

**Supplementary Figure 1.** A) List of previously known and newly identified binding partners of EZH2 after LC-MS/MS analysis of EZH2-interactome. B) Co-immunoprecipitation. HA-TRIM28 was overexpressed in HEK-293T cells, HA beads were used to immunoprecipitate TRIM28, and EZH2 was analyzed by western blotting. C) *in vitro* binding assay, *E. coli*. purified MBP-EZH2 was incubated with GST-TRIM28 full length, and RBCC fragment, MBP beads were used to pull down MBP-EZH2, and immunoblotted with GST antibody. D) *E. coli*-purified GST-EZH2 was incubated with MCF7 cell lysates followed by GST-pull down, and immunoblotting with TRIM28 and GST antibodies (\*non-specific band). E) Distribution of co-occupied 10,882 genomic sites of TRIM28 and EZH2. Peaks are categorized as TSS (+/-3Kb), 5'UTR, 3'UTR, genic (coding exon + intron), or intergenic. F) Histogram of the count of overlapping nucleotides between EZH2 and TRIM28 co-occupancy from ChIP-seq.

**Supplementary Figure 2.** A) EZH2, TRIM28, RBBP4, EED, SUZ12 protein levels were analyzed by western blotting in shControl and sh*EZH2* MCF7 cells. B) TRIM28, EZH2, and TRIM33 protein levels were analyzed by western blotting in shControl and sh*TRIM28* MCF7 cells. C) Functional annotation analysis of down-regulated genes in sh*EZH2* cells (EZH2 activated genes). D) Functional annotation analysis of up-regulated genes in sh*EZH2* RNA-seq (EZH2 repressed genes). E) Functional annotation analysis of down-regulated genes in sh*TRIM28* cells (TRIM28 activated genes). F) Functional annotation analysis of up-regulated genes in sh*TRIM28* RNA-seq (TRIM28 repressed genes). G) KEGG pathway analysis of down-regulated genes in sh*EZH2* cells (EZH2 activated genes). H) KEGG pathway analysis of down-regulated genes in sh*TRIM28* cells (TRIM28 activated genes). I) List of TRIM28/EZH2 co-activated genes and its association with cancer.

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QPRT	-1.386	2.72E-87	1.08E-83	1666	1890	4736	4555
DDIT4	-1.284	5.43E-87	1.88E-83	4038	5266	11541	11115
FAM210B	-1.662	5.23E-86	1.61E-82	1029	1506	4088	3935
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C14orf132	-1.653	4.56E-79	9.71E-76	579	753	2032	2158
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MYC	-1.092	1.15E-70	1.65E-67	6679	8259	16440	15402
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RIMS3	-1.474	1.04E-60	8.75E-58	472	565	1459	1423
GALNT5	-2.787	1.01E-59	8.24E-57	49	66	396	399
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BBC3	-1.385	3.26E-40	8.83E-38	382	442	1140	1012
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SPATA18	-1.783	6.35E-40	1.66E-37	134	194	578	551
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ZDHHC22	-1.38	2.24E-39	5.74E-37	444	515	1358	1139
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ABCG1	-1.991	1.08E-32	1.73E-30	73	80	314	295
ST8SIA4	-1.518	1.15E-32	1.85E-30	215	222	617	635
EGFR	-1.074	1.30E-32	2.06E-30	507	589	1170	1137
ACVR1C	-1.377	1.32E-32	2.08E-30	294	401	851	955
NRCAM	-1.04	1.79E-32	2.79E-30	677	738	1488	1421
NTRK2	-1.931	2.84E-32	4.42E-30	86	146	464	421
GPR160	-1.031	3.08E-32	4.75E-30	610	728	1329	1406
LRRTM4	-1.101	3.09E-32	4.75E-30	668	701	1444	1492
NOG	-2.397	3.46E-32	5.29E-30	66	51	330	287
AMIGO2	-1.985	1.03E-31	1.52E-29	76	102	386	319
FAS	-1.414	1.06E-31	1.56E-29	196	264	609	617
GLRX	-1.294	3.92E-31	5.58E-29	253	316	692	704
GALNT12	-1.486	5.75E-31	8.07E-29	184	205	531	559
SLITRK1	-3.028	6.39E-31	8.92E-29	20	29	234	167
RP11-558F24.4	-1.297	8.31E-31	1.14E-28	287	391	802	864
TNFAIP8	-1.082	9.97E-31	1.36E-28	474	542	1109	1042
CD24P4	-1.374	1.21E-30	1.65E-28	223	251	631	598
SULF1	-1.261	1.51E-30	2.04E-28	472	683	1515	1254
AK7	-2.015	2.20E-30	2.93E-28	71	107	398	322
NDNF	-1.073	3.79E-30	4.99E-28	595	644	1365	1242

BTG2	-1.087	4.10E-30	5.35E-28	813	917	2018	1657
TSPAN2	-1.954	4.79E-30	6.19E-28	72	75	293	277
ASIC1	-1.469	4.88E-30	6.27E-28	335	309	904	879
SLC25A27	-1.626	6.59E-30	8.36E-28	250	291	729	941
DISC1	-1.171	6.93E-30	8.75E-28	470	566	1084	1249
IGFBP5	-1.562	7.36E-30	9.26E-28	1116	909	3232	2749
42252	-1.022	9.49E-30	1.19E-27	477	580	1087	1060
SOSTDC1	-1.736	1.37E-29	1.69E-27	100	110	345	355
PCK2	-1.139	1.76E-29	2.14E-27	652	646	1412	1446
RP4-717I23.3	-1.133	1.97E-29	2.39E-27	526	571	1145	1261
S1PR1	-1.481	2.75E-29	3.31E-27	147	186	481	449
LPL	-1.862	4.26E-29	5.04E-27	75	83	293	282
IFIT1	-1.45	5.24E-29	6.12E-27	203	208	567	556
RGS16	-1.035	6.22E-29	7.19E-27	526	614	1130	1206
RNASE4	-1.589	6.40E-29	7.38E-27	151	172	528	444
FZD4	-1.043	7.19E-29	8.25E-27	507	638	1132	1228
LPPR3	-1.805	8.65E-29	9.80E-27	92	93	323	324
MT2A	-1.276	8.70E-29	9.82E-27	342	357	890	803
ZNF83	-1.62	1.43E-28	1.57E-26	108	161	413	414
MAML2	-1.892	1.61E-28	1.76E-26	132	119	428	504
GNG2	-1.784	2.07E-28	2.24E-26	93	95	322	326
C16orf74	-1.967	2.36E-28	2.53E-26	65	76	299	253
NR5A2	-1.34	5.39E-28	5.54E-26	225	267	665	581
CFHR3	-2.641	6.18E-28	6.33E-26	25	25	165	148
PLD1	-1.307	1.19E-27	1.20E-25	259	285	713	633
PRODH	-2.216	1.50E-27	1.50E-25	35	55	222	197
CCDC74B	-1.283	1.70E-27	1.67E-25	287	297	727	694
TMCC3	-1.101	1.74E-27	1.70E-25	379	430	869	866
LIG1	-1.175	1.79E-27	1.75E-25	276	356	718	709
CDH10	-2.393	2.01E-27	1.95E-25	26	42	187	171
ACSF2	-1.288	2.46E-27	2.37E-25	262	286	648	690
HPGD	-1.334	3.01E-27	2.90E-25	181	237	522	532
FAM129A	-1.008	3.84E-27	3.67E-25	444	587	1036	1037
CNTNAP2	-1.089	4.13E-27	3.91E-25	841	884	2018	1653
COMTD1	-1.068	6.51E-27	6.10E-25	435	514	1053	937
DPM3	-1.097	7.14E-27	6.65E-25	392	486	998	880
CCBL1	-1.47	9.93E-27	9.15E-25	131	158	411	390
HTRA1	-1.753	1.20E-26	1.10E-24	81	90	300	277
DCHS2	-1.883	1.25E-26	1.15E-24	56	80	256	246
ANKRD34B	-1.355	1.56E-26	1.42E-24	202	272	652	561
ST3GAL1	-1.028	1.66E-26	1.49E-24	482	577	1152	1008

CTD-2267D19.3	-1.081	2.12E-26	1.89E-24	349	418	808	815
PDE7B	-2.68	3.34E-26	2.94E-24	22	22	149	134
PROCR	-1.001	3.60E-26	3.15E-24	424	552	1002	951
CORO6	-1.594	3.93E-26	3.43E-24	123	184	503	424
NEAT1	-1.217	4.68E-26	4.07E-24	7904	8980	16343	22896
COL4A4	-1.417	4.88E-26	4.23E-24	151	198	447	485
MSTN	-2.345	6.04E-26	5.19E-24	29	35	161	165
CRYL1	-2.046	7.15E-26	6.12E-24	48	56	205	225
CORO2A	-1.327	8.80E-26	7.46E-24	230	360	759	722
CAMK2B	-1.439	9.22E-26	7.80E-24	137	182	418	447
CGNL1	-1.162	1.16E-25	9.72E-24	312	445	825	869
SLITRK3	-1.151	1.27E-25	1.05E-23	268	356	689	697
GPRC5B	-1.014	1.46E-25	1.20E-23	459	521	1036	944
FAM81A	-1.322	1.52E-25	1.25E-23	189	208	501	492
TRIM7	-1.13	1.63E-25	1.33E-23	285	377	747	702
YPEL3	-1.36	2.56E-25	2.08E-23	207	218	577	514
EFEMP1	-1.271	3.22E-25	2.60E-23	189	232	525	491
EPAS1	-1.031	3.23E-25	2.60E-23	398	459	866	886
TMEM74B	-1.465	5.87E-25	4.66E-23	124	144	365	375
TFCP2L1	-1.138	8.19E-25	6.42E-23	260	337	653	661
LMOD1	-1.281	1.57E-24	1.20E-22	261	414	808	833
DKK2	-2.365	1.92E-24	1.46E-22	39	35	214	168
HMCN1	-1.274	2.10E-24	1.60E-22	248	262	654	580
C1QL4	-1.571	2.26E-24	1.71E-22	104	111	320	319
MBL1P	-1.03	2.37E-24	1.79E-22	497	648	1088	1251
MRAP2	-1.654	3.55E-24	2.62E-22	97	96	303	305
HIST1H3F	-1.045	4.10E-24	3.00E-22	563	635	1357	1115
IPCEF1	-2.212	7.22E-24	5.12E-22	32	38	158	167
BAI2	-1.031	8.07E-24	5.70E-22	345	409	762	779
SSH3	-1.197	8.48E-24	5.97E-22	252	325	712	611
SPOCK3	-1.165	9.67E-24	6.74E-22	290	425	775	829
KIAA1456	-1.146	1.02E-23	7.11E-22	242	331	633	635
ERAP2	-2.54	1.63E-23	1.12E-21	19	24	129	122
DPP4	-1.303	1.95E-23	1.33E-21	182	233	552	472
PPAPDC2	-1.036	2.01E-23	1.37E-21	318	417	771	736
RP11-551L14.1	-1.195	2.05E-23	1.39E-21	232	254	569	544
NYNRIN	-1.113	2.20E-23	1.49E-21	558	531	1219	1137
KIFC2	-1.123	2.92E-23	1.95E-21	242	318	608	612
NDST4	-1.619	3.01E-23	2.01E-21	75	102	283	261
BMP3	-1.621	3.54E-23	2.34E-21	120	109	350	355
SOWAHA	-1.276	4.56E-23	2.99E-21	244	247	626	563

TCF24	-1.111	6.61E-23	4.31E-21	277	314	664	613
PLEKHH2	-1.29	8.03E-23	5.19E-21	274	427	797	918
NPY1R	-1.005	8.17E-23	5.27E-21	457	485	977	914
JAKMIP1	-1.795	8.61E-23	5.54E-21	72	95	258	322
GBP1P1	-1.609	1.16E-22	7.36E-21	98	96	294	298
PLA2G4A	-1.093	1.21E-22	7.63E-21	598	865	1403	1718
GCNT2	-1.691	1.21E-22	7.66E-21	110	97	323	346
YPEL5	-1.013	1.37E-22	8.61E-21	564	753	1213	1445
EDIL3	-1.019	1.60E-22	1.01E-20	564	809	1287	1496
TSLP	-1.62	1.75E-22	1.09E-20	71	102	276	256
KIAA0226L	-1.361	2.01E-22	1.25E-20	152	168	394	428
NMRK1	-1.527	2.19E-22	1.36E-20	146	204	445	564
ARHGAP24	-1.281	2.81E-22	1.73E-20	147	183	408	394
RNF165	-1.986	3.23E-22	1.97E-20	35	56	179	182
NOXA1	-1.176	3.58E-22	2.18E-20	189	245	490	491
SLC46A3	-1.072	4.64E-22	2.80E-20	310	435	756	810
HAGHL	-1.288	5.26E-22	3.14E-20	238	228	573	565
FAM78A	-1.235	7.04E-22	4.15E-20	222	264	625	519
CCDC85A	-1.947	8.16E-22	4.78E-20	43	65	192	225
SH2D5	-1.083	9.70E-22	5.63E-20	241	307	575	586
HES7	-1.652	2.21E-21	1.25E-19	119	110	397	323
FILIP1	-2.571	2.89E-21	1.63E-19	19	31	127	171
SLFN5	-1.491	3.51E-21	1.97E-19	139	224	465	556
TTYH2	-1.168	3.77E-21	2.11E-19	188	261	519	490
PLA2G7	-2.965	5.50E-21	3.02E-19	9	14	94	87
EFNB3	-1.192	6.06E-21	3.32E-19	209	235	541	474
SNCAIP	-1.564	6.67E-21	3.64E-19	70	97	251	243
PALMD	-1.878	7.26E-21	3.95E-19	47	50	184	173
SYTL4	-1.431	7.52E-21	4.08E-19	155	143	406	398
TCP11L2	-1.591	8.65E-21	4.66E-19	99	96	315	273
PPARGC1A	-1.67	9.00E-21	4.84E-19	60	96	261	236
FLJ23152	-2.965	1.02E-20	5.47E-19	13	10	90	91
MYT1	-1.75	1.36E-20	7.24E-19	57	93	234	271
MME	-1.201	1.39E-20	7.34E-19	166	238	464	465
PPFIA4	-1.122	1.61E-20	8.46E-19	207	294	548	543
RP11-124L5.7	-1.129	1.69E-20	8.84E-19	221	250	500	530
OXGR1	-2.016	1.85E-20	9.64E-19	32	64	188	201
PADI2	-1.574	2.17E-20	1.13E-18	70	85	232	230
NTNG1	-1.317	2.25E-20	1.16E-18	150	185	387	448
RNF144B	-1.199	2.48E-20	1.27E-18	231	372	700	685
BTN3A3	-1.075	2.89E-20	1.47E-18	227	267	517	524

KCNAB2	-1.763	3.12E-20	1.58E-18	55	83	259	210
BCKDHB	-1.05	4.51E-20	2.24E-18	349	544	939	910
NTN4	-1.629	6.45E-20	3.13E-18	68	79	215	240
ZNF467	-1.669	1.01E-19	4.85E-18	69	68	214	222
TLR1	-1.363	1.14E-19	5.45E-18	98	132	293	299
LRRC3	-1.015	1.20E-19	5.71E-18	256	312	595	553
KIAA1217	-1.299	1.37E-19	6.44E-18	117	154	326	341
DLX6-AS1	-1.023	1.53E-19	7.22E-18	265	298	582	562
FRY	-1.347	1.56E-19	7.35E-18	108	145	310	334
SLC9A9	-1.613	3.13E-19	1.43E-17	86	130	291	370
FMNL1	-1.181	3.41E-19	1.56E-17	156	217	440	406
C12orf39	-1.491	3.88E-19	1.76E-17	76	90	241	226
DOC2A	-1.055	4.10E-19	1.85E-17	321	323	679	659
RP11-445F12.1	-1.523	4.26E-19	1.92E-17	103	122	287	360
SERINC4	-1.267	4.77E-19	2.14E-17	124	153	349	318
NOTCH3	-1.213	5.45E-19	2.43E-17	318	292	748	666
ANKRD63	-1.224	7.17E-19	3.17E-17	148	166	384	350
LBH	-1.303	7.34E-19	3.24E-17	122	171	388	335
TTC18	-1.21	7.91E-19	3.48E-17	171	262	481	521
PDK4	-1.729	8.25E-19	3.62E-17	146	119	501	378
MAPK15	-1.226	1.11E-18	4.80E-17	133	155	336	338
ARHGEF17	-1.046	1.18E-18	5.09E-17	292	433	797	700
TRAM1L1	-1.286	1.21E-18	5.23E-17	153	156	362	392
CCDC74A	-1.035	1.42E-18	6.02E-17	363	390	841	702
PIK3CD	-1.183	1.48E-18	6.28E-17	152	210	397	425
OGDHL	-1.094	1.55E-18	6.55E-17	250	273	601	516
ROR2	-1.195	1.62E-18	6.80E-17	170	182	423	383
HBQ1	-1.561	1.65E-18	6.94E-17	100	94	313	260
TNS3	-1.038	2.17E-18	8.98E-17	302	470	783	802
NKX1-2	-1.032	2.72E-18	1.12E-16	302	323	681	597
HPSE	-1.188	3.34E-18	1.36E-16	151	172	358	378
ADAMTS6	-1.347	3.69E-18	1.50E-16	135	155	334	404
CDH1	-1.506	3.78E-18	1.54E-16	81	102	288	232
RP11-347C18.3	-2.117	3.90E-18	1.58E-16	21	36	122	126
PDE3A	-1.116	4.38E-18	1.77E-16	176	258	467	474
MIR34A	-2.007	6.27E-18	2.50E-16	29	43	161	129
PRSS35	-1.201	6.37E-18	2.53E-16	138	159	334	349
FST	-2.365	6.56E-18	2.60E-16	14	33	132	111
CCDC110	-1.515	6.72E-18	2.66E-16	68	89	242	207
CCDC3	-1.278	8.46E-18	3.32E-16	166	250	562	447
UNC5A	-2.414	8.99E-18	3.49E-16	12	25	100	98

SDAD1P1	-1.601	1.12E-17	4.34E-16	93	77	264	252
CFD	-1.225	1.12E-17	4.34E-16	296	262	684	621
HMGCLL1	-1.83	1.40E-17	5.37E-16	46	101	254	269
FXYD6	-1.529	1.57E-17	6.01E-16	74	79	209	233
BMP4	-1.044	1.72E-17	6.54E-16	252	289	605	511
MAPK4	-1.408	1.72E-17	6.54E-16	73	104	237	233
GDF10	-2.632	2.10E-17	7.89E-16	8	22	92	95
RP11-660L16.2	-1.151	2.28E-17	8.55E-16	156	170	366	358
ALS2CL	-2.398	2.38E-17	8.86E-16	24	39	130	203
IMPA2	-1.045	2.44E-17	9.08E-16	224	242	500	462
SLCO4C1	-1.1	3.20E-17	1.17E-15	265	255	555	560
IGSF10	-1.382	3.20E-17	1.17E-15	144	126	359	345
CDA	-2.375	3.30E-17	1.21E-15	12	26	101	97
RP11-12A2.3	-3.076	3.76E-17	1.37E-15	17	5	90	97
SCN4B	-2.02	3.99E-17	1.45E-15	37	41	184	133
RP11-326C3.7	-1.765	4.96E-17	1.79E-15	51	48	159	178
GLT8D2	-1.031	5.23E-17	1.88E-15	181	227	424	410
ABCC6P1	-1.465	5.36E-17	1.92E-15	80	80	224	218
PTP4A3	-1.42	5.60E-17	1.99E-15	95	106	297	241
DNAH6	-1.41	7.02E-17	2.48E-15	139	160	341	454
NKX2-1	-1.233	1.04E-16	3.59E-15	111	139	311	277
PGM5	-1.883	1.23E-16	4.25E-15	27	42	128	127
LYPD6	-1.044	1.32E-16	4.53E-15	277	304	552	646
AC116614.1	-1.568	1.37E-16	4.71E-15	49	75	189	179
TFEB	-1.209	2.32E-16	7.75E-15	106	137	289	273
PDE1A	-1.648	3.08E-16	1.02E-14	63	61	178	211
KCNJ4	-1.921	3.56E-16	1.17E-14	34	34	139	119
HHAT	-1.022	4.04E-16	1.32E-14	210	242	491	427
SIDT1	-1.743	4.25E-16	1.38E-14	45	43	151	144
GPR137C	-1.133	4.29E-16	1.39E-14	218	231	450	535
COL24A1	-1.277	5.02E-16	1.61E-14	187	164	447	404
PIK3IP1	-1.379	5.28E-16	1.68E-14	74	117	262	235
INPP4B	-1.034	5.51E-16	1.75E-14	181	235	407	445
FTLP12	-1.214	5.83E-16	1.85E-14	111	132	298	266
LONRF3	-1.028	6.08E-16	1.93E-14	169	207	380	387
COL21A1	-1.93	6.87E-16	2.17E-14	28	33	122	111
ELFN1	-1.825	7.31E-16	2.29E-14	69	55	251	189
TMEM37	-1.636	7.35E-16	2.30E-14	44	53	158	144
KCNK1	-1.168	7.61E-16	2.38E-14	131	147	330	295
ABCC6P2	-1.691	8.44E-16	2.62E-14	53	59	160	202
FAM70A	-1.2	9.02E-16	2.79E-14	200	183	463	417

