, FBLN5, SERPINE1, F2, TFPI2, ENTPD2, PAPSS2
GO:0007548~sex differentiation	8.56E-05	RBP4, HMGB2, STAT5A, SOX2, TP63, VGF, MMP14, SOX9, SYCP2, CDKL2, SHH, GJB2, INHBB, WNT4, AGT, BCL2, ADAMTS1, ANGPT1, FOXC1, BMPR1B, LHX8, LFNG
GO:0050878~regulation of body fluid levels	9.49E-05	KCNMA1, IL6, C4BPB, F7, SHH, IL11, PLAUR, KCNN4, FGG, THBD, PLSCR4, F5, HNF4A, FGB, FBLN5, F2, SERPINE1, GUCA2B, TFPI2, ENTPD2, PAPSS2
GO:0016323~basolateral plasma membrane	1.13E-04	DLC1, TF, CAV2, LIMA1, LIMS2, ERBB3, NPY2R, ITGB4, APBB1IP, AQP3, EPCAM, P2RY6, CD44, SLC23A2, ANK3, CEACAM5, DIXDC1, MYO1A, SLC12A2, LPP, CTNNA2, TNS4, LAMA3, RHCG, CDH17, MAP7, CA2
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	1.13E-04	FGFR2, FGFR4, NRTN, CCL2, ERBB3, GRIK2, STAT5A, BDKRB2, PHIP, ANGPT1, EGF, PIK3R3, IRS2, BAIAP2, ARID5B, IGF2, EPHA2, NTRK3, VEGFC, EPHA4, PLCE1, EPHA7, EPS8, DOK5, FOXC1, IGFBP1, AREG, MST1R
GO:0007586~digestion	1.29E-04	KCNMA1, RBP4, VIPR1, PPARGC1A, UGT1A1, KCNN4, UGT1A6, ACE, MUC3A, CYP39A1, ACSL1, BAAT, CHRM3, UGT1A4, PRSS3, TFF3, MUC5AC, TFF1
GO:0060429~epithelium development	1.42E-04	DLC1, SHROOM3, ONECUT1, ONECUT2, TP63, HOXB13, EHF, ZEB2, SFN, GREM1, SHH, WNT4, CD44, AGT, BCL2, UPK1B, KRT4, F11R, MECOM, SCEL, VEGFC, LAMA3, RHCG, FLG, CA2, BMP7, TBX18, EMP1
GO:0040012~regulation of locomotion	1.53E-04	DLC1, DRD1, ONECUT1, TACR1, SNCA, ONECUT2, GREM1, SHH, ACE, APOE, AGT, BCL2, HMOX1, UNC5C, SCG2, IL6, IRS2, IGF2, F7, HDAC5, VEGFC, LAMA3, DLL4, TGFBR3, MUC5AC
GO:0048545~response to steroid hormone stimulus	1.53E-04	CALCR, CAV2, HMGB2, CCL2, SHH, CPN1, UGT1A6, BCHE, HMOX1, BCL2, UGT1A4, ANGPT1, LOX, TFF1, NEFL, KCNMA1, IL6, CRYAB, CPS1, MMP14, TAT, UGT1A1, KRT19, ADM, COL1A1, CA2, BMP7
GO:0004857~enzyme inhibitor activity	1.54E-04	CAST, PPP1R14D, C3, LXN, SNCA, C5, PRKAG2, APOC1, TNFSF14, SFN, COL7A1, PPP1R1C, CDKN2C, AGT, SERPINE1, ITIH5, PPP1R14C, TFPI2, ANGPTL4, RHOH, COL4A3, PHACTR2, CST2, SPINT1, CST1, PKIB, CAMK2N1, RENBP, SERPINF2, ARRB1, PI3, SLPI
GO:0030334~regulation of cell migration	1.58E-04	DLC1, DRD1, IRS2, IL6, ONECUT1, TACR1, ONECUT2, IGF2, F7, GREM1, SHH, HDAC5, VEGFC, ACE, LAMA3, APOE, HMOX1, AGT, DLL4, BCL2, TGFBR3, MUC5AC, UNC5C
GO:0007242~intracellular signaling cascade	1.62E-04	CYP24A1, ADCY1, NRTN, STAT5A, TNFSF15, TNFSF14, VIPR1, RGL1, S1PR3, AGTR1, DIRAS2, STAC, APOE, BHLHA15, CHRNA7, RAPGEF4, HTR1D, RAB27B, DDAH1, NET1, DEPDC7, MAGI3, CRYAB, DCDC2, PPARGC1A, DCDC1, LAT2, PLCE1, RND1, RASGRF2, ZWINT, F2, LRRK2, ASB4, DRD1, HMGB2, CCL2, ADORA2B, ERBB3, ABCA1,

		RAB40B, CORO2A, P2RY6, PLCH1, ADRA2A, DYRK2, EGF, STK38L, FGD4, ARHGDIB, BRIP1, RERG, CDC42BPG, PLCG2, PCNA, TGFBR3, ADRA1D, TACR1, PRKAG2, TP63, RHOV, MCF2L, PLCB4, HMOX1, SHC2, RHOF, RHOH, CDK1, PRKCI, FMN2, ADM, DOK5, GADD45G, PDE9A, GADD45B, CALCR, RAB3B, PLEK2, NPY2R, C5, SFN, EFCAB4B, DGKA, PLCL2, HRH1, AGT, RASGRP2, TGM2, SH2B3, TNFRSF19, SCG2, NFATC1, BIRC7, IGF2, NPR3, MAPK10, NUPR1, JAK3, CIT, DUSP6
GO:0008585~female gonad development	1.72E-04	STAT5A, VGF, MMP14, INHBB, WNT4, BCL2, AGT, ANGPT1, ADAMTS1, FOXC1, LHX8, BMPR1B, LFNG
GO:0030198~extracellular matrix organization	1.79E-04	MPZL3, NID1, COL5A2, COL5A1, COL14A1, KAZALD1, FBLN5, AGT, TGFBI, FOXF2, COL12A1, FOXC1, MUC5AC, LOX, COL1A1, VWA1, CYR61
GO:0001558~regulation of cell growth	1.80E-04	IGFBPL1, TP63, SFN, GREM1, AGTR1, WISP2, TSPYL2, CD44, CDKN2C, APOE, AGT, BCL2, RASGRP2, CDA, CYR61, NET1, CRYAB, IGF2, NTRK3, RERG, PLCE1, HNF4A, KAZALD1, IGFBP1, IGFBP4
GO:0048608~reproductive structure development	1.91E-04	RBP4, HMGB2, STAT5A, TP63, HOXB13, VGF, SOX9, MMP14, SHH, INHBB, WNT4, AGT, BCL2, ADAMTS1, ANGPT1, FOXC1, BMPR1B, LHX8, LFNG
GO:0031667~response to nutrient levels	2.27E-04	RBP4, CYP24A1, CCK, CCL2, SOX2, SHH, AQP3, UGT1A6, ACSL1, CD44, BCHE, HMOX1, BCL2, UGT1A4, ANGPT1, MUC1, GATM, STC2, HRK, CPS1, PPARGC1A, UGT1A1, ADM, CTSD, COL1A1, ALOX5, BMP7
GO:0048514~blood vessel morphogenesis	2.62E-04	NRP2, TNFSF13, PRRX2, ENPEP, SHH, TYMP, ACE, HEY1, APOE, HMOX1, AGT, TGM2, ANGPT1, SOX17, EGF, CEACAM1, CYR61, ANGPTL4, SCG2, KLF5, NOX1, MMP14, VEGFC, ID1, DLL4, FOXC1
GO:0007267~cell-cell signaling	2.70E-04	NAMPT, INSL4, GRIK2, SNCA, TP63, IL15, ENPEP, VGF, VIPR1, SHH, IL11, KCNQ5, WISP2, WNT4, BDNF, APOE, BHLHA15, CEACAM6, SEMA3B, RAPGEF4, WNT6, HTR1D, KCNMA1, GABRG3, GPR176, STC2, EFNB2, CTNNA2, ADM, CAV2, DRD1, FGFR4, CXCL5, SOX2, CD70, GREM1, NPTX1, HRH1, AGT, FGFBP1, DTNA, HCN2, IL6, NOS1, IGF2, PARK2, TNFSF9, KCNK3, GJB1, GJB2, SLC17A7, TNFSF10, AREG, MERTK, ADRA1D
GO:0004114~3',5'-cyclic-nucleotide phosphodiesterase activity	2.77E-04	PDE2A, PDE1C, PDE1A, PDE3B, PDE11A, PDE9A, PDE10A, PDE3A
GO:0004112~cyclic-nucleotide phosphodiesterase activity	3.67E-04	PDE2A, PDE1C, PDE1A, PDE3B, PDE11A, PDE9A, PDE10A, PDE3A
GO:0048762~mesenchymal cell differentiation	4.07E-04	NRP2, S100A4, NRTN, BCL2, TGFBR3, ZEB2, FOXC1, SOX9, BMP7, SHH, NFATC1
GO:0014031~mesenchymal cell development	4.07E-04	NRP2, S100A4, NRTN, BCL2, TGFBR3, ZEB2, FOXC1, SOX9, BMP7, SHH, NFATC1
GO:0051270~regulation of cell motion	4.19E-04	DLC1, PARD3, DRD1, IRS2, IL6, ONECUT1, TACR1, ONECUT2, IGF2, F7, GREM1, SHH, HDAC5, VEGFC, ACE, LAMA3, APOE, HMOX1, AGT, DLL4, BCL2, TGFBR3, MUC5AC, UNC5C

GO:0060485~mesenchyme development	4.79E-04	NRP2, S100A4, NRTN, BCL2, TGFBR3, ZEB2, FOXC1, SOX9, BMP7, SHH, NFATC1
GO:0035295~tube development	4.95E-04	DLC1, RBP4, CAV2, FGFR4, SHROOM3, TP63, HOXB13, ZEB2, GREM1, SHH, WNT4, BDNF, CD44, BCL2, AGT, LOX, RARB, EGF, TRAF4, SIM2, CYR61, NR4A3, MMP14, FOXP2, FOXC1, BMP7
GO:0009991~response to extracellular stimulus	4.95E-04	RBP4, CYP24A1, CCK, CCL2, ADORA2B, SOX2, SHH, AQP3, UGT1A6, ACSL1, CD44, BCHE, HMOX1, BCL2, UGT1A4, ANGPT1, MUC1, GATM, STC2, HRK, CPS1, PPARGC1A, UGT1A1, ADM, CTSD, COL1A1, ALOX5, BMP7
GO:0055080~cation homeostasis	5.63E-04	CALCR, TF, DRD1, CCL2, GRIK2, TACR1, SLC9A2, BDKRB2, S1PR3, AGTR1, APOE, HMOX1, AGT, BCL2, TGM2, CHRNA7, KCNMA1, TRPC6, NOX1, TMPRSS3, CCR7, PLCE1, RHCG, ADM, HPX, SLC26A9, F2, MT2A, PLCG2, CACNA1G, SCARA5
GO:0019932~second-messenger-mediated signaling	5.82E-04	CALCR, ADCY1, DRD1, HMGB2, CCL2, ADORA2B, NPY2R, TACR1, VIPR1, AGTR1, S1PR3, HRH1, P2RY6, APOE, BHLHA15, AGT, TGM2, RAPGEF4, HTR1D, NPR3, PLCE1, LAT2, ADM, ZWINT, PCNA, PDE9A, ADRA1D
GO:0051271~negative regulation of cell motion	6.04E-04	DLC1, HDAC5, DRD1, PARD3, APOE, HMOX1, BCL2, DLL4, TGFBR3, MUC5AC, GREM1, SHH
GO:0045765~regulation of angiogenesis	6.04E-04	HDAC5, COL4A3, IL6, ADORA2B, ID1, HMOX1, SERPINE1, CHRNA7, TNFSF13, DDAH1, IL1A, ANGPTL4
GO:0045177~apical part of cell	6.56E-04	MUC1, KCNMA1, CAV2, PARD3, MYO1A, SHROOM3, SLC12A2, ERBB3, GPR64, PRKCI, ENPEP, EPCAM, ANXA6, P2RY6, MUC3A, RHCG, CD44, SLC23A2, SLC26A9, USH1C, CTSB, CA2, ATP6V0D2
GO:0043062~extracellular structure organization	6.71E-04	MPZL3, DNM3, DRD1, NID1, COL5A2, COL5A1, GPHN, COL14A1, ANK3, KAZALD1, FBLN5, AGT, TGFBI, FOXF2, COL12A1, FOXC1, MUC5AC, LOX, COL1A1, VWA1, CYR61
GO:0016477~cell migration	6.74E-04	NRP2, CAV2, DRD1, NRTN, CCK, CCL2, PLXNA2, CXCL3, ITGA11, TNFSF13, ZEB2, ENPEP, CX3CL1, SHH, CD44, PRSS3, CEACAM1, SCG2, IL6, ARID5B, PODXL, NOX1, DCDC2, MMP14, COL5A1, CTNNA2, VEGFC, ID1, TGFBR3, FOXC1
GO:0048511~rhythmic process	6.76E-04	KCNMA1, PHLPP1, HLF, DDC, DRD1, ERBB3, STAT5A, VGF, MMP14, INHBB, AGT, BCL2, PER2, ANGPT1, FOXC1, ADAMTS1, BMPR1B, LFNG
GO:0001763~morphogenesis of a branching structure	6.94E-04	CTNND2, SPINT1, HOXB13, MMP14, GREM1, SHH, EPHA7, CD44, BCL2, AGT, EGF, BMP7, CYR61
GO:0007584~response to nutrient	7.05E-04	MUC1, RBP4, CYP24A1, CCL2, GATM, STC2, SOX2, UGT1A1, SHH, AQP3, UGT1A6, ACSL1, CD44, BCHE, HMOX1, BCL2, UGT1A4, ANGPT1, COL1A1, ALOX5, BMP7
GO:0030054~cell junction	7.81E-04	DLC1, LIMA1, CLDN4, GRIK2, SYT6, CALB2, CD44, CHRNA7, GRID1, F11R, GABRG3, MAGI3, CTNNA2, TNS4, RND1, CHRM3, DOK7, VAMP1, ADD3, CGNL1, CAV2, PARD3, SHROOM3, LIMS2, NPY2R, CTNND2, APBB1IP, RIMS3, GPHN, PVRL3,

		RASGRP2, SLC30A3, DTNA, GABRP, DIXDC1, LPP, SYT11, SYT12, GJB1, CAMK2N1, GJB2, SLC17A7, TMEM47, LAMA3, DSG2, PKP2, DSC2, TJP3, TJP2
GO:0051046~regulation of secretion	7.96E-04	RBP4, RAB3B, IL6, ADORA2B, ERBB3, TACR1, SNCA, TNFSF15, PDE3B, IGF2, KRT20, PARK2, IL11, INHBB, AGTR1, KCNN4, VEGFC, HMOX1, AGT, SCIN, RAPGEF4, EGF, RAB27B, IL1A
GO:0050727~regulation of inflammatory response	8.86E-04	IL6, ADORA2B, C3, STAT5A, IGF2, CX3CL1, GPX2, AGTR1, APOE, AGT, TGM2, CHRNA7, NT5E
GO:0033273~response to vitamin	9.06E-04	MUC1, RBP4, CYP24A1, CCL2, CD44, BCHE, BCL2, SOX2, ANGPT1, BMP7, AQP3, SHH
GO:0002526~acute inflammatory response	9.56E-04	TF, IL6, C3, TACR1, C5, C4BPB, IGF2, C4BPA, APOL2, NUPR1, SERPINF2, F2, CFH, CFD, IL1A
GO:0010035~response to inorganic substance	9.75E-04	KCNMA1, PXDN, S100A16, GATM, CRYAB, EEF1A2, SNCA, TAT, AQP3, MT1X, FGG, NPTXR, APOE, FGB, HMOX1, BCL2, GPX3, SERPINE1, PLCG2, CACNA1G, COL1A1, TFF1, CA2, MB
GO:0043067~regulation of programmed cell death	9.77E-04	DLC1, GRIK2, STAT5A, SNCA, TNFSF15, TNFSF14, TP63, TNFSF13, MCF2L, SHH, BDNF, CD44, BOK, CDKN2C, APOE, HMOX1, RARB, ALX4, IL1A, NET1, KCNMA1, CDK1, CRYAB, PRKCI, HRK, F7, RASGRF2, SCIN, F2, FOXC1, CTSB, LRRK2, PRODH, CCL2, CCK, ERBB3, SOX4, CD70, SFN, BDKRB2, SOX9, AGT, BCL2, TGM2, TNFRSF19, DYRK2, NEFL, BMF, TRAF4, HELLS, FGD4, SCG2, ANGPTL4, COL4A3, IL6, EEF1A2, BIRC7, IGF2, PDE3A, SLAMF7, BIRC3, EPHA7, TNFSF10, NUPR1, PLCG2, MUC5AC, BMP7
GO:0006928~cell motion	9.80E-04	NRP2, CAV2, NRTN, DRD1, CCK, CCL2, PLXNA2, CXCL3, ITGA11, SPOCK1, TNFSF13, ZEB2, ENPEP, CX3CL1, SHH, BDNF, CD44, ANK3, PRSS3, ADRA2A, SEMA3B, UNC5C, ROBO3, CEACAM1, SCG2, ARHGDIB, IL6, ARID5B, PODXL, NOX1, DCDC2, MMP14, COL5A1, PLAUR, CTNNA2, EPHA4, VEGFC, EPHA7, ID1, TGFBR3, FOXC1, MST1R, BMPR1B, BMP7
GO:0046700~heterocycle catabolic process	9.98E-04	ALDH1L1, PDE3B, UGT1A1, AMPD3, MOXD1, FRRS1, UGT1A6, HMOX1, UGT1A4, PRODH2, CDA, DPYD, ENTPD2, NT5E, PRODH
GO:0030336~negative regulation of cell migration	0.001019734	DLC1, HDAC5, DRD1, APOE, HMOX1, BCL2, DLL4, TGFBR3, MUC5AC, GREM1, SHH
GO:0050729~positive regulation of inflammatory response	0.001021761	AGTR1, IL6, ADORA2B, C3, STAT5A, AGT, TGM2, CX3CL1
GO:0010941~regulation of cell death	0.001069339	DLC1, GRIK2, STAT5A, SNCA, TNFSF15, TNFSF14, TP63, TNFSF13, MCF2L, SHH, BDNF, CD44, BOK, CDKN2C, APOE, HMOX1, RARB, ALX4, IL1A, NET1, KCNMA1, CDK1, CRYAB, PRKCI, HRK, F7, RASGRF2, SCIN, F2, FOXC1, CTSB, LRRK2, PRODH, CCL2, CCK, ERBB3, SOX4, CD70, SFN, BDKRB2, SOX9, AGT, BCL2, TGM2, TNFRSF19, DYRK2, NEFL, BMF, TRAF4, HELLS, FGD4, SCG2, ANGPTL4, COL4A3, IL6, EEF1A2, BIRC7, IGF2, PDE3A, SLAMF7, BIRC3, EPHA7, TNFSF10, NUPR1, PLCG2, MUC5AC, BMP7