KCNV1	-1.976	1.04E-15	3.21E-14	61	38	194	196
LAMP3	-1.512	1.22E-15	3.74E-14	53	64	169	165
CDH3	-2.312	1.36E-15	4.13E-14	44	34	243	145
CLYBL	-1.468	1.88E-15	5.67E-14	92	137	272	362
TSPAN11	-1.616	2.34E-15	6.96E-14	63	69	177	228
RP11-657O9.1	-1.567	2.53E-15	7.51E-14	78	143	288	367
ABAT	-1.112	3.27E-15	9.61E-14	148	233	405	419
RP11-182J1.14	-1.136	3.66E-15	1.07E-13	186	203	388	467
C11orf45	-1.525	3.83E-15	1.12E-13	72	71	228	184
NEURL1B	-1.187	4.97E-15	1.44E-13	113	143	316	267
BIRC3	-1.754	5.97E-15	1.71E-13	41	38	130	137
RP11-696N14.1	-1.266	6.07E-15	1.74E-13	110	107	258	264
ST8SIA6	-2.023	6.75E-15	1.92E-13	27	25	113	99
DENND1C	-1.535	6.79E-15	1.93E-13	60	70	211	166
USH1G	-1.777	6.80E-15	1.93E-13	36	47	161	124
RP1-45C12.1	-2.256	7.45E-15	2.11E-13	14	25	84	103
PROX1	-1.082	9.23E-15	2.59E-13	191	194	436	379
RCAN2	-1.645	9.52E-15	2.66E-13	37	70	165	170
EDNRB	-2.025	1.06E-14	2.93E-13	19	30	107	93
MRPL23-AS1	-3.38	1.19E-14	3.27E-13	3	7	48	58
SIRT4	-1.194	1.22E-14	3.36E-13	99	119	241	258
SNAP91	-1.261	1.37E-14	3.75E-13	90	101	220	238
STAT4	-2.017	1.46E-14	3.97E-13	17	33	105	98
SLC38A4	-2.669	1.82E-14	4.88E-13	6	16	78	63
PLA2G6	-1.17	1.84E-14	4.94E-13	195	316	514	636
ASNAP1	-1.076	2.50E-14	6.55E-13	178	228	386	470
CNPY1	-1.168	2.58E-14	6.78E-13	93	128	250	247
KCNH7	-1.596	3.46E-14	8.97E-13	52	66	155	202
<b>SOX21</b>	<b>-1.198</b>	<b>3.48E-14</b>	<b>9.01E-13</b>	<b>115</b>	<b>196</b>	<b>373</b>	<b>341</b>
ADAMTS7	-1.213	4.03E-14	1.04E-12	97	103	236	228
LINC00621	-1.023	5.06E-14	1.29E-12	198	203	433	382
RP11-461C13.1	-2.48	5.29E-14	1.35E-12	14	12	67	79
GNG7	-1.063	6.05E-14	1.53E-12	205	198	404	438
ICAM1	-1.418	7.45E-14	1.85E-12	122	95	292	288
IFI35	-1.463	8.46E-14	2.09E-12	84	70	204	221
FBXO2	-1.724	9.58E-14	2.35E-12	41	40	149	119
PQLC3	-1.352	1.02E-13	2.49E-12	67	77	197	171
RPRML	-1.5	1.06E-13	2.59E-12	65	59	189	162
FRMPD1	-1.414	1.06E-13	2.59E-12	54	69	157	171
RP11-627G18.3	-1.982	1.07E-13	2.60E-12	20	32	115	91
PPP4R4	-1.145	1.12E-13	2.74E-12	117	147	268	316



RP11-136K7.2	-2.884	1.82E-13	4.36E-12	9	6	55	57
PLSCR4	-1.009	1.88E-13	4.48E-12	149	165	323	309
ONECUT1	-1.172	1.91E-13	4.56E-12	91	109	237	214
ART5	-1.084	2.05E-13	4.87E-12	108	131	258	249
AQP4	-1.753	2.41E-13	5.68E-12	44	44	173	124
MDGA1	-1.425	2.97E-13	6.93E-12	50	78	161	183
C4orf34	-1.116	3.11E-13	7.24E-12	154	237	382	466
FIBIN	-2.303	3.58E-13	8.29E-12	14	14	72	67
PTPRZ1	-1.501	3.85E-13	8.85E-12	61	124	242	282
FBXO36	-1.096	4.19E-13	9.56E-12	100	124	240	239
ALPL	-1.286	4.23E-13	9.63E-12	78	115	263	208
MEGF10	-1.509	4.72E-13	1.07E-11	42	71	175	147
LINC00173	-1.951	4.78E-13	1.08E-11	22	35	129	92
KCNJ3	-1.761	5.43E-13	1.22E-11	29	70	175	161
CCDC64	-1.281	7.82E-13	1.73E-11	61	80	175	168
RORB	-1.069	7.91E-13	1.75E-11	117	157	311	264
GAS6	-1.178	8.13E-13	1.79E-11	81	108	205	223
DRAM1	-1.453	9.41E-13	2.05E-11	58	54	151	156
MLXIPL	-1.194	9.97E-13	2.17E-11	111	114	236	279
ITGA8	-1.272	1.01E-12	2.20E-11	65	103	196	210
GRID2	-1.379	1.03E-12	2.25E-11	92	89	206	265
CHRNA4	-1.755	1.22E-12	2.63E-11	29	31	97	106
STYK1	-2.948	1.30E-12	2.79E-11	5	14	55	93
LIF	-1.092	1.47E-12	3.15E-11	111	160	315	263
SLC2A4	-1.126	1.56E-12	3.33E-11	117	129	247	290
MIR210HG	-1.145	1.71E-12	3.61E-11	100	150	304	249
EML2	-1.031	1.80E-12	3.79E-11	119	176	293	310
PDE4B	-1.299	2.07E-12	4.32E-11	56	78	172	158
AC011242.6	-1.627	2.21E-12	4.61E-11	33	42	107	125
TRPM6	-1.509	2.31E-12	4.80E-11	36	51	126	122
GRB14	-1.085	2.83E-12	5.79E-11	129	125	272	267
SLC24A4	-1.276	2.89E-12	5.90E-11	90	80	209	203
RTN2	-1.067	3.61E-12	7.29E-11	100	128	254	224
ERICH2	-1.337	5.81E-12	1.15E-10	51	91	182	177
DLX5	-1.033	5.81E-12	1.15E-10	105	150	273	249
CR2	-1.011	6.39E-12	1.25E-10	106	138	254	238
TLR3	-2.531	6.40E-12	1.25E-10	8	10	55	50
RASSF6	-1.929	6.42E-12	1.26E-10	26	24	83	108
ZNF385B	-1.176	7.41E-12	1.44E-10	80	104	192	224
THSD7A	-1.62	7.63E-12	1.48E-10	40	36	126	108
AFAP1L2	-1.457	8.55E-12	1.64E-10	52	75	149	200

FUT9	-1.845	8.77E-12	1.68E-10	39	26	109	125
PIK3R5	-1.79	9.18E-12	1.75E-10	20	38	110	91
RP11-159H10.3	-1.542	9.39E-12	1.79E-10	30	53	126	116
FREM1	-2.572	1.00E-11	1.91E-10	10	9	64	50
TDRD6	-1.557	1.03E-11	1.96E-10	40	72	143	187
ADAMTS2	-1.015	1.13E-11	2.14E-10	134	141	266	290
SYNPO	-1.352	1.14E-11	2.15E-10	45	63	135	141
RP11-480I12.4	-2.13	1.27E-11	2.38E-10	14	16	67	65
GAP43	-1.109	1.38E-11	2.56E-10	103	150	247	299
SPOCD1	-1.408	1.44E-11	2.67E-10	39	60	132	131
CEACAM1	-2.03	1.63E-11	3.00E-10	19	21	70	94
C1QTNF1	-1.558	1.65E-11	3.03E-10	50	48	167	122
AC009299.3	-1.127	1.72E-11	3.16E-10	84	132	254	218
PTPRB	-1.406	1.91E-11	3.47E-10	44	60	127	149
MIR148A	-1.096	2.01E-11	3.65E-10	161	165	306	391
TPTE2P1	-1.523	2.07E-11	3.76E-10	44	46	116	143
TMEM187	-1.203	2.12E-11	3.83E-10	79	79	191	173
CLUL1	-1.235	2.16E-11	3.89E-10	90	113	278	200
LRRK1	-1.068	2.18E-11	3.92E-10	88	107	206	203
HERC6	-1.367	2.27E-11	4.08E-10	50	53	134	132
SSPO	-1.409	2.49E-11	4.46E-10	40	54	134	116
MT1F	-2.44	2.59E-11	4.63E-10	7	12	52	52
CDKN1C	-1.055	2.81E-11	4.99E-10	96	107	213	209
RASGRP2	-1.362	2.83E-11	5.03E-10	56	54	139	144
ITGA2B	-1.329	3.05E-11	5.39E-10	64	72	194	148
HOPX	-1.448	3.17E-11	5.58E-10	57	47	145	139
AC005281.1	-1.434	4.01E-11	6.97E-10	39	56	142	115
C1orf129	-3.501	4.01E-11	6.97E-10	2	4	40	30
RP11-365D9.1	-1.531	4.30E-11	7.41E-10	48	65	133	194
HGF	-3.176	4.36E-11	7.51E-10	8	2	51	41
WBSCR27	-1.049	4.58E-11	7.88E-10	106	109	223	222
PRR15	-1.173	5.09E-11	8.69E-10	62	82	169	156
CCDC88B	-1.171	5.13E-11	8.74E-10	75	87	199	166
SYNE3	-1.063	5.19E-11	8.84E-10	85	102	194	197
CDC42BPG	-1.417	6.04E-11	1.02E-09	55	52	130	156
RP11-830F9.7	-1.655	6.33E-11	1.06E-09	33	38	131	93
CTD-2311B13.7	-2.417	6.39E-11	1.07E-09	5	16	57	56
DUX4L13	-1.519	6.52E-11	1.09E-09	31	39	104	97
C18orf56	-1.482	6.71E-11	1.12E-09	65	48	165	151
CBR3	-1.428	7.67E-11	1.27E-09	41	44	118	111
RP6-24A23.3	-1.031	8.00E-11	1.32E-09	121	149	311	241

LHX9	-1.032	8.79E-11	1.45E-09	131	223	393	331
RAG1	-1.793	9.15E-11	1.50E-09	22	22	78	75
C3	-1.293	9.94E-11	1.62E-09	45	63	138	127
OLFM2	-1.209	1.01E-10	1.65E-09	93	169	341	265
RP11-402J6.1	-1.048	1.07E-10	1.73E-09	85	105	192	201
AGTR1	-1.23	1.11E-10	1.78E-09	56	85	180	151
RP11-17G12.2	-1.777	1.11E-10	1.79E-09	21	27	74	91
FAM198B	-2.024	1.13E-10	1.82E-09	15	20	83	60
SEMA6D	-1.074	1.24E-10	2.00E-09	301	237	599	534
RGCC	-1.15	1.28E-10	2.05E-09	61	93	171	171
RIN2	-1.095	1.30E-10	2.08E-09	106	98	225	211
PDE9A	-1.23	1.31E-10	2.09E-09	88	82	181	218
H2AFJ	-1.041	1.51E-10	2.39E-09	155	171	387	284
SYT6	-1.196	1.73E-10	2.72E-09	92	113	276	194
AGXT2L1	-1.31	1.89E-10	2.95E-09	41	67	133	135
ANGPT1	-2.04	1.94E-10	3.01E-09	15	24	65	96
ACTA2	-1.202	1.98E-10	3.08E-09	77	75	164	186
NHS	-1.796	2.03E-10	3.15E-09	42	33	159	102
WDR96	-1.557	2.25E-10	3.46E-09	27	48	123	98
LMO2	-1.575	2.27E-10	3.49E-09	36	31	106	94
HMGB1P1	-1.631	2.43E-10	3.73E-09	25	33	82	98
RP11-403I13.4	-1.122	2.46E-10	3.77E-09	76	99	173	208
CLIC5	-1.643	2.74E-10	4.17E-09	20	41	100	91
USH1C	-1.462	2.94E-10	4.45E-09	32	59	116	135
NUDT7	-1.349	3.73E-10	5.56E-09	41	70	129	154
SCIN	-1.777	4.04E-10	5.99E-09	18	23	73	68
NUDT8	-1.117	4.07E-10	6.04E-09	64	83	168	151
RP11-611D20.2	-1.249	4.13E-10	6.11E-09	103	101	287	198
MEOX1	-1.816	4.17E-10	6.16E-09	17	32	100	73
FAM220CP	-1.415	4.64E-10	6.83E-09	40	42	103	116
FRK	-1.251	4.89E-10	7.16E-09	54	56	136	126
OLFML2A	-1.253	5.91E-10	8.60E-09	43	63	132	121
CCDC151	-1.338	7.02E-10	1.01E-08	103	80	264	199
GPR12	-2.147	8.96E-10	1.28E-08	8	16	55	52
FRMPD3	-1.645	9.03E-10	1.29E-08	26	26	77	86
ARL5C	-1.558	9.94E-10	1.41E-08	25	36	81	99
RP11-666A20.4	-1.022	1.02E-09	1.44E-08	114	106	231	216
PNCK	-1.628	1.07E-09	1.50E-08	29	32	110	79
TRPA1	-2.099	1.10E-09	1.54E-08	12	21	56	86
C2CD4C	-1.543	1.10E-09	1.55E-08	27	47	124	92
KCND2	-1.208	1.11E-09	1.56E-08	81	141	219	294

RP11-333E1.1	-1.198	1.26E-09	1.77E-08	57	102	170	195
RP11-168O16.1	-1.477	1.33E-09	1.85E-08	26	36	85	88
TCF21	-3.222	1.54E-09	2.13E-08	3	4	27	40
FBLN2	-1.378	1.63E-09	2.23E-08	37	51	129	100
ABLIM2	-2.216	1.66E-09	2.28E-08	20	16	109	59
NXNL2	-1.673	1.72E-09	2.35E-08	32	24	82	97
RP11-53O19.1	-1.315	1.74E-09	2.38E-08	53	49	139	115
RASSF9	-1.502	1.96E-09	2.66E-08	24	38	83	93
SGK223	-1.036	2.03E-09	2.74E-08	83	91	169	188
ALDH1A1	-1.751	2.04E-09	2.75E-08	24	24	69	93
FAM167A	-1.384	2.27E-09	3.04E-08	78	59	203	155
DKK3	-1.285	2.39E-09	3.19E-08	50	80	136	181
TLCD2	-1.274	2.48E-09	3.29E-08	88	69	174	206
AC073043.2	-1.226	2.59E-09	3.43E-08	63	57	148	133
RP11-761I4.3	-1.235	2.61E-09	3.45E-08	41	60	123	115
SLCO2A1	-3.385	2.86E-09	3.77E-08	7	0	32	43
ADAMTSL1	-2.182	3.00E-09	3.95E-08	8	13	53	43
CLEC4F	-1.535	3.13E-09	4.10E-08	22	41	85	98
DNAJC27-AS1	-2.078	3.42E-09	4.45E-08	11	13	47	55
TMEM198B	-1.135	3.48E-09	4.51E-08	125	98	235	255
ANKRD19P	-1.115	3.54E-09	4.59E-08	64	67	148	136
RP11-313D6.4	-1.307	4.22E-09	5.40E-08	37	51	101	117
CHRD	-1.195	4.28E-09	5.47E-08	44	59	118	118
GDNF-AS1	-1.778	4.33E-09	5.53E-08	50	28	154	114
C9orf106	-2.067	5.08E-09	6.42E-08	12	11	50	47
DIRC3	-1.177	5.42E-09	6.82E-08	49	61	134	115
COL9A3	-1.431	5.83E-09	7.32E-08	62	58	198	126
SFRP4	-2.533	6.05E-09	7.58E-08	6	8	48	34
ELFN2	-1.223	6.65E-09	8.26E-08	46	70	152	119
RILP	-1.214	7.41E-09	9.13E-08	82	105	265	169
SALL4	-1.059	7.69E-09	9.47E-08	77	75	159	158
C20orf96	-1.1	8.49E-09	1.04E-07	62	117	192	192
SLC35D3	-1.743	8.50E-09	1.04E-07	14	22	61	60
AC079776.7	-2.193	8.56E-09	1.05E-07	12	13	44	71
AC105020.1	-1.624	9.44E-09	1.15E-07	18	25	67	66
MYOM2	-1.092	1.03E-08	1.25E-07	72	85	191	144
XKR5	-1.535	1.20E-08	1.44E-07	18	35	76	78
CT476828.12	-2.064	1.21E-08	1.45E-07	14	10	52	49
MAF	-1.185	1.23E-08	1.47E-07	65	69	176	129
SECTM1	-1.109	1.47E-08	1.74E-07	49	64	121	123
MYOD1	-1.591	1.50E-08	1.77E-07	20	24	69	64

NOTUM	-1.699	1.54E-08	1.81E-07	29	22	97	69
UGT2B4	-2.139	1.55E-08	1.82E-07	15	8	53	49
FAM159B	-1.438	1.66E-08	1.94E-07	28	35	77	94
FAM123A	-1.868	1.69E-08	1.98E-07	11	22	53	68
CCM2L	-3.663	1.78E-08	2.07E-07	1	3	19	34
FOXL1	-1.539	1.84E-08	2.14E-07	49	30	121	109
PPP1R14A	-1.083	1.98E-08	2.29E-07	51	66	127	121
NEGR1	-1.029	2.13E-08	2.44E-07	58	87	145	151
FAM131B	-2.139	2.13E-08	2.44E-07	14	9	58	44
KLHL32	-1.143	2.20E-08	2.52E-07	118	96	208	265
CFHR1	-1.936	2.49E-08	2.82E-07	11	21	50	73
COL4A3	-1.433	2.65E-08	2.99E-07	23	48	90	102
RP11-806O11.1	-1.387	2.72E-08	3.06E-07	24	47	97	89
RFX6	-1.704	3.06E-08	3.42E-07	13	24	58	63
FBXL16	-1.08	3.21E-08	3.59E-07	70	68	159	133
RNF175	-1.497	3.56E-08	3.95E-07	19	34	79	71
ATOH1	-1.942	3.72E-08	4.11E-07	13	16	67	45
SOCS3	-1.24	4.06E-08	4.46E-07	48	45	120	100
RP11-490M8.1	-1.794	4.10E-08	4.49E-07	13	18	51	57
AC012123.1	-1.442	4.66E-08	5.05E-07	36	29	82	95
AC068057.1	-2.777	4.70E-08	5.08E-07	4	4	30	26
CXCL3	-1.551	4.96E-08	5.33E-07	22	27	82	62
ACPP	-3.521	4.99E-08	5.36E-07	2	2	22	26
ADRB2	-1.155	5.15E-08	5.53E-07	47	49	111	103
DUX4L6	-2.093	5.19E-08	5.57E-07	11	9	44	42
ABCB4	-1.279	5.27E-08	5.65E-07	29	57	106	103
TMEM178A	-1.08	5.46E-08	5.82E-07	51	70	119	137
NMNAT3	-1.069	5.47E-08	5.83E-07	66	64	145	128
TGM2	-1.813	6.00E-08	6.35E-07	14	24	53	81
PTPN5	-1.854	6.23E-08	6.59E-07	15	15	63	46
ST8SIA1	-1.206	6.31E-08	6.66E-07	34	50	95	99
C17orf72	-1.801	6.40E-08	6.75E-07	10	22	51	61
ENPP3	-3.279	6.44E-08	6.78E-07	3	3	20	40
AC007255.8	-2.166	6.61E-08	6.94E-07	5	12	38	39
C8orf73	-1.133	6.82E-08	7.16E-07	51	51	108	116
GRID2IP	-1.435	7.00E-08	7.34E-07	20	35	73	76
MATN1-AS1	-1.263	7.05E-08	7.39E-07	32	60	102	119
INSC	-1.395	7.34E-08	7.67E-07	23	40	91	75
FAM26E	-3.911	8.60E-08	8.87E-07	2	2	18	45
RP11-42I10.1	-2.345	8.81E-08	9.06E-07	8	7	32	45
CT476828.13	-1.93	8.98E-08	9.22E-07	8	16	47	45

CSRP1	-1.866	9.07E-08	9.30E-07	40	18	94	118
RP11-61L23.2	-1.338	9.21E-08	9.45E-07	30	32	82	75
BCL11B	-1.62	9.53E-08	9.75E-07	91	51	265	172
CXCL12	-1.165	1.04E-07	1.05E-06	123	103	305	202
OLFML2B	-1.179	1.06E-07	1.08E-06	37	49	105	90
POM121L2	-3.017	1.07E-07	1.08E-06	2	4	22	28
SEPP1	-1.268	1.08E-07	1.09E-06	32	58	122	95
KNDC1	-1.609	1.15E-07	1.16E-06	14	37	86	70
CTB-52I2.8	-1.005	1.40E-07	1.39E-06	59	66	132	119
PRR16	-1.08	1.40E-07	1.39E-06	70	112	228	157
XX-2136C48.9	-1.481	1.41E-07	1.40E-06	26	33	99	66
DUX4L2	-1.73	1.41E-07	1.40E-06	13	17	50	50
RASA4CP	-1.063	1.42E-07	1.41E-06	91	74	186	159
RP11-115D19.1	-1.264	1.46E-07	1.45E-06	43	36	95	95
PAX2	-1.593	1.54E-07	1.52E-06	16	21	58	54
RNA5SP93	-3.459	1.54E-07	1.52E-06	2	2	20	26
AP003774.4	-3.416	1.57E-07	1.54E-06	4	2	46	20
LIPH	-1.694	1.77E-07	1.73E-06	11	21	54	50
CTD-3105H18.8	-1.379	1.85E-07	1.80E-06	32	34	73	99
HECW1	-1.418	1.99E-07	1.92E-06	21	44	99	75
SPATA6L	-1.01	2.01E-07	1.94E-06	55	75	144	118
TTLL1	-1.074	2.02E-07	1.94E-06	42	60	112	103
RP11-680F8.1	-1.036	2.04E-07	1.96E-06	46	68	122	112
AP003068.23	-1.233	2.05E-07	1.97E-06	36	43	83	103
FER1L4	-1.125	2.05E-07	1.97E-06	66	104	150	221
VN1R20P	-7.375	2.22E-07	2.12E-06	0	0	11	22
KB-431C1.4	-1.464	2.23E-07	2.13E-06	59	34	139	118
TMEM155	-1.203	2.25E-07	2.15E-06	63	65	179	116
GHR	-1.218	2.28E-07	2.17E-06	29	56	100	98
NIPSNAP3B	-1.291	2.39E-07	2.28E-06	31	40	100	74
NPFFR2	-2.005	2.45E-07	2.33E-06	5	23	61	52
RP11-345F18.1	-1.815	2.47E-07	2.35E-06	9	17	44	48
CT476828.10	-1.779	2.50E-07	2.37E-06	17	12	48	52
RP11-458I7.1	-1.024	2.55E-07	2.42E-06	55	58	117	113
AC009831.1	-1.866	2.72E-07	2.56E-06	10	14	40	48
EBF2	-1.448	2.75E-07	2.59E-06	75	44	186	139
CT476828.3	-1.846	2.75E-07	2.59E-06	15	11	47	47
AC073109.2	-3.608	2.86E-07	2.69E-06	2	2	17	34
KREMEN2	-1.282	2.87E-07	2.69E-06	57	49	154	104
CXCL6	-1.833	2.96E-07	2.77E-06	10	14	45	41
RP11-1C8.4	-1.145	3.00E-07	2.80E-06	40	44	94	92

SYNPO2	-1.045	3.02E-07	2.82E-06	42	64	112	107
WNT2	-2.395	3.06E-07	2.86E-06	7	9	56	29
AC135983.1	-1.005	3.07E-07	2.86E-06	49	77	122	131
FAM90A12P	-1.984	3.36E-07	3.11E-06	17	19	97	46
RP11-1114A5.4	-1.124	3.37E-07	3.11E-06	69	135	185	260
PIGZ	-1.377	3.37E-07	3.11E-06	29	29	84	67
CFH	-1.678	3.70E-07	3.39E-06	15	18	47	59
RP11-81N13.1	-1.081	3.72E-07	3.41E-06	40	71	125	110
RP11-433A10.1	-1.739	4.15E-07	3.78E-06	25	18	56	88
FMO6P	-2.327	4.34E-07	3.94E-06	5	7	28	33
AMBN	-1.076	4.91E-07	4.42E-06	40	51	98	94
CTD-2206N4.4	-1.358	5.02E-07	4.51E-06	23	28	67	64
HS3ST5	-1.725	5.23E-07	4.70E-06	10	18	49	44
RP11-771K4.1	-2.234	5.51E-07	4.93E-06	6	10	47	29
DUX4L15	-1.545	5.57E-07	4.97E-06	18	23	70	50
RP11-307C12.11	-1.146	5.68E-07	5.05E-06	42	65	139	98
EMID2	-1.159	5.73E-07	5.09E-06	60	149	245	222
FOXQ1	-1.467	5.83E-07	5.17E-06	23	21	57	65
APLN	-1.82	5.95E-07	5.27E-06	11	37	105	65
RP3-525N10.2	-2.085	6.11E-07	5.39E-06	12	6	38	39
PRPH	-1.066	6.24E-07	5.50E-06	39	65	117	101
BCAS4	-1.309	6.25E-07	5.50E-06	24	32	75	64
RP11-63P12.6	-1.319	6.45E-07	5.67E-06	24	42	72	93
AC011841.1	-1.69	7.11E-07	6.22E-06	11	18	44	50
LPPR5	-1.474	7.15E-07	6.26E-06	30	21	67	75
STX11	-1.271	7.45E-07	6.49E-06	26	63	110	105
CT476828.11	-1.713	7.48E-07	6.52E-06	12	15	43	46
RNF144A-AS1	-1.75	7.67E-07	6.66E-06	14	15	41	57
CDNF	-1.306	7.73E-07	6.71E-06	26	39	69	92
DKK1	-1.406	7.87E-07	6.82E-06	30	48	131	76
AC131097.3	-2.654	7.99E-07	6.91E-06	2	8	41	23
TNS1	-1.382	8.06E-07	6.96E-06	36	31	104	71
PDCL3P4	-1.074	8.37E-07	7.20E-06	44	58	95	120
SRPX	-2.195	8.65E-07	7.43E-06	6	10	29	45
GCNT4	-1.272	9.34E-07	7.99E-06	23	51	92	87
RP11-293M10.6	-1.223	9.42E-07	8.04E-06	51	38	113	95
PTGDS	-1.991	9.57E-07	8.16E-06	18	7	47	53
OTOG	-2.402	9.70E-07	8.26E-06	2	9	28	31
DUX4L4	-1.624	9.98E-07	8.45E-06	16	15	46	50
RP11-328M4.2	-1.204	1.01E-06	8.55E-06	50	38	108	95
LCP1	-1.955	1.03E-06	8.73E-06	12	17	75	38

RP13-401N8.1	-1.105	1.07E-06	9.07E-06	52	52	97	127
CTD-2349P21.6	-1.041	1.12E-06	9.39E-06	56	96	133	180
CACNA1G	-1.297	1.20E-06	1.00E-05	26	28	65	68
SCN3A	-1.153	1.26E-06	1.05E-05	35	40	76	91
DUX4L5	-1.697	1.27E-06	1.06E-05	14	13	47	41
AC140061.9	-1.45	1.32E-06	1.10E-05	24	22	55	71
ARHGAP23	-1.233	1.35E-06	1.12E-05	27	35	79	67
RASGEF1C	-1.168	1.36E-06	1.12E-05	28	40	80	73
HTR1D	-1.152	1.37E-06	1.13E-05	38	87	129	149
RP11-44F21.3	-1.084	1.39E-06	1.15E-05	53	45	102	106
DSCR6	-1.373	1.40E-06	1.15E-05	40	39	129	76
CTD-2536I1.1	-1.405	1.45E-06	1.19E-05	30	22	73	65
ARMC3	-1.632	1.46E-06	1.20E-05	20	16	47	65
COL23A1	-1.569	1.48E-06	1.21E-05	24	18	73	52
SLC25A48	-1.116	1.49E-06	1.22E-05	34	48	81	97
NTNG2	-1.886	1.61E-06	1.32E-05	16	12	65	39
GREM1	-2.65	1.63E-06	1.33E-05	2	5	22	23
DUX4L3	-1.645	1.67E-06	1.36E-05	12	16	43	45
PDE1B	-1.013	1.73E-06	1.41E-05	43	56	93	107
RP11-360O19.4	-2.327	1.74E-06	1.41E-05	2	10	36	25
LINC00403	-1.534	1.77E-06	1.44E-05	22	20	51	71
RP11-315O6.1	-2.559	1.79E-06	1.45E-05	5	4	34	20
CT476828.4	-1.643	1.81E-06	1.46E-05	16	13	46	45
KIAA1211L	-1.187	1.82E-06	1.47E-05	26	38	77	69
RP11-24M17.7	-1.22	1.83E-06	1.48E-05	26	37	66	81
IDH1-AS1	-1.773	1.85E-06	1.49E-05	20	10	52	51
RP11-392A22.2	-1.5	1.88E-06	1.52E-05	14	23	58	47
RP11-553L6.5	-1.382	1.94E-06	1.56E-05	18	31	56	72
C5	-1.046	1.99E-06	1.60E-05	36	54	95	91
TTLL6	-1.437	2.00E-06	1.61E-05	19	30	54	79
RBM24	-1.764	2.02E-06	1.62E-05	8	16	38	44
ADSSL1	-1.037	2.09E-06	1.67E-05	35	57	94	95
RP1-67M12.2	-4	2.20E-06	1.75E-05	0	2	22	13
TMEM169	-1.027	2.23E-06	1.77E-05	37	65	110	98
FLJ22184	-1.411	2.27E-06	1.80E-05	20	25	52	68
CNTN5	-1.181	2.27E-06	1.80E-05	27	47	75	93
STAB1	-1.193	2.28E-06	1.81E-05	29	40	90	68
CTD-2325P2.3	-2.877	2.28E-06	1.81E-05	2	3	20	18
ZBBX	-1.237	2.30E-06	1.82E-05	43	32	84	93
NMRK2	-2.44	2.34E-06	1.85E-05	10	2	34	32
CT476828.9	-1.664	2.51E-06	1.97E-05	13	14	39	47



RP11-16E12.1	-2.834	2.57E-06	2.02E-05	1	5	18	26
SLC2A1-AS1	-1.021	2.66E-06	2.09E-05	47	49	106	89
RP5-1109J22.1	-1.279	2.76E-06	2.15E-05	21	44	89	69
RP11-685M7.3	-1.318	2.86E-06	2.23E-05	23	25	57	63
CT476828.8	-1.611	2.91E-06	2.26E-05	15	14	48	41
CRIP3	-1.765	2.93E-06	2.28E-05	16	18	41	75
DCN	-1.522	2.93E-06	2.28E-05	18	16	47	51
KLRC4	-1.367	2.93E-06	2.28E-05	20	26	53	66
FBLL1	-1.556	2.95E-06	2.29E-05	20	20	72	46
RP11-241F15.1	-1.088	3.22E-06	2.49E-05	46	48	115	85
LINC00473	-1.889	3.22E-06	2.49E-05	8	14	32	50
ABCD2	-1.128	3.36E-06	2.59E-05	27	42	75	76
VGLL2	-1.116	3.40E-06	2.62E-05	29	41	73	79
AC079341.1	-2.697	3.41E-06	2.62E-05	2	4	20	20
C10orf54	-1.818	3.67E-06	2.80E-05	7	13	33	38
DAND5	-2.914	3.88E-06	2.96E-05	0	5	19	20
COL13A1	-1.07	3.94E-06	2.99E-05	80	68	186	125
AC104655.3	-1.85	3.95E-06	3.00E-05	6	13	37	32
CSDC2	-1.025	4.10E-06	3.11E-05	56	51	122	96
RP1-151F17.1	-1.189	4.21E-06	3.17E-05	27	40	88	65
RASL10A	-1.055	4.25E-06	3.20E-05	90	62	154	162
MDH1B	-1.049	4.27E-06	3.22E-05	53	46	95	110
DYNC111	-1.084	4.49E-06	3.37E-05	41	41	79	95
HTR6	-1.841	4.52E-06	3.39E-05	7	11	35	30
CT476828.7	-1.579	4.63E-06	3.47E-05	17	13	45	45
GAPDHP21	-1.026	4.89E-06	3.65E-05	55	76	107	160
TJP3	-1.208	5.13E-06	3.80E-05	24	30	65	60
LINC00341	-1.186	5.32E-06	3.93E-05	22	46	75	80
DUX4L10	-1.546	5.52E-06	4.07E-05	14	16	41	47
TCN2	-1.287	5.60E-06	4.12E-05	20	27	55	60
OPRL1	-1.154	5.67E-06	4.17E-05	25	36	69	67
RP11-447H19.3	-2.084	5.79E-06	4.26E-05	6	8	25	35
CALY	-1.165	5.97E-06	4.37E-05	23	38	73	64
PITX3	-1.418	6.03E-06	4.42E-05	36	20	75	75
RP11-449H11.1	-1.123	6.07E-06	4.44E-05	27	45	73	84
TNFSF4	-1.385	6.09E-06	4.45E-05	22	20	51	59
ZMAT1	-2.193	6.10E-06	4.46E-05	5	6	25	26
IGBP1P1	-1.627	6.21E-06	4.53E-05	15	14	53	37
CTC-459M5.1	-1.788	6.52E-06	4.74E-05	9	12	43	30
TRPC4	-1.641	6.80E-06	4.92E-05	14	16	37	57
KCNK13	-1.014	6.98E-06	5.05E-05	42	48	102	80

RP11-61J19.4	-1.134	7.17E-06	5.17E-05	40	36	74	93
TEPP	-1.092	7.40E-06	5.32E-05	27	55	86	89
CRB1	-1.465	7.79E-06	5.56E-05	17	43	65	101
STRA6	-1.545	8.03E-06	5.72E-05	23	31	107	51
IKZF1	-1.43	8.12E-06	5.78E-05	19	18	55	45
ZMYND15	-3.375	8.33E-06	5.92E-05	0	3	21	12
FNDC1	-1.659	8.35E-06	5.93E-05	15	14	36	56
SLC2A14	-1.105	9.37E-06	6.59E-05	37	34	72	81
CTD-3105H18.11	-1.046	9.40E-06	6.61E-05	30	44	75	78
RASAL1	-4.155	9.72E-06	6.82E-05	2	0	29	10
C1orf147	-1.948	9.88E-06	6.91E-05	6	12	26	44
ISM2	-1.047	1.00E-05	6.99E-05	48	40	93	89
CNFN	-1.067	1.06E-05	7.34E-05	66	69	177	106
RP11-317J10.2	-2.623	1.07E-05	7.43E-05	1	5	19	19
GAL3ST1	-1.122	1.09E-05	7.56E-05	27	34	63	70
RP11-573I11.2	-2.108	1.11E-05	7.72E-05	7	7	23	38
ZDHHC19	-2.504	1.12E-05	7.78E-05	4	5	35	17
CHST13	-2.799	1.14E-05	7.85E-05	1	4	15	21
HES2	-1.436	1.15E-05	7.91E-05	26	16	61	53
FMO3	-1.87	1.15E-05	7.92E-05	5	11	27	32
RP11-174O3.3	-1.894	1.24E-05	8.51E-05	6	10	33	27
RXRG	-1.931	1.26E-05	8.62E-05	4	15	30	43
PMP2	-2.279	1.26E-05	8.67E-05	7	5	39	20
RP11-315I14.5	-1.033	1.37E-05	9.35E-05	58	47	96	119
FGD5	-1.079	1.38E-05	9.43E-05	27	42	79	67
ATP8B3	-1.524	1.40E-05	9.51E-05	19	16	61	40
OGFR-AS1	-1.615	1.40E-05	9.57E-05	12	13	33	44
RP11-192P9.1	-1.67	1.41E-05	9.59E-05	8	17	34	46
CT476828.5	-1.513	1.47E-05	9.98E-05	15	15	38	48
SNCB	-1.11	1.53E-05	0.000103	80	64	193	118
CTD-2267D19.2	-1.117	1.60E-05	0.000108	25	33	64	62
FAM179A	-1.688	1.64E-05	0.00011	16	9	38	43
GDF15	-1.68	1.64E-05	0.00011	20	12	63	40
TP53TG3B	-1.746	1.65E-05	0.000111	14	10	33	48
RP11-610P16.1	-1.17	1.66E-05	0.000111	54	37	89	116
AP000351.10	-6.728	1.75E-05	0.000117	0	0	9	12
CTD-2270N23.1	-1.371	1.81E-05	0.000121	30	24	87	53
SLC22A31	-1.658	1.82E-05	0.000122	12	11	33	40
LPA	-7.651	1.83E-05	0.000122	0	0	0	40
WDR63	-1.279	1.85E-05	0.000123	26	81	118	142
DLGAP1-AS1	-1.49	1.92E-05	0.000128	14	14	38	41

DOK7	-1.295	1.99E-05	0.000132	16	23	47	49
STC1	-1.486	2.06E-05	0.000136	15	17	53	37
FMO2	-1.842	2.09E-05	0.000138	16	7	49	34
RP11-410L14.2	-1.268	2.10E-05	0.000138	18	23	48	51
LRRC9	-1.039	2.25E-05	0.000147	39	49	74	107
LRRC17	-1.211	2.27E-05	0.000148	39	27	69	84
PZP	-2.661	2.31E-05	0.000151	2	4	14	25
BCMO1	-2.585	2.46E-05	0.000159	6	1	22	21
SLC5A12	-1.059	2.46E-05	0.00016	34	35	79	65
RP11-881M11.2	-1.067	2.49E-05	0.000161	29	32	63	65
DHDH	-1.404	2.63E-05	0.000169	13	19	42	43
RP11-60I3.5	-1.577	2.63E-05	0.00017	9	14	36	33
HAPLN2	-1.709	2.65E-05	0.000171	20	8	44	48
AC093818.1	-1.008	2.69E-05	0.000173	30	38	71	66
FAM189A2	-1.27	2.70E-05	0.000174	21	27	48	68
TMEM221	-1.091	2.71E-05	0.000174	26	41	62	81
RP1-125I3.4	-2.551	2.75E-05	0.000176	0	7	23	19
LINC00308	-1.41	2.76E-05	0.000177	13	23	40	56
GPNMB	-1.208	2.79E-05	0.000179	27	27	53	72
CTD-2058B24.2	-2.282	3.02E-05	0.000192	2	11	21	43
RP11-390G14.1	-1.53	3.14E-05	0.000199	12	18	53	34
MMP2	-1.047	3.28E-05	0.000207	38	35	84	67
POU4F2	-1.557	3.29E-05	0.000208	27	15	49	75
RAPGEF4-AS1	-1.341	3.49E-05	0.00022	17	18	44	45
FGL1	-1.932	3.50E-05	0.00022	4	10	24	30
BAI1	-1.077	3.54E-05	0.000222	64	61	168	96
PCOLCE-AS1	-1.491	3.71E-05	0.000232	10	29	66	44
RP11-383H13.1	-1.324	3.72E-05	0.000233	22	29	81	47
KLRC1	-2.27	3.83E-05	0.000238	2	8	19	30
GRM4	-1.75	3.83E-05	0.000238	10	8	34	27
AC147651.3	-1.415	3.84E-05	0.000239	17	14	40	43
PCDH8	-1.295	3.90E-05	0.000242	13	26	48	48
CT476828.6	-1.729	3.96E-05	0.000246	17	7	38	42
FAM163A	-1.134	4.00E-05	0.000248	22	28	56	54
C20orf166-AS1	-1.748	4.02E-05	0.000249	12	9	43	28
TYRP1	-2.585	4.03E-05	0.00025	4	2	20	17
CTD-2281M20.1	-6.728	4.09E-05	0.000253	0	0	7	14
CT476828.14	-1.398	4.10E-05	0.000253	16	15	39	43
LMO1	-1.325	4.14E-05	0.000255	20	19	56	42
GRIA2	-3.026	4.31E-05	0.000265	2	2	22	12
GREM2	-1.652	4.33E-05	0.000266	7	11	29	28