GO:0005201~extracellular matrix structural constituent	0.001093527	MATN3, COL4A3, FBN1, COL5A2, COL5A1, WNT4, MUC3A, COL14A1, COL12A1, COL1A1, MUC5AC, WNT6, TFPI2, MFAP5
GO:0006954~inflammatory response	0.001125141	TF, CCL2, C3, CXCL3, TACR1, C5, IL15, BDKRB2, S1PR3, HRH1, CD44, HMOX1, CFH, CFD, IL1A, SCG2, F11R, IL6, NOX1, CHST2, IGF2, C4BPB, C4BPA, MECOM, HDAC5, APOL2, CCR7, NUPR1, SERPINF2, F2, ALOX5, BMPR1B, IGFBP4
GO:0007010~cytoskeleton organization	0.001140432	DLC1, CAV2, TPPP3, LIMA1, SHROOM3, PDLIM7, PLEK2, ABLIM3, DIAPH3, KRT20, HOOK2, CDC42EP2, ANK3, APOE, BCL2, ADRA2A, KRT4, TUBA1B, NEFL, RHOF, FGD4, ARHGDIB, KIF11, CRYAB, VIL1, PRKCI, ESPL1, FMN2, PLCE1, CDC42BPG, KRT19, EPB41L1, RND1, EPS8, ZWINT, TPPP, MAP2, SCIN, SGCD, MAP7, TMSB4Y
GO:0003018~vascular process in circulatory system	0.00117233	KCNMA1, CAV2, AGTR1, ADORA2B, NTS, APOE, AGT, CACNA1G, FOXC1, BDKRB2, ADRA1D
GO:0008406~gonad development	0.001257547	RBP4, HMGB2, STAT5A, VGF, SOX9, MMP14, INHBB, WNT4, BCL2, AGT, ANGPT1, FOXC1, ADAMTS1, LHX8, BMPR1B, LFNG
GO:0019216~regulation of lipid metabolic process	0.001257547	KCNMA1, IRS2, STAT5A, PRKAG2, SNCA, RBL1, APOC1, PDE3B, IGF2, PPARGC1A, AGTR1, ACSL1, HNF4A, APOE, AGT, NR1H3
GO:0019217~regulation of fatty acid metabolic process	0.00128674	IRS2, ACSL1, HNF4A, AGT, PRKAG2, SNCA, APOC1, IGF2, PPARGC1A, NR1H3
GO:0007167~enzyme linked receptor protein signaling pathway	0.001309453	FGFR2, NRTN, FGFR4, CCL2, ERBB3, GRIK2, USP9Y, STAT5A, BDKRB2, PHIP, ANGPT1, EGF, PIK3R3, IRS2, BAIAP2, ARID5B, IGF2, EPHA2, NTRK3, VEGFC, EPHA4, PLCE1, EPHA7, EPS8, ID1, DOK5, TGFBR3, FOXC1, MST1R, JAK3, IGFBP1, AREG, BMPR1B, BMP7
GO:0031099~regeneration	0.001324106	CCL2, GATM, ADM, BCL2, SERPINE1, ANGPT1, IGFBP1, NR4A3, NEFL, GAS6, TM4SF4, PLAUR
GO:0001525~angiogenesis	0.001352651	KLF5, NRP2, NOX1, TNFSF13, ENPEP, MMP14, SHH, VEGFC, TYMP, ID1, HMOX1, DLL4, ANGPT1, SOX17, EGF, CEACAM1, CYR61, ANGPTL4, SCG2
GO:0030155~regulation of cell adhesion	0.001458475	ONECUT1, ERBB3, PODXL, STAT5A, ONECUT2, PDE3B, NID1, CX3CL1, EDIL3, MMP14, LAMA3, RND1, BCL2, TGFBI, TGM2, COL1A1, CYR61, ARHGDIB
GO:0003013~circulatory system process	0.001469606	KCNMA1, COL4A3, CAV2, ADORA2B, TACR1, NOX1, NPR3, BDKRB2, AGTR1, RENBP, ACE, F5, ADM, NTS, APOE, HMOX1, AGT, DLL4, CACNA1G, FOXC1, GUCA2B, ADRA1D
GO:0008015~blood circulation	0.001469606	KCNMA1, COL4A3, CAV2, ADORA2B, TACR1, NOX1, NPR3, BDKRB2, AGTR1, RENBP, ACE, F5, ADM, NTS, APOE, HMOX1, AGT, DLL4, CACNA1G, FOXC1, GUCA2B, ADRA1D
GO:0004866~endopeptidase inhibitor activity	0.001474756	CAST, COL4A3, LXN, C3, C5, SNCA, SPINT1, CST2, TNFSF14, CST1, RENBP, COL7A1, SERPINF2, AGT, SERPINE1, PI3, ITIH5, SLPI, TFPI2
GO:0008284~positive regulation of cell proliferation	0.001482115	FGFR2, NAMPT, FGFR4, CCL2, CXCL5, MARCKSL1, STAT5A, TACR1, SOX2, SOX4, TP63, TNFSF13, PRRX2, IL15, VIPR1, SHH, IL11, S1PR3, HLX, BCL2,

		AGT, TGM2, ADRA2A, CHRNA7, EGF, RUNX2, SCG2, KLF5, IL6, IRS2, CRIP2, NOX1, IGF2, FOXP2, VEGFC, ADM, MST1R, TBX18, ADRA1D
GO:0040013~negative regulation of locomotion	0.001745228	DLC1, HDAC5, DRD1, APOE, HMOX1, BCL2, DLL4, TGFBR3, MUC5AC, GREM1, SHH
GO:0002053~positive regulation of mesenchymal cell proliferation	0.001807188	IRS2, TP63, PRRX2, TBX18, SHH, FOXP2
GO:0030003~cellular cation homeostasis	0.001819434	CALCR, TF, DRD1, CCL2, GRIK2, TACR1, BDKRB2, AGTR1, S1PR3, APOE, AGT, BCL2, TGM2, CHRNA7, KCNMA1, TRPC6, NOX1, TMPRSS3, CCR7, PLCE1, ADM, HPX, F2, MT2A, PLCG2, CACNA1G, SCARA5
GO:0044057~regulation of system process	0.001942205	TF, DRD1, CCK, CCL2, ADORA2B, GRIK2, TACR1, SNCA, CTNND2, BDKRB2, VGF, ANXA6, AGTR1, BDNF, ACE, BCHE, APOE, HMOX1, AGT, KCNMA1, NOS1, IGF2, PARK2, CPS1, INHBB, PLCE1, ADM, CHRM3, CACNA1G, ALOX5, ADRA1D
GO:0022602~ovulation cycle process	0.001980013	INHBB, BCL2, STAT5A, AGT, ANGPT1, ADAMTS1, FOXC1, MMP14, BMPR1B, VGF, LFNG
GO:0042981~regulation of apoptosis	0.001980279	DLC1, GRIK2, STAT5A, SNCA, TNFSF15, TNFSF14, TP63, TNFSF13, MCF2L, SHH, BDNF, CD44, BOK, APOE, CDKN2C, HMOX1, RARB, ALX4, IL1A, NET1, KCNMA1, CDK1, CRYAB, PRKCI, HRK, F7, RASGRF2, SCIN, F2, FOXC1, CTSB, PRODH, CCL2, CCK, ERBB3, SOX4, CD70, SFN, BDKRB2, SOX9, AGT, BCL2, TGM2, TNFRSF19, DYRK2, NEFL, BMF, TRAF4, HELLS, FGD4, SCG2, ANGPTL4, COL4A3, IL6, EEF1A2, BIRC7, IGF2, PDE3A, SLAMF7, BIRC3, EPHA7, TNFSF10, NUPR1, MUC5AC, BMP7
GO:0019935~cyclic-nucleotide-mediated signaling	0.002162298	CALCR, DRD1, ADCY1, CCL2, ADORA2B, NPY2R, NPR3, VIPR1, S1PR3, ADM, APOE, AGT, TGM2, RAPGEF4, PDE9A, HTR1D, ADRA1D
GO:0042325~regulation of phosphorylation	0.002174317	PARD3, DRD1, ADCY1, PPP1R14D, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, BDKRB2, SFN, IL11, DGKA, TSPYL2, APOE, CDKN2C, BCL2, AGT, ADRA2A, CHRNA7, RAPGEF4, PPP1R14C, EGF, FGD4, CDC6, IL6, RBL1, BIRC7, IGF2, PKIB, CDC25A, VEGFC, PLCE1, CCND3, HNF4A, HPX, GADD45G, F2, GADD45B, BMP7, DUSP6
GO:0050801~ion homeostasis	0.002178986	CALCR, TF, DRD1, CCK, CCL2, GRIK2, TACR1, SNCA, SLC9A2, BDKRB2, CKB, S1PR3, AGTR1, APOE, HMOX1, BCL2, AGT, TGM2, CHRNA7, KCNMA1, HCN2, TRPC6, NOX1, CPS1, TMPRSS3, CCR7, PLCE1, RHCG, ADM, HPX, NAB1, PLCG2, SLC26A9, F2, MT2A, CACNA1G, PLLP, SCARA5
GO:0051240~positive regulation of multicellular organismal process	0.002181493	TF, DRD1, CCL2, ADORA2B, GRIK2, TACR1, STAT5A, SNCA, SHH, HMOX1, AGT, BCL2, IL1A, IL6, NOS1, NOX1, IGF2, CPS1, ADM, CHRM3, SERPINF2, F2, CA2, ALOX5, BMP7, BMPR1B
GO:0070161~anchoring junction	0.002223413	DLC1, CAV2, DIXDC1, PARD3, LIMA1, SHROOM3, LIMS2, LPP, NPY2R, CTNND2, APBB1IP, CTNNA2, TNS4, LAMA3, RND1, DSG2, CD44, PKP2, PVRL3, DSC2, TJP2
GO:0019229~regulation of vasoconstriction	0.002227226	AGTR1, ACE, CHRM3, ADM, TACR1, AGT, BDKRB2, ALOX5

GO:0050880~regulation of blood vessel size	0.002279145	KCNMA1, CAV2, AGTR1, ADORA2B, NTS, APOE, AGT, CACNA1G, FOXC1, ADRA1D
GO:0035150~regulation of tube size	0.002279145	KCNMA1, CAV2, AGTR1, ADORA2B, NTS, APOE, AGT, CACNA1G, FOXC1, ADRA1D
GO:0005520~insulin-like growth factor binding	0.002322628	WISP2, IGFBPL1, KAZALD1, IGF2, IGFBP1, IGFBP4, CYR61
GO:0004435~phosphoinositide phospholipase C activity	0.002322628	PLCL2, PLCE1, PLCB4, CHRM3, PLCG2, PLCH1, BDKRB2
GO:0031960~response to corticosteroid stimulus	0.002388866	KCNMA1, CALCR, IL6, CCL2, CPS1, TAT, UGT1A1, CPN1, UGT1A6, ADM, BCHE, BCL2, UGT1A4, COL1A1, NEFL
GO:0010464~regulation of mesenchymal cell proliferation	0.002389595	IRS2, TP63, PRRX2, TBX18, SHH, FOXP2
GO:0040008~regulation of growth	0.002405944	RBP4, IGFBPL1, STAT5A, TP63, HOXB13, SFN, VGF, GREM1, AGTR1, IGSF11, WISP2, TSPYL2, CD44, APOE, CDKN2C, AGT, HLX, BCL2, RASGRP2, CDA, NET1, CYR61, CRYAB, IGF2, GAS6, RERG, NTRK3, PLCE1, HNF4A, KAZALD1, FOXC1, IGFBP1, IGFBP4
GO:0019838~growth factor binding	0.00245652	IL1R2, FGFR4, IGFBPL1, ERBB3, IGF2, COL5A1, NTRK3, WISP2, KAZALD1, TGFBR3, IGFBP1, COL1A1, FGFBP1, IGFBP4, CYR61
GO:0032103~positive regulation of response to external stimulus	0.002525884	NTRK3, AGTR1, IL6, ADORA2B, C3, STAT5A, AGT, TGM2, F7, CX3CL1, SCG2
GO:0051174~regulation of phosphorus metabolic process	0.002596525	DLC1, PARD3, DRD1, ADCY1, PPP1R14D, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, BDKRB2, SFN, IL11, DGKA, TSPYL2, APOE, CDKN2C, BCL2, AGT, ADRA2A, CHRNA7, RAPGEF4, PPP1R14C, EGF, FGD4, CDC6, IL6, RBL1, BIRC7, IGF2, PKIB, CDC25A, VEGFC, PLCE1, CCND3, HNF4A, HPX, GADD45G, F2, GADD45B, BMP7, DUSP6
GO:0019220~regulation of phosphate metabolic process	0.002596525	DLC1, PARD3, DRD1, ADCY1, PPP1R14D, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, BDKRB2, SFN, IL11, DGKA, TSPYL2, APOE, CDKN2C, BCL2, AGT, ADRA2A, CHRNA7, RAPGEF4, PPP1R14C, EGF, FGD4, CDC6, IL6, RBL1, BIRC7, IGF2, PKIB, CDC25A, VEGFC, PLCE1, CCND3, HNF4A, HPX, GADD45G, F2, GADD45B, BMP7, DUSP6
GO:0001657~ureteric bud development	0.002653536	BDNF, CD44, BCL2, AGT, FOXC1, RARB, GREM1, SHH
GO:0030414~peptidase inhibitor activity	0.00269435	CAST, COL4A3, LXN, C3, C5, SNCA, SPINT1, CST2, TNFSF14, CST1, RENBP, COL7A1, SERPINF2, AGT, SERPINE1, PI3, ITIH5, SLPI, TFPI2
GO:0006875~cellular metal ion homeostasis	0.002798583	CALCR, KCNMA1, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, TMPRSS3, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, AGT, BCL2, F2, PLCG2, TGM2, CACNA1G, CHRNA7
GO:0051050~positive regulation of transport	0.002952156	RBP4, IL6, DRD1, IRS2, ADORA2B, ERBB3, C3, TACR1, SNCA, PRKCI, TNFSF15, TNFSF14, IGF2, SYNGR3, SHH, INHBB, KCNN4, VEGFC, APOE, SCIN, F2, PLCG2, IL1A, NR1H3
GO:0042596~fear response	0.003097221	DRD1, BDNF, CCK, GRIK2, BCL2, ADRA2A
GO:0045909~positive regulation of	0.003211193	NOS1, ADM, HMOX1, IGF2, CPS1

vasodilation		
GO:0045937~positive regulation of phosphate metabolic process	0.003376094	DLC1, IL6, CCK, PRKAG2, IGF2, IL11, VEGFC, CCND3, HPX, BCL2, AGT, F2, EGF, BMP7
GO:0032868~response to insulin stimulus	0.003376094	RBP4, IRS2, DRD1, ERBB3, BAIAP2, PRKCI, PDE3B, IGF2, VGF, PHIP, HDAC5, ADM, IGFBP1, PIK3R3
GO:0010562~positive regulation of phosphorus metabolic process	0.003376094	DLC1, IL6, CCK, PRKAG2, IGF2, IL11, VEGFC, CCND3, HPX, BCL2, AGT, F2, EGF, BMP7
GO:0045834~positive regulation of lipid metabolic process	0.003383711	AGTR1, IRS2, HNF4A, APOE, AGT, APOC1, IGF2, PPARGC1A, NR1H3
GO:0005581~collagen	0.003404915	COL4A3, COL14A1, COL7A1, COL12A1, COL1A1, LOX, COL5A2, COL5A1
GO:0051674~localization of cell	0.003461773	NRP2, CAV2, DRD1, NRTN, CCK, CCL2, PLXNA2, CXCL3, ITGA11, TNFSF13, ZEB2, ENPEP, CX3CL1, SHH, CD44, PRSS3, CEACAM1, SCG2, IL6, ARID5B, PODXL, NOX1, DCDC2, MMP14, COL5A1, CTNNA2, VEGFC, ID1, TGFBR3, FOXC1
GO:0048870~cell motility	0.003461773	NRP2, CAV2, DRD1, NRTN, CCK, CCL2, PLXNA2, CXCL3, ITGA11, TNFSF13, ZEB2, ENPEP, CX3CL1, SHH, CD44, PRSS3, CEACAM1, SCG2, IL6, ARID5B, PODXL, NOX1, DCDC2, MMP14, COL5A1, CTNNA2, VEGFC, ID1, TGFBR3, FOXC1
GO:0003779~actin binding	0.00350112	LIMA1, SHROOM3, PDLIM5, ABLIM3, DIAPH3, KLHL4, CORO2A, ACE, PLS1, PIP, STK38L, FGD4, MYO5C, KCNMA1, DIXDC1, MYO1A, PHACTR2, NCALD, VIL1, MYO1D, SYNPO2, TNS4, FMN2, EPB41L1, MYPN, SCIN, CAPG, POF1B, MARCKS, TMSB4Y, ADD3, SPTB
GO:0042698~ovulation cycle	0.003564198	INHBB, BCL2, STAT5A, AGT, ANGPT1, ADAMTS1, FOXC1, MMP14, BMPR1B, VGF, LFNG
GO:0005912~adherens junction	0.003657947	DLC1, CAV2, DIXDC1, LIMA1, PARD3, SHROOM3, LIMS2, LPP, NPY2R, CTNND2, APBB1IP, CTNNA2, TNS4, LAMA3, RND1, CD44, PKP2, PVRL3, TJP2
GO:0030855~epithelial cell differentiation	0.003683739	F11R, SHROOM3, ONECUT1, ONECUT2, TP63, HOXB13, EHF, SFN, SCEL, LAMA3, RHCG, FLG, AGT, UPK1B, KRT4, BMP7, EMP1
GO:0005125~cytokine activity	0.003684249	NAMPT, IL6, CCL2, CXCL5, CXCL3, C5, TNFSF15, TNFSF14, CD70, TNFSF13, CX3CL1, IL15, GREM1, TNFSF9, IL11, INHBB, TNFSF10, PPBP, AREG, BMP7, IL1A, SCG2
GO:0002009~morphogenesis of an epithelium	0.003684276	DLC1, SHROOM3, TP63, HOXB13, ZEB2, GREM1, SHH, VEGFC, WNT4, CD44, BCL2, AGT, CA2, TBX18
GO:0010565~regulation of cellular ketone metabolic process	0.003801365	IRS2, ACSL1, HNF4A, AGT, PRKAG2, SNCA, APOC1, IGF2, PPARGC1A, NR1H3
GO:0055082~cellular chemical homeostasis	0.003851712	CALCR, TF, DRD1, CCK, CCL2, GRIK2, TACR1, SNCA, BDKRB2, CKB, S1PR3, AGTR1, APOE, AGT, BCL2, TGM2, CHRNA7, KCNMA1, HCN2, TRPC6, NOX1, PPARGC1A, TMPRSS3, CCR7, PLCE1, RHCG, ADM, HPX, NAB1, PLCG2, F2, MT2A, CACNA1G, PLLP, SCARA5
GO:0032869~cellular response to insulin stimulus	0.003976953	PHIP, HDAC5, IRS2, DRD1, ERBB3, BAIAP2, PRKCI, PDE3B, IGF2, IGFBP1, PIK3R3
GO:0006260~DNA replication	0.004262368	GINS1, CLSPN, CDC6, HMGB2, DTL, POLE, RAD9B, MCM10, MCM4, MCM5, CDC25A, TK1, MCM6,