RP11-923I11.6	-2.464	4.34E-05	0.000266	2	4	19	15
PROX1-AS1	-1.096	4.65E-05	0.000284	41	30	81	71
AC012354.6	-2.986	4.66E-05	0.000284	3	2	29	12
CASC1	-1.597	4.66E-05	0.000284	13	10	37	33
R3HDM2P1	-1.145	4.77E-05	0.00029	19	32	52	61
ST14	-3.185	5.02E-05	0.000304	1	3	29	9
RP11-1109M24.5	-1.302	5.22E-05	0.000315	19	19	53	41
AC073464.11	-1.692	5.58E-05	0.000335	14	10	30	48
AF131216.5	-1.083	5.85E-05	0.00035	20	37	58	63
PARK2	-1.035	5.95E-05	0.000355	39	38	67	91
GABRP	-3.19	6.04E-05	0.00036	0	3	10	19
GRM8	-1.878	6.05E-05	0.00036	6	8	30	22
EMP1	-1.167	6.19E-05	0.000368	30	34	90	54
BMP5	-1.597	6.22E-05	0.000369	14	9	36	34
MMD2	-2.893	6.22E-05	0.000369	2	2	16	15
SEMA4A	-1.013	6.30E-05	0.000374	35	66	83	121
RP11-594N15.3	-1.185	6.35E-05	0.000376	20	23	46	52
PDGFB	-2.221	6.76E-05	0.000399	9	2	23	29
CT476828.2	-1.499	6.80E-05	0.000401	20	11	42	46
CHRNA9	-2.125	6.81E-05	0.000401	7	5	35	18
SEL1L2	-1.191	6.90E-05	0.000406	26	26	49	70
AC006445.8	-3.147	7.07E-05	0.000415	0	4	10	27
RNA5SP162	-6.585	7.12E-05	0.000418	0	0	7	12
TCAM1P	-1.387	7.19E-05	0.000422	18	14	38	46
ODF3L2	-3.574	7.20E-05	0.000422	0	2	11	15
FAM107A	-6.508	7.21E-05	0.000423	0	0	10	8
CDK15	-3.185	7.28E-05	0.000426	2	2	28	10
RP11-444D3.1	-2.29	7.36E-05	0.000431	2	5	17	18
RSPH1	-3.14	7.47E-05	0.000437	1	2	15	13
CTC-281F24.1	-1.085	7.81E-05	0.000454	41	40	67	105
SHD	-1.131	7.83E-05	0.000456	34	28	58	78
FAM150A	-1.271	8.21E-05	0.000476	31	24	83	50
RP11-162A12.2	-1.223	8.26E-05	0.000479	16	31	46	64
DNAH10OS	-1.434	8.43E-05	0.000487	45	20	76	100
TPTE2P3	-2.43	8.76E-05	0.000505	4	4	31	13
MCF2L-AS1	-1.229	8.94E-05	0.000515	15	22	42	45
SPINK2	-1.009	9.02E-05	0.000519	25	37	60	65
PCDH11X	-1.597	9.02E-05	0.000519	5	18	35	35
SCGB3A2	-1.68	9.09E-05	0.000522	32	15	51	100
CTNNA3	-2.091	9.11E-05	0.000524	3	6	19	20
RP11-689P11.2	-1.575	9.24E-05	0.00053	8	12	26	34

RP11-396M11.1	-1.526	9.29E-05	0.000533	16	12	33	48
BATF2	-1.022	9.32E-05	0.000534	28	30	63	55
RP4-595K12.1	-1.044	9.42E-05	0.00054	52	41	79	113
CATSPERG	-1.072	9.46E-05	0.000541	22	54	74	86
FUT7	-2.364	9.54E-05	0.000546	0	8	20	22
RP11-524O24.2	-1.508	0.000101	0.000573	12	16	30	50
SULT2B1	-1.271	0.000106	0.000601	14	24	54	38
ALPK2	-1.408	0.000108	0.000611	14	13	32	40
FAM201A	-1.317	0.000108	0.000614	22	14	46	44
UBE2E1-AS1	-1.156	0.00011	0.000621	19	28	60	45
CYP27A1	-1.152	0.000111	0.000627	18	26	45	53
RP11-84E24.3	-1.554	0.000112	0.000634	7	15	28	37
RP11-436H11.4	-1.1	0.000123	0.000687	20	34	67	49
RP11-485G7.5	-1.073	0.000124	0.000693	22	34	68	50
RPS11P6	-2.747	0.000124	0.000693	1	3	11	17
Z83851.1	-1.095	0.000124	0.000696	27	45	96	58
RP11-699L21.1	-4.209	0.000126	0.000706	0	1	14	8
FEZF1-AS1	-1.078	0.000133	0.000739	26	26	50	60
RP11-303G3.6	-1.174	0.000133	0.00074	14	28	44	51
SIDT1-AS1	-1.932	0.000134	0.000744	8	6	19	35
AC020907.1	-4.143	0.000136	0.000757	1	0	9	12
AC139103.1	-1.446	0.000137	0.00076	9	14	34	29
THBS4	-1.077	0.000139	0.000771	22	31	48	64
EDA2R	-1.128	0.000139	0.000772	46	39	119	67
WNT7B	-1.452	0.000141	0.000779	8	16	31	35
RP13-371D18.2	-1.036	0.000143	0.000788	28	27	55	58
RP11-266L9.6	-1.09	0.000149	0.000819	27	72	124	87
MYEOV	-2.697	0.000149	0.00082	6	0	25	15
FTH1P20	-3.087	0.00015	0.000823	1	2	16	11
SYNE2	-6.508	0.000153	0.000839	0	0	6	12
MIR1289-1	-1.084	0.000156	0.000851	38	27	62	76
AC003090.1	-1.629	0.000157	0.000858	9	8	28	25
ISCA1P4	-1.78	0.000164	0.000893	4	11	20	32
CREB3L1	-1.207	0.000164	0.000893	13	25	46	42
RP11-736K20.5	-2.142	0.000164	0.000894	2	6	16	20
DENND6B	-1.214	0.000167	0.000906	12	31	48	52
FCGR2B	-3.087	0.000167	0.000908	3	0	13	14
RP11-366M4.3	-3.363	0.000168	0.000914	2	2	8	35
RANP4	-1.17	0.000183	0.00099	33	26	52	81
DBX2	-1.344	0.000186	0.001	16	15	47	32
MLLT4-AS1	-1.248	0.000188	0.00101	34	24	53	85

RP11-496I9.1	-1.175	0.000193	0.00104	66	38	143	92
MIR375	-1.401	0.000193	0.00104	10	16	30	39
RP11-129B22.6	-1.173	0.000195	0.00105	26	20	58	46
DUX4L7	-1.107	0.000206	0.0011	15	29	50	45
GPRC6A	-6.34	0.000209	0.00112	0	0	7	9
CHST4	-1.203	0.000213	0.00113	25	27	77	43
RP11-666A1.5	-1.01	0.000213	0.00114	20	36	55	58
ALOX5	-1.201	0.000215	0.00115	17	29	66	40
WTAPP1	-1.049	0.000224	0.00119	31	24	60	54
CHAD	-1.477	0.000227	0.0012	23	11	56	39
CTC-430J12.2	-2.329	0.000228	0.00121	0	8	17	24
CDH22	-2.331	0.000237	0.00125	2	4	13	18
IRAK3	-1.325	0.00024	0.00126	16	17	51	32
SEMA5B	-1.627	0.000242	0.00127	9	9	34	22
RP11-66N11.8	-1.04	0.000249	0.00131	23	27	48	55
DUX4L8	-1.257	0.000249	0.00131	15	15	36	36
AP000640.10	-1.599	0.000249	0.00131	7	13	39	22
RP11-177H13.2	-1.446	0.00025	0.00131	8	15	27	36
RP5-1092L12.2	-3.399	0.00025	0.00131	2	0	13	10
AC115115.3	-1.337	0.000251	0.00131	10	16	33	33
RP11-15I11.2	-1.632	0.000268	0.00139	4	12	26	24
C1orf228	-1.632	0.000279	0.00145	6	10	24	26
RPS26P21	-1.415	0.000305	0.00157	10	12	34	25
PDGFRB	-2.747	0.000305	0.00157	3	1	16	12
FRMPD2	-2.421	0.000308	0.00159	5	1	15	18
CTD-2555K7.2	-1.463	0.00031	0.00159	13	9	30	31
RP11-69H7.4	-6.248	0.000319	0.00163	0	0	7	8
RP11-330L19.2	-3.399	0.000332	0.00169	0	2	9	14
IFIH1	-1.655	0.000342	0.00174	18	6	36	40
SOWAHD	-1.491	0.000345	0.00175	13	10	39	26
CTC-236F12.4	-1.844	0.000355	0.0018	3	8	19	21
CTD-2514C3.1	-1.114	0.000363	0.00184	19	22	51	38
AC099684.1	-2.695	0.000367	0.00185	2	2	12	15
PLAU	-1.095	0.000369	0.00186	15	35	58	49
RP4-773A18.4	-1.17	0.000389	0.00196	17	18	43	36
KCNA3	-1.011	0.000392	0.00196	19	31	56	45
PPIAL4B	-6.34	0.000405	0.00203	0	0	11	5
PPIAL4C	-6.34	0.000406	0.00203	0	0	11	5
GRM5	-2.839	0.000416	0.00208	3	2	9	28
MGAT4C	-2.21	0.000417	0.00208	5	5	12	35
NMUR1	-1.574	0.000424	0.00212	10	8	22	32

TCHH	-1.976	0.000425	0.00212	5	4	22	14
AC010983.1	-6.34	0.000436	0.00217	0	0	5	11
RP11-307O13.1	-1.458	0.000441	0.00219	24	9	46	45
RP11-46H11.3	-1.45	0.000457	0.00226	11	9	29	26
RP11-391M20.1	-1.93	0.000468	0.00231	12	12	72	20
RP11-284F21.7	-1.181	0.000469	0.00231	12	43	66	59
RP11-526A4.1	-1.217	0.000474	0.00234	11	22	33	44
ICAM5	-1.08	0.000478	0.00235	16	26	49	40
RP11-356C4.5	-1.66	0.000491	0.00241	7	9	32	19
AL353662.3	-1.18	0.000506	0.00247	12	21	43	32
DUX4	-1.156	0.000529	0.00258	18	16	38	38
CTD-2269F5.1	-1.921	0.00055	0.00267	4	8	15	31
RP11-347E10.1	-6.15	0.000578	0.00279	0	0	6	8
NRXN3	-1.034	0.000625	0.003	139	69	239	187
RP4-811H24.9	-1.744	0.000632	0.00303	2	11	19	25
CBFA2T3	-1.202	0.000637	0.00305	14	15	34	33
ZNF469	-2.185	0.00064	0.00306	2	4	16	12
RP4-613B23.1	-1.196	0.000641	0.00307	15	15	36	33
TUBB7P	-1.509	0.000654	0.00312	11	11	41	22
C6orf99	-1.575	0.000656	0.00313	12	8	22	38
RP1-118J21.25	-1.098	0.00066	0.00314	35	20	58	60
HHIP-AS1	-1.025	0.000665	0.00316	50	31	96	69
KCNJ9	-2.439	0.000683	0.00324	0	5	17	11
RP11-406A9.2	-2.333	0.000691	0.00328	1	4	11	15
TRPV4	-1.37	0.000732	0.00346	8	12	30	22
CD36	-1.365	0.000733	0.00346	8	14	34	23
RP11-214C8.2	-6.15	0.000744	0.0035	0	0	9	5
RP11-809O17.1	-1.119	0.000747	0.00352	34	23	49	75
CCDC170	-1.084	0.000759	0.00357	13	27	41	44
CCT8P1	-1.272	0.000771	0.00362	10	23	50	30
MYLK4	-1.043	0.000784	0.00367	26	20	45	50
ITGB8	-1.684	0.000787	0.00368	5	7	22	17
GRIN1	-1.108	0.000804	0.00375	30	33	92	44
MIR221	-1.346	0.00081	0.00378	174	84	472	184
SIX3	-1.715	0.000821	0.00382	2	14	32	21
LGI1	-1.894	0.000831	0.00386	5	4	21	13
RP11-615I2.3	-6.585	0.000837	0.00388	0	0	18	1
GBP1	-1.111	0.000854	0.00396	13	23	45	33
OLIG3	-2.585	0.000858	0.00397	0	4	9	16
RP11-807H7.1	-1.354	0.000872	0.00403	10	20	26	51
RP11-87C12.4	-1.72	0.000874	0.00403	7	5	24	16

TEX36	-2.387	0.000874	0.00403	2	3	15	12
RP11-23F23.2	-2.236	0.000877	0.00404	3	3	15	14
THRB-IT1	-1.047	0.000883	0.00407	45	27	64	85
KRT6A	-6.044	0.000898	0.00413	0	0	6	7
FAM90A8P	-1.928	0.0009	0.00414	2	6	14	17
AC034243.1	-3.199	0.00092	0.00422	2	0	9	11
AC116609.2	-1.231	0.000926	0.00425	12	16	39	27
PTH1R	-1.014	0.000931	0.00427	16	25	44	39
ESPNP	-3.923	0.00094	0.0043	0	1	6	12
MRO	-1.928	0.000949	0.00434	4	4	17	14
TPTEP1	-1.456	0.000954	0.00436	5	12	26	21
F2RL2	-1.014	0.000964	0.0044	16	24	43	38
LINC00238	-6.248	0.000968	0.00441	0	0	4	11
EPSTI1	-1.315	0.00104	0.00472	14	12	39	26
RP13-401N8.3	-1.512	0.00105	0.00476	5	11	22	24
PACRG	-1.193	0.00105	0.00477	11	16	34	28
EFCAB3	-1.288	0.00107	0.00482	12	19	27	49
AC026150.8	-1.274	0.00107	0.00482	17	11	32	36
PPIAL4A	-6.044	0.00107	0.00485	0	0	8	5
CTD-2522E6.4	-1.48	0.00109	0.0049	4	12	22	23
HCRTR2	-2.527	0.0011	0.00496	2	2	11	13
AC021016.8	-1.114	0.00111	0.00499	20	15	41	35
CPAMD8	-1.181	0.00112	0.00504	13	16	38	28
RP11-230B22.1	-1.524	0.00113	0.00507	12	7	21	34
AC064834.1	-2.728	0.00118	0.00528	0	3	14	7
GPR1	-1.327	0.0012	0.00536	6	15	29	24
AMOT	-1.119	0.00123	0.00545	4383	2127	9962	4175
CD164L2	-1.97	0.00123	0.00547	3	4	15	13
PRSS45	-1.261	0.00127	0.00563	8	14	29	24
HTR2C	-1.442	0.00127	0.00563	4	22	31	40
FAM154A	-2.387	0.00128	0.00565	0	5	10	17
F10	-2.115	0.00132	0.00582	5	2	17	14
RASA4DP	-1.033	0.00136	0.00596	13	26	43	37
RP11-74C13.3	-2.079	0.00136	0.00597	2	4	15	11
HNRNPA1P25	-1.218	0.00138	0.00604	14	22	28	56
RP11-593F23.1	-1.337	0.00139	0.00609	16	10	27	39
RAB37	-1.302	0.00144	0.00627	14	9	29	28
RP11-127L20.6	-2.02	0.00145	0.0063	2	5	18	11
RP11-586D19.2	-1.072	0.00147	0.0064	30	17	49	50
RP11-307C19.1	-1.075	0.00147	0.0064	13	32	57	38
LINC00494	-1.443	0.0015	0.0065	13	6	24	28



RP11-184E9.1	-3.126	0.0015	0.00652	2	0	11	8
FAM84B	-1.261	0.00151	0.00654	308	152	809	294
C16orf11	-1.861	0.00157	0.00677	21	5	66	29
RP11-86H7.7	-1.537	0.00158	0.00682	4	10	20	21
RP11-363D14.1	-5.931	0.00163	0.00699	0	0	7	5
TNFRSF13C	-1.2	0.00163	0.007	13	13	25	35
RP11-274J7.3	-1.358	0.00164	0.00703	10	9	24	25
AC102953.4	-5.931	0.00166	0.0071	0	0	5	7
PDZK1IP1-AS1	-2.858	0.00169	0.00721	2	1	16	7
AC129929.5	-1.607	0.00171	0.00731	8	5	24	16
AC026877.1	-1.54	0.00173	0.00739	8	7	17	27
RP11-656E20.4	-2.22	0.00174	0.0074	1	7	10	28
RP11-314D7.3	-2.466	0.00175	0.00745	0	4	15	8
ADAMTS14	-2.158	0.00175	0.00745	1	4	12	11
MLC1	-2.333	0.0018	0.00762	3	2	16	10
TMIE	-1.208	0.0018	0.00765	13	12	31	27
C1QTNF9B	-1.607	0.00186	0.00786	3	10	23	17
LIMS2	-1.573	0.00187	0.00789	2	14	26	22
SERHL	-1.247	0.00187	0.00789	14	20	55	26
LINC00357	-1.571	0.00188	0.00793	5	9	16	26
LDLRAD2	-2.387	0.00189	0.00794	4	1	17	10
PPIAL4G	-3.126	0.00192	0.00809	2	0	12	7
AC005152.2	-1.224	0.002	0.00836	14	12	26	35
RP11-264L1.3	-3.663	0.00202	0.00843	1	0	7	8
KB-1980E6.3	-3.663	0.00202	0.00843	1	0	7	8
INPP5D	-1.486	0.00202	0.00843	37	10	58	74
RP11-830F9.6	-3.048	0.00207	0.00863	0	2	10	8
NTS	-1.051	0.00208	0.00865	12	27	35	46
RP5-940J5.3	-1.151	0.00215	0.00894	11	15	25	33
AC096670.3	-2.182	0.00222	0.00919	3	5	8	29
TM4SF19-AS1	-1.387	0.00222	0.00919	12	7	21	29
EIF4BP2	-1.206	0.00222	0.0092	23	12	35	46
YBX2	-1.083	0.00225	0.00931	14	18	28	40
GJA5	-5.931	0.00228	0.0094	0	0	4	8
RP11-259G18.1	-1.039	0.0023	0.00948	16	17	36	32
NPSR1-AS1	-1.894	0.00232	0.00956	12	4	17	43
GPRIN2	-3.199	0.00233	0.00958	2	0	6	14
RP11-778D9.4	-1.658	0.00239	0.0098	6	4	14	18
AC097724.3	-1.381	0.00242	0.00992	4	12	21	21
ZCCHC12	2.274	7.85E-153	2.17E-148	3935	4697	905	879
HCFC1	1.645	6.43E-91	2.96E-87	11617	13185	3982	3948