		TYMP, MCM8, CDC45, POLE2, RRM2, RRM1, PCNA, EGF
GO:0035239~tube morphogenesis	0.004353686	DLC1, SHROOM3, TP63, HOXB13, ZEB2, NR4A3, GREM1, MMP14, SHH, WNT4, CD44, BCL2, AGT, EGF, BMP7, CYR61
GO:0070633~transepithelial transport	0.004437395	CAV2, P2RY6, RHCG, SLC12A2, SLC23A2
GO:0030199~collagen fibril organization	0.004455077	COL14A1, COL12A1, FOXC1, COL1A1, LOX, COL5A2, COL5A1
GO:0070085~glycosylation	0.004687373	GCNT4, MGAT4A, GALNT1, ST6GAL2, GALNT7, TSPAN7, TSPAN8, ST6GALNAC1, LARGE, ST8SIA4, B3GNT7, B3GALNT1, FUT1, B3GNT3, GALNT9, TM4SF4
GO:0043413~biopolymer glycosylation	0.004687373	GCNT4, MGAT4A, GALNT1, ST6GAL2, GALNT7, TSPAN7, TSPAN8, ST6GALNAC1, LARGE, ST8SIA4, B3GNT7, B3GALNT1, FUT1, B3GNT3, GALNT9, TM4SF4
GO:0006486~protein amino acid glycosylation	0.004687373	GCNT4, MGAT4A, GALNT1, ST6GAL2, GALNT7, TSPAN7, TSPAN8, ST6GALNAC1, LARGE, ST8SIA4, B3GNT7, B3GALNT1, FUT1, B3GNT3, GALNT9, TM4SF4
GO:0055065~metal ion homeostasis	0.004746745	CALCR, KCNMA1, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, TMPRSS3, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, AGT, BCL2, F2, PLCG2, TGM2, CACNA1G, CHRNA7
GO:0002064~epithelial cell development	0.004944797	SHROOM3, ONECUT1, AGT, ONECUT2, TP63, HOXB13
GO:0043255~regulation of carbohydrate biosynthetic process	0.004944797	IRS2, PPP1R3C, HNF4A, IGF2, DYRK2, PPARGC1A
GO:0010873~positive regulation of cholesterol esterification	0.004982544	AGTR1, APOE, AGT, APOC1
GO:0035112~genitalia morphogenesis	0.004982544	RBP4, TP63, SYCP2, SHH
GO:0033555~multicellular organismal response to stress	0.005011398	DRD1, BDNF, CCK, NOS1, GRIK2, TACR1, BCL2, ADRA2A
GO:0005604~basement membrane	0.005030565	TF, COL4A3, LAMB3, LAMA3, COL7A1, FBN1, LAMC2, ADAMTS1, NID1, VWA1, ENTPD2, COL5A1
GO:0048729~tissue morphogenesis	0.005105707	DLC1, SHROOM3, TP63, HOXB13, ZEB2, NR4A3, GREM1, SHH, VEGFC, FOXQ1, WNT4, CD44, AGT, BCL2, TGFBR3, FOXC1, COL1A1, CA2, BMP7, TBX18
GO:0043069~negative regulation of programmed cell death	0.005237339	CCL2, GRIK2, ERBB3, STAT5A, SNCA, SOX4, TP63, BDKRB2, SHH, BDNF, APOE, HMOX1, BCL2, AGT, TGM2, NEFL, HELLS, IL1A, SCG2, ANGPTL4, CDK1, IL6, CRYAB, EEF1A2, HRK, BIRC7, PRKCI, IGF2, PDE3A, F7, BIRC3, PLCG2, FOXC1
GO:0005792~microsome	0.005343964	CYP3A5, CYP1B1, OAS3, TP63, PDE3B, OAS1, UGT1A6, PPP1R3C, CYP39A1, ACSL1, PTGES, BCL2, HMOX1, UGT1A4, DTNA, FA2H, CYP4F12, UGT1A1, POR, AADAC, CYP4F8, DGAT2, MAP2, CYP4F3, CPD, UGT2B15, LRRK2
GO:0006873~cellular ion homeostasis	0.005421065	CALCR, TF, DRD1, CCK, CCL2, GRIK2, TACR1, SNCA, BDKRB2, CKB, S1PR3, AGTR1, APOE, AGT, BCL2, TGM2, CHRNA7, KCNMA1, HCN2, TRPC6, NOX1, TMPRSS3, CCR7, PLCE1, RHCG, ADM, HPX,

		NAB1, F2, MT2A, PLCG2, CACNA1G, PLLP, SCARA5
GO:0060548~negative regulation of cell death	0.005465262	CCL2, GRIK2, ERBB3, STAT5A, SNCA, SOX4, TP63, BDKRB2, SHH, BDNF, APOE, HMOX1, BCL2, AGT, TGM2, NEFL, HELLS, IL1A, SCG2, ANGPTL4, CDK1, IL6, CRYAB, EEF1A2, HRK, BIRC7, PRKCI, IGF2, PDE3A, F7, BIRC3, PLCG2, FOXC1
GO:0005164~tumor necrosis factor receptor binding	0.00559134	TNFSF10, TNFSF15, TNFSF14, CD70, TNFSF13, TNFSF9
GO:0032102~negative regulation of response to external stimulus	0.005734775	GPX2, DRD1, CCK, APOE, CHRNA7, IGF2, GREM1, NT5E, CTNNA2
GO:0009266~response to temperature stimulus	0.005826723	NOS1, CCL2, DIO2, STAC, ADM, LXN, CRYAB, TACR1, BCL2, AGT, VGF, SCARA5
GO:0040007~growth	0.006092667	FGFR2, GINS1, ST6GAL2, GATM, ARID5B, SHH, PLAUR, FOXP2, INHBB, NUPR1, BCL2, SERPINE1, TGFBR3, FOXC1, IGFBP1, SEPP1, BMP7, BMPR1B, TM4SF4, EMP1
GO:0030001~metal ion transport	0.006221247	KCNH1, FXYD2, TF, KCNAB2, SLC9A2, KCNJ2, ANXA6, KCNQ5, BHLHA15, SLC23A2, KCNK5, SLC4A8, CHRNA7, SLC30A3, SLC4A4, KCNG1, NFATC1, KCNMA1, HCN2, CACNA2D1, SLC12A8, SGK1, SLC12A2, TRPC6, CACNG7, SLC10A7, KCNK1, TCN1, KCNK3, SLC17A7, KCNN4, KCNJ6, SLC17A3, ATP2A3, SLC17A1, F2, CACNA1G, SLC13A2, ABCC8, SCARA5
GO:0019725~cellular homeostasis	0.006392832	CALCR, TF, DRD1, CCK, CCL2, GRIK2, TACR1, SNCA, BDKRB2, CKB, S1PR3, AGTR1, APOE, BCL2, AGT, TGM2, CHRNA7, GLRX, KCNMA1, HCN2, SLC12A2, TRPC6, NOX1, PPARGC1A, TMPRSS3, KCNN4, CCR7, PLCE1, RHCG, NXN, LARGE, ADM, HPX, NAB1, PLCG2, F2, MT2A, CACNA1G, PLLP, SCARA5
GO:0001541~ovarian follicle development	0.006658012	INHBB, BCL2, ANGPT1, FOXC1, MMP14, BMPR1B, VGF, LFNG
GO:0055066~di-, tri-valent inorganic cation homeostasis	0.006880564	CALCR, TF, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, HPX, HMOX1, BCL2, MT2A, F2, PLCG2, TGM2, CACNA1G, CHRNA7, SCARA5
GO:0042327~positive regulation of phosphorylation	0.007093534	IL6, CCK, PRKAG2, IGF2, IL11, VEGFC, CCND3, HPX, BCL2, AGT, F2, EGF, BMP7
GO:0004629~phospholipase C activity	0.007221679	PLCL2, PLCE1, PLCB4, CHRM3, PLCG2, PLCH1, BDKRB2
GO:0007200~activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	0.007297389	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3
GO:0001932~regulation of protein amino acid phosphorylation	0.007311114	IL6, CCK, PRKAG2, BIRC7, IGF2, ZEB2, BDKRB2, IL11, VEGFC, CCND3, HNF4A, HPX, AGT, BCL2, F2, RAPGEF4, EGF, BMP7, FGD4
GO:0048806~genitalia development	0.00746178	RBP4, SOX2, TP63, SYCP2, SHH, GJB2
GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	0.007474841	CALCR, TF, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, HPX, BCL2, MT2A, F2, PLCG2, TGM2, CACNA1G, CHRNA7, SCARA5

GO:0030030~cell projection organization	0.007491273	NRP2, PARD3, NRTN, LIMA1, CCK, ONECUT1, ERBB3, ONECUT2, ITGB4, SHH, BDNF, CD44, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, NEFL, FGD4, KLF5, DNM3, IL6, MYO1A, BAIAP2, CTNNA2, EPHA4, EPHA7, ADM, CAPG, MAP2, BMPR1B, BMP7, SLITRK6
GO:0007204~elevation of cytosolic calcium ion concentration	0.007611095	CALCR, DRD1, TRPC6, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, PLCG2, F2, CACNA1G, TGM2
GO:0042598~vesicular fraction	0.007618677	CYP3A5, CYP1B1, OAS3, TP63, PDE3B, OAS1, UGT1A6, PPP1R3C, CYP39A1, ACSL1, PTGES, BCL2, HMOX1, UGT1A4, DTNA, FA2H, CYP4F12, UGT1A1, POR, AADAC, CYP4F8, DGAT2, MAP2, CYP4F3, CPD, UGT2B15, LRRK2
GO:0043066~negative regulation of apoptosis	0.007633106	CCL2, GRIK2, ERBB3, STAT5A, SNCA, SOX4, TP63, BDKRB2, SHH, BDNF, APOE, HMOX1, BCL2, AGT, TGM2, NEFL, HELLS, IL1A, SCG2, ANGPTL4, CDK1, IL6, CRYAB, EEF1A2, HRK, BIRC7, PRKCI, IGF2, PDE3A, F7, BIRC3, FOXC1
GO:0010872~regulation of cholesterol esterification	0.007646488	AGTR1, APOE, AGT, APOC1
GO:0060343~trabecula formation	0.007646488	RBP4, TGFBR3, ADAMTS1, COL1A1
GO:0007507~heart development	0.008110507	DLC1, NRP2, RBP4, ERBB3, FBN1, SOX4, EGLN1, MECOM, SOX9, COL5A1, SHH, HDAC5, PLCE1, ADM, PKP2, ID1, TGFBR3, FOXC1, ADAMTS1, RARB, NFATC1, MB
GO:0008092~cytoskeletal protein binding	0.008201678	TPPP3, LIMA1, SHROOM3, PDLIM5, ABLIM3, DIAPH3, SNCA, EPB41L4A, KLHL4, SDC2, FRMD3, HOOK2, CORO2A, ACE, APOE, PLS1, PIP, STK38L, FGD4, MYO5C, KCNMA1, DIXDC1, PHACTR2, MYO1A, NCALD, CRYAB, BAIAP2, VIL1, MYO1D, SYNPO2, TNS4, FMN2, EPB41L1, RHCG, MYPN, TPPP, CAPG, SCIN, POF1B, MARCKS, TMSB4Y, ADD3, SPTB
GO:0060191~regulation of lipase activity	0.008287963	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, APOC1, TGM2, NPR3, ANGPTL4, NR1H3
GO:0032535~regulation of cellular component size	0.008410034	FGFR2, LIMA1, TP63, SFN, GREM1, CDC42EP2, TSPYL2, CDKN2C, AGT, BCL2, CDA, NEFL, CRYAB, VIL1, IGF2, NTRK3, RERG, HNF4A, NUPR1, CAPG, SCIN, TGFBR3, TMSB4Y, IGFBP1, EMP1, SPTB
GO:0031093~platelet alpha granule lumen	0.008433323	VEGFC, FGG, F5, PPBP, FGB, SERPINF2, EGF, CFD
GO:0006939~smooth muscle contraction	0.00861194	KCNMA1, DRD1, CHRM3, TACR1, AGT, CACNA1G, BDKRB2
GO:0007162~negative regulation of cell adhesion	0.008675897	RND1, ERBB3, PODXL, TGFBI, PDE3B, COL1A1, MMP14, ARHGDIB
GO:0048015~phosphoinositide-mediated signaling	0.009013769	AGTR1, P2RY6, HMGB2, DRD1, HRH1, PLCE1, TACR1, ZWINT, AGT, TGM2, PCNA, NPR3
GO:0048754~branching morphogenesis of a tube	0.0091336	CD44, BCL2, AGT, HOXB13, MMP14, EGF, GREM1, BMP7, SHH, CYR61
GO:0051241~negative regulation of multicellular organismal process	0.009307355	KCNMA1, RBP4, DRD1, IL6, ADORA2B, GRIK2, APOC1, TSPAN8, IGF2, SOX9, ADM, BCHE, APOE, HMOX1, F2, SERPINE1, CHRNA7, ADRA1D
GO:0006979~response to oxidative stress	0.009307355	PXDN, GATM, CRYAB, SNCA, MMP14, TAT, GPX2,

		NPTXR, APOE, SLC23A2, HMOX1, BCL2, GPX3, SERPINE1, SCARA3, SEPP1, COL1A1, MB
GO:0006952~defense response	0.009657901	KLRC2, GRIK2, TACR1, SNCA, IL15, S1PR3, CD44, HMOX1, CFH, CFD, IL1A, F11R, CHST2, DCDC2, MECOM, INHBB, CCR7, PPBP, SERPINF2, F2, MST1R, TF, DRD1, CCK, CCL2, ADORA2B, C3, CXCL3, C5, BDKRB2, CX3CL1, HRH1, BCL2, TFF3, SCG2, IL6, NOX1, IGF2, C4BPB, C4BPA, SLAMF7, HDAC5, APOL2, KCNN4, APOL1, NUPR1, ALOX5, BMPR1B, IGFBP4
GO:0005506~iron ion binding	0.009691963	CYP24A1, CYP3A5, TF, PXDN, CYP1B1, UTY, SNCA, EGLN1, CYP39A1, HMOX1, P4HA3, NT5E, KDM5D, MOCS1, MB, NOS1, FA2H, NOX1, FADS3, CYP4F12, POR, FRRS1, CYP4F8, HPX, RRM2, CYP4F3, ALOX5, DPYD, SCARA5
GO:0001934~positive regulation of protein amino acid phosphorylation	0.009787724	VEGFC, IL6, CCK, CCND3, HPX, BCL2, AGT, PRKAG2, F2, IGF2, BMP7, IL11
GO:0001656~metanephros development	0.009838074	BDNF, CD44, BCL2, AGT, FOXC1, RARB, GREM1, SHH
GO:0051384~response to glucocorticoid stimulus	0.010511703	CALCR, IL6, CCL2, CPS1, UGT1A1, TAT, CPN1, UGT1A6, ADM, BCHE, BCL2, UGT1A4, NEFL
GO:0060341~regulation of cellular localization	0.010540416	RBP4, RAB3B, IL6, ADORA2B, CRYAB, SNCA, TNFSF15, PDE3B, TNFSF14, IGF2, KRT20, PARK2, SHH, IL11, INHBB, KCNN4, VEGFC, HNF4A, HMOX1, AGT, RAPGEF4, RAB27B, EGF, IL1A
GO:0003006~reproductive developmental process	0.010686019	RBP4, HMGB2, STAT5A, SOX2, TP63, HOXB13, SOX9, VGF, SYCP2, SHH, WNT4, AGT, BCL2, ANGPT1, LHX8, LFNG, PCSK4, PDE3A, MMP14, CDKL2, GJB2, INHBB, ADAMTS1, FOXC1, BMPR1B
GO:0031420~alkali metal ion binding	0.010783097	KCNH1, KCNMA1, HCN2, FXYD2, SLC12A8, SLC12A2, KCNAB2, SLC9A2, SLC10A7, KCNJ2, KCNK1, KCNK3, SLC17A7, KCNQ5, KCNJ6, SLC17A3, SLC23A2, SLC17A1, KCNK5, SLC4A8, SLC13A2, SLC4A4, KCNG1
GO:0010574~regulation of vascular endothelial growth factor production	0.011002689	IL6, ADORA2B, NOX1, IL1A
GO:0015293~symporter activity	0.011183541	SLC16A14, SLC2A13, SLC12A8, SLC12A2, SLC6A14, SLC10A7, SLC6A17, SLC17A7, SLC16A2, SLC17A3, SLC16A7, SLC2A3, SLC23A2, SLC17A1, SLC13A2, SLC4A4
GO:0051130~positive regulation of cellular component organization	0.011430518	CAV2, CCK, C3, TACR1, NOX1, SNCA, PRKCI, IGF2, ESPL1, PPARGC1A, AHR, NTRK3, METRN, CDC42EP2, TPPP, DNMT1, EGF, NEFL, IL1A
GO:0010906~regulation of glucose metabolic process	0.011495933	IRS2, PPP1R3C, HNF4A, PRKAG2, IGF2, DYRK2, PPARGC1A
GO:0060205~cytoplasmic membrane-bounded vesicle lumen	0.012381802	VEGFC, FGG, F5, PPBP, FGB, SERPINF2, EGF, CFD
GO:0010810~regulation of cell-substrate adhesion	0.012496536	ONECUT1, BCL2, ONECUT2, NID1, EDIL3, COL1A1, MMP14, CYR61
GO:0006874~cellular calcium ion homeostasis	0.012704594	CALCR, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, BCL2, F2, PLCG2, CACNA1G, TGM2, CHRNA7

GO:0004714~transmembrane receptor protein tyrosine kinase activity	0.013211971	NRP2, NTRK3, FGFR2, EPHA4, EPHA7, FGFR4, ERBB3, MST1R, MERTK, EPHA2
GO:0051480~cytosolic calcium ion homeostasis	0.013374002	CALCR, DRD1, TRPC6, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, PLCG2, F2, CACNA1G, TGM2
GO:0000165~MAPKKK cascade	0.01338233	NRTN, ADORA2B, CRYAB, C5, BIRC7, IGF2, MAPK10, PLCE1, DOK5, GADD45G, ADRA2A, TNFRSF19, CHRNA7, LRRK2, GADD45B, EGF, FGD4, DUSP6, SCG2
GO:0050708~regulation of protein secretion	0.013921021	KCNN4, VEGFC, RBP4, IL6, TNFSF15, IGF2, KRT20, EGF, IL1A
GO:0009101~glycoprotein biosynthetic process	0.014064419	MGAT4A, GCNT4, GALNT1, ST6GAL2, GALNT7, TSPAN7, TSPAN8, ST6GALNAC1, LARGE, ST8SIA4, B3GNT7, B3GALNT1, CHST13, FUT1, B3GNT3, GALNT9, TM4SF4
GO:0010639~negative regulation of organelle organization	0.014686128	DLC1, LIMA1, SCIN, MAP2, SNCA, CAPG, VIL1, DNMT1, ESPL1, TMSB4Y, SPTB
GO:0031175~neuron projection development	0.01497966	NRP2, PARD3, NRTN, IL6, CCK, ERBB3, BAIAP2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ADM, CD44, ANK3, BCL2, MAP2, SEMA3B, UNC5C, ROBO3, BMP7, BMPR1B, SLITRK6, NEFL
GO:0001837~epithelial to mesenchymal transition	0.015239101	S100A4, TGFBR3, SOX9, BMP7, NFATC1
GO:0043068~positive regulation of programmed cell death	0.015515219	DLC1, CCK, GRIK2, SOX4, TP63, TNFSF14, CD70, TNFSF13, SFN, MCF2L, CD44, APOE, CDKN2C, BOK, HMOX1, AGT, BCL2, TGM2, TNFRSF19, DYRK2, RARB, NET1, FGD4, KCNMA1, COL4A3, HRK, SLAMF7, TNFSF10, EPHA7, NUPR1, RASGRF2, SCIN, MUC5AC, BMP7, LRRK2, PRODH
GO:0031983~vesicle lumen	0.015661119	VEGFC, FGG, F5, PPBP, FGB, SERPINF2, EGF, CFD
GO:0001666~response to hypoxia	0.016212915	KCNMA1, TF, CCL2, NOS1, EGLN1, MMP14, SHH, ACE, ADM, HMOX1, BCL2, CHRNA7, ANGPT1, ANGPTL4, MB
GO:0055074~calcium ion homeostasis	0.016382308	CALCR, DRD1, CCL2, TRPC6, GRIK2, TACR1, BDKRB2, AGTR1, S1PR3, PLCE1, CCR7, ADM, APOE, BCL2, F2, PLCG2, CACNA1G, TGM2, CHRNA7
GO:0010942~positive regulation of cell death	0.016427967	DLC1, CCK, GRIK2, SOX4, TP63, TNFSF14, CD70, TNFSF13, SFN, MCF2L, CD44, APOE, CDKN2C, BOK, HMOX1, AGT, BCL2, TGM2, TNFRSF19, DYRK2, RARB, NET1, FGD4, KCNMA1, COL4A3, HRK, SLAMF7, TNFSF10, EPHA7, NUPR1, RASGRF2, SCIN, MUC5AC, BMP7, LRRK2, PRODH
GO:0000904~cell morphogenesis involved in differentiation	0.016483149	S100A4, NRP2, PARD3, CCK, ERBB3, BAIAP2, SOX9, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ANK3, BCL2, TGFBR3, SEMA3B, UNC5C, ROBO3, BMP7, SLITRK6, BMPR1B, NEFL, NFATC1
GO:0008202~steroid metabolic process	0.016533689	ACOX2, CYP24A1, CYP3A5, CYP1B1, HSD17B14, PRKAG2, SORL1, APOC1, ABCA1, UGT1A1, SHH, APOL2, UGT1A6, CYP39A1, APOL1, BAAT, ADM, APOE, UGT1A4, OSBPL10, UGT2B15, NR5A2
GO:0004653~polypeptide N-acetylgalactosaminyltransferase activity	0.016800519	GALNT1, GALNT7, GALNT5, GALNT4, GALNT9

GO:0033860~regulation of NAD(P)H oxidase activity	0.017001128	AGTR1, AGT, IGF2
GO:0010675~regulation of cellular carbohydrate metabolic process	0.017005191	IRS2, PPP1R3C, HNF4A, PRKAG2, IGF2, DYRK2, PPARGC1A
GO:0006468~protein amino acid phosphorylation	0.017408243	STAT5A, AURKB, FES, CAMKK1, PRKY, PAK3, MAP3K8, MLKL, CHRNA7, CDK1, SGK1, PRKCI, CDKL2, PLCE1, F2, GADD45G, MST1R, LRRK2, GADD45B, FGFR2, FRK, CAV2, FGFR4, CCL2, ADORA2B, ERBB3, C5, BCL2, ADRA2A, DYRK2, EGF, STK38L, FGD4, PDK4, BIRC7, MAPK10, EPHA2, RPS6KL1, NTRK3, GLYCTK, EPHA4, IKBKE, CDC42BPG, EPHA7, MAP2, TGFBR3, JAK3, MERTK, BMP7, CIT, BMPR1B
GO:0015672~monovalent inorganic cation transport	0.017683747	KCNH1, FXYD2, KCNAB2, SLC9A2, KCNJ2, KCNQ5, SLC23A2, KCNK5, SLC4A8, SLC4A4, ATP6V0D2, KCNG1, KCNMA1, HCN2, SGK1, SLC12A8, SLC12A2, NOX1, SLC10A7, KCNK1, KCNK3, SLC17A7, KCNN4, KCNJ6, SLC17A3, SLC17A1, SLC13A2, ABCC8
GO:0060348~bone development	0.01839348	CYP24A1, PDLIM7, IGF2, SOX9, MMP14, COL5A2, SHH, KAZALD1, BCL2, NAB1, FOXC1, COL1A1, BMP7, RUNX2
GO:0010907~positive regulation of glucose metabolic process	0.018476935	IRS2, HNF4A, IGF2, DYRK2, PPARGC1A
GO:0046661~male sex differentiation	0.018803265	RBP4, HMGB2, WNT4, BCL2, STAT5A, SOX2, SOX9, SYCP2, SHH, GJB2
GO:0008219~cell death	0.019137368	DLC1, E2F1, E2F2, GRIK2, TNFSF15, TP63, TNFSF13, MCF2L, BOK, HMOX1, C8ORF4, UNC5C, MAGEH1, IL1A, NET1, HYAL1, MAGI3, SGK1, FA2H, HRK, ESPL1, AHR, TNS4, RASGRF2, GADD45G, F2, CTSD, GADD45B, PHLPP1, CCK, ERBB3, C5, SFN, KRT20, SYCP2, GREM1, GRAMD4, BCL2, TGM2, TNFRSF19, DYRK2, BMF, TRAF4, FGD4, RNF144B, COL4A3, IL6, BIRC7, IGF2, BIRC3, TNFSF9, TNFSF10, APOL1, MUC5AC
GO:0006109~regulation of carbohydrate metabolic process	0.019185881	IRS2, PPP1R3C, HNF4A, PRKAG2, IGF2, DYRK2, PPARGC1A
GO:0040017~positive regulation of locomotion	0.019252145	VEGFC, IRS2, DRD1, IL6, ONECUT1, TACR1, BCL2, AGT, ONECUT2, IGF2, F7, SCG2
GO:0006811~ion transport	0.019617202	KCNH1, SLC22A17, KCNAB2, GRIK2, SLC9A2, KCNQ5, BHLHA15, SLC23A2, KCNK5, CHRNA7, SLC4A4, ATP6V0D2, SLC4A3, KCNG1, ANO9, GRID1, KCNMA1, SLC12A8, GABRG3, SGK1, CACNG7, TCN1, RHCG, F2, SLC26A9, PLLP, FXYD2, TF, CAV2, KCNJ2, PKD1L2, ANXA6, P2RY6, SLC4A8, SLC30A3, GABRP, NFATC1, HCN2, CACNA2D1, TRPC6, SLC12A2, NOX1, SLC10A7, KCNK1, KCNK3, SLC17A7, KCNN4, KCNJ6, APOL1, SLC17A3, SLC16A7, ATP2A3, SLC17A1, CACNA1G, SLC13A2, ABCC8, SCARA5
GO:0006916~anti-apoptosis	0.0199148	CDK1, CCL2, CRYAB, EEF1A2, STAT5A, SNCA, HRK, PRKCI, BIRC7, TP63, F7, BIRC3, BDNF, APOE, HMOX1, BCL2, TGM2, FOXC1, HELLS, IL1A
GO:0043588~skin development	0.020049404	TP63, SFN, COL1A1, COL5A2, COL5A1, SHH

GO:0012501~programmed cell death	0.020131463	DLC1, PHLPP1, E2F1, E2F2, CCK, GRIK2, ERBB3, TNFSF15, TP63, TNFSF13, KRT20, SFN, SYCP2, GREM1, GRAMD4, MCF2L, BOK, BCL2, TGM2, C8ORF4, TNFRSF19, DYRK2, UNC5C, BMF, MAGEH1, IL1A, TRAF4, NET1, FGD4, RNF144B, COL4A3, MAGI3, IL6, SGK1, HRK, BIRC7, ESPL1, TNFSF9, BIRC3, AHR, TNS4, TNFSF10, RASGRF2, GADD45G, F2, MUC5AC, GADD45B
GO:0051094~positive regulation of developmental process	0.020392464	PDLIM7, STAT5A, SOX2, TNFSF13, SHH, AGTR1, BDNF, METRN, AGT, HLX, BCL2, CHRNA7, DDAH1, RUNX2, NEFL, IL1A, ANGPTL4, IL6, IGF2, NTRK3, VEGFC, SCIN, CA2, BMP7, BMPR1B
GO:0007409~axonogenesis	0.020840096	NRP2, PARD3, CCK, ERBB3, BAIAP2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ANK3, BCL2, SEMA3B, ROBO3, UNC5C, BMP7, SLITRK6, BMPR1B, NEFL
GO:0006953~acute-phase response	0.021549665	APOL2, TF, IL6, SERPINF2, F2, IGF2, IL1A
GO:0016265~death	0.021700881	DLC1, E2F1, E2F2, GRIK2, TNFSF15, TP63, TNFSF13, MCF2L, BOK, HMOX1, C8ORF4, UNC5C, MAGEH1, IL1A, NET1, HYAL1, MAGI3, SGK1, FA2H, HRK, ESPL1, AHR, TNS4, RASGRF2, GADD45G, F2, CTSD, GADD45B, PHLPP1, CCK, ERBB3, C5, SFN, KRT20, SYCP2, GREM1, GRAMD4, BCL2, TGM2, TNFRSF19, DYRK2, BMF, TRAF4, FGD4, RNF144B, COL4A3, IL6, BIRC7, IGF2, BIRC3, TNFSF9, TNFSF10, APOL1, MUC5AC
GO:0031224~intrinsic to membrane	0.021916889	KLRC2, ADCY1, GPR124, CADM2, VTCN1, SLC9A2, SYT6, SIDT1, MEGF11, AQP3, SHH, LPHN2, AGTR1, S1PR3, LPHN3, MALL, CD44, KCNK5, S1PR5, CREB3L1, CHRNA7, HTR1D, RAB27B, MUC13, GRID1, F11R, SLC12A8, ATRNL1, EFNB2, PTPRR, LHFP, SIRPA, PTPRO, PLAUR, TMEM133, AADAC, CCR7, VSIG1, RHCG, LPAR5, KIAA1524, MGAM, FER1L6, MST1R, GCNT4, SLC2A13, IL1R2, CATSPERB, ERBB3, TMEM121, ITGA11, FCGRT, CD70, BDKRB2, KCNJ2, MANSC1, ITGBL1, TMCC2, ACE, LPCAT1, PVRL3, UPK1B, LFNG, MGAT4A, ST6GAL2, BRI3BP, TRPC6, PCDH10, SLAMF7, KCNK1, SYNGR3, EPHA2, KCNK3, ABCG2, NTRK3, EPHA4, GGT5, SEMA6B, EPHA7, APOL1, KCNJ6, NLGN4Y, EPS8, ATP2A3, PKP2, GOLGA7B, TGFBR3, MARCKS, AREG, BTBD11, NRP2, KCNH1, SLC16A14, KCNAB2, SUSD2, C14ORF132, PTGES, SLC23A2, CHST13, CEACAM6, CEACAM5, NT5E, CEACAM1, KCNG1, DPEP1, KCNMA1, ADAM11, GPR176, LPGAT1, CACNG7, CDS1, MMP14, ST6GALNAC1, KIAA1161, SEMA4G, ALG10B, SLC26A9, SGCD, SUSD4, MOSPD1, GRAMD1B, PARD3, FAM69A, NPY2R, GPR64, C5, SLC19A3, XKRX, C2ORF82, IGSF11, FNDC4, GLIPR2, ACSL1, BCL2, SLC4A8, CD22, FUT1, ARMCX1, UGT8, PCSK4, FLRT2, PLA2G16, IL6, FADS3, CYP4F12, NPR3, FAAH2, TMPRSS3, GJB1, GJB2, SLC16A2, CDH15, LARGE, SLC16A7, PLSCR4, CDH17,

		TMTC1, GFRA1, TMTC2, ABCC8, GREB1L, CDH10, SLC22A17, MPZL3, TSPAN1, SLC44A3, GRIK2, PLXNA2, TNFSF15, LRRC4B, TNFSF14, TSPAN7, PDE3B, TSPAN8, TNFSF13, ENPEP, IL15, VIPR1, IL17RD, SLC7A7, SLC2A3, ELOVL4, B3GALNT1, SLC25A29, TMEM98, ROBO3, UNC5C, SLC4A4, SLC4A3, SPTLC3, FA2H, BASP1, FIBCD1, MOXD1, LAT2, THBD, VAMP8, DLL4, CPD, VAMP1, SLITRK6, GBP3, EMP1, SPTB, ABCA8, FGFR2, CAV2, FXYD2, PAM, FGFR4, DRD1, ADORA2B, IFITM3, ITGB4, NKAIN4, ABCA1, CX3CL1, ABCA4, P2RY6, ITGB8, FOLR1, ENTPD7, B3GNT7, MSLN, FAM189A2, PTPLA, ADRA2A, HEG1, SDR16C5, B3GNT3, SLC30A3, PCDHA13, EGF, ENTPD2, GABRP, B4GALT5, ADAM28, MUC1, HCN2, CACNA2D1, ADAM23, UST, PODXL, SYT11, MRC2, SYT12, GOLIM4, SLC6A14, SLC6A17, REEP2, THSD7A, TNFSF10, GPR37, DIO2, DSG2, SLC7A2, ST8SIA4, CD274, CACNA1G, SLC13A2, TMPO, SCARA3, MERTK, CEND1, SCARA5, ADRA1D, CLDN4, SGPP2, TACR1, SORL1, BCAM, LGR6, SYNGR2, SDC2, CCRL2, EPCAM, FRMD3, TSPAN12, KCNQ5, PLEKHB1, GPC6, DENND5B, SLC43A1, ANO9, CSF2RA, SLC43A2, KIRREL3, PARM1, GABRG3, NRXN2, CHST2, PCDH9, WLS, MAN1A1, PCDH7, UGT1A1, MUC3A, NPTXR, CHRM3, DGAT2, CD82, CNTN1, PLLP, UGT2B15, GALNT9, TM4SF4, CALCR, GALNT1, GALNT7, MAL2, GALNT5, GALNT4, PCDHGC3, GPRC5A, GRAMD4, PKD1L2, UGT1A6, CDH7, HRH1, PRRG4, UGT1A4, RNF128, PALM3, TNFRSF19, PLA2R1, PTPRB, RNF144B, TMEM45B, SLC12A2, NOX1, TSPAN13, SLC10A7, TMEM52, GDPD5, TNFSF9, SLC17A7, FRRS1, KCNN4, CYP4F8, TMEM47, SLC17A3, SLC17A1, DSC2, CYP4F3, TMEM86A, BMPR1B, GPR115
GO:0060193~positive regulation of lipase activity	0.022081763	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3, NR1H3
GO:0000302~response to reactive oxygen species	0.022081763	PXDN, NPTXR, APOE, CRYAB, HMOX1, BCL2, GPX3, SERPINE1, COL1A1, MB
GO:0010676~positive regulation of cellular carbohydrate metabolic process	0.022110107	IRS2, HNF4A, IGF2, DYRK2, PPARGC1A
GO:0045913~positive regulation of carbohydrate metabolic process	0.022110107	IRS2, HNF4A, IGF2, DYRK2, PPARGC1A
GO:0009065~glutamine family amino acid catabolic process	0.022110107	NOS1, PRODH2, ASRGL1, DDAH1, PRODH
GO:0048666~neuron development	0.022271462	NRP2, PARD3, DRD1, NRTN, CCK, ERBB3, ONECUT2, SHH, BDNF, CD44, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, LHX8, NEFL, IL6, BAIAP2, PRKCI, CTNNA2, EPHA4, EPHA7, RND1, ADM, MAP2, BMP7, SLITRK6, BMPR1B
GO:0006812~cation transport	0.022674233	KCNH1, FXYD2, TF, KCNAB2, SLC9A2, KCNJ2, ANXA6, KCNQ5, BHLHA15, SLC23A2, KCNK5, SLC4A8, CHRNA7, SLC30A3, SLC4A4, ATP6V0D2, KCNG1, NFATC1, KCNMA1, HCN2, CACNA2D1,

		SLC12A8, SGK1, SLC12A2, TRPC6, CACNG7, NOX1, SLC10A7, KCNK1, TCN1, KCNK3, SLC17A7, KCNN4, KCNJ6, RHCG, SLC17A3, ATP2A3, SLC17A1, F2, CACNA1G, SLC13A2, ABCC8, SCARA5
GO:0009891~positive regulation of biosynthetic process	0.023308998	E2F1, STAT5A, TP63, SHH, IL11, BHLHA15, APOE, HMOX1, FOXF2, RARB, ALX4, DDAH1, IL1A, IRS2, MECOM, PPARGC1A, AHR, HNF4A, F2, FOXC1, SMARCA2, DRD1, HMGB2, ADORA2B, ABLIM3, SOX2, ONECUT2, SOX4, EHF, ABCA1, SOX9, HRH1, AGT, DYRK2, TCF4, RUNX2, NR1H3, KLF5, IL6, IKZF2, MAML2, NOX1, IGF2, CREB5, NR4A3, CENPK, HDAC5, ETS2, AREG, JAK3, NR5A2, BMP7
GO:0032844~regulation of homeostatic process	0.023600813	TF, DRD1, NOS1, CCK, TACR1, STAT5A, AGTR1, CD44, BCL2, AGT, F2, CACNA1G, CA2
GO:0006915~apoptosis	0.023929097	DLC1, PHLPP1, E2F1, E2F2, CCK, GRIK2, ERBB3, TNFSF15, TP63, TNFSF13, KRT20, SFN, SYCP2, GREM1, GRAMD4, MCF2L, BOK, BCL2, C8ORF4, TNFRSF19, DYRK2, UNC5C, BMF, MAGEH1, IL1A, TRAF4, NET1, FGD4, RNF144B, COL4A3, MAGI3, IL6, SGK1, HRK, BIRC7, ESPL1, TNFSF9, BIRC3, AHR, TNS4, TNFSF10, RASGRF2, GADD45G, F2, MUC5AC, GADD45B
GO:0005200~structural constituent of cytoskeleton	0.02407956	KRT19, KRT15, PLS1, KRT20, NEFL, TUBA1B, ADD3, BICD1, SPTB, CTNNA2
GO:0050714~positive regulation of protein secretion	0.024102519	KCNN4, VEGFC, RBP4, IL6, TNFSF15, IGF2, IL1A
GO:0005625~soluble fraction	0.02411646	CAV2, INSL4, TAC3, WISP2, PPP1R3C, ACSL1, STAC, FGB, AGT, SERPINE1, GPX3, EGF, CRYAB, PDE3A, POR, DOCK3, TNFSF10, ADM, NTS, ARRB1, FBLN5, TPPP, F2, LAMC2, CTSB, ALOX5, MERTK, DUSP6
GO:0070482~response to oxygen levels	0.024147991	KCNMA1, TF, CCL2, NOS1, EGLN1, MMP14, SHH, ACE, ADM, HMOX1, BCL2, CHRNA7, ANGPT1, ANGPTL4, MB
GO:0007160~cell-matrix adhesion	0.024794748	DLC1, CD44, ITGB8, FBLN5, BCL2, AGT, ITGB4, ITGA11, BCAM, NID1, ITGBL1
GO:0030335~positive regulation of cell migration	0.024794748	VEGFC, IRS2, DRD1, IL6, ONECUT1, TACR1, BCL2, AGT, ONECUT2, IGF2, F7
GO:0001503~ossification	0.025078849	CYP24A1, PDLIM7, IGF2, MMP14, COL5A2, SHH, BCL2, KAZALD1, NAB1, FOXC1, COL1A1, BMP7, RUNX2
GO:0000768~syncytium formation by plasma membrane fusion	0.025457301	KCNH1, CAST, NOS1, CD44
GO:0051129~negative regulation of cellular component organization	0.025483096	DLC1, LIMA1, VIL1, SNCA, APOC1, ESPL1, MMP14, SCIN, MAP2, CAPG, TGFBR3, DNMT1, TMSB4Y, SPTB, NR1H3
GO:0030036~actin cytoskeleton organization	0.025641764	DLC1, LIMA1, SHROOM3, PDLIM7, PLEK2, DIAPH3, PRKCI, FMN2, KRT19, CDC42BPG, CDC42EP2, RND1, EPB41L1, EPS8, BCL2, SCIN, ADRA2A, TMSB4Y, RHOF, FGD4, ARHGDIB
GO:0045923~positive regulation of fatty acid metabolic process	0.026149003	IRS2, HNF4A, AGT, PPARGC1A, NR1H3
GO:0010038~response to metal ion	0.026154468	KCNMA1, S100A16, GATM, SNCA, TAT, AQP3, MT1X, FGG, FGB, BCL2, PLCG2, CACNA1G, TFF1,