DNAJB1	1.442	1.82E-73	2.80E-70	13101	16303	5396	5428
HSPA8	1.571	7.56E-59	5.97E-56	378753	542269	2E+05	2E+05
IRAK1	1.317	5.43E-58	4.06E-55	10934	13018	4997	4617
CCDC86	1.257	1.10E-47	5.05E-45	4244	5011	1970	1901
RRP12	1.442	4.42E-47	1.88E-44	2094	2594	852	873
HSPH1	1.106	4.11E-42	1.26E-39	10556	12645	5468	5314
HSP90AA1	1.095	1.54E-41	4.40E-39	171887	214463	89518	91364
CLU	1.747	1.89E-40	5.23E-38	1451	2159	541	534
NAALAD2	1.127	2.97E-40	8.13E-38	7875	9339	3866	4013
DPH2	1.16	5.85E-39	1.46E-36	4564	5855	2397	2264
EIF4G2	1.05	1.84E-38	4.42E-36	72749	91676	40149	39254
CBX6	1.101	7.84E-38	1.85E-35	18777	24220	9874	10176
CDC20	1.097	4.12E-37	8.97E-35	6742	8623	3579	3605
DHX37	1.21	1.16E-36	2.48E-34	3019	3961	1493	1524
BRPF3	1.343	2.55E-36	5.35E-34	2048	2760	936	959
BCYRN1	1.089	3.32E-34	5.96E-32	8044	10694	4460	4351
LANCL2	1.325	4.70E-34	8.28E-32	2205	3044	1081	1014
RP11-442N24__B.1	1.279	5.63E-34	9.80E-32	2066	2335	892	921
DNAJA1	1.192	7.19E-34	1.24E-31	23392	32430	11790	12644
TUBB4B	1.131	1.19E-32	1.88E-30	43045	60060	23472	23595
ZNF503	1.11	3.67E-31	5.28E-29	3154	4062	1631	1711
NOL6	1.158	1.95E-30	2.61E-28	2707	3534	1354	1443
DUS3L	1.107	4.83E-29	5.66E-27	2492	3245	1356	1307
ANKRD52	1.001	1.25E-28	1.40E-26	3937	4936	2269	2165
ADI1	1.166	2.89E-28	3.08E-26	4985	6739	2450	2773
CREBBP	1.079	1.23E-25	1.02E-23	3385	3851	1616	1808
ARSB	1.106	2.20E-25	1.79E-23	1989	2601	1046	1087
TNFRSF12A	1.78	3.37E-25	2.71E-23	1010	1672	417	364
MPDU1	1.006	1.83E-24	1.40E-22	4704	6452	2831	2725
BAG3	1.146	2.74E-24	2.05E-22	1683	2169	837	903
TAGLN2	1.115	4.47E-24	3.26E-22	11227	16659	6615	6258
GCLM	1.134	4.54E-24	3.30E-22	4153	5413	1994	2366
LRRC41	1.017	4.93E-24	3.56E-22	3991	5465	2305	2366
RNU4-2	1.447	3.20E-23	2.13E-21	1381	1375	552	459
PARVA	1.301	1.68E-22	1.05E-20	960	1299	445	472
PNO1	1.043	7.12E-22	4.19E-20	2518	3391	1378	1489
POLR2A	1.121	4.41E-20	2.19E-18	2808	2763	1262	1299
CTD-2651B20.6	1.325	1.18E-19	5.63E-18	1206	1618	638	489
HSPA6	2.271	1.23E-19	5.85E-18	275	469	90	64
MAGED2	1.04	4.31E-19	1.94E-17	5147	7707	3107	3146
POLE4	1.063	1.31E-18	5.58E-17	1166	1509	638	642

DOHH	1.128	1.57E-18	6.62E-17	945	1108	487	452
C7orf26	1.161	5.41E-17	1.93E-15	766	1017	403	394
THOC6	1.006	1.53E-16	5.23E-15	1150	1347	644	599
GTPBP6	1.015	3.19E-16	1.05E-14	1123	1333	640	575
PRSS23	1.099	3.32E-16	1.10E-14	1379	1957	734	823
RRP9	1.056	3.35E-16	1.10E-14	1048	1405	614	566
RP11-1033A18.1	1.342	3.69E-16	1.21E-14	550	573	223	220
PRR22	1.708	1.66E-15	5.02E-14	283	446	119	104
RNU5A-8P	1.428	2.45E-15	7.29E-14	569	787	220	284
RCBTB2	1.425	7.07E-15	2.01E-13	309	403	139	126
RP11-473M20.16	1.5	1.62E-14	4.37E-13	290	409	132	115
CTGF	1.87	2.60E-14	6.80E-13	201	337	71	76
RNU5B-1	1.254	3.17E-14	8.24E-13	486	628	217	250
TESK1	1.134	7.08E-14	1.77E-12	651	907	361	349
AVEN	1.09	7.42E-14	1.84E-12	661	806	331	358
IGFBP4	1.477	5.43E-13	1.22E-11	288	308	119	95
LY6K	8.209	6.41E-13	1.43E-11	27	32	0	0
ANXA1	2.384	6.55E-13	1.46E-11	112	223	34	30
SYTL5	1.773	2.06E-12	4.30E-11	142	207	49	53
RNU4-1	1.281	7.31E-12	1.42E-10	809	717	334	294
RNU5A-1	1.009	1.20E-11	2.25E-10	647	834	354	382
FAM102A	1.092	4.11E-11	7.12E-10	490	689	285	268
AC114776.1	1.153	4.12E-11	7.13E-10	358	443	173	187
GLYCTK	1.139	5.79E-11	9.79E-10	391	543	218	206
MIR22HG	1.376	5.92E-11	1.00E-09	225	323	102	109
FOXD4	1.227	1.00E-10	1.63E-09	266	329	128	126
DOK3	1.476	1.31E-10	2.10E-09	230	285	111	74
RP11-295G20.2	1.071	3.44E-10	5.16E-09	943	1541	583	599
TAGLN	1.375	3.50E-10	5.24E-09	235	367	114	118
SLC25A21	1.273	3.68E-10	5.50E-09	258	274	111	109
RP11-279N8.3	1.038	1.25E-09	1.75E-08	463	517	224	253
DNAJA4	1.018	1.61E-09	2.21E-08	388	477	210	217
CT47A1	3.377	2.11E-09	2.84E-08	30	55	4	4
CGA	4.134	2.39E-09	3.19E-08	24	32	1	2
GADD45B	1.033	3.05E-09	4.00E-08	547	796	354	302
RP5-875O13.1	1.035	3.73E-09	4.82E-08	366	415	196	185
AC016910.1	1.572	4.52E-09	5.74E-08	135	136	44	47
RP4-564F22.5	1.48	7.95E-09	9.77E-08	166	158	57	59
CPA4	4.055	1.28E-08	1.53E-07	21	32	1	2
RP11-47K11.2	1.078	1.82E-08	2.12E-07	357	418	164	203
SYT14	1.243	1.90E-08	2.20E-07	186	238	83	96

SGK1	1.03	2.04E-08	2.35E-07	630	1018	413	394
CT47A5	3.272	2.07E-08	2.38E-07	27	52	4	4
RP11-109N23.1	1.583	2.46E-08	2.80E-07	135	234	70	53
KCNJ14	1.359	4.48E-08	4.87E-07	142	197	74	58
RP11-305N23.1	1.311	4.54E-08	4.93E-07	155	205	81	64
NUBP1	1.227	4.71E-08	5.09E-07	169	227	83	86
RP11-145G20.1	1.083	5.71E-08	6.07E-07	416	512	186	252
FOXD4L4	1.112	7.37E-08	7.70E-07	232	326	127	131
FOXD4L2	1.112	7.41E-08	7.73E-07	232	326	127	131
CTD-2561B21.5	1.288	8.30E-08	8.59E-07	147	183	63	72
RP11-452H21.4	1.086	1.99E-07	1.92E-06	406	456	170	236
ETS1	4.915	3.46E-07	3.19E-06	15	21	1	0
HSPA7	2.417	3.56E-07	3.27E-06	40	73	15	6
TSACC	1.116	5.89E-07	5.21E-06	175	237	95	95
RP11-15N24.4	1.332	6.36E-07	5.60E-06	160	150	69	54
AC017104.2	1.315	7.72E-07	6.71E-06	130	149	65	47
FOXD4L5	1.168	9.13E-07	7.82E-06	176	240	81	104
RP11-540O11.7	1.104	9.80E-07	8.32E-06	408	349	167	185
KCNH6	1.459	1.50E-06	1.23E-05	88	102	40	29
HOXA7	1.179	1.91E-06	1.54E-05	162	178	86	64
RP11-368I7.4	1.906	2.18E-06	1.74E-05	46	67	18	12
TMEM217	1.492	2.18E-06	1.74E-05	76	96	27	34
RP11-23E10.3	2.358	2.19E-06	1.75E-05	50	38	6	11
SOX15	1.541	2.25E-06	1.79E-05	88	87	35	25
ANKRD1	1.552	2.73E-06	2.13E-05	92	181	48	45
CT47A7	4	3.55E-06	2.72E-05	15	20	0	2
RP5-1074L1.1	1.289	3.80E-06	2.90E-05	103	149	48	55
AC105396.3	1.056	4.09E-06	3.10E-05	193	198	94	94
CT47A12	3.396	4.09E-06	3.10E-05	15	29	2	2
MIP	1.103	4.74E-06	3.55E-05	149	167	71	76
CT47A9	3.294	5.87E-06	4.31E-05	15	26	2	2
CT47A8	3.294	5.88E-06	4.32E-05	15	26	2	2
CT47A4	3.294	5.89E-06	4.32E-05	15	26	2	2
CT47A11	3.294	5.89E-06	4.32E-05	15	26	2	2
CT47A3	3.294	5.89E-06	4.32E-05	15	26	2	2
CT47A10	3.294	5.90E-06	4.33E-05	15	26	2	2
RYR3	1.054	5.93E-06	4.35E-05	177	249	113	92
INHBA	1.704	6.43E-06	4.68E-05	72	62	19	22
DPYSL3	1.599	7.78E-06	5.56E-05	60	101	24	29
ANKDD1B	1.957	1.12E-05	7.72E-05	41	45	13	9
PTGDR2	1.244	1.35E-05	9.22E-05	99	150	49	56

RP11-697M17.2	1.3	1.94E-05	0.000129	79	106	36	39
REC8	1.096	1.99E-05	0.000132	130	178	80	64
AC079613.1	1.21	2.26E-05	0.000148	98	122	42	53
RP4-694A7.4	1.842	3.02E-05	0.000192	73	53	12	23
RP11-589M4.2	1.471	3.94E-05	0.000244	74	65	24	26
RP13-15E13.1	1.344	4.05E-05	0.000251	85	159	51	45
SRCRB4D	1.272	4.24E-05	0.000261	86	93	42	32
EEF1A1P14	2.019	4.38E-05	0.000269	32	74	13	13
TRIM64EP	1.165	4.44E-05	0.000272	197	180	67	101
ETV4	1.842	5.19E-05	0.000314	36	47	14	9
RP11-318C24.1	1.347	6.13E-05	0.000365	63	95	30	32
ATP4A	1.476	6.26E-05	0.000372	53	67	24	19
RP11-150O12.1	1.102	6.91E-05	0.000407	165	301	116	101
AC126118.1	1.339	7.55E-05	0.000441	69	73	27	29
WNK4	1.113	7.96E-05	0.000463	95	128	56	47
MYO1G	2.512	8.32E-05	0.000482	31	27	9	1
RP11-425D10.10	1.419	8.39E-05	0.000486	70	64	28	22
RP4-794H19.2	1.265	8.78E-05	0.000507	74	121	43	38
RP11-295D4.1	1.301	9.62E-05	0.00055	112	147	36	69
COL12A1	1.254	0.00012	0.000674	70	102	32	40
PCDHB15	1.011	0.000132	0.000734	115	131	60	62
RP4-635E18.6	1.275	0.000133	0.00074	65	95	37	29
FN3K	1.379	0.000147	0.000807	77	69	23	33
RP11-96A1.5	2.06	0.00016	0.000873	28	31	4	10
ATP5G1P4	1.941	0.00017	0.000922	34	28	8	8
FOSB	1.256	0.000184	0.000995	88	175	56	54
GAL3ST4	1.149	0.000234	0.00124	84	87	36	41
AC004019.13	2.21	0.000236	0.00124	24	23	5	5
AVPR2	6.426	0.000294	0.00152	8	9	0	0
ADM5	1.237	0.000298	0.00154	66	71	28	30
RP5-875H3.2	2.06	0.000309	0.00159	33	26	4	10
RNF180	2.846	0.000311	0.0016	16	14	3	1
FAM166A	1.402	0.000361	0.00183	47	67	26	17
RP11-174O3.1	2.204	0.000368	0.00186	18	38	8	4
RPS3AP44	1.886	0.000381	0.00192	29	27	9	6
RPL31P52	1.099	0.00046	0.00227	74	104	45	38
RP11-473M20.11	1.05	0.000471	0.00232	91	110	42	55
RP11-184D12.1	2.408	0.000494	0.00242	16	22	4	3
TSSK5P1	1.542	0.000499	0.00244	34	45	12	15
CNTN4	1.252	0.000517	0.00252	51	66	24	25
SERPINB8	2.231	0.000517	0.00252	17	26	3	6

SLC27A4	1.314	0.000605	0.00291	51	96	30	29
AC013400.2	1.29	0.000662	0.00315	58	67	19	32
AC004840.8	1.697	0.0007	0.00332	53	35	17	10
H2BFM	1.878	0.000713	0.00337	21	31	8	6
HGD	2.505	0.000718	0.00339	19	16	4	2
NDST1	3.285	0.000777	0.00364	7	24	2	1
ELSPBP1	6.248	0.000817	0.0038	7	8	0	0
HSPB8	1.503	0.000865	0.004	89	209	33	72
FAM109B	1.247	0.000873	0.00403	89	75	44	25
RP11-415J8.3	1.898	0.000945	0.00432	22	27	5	8
HCLS1	2.464	0.000973	0.00444	14	20	3	3
RP11-334L9.1	1.196	0.000991	0.00451	53	87	31	30
AC012442.6	2.919	0.00104	0.00472	9	15	1	2
RP11-521D12.5	6.15	0.00112	0.00504	8	6	0	0
NIPA2P4	6.34	0.00113	0.00508	4	12	0	0
FOXD4L1	1.162	0.00114	0.00509	62	115	39	40
RP11-632F7.1	1.282	0.00124	0.00549	51	66	31	17
C15orf26	1.167	0.0014	0.00612	69	66	36	24
AF230666.2	1.793	0.00141	0.00617	21	28	7	7
GALR2	1.508	0.00152	0.00658	46	34	13	15
RP11-158M2.5	1.36	0.00152	0.0066	38	65	23	17
C7orf71	1.898	0.0016	0.00689	27	22	4	9
FAM71F2	1.575	0.00161	0.00692	31	29	9	11
SETP20	1.448	0.00162	0.00695	33	41	16	11
RP11-758P17.3	2.377	0.00164	0.00704	17	15	3	3
RP11-65D17.1	6.34	0.00171	0.0073	12	4	0	0
RP11-403P17.4	1.309	0.00186	0.00784	49	43	16	21
RNA5SP491	1.513	0.00193	0.00811	52	34	13	17
RP11-59H1.1	1.062	0.00203	0.00846	69	69	35	31
HIGD1B	1.36	0.00207	0.00861	44	41	13	20
HNRNPA1P15	1.506	0.00213	0.00884	25	35	9	12
RP11-23E19.1	6.15	0.00217	0.00901	4	10	0	0
RP11-383J24.1	6.15	0.00217	0.00901	4	10	0	0
NUFIP1P	6.044	0.00224	0.00927	8	5	0	0
AC017074.2	1.879	0.00224	0.00928	19	22	5	6
LA16c-390H2.4	2.799	0.00238	0.00979	7	29	1	4

**Table S3: Functional annotation of EZH2 regulated genes**

Functional annotation (GO) analysis of EZH2 activated genes				
Identifier	GO Term	Genes in the list	Total genes	PValue
GO:0030182	neuron differentiation	42	438	9.52E-08
GO:0048666	neuron development	35	339	2.48E-07
GO:0000904	cell morphogenesis involved in differentiation	28	244	6.46E-07
GO:0007409	axonogenesis	24	193	1.21E-06
GO:0048667	cell morphogenesis involved in neuron differentiation	25	209	1.40E-06
GO:0048812	neuron projection morphogenesis	25	213	1.97E-06
GO:0048858	cell projection morphogenesis	26	245	7.25E-06
GO:0031099	regeneration	13	69	9.93E-06
GO:0031175	neuron projection development	26	256	1.55E-05
GO:0032990	cell part morphogenesis	26	256	1.55E-05
GO:0000902	cell morphogenesis	32	356	1.58E-05
GO:0030030	cell projection organization	32	368	3.01E-05
GO:0007423	sensory organ development	23	229	6.40E-05
GO:0060348	bone development	16	123	6.62E-05
GO:0019932	second-messenger-mediated signaling	23	235	9.40E-05
GO:0007155	cell adhesion	48	700	1.10E-04
GO:0022610	biological adhesion	48	701	1.10E-04
GO:0001503	ossification	15	115	1.17E-04
GO:0032989	cellular component morphogenesis	32	397	1.23E-04
GO:0007626	locomotory behavior	25	274	1.30E-04
GO:0042471	ear morphogenesis	11	66	1.82E-04
GO:0001501	skeletal system development	27	319	2.19E-04
GO:0040008	regulation of growth	28	341	2.70E-04
GO:0048638	regulation of developmental growth	9	47	3.54E-04
GO:0031100	organ regeneration	7	26	3.55E-04
GO:0007267	cell-cell signaling	41	600	4.07E-04
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	29	371	4.55E-04
GO:0050954	sensory perception of mechanical stimulus	13	103	5.33E-04
GO:0009891	positive regulation of biosynthetic process	45	695	6.31E-04

GO:0007200	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	9	52	7.18E-04
GO:0010863	positive regulation of phospholipase C activity	10	65	7.49E-04
GO:0007202	activation of phospholipase C activity	10	65	7.49E-04
GO:0031328	positive regulation of cellular biosynthetic process	44	685	8.65E-04
GO:0046928	regulation of neurotransmitter secretion	6	21	9.61E-04
GO:0051094	positive regulation of developmental process	23	278	9.91E-04
GO:0007610	behavior	33	469	0.0010403
GO:0040012	regulation of locomotion	18	192	0.0010731
GO:0048545	response to steroid hormone stimulus	18	192	0.0010731
GO:0007605	sensory perception of sound	12	97	0.0011283
GO:0010518	positive regulation of phospholipase activity	10	69	0.0011614
GO:0042472	inner ear morphogenesis	9	56	0.0011867
GO:0045893	positive regulation of transcription, DNA-dependent	33	477	0.0013707
GO:0010517	regulation of phospholipase activity	10	71	0.0014273
GO:0051254	positive regulation of RNA metabolic process	33	481	0.001567
GO:0044057	regulation of system process	24	309	0.0017223
GO:0048015	phosphoinositide-mediated signaling	11	88	0.0018425
GO:0009100	glycoprotein metabolic process	18	202	0.0018636
GO:0009611	response to wounding	35	530	0.0019955
GO:0009968	negative regulation of signal transduction	19	221	0.0019993
GO:0030335	positive regulation of cell migration	11	89	0.0020069
GO:0030334	regulation of cell migration	16	169	0.0020182
GO:0016477	cell migration	22	276	0.0020447
GO:0060193	positive regulation of lipase activity	10	75	0.0021053
GO:0031644	regulation of neurological system process	15	153	0.0021182
GO:0048568	embryonic organ development	16	172	0.0023962
GO:0051588	regulation of neurotransmitter transport	6	26	0.0026563
GO:0051384	response to glucocorticoid stimulus	10	78	0.0027652
GO:0051270	regulation of cell motion	17	193	0.0029131
GO:0032101	regulation of response to external stimulus	15	159	0.0030231
GO:0010648	negative regulation of cell communication	20	248	0.0030404
GO:0043583	ear development	11	95	0.003258
GO:0048870	cell motility	23	307	0.0033961
GO:0051674	localization of cell	23	307	0.0033961
GO:0010557	positive regulation of macromolecule biosynthetic process	40	654	0.0036638
GO:0040017	positive regulation of locomotion	11	98	0.0040822



GO:0051272	positive regulation of cell motion	11	98	0.0040822
GO:0001654	eye development	13	132	0.0045175
GO:0006140	regulation of nucleotide metabolic process	12	116	0.0046788
GO:0048562	embryonic organ morphogenesis	13	133	0.0047994
GO:0051173	positive regulation of nitrogen compound metabolic process	39	644	0.0048863
GO:0031960	response to corticosteroid stimulus	10	85	0.0049432
GO:0045637	regulation of myeloid cell differentiation	9	70	0.0049635
GO:0010628	positive regulation of gene expression	36	581	0.0049648
GO:0030817	regulation of cAMP biosynthetic process	11	101	0.005063
GO:0045941	positive regulation of transcription	35	564	0.0053845
GO:0050804	regulation of synaptic transmission	13	136	0.0057303
GO:0060191	regulation of lipase activity	10	87	0.0057615
GO:0030814	regulation of cAMP metabolic process	11	103	0.0058133
GO:0007167	enzyme linked receptor protein signaling pathway	24	342	0.006012
GO:0030855	epithelial cell differentiation	13	137	0.0060705
GO:0003018	vascular process in circulatory system	8	58	0.0062322
GO:0043627	response to estrogen stimulus	11	105	0.0066477
GO:0051216	cartilage development	9	74	0.0069469
GO:0048598	embryonic morphogenesis	22	307	0.0070132
GO:0010885	regulation of cholesterol storage	4	11	0.0072007
GO:0008038	neuron recognition	5	21	0.007417
GO:0030514	negative regulation of BMP signaling pathway	5	21	0.007417
GO:0019226	transmission of nerve impulse	24	350	0.0078729
GO:0006928	cell motion	30	475	0.0084336
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	37	624	0.0085701
GO:0030808	regulation of nucleotide biosynthetic process	11	110	0.0091411
GO:0030802	regulation of cyclic nucleotide biosynthetic process	11	110	0.0091411
GO:0048839	inner ear development	9	79	0.0102052
GO:0002088	lens development in camera-type eye	5	23	0.0103351
GO:0051969	regulation of transmission of nerve impulse	13	147	0.0104265
GO:0001764	neuron migration	8	64	0.010602
GO:0019935	cyclic-nucleotide-mediated signaling	12	130	0.0107866
GO:0001822	kidney development	10	96	0.0108034
GO:0045761	regulation of adenylate cyclase activity	10	96	0.0108034
GO:0030799	regulation of cyclic nucleotide metabolic process	11	113	0.0109476
GO:0030001	metal ion transport	29	465	0.0111553