		CA2
GO:0007202~activation of phospholipase C activity	0.026218317	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3
GO:0046546~development of primary male sexual characteristics	0.026218317	RBP4, HMGB2, WNT4, BCL2, SOX2, SOX9, SYCP2, SHH, GJB2
GO:0010863~positive regulation of phospholipase C activity	0.026218317	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3
GO:0008544~epidermis development	0.026267731	TP63, HOXB13, SFN, SOX9, COL5A2, COL5A1, SHH, SCEL, FOXQ1, LAMB3, LAMA3, COL7A1, FLG, BCL2, KRT15, LAMC2, COL1A1, EMP1
GO:0030029~actin filament-based process	0.026283491	DLC1, LIMA1, SHROOM3, PDLIM7, PLEK2, DIAPH3, VIL1, PRKCI, FMN2, KRT19, CDC42BPG, CDC42EP2, RND1, EPB41L1, EPS8, BCL2, SCIN, ADRA2A, TMSB4Y, RHOF, FGD4, ARHGDIB
GO:0048812~neuron projection morphogenesis	0.027086356	NRP2, PARD3, CCK, ERBB3, BAIAP2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ADM, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, BMP7, SLITRK6, BMPR1B, NEFL
GO:0032835~glomerulus development	0.027303231	PLCE1, BCL2, NID1
GO:0043296~apical junction complex	0.027501084	F11R, CGNL1, MAGI3, PARD3, SHROOM3, DSG2, CLDN4, PKP2, PVRL3, DSC2, TJP3, TJP2
GO:0009310~amine catabolic process	0.027738625	FRRS1, NOS1, DIO2, PRODH2, ASRGL1, TAT, DDAH1, MOXD1, PRODH, GLDC
GO:0051726~regulation of cell cycle	0.028045464	E2F1, E2F2, CAV2, STAT5A, KNTC1, SFN, CDC45, TSPYL2, CDKN2C, BCL2, EGF, IL1A, CDC6, CDK1, PLA2G16, BRIP1, PDE3A, ESPL1, IGF2, CDC25A, HNF4A, CCND3, ZWINT, GADD45G, KIF20B, FOXC1, BMP7, GADD45B
GO:0042476~odontogenesis	0.028341466	ERBB3, TP63, FOXC1, CA2, COL1A1, LHX8, BMP7, SHH
GO:0005516~calmodulin binding	0.028369557	KCNH1, MYO1A, ADCY1, NOS1, MARCKSL1, MYO1D, CAMKK1, KCNN4, PDE1C, PDE1A, MAP2, MARCKS, NRGN, ADD3, MYO5C
GO:0001775~cell activation	0.028502975	ONECUT1, STAT5A, SNCA, SOX4, TNFSF14, IL15, CX3CL1, IL11, FGG, FGB, AGT, BCL2, ENTPD2, HELLS, RHOH, KIF13B, EXO1, IL6, IGF2, SLAMF7, HDAC5, LAT2, CCND3, F2, PLCG2
GO:0030182~neuron differentiation	0.028644673	NRP2, PARD3, NRTN, DRD1, CCK, ERBB3, SOX2, ONECUT2, SHH, BDNF, CD44, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, LHX8, NEFL, KCNMA1, DFNA5, IL6, BAIAP2, PTPRR, PRKCI, EPHA2, CTNNA2, NTRK3, EPHA4, EPHA7, RND1, ADM, MAP2, BMPR1B, BMP7, SLITRK6
GO:0008376~acetylgalactosaminyltransferase activity	0.029249203	GALNT1, GALNT7, GALNT5, B3GALNT1, GALNT4, GALNT9
GO:0032813~tumor necrosis factor receptor superfamily binding	0.029249203	TNFSF10, TNFSF15, TNFSF14, CD70, TNFSF13, TNFSF9
GO:0001936~regulation of endothelial cell proliferation	0.029696418	CAV2, CCL2, APOE, TNFSF15, TNFSF13, SCG2
GO:0030168~platelet activation	0.029696418	FGG, IL6, FGB, F2, ENTPD2, IL11
GO:0006959~humoral immune response	0.029831819	EXO1, IL6, CCL2, C3, BCL2, C5, CFH, C4BPB, C4BPA, CFD
GO:0030955~potassium ion binding	0.030320955	KCNMA1, KCNH1, FXYD2, HCN2, SLC12A8,

		SLC12A2, KCNAB2, KCNJ2, KCNK1, KCNK3, KCNQ5, KCNJ6, KCNK5, KCNG1
GO:0043627~response to estrogen stimulus	0.03035127	KCNMA1, CAV2, KRT19, CRYAB, HMOX1, BCL2, ANGPT1, CA2, TFF1, MMP14, BMP7, SHH
GO:0001658~branching involved in ureteric bud morphogenesis	0.030601497	CD44, BCL2, AGT, GREM1, SHH
GO:0060675~ureteric bud morphogenesis	0.030601497	CD44, BCL2, AGT, GREM1, SHH
GO:0048858~cell projection morphogenesis	0.030734999	NRP2, PARD3, CCK, ONECUT1, ERBB3, BAIAP2, ONECUT2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ADM, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, BMP7, SLITRK6, BMPR1B, NEFL
GO:0060562~epithelial tube morphogenesis	0.030799567	DLC1, WNT4, SHROOM3, CD44, BCL2, AGT, ZEB2, GREM1, SHH
GO:0051222~positive regulation of protein transport	0.030799567	KCNN4, VEGFC, RBP4, IL6, TNFSF15, TNFSF14, IGF2, SHH, IL1A
GO:0044270~nitrogen compound catabolic process	0.030799567	UGT1A6, ALDH1L1, HMOX1, UGT1A4, CDA, PDE3B, DPYD, NT5E, AMPD3, UGT1A1, ENTPD2
GO:0001501~skeletal system development	0.030835415	RBP4, CYP24A1, PDLIM7, TP63, PRRX2, SOX9, SHH, BCL2, COL12A1, ALX4, PAPSS2, RUNX2, MATN3, ARID5B, FBN1, IGF2, NPR3, MMP14, COL5A2, KAZALD1, ETS2, NAB1, FOXC1, COL1A1, BMP7, BMPR1B, IGFBP4
GO:0051494~negative regulation of cytoskeleton organization	0.030984793	DLC1, LIMA1, SCIN, MAP2, CAPG, VIL1, TMSB4Y, SPTB
GO:0030246~carbohydrate binding	0.031129019	FGFR2, GALNT1, KLRC2, CCL2, GALNT7, GALNT5, LGALS9C, SUSD2, LGALS9B, GALNT4, PKD1L2, ZG16B, LPHN2, LPHN3, CD44, APOE, RSPO3, CD22, PLA2R1, FGFBP1, CYR61, ATRNL1, LGALS2, MRC2, COL5A1, TGFBR3, ADAMTS1, LAMC2, BMP7, GALNT9
GO:0006813~potassium ion transport	0.03162077	KCNH1, KCNMA1, FXYD2, HCN2, SLC12A8, SLC12A2, KCNAB2, KCNJ2, KCNK1, KCNK3, KCNQ5, KCNN4, KCNJ6, KCNK5, ABCC8, KCNG1
GO:0046906~tetrapyrrole binding	0.032038789	CYP24A1, CYP3A5, PXDN, CYP1B1, NOS1, FA2H, FADS3, CYP4F12, TCN1, CYP4F8, CYP39A1, HMOX1, CYP4F3, MB
GO:0016337~cell-cell adhesion	0.032633815	PARD3, CLDN4, GMDS, PCDH10, CTNND2, PCDH9, PCDHGC3, PCDH7, SOX9, CTNNA2, CDH7, CDH15, COL14A1, CD44, DSG2, PKP2, CDH17, BCL2, PVRL3, DSC2, PCDHA13, BMPR1B, CDH10, CEACAM1
GO:0009063~cellular amino acid catabolic process	0.033283973	FRRS1, NOS1, PRODH2, ASRGL1, TAT, DDAH1, MOXD1, PRODH, GLDC
GO:0016327~apicolateral plasma membrane	0.03332306	F11R, CGNL1, MAGI3, PARD3, SHROOM3, DSG2, CLDN4, PKP2, PVRL3, DSC2, TJP3, TJP2
GO:0014033~neural crest cell differentiation	0.033461504	NRP2, NRTN, ZEB2, FOXC1, SOX9, SHH
GO:0014032~neural crest cell development	0.033461504	NRP2, NRTN, ZEB2, FOXC1, SOX9, SHH
GO:0042542~response to hydrogen peroxide	0.033788612	PXDN, NPTXR, CRYAB, HMOX1, BCL2, GPX3, COL1A1, MB
GO:0043065~positive regulation of apoptosis	0.035309994	DLC1, CCK, SOX4, TP63, TNFSF14, CD70, TNFSF13, SFN, MCF2L, CD44, APOE, CDKN2C, BOK, HMOX1, AGT, BCL2, TGM2, TNFRSF19, DYRK2, RARB, NET1, FGD4, KCNMA1, COL4A3, HRK, SLAMF7,

		TNFSF10, EPHA7, NUPR1, RASGRF2, SCIN, MUC5AC, BMP7, PRODH
GO:0070201~regulation of establishment of protein localization	0.035398979	RBP4, IL6, PRKCI, TNFSF15, TNFSF14, IGF2, KRT20, SHH, VEGFC, KCNN4, HNF4A, EGF, IL1A
GO:0042558~pteridine and derivative metabolic process	0.035473017	MOCOS, GPHN, ALDH1L1, FOLR1, MOCS1
GO:0017156~calcium ion-dependent exocytosis	0.035473017	SCIN, SYT6, RAPGEF4, PCSK4, RIMS3
GO:0010518~positive regulation of phospholipase activity	0.035901215	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3
GO:0051051~negative regulation of transport	0.036089728	IRS2, NOS1, CRYAB, ERBB3, SNCA, APOC1, IGF2, IL11, INHBB, HNF4A, HMOX1, BCL2, EGF, NR1H3
GO:0055067~monovalent inorganic cation homeostasis	0.036308371	KCNMA1, RHCG, AGT, NOX1, SLC9A2, SLC26A9, TMPRSS3
GO:0007243~protein kinase cascade	0.036802146	NRTN, CCL2, ADORA2B, ERBB3, STAT5A, C5, PRKAG2, TNFSF15, TNFSF14, HMOX1, ADRA2A, TNFRSF19, CHRNA7, EGF, STK38L, FGD4, SCG2, CRYAB, BIRC7, IGF2, MAPK10, PLCE1, DOK5, GADD45G, F2, TGFBR3, JAK3, LRRK2, GADD45B, DUSP6
GO:0019933~cAMP-mediated signaling	0.036804011	CALCR, S1PR3, ADCY1, DRD1, ADORA2B, ADM, NPY2R, TGM2, RAPGEF4, NPR3, ADRA1D
GO:0016021~integral to membrane	0.037144987	KLRC2, ADCY1, CADM2, VTCN1, GPR124, SLC9A2, SYT6, SIDT1, MEGF11, AQP3, LPHN2, AGTR1, S1PR3, LPHN3, MALL, CD44, KCNK5, S1PR5, CREB3L1, CHRNA7, HTR1D, MUC13, GRID1, F11R, SLC12A8, ATRNL1, EFNB2, PTPRR, LHFP, SIRPA, PTPRO, PLAUR, TMEM133, AADAC, CCR7, VSIG1, RHCG, LPAR5, KIAA1524, MGAM, FER1L6, MST1R, GCNT4, IL1R2, SLC2A13, CATSPERB, ERBB3, TMEM121, ITGA11, FCGRT, CD70, BDKRB2, KCNJ2, MANSC1, ITGBL1, TMCC2, ACE, LPCAT1, PVRL3, UPK1B, LFNG, MGAT4A, ST6GAL2, BRI3BP, TRPC6, PCDH10, SLAMF7, KCNK1, SYNGR3, EPHA2, KCNK3, ABCG2, NTRK3, EPHA4, GGT5, SEMA6B, EPHA7, KCNJ6, NLGN4Y, EPS8, ATP2A3, PKP2, TGFBR3, AREG, BTBD11, NRP2, KCNH1, SLC16A14, KCNAB2, SUSD2, C14ORF132, PTGES, SLC23A2, CHST13, CEACAM6, CEACAM5, CEACAM1, KCNG1, KCNMA1, ADAM11, GPR176, LPGAT1, CACNG7, CDS1, MMP14, ST6GALNAC1, KIAA1161, SEMA4G, ALG10B, SLC26A9, SGCD, SUSD4, MOSPD1, GRAMD1B, PARD3, FAM69A, NPY2R, GPR64, C5, SLC19A3, XKRX, C2ORF82, IGSF11, FNDC4, ACSL1, BCL2, SLC4A8, CD22, FUT1, ARMCX1, UGT8, PCSK4, FLRT2, PLA2G16, IL6, FADS3, CYP4F12, NPR3, FAAH2, TMPRSS3, GJB1, GJB2, SLC16A2, CDH15, LARGE, SLC16A7, PLSCR4, CDH17, TMTC1, TMTC2, ABCC8, GREB1L, CDH10, SLC22A17, MPZL3, TSPAN1, SLC44A3, GRIK2, PLXNA2, TNFSF15, LRRC4B, TNFSF14, TSPAN7, PDE3B, TSPAN8, TNFSF13, ENPEP, IL15, VIPR1, IL17RD, SLC7A7, SLC2A3, ELOVL4, B3GALNT1, SLC25A29, TMEM98, ROBO3, UNC5C,

		SLC4A4, SLC4A3, SPTLC3, FA2H, FIBCD1, MOXD1, LAT2, THBD, VAMP8, DLL4, CPD, VAMP1, SLITRK6, GBP3, EMP1, ABCA8, FGFR2, CAV2, FXYD2, PAM, FGFR4, DRD1, ADORA2B, IFITM3, ITGB4, NKAIN4, ABCA1, CX3CL1, ABCA4, P2RY6, ITGB8, FOLR1, ENTPD7, B3GNT7, FAM189A2, PTPLA, ADRA2A, HEG1, SDR16C5, B3GNT3, SLC30A3, PCDHA13, EGF, ENTPD2, GABRP, B4GALT5, ADAM28, MUC1, HCN2, CACNA2D1, ADAM23, UST, PODXL, SYT11, MRC2, SYT12, GOLIM4, SLC6A14, SLC6A17, REEP2, THSD7A, TNFSF10, GPR37, DIO2, DSG2, SLC7A2, ST8SIA4, CD274, CACNA1G, SLC13A2, TMPO, SCARA3, MERTK, CEND1, SCARA5, ADRA1D, CLDN4, SGPP2, TACR1, SORL1, BCAM, LGR6, SYNGR2, SDC2, CCRL2, EPCAM, FRMD3, TSPAN12, KCNQ5, PLEKHB1, GPC6, DENND5B, SLC43A1, ANO9, CSF2RA, SLC43A2, KIRREL3, PARM1, GABRG3, NRXN2, CHST2, PCDH9, WLS, MAN1A1, PCDH7, UGT1A1, MUC3A, NPTXR, CHRM3, DGAT2, CD82, PLLP, UGT2B15, GALNT9, TM4SF4, CALCR, GALNT1, GALNT7, MAL2, GALNT5, GALNT4, PCDHGC3, GPRC5A, GRAMD4, PKD1L2, UGT1A6, CDH7, HRH1, PRRG4, UGT1A4, RNF128, TNFRSF19, PLA2R1, PTPRB, RNF144B, TMEM45B, SLC12A2, NOX1, TSPAN13, SLC10A7, TMEM52, GDPD5, TNFSF9, SLC17A7, FRRS1, KCNN4, CYP4F8, TMEM47, SLC17A3, SLC17A1, DSC2, CYP4F3, TMEM86A, BMPR1B, GPR115
GO:0031328~positive regulation of cellular biosynthetic process	0.037421909	E2F1, STAT5A, TP63, SHH, IL11, BHLHA15, APOE, HMOX1, FOXF2, RARB, ALX4, DDAH1, IL1A, IRS2, MECOM, PPARGC1A, AHR, HNF4A, FOXC1, SMARCA2, HMGB2, DRD1, ADORA2B, ABLIM3, ONECUT2, SOX2, SOX4, EHF, ABCA1, SOX9, HRH1, AGT, DYRK2, TCF4, RUNX2, NR1H3, KLF5, IL6, IKZF2, MAML2, IGF2, CREB5, NR4A3, CENPK, HDAC5, ETS2, AREG, JAK3, NR5A2, BMP7
GO:0031399~regulation of protein modification process	0.037558948	DLC1, CCK, SNCA, PRKAG2, ZEB2, BDKRB2, IL11, AGT, BCL2, RAPGEF4, EGF, FGD4, CDK1, IL6, BIRC7, IGF2, PPARGC1A, VEGFC, HNF4A, CCND3, HPX, F2, DNMT1, LRRK2, BMP7
GO:0048584~positive regulation of response to stimulus	0.038046072	IL6, ADORA2B, C3, STAT5A, C5, C4BPB, IGF2, CX3CL1, C4BPA, F7, IL15, NTRK3, AGTR1, LAT2, HPX, AGT, PLCG2, TGM2, CFH, CFD, SCG2
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.038047833	E2F1, HMGB2, STAT5A, ABLIM3, SOX2, ONECUT2, TP63, SOX9, SHH, IL11, BHLHA15, RARB, ALX4, RUNX2, NR1H3, IL6, IKZF2, MAML2, NR4A3, MECOM, CENPK, PPARGC1A, AHR, HDAC5, HNF4A, FOXC1, JAK3, BMP7, NR5A2, SMARCA2
GO:0000902~cell morphogenesis	0.038129851	S100A4, NRP2, PARD3, CCK, SHROOM3, ONECUT1, ERBB3, ONECUT2, SOX9, SHH, BDNF, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, NEFL, NFATC1, BAIAP2, PRKCI, CTNNA2, EPHA4, EPHA7, ADM, TGFBR3, MAP7, BMP7, SLITRK6, BMPR1B