GO:0007166	cell surface receptor linked signal transduction	90	1856	0.0117488
GO:0003013	circulatory system process	15	186	0.0117513
GO:0008015	blood circulation	15	186	0.0117513
GO:0031279	regulation of cyclase activity	10	99	0.013061
GO:0060429	epithelium development	17	227	0.013327
GO:0009725	response to hormone stimulus	24	367	0.0133298
GO:0010743	regulation of foam cell differentiation	5	25	0.0139076
GO:0045597	positive regulation of cell differentiation	17	229	0.0143848
GO:0006334	nucleosome assembly	9	84	0.0144795
GO:0042060	wound healing	15	191	0.0145575
GO:0035249	synaptic transmission, glutamatergic	4	14	0.0145926
GO:0051339	regulation of lyase activity	10	101	0.0147493
GO:0050880	regulation of blood vessel size	7	53	0.0149175
GO:0035150	regulation of tube size	7	53	0.0149175
GO:0001944	vasculature development	18	251	0.0157627
GO:0046888	negative regulation of hormone secretion	5	26	0.0159533
GO:0032355	response to estradiol stimulus	7	54	0.0162597
GO:0043279	response to alkaloid	7	54	0.0162597
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	10	103	0.0165933
GO:0048589	developmental growth	9	87	0.0175976
GO:0031497	chromatin assembly	9	87	0.0175976
GO:0008037	cell recognition	7	55	0.0176829
GO:0006957	complement activation, alternative pathway	4	15	0.017734
GO:0007601	visual perception	16	216	0.0183161
GO:0050953	sensory perception of light stimulus	16	216	0.0183161
GO:0009612	response to mechanical stimulus	7	56	0.0191892
GO:0007268	synaptic transmission	20	298	0.0197822
GO:0007411	axon guidance	10	107	0.0207787
GO:0001649	osteoblast differentiation	6	42	0.0209025
GO:0006956	complement activation	6	42	0.0209025
GO:0048639	positive regulation of developmental growth	4	16	0.0212214
GO:0048878	chemical homeostasis	30	512	0.021497
GO:0009719	response to endogenous stimulus	25	405	0.0215791
GO:0042110	T cell activation	11	126	0.0220356
GO:0065004	protein-DNA complex assembly	9	91	0.0224685
GO:0051046	regulation of secretion	15	202	0.0225255
GO:0006874	cellular calcium ion homeostasis	14	183	0.0228491
GO:0003006	reproductive developmental process	18	262	0.022928
GO:0002541	activation of plasma proteins involved in acute inflammatory response	6	43	0.0229365
GO:0006029	proteoglycan metabolic process	6	43	0.0229365

GO:0001655	urogenital system development	10	110	0.0243817
GO:0009628	response to abiotic stimulus	23	368	0.0247771
GO:0001656	metanephros development	6	44	0.0250944
GO:0034728	nucleosome organization	9	93	0.0252301
GO:0001568	blood vessel development	17	245	0.0253771
GO:0030510	regulation of BMP signaling pathway	5	30	0.0259672
GO:0010604	positive regulation of macromolecule metabolic process	45	857	0.0262979
GO:0006811	ion transport	41	768	0.026826
GO:0007389	pattern specification process	18	267	0.0268493
GO:0030005	cellular di-, tri-valent inorganic cation homeostasis	16	227	0.027196
GO:0055074	calcium ion homeostasis	14	188	0.0277221
GO:0048661	positive regulation of smooth muscle cell proliferation	5	31	0.0289447
GO:0006664	glycolipid metabolic process	5	31	0.0289447
GO:0048660	regulation of smooth muscle cell proliferation	6	46	0.02979
GO:0050905	neuromuscular process	7	62	0.0300806
GO:0030900	forebrain development	12	152	0.0307499
GO:0042246	tissue regeneration	5	32	0.0321164
GO:0032103	positive regulation of response to external stimulus	7	64	0.0344568
GO:0030324	lung development	9	99	0.0349177
GO:0016337	cell-cell adhesion	18	276	0.0351314
GO:0001709	cell fate determination	5	33	0.0354837
GO:0045639	positive regulation of myeloid cell differentiation	5	33	0.0354837
GO:0006939	smooth muscle contraction	5	33	0.0354837
GO:0051480	cytosolic calcium ion homeostasis	10	118	0.0361192
GO:0030155	regulation of cell adhesion	11	137	0.0364431
GO:0048584	positive regulation of response to stimulus	16	236	0.0365388
GO:0048585	negative regulation of response to stimulus	9	100	0.0367466
GO:0045596	negative regulation of cell differentiation	15	216	0.0368825
GO:0006875	cellular metal ion homeostasis	14	196	0.0370389
GO:0021700	developmental maturation	9	101	0.0386388
GO:0050806	positive regulation of synaptic transmission	5	34	0.0390475
GO:0009101	glycoprotein biosynthetic process	12	158	0.0391144
GO:0045165	cell fate commitment	11	139	0.0396336
GO:0055066	di-, tri-valent inorganic cation homeostasis	16	239	0.0402804
GO:0030323	respiratory tube development	9	102	0.0405952
GO:0051345	positive regulation of hydrolase activity	13	179	0.0410699
GO:0035295	tube development	15	220	0.0420766
GO:0006935	chemotaxis	12	160	0.042224

GO:0006813	potassium ion transport	12	160	0.042224
GO:0042330	taxis	12	160	0.042224
GO:0001657	ureteric bud development	5	35	0.0428081
GO:0070482	response to oxygen levels	11	141	0.0430111
GO:0014829	vascular smooth muscle contraction	3	9	0.0436057
GO:0010883	regulation of lipid storage	4	21	0.0438306
GO:0006816	calcium ion transport	11	142	0.0447713
GO:0051240	positive regulation of multicellular organismal process	16	244	0.0465488
GO:0032675	regulation of interleukin-6 production	5	36	0.0467655
GO:0048592	eye morphogenesis	7	69	0.0471262
GO:0040007	growth	13	183	0.0472428
GO:0048286	lung alveolus development	4	22	0.0493622
GO:0001658	branching involved in ureteric bud morphogenesis	4	22	0.0493622
GO:0060675	ureteric bud morphogenesis	4	22	0.0493622
GO:0055065	metal ion homeostasis	14	205	0.0499698

Functional annotation (GO) analysis of EZH2 repressed genes				
Identifier	GO Term	Genes in the list	Total genes	PValue
GO:0006986	response to unfolded protein	6	71	6.49E-05
GO:0051789	response to protein stimulus	6	107	4.48E-04
GO:0006457	protein folding	7	177	6.64E-04
GO:0010033	response to organic substance	10	721	0.0280265
GO:0045683	negative regulation of epidermis development	2	5	0.0295859
GO:0010604	positive regulation of macromolecule metabolic process	11	857	0.0314504
GO:0006790	sulfur metabolic process	4	115	0.0316331
GO:0016573	histone acetylation	3	48	0.0334414
GO:0006916	anti-apoptosis	5	206	0.0350326
GO:0015718	monocarboxylic acid transport	3	50	0.0360406
GO:0044272	sulfur compound biosynthetic process	3	50	0.0360406
GO:0006473	protein amino acid acetylation	3	52	0.0387155
GO:0001501	skeletal system development	6	319	0.0423512

KEGG pathway analysis s of EZH2 activated genes				
Identifier	GO Term	Genes in the list	Total genes	PValue
hsa04080	Neuroactive ligand-receptor interaction	23	256	0.0012679
hsa05200	Pathways in cancer	25	328	0.0064785
hsa04360	Axon guidance	13	129	0.0088458
hsa05322	Systemic lupus erythematosus	10	99	0.0252471
hsa04512	ECM-receptor interaction	9	84	0.0266016
hsa05218	Melanoma	8	71	0.0313681
hsa04350	TGF-beta signaling pathway	9	87	0.0319931
hsa04510	Focal adhesion	15	201	0.0485787
hsa04930	Type II diabetes mellitus	6	47	0.0492058
hsa04666	Fc gamma R-mediated phagocytosis	9	95	0.0498986

## KEGG pathway analysis s of EZH2 repressed genes

Identifier	GO Term	Genes in the list	Total g PValue
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No significantly enriched KEGG-pathways

Gene_ID	log2(Fold_change)	PValue	FDR	shTRIM28_rep1	shTRIM28_rep2	shCtrl_rep1	shCtrl_rep2
GUCY1A3	-11.177	7.44E-199	1.98E-194	1	0	1496	1282
XIST	-6.857	8.71E-184	1.16E-179	29	59	5350	4872
NCAM2	-4.191	1.32E-132	1.17E-128	157	133	2827	2475
SYBU	-5.102	1.95E-132	1.29E-128	49	51	1940	1502
SULF1	-4.511	2.02E-125	8.95E-122	83	70	1916	1577
CA2	-4.135	7.44E-120	2.82E-116	204	215	4108	3255
FAM5C	-12.326	2.59E-117	8.60E-114	0	0	564	463
GPR179	-5.594	2.29E-110	6.08E-107	16	23	1080	813
LINC00472	-3.914	6.45E-102	1.43E-98	333	364	5975	4536
PVRL3	-4.675	3.02E-93	5.73E-90	24	28	715	618
CALML5	-3.684	9.69E-93	1.71E-89	97	98	1318	1191
PLCXD3	-4.486	1.22E-84	1.90E-81	25	26	615	532
KLK11	-4.006	6.93E-84	1.02E-80	54	46	888	722
SOX2	-3.284	7.39E-77	9.35E-74	248	281	2873	2282
RPL35AP31	-11.214	1.58E-71	1.75E-68	0	0	266	209
GUCY1B3	-10.79	2.10E-61	1.69E-58	0	0	188	166
HS6ST2	-3.727	2.25E-59	1.66E-56	37	36	546	423
LRFN5	-10.604	1.63E-55	1.11E-52	0	0	156	155
PRODH	-3.884	1.05E-53	6.82E-51	22	19	325	283
AC010729.1	-7.153	7.01E-53	4.33E-50	2	0	164	149
GPX2	-2.695	3.90E-52	2.30E-49	142	145	1011	848
HS3ST3A1	-3.006	2.00E-51	1.16E-48	119	152	1212	967
ROBO1	-2.384	6.28E-51	3.55E-48	400	388	2265	1849
TCEAL8	-10.41	1.01E-49	5.59E-47	0	0	149	123
SYNPO2	-2.561	1.41E-49	7.64E-47	191	209	1269	1093
PDE4D	-3.991	1.84E-49	9.77E-47	17	14	261	235
UGT1A6	-2.333	1.65E-48	8.42E-46	292	278	1459	1414
PHGDH	-2.715	1.92E-48	9.61E-46	135	154	1043	856
UBE2QL1	-2.427	1.50E-47	7.24E-45	282	300	1713	1418
CNTNAP2	-3.846	4.25E-47	2.01E-44	19	27	380	284
C9orf152	-5.277	1.96E-46	9.13E-44	4	7	258	176
CXCR4	-2.718	6.35E-46	2.91E-43	133	140	1024	773
BST2	-3.48	1.08E-45	4.79E-43	30	44	465	363
VAV3	-2.163	1.14E-45	4.96E-43	720	726	3444	3033
DACH1	-10.212	2.31E-45	9.91E-43	0	0	121	116
HEY2	-2.928	2.94E-45	1.24E-42	68	89	620	576
PALLD	-2.262	1.71E-44	6.88E-42	300	267	1485	1235
CTA-392E5.1	-5.185	2.31E-44	9.16E-42	4	4	157	141
SLITRK6	-2.2	5.61E-44	2.10E-41	832	838	4271	3402

CORO1A	-2.718	6.58E-42	2.33E-39	137	169	1146	869
ZIC2	-4.262	9.35E-42	3.27E-39	10	8	172	177
DIO2	-5.639	2.09E-41	7.04E-39	1	4	138	121
ZNF827	-3.887	3.06E-41	1.02E-38	16	12	200	217
S100P	-2.92	1.16E-40	3.76E-38	141	210	1289	1369
BMPER	-4.223	1.57E-39	4.91E-37	8	9	166	155
MITF	-2.63	2.88E-39	8.90E-37	82	90	589	477
NAALADL2	-2.453	7.41E-39	2.26E-36	115	116	699	567
PPM1K	-1.927	2.29E-38	6.75E-36	617	559	2417	2056
TRIM28	-2.066	1.80E-37	5.13E-35	1736	1867	8343	6740
AXIN2	-2.52	3.10E-37	8.65E-35	79	75	478	406
RP11-124N14.4	-3.316	3.64E-37	1.01E-34	26	19	247	203
SLC1A1	-2.857	1.18E-36	3.23E-34	56	74	531	412
RP11-1081M5.1	-3.674	2.98E-36	8.00E-34	11	20	218	180
PLCB4	-2.437	3.67E-36	9.76E-34	128	125	785	586
SHH	-1.92	3.89E-36	1.02E-33	645	572	2558	2048
CECR2	-3.996	1.56E-35	4.03E-33	10	14	227	159
KIAA0226L	-3.28	3.32E-35	8.48E-33	21	20	216	184
VIM	-3.378	3.57E-35	9.02E-33	23	20	258	191
TIMP3	-1.922	4.41E-35	1.10E-32	706	646	2889	2235
C9orf47	-1.916	4.49E-35	1.11E-32	479	461	1949	1600
ELOVL2	-1.932	2.28E-34	5.56E-32	622	624	2666	2090
S100A16	-2.234	3.16E-34	7.63E-32	900	1145	5221	4402
SLC16A1	-2.126	5.45E-34	1.29E-31	186	185	893	727
RP1-140K8.5	-3.293	5.07E-33	1.16E-30	21	18	215	169
HS3ST3B1	-2.275	8.52E-33	1.92E-30	139	131	745	563
OLFML3	-2.285	1.66E-32	3.55E-30	169	200	1014	785
BCL11B	-2.35	3.63E-32	7.64E-30	96	92	539	420
RIMS2	-3.152	4.25E-32	8.88E-30	28	48	385	292
WDR72	-2.447	7.40E-32	1.54E-29	81	58	411	348
CPNE4	-6.38	2.28E-31	4.69E-29	2	0	84	99
AMPH	-4.588	3.09E-30	6.16E-28	2	7	122	99
DNAJC22	-1.929	4.58E-30	9.07E-28	637	760	2883	2439
LCN2	-1.88	1.97E-29	3.85E-27	254	266	1018	897
ZIC5	-3.082	4.16E-29	8.06E-27	38	21	294	207
TFF3	-1.728	4.65E-29	8.95E-27	582	614	2109	1854
KCNMA1	-4.797	6.36E-29	1.21E-26	4	3	116	84
EFNA5	-2.257	1.41E-28	2.64E-26	109	86	531	402
UNC5C	-2.671	1.44E-28	2.65E-26	44	37	296	221
C4orf19	-1.678	2.04E-28	3.71E-26	587	600	2008	1791
AP004372.1	-5.298	9.50E-28	1.64E-25	2	2	93	72



TNFRSF19	-4.31	1.04E-27	1.78E-25	7	4	131	91
CAMK2D	-1.756	1.46E-27	2.48E-25	308	291	1097	926
KLK6	-2.891	4.16E-27	6.85E-25	29	52	332	270
BMP5	-2.316	4.69E-27	7.63E-25	83	64	417	316
RP11-400K9.4	-2.361	5.44E-27	8.80E-25	62	76	392	318
SBK1	-2.118	1.02E-26	1.63E-24	104	117	529	431
CHST1	-2.694	1.18E-26	1.87E-24	29	30	210	173
AC005301.8	-3.797	1.44E-26	2.26E-24	9	7	129	96
GP2	-4.727	1.94E-26	3.01E-24	4	2	89	75
BMPR1B	-1.802	2.43E-26	3.73E-24	216	216	811	696
REG4	-9.433	4.33E-26	6.57E-24	0	0	60	78
MUC5B	-3.281	1.00E-25	1.50E-23	18	46	309	315
HIST1H2BB	-1.694	1.22E-25	1.82E-23	491	402	1392	1498
MPPED2	-2.732	1.37E-25	2.04E-23	26	25	186	154
FAM129A	-3.642	1.85E-25	2.72E-23	9	7	108	94
AKAP5	-1.609	2.16E-25	3.15E-23	640	638	2150	1750
ANKRD35	-2.888	3.11E-25	4.48E-23	36	18	228	173
PLEKHO1	-2.295	3.24E-25	4.65E-23	64	87	380	362
PADI2	-2.708	3.69E-25	5.26E-23	50	38	349	227
AP001137.1	-9.443	4.23E-25	5.97E-23	0	0	58	81
MALL	-1.755	5.73E-25	8.05E-23	242	217	857	693
LPHN2	-2.75	5.76E-25	8.06E-23	23	25	176	148
RP11-573G6.2	-9.17	1.68E-24	2.31E-22	0	0	64	51
ADAMTS19	-1.7	1.93E-24	2.63E-22	390	439	1413	1280
ARAP1	-1.599	2.21E-24	2.99E-22	4077	4257	13904	11340
CAPN9	-2.567	2.23E-24	3.00E-22	33	33	221	171
CRAT	-2.848	3.12E-24	4.18E-22	28	56	319	287
RP11-493K23.4	-4.052	4.81E-24	6.36E-22	7	3	85	84
MAOB	-2.133	5.24E-24	6.89E-22	69	64	320	264
KIF1A	-2.23	5.34E-24	6.98E-22	165	130	849	536
DIRAS2	-2.246	6.35E-24	8.26E-22	72	90	435	334
EGLN3	-1.765	8.48E-24	1.09E-21	235	261	914	772
PKHD1L1	-5.369	1.15E-23	1.46E-21	2	1	73	59
SERPINE1	-2.585	2.04E-23	2.58E-21	39	33	255	178
UST	-1.92	2.12E-23	2.66E-21	120	104	411	437
KCNJ3	-1.662	2.85E-23	3.55E-21	324	326	1142	915
NPY1R	-1.474	3.01E-23	3.70E-21	1913	1891	5646	4921
CXCL12	-1.555	3.02E-23	3.70E-21	830	882	2765	2266
HOXD8	-3.07	6.37E-23	7.59E-21	11	18	130	115
MAPK8IP2	-2.633	8.12E-23	9.63E-21	34	35	256	173
GPR139	-3.973	8.84E-23	1.04E-20	4	6	80	80

GCNT2	-2.452	8.94E-23	1.05E-20	36	30	200	162
ZNF804B	-3.309	1.21E-22	1.42E-20	13	7	106	94
CBX2	-1.546	1.77E-22	2.05E-20	1830	1970	6080	5018
NBPF6	-1.721	3.21E-22	3.71E-20	314	350	1230	959
RASGRP1	-1.557	3.88E-22	4.44E-20	355	329	1102	911
MUCL1	-4.668	4.25E-22	4.80E-20	1	4	68	64
MARCKS	-1.618	6.74E-22	7.49E-20	836	905	3065	2278
CTSD	-1.549	7.99E-22	8.84E-20	17061	17852	57507	44651
UGT2B15	-1.66	1.44E-21	1.58E-19	210	226	706	672
CDCA7	-1.936	1.72E-21	1.88E-19	90	81	363	292
KRT6A	-3.606	2.96E-21	3.19E-19	12	4	115	82
CRLF1	-1.801	4.19E-21	4.48E-19	121	130	474	401
CKMT1B	-1.566	4.85E-21	5.15E-19	549	588	1895	1472
SUSD3	-2.25	6.08E-21	6.43E-19	42	47	237	187
EHF	-2.228	6.27E-21	6.61E-19	41	50	212	215
SCNN1A	-1.68	1.20E-20	1.26E-18	153	154	526	458
PTHLH	-2.964	1.25E-20	1.30E-18	16	11	103	109
B3GNT5	-2.845	2.52E-20	2.59E-18	18	24	181	122
RP11-162J8.3	-3.844	1.10E-19	1.11E-17	5	7	108	67
SEMA6A	-1.802	1.34E-19	1.34E-17	113	130	464	384
U91328.2	-1.571	1.52E-19	1.52E-17	182	170	534	512
FIBCD1	-1.498	1.64E-19	1.62E-17	370	362	1156	912
MUC13	-5.735	1.88E-19	1.85E-17	0	2	49	68
SPSB4	-2.462	2.00E-19	1.96E-17	30	23	166	127
AC068580.6	-1.67	2.78E-19	2.72E-17	244	264	927	690
SLC12A2	-1.366	2.96E-19	2.87E-17	2809	2779	7933	6470
MSX2	-1.382	3.28E-19	3.17E-17	853	858	2474	1987
EMCN	-2.752	4.57E-19	4.38E-17	19	12	105	105
ANKRD62P1-PAR	-1.649	6.00E-19	5.71E-17	136	112	407	371
KLK12	-3.76	6.31E-19	5.98E-17	5	5	78	60
TRIM3	-1.475	6.55E-19	6.19E-17	253	224	709	617
FAM5B	-1.641	8.55E-19	8.02E-17	182	195	655	521
FAM169A	-1.495	1.45E-18	1.35E-16	217	186	592	544
RASSF2	-2.052	1.45E-18	1.35E-16	54	44	228	179
ARSJ	-2.007	1.97E-18	1.82E-16	53	65	260	215
SALL2	-1.662	3.81E-18	3.45E-16	168	158	592	440
FAT1	-1.302	4.85E-18	4.35E-16	1796	1826	4764	4165
GRIK3	-2.465	6.22E-18	5.52E-16	47	91	419	344
10-Sep	-1.542	6.92E-18	6.13E-16	223	244	746	614
C3	-1.8	7.50E-18	6.61E-16	87	82	331	258
CREB3L1	-4.91	1.12E-17	9.82E-16	2	1	50	46

BAMBI	-1.383	1.15E-17	1.00E-15	2273	2429	6857	5406
MIR375	-2.619	1.30E-17	1.12E-15	15	20	106	110
C5orf4	-1.43	1.67E-17	1.43E-15	406	435	1255	1011
SERPINB5	-2.955	1.92E-17	1.65E-15	16	14	146	88
RP11-109N23.1	-1.755	2.05E-17	1.75E-15	78	70	262	238
ZFP37	-5.48	2.42E-17	2.06E-15	0	2	59	39
PSCA	-2.118	3.28E-17	2.77E-15	34	43	179	156
LRIG3	-1.562	4.52E-17	3.79E-15	178	207	594	543
DPYSL5	-2.736	5.55E-17	4.62E-15	14	19	130	91
CTTNBP2	-8.665	5.82E-17	4.83E-15	0	0	35	46
RP11-346A9.1	-1.985	5.99E-17	4.95E-15	45	44	194	159
PLCH1	-1.772	6.08E-17	5.02E-15	222	319	986	862
COL3A1	-2.416	7.32E-17	6.01E-15	21	24	136	105
HPGD	-2.137	1.17E-16	9.52E-15	49	27	177	158
TNNT1	-1.77	1.21E-16	9.85E-15	138	178	612	466
PTMS	-1.713	1.22E-16	9.88E-15	388	426	1640	1029
PKP1	-1.481	1.57E-16	1.25E-14	339	353	1113	819
SPDEF	-1.306	1.63E-16	1.30E-14	2529	2674	7114	5749
LARGE	-1.301	1.66E-16	1.31E-14	1433	1538	4000	3323
SLCO4C1	-2.069	1.66E-16	1.31E-14	37	31	147	139
ALDH3A1	-2.001	1.73E-16	1.37E-14	46	58	234	183
IKZF2	-1.28	2.18E-16	1.71E-14	558	541	1465	1205
KIAA1217	-1.361	2.55E-16	2.00E-14	275	232	695	608
ASB9	-1.934	2.67E-16	2.08E-14	55	60	252	188
ZNF583	-2.731	3.62E-16	2.82E-14	12	16	88	99
MIR205HG	-1.942	4.01E-16	3.11E-14	55	37	183	171
LMO4	-1.405	6.04E-16	4.65E-14	201	187	517	511
RHOBTB1	-1.261	6.12E-16	4.69E-14	427	382	1034	905
PALMD	-4.311	6.26E-16	4.79E-14	2	3	61	42
SLC9A3R2	-1.333	6.37E-16	4.86E-14	651	677	1895	1450
ATP11B	-1.238	6.80E-16	5.17E-14	1691	1760	4390	3748
HES2	-1.806	8.94E-16	6.77E-14	75	91	328	253
RP11-347C12.3	-1.955	9.09E-16	6.85E-14	39	39	156	147
RP13-895J2.7	-8.592	1.01E-15	7.59E-14	0	0	48	29
RP11-865I6.2	-2.457	1.03E-15	7.76E-14	30	23	180	112
HS3ST5	-4.075	1.07E-15	7.97E-14	2	6	89	49
BCYRN1	-1.424	1.23E-15	9.16E-14	3172	3525	8188	9786
TPTEP1	-1.771	1.29E-15	9.51E-14	81	58	230	245
PDGFC	-2.311	1.31E-15	9.63E-14	21	27	134	105
LRP1B	-1.444	1.56E-15	1.14E-13	264	313	835	735
IGFBP2	-1.389	1.63E-15	1.19E-13	1580	1947	4886	4352

RECK	-3.681	2.04E-15	1.47E-13	3	5	53	52
ZNF365	-1.804	2.19E-15	1.58E-13	61	48	208	173
ELF5	-1.667	3.34E-15	2.37E-13	74	72	251	213
PCDH9	-1.185	3.46E-15	2.45E-13	573	505	1277	1175
OLFM1	-1.203	3.46E-15	2.45E-13	947	875	2344	1850
LPAR1	-4.203	4.14E-15	2.91E-13	6	0	70	44
3-Sep	-1.728	4.74E-15	3.32E-13	90	68	299	225
GPR173	-2.668	4.96E-15	3.47E-13	11	14	85	75
SPOCK1	-1.732	5.37E-15	3.73E-13	80	74	295	217
IL8	-4.441	8.94E-15	6.19E-13	4	0	42	49
REEP1	-1.499	9.44E-15	6.53E-13	113	97	308	286
GPNMB	-1.858	1.09E-14	7.50E-13	63	80	299	220
A4GALT	-1.301	1.11E-14	7.65E-13	387	384	1068	832
HIST1H2BM	-1.179	1.19E-14	8.13E-13	2555	2702	6183	5721
MEGF9	-1.2	1.21E-14	8.26E-13	921	947	2376	1917
SLC29A4	-1.358	1.25E-14	8.47E-13	198	180	527	442
LEF1	-5.095	1.59E-14	1.07E-12	2	0	40	35
ONECUT1	-1.377	1.73E-14	1.16E-12	191	198	547	464
IQCK	-1.4	2.61E-14	1.73E-12	186	197	556	455
FILIP1L	-1.259	3.59E-14	2.36E-12	331	320	858	700
OR7E13P	-1.185	3.79E-14	2.49E-12	646	623	1599	1286
BMP7	-1.16	3.92E-14	2.57E-12	6292	6536	15476	13197
RTN4RL1	-1.348	3.98E-14	2.61E-12	620	718	1944	1463
STON2	-1.166	4.43E-14	2.88E-12	743	668	1763	1404
PVRL1	-1.248	4.53E-14	2.94E-12	604	520	1531	1139
RP11-129B22.6	-1.819	4.63E-14	2.99E-12	43	45	169	142
LRG1	-2.542	4.95E-14	3.18E-12	11	23	97	102
LAMB3	-1.367	5.22E-14	3.33E-12	163	168	448	406
ARNT2	-1.326	5.34E-14	3.40E-12	457	479	1356	991
SGK1	-1.108	5.79E-14	3.68E-12	897	845	2018	1738
LTBP1	-1.195	6.97E-14	4.39E-12	770	776	1992	1548
DHRS3	-1.592	7.05E-14	4.44E-12	95	80	299	229
PITX1	-1.44	8.66E-14	5.42E-12	197	244	636	561
SIM1	-8.304	9.84E-14	6.13E-12	0	0	38	25
EDARADD	-2.956	9.99E-14	6.21E-12	10	8	86	55
RP11-345J4.3	-1.863	1.11E-13	6.89E-12	37	36	137	129
TTC22	-8.209	1.12E-13	6.91E-12	0	0	32	27
NTSR1	-2.069	1.75E-13	1.07E-11	47	36	215	134
ZMAT4	-2.222	1.79E-13	1.09E-11	21	17	96	82
ANXA8L1	-1.387	2.07E-13	1.26E-11	140	149	402	354
RP11-677N16.1	-3.663	2.26E-13	1.37E-11	5	2	51	40

SHC4	-1.324	3.04E-13	1.82E-11	165	154	431	368
ADAMTS9	-1.214	3.30E-13	1.97E-11	377	368	962	766
ST6GAL1	-1.182	5.13E-13	3.02E-11	416	429	1044	874
PRSS23	-1.124	5.14E-13	3.03E-11	10929	11432	26642	22089
TUFMP1	-8.304	5.42E-13	3.19E-11	0	0	25	38
VGF	-1.351	5.53E-13	3.24E-11	218	164	543	432
ANXA8	-1.39	5.60E-13	3.28E-11	162	190	495	428
SOWAHC	-1.218	5.65E-13	3.30E-11	575	622	1566	1218
ALG1L2	-1.793	6.02E-13	3.51E-11	63	78	289	200
CD109	-1.456	6.99E-13	4.06E-11	108	85	286	244
SLC25A1P1	-2.49	7.33E-13	4.23E-11	15	11	84	63
FAXC	-1.803	8.80E-13	5.06E-11	40	47	169	135
SLC27A6	-1.556	9.18E-13	5.25E-11	106	135	343	366
ANXA6	-1.315	9.36E-13	5.34E-11	275	275	791	578
AL603965.1	-1.354	1.12E-12	6.36E-11	171	195	507	429
INHBB	-1.272	1.13E-12	6.39E-11	516	601	1523	1175
UGT2B17	-1.75	1.14E-12	6.45E-11	44	37	138	135
AREG	-1.199	1.16E-12	6.53E-11	442	476	1171	937
DNAAF3	-1.867	1.41E-12	7.91E-11	51	67	257	174
SCML1	-1.576	1.42E-12	7.94E-11	103	140	393	332
FKBP10	-1.595	1.45E-12	8.08E-11	86	92	313	225
ITGA2	-1.163	1.50E-12	8.34E-11	702	765	1822	1463
PLA2G3	-3.565	1.51E-12	8.39E-11	2	5	44	41
ARSB	-1.35	1.65E-12	9.11E-11	179	177	517	391
MARK1	-2.709	1.72E-12	9.48E-11	7	15	83	62
ITM2C	-1.542	1.75E-12	9.65E-11	93	116	336	273
RP11-284F21.7	-1.426	2.49E-12	1.36E-10	132	112	376	280
AREGB	-1.206	2.56E-12	1.40E-10	415	444	1112	870
HSD17B12	-1.13	2.83E-12	1.54E-10	488	522	1175	1035
RP11-57A19.2	-1.66	2.96E-12	1.61E-10	49	55	179	150
MUC5AC	-4.376	4.62E-12	2.49E-10	0	4	56	31
GPRC5B	-1.758	4.65E-12	2.51E-10	45	35	151	120
C8orf48	-3.052	5.17E-12	2.75E-10	8	4	47	54
PRKAR2B	-1.479	5.73E-12	3.05E-10	181	187	621	405
TMPRSS4	-1.314	6.01E-12	3.19E-10	140	151	388	336
SNCG	-2.46	6.42E-12	3.40E-10	9	17	73	71
FAR2	-2.265	6.67E-12	3.53E-10	15	20	97	72
PCCA	-1.498	6.85E-12	3.61E-10	89	106	306	245
FRMD6	-1.044	8.40E-12	4.41E-10	920	902	2069	1688
SLC28A3	-5.6	8.49E-12	4.44E-10	1	0	34	24
RP11-161I10.1	-4.798	8.49E-12	4.44E-10	2	0	32	29

LGALS1	-1.117	8.61E-12	4.49E-10	764	868	1781	1758
TOX3	-7.972	1.06E-11	5.52E-10	0	0	28	22
DEFB4A	-5.524	1.28E-11	6.58E-10	0	1	29	26
POC1B	-1.06	1.28E-11	6.58E-10	3459	3580	8100	6574
CYBRD1	-2.773	1.37E-11	7.06E-10	7	12	79	52
FBXO32	-1.254	1.39E-11	7.16E-10	149	151	373	343
MAPK8IP1	-1.167	1.43E-11	7.33E-10	377	417	978	805
RP11-389K14.3	-2.035	1.75E-11	8.82E-10	24	21	87	98
SEL1L3	-1.505	1.77E-11	8.90E-10	135	182	509	391
EPHA3	-2.009	1.79E-11	8.99E-10	32	61	206	169
SYT17	-1.173	1.90E-11	9.46E-10	517	527	1363	991
RPRM	-1.546	2.19E-11	1.09E-09	69	48	176	166
EXPH5	-1.11	2.30E-11	1.14E-09	715	656	1710	1250
CAPN13	-1.386	2.30E-11	1.14E-09	97	111	278	266
TP63	-1.513	2.41E-11	1.19E-09	139	82	347	284
RP11-744O11.2	-7.883	2.50E-11	1.23E-09	0	0	24	23
CXXC4	-1.761	2.70E-11	1.33E-09	35	51	151	141
KCNH2	-1.486	2.76E-11	1.35E-09	64	74	201	186
MYO10	-1.122	2.81E-11	1.38E-09	789	774	1979	1424
RP11-1C8.4	-2.527	2.92E-11	1.42E-09	14	7	58	64
PEG10	-7.883	2.92E-11	1.42E-09	0	0	23	24
KDEL1C1	-1.519	3.15E-11	1.53E-09	59	64	175	178
CD36	-1.213	3.24E-11	1.57E-09	191	210	486	444
FOXD1	-1.402	3.44E-11	1.66E-09	114	80	280	233
EGR1	-1.37	3.58E-11	1.72E-09	122	132	373	284
CP	-2.202	3.72E-11	1.78E-09	21	11	78	70
SNAI2	-4.844	3.78E-11	1.81E-09	2	0	39	24
S100A2	-2.721	3.85E-11	1.83E-09	9	6	50	50
PRAME	-4	4.32E-11	2.05E-09	4	0	36	31
TFF1	-1.071	4.89E-11	2.31E-09	22389	24924	54369	45061
TSKU	-1.112	4.89E-11	2.31E-09	1412	1616	3638	2909
TNFSF10	-1.528	5.37E-11	2.53E-09	157	232	627	495
NGFRAP1	-1.004	5.37E-11	2.53E-09	3970	4054	8727	7361
CDH13	-1.877	6.56E-11	3.07E-09	38	25	136	96
CARD10	-1.146	7.05E-11	3.29E-09	201	193	446	426
CSRP2	-1.567	7.10E-11	3.31E-09	50	44	151	128
CBLB	-1.083	7.15E-11	3.32E-09	342	329	780	642
HIST1H3I	-1.036	7.30E-11	3.38E-09	1509	1657	3259	3232
CT62	-1.355	7.33E-11	3.39E-09	102	120	289	279
KCNH3	-1.914	7.42E-11	3.43E-09	22	28	94	95
TMTC1	-1.3	7.51E-11	3.46E-09	312	302	915	597

SLC2A10	-1.086	7.98E-11	3.67E-09	868	855	2121	1537
RP11-225N10.1	-5.807	8.47E-11	3.87E-09	0	1	47	20
LRRC10B	-1.265	8.50E-11	3.88E-09	161	166	444	342
DLX1	-1.243	8.66E-11	3.94E-09	164	182	446	373
FIGN	-1.034	8.75E-11	3.98E-09	465	461	1027	869
TMCC3	-1.12	9.72E-11	4.40E-09	262	275	620	547
ZNF880	-1.168	9.83E-11	4.45E-09	170	156	379	354
FBLN2	-3.565	1.06E-10	4.77E-09	6	1	35	50
ARMCX2	-1.057	1.22E-10	5.51E-09	734	832	1746	1513
DGKG	-1.695	1.61E-10	7.18E-09	38	44	153	113
DLG4	-1.628	1.73E-10	7.72E-09	47	48	171	123
HS6ST3	-1.173	1.76E-10	7.86E-09	249	220	605	453
ZFP82	-7.852	2.07E-10	9.15E-09	0	0	28	18
RP11-393B14.1	-1.292	2.24E-10	9.88E-09	108	119	299	257
FGFR1	-1.343	2.63E-10	1.16E-08	159	157	479	323
FAM19A5	-1.44	2.73E-10	1.20E-08	89	114	309	242
ASPH	-1.009	2.84E-10	1.24E-08	489	421	1008	823
GBE1	-1.006	3.50E-10	1.52E-08	523	524	1151	952
LMOD3	-3.501	3.64E-10	1.58E-08	2	4	41	29
KREMEN2	-1.265	3.69E-10	1.60E-08	104	96	261	220
SUSD2	-1.743	3.84E-10	1.65E-08	80	68	320	176
LINC00284	-1.583	3.90E-10	1.68E-08	46	53	169	128
ASMTL	-1.086	4.07E-10	1.75E-08	412	454	1020	819
CHST8	-1.235	4.43E-10	1.90E-08	140	153	380	310
KLK8	-3.865	5.07E-10	2.16E-08	3	1	35	26
TFPI2	-1.21	5.10E-10	2.17E-08	238	279	675	521
MTFP1	-1.004	5.61E-10	2.38E-08	751	811	1717	1416
STEAP4	-1.859	5.78E-10	2.44E-08	29	18	93	78
FAM178B	-1.378	7.20E-10	3.02E-08	121	157	410	313
RAB36	-2.446	8.05E-10	3.36E-08	8	10	54	45
ARHGEF38	-2.226	8.60E-10	3.57E-08	12	12	62	51
PTPRN2	-3.339	9.03E-10	3.74E-08	3	7	70	33
TNIK	-1.365	9.13E-10	3.77E-08	67	61	173	157
CAMK2N1	-1.146	9.74E-10	4.00E-08	270	293	710	536
CTA-714B7.5	-1.934	1.11E-09	4.50E-08	17	25	82	79
ZMYND10	-1.895	1.15E-09	4.69E-08	20	21	77	76
PADI3	-2.486	1.16E-09	4.71E-08	14	6	67	46
KCTD17	-1.913	1.19E-09	4.80E-08	22	23	99	71
GAS6	-1.344	1.27E-09	5.11E-08	77	84	226	183
LMO3	-1.619	1.29E-09	5.20E-08	34	45	127	116
ZNF488	-1.433	1.32E-09	5.32E-08	68	93	231	204

WNT5A	-2.287	1.42E-09	5.69E-08	16	7	58	55
HOXA13	-1.773	1.64E-09	6.54E-08	27	22	90	78
SPRED1	-1.096	1.75E-09	6.95E-08	218	230	524	434
ABCC2	-1.723	1.76E-09	6.97E-08	33	22	91	91
CBLN4	-7.615	1.83E-09	7.23E-08	0	0	22	17
PROSAPIP1	-1.198	2.20E-09	8.66E-08	121	109	292	236
CCNO	-2.255	2.26E-09	8.90E-08	34	79	341	199
RP11-195F19.9	-1.529	2.56E-09	9.96E-08	52	66	198	143
DEFB4B	-5.17	2.64E-09	1.03E-07	0	1	22	21
NTN1	-1.003	2.69E-09	1.04E-07	263	237	526	476
COL4A6	-1.436	2.93E-09	1.13E-07	57	43	147	124
FOLR1	-2.111	2.95E-09	1.14E-07	13	13	61	52
AFF3	-1.467	3.18E-09	1.22E-07	71	58	157	200
FOXI3	-3.625	3.20E-09	1.23E-07	11	0	96	42
KIF12	-2.126	3.25E-09	1.24E-07	21	54	178	150
RP11-260A9.6	-7.721	3.28E-09	1.25E-07	0	0	27	15
DOCK10	-1.173	3.32E-09	1.26E-07	138	104	287	259
ITGA6	-1.098	3.56E-09	1.35E-07	294	346	752	618
KLF12	-1.167	3.61E-09	1.37E-07	192	161	460	333
RP11-18B16.2	-5.328	3.70E-09	1.40E-07	1	0	31	17
LINC00478	-1.224	3.72E-09	1.40E-07	90	88	210	206
CTXN1	-1.181	3.83E-09	1.44E-07	126	139	326	275
IL20RA	-2.602	4.23E-09	1.58E-07	8	6	50	36
IFT57	-1.004	4.26E-09	1.59E-07	447	508	1023	893
PYGO1	-2.046	4.54E-09	1.69E-07	12	22	74	67
HRNR	-3.122	5.56E-09	2.05E-07	0	12	56	50
MAF	-1.422	5.98E-09	2.19E-07	47	51	139	124
ZNF618	-1.038	6.41E-09	2.34E-07	387	424	938	727
LIMA1	-1.032	6.43E-09	2.34E-07	532	628	1308	1065
ZNF559	-1.227	6.66E-09	2.42E-07	107	77	229	202
RASGEF1B	-1.106	7.94E-09	2.87E-07	136	125	301	261
RHOH	-1.876	8.32E-09	3.00E-07	24	14	76	64
RP11-347E10.1	-1.064	8.45E-09	3.04E-07	505	627	1296	1071
PLAGL1	-2.049	8.88E-09	3.19E-07	12	27	87	75
MEIS1	-1.093	8.93E-09	3.20E-07	353	403	928	685
ADRB1	-1.521	9.24E-09	3.30E-07	37	50	132	118
RP1-212P9.2	-7.651	9.87E-09	3.51E-07	0	0	15	25
SYN3	-4.028	1.09E-08	3.83E-07	2	1	32	20
TPK1	-1.247	1.16E-08	4.07E-07	77	75	177	184
TNFRSF11B	-1.179	1.21E-08	4.24E-07	99	97	241	203
TRPC6	-1.791	1.27E-08	4.45E-07	27	48	119	141