GO:0044271~nitrogen compound biosynthetic process	0.038154896	MOCOS, NAMPT, ADCY1, RP2, SNCA, PRKAG2, GPHN, CDA, GUCA2B, ATP6V0D2, NT5E, MOCS1, DDC, NMNAT2, NOS1, PADI2, AK5, CPS1, AMPD3, ADM, ATP2A3, RRM2, RRM1, PRODH2, QPRT, DPYD, PRODH
GO:0051047~positive regulation of secretion	0.038433128	INHBB, KCNN4, VEGFC, RBP4, IL6, ADORA2B, TACR1, SCIN, SNCA, TNFSF15, IGF2, IL1A
GO:0033135~regulation of peptidyl-serine phosphorylation	0.038804973	IL6, BCL2, BDKRB2, IL11
GO:0045940~positive regulation of steroid metabolic process	0.038804973	AGTR1, APOE, AGT, APOC1
GO:0006949~syncytium formation	0.038804973	KCNH1, CAST, NOS1, CD44
GO:0010962~regulation of glucan biosynthetic process	0.038804973	IRS2, PPP1R3C, IGF2, DYRK2
GO:0005979~regulation of glycogen biosynthetic process	0.038804973	IRS2, PPP1R3C, IGF2, DYRK2
GO:0032885~regulation of polysaccharide biosynthetic process	0.038804973	IRS2, PPP1R3C, IGF2, DYRK2
GO:0055114~oxidation reduction	0.039269141	ACOX2, CYP3A5, CYP24A1, PAM, PXDN, ALDH1L1, CYP1B1, KCNAB2, UTY, HSD17B14, SNCA, EGLN1, ALDH3A1, GLDC, GPX2, CYP39A1, HMOX1, P4HA3, GPX3, SDR16C5, LOX, LOXL2, PCSK4, GLRX, KDM5D, NOS1, FA2H, MICAL2, NOX1, FADS3, CYP4F12, PPARGC1A, POR, MOXD1, FRRS1, CYP4F8, DIO2, NXN, F5, RRM2, RRM1, AKR1B1, PRODH2, CYP4F3, DPYD, ALOX5, PRODH
GO:0043549~regulation of kinase activity	0.039357191	ADCY1, DRD1, PARD3, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, SFN, DGKA, TSPYL2, APOE, CDKN2C, ADRA2A, CHRNA7, EGF, FGD4, CDC6, RBL1, BIRC7, PKIB, IGF2, CDC25A, PLCE1, CCND3, GADD45G, GADD45B, DUSP6
GO:0010669~epithelial structure maintenance	0.039470462	RBP4, MUC3A, TFF1
GO:0060347~heart trabecula formation	0.039470462	RBP4, TGFBR3, ADAMTS1
GO:0030277~maintenance of gastrointestinal epithelium	0.039470462	RBP4, MUC3A, TFF1
GO:0007588~excretion	0.039890399	KCNMA1, ADORA2B, HMOX1, TACR1, AGT, KCNK5, GUCA2B, AQP3
GO:0030835~negative regulation of actin filament depolymerization	0.040766632	LIMA1, SCIN, CAPG, VIL1, SPTB
GO:0008083~growth factor activity	0.041095663	IL6, NRTN, IGF2, VGF, IL11, INHBB, VEGFC, TYMP, BDNF, PPBP, INHBE, AGT, TFF1, AREG, EGF, BMP7
GO:0048667~cell morphogenesis involved in neuron differentiation	0.041450383	NRP2, PARD3, CCK, ERBB3, BAIAP2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ANK3, BCL2, SEMA3B, ROBO3, UNC5C, BMP7, SLITRK6, BMPR1B, NEFL
GO:0031091~platelet alpha granule	0.041473018	VEGFC, FGG, F5, PPBP, FGB, SERPINF2, EGF, CFD
GO:0010517~regulation of phospholipase activity	0.041544065	AGTR1, P2RY6, DRD1, HRH1, PLCE1, TACR1, AGT, TGM2, NPR3
GO:0016715~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced ascorbate as one donor, and incorporation of	0.041643473	FRRS1, PAM, MOXD1

one atom of oxygen		
GO:0031016~pancreas development	0.041845704	IL6, ONECUT1, ONECUT2, PDE3B, SOX4, SHH
GO:0032880~regulation of protein localization	0.041957408	RBP4, IL6, PRKCI, TNFSF15, TNFSF14, IGF2, KRT20, SHH, KCNN4, VEGFC, HNF4A, BCL2, EGF, IL1A
GO:0010647~positive regulation of cell communication	0.042467775	CAV2, DRD1, CCL2, ERBB3, GRIK2, TACR1, SNCA, SOX2, SOX4, TP63, ZEB2, PRRX2, IL11, HMOX1, AGT, TGM2, EGF, IL6, IGF2, WLS, F7, ECM1, IKBKE, TNFSF10, HPX, KCP, BMP7
GO:0020037~heme binding	0.042635113	CYP24A1, CYP3A5, PXDN, CYP1B1, NOS1, FA2H, FADS3, CYP4F12, CYP4F8, CYP39A1, HMOX1, CYP4F3, MB
GO:0005641~nuclear envelope lumen	0.042858934	PTGES, BCHE, ALOX5
GO:0007166~cell surface receptor linked signal transduction	0.042944329	ADCY1, NRTN, GPR124, GRIK2, PLXNA2, STAT5A, VIPR1, SHH, LPHN2, LPHN3, S1PR3, AGTR1, WNT4, APOE, BHLHA15, S1PR5, RAPGEF4, HTR1D, WNT6, CFD, IRS2, STC2, ATRNL1, BAIAP2, VEGFC, CCR7, PLCE1, LAT2, PPBP, LPAR5, DLL4, F2, ADAMTS1, MST1R, FGFR2, FGFR4, DRD1, CCL2, ADORA2B, ERBB3, ITGA11, ITGB4, SOX4, CXXC4, BDKRB2, ABCA1, ITGBL1, P2RY6, ITGB8, ADRA2A, CDA, EGF, ENTPD2, DIXDC1, ADAM23, MAML2, EPHA2, NTRK3, EPHA4, EPHA7, LAMA3, GPR37, NXN, EPS8, CD274, PLCG2, TGFBR3, AREG, MERTK, BMP7, ADRA1D, NXPH4, TACR1, TP63, LGR6, CCRL2, HEY1, RSPO3, ANGPT1, CEACAM1, GABRG3, ADAM11, GPR176, ARID5B, TLE3, CHRM3, ADM, DOK5, CNTN1, FOXC1, CALCR, PARD3, CCK, CXCL5, USP9Y, C3, CXCL3, NPY2R, GPR64, C5, GPRC5A, PKD1L2, TAC3, PHIP, DGKA, HRH1, AGT, TGM2, PIK3R3, COL4A3, SLC12A2, IGF2, NPR3, BIRC3, ID1, GFRA1, JAK3, IGFBP1, BMPR1B, GPR115
GO:0045859~regulation of protein kinase activity	0.043359009	ADCY1, DRD1, PARD3, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, SFN, DGKA, TSPYL2, APOE, CDKN2C, ADRA2A, CHRNA7, EGF, FGD4, CDC6, BIRC7, PKIB, IGF2, CDC25A, PLCE1, CCND3, GADD45G, GADD45B, DUSP6
GO:0015294~solute:cation symporter activity	0.043433533	SLC17A7, SLC2A13, SLC12A2, SLC17A3, SLC23A2, SLC2A3, SLC6A14, SLC10A7, SLC13A2, SLC6A17, SLC4A4
GO:0007610~behavior	0.043514062	NRP2, ADCY1, DRD1, CCK, CCL2, CXCL5, GRIK2, TACR1, NPY2R, CXCL3, SNCA, C5, CTNND2, CX3CL1, CCRL2, TYMP, BDNF, BCHE, BCL2, AGT, CHRNA7, SEPP1, ROBO3, LHX8, SCG2, CYR61, KCNMA1, IL6, NR4A3, PARK2, PLAUR, FOXP2, EPHA4, CCR7, PPBP, EPS8
GO:0051272~positive regulation of cell motion	0.044110664	VEGFC, IRS2, DRD1, IL6, ONECUT1, TACR1, BCL2, AGT, ONECUT2, IGF2, F7
GO:0031589~cell-substrate adhesion	0.044110664	DLC1, CD44, ITGB8, FBLN5, BCL2, AGT, ITGB4, ITGA11, BCAM, NID1, ITGBL1
GO:0016208~AMP binding	0.044606472	HCN2, PDE1C, PRKAG2, PDE10A, RAPGEF4
GO:0032990~cell part morphogenesis	0.045889018	NRP2, PARD3, CCK, ONECUT1, ERBB3, BAIAP2,

		ONECUT2, SHH, CTNNA2, EPHA4, BDNF, EPHA7, ADM, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, BMP7, SLITRK6, BMPR1B, NEFL
GO:0010604~positive regulation of macromolecule metabolic process	0.046233918	DLC1, E2F1, STAT5A, PRKAG2, SNCA, TP63, TNFSF13, SHH, IL11, AGTR1, APOE, BHLHA15, HMOX1, FOXF2, RARB, ALX4, IL1A, CDK1, IRS2, MECOM, PPARGC1A, AHR, VEGFC, HNF4A, CCND3, F2, FOXC1, LRRK2, SMARCA2, HMGB2, CCK, ABLIM3, SOX2, ONECUT2, SOX4, EHF, SOX9, AGT, BCL2, DYRK2, TCF4, RUNX2, NR1H3, KLF5, IL6, IKZF2, NOX1, MAML2, CREB5, IGF2, NR4A3, CENPK, HDAC5, HPX, ETS2, DNMT1, JAK3, AREG, NR5A2, BMP7
GO:0048168~regulation of neuronal synaptic plasticity	0.046471276	DRD1, GRIK2, APOE, AGT, SNCA, VGF
GO:0019218~regulation of steroid metabolic process	0.046471276	KCNMA1, AGTR1, APOE, STAT5A, AGT, APOC1
GO:0048730~epidermis morphogenesis	0.046483164	FOXQ1, BCL2, TP63, COL1A1, SHH
GO:0045669~positive regulation of osteoblast differentiation	0.046483164	IL6, PDLIM7, BMP7, BMPR1B, RUNX2
GO:0010594~regulation of endothelial cell migration	0.046483164	HDAC5, VEGFC, APOE, AGT, DLL4
GO:0030810~positive regulation of nucleotide biosynthetic process	0.046567396	DRD1, ADORA2B, APOE, ABCA1
GO:0030804~positive regulation of cyclic nucleotide biosynthetic process	0.046567396	DRD1, ADORA2B, APOE, ABCA1
GO:0006957~complement activation, alternative pathway	0.046567396	C3, C5, CFH, CFD
GO:0042304~regulation of fatty acid biosynthetic process	0.046567396	HNF4A, AGT, APOC1, NR1H3
GO:0046847~filopodium assembly	0.046567396	DNM3, BAIAP2, ITGB4, FGD4
GO:0030801~positive regulation of cyclic nucleotide metabolic process	0.046567396	DRD1, ADORA2B, APOE, ABCA1
GO:0001662~behavioral fear response	0.046567396	DRD1, CCK, GRIK2, BCL2
GO:0032881~regulation of polysaccharide metabolic process	0.046567396	IRS2, PPP1R3C, IGF2, DYRK2
GO:0002209~behavioral defense response	0.046567396	DRD1, CCK, GRIK2, BCL2
GO:0045981~positive regulation of nucleotide metabolic process	0.046567396	DRD1, ADORA2B, APOE, ABCA1
GO:0008217~regulation of blood pressure	0.049494271	AGTR1, ACE, RENBP, HMOX1, TACR1, AGT, NOX1, BDKRB2, NPR3, GUCA2B, ADRA1D
GO:0007398~ectoderm development	0.049595895	TP63, HOXB13, SFN, SOX9, COL5A2, COL5A1, SHH, SCEL, FOXQ1, LAMB3, LAMA3, COL7A1, FLG, BCL2, KRT15, LAMC2, COL1A1, EMP1
GO:0030552~cAMP binding	0.050059738	HCN2, PDE1C, PDE10A, RAPGEF4
GO:0030425~dendrite	0.050303854	DNM3, DRD1, CCK, NOS1, GRIK2, TACR1, TP63, KCNJ2, CAMK2N1, EPHA7, CHRM3, APOE, MAP2, CACNA1G, ALOX5, LRRK2
GO:0051223~regulation of protein transport	0.050502267	KCNN4, VEGFC, RBP4, IL6, HNF4A, TNFSF15, TNFSF14, IGF2, KRT20, EGF, SHH, IL1A
GO:0007423~sensory organ development	0.050579885	KCNMA1, RBP4, DFNA5, ERBB3, CRYAB, SOX2, PRKCI, NR4A3, PRRX2, COL5A2, COL5A1, SHH,

		FOXP2, BDNF, BCL2, PVRL3, FOXC1, RARB, BMP7, BMPR1B
GO:0045597~positive regulation of cell differentiation	0.050579885	IL6, PDLIM7, STAT5A, SOX2, IGF2, SHH, NTRK3, AGTR1, VEGFC, BDNF, METRN, AGT, BCL2, HLX, SCIN, CA2, BMPR1B, BMP7, RUNX2, NEFL
GO:0007626~locomotory behavior	0.050728483	NRP2, KCNMA1, IL6, DRD1, CCL2, CXCL5, NPY2R, CXCL3, C5, SNCA, PARK2, CX3CL1, PLAUR, CCRL2, EPHA4, TYMP, CCR7, PPBP, EPS8, ROBO3, SEPP1, CYR61, SCG2
GO:0004713~protein tyrosine kinase activity	0.051348675	FGFR2, NRP2, FRK, CAV2, FGFR4, ERBB3, FES, EPHA2, NTRK3, EPHA4, EPHA7, MLKL, JAK3, DYRK2, MST1R, MERTK
GO:0008286~insulin receptor signaling pathway	0.051388474	PHIP, IRS2, BAIAP2, IGF2, IGFBP1, PIK3R3
GO:0033500~carbohydrate homeostasis	0.051895284	RBP4, BHLHA15, SERPINE1, PDE3B, IGF2, VGF, PPARGC1A
GO:0042593~glucose homeostasis	0.051895284	RBP4, BHLHA15, SERPINE1, PDE3B, IGF2, VGF, PPARGC1A
GO:0031100~organ regeneration	0.052621297	CCL2, ADM, ANGPT1, NR4A3, GAS6
GO:0045766~positive regulation of angiogenesis	0.052621297	CHRNA7, TNFSF13, DDAH1, IL1A, ANGPTL4
GO:0045893~positive regulation of transcription, DNA-dependent	0.052929721	E2F1, HMGB2, STAT5A, ABLIM3, SOX2, ONECUT2, SOX4, TP63, EHF, SOX9, SHH, IL11, BHLHA15, FOXF2, RARB, TCF4, ALX4, RUNX2, NR1H3, IL6, IKZF2, MAML2, CREB5, NR4A3, CENPK, MECOM, PPARGC1A, AHR, HDAC5, HNF4A, ETS2, FOXC1, JAK3, BMP7, NR5A2, SMARCA2
GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger	0.053191283	CALCR, S1PR3, ADCY1, DRD1, CCL2, ADORA2B, AGT, NPY2R, NPR3, VIPR1, HTR1D, ADRA1D
GO:0051189~prosthetic group metabolic process	0.05326563	MOCOS, GPHN, MOCS1
GO:0019720~Mo-molybdopterin cofactor metabolic process	0.05326563	MOCOS, GPHN, MOCS1
GO:0043545~molybdopterin cofactor metabolic process	0.05326563	MOCOS, GPHN, MOCS1
GO:0032324~molybdopterin cofactor biosynthetic process	0.05326563	MOCOS, GPHN, MOCS1
GO:0006777~Mo-molybdopterin cofactor biosynthetic process	0.05326563	MOCOS, GPHN, MOCS1
GO:0031410~cytoplasmic vesicle	0.053492051	CALCR, CAV2, TF, PAM, RAB3B, CXXC4, SYT6, ABCA1, ENPEP, VGF, GPRC5A, SHH, ANXA6, AP1S3, BDNF, NPTX1, FGG, MALL, FGB, ENTPD7, TFF3, SLC30A3, RAB27B, CFD, EGF, PCSK4, ARHGDIB, NCALD, SYT11, SYT12, GOLIM4, MMP14, SYNGR3, SLC17A7, SH3BP4, VEGFC, RHCG, PPBP, NTS, F5, FLG, SERPINF2, CAPG, CTSD, ADAMTS1, CTSB, VAMP1, LRRK2
GO:0050905~neuromuscular process	0.054142423	KCNMA1, DRD1, SOX2, USH1C, NR4A3, PARK2, NEFL, CTNNA2
GO:0031401~positive regulation of protein modification process	0.054938546	DLC1, CDK1, IL6, CCK, PRKAG2, IGF2, PPARGC1A, IL11, VEGFC, CCND3, HPX, BCL2, AGT, F2, DNMT1, BMP7, LRRK2
GO:0032403~protein complex binding	0.054961927	PDP1, COL4A3, ADAM11, IRS2, ADAM23, FCGRT,

		IGF2, EDIL3, CPS1, COL5A1, PHIP, LAMB3, NPTXR, DOK5, FBLN5, TGFBI, DOK7, PCNA
GO:0043535~regulation of blood vessel endothelial cell migration	0.055030239	HDAC5, VEGFC, APOE, DLL4
GO:0030035~microspike assembly	0.055030239	DNM3, BAIAP2, ITGB4, FGD4
GO:0060350~endochondral bone morphogenesis	0.055030239	NAB1, COL1A1, SOX9, RUNX2
GO:0030539~male genitalia development	0.055030239	SOX2, SYCP2, SHH, GJB2
GO:0022612~gland morphogenesis	0.055030239	ERBB3, BCL2, BMP7, SHH
GO:0006270~DNA replication initiation	0.055030239	CDC45, MCM4, MCM5, MCM6
GO:0009100~glycoprotein metabolic process	0.055615209	MGAT4A, GCNT4, GALNT1, ST6GAL2, GALNT7, TSPAN7, TSPAN8, EDEM3, ST6GALNAC1, LARGE, ST8SIA4, B3GNT7, B3GALNT1, CHST13, FUT1, B3GNT3, GALNT9, TM4SF4
GO:0006140~regulation of nucleotide metabolic process	0.055974571	CALCR, S1PR3, ADCY1, DRD1, ADORA2B, APOE, NPY2R, ADRA2A, CDA, ABCA1, NPR3, GUCA2B
GO:0006814~sodium ion transport	0.056031729	FXYD2, HCN2, SGK1, SLC12A2, SLC9A2, SLC10A7, SLC17A7, SLC17A3, SLC23A2, SLC17A1, SLC4A8, SLC13A2, SLC4A4
GO:0033043~regulation of organelle organization	0.056033221	DLC1, CAV2, LIMA1, TACR1, VIL1, SNCA, IGF2, ESPL1, PPARGC1A, CDC42EP2, SCIN, MAP2, CAPG, KIF20B, DNMT1, TMSB4Y, EGF, IL1A, SPTB
GO:0047555~3',5'-cyclic-GMP phosphodiesterase activity	0.056137568	PDE11A, PDE9A, PDE10A
GO:0016725~oxidoreductase activity, acting on CH or CH2 groups	0.056137568	ACOX2, RRM2, RRM1
GO:0006638~neutral lipid metabolic process	0.056340287	PLCE1, DGAT2, APOE, SNCA, APOC1, CPS1, NR1H3
GO:0019210~kinase inhibitor activity	0.056910737	CDKN2C, PRKAG2, PKIB, SFN, CAMK2N1, RHOH
GO:0030141~secretory granule	0.057329913	CALCR, PAM, TF, VGF, VEGFC, FGG, NPTX1, F5, NTS, PPBP, SERPINF2, FGB, TFF3, EGF, CFD, RAB27B, PCSK4
GO:0005577~fibrinogen complex	0.057741807	FGG, FGB, FGL1
GO:0032270~positive regulation of cellular protein metabolic process	0.058214579	DLC1, CDK1, IL6, CCK, PRKAG2, IGF2, PPARGC1A, IL11, AGTR1, VEGFC, CCND3, HPX, APOE, BCL2, AGT, F2, DNMT1, BMP7, LRRK2, NR1H3
GO:0051254~positive regulation of RNA metabolic process	0.058296337	E2F1, HMGB2, STAT5A, ABLIM3, SOX2, ONECUT2, SOX4, TP63, EHF, SOX9, SHH, IL11, BHLHA15, FOXF2, RARB, TCF4, ALX4, RUNX2, NR1H3, IL6, IKZF2, MAML2, CREB5, NR4A3, CENPK, MECOM, PPARGC1A, AHR, HDAC5, HNF4A, ETS2, FOXC1, JAK3, BMP7, NR5A2, SMARCA2
GO:0051259~protein oligomerization	0.058524473	CAV2, CRYAB, HR, TP63, BIRC3, GJB1, RRM2, GPX3, RRM1, TGM2, CDA, QPRT, ANGPT1, SKIL, SCARA5, ANGPTL4
GO:0007156~homophilic cell adhesion	0.058736368	PCDH10, PCDH9, PCDHGC3, PCDH7, CDH7, CDH15, DSG2, CDH17, PVRL3, DSC2, PCDHA13, CEACAM1, CDH10
GO:0030834~regulation of actin filament depolymerization	0.059177709	LIMA1, SCIN, CAPG, VIL1, SPTB
GO:0042330~taxis	0.05977218	NRP2, IL6, CCL2, CXCL5, CXCL3, C5, CX3CL1, PLAUR, CCRL2, TYMP, CCR7, PPBP, ROBO3, CYR61, SCG2

GO:0006935~chemotaxis	0.05977218	NRP2, IL6, CCL2, CXCL5, CXCL3, C5, CX3CL1, PLAUR, CCRL2, TYMP, CCR7, PPBP, ROBO3, CYR61, SCG2
GO:0051338~regulation of transferase activity	0.060261604	ADCY1, DRD1, PARD3, CCK, ADORA2B, C5, PRKAG2, TNFSF15, ZEB2, SFN, DGKA, TSPYL2, APOE, CDKN2C, ADRA2A, CHRNA7, EGF, FGD4, CDC6, RBL1, BIRC7, PKIB, IGF2, CDC25A, PLCE1, CCND3, GADD45G, GADD45B, DUSP6
GO:0043254~regulation of protein complex assembly	0.060420236	CAV2, CDC42EP2, CCK, TPPP, SCIN, CAPG, VIL1, TMSB4Y, AHR, SPTB
GO:0051173~positive regulation of nitrogen compound metabolic process	0.06056501	E2F1, HMGB2, DRD1, ADORA2B, STAT5A, ABLIM3, SOX2, ONECUT2, SOX4, TP63, EHF, TNFSF13, ABCA1, SOX9, SHH, IL11, HRH1, BHLHA15, APOE, FOXF2, RARB, TCF4, ALX4, RUNX2, DDAH1, NR1H3, KLF5, IL6, IKZF2, MAML2, IGF2, CREB5, NR4A3, CENPK, MECOM, PPARGC1A, AHR, HDAC5, HNF4A, ETS2, FOXC1, AREG, JAK3, BMP7, NR5A2, SMARCA2
GO:0043005~neuron projection	0.060972641	S100A4, CALCR, NRP2, DRD1, CCK, GRIK2, TACR1, SNCA, TP63, KCNJ2, VGF, APOE, ANK3, NEFL, KCNMA1, DNM3, NOS1, PARK2, BASP1, CAMK2N1, CTNNA2, EPHA7, CHRM3, MAP2, CACNA1G, CA2, ALOX5, LRRK2
GO:0055088~lipid homeostasis	0.061007279	IRS2, MALL, HNF4A, APOE, IGF2, ABCA1, NR5A2
GO:0043524~negative regulation of neuron apoptosis	0.061007279	BDNF, GRIK2, ERBB3, BCL2, AGT, SNCA, NEFL
GO:0001654~eye development	0.061526725	RBP4, CRYAB, SOX2, PRKCI, COL5A2, SHH, COL5A1, FOXP2, PVRL3, FOXC1, RARB, BMPR1B, BMP7
GO:0031646~positive regulation of neurological system process	0.062099854	TF, DRD1, CCL2, GRIK2, TACR1, SNCA
GO:0042475~odontogenesis of dentine-containing tooth	0.062099854	TP63, FOXC1, CA2, LHX8, BMP7, SHH
GO:0045471~response to ethanol	0.062322351	UGT1A6, RBP4, CCL2, EPS8, APOE, TACR1, BCL2, UGT1A4, UGT1A1, SHH
GO:0048167~regulation of synaptic plasticity	0.062322351	DRD1, BDNF, GRIK2, APOE, AGT, SNCA, CTNND2, VGF
GO:0031018~endocrine pancreas development	0.064168793	IL6, ONECUT1, ONECUT2, PDE3B
GO:0035094~response to nicotine	0.064168793	HMOX1, TACR1, BCL2, CHRNA7
GO:0032870~cellular response to hormone stimulus	0.064403507	IRS2, DRD1, ADCY1, ERBB3, STAT5A, BAIAP2, PRKCI, PDE3B, IGF2, PHIP, HDAC5, IGFBP1, PIK3R3
GO:0008361~regulation of cell size	0.064405892	FGFR2, CRYAB, TP63, IGF2, SFN, GREM1, NTRK3, RERG, TSPYL2, NUPR1, HNF4A, CDKN2C, BCL2, AGT, TGFBR3, CDA, IGFBP1, EMP1
GO:0050840~extracellular matrix binding	0.064514355	TGFBI, BCAM, NID1, SHH, CYR61
GO:0030278~regulation of ossification	0.065783849	CALCR, IL6, PDLIM7, BCL2, SOX2, SOX9, BMP7, BMPR1B, RUNX2
GO:0007219~Notch signaling pathway	0.065896675	HEY1, DLL4, MAML2, CNTN1, TP63, FOXC1, CFD
GO:0030837~negative regulation of actin filament polymerization	0.066147206	SCIN, CAPG, VIL1, TMSB4Y, SPTB
GO:0003014~renal system process	0.066147206	KCNMA1, AGTR1, TACR1, BCL2, AGT

GO:0019842~vitamin binding	0.066666837	MOCOS, RBP4, DDC, PAM, CRABP1, SPTLC3, EGLN1, SLC19A3, TCN1, TAT, GLDC, FOLR1, P4HA3
GO:0042063~gliogenesis	0.066679734	METRN, DRD1, CDKN2C, ERBB3, AGT, NAB1, MMP14, SHH
GO:0009582~detection of abiotic stimulus	0.066679734	RBP4, PLEKHB1, SLC12A2, LXN, ARRB1, TACR1, SOX2, ABCA4
GO:0030308~negative regulation of cell growth	0.06756935	RERG, TSPYL2, HNF4A, CDKN2C, CRYAB, BCL2, AGT, CDA, TP63, GREM1
GO:0006767~water-soluble vitamin metabolic process	0.067892738	NAMPT, NMNAT2, SLC23A2, FOLR1, SLC19A3, QPRT
GO:0008201~heparin binding	0.068144523	FGFR2, CCL2, APOE, RSPO3, TGFBR3, LAMC2, ADAMTS1, BMP7, FGFBP1, COL5A1, CYR61
GO:0010575~positive regulation vascular endothelial growth factor production	0.06847201	ADORA2B, NOX1, IL1A
GO:0033032~regulation of myeloid cell apoptosis	0.06847201	CD44, BCL2, STAT5A
GO:0002016~regulation of blood volume by renin-angiotensin	0.06847201	AGTR1, ACE, AGT
GO:0002052~positive regulation of neuroblast proliferation	0.06847201	VEGFC, SOX2, SHH
GO:0009263~deoxyribonucleotide biosynthetic process	0.06847201	RRM2, RRM1, AK5
GO:0003078~regulation of natriuresis	0.06847201	AGTR1, TACR1, AGT
GO:0006111~regulation of gluconeogenesis	0.06847201	HNF4A, IGF2, PPARGC1A
GO:0030291~protein serine/threonine kinase inhibitor activity	0.068820534	CDKN2C, PRKAG2, PKIB, SFN
GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process	0.06894165	NMNAT2, NAMPT, ADCY1, RP2, PRKAG2, AK5, AMPD3, ADM, ATP2A3, RRM2, RRM1, CDA, QPRT, DPYD, GUCA2B, NT5E, ATP6V0D2
GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	0.06894165	NMNAT2, NAMPT, ADCY1, RP2, PRKAG2, AK5, AMPD3, ADM, ATP2A3, RRM2, RRM1, CDA, QPRT, DPYD, GUCA2B, NT5E, ATP6V0D2
GO:0045860~positive regulation of protein kinase activity	0.069090171	ADCY1, PARD3, CCK, ADORA2B, PRKAG2, C5, TNFSF15, BIRC7, IGF2, ZEB2, DGKA, PLCE1, CCND3, GADD45G, ADRA2A, CHRNA7, GADD45B, EGF, FGD4
GO:0031402~sodium ion binding	0.069324597	SLC17A7, FXYD2, HCN2, SLC12A2, SLC17A3, SLC23A2, SLC17A1, SLC9A2, SLC4A8, SLC10A7, SLC13A2, SLC4A4
GO:0031982~vesicle	0.069951272	SYT6, ENPEP, VGF, SHH, AP1S3, BDNF, MALL, RAB27B, CFD, NCALD, MMP14, VEGFC, F5, RHCG, PPBP, SERPINF2, CTSD, ADAMTS1, CTSB, LRRK2, VAMP1, CALCR, PAM, TF, CAV2, RAB3B, CXXC4, ABCA1, GPRC5A, ANXA6, FGG, NPTX1, FGB, ENTPD7, TFF3, SLC30A3, EGF, PCSK4, ARHGDIB, SYT11, SYT12, GOLIM4, SYNGR3, SLC17A7, SH3BP4, NTS, FLG, CAPG, BMP7
GO:0005925~focal adhesion	0.07021536	TNS4, DLC1, CAV2, DIXDC1, LIMA1, LIMS2, LAMA3, CD44, LPP, NPY2R, APBB1IP
GO:0046903~secretion	0.070486262	KCNMA1, IL6, ADORA2B, TACR1, PRKCI, SYT6, ABCA1, BDKRB2, VGF, AQP3, RIMS3, KCNN4, BDNF, ACE, LAT2, HMOX1, AGT, SCIN, KCNK5,

		RAPGEF4, CA2, GUCA2B, PCSK4, SCG2
GO:0010001~glial cell differentiation	0.071008365	METRN, DRD1, CDKN2C, ERBB3, AGT, NAB1, SHH
GO:0007411~axon guidance	0.071718002	NRP2, EPHA4, EPHA7, BDNF, ANK3, SEMA3B, ROBO3, UNC5C, BMP7, BMPR1B, SHH
GO:0009986~cell surface	0.071969383	FGFR2, CAV2, PARD3, TACR1, BCAM, ENPEP, CX3CL1, GREM1, SHH, WISP2, FGG, ACE, CD44, FGB, APOE, GPC6, CD22, KCNMA1, CRYAB, PTPRR, PLAUR, CD274, CNTN1, TGFBR3, AREG, CTSB, SCARA5, SPTB
GO:0005158~insulin receptor binding	0.072025178	PHIP, IRS2, DOK5, DOK7, IGF2
GO:0032272~negative regulation of protein polymerization	0.073522855	SCIN, CAPG, VIL1, TMSB4Y, SPTB
GO:0001937~negative regulation of endothelial cell proliferation	0.073954731	CAV2, APOE, TNFSF15, SCG2
GO:0043242~negative regulation of protein complex disassembly	0.073974713	LIMA1, SCIN, MAP2, CAPG, VIL1, SPTB
GO:0051186~cofactor metabolic process	0.074096621	GSTA1, MOCOS, NMNAT2, NAMPT, ALDH1L1, NOX1, UGT1A1, GGT5, UGT1A6, GPHN, BAAT, HNF4A, FOLR1, HPX, HMOX1, GPX3, UGT1A4, QPRT, MOCS1
GO:0043205~fibril	0.074103452	FBN1, MUC5AC, MFAP5
GO:0008509~anion transmembrane transporter activity	0.075896716	GABRG3, SLC12A2, ABCA1, SLC17A7, APOL1, SLC17A3, SLC17A1, SLC26A9, SLC4A8, SLC13A2, SLC4A4, SLC4A3, ANO9, GABRP
GO:0032989~cellular component morphogenesis	0.076359297	S100A4, NRP2, PARD3, CCK, SHROOM3, ONECUT1, ERBB3, ONECUT2, SOX9, SHH, BDNF, ANK3, BCL2, SEMA3B, UNC5C, ROBO3, NEFL, NFATC1, BAIAP2, PRKCI, CTNNA2, EPHA4, KRT19, EPHA7, ADM, TGFBR3, MAP7, BMPR1B, BMP7, SLITRK6
GO:0016023~cytoplasmic membrane-bounded vesicle	0.076647199	CALCR, CAV2, TF, PAM, RAB3B, CXXC4, SYT6, ABCA1, VGF, SHH, ANXA6, AP1S3, BDNF, NPTX1, FGG, MALL, FGB, TFF3, SLC30A3, RAB27B, CFD, EGF, PCSK4, ARHGDIB, NCALD, SYT11, GOLIM4, MMP14, SYNGR3, SLC17A7, SH3BP4, VEGFC, PPBP, NTS, F5, FLG, SERPINF2, CAPG, CTSD, CTSB, LRRK2
GO:0007346~regulation of mitotic cell cycle	0.078177379	CAV2, CDK1, CDC6, STAT5A, KNTC1, ESPL1, IGF2, HNF4A, ZWINT, BCL2, KIF20B, FOXC1, EGF, IL1A
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.079073326	E2F1, HMGB2, DRD1, ADORA2B, STAT5A, ABLIM3, SOX2, ONECUT2, SOX4, TP63, EHF, TNFSF13, ABCA1, SOX9, SHH, IL11, BHLHA15, APOE, FOXF2, RARB, TCF4, ALX4, RUNX2, NR1H3, KLF5, IL6, IKZF2, MAML2, IGF2, CREB5, NR4A3, CENPK, MECOM, PPARGC1A, AHR, HDAC5, HNF4A, ETS2, FOXC1, AREG, JAK3, BMP7, NR5A2, SMARCA2
GO:0051015~actin filament binding	0.079245513	LIMA1, SCIN, PLS1, MARCKS, SPTB, MYO5C, FGD4
GO:0031988~membrane-bounded vesicle	0.080059061	CALCR, CAV2, TF, PAM, RAB3B, CXXC4, SYT6, ABCA1, VGF, SHH, ANXA6, AP1S3, BDNF, NPTX1, FGG, MALL, FGB, TFF3, SLC30A3, RAB27B, CFD, EGF, PCSK4, ARHGDIB, NCALD, SYT11, GOLIM4, MMP14, SYNGR3, SLC17A7, SH3BP4, VEGFC, PPBP, NTS, F5, FLG, SERPINF2, CAPG, CTSD, CTSB, BMP7, LRRK2

GO:0033189~response to vitamin A	0.080342919	MUC1, RBP4, CD44, SOX2, AQP3, SHH
GO:0042594~response to starvation	0.080342919	UGT1A6, ADM, UGT1A4, HRK, CTSD, CPS1, PPARGC1A, UGT1A1
GO:0006956~complement activation	0.080342919	C3, C5, CFH, C4BPB, C4BPA, CFD
GO:0051247~positive regulation of protein metabolic process	0.080737646	DLC1, CDK1, IL6, CCK, PRKAG2, IGF2, PPARGC1A, IL11, AGTR1, VEGFC, CCND3, HPX, APOE, BCL2, AGT, F2, DNMT1, BMP7, LRRK2, NR1H3
GO:0050730~regulation of peptidyl-tyrosine phosphorylation	0.080825229	IL6, CCK, HNF4A, HPX, AGT, IGF2, EGF, IL11
GO:0032271~regulation of protein polymerization	0.080825229	CAV2, CDC42EP2, TPPP, SCIN, CAPG, VIL1, TMSB4Y, SPTB
GO:0009628~response to abiotic stimulus	0.081253493	RBP4, DRD1, CCL2, LXN, TACR1, SOX2, BDKRB2, ABCA4, VGF, PLEKHB1, STAC, BCL2, AGT, KCNMA1, NOS1, SLC12A2, CRYAB, NOX1, MMP14, FOXP2, THBD, DIO2, ADM, ARRB1, SCARA3, CA2, COL1A1, SCARA5
GO:0043467~regulation of generation of precursor metabolites and energy	0.081296124	IRS2, PPP1R3C, PRKAG2, IGF2, DYRK2
GO:0006732~coenzyme metabolic process	0.081353349	GSTA1, MOCOS, NMNAT2, NAMPT, ALDH1L1, NOX1, GGT5, GPHN, BAAT, HNF4A, FOLR1, GPX3, QPRT, MOCS1
GO:0031644~regulation of neurological system process	0.081353349	TF, DRD1, CCL2, CCK, GRIK2, TACR1, SNCA, CTNND2, PARK2, VGF, BDNF, APOE, BCHE, AGT
GO:0008227~amine receptor activity	0.081517675	DRD1, HRH1, CHRM3, ADRA2A, HTR1D, ADRA1D
GO:0012502~induction of programmed cell death	0.082040769	DLC1, GRIK2, TP63, TNFSF14, TNFSF13, CD70, SFN, MCF2L, BOK, CDKN2C, APOE, HMOX1, TGM2, TNFRSF19, DYRK2, FGD4, NET1, COL4A3, HRK, SLAMF7, TNFSF10, RASGRF2, NUPR1, MUC5AC, PRODH
GO:0003012~muscle system process	0.082063965	KCNMA1, HCN2, DRD1, ADORA2B, CRYAB, TACR1, BDKRB2, VIPR1, HDAC5, CHRM3, HMOX1, AGT, CACNA1G, MB, DTNA
GO:0019207~kinase regulator activity	0.082109869	CDKN2C, ERBB3, PRKAG2, RAPGEF4, PKIB, SFN, PIK3R3, EGF, CAMK2N1, RHOH
GO:0030802~regulation of cyclic nucleotide biosynthetic process	0.082900181	CALCR, S1PR3, ADCY1, DRD1, ADORA2B, APOE, NPY2R, ADRA2A, ABCA1, NPR3, GUCA2B
GO:0030808~regulation of nucleotide biosynthetic process	0.082900181	CALCR, S1PR3, ADCY1, DRD1, ADORA2B, APOE, NPY2R, ADRA2A, ABCA1, NPR3, GUCA2B
GO:0005911~cell-cell junction	0.083902321	F11R, CGNL1, MAGI3, PARD3, SHROOM3, CLDN4, CALB2, GJB1, CTNNA2, GJB2, DSG2, PKP2, PVRL3, DSC2, TJP3, ADD3, TJP2
GO:0035272~exocrine system development	0.084356818	SOX4, FOXC1, BMP7, SHH
GO:0051402~neuron apoptosis	0.084356818	GRIK2, ERBB3, BCL2, TP63
GO:0008206~bile acid metabolic process	0.084356818	ACOX2, BAAT, CYP39A1, NR5A2
GO:0031069~hair follicle morphogenesis	0.084356818	FOXQ1, BCL2, TP63, SHH
GO:0001963~synaptic transmission, dopaminergic	0.084891816	DRD1, SNCA, PARK2
GO:0006599~phosphagen metabolic process	0.084891816	GATM, STAT5A, CKB
GO:0030321~transepithelial chloride transport	0.084891816	CAV2, P2RY6, SLC12A2
GO:0006600~creatine metabolic process	0.084891816	GATM, STAT5A, CKB
GO:0044062~regulation of excretion	0.084891816	AGTR1, TACR1, AGT

GO:0019934~cGMP-mediated signaling	0.084891816	APOE, AGT, PDE9A
GO:0051145~smooth muscle cell differentiation	0.084891816	WNT4, AGT, TBX18
GO:0043537~negative regulation of blood vessel endothelial cell migration	0.084891816	HDAC5, APOE, DLL4
GO:0033002~muscle cell proliferation	0.084891816	AGT, TGFBR3, FOXC1
GO:0007164~establishment of tissue polarity	0.084891816	HNF4A, FOXF2, TP63
GO:0009125~nucleoside monophosphate catabolic process	0.084891816	PDE3B, NT5E, AMPD3
GO:0009435~NAD biosynthetic process	0.084891816	NAMPT, NMNAT2, QPRT
GO:0060004~reflex	0.084891816	KCNMA1, NR4A3, FOXP2
GO:0046649~lymphocyte activation	0.085155552	EXO1, ONECUT1, STAT5A, SOX4, TNFSF14, IGF2, SLAMF7, IL15, IL11, HDAC5, LAT2, CCND3, BCL2, PLCG2, HELLS, RHOH, KIF13B
GO:0048592~eye morphogenesis	0.085897295	RBP4, PVRL3, SOX2, PRKCI, RARB, BMP7, COL5A2, COL5A1
GO:0005924~cell-substrate adherens junction	0.08590642	TNS4, DLC1, CAV2, DIXDC1, LIMA1, LIMS2, LAMA3, CD44, LPP, NPY2R, APBB1IP
GO:0045202~synapse	0.086234505	RAB3B, ERBB3, GRIK2, SYT6, RIMS3, GPHN, ANK3, RASGRP2, CHRNA7, SLC30A3, GABRP, DTNA, GRID1, KCNMA1, DNM3, GABRG3, SYT11, SYT12, CAMK2N1, SYNGR3, SLC17A7, EPHA7, CDH15, EPS8, CHRM3, DOK7, LRRK2, VAMP1
GO:0016054~organic acid catabolic process	0.08685165	FRRS1, ACOX2, CYP39A1, NOS1, PRODH2, ASRGL1, TAT, DDAH1, MOXD1, PRODH, GLDC
GO:0046395~carboxylic acid catabolic process	0.08685165	FRRS1, ACOX2, CYP39A1, NOS1, PRODH2, ASRGL1, TAT, DDAH1, MOXD1, PRODH, GLDC
GO:0002541~activation of plasma proteins involved in acute inflammatory response	0.086993681	C3, C5, CFH, C4BPB, C4BPA, CFD
GO:0042633~hair cycle	0.086993681	MPZL3, FOXQ1, BCL2, TP63, SOX9, SHH
GO:0042303~molting cycle	0.086993681	MPZL3, FOXQ1, BCL2, TP63, SOX9, SHH
GO:0045667~regulation of osteoblast differentiation	0.086993681	IL6, PDLIM7, SOX2, BMP7, BMPR1B, RUNX2
GO:0030031~cell projection assembly	0.087532136	KLF5, DNM3, MYO1A, ONECUT1, BAIAP2, CAPG, ONECUT2, ITGB4, FGD4
GO:0010638~positive regulation of organelle organization	0.087532136	CAV2, CDC42EP2, TACR1, DNMT1, IGF2, ESPL1, EGF, PPARGC1A, IL1A
GO:0009612~response to mechanical stimulus	0.08766848	CCL2, SLC12A2, TACR1, SOX2, COL1A1, MMP14, FOXP2
GO:0009408~response to heat	0.08766848	NOS1, CCL2, STAC, CRYAB, TACR1, BCL2, SCARA5
GO:0050728~negative regulation of inflammatory response	0.089457027	GPX2, APOE, CHRNA7, IGF2, NT5E
GO:0002455~humoral immune response mediated by circulating immunoglobulin	0.089457027	EXO1, C3, C5, C4BPB, C4BPA
GO:0033674~positive regulation of kinase activity	0.089495236	ADCY1, PARD3, CCK, ADORA2B, PRKAG2, C5, TNFSF15, BIRC7, IGF2, ZEB2, DGKA, PLCE1, CCND3, GADD45G, ADRA2A, CHRNA7, GADD45B, EGF, FGD4
GO:0005529~sugar binding	0.090079526	KLRC2, GALNT1, ATRNL1, GALNT7, GALNT5, LGALS9C, LGALS2, GALNT4, MRC2, LGALS9B, PKD1L2, LPHN2, ZG16B, LPHN3, CD22, PLA2R1, GALNT9

GO:0002020~protease binding	0.090264596	SERPINF2, BCL2, SERPINE1, BDKRB2
GO:0007229~integrin-mediated signaling pathway	0.091146572	ADAM11, ADAM23, ITGB8, ITGB4, ITGA11, ADAMTS1, CEACAM1, ITGBL1
GO:0009165~nucleotide biosynthetic process	0.091504978	NMNAT2, NAMPT, ADCY1, RP2, PRKAG2, AK5, AMPD3, ADM, ATP2A3, RRM2, RRM1, QPRT, DPYD, GUCA2B, NT5E, ATP6V0D2
GO:0030934~anchoring collagen	0.09172363	COL14A1, COL7A1, COL12A1
GO:0070661~leukocyte proliferation	0.093922542	ACE, CCND3, BCL2, TNFSF14, IL15, HELLS
GO:0032943~mononuclear cell proliferation	0.093922542	ACE, CCND3, BCL2, TNFSF14, IL15, HELLS
GO:0044087~regulation of cellular component biogenesis	0.094265439	DLC1, CAV2, CCK, TACR1, VIL1, MMP14, AHR, CDC42EP2, TPPP, CAPG, SCIN, TMSB4Y, SPTB
GO:0010876~lipid localization	0.09486806	RBP4, STAT5A, SORL1, APOC1, ABCA1, BDKRB2, ABCA4, APOL2, KCNN4, ACE, APOL1, PLIN2, APOE, OSBPL10
GO:0030799~regulation of cyclic nucleotide metabolic process	0.095090855	CALCR, S1PR3, ADCY1, DRD1, ADORA2B, APOE, NPY2R, ADRA2A, ABCA1, NPR3, GUCA2B
GO:0034367~macromolecular complex remodeling	0.095341532	AGTR1, APOE, AGT, APOC1
GO:0006044~N-acetylglucosamine metabolic process	0.095341532	UAP1, RENBP, LARGE, CHST2
GO:0002685~regulation of leukocyte migration	0.095341532	IL6, HMOX1, F7, GREM1
GO:0034368~protein-lipid complex remodeling	0.095341532	AGTR1, APOE, AGT, APOC1
GO:0034369~plasma lipoprotein particle remodeling	0.095341532	AGTR1, APOE, AGT, APOC1
GO:0060349~bone morphogenesis	0.095341532	NAB1, COL1A1, SOX9, RUNX2
GO:0006041~glucosamine metabolic process	0.095341532	UAP1, RENBP, LARGE, CHST2
GO:0019205~nucleobase, nucleoside, nucleotide kinase activity	0.095629658	MAGI3, RP2, DLG3, AK5, TJP2, TK1
GO:0043176~amine binding	0.095907272	DRD1, NOS1, CHRM3, BCHE, FOLR1, APOC1, CHRNA7, SLC19A3, HTR1D, TAT, DDAH1
GO:0045792~negative regulation of cell size	0.096613842	RERG, TSPYL2, HNF4A, CDKN2C, CRYAB, BCL2, AGT, CDA, TP63, GREM1
GO:0044093~positive regulation of molecular function	0.097039808	DLC1, CALCR, PARD3, DRD1, ADCY1, CCK, ADORA2B, TACR1, C5, PRKAG2, TNFSF15, ZEB2, SHH, DGKA, AGTR1, P2RY6, HRH1, APOE, BCL2, AGT, TGM2, ADRA2A, CHRNA7, EGF, FGD4, NR1H3, COL4A3, CDK1, IL6, BIRC7, IGF2, NPR3, SYNGR3, HDAC5, PLCE1, CCND3, GADD45G, PLCG2, F2, TGFBR3, GADD45B
GO:0015296~anion:cation symporter activity	0.097057789	SLC17A7, SLC12A2, SLC17A3, SLC13A2, SLC4A4
GO:0042246~tissue regeneration	0.097994257	GATM, SERPINE1, IGFBP1, TM4SF4, PLAUR
GO:0004620~phospholipase activity	0.099322882	PLCL2, PLCE1, PLA2G16, PLCB4, CHRM3, HMOX1, PLCG2, PLCH1, BDKRB2
GO:0016331~morphogenesis of embryonic epithelium	0.099862138	DLC1, VEGFC, WNT4, SHROOM3, ZEB2, TBX18, SHH

Table S9. Genes positively regulated by EHF in Calu-3 and A549 cells. These transcripts showed a significant decrease in expression in EHF-depleted Calu-3 cells and an increase in expression in EHF-overexpressing A549 clones.

ALDH3A1
AQP3
AREG
ARHGDIB
ARL5B
BACH1
BASP1
BCAS1
BDNF
BHLHA15
BPIFB1
CCAT1
CDC37L1
CHST2
CMTM4
CPNE8
CXCL5
CYP24A1
DSC2
E2F7
EHF
ELK3
FA2H
FAM83A
FERMT1
FOXA1
FRRS1
GALNT7
IFI16
KRAS
KRT4
LIN7C
MIR205HG
MIR3648
MSN
NCEH1
PADI2
PIK3R3
PRSS23
RNF128

SCEL
SEC23A
SEC24D
SESN3
SLC39A10
SLC4A7
SLCO1B3
SOX4
SPDEF
SPTY2D1
STK38L
SYT12
TJP2
TNFSF15
TNS4
TOB1
TRIM29
TSPYL2
UGDH

Table S10. List of enriched gene pathways from DAVID gene ontology analysis of genes positively regulated by EHF in Calu-3 and A549 cells.

Term	P Value	Genes
GO:0030855~epithelial cell differentiation	0.01190634	FOXA1, EHF, KRT4, SCEL
GO:0070161~anchoring junction	0.015347644	TNS4, FERMT1, DSC2, TJP2
GO:0042127~regulation of cell proliferation	0.018073213	BDNF, KRAS, CXCL5, E2F7, TNFSF15, SOX4, KRT4, TOB1
GO:0030054~cell junction	0.019804694	TNS4, SYT12, FERMT1, LIN7C, DSC2, TJP2
GO:0016323~basolateral plasma membrane	0.023719142	TNS4, FERMT1, MSN, AQP3
GO:0012507~ER to Golgi transport vesicle membrane	0.024156786	SEC23A, SEC24D
GO:0030127~COPII vesicle coat	0.024156786	SEC23A, SEC24D
GO:0005125~cytokine activity	0.029844065	CXCL5, TNFSF15, AREG, CMTM4
GO:0030528~transcription regulator activity	0.031446214	BACH1, BHLHA15, E2F7, TRIM29, FOXA1, SPDEF, SOX4, EHF, ELK3, IFI16, TOB1
GO:0030134~ER to Golgi transport vesicle	0.033068193	SEC23A, SEC24D
GO:0008285~negative regulation of cell proliferation	0.036171566	BDNF, E2F7, TNFSF15, KRT4, TOB1
GO:0043296~apical junction complex	0.036548015	LIN7C, DSC2, TJP2
GO:0016327~apicolateral plasma membrane	0.038588153	LIN7C, DSC2, TJP2
GO:0060429~epithelium development	0.044055138	FOXA1, EHF, KRT4, SCEL
GO:0003700~transcription factor activity	0.048932898	BACH1, E2F7, TRIM29, FOXA1, SPDEF, SOX4, EHF, ELK3
GO:0033280~response to vitamin D	0.054192433	CYP24A1, AQP3
GO:0043565~sequence-specific DNA binding	0.057659769	BACH1, TSPYL2, FOXA1, SPDEF, EHF, ELK3
GO:0009898~internal side of plasma membrane	0.071226533	KRAS, FERMT1, MSN, TJP2
GO:0030658~transport vesicle membrane	0.076449226	SEC23A, SEC24D
GO:0045666~positive regulation of neuron differentiation	0.080199987	BDNF, FOXA1
GO:0005912~adherens junction	0.080909028	TNS4, FERMT1, TJP2
GO:0043232~intracellular non-membrane-bounded organelle	0.081345558	BACH1, FERMT1, IFI16, BASP1, ELK3, SCEL, TNS4, TSPYL2, SLC4A7, MSN, KRT4, STK38L, ARHGDIB
GO:0043228~non-membrane-bounded organelle	0.081345558	BACH1, FERMT1, IFI16, BASP1, ELK3, SCEL, TNS4, TSPYL2, SLC4A7, MSN, KRT4, STK38L, ARHGDIB
GO:0016564~transcription repressor activity	0.096051251	E2F7, ELK3, IFI16, TOB1

Table S11. Genes negatively regulated by EHF in Calu-3 and A549 cells. These transcripts showed a significant increase in expression in EHF-depleted Calu-3 cells and a significant decrease in expression in EHF-overexpressing A549 clones.

ACSL1
ADAMTS15
AK5
C10orf10
CD22
CYS1
DMKN
EFEMP1
FGFR2
FJX1
FUT1
GLIPR2
GPC1
H1F0
HSPB1
ID2
KCNMA1
MAP2
MT2A
NEFL
NRTN
PMP22
PPP1R14C
REEP2
SERPINE1
SUSD2
TNNT1
TYMP
VAT1

Supplementary Methods

ChIP-seq. ChIP-seq was performed as described previously (1, 2) with modifications. Briefly, cells were cross-linked for 10 min in 1% formaldehyde, neutralized and scraped into lysis buffer (5mM PIPEs pH 8.0, 85mM KCL, 0.5% NP-40, 1x Protese Inhibitor Cocktail (Roche)). Nuclear preparation was isolated by centrifugation, lysed in RIPA buffer (1x PBS, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS, Protease Inhibitor Cocktail), and sonicated at 40% amplitude with the Cole Palmer Ultrasonic Processor probe sonicator 16 times for 25s each in an ice water bath to produce an average fragment size of 250bp. Sonicated chromatin was incubated with antibody coupled to Protein G beads (Dynabeads) overnight at 4°C. For EHF, 10 million Calu-3 cells and 10μg of antibody were used; for histone modifications, 1.25 million Calu-3 cells and 5μg were used. Magnetic beads were washed 5x with wash buffer (100mM Tris pH 7.5, 500mM LiCl, 1% NP-40, 1% sodium deoxycholate) and once with TE (10mM Tris-HCL pH 7.5, 0.1 mM Na_2EDTA). Bound DNA was eluted with elution buffer (1% SDS, 0.1M $NaHCO_3$) at 65°C. Input library was prepared from chromatin that was not immunoprecipitated. Eluted DNA and input were incubated at 65°C overnight to reverse cross-links. DNA was purified with QIAquick PCR cleanup kit (Qiagen).

Sequencing libraries were prepared as previously described (3) with modifications. DNA ends were blunted using T4 DNA polymerase, Klenow DNA polymerase, and T4 polynucleotide kinase. DNA was then incubated with Klenow exo- to add 5' adenine overhangs. Multiplex adaptors were ligated to the ends and converted to dsDNA using 5 cycles of PCR. DNA was size-selected to contain fragments between 200 and 300bp and PCR amplified for 5 cycles. DNA was purified with 1.2x AMPusreXP beads and analyzed on Bioanalyzer (Agilent). Sequencing was preformed on an Illumina Hi-Seq, which generated 14 to 41.7 million reads per samples (Table S10).

Fastq files were aligned to the hg19 version of the human genome using Bowtie (v 1.0.0) (4) with a seed length of 40 and a maximum number of 3 mismatches allowed in the seed. Only unique reads were used. The --best argument was used to ensure that Bowtie kept the alignment in the best stratum. In Homer, tag directories were created from the Bowtie alignment files. Then peaks were called using the Homer FindPeaks command in the factor style (EHF ChIP-seq) or histone style (H3K4Me1 and H3K27ac ChIP-seq) with the chromatin input tag directory as the control. The FDR was calculated using the input sequences assuming that the local density of tags followed a Poisson distribution. Using this distribution, Homer calculates the assumed number of false positives for a given tag threshold. It then sets the tag threshold based on the FDR specified by the user (here 0.01). All other parameters for peak calling were the default settings for the FindPeaks command. To identify high-confidence binding sites for EHF, we intersected the peaks from the replicate experiments using Bedtools, and only selected overlapping peaks present in both. This yielded a final list of 768 high-confidence binding sites. To determine the transcription factor binding motifs that were enriched within EHF ChIP-seq peaks, the findMotifsGenome.pl command in HOMER was used with the hg19 genome build and a 200bp window. HOMER uses a differential discovery algorithm to compare the ChIP-seq peaks with the genome.

Motif enrichment is calculated using the cumulative binomial distributions, and the p-value represents the probability of observing the motif sequences by chance. Histone modification enrichment and peak annotation were performed using the Homer software annotatePeaks.pl command and the high-confidence sites. Biological processes enriched among annotated genes were identified using DAVID (6).

RNA-seq. Total RNA purity and quality was assessed by Nanodrop (Thermo Scientific) and Bioanalyzer (Agilent). RNA libraries were prepared from 2 μg of total RNA from four samples of control and EHF-siRNA transfected cells, using TruSeq™ RNA sample preparation kit as per the manufacturer's protocol (Illumina, San Diego, CA). The libraries were sequenced on Illumina HiSeq2500 machines at the UNC High -Throughput Sequencing Facility for paired-end 2 x 100 base reads using standard protocols. Data in fastq format were mapped to the reference human genome (hg19) with ENSEMBL Release 74 of human genome annotation as transcriptome mapping, using TopHat (v2.0.10) (7). Quantification and differential expression of transcripts from the aligned reads were performed using Cufflinks (v2.1.1) with FDR ≤ 0.1 as differential expression threshold. Samples were then normalized and expressed as fragments per kilobase of transcript per million fragments mapped (FPKM). Genes with a fold change ≥ 1.5 were considered differentially expressed. Biological processes enriched among differentially expressed genes were identified using DAVID (6).

1. Mortazavi A, Leeper Thompson EC, Garcia ST, Myers RM, & Wold B (2006) Comparative genomics modeling of the NRSF/REST repressor network: from single conserved sites to genome-wide repertoire. *Genome research* 16(10):1208-1221.
2. Johnson DS, Mortazavi A, Myers RM, & Wold B (2007) Genome-wide mapping of in vivo protein-DNA interactions. *Science* 316(5830):1497-1502.
3. Ford E, Nikopoulou C, Kokkalis A, & Thanos D (2014) A method for generating highly multiplexed ChIP-seq libraries. *BMC Research Notes* 7(312).
4. Langmead B, Trapnell C, Pop M, & Salzberg SL (2009) Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol* 10(3):R25.
5. Heinz S*, et al.* (2010) Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. *Mol Cell* 38(4):576-589.
6. Dennis Jr. G*, et al.* (2003) DAVID: Database for Annotation, Visualization, and Integrated Discovery. *Genome Biology* 4(5):P3.
7. Trapnell C*, et al.* (2012) Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nature protocols* 7(3):562-578.