PDE10A	-3.742	1.34E-08	4.67E-07	2	2	35	21
ELOVL2-AS1	-1.62	1.37E-08	4.75E-07	38	65	166	151
DENND5B	-1.105	1.39E-08	4.82E-07	246	264	635	462
IGHE	-1.596	1.44E-08	4.99E-07	36	31	93	110
TTC12	-1.292	1.48E-08	5.10E-07	71	80	205	165
RNF157	-1.739	1.48E-08	5.11E-07	55	68	268	143
AC009336.1	-2.783	1.51E-08	5.22E-07	6	4	39	31
NR2F1	-3.111	1.52E-08	5.23E-07	4	3	28	34
MIR203	-1.553	1.69E-08	5.80E-07	30	37	102	95
RP11-210M15.2	-1.993	1.77E-08	6.03E-07	12	19	63	61
TNS4	-1.895	1.93E-08	6.56E-07	15	19	67	60
RP11-61L23.2	-1.116	2.03E-08	6.87E-07	137	155	321	312
PRSS16	-1.439	2.19E-08	7.37E-07	56	35	133	114
SOBP	-2.571	2.71E-08	9.02E-07	15	2	51	51
AC144450.1	-1.06	2.85E-08	9.48E-07	137	131	285	274
CYB561D2	-1.006	2.93E-08	9.74E-07	270	309	607	556
AC135776.1	-2.184	2.99E-08	9.90E-07	11	19	57	80
RUNX1T1	-2.034	3.10E-08	1.02E-06	12	13	56	47
ZCCHC11	-1.14	3.29E-08	1.08E-06	96	94	219	200
PABPC1L2B	-2.972	3.33E-08	1.10E-06	5	4	46	26
GNB4	-1.193	3.38E-08	1.11E-06	131	88	276	225
NMNAT2	-1.193	3.89E-08	1.27E-06	91	93	201	220
RP11-214O1.2	-1.535	4.00E-08	1.29E-06	45	76	186	165
RP11-830F9.7	-1.333	4.07E-08	1.31E-06	72	87	233	168
SORL1	-1.066	4.15E-08	1.34E-06	195	156	417	318
KLK10	-2.972	4.40E-08	1.42E-06	5	4	28	44
AP000330.8	-3.154	4.53E-08	1.45E-06	2	4	27	28
ZNF256	-1.035	4.54E-08	1.45E-06	233	258	561	445
AL391421.1	-1.651	4.59E-08	1.47E-06	28	47	132	104
BAI2	-1.503	4.64E-08	1.48E-06	37	56	143	121
RP4-813D12.3	-2.643	4.73E-08	1.51E-06	4	8	45	31
DENND1A	-1.009	5.18E-08	1.64E-06	225	256	498	470
RP11-422N16.3	-7.577	5.26E-08	1.66E-06	0	0	13	25
SLC14A1	-2.325	5.82E-08	1.83E-06	9	7	45	36
RP4-625H18.2	-1.203	5.94E-08	1.86E-06	106	138	301	261
C3orf70	-1.133	6.36E-08	1.99E-06	105	121	263	233
OPRD1	-2.68	6.61E-08	2.06E-06	3	9	44	34
PABPC1L2A	-2.728	6.61E-08	2.06E-06	7	4	46	28
HMOX1	-1.017	6.89E-08	2.14E-06	186	186	419	334
SLC2A12	-1.207	7.46E-08	2.30E-06	90	87	237	172
KLK13	-7.5	7.75E-08	2.39E-06	0	0	24	12

RP11-153K16.1	-3.382	8.16E-08	2.50E-06	0	5	29	25
NXN	-1.07	8.63E-08	2.63E-06	156	152	369	278
C16orf62	-1.022	8.77E-08	2.67E-06	194	222	452	393
EEFSEC	-1.044	1.05E-07	3.18E-06	183	198	443	343
KIT	-1.498	1.06E-07	3.19E-06	34	31	104	80
TMPRSS3	-1.254	1.10E-07	3.30E-06	145	176	463	303
CPE	-1.033	1.25E-07	3.72E-06	223	271	545	466
RNASE4	-1.657	1.27E-07	3.77E-06	26	49	127	110
GK	-1.202	1.32E-07	3.90E-06	66	73	170	150
EGFR	-1.126	1.48E-07	4.32E-06	123	144	327	256
CHRM1	-2.471	1.63E-07	4.74E-06	8	5	33	40
RP11-145G20.1	-1.217	1.80E-07	5.20E-06	96	131	261	267
DNAJB5	-1.134	1.82E-07	5.26E-06	113	138	303	248
F7	-2.676	1.88E-07	5.41E-06	8	2	34	31
PITPNM3	-1.341	1.93E-07	5.54E-06	82	71	240	148
RP11-206M11.7	-1.831	2.01E-07	5.74E-06	18	17	74	51
DAPK1	-1.881	2.09E-07	5.95E-06	13	14	52	48
SOWAHA	-2.073	2.26E-07	6.39E-06	13	8	43	46
HMGB3P14	-1.272	2.29E-07	6.47E-06	55	43	126	111
AC021218.2	-2.395	2.32E-07	6.55E-06	4	12	43	42
KCNH1	-2.654	2.40E-07	6.76E-06	6	4	28	36
KDELCP1	-1.814	2.50E-07	7.02E-06	19	13	53	60
FBXO15	-2.271	2.93E-07	8.16E-06	8	8	46	32
MAPK10	-1.264	3.34E-07	9.16E-06	52	42	115	111
PGBD5	-1.312	3.52E-07	9.59E-06	46	63	141	130
TFAP2B	-7.19	3.55E-07	9.66E-06	0	0	13	16
SIGLEC15	-1.124	3.71E-07	1.01E-05	186	263	513	466
ZNF608	-2.608	3.76E-07	1.02E-05	3	7	33	29
TEX14	-1.136	3.76E-07	1.02E-05	92	69	197	157
RUNDC3B	-1.298	3.77E-07	1.02E-05	80	48	179	136
NPY5R	-2.122	3.79E-07	1.02E-05	10	8	40	39
FAM43A	-1.047	3.81E-07	1.03E-05	135	121	302	227
ETV4	-2.006	3.82E-07	1.03E-05	14	8	45	44
APCDD1	-1.614	4.48E-07	1.19E-05	20	22	68	61
RP11-317J10.2	-2.648	5.42E-07	1.42E-05	2	9	35	35
TMEM31	-5.203	5.58E-07	1.46E-05	0	1	33	11
GNAZ	-1.195	5.66E-07	1.48E-05	229	331	753	529
CCDC110	-1.846	5.97E-07	1.55E-05	14	12	50	44
AMMECR1LP1	-2.072	6.05E-07	1.57E-05	10	21	82	49
KCNN4	-1.013	6.26E-07	1.62E-05	112	106	236	204
PDZK1	-1.085	7.07E-07	1.81E-05	124	161	319	286

SPOCD1	-1.043	7.44E-07	1.89E-05	96	81	192	173
SLC22A17	-1.014	7.46E-07	1.89E-05	138	100	258	223
CLCA2	-1.929	7.93E-07	2.01E-05	16	13	70	41
SOX9	-1.046	8.36E-07	2.11E-05	130	116	294	214
RP11-347D21.4	-1.007	8.52E-07	2.15E-05	158	140	346	253
TTLL11	-1.457	9.14E-07	2.28E-05	38	50	104	138
HOXD-AS1	-1.492	1.01E-06	2.50E-05	25	25	76	65
RP11-124N14.3	-3.721	1.07E-06	2.64E-05	1	2	27	15
STRA6	-1.918	1.09E-06	2.68E-05	17	8	54	41
ZIC3	-1.675	1.14E-06	2.78E-05	20	14	60	49
C10orf107	-2.959	1.18E-06	2.88E-05	3	3	21	27
PIK3C2G	-3.363	1.20E-06	2.92E-05	4	0	20	23
TH	-2.35	1.23E-06	2.98E-05	6	6	31	31
RP11-22P6.3	-2.038	1.32E-06	3.17E-05	16	6	42	49
RP11-483P21.2	-2.058	1.36E-06	3.24E-05	12	21	91	47
RP11-1223D19.1	-1.443	1.36E-06	3.24E-05	28	30	90	68
SMOC2	-1.452	1.40E-06	3.33E-05	40	37	131	80
CDC42EP3	-1.863	1.44E-06	3.42E-05	10	19	52	54
BAG2	-1.006	1.45E-06	3.43E-05	160	193	395	314
DNAH7	-1.204	1.72E-06	4.04E-05	48	53	126	107
MYEOV	-1.52	1.73E-06	4.06E-05	28	50	127	97
OSCP1	-1.413	1.75E-06	4.11E-05	32	49	103	113
AP002348.1	-2.773	1.81E-06	4.24E-05	3	4	27	22
PDLIM3	-3.3	1.85E-06	4.31E-05	5	0	33	18
Z83851.1	-3.615	1.96E-06	4.56E-05	0	3	17	22
ANK1	-1.256	1.98E-06	4.60E-05	47	58	143	108
PPP1R14C	-2.234	2.05E-06	4.74E-05	13	3	39	37
HMGCS2	-7.033	2.08E-06	4.80E-05	0	0	11	15
ELOVL3	-2.004	2.13E-06	4.92E-05	9	24	80	53
LL22NC03-104C7	-2.532	2.58E-06	5.87E-05	4	5	29	24
MRAS	-1.091	2.62E-06	5.95E-05	88	111	235	189
OLFM2	-1.227	2.72E-06	6.17E-05	67	41	142	111
AL583842.3	-1.189	2.74E-06	6.19E-05	58	48	139	103
RP11-27K13.3	-1.41	2.74E-06	6.19E-05	47	24	105	84
DTX4	-1.059	2.75E-06	6.22E-05	94	107	196	223
SLC43A1	-1.794	2.82E-06	6.35E-05	15	16	46	62
FSCN1	-1.053	3.09E-06	6.94E-05	144	187	390	297
LINC00665	-1.098	3.15E-06	7.05E-05	63	70	154	131
CLIC6	-2.243	3.33E-06	7.38E-05	7	7	41	26
RGAG1	-2.378	3.85E-06	8.46E-05	8	3	32	26
FSD1	-1.447	3.94E-06	8.63E-05	26	41	103	80

SPRY1	-1.198	4.53E-06	9.77E-05	42	49	110	99
CHST11	-1.279	4.63E-06	9.96E-05	99	123	344	195
MIR148A	-1.73	4.79E-06	0.000103	13	14	51	39
C17orf97	-1.073	4.84E-06	0.000103	85	96	220	161
FLJ27352	-1.315	5.06E-06	0.000108	35	28	76	81
SH3TC2	-1.159	5.68E-06	0.00012	45	44	102	97
PCOLCE2	-3.222	6.13E-06	0.000128	4	0	18	21
ACE2	-2.41	6.59E-06	0.000137	3	7	29	25
PLEKHS1	-2.378	7.53E-06	0.000155	9	2	32	26
GPR39	-1.079	8.44E-06	0.000172	86	108	236	174
RP11-493K23.1	-3.826	8.90E-06	0.000181	2	0	14	17
AMBP	-3.779	1.12E-05	0.000222	0	2	15	15
SNCB	-3.375	1.17E-05	0.00023	1	2	19	14
GLIPR2	-1.356	1.18E-05	0.00023	46	73	185	120
LINC00327	-4.448	1.19E-05	0.000232	1	0	13	13
RP11-1286E23.1	-2.561	1.24E-05	0.000241	1	9	32	28
RP11-127O4.3	-3.826	1.24E-05	0.000242	2	0	13	18
MIR30C2	-3.779	1.28E-05	0.000247	2	0	14	16
AC084125.1	-1.746	1.33E-05	0.000255	11	13	38	43
DACT3	-2.115	1.45E-05	0.000277	8	5	30	27
CTA-392C11.2	-1.145	1.46E-05	0.000278	46	57	127	101
HAR1B	-1.779	1.46E-05	0.000278	11	11	36	40
CTHRC1	-1.518	1.64E-05	0.000308	19	35	91	64
RAI2	-1.47	1.68E-05	0.000315	21	24	55	70
FAM149A	-1.282	1.69E-05	0.000317	32	39	101	72
FREM1	-2.698	1.81E-05	0.000339	8	0	31	22
CENPC1P1	-2.178	1.87E-05	0.000348	8	4	25	30
RP11-567G11.1	-1.13	1.88E-05	0.000349	52	42	118	88
APOBR	-1.857	1.95E-05	0.000361	10	10	44	29
AC104655.3	-1.214	2.03E-05	0.000375	33	35	86	72
IL17REL	-2.661	2.12E-05	0.000388	3	3	21	18
GNAQP1	-1.085	2.13E-05	0.000389	54	59	136	104
DCPS	-1.066	2.17E-05	0.000396	79	68	185	123
RP1-310O13.12	-2.869	2.21E-05	0.000403	0	9	43	24
KRT6B	-2.697	2.29E-05	0.000415	5	1	20	20
RNU4-4P	-1.063	2.30E-05	0.000416	63	46	126	102
BEX5	-1.771	2.33E-05	0.000421	14	9	34	45
INPP5D	-3.147	2.36E-05	0.000426	4	0	22	15
NYAP2	-2.359	2.37E-05	0.000427	4	5	26	21
LHX6	-1.023	2.40E-05	0.000431	67	50	121	117
RP11-247A12.2	-2.27	2.57E-05	0.000457	6	4	27	22

LAMP3	-1.838	2.59E-05	0.000461	8	12	42	30
FOSL1	-1.458	2.60E-05	0.000461	22	15	57	45
FAM83E	-1.129	2.72E-05	0.000481	42	42	88	96
GABBR2	-1.388	2.77E-05	0.00049	22	18	55	50
STK32A	-2.983	3.07E-05	0.000534	2	2	17	16
FYB	-6.658	3.19E-05	0.000552	0	0	11	9
RP11-273G15.2	-1.652	3.22E-05	0.000558	14	11	45	34
C1orf127	-6.658	3.63E-05	0.00062	0	0	9	11
HPD	-1.458	3.72E-05	0.000634	23	14	58	44
CLDN1	-1.086	3.84E-05	0.000651	47	57	123	98
RP11-262H14.7	-1.692	4.22E-05	0.00071	13	11	47	31
RP11-150O12.3	-1.194	4.24E-05	0.000713	64	53	171	97
KLF15	-1.894	4.25E-05	0.000713	7	9	28	32
KIAA1239	-3.628	4.39E-05	0.000734	2	0	15	12
GJA1	-2.165	4.60E-05	0.000765	5	8	38	21
PEX11G	-1.012	4.64E-05	0.00077	59	46	107	105
FAM81A	-1.239	4.69E-05	0.000777	27	36	82	67
RAB39A	-1.751	4.90E-05	0.00081	19	7	53	35
MAPRE2	-1.081	5.13E-05	0.000843	72	109	213	170
LDHB	-1.962	5.17E-05	0.000847	10	5	34	25
NPW	-2.445	5.65E-05	0.000918	4	3	19	20
RP1-102D24.5	-1.596	5.70E-05	0.000926	12	15	41	41
ATP6V0D2	-2.213	5.80E-05	0.00094	5	8	41	20
SARDH	-1.779	5.83E-05	0.000942	8	14	44	32
VEGFC	-1.424	6.10E-05	0.000979	18	24	66	47
SLC13A3	-1.137	6.30E-05	0.00101	35	34	82	70
JAKMIP1	-1.293	6.49E-05	0.00103	23	23	58	55
AKR1B10	-2.366	6.72E-05	0.00107	10	4	53	20
TIGD3	-1.01	6.73E-05	0.00107	59	67	118	136
PRSS30P	-1.039	7.01E-05	0.00111	48	40	95	86
F2R	-1.202	7.02E-05	0.00111	27	32	68	68
TRPM6	-3.238	7.02E-05	0.00111	1	2	19	11
HLA-DRB6	-1.306	7.32E-05	0.00115	31	34	101	60
DUSP7	-1.242	7.35E-05	0.00115	84	107	300	152
CLEC7A	-1.131	8.15E-05	0.00126	37	30	76	71
RP11-279F6.1	-1.286	8.19E-05	0.00127	36	18	70	62
PTPN22	-1.056	8.29E-05	0.00128	45	54	99	107
C1QL4	-1.559	8.66E-05	0.00133	16	10	38	39
RP4-813D12.2	-1.385	8.80E-05	0.00135	18	24	63	47
SDR16C5	-1.448	9.10E-05	0.00138	30	30	110	54
AUTS2	-1.426	9.17E-05	0.00139	20	13	44	45

RP11-3P17.4	-1.137	9.20E-05	0.0014	42	27	83	69
RP11-483C6.1	-2.084	9.24E-05	0.0014	11	3	37	23
AC068580.5	-1.325	9.39E-05	0.00142	21	18	49	49
ADAM19	-1.228	0.000106	0.00158	47	31	115	68
OSBPL6	-1.06	0.000117	0.00171	48	32	89	78
ZNF804A	-2.397	0.000122	0.00178	6	2	17	26
NTNG1	-1.524	0.000128	0.00185	11	24	53	48
C11orf70	-2.585	0.000137	0.00196	2	4	23	14
ADM2	-1.226	0.000138	0.00198	27	34	85	58
SLC7A8	-1.033	0.000139	0.00199	40	41	85	81
ARMCX4	-1.454	0.000148	0.0021	16	16	38	50
RIBC1	-1.109	0.000152	0.00215	34	47	96	79
RP11-324I22.2	-6.426	0.000154	0.00216	0	0	9	8
CCBL1	-1.015	0.000157	0.00222	44	40	93	77
GLIS3	-1.089	0.00016	0.00224	38	47	103	78
CCM2L	-1.157	0.000165	0.00231	48	29	103	69
RP11-116G8.4	-1.102	0.000169	0.00235	37	43	101	71
FAM171A1	-1.076	0.000172	0.00239	45	46	116	76
DNER	-1.769	0.000173	0.0024	9	7	28	27
PPP2R2B	-2.464	0.000175	0.00242	2	4	18	16
C1orf64	-3.871	0.000185	0.00254	2	0	25	7
TMC7	-1.016	0.000187	0.00257	41	42	83	85
KRT6C	-2.798	0.000197	0.0027	3	1	14	15
RP5-998N21.7	-6.426	0.000208	0.00282	0	0	7	10
BX571672.1	-1.018	0.000216	0.00291	74	117	188	199
HMX3	-6.585	0.000218	0.00293	0	0	14	5
RP1-34B20.4	-1.007	0.000238	0.00317	40	45	84	87
RP4-622L5.7	-2.585	0.000248	0.00328	3	2	14	17
ZPLD1	-1.698	0.000251	0.00332	10	29	51	76
CCDC28B	-1.147	0.000255	0.00336	25	30	65	57
RP11-49C9.2	-6.34	0.000257	0.00338	0	0	8	8
FST	-6.34	0.000257	0.00339	0	0	8	8
CCDC33	-1.868	0.000266	0.00348	9	4	24	24
RP3-426I6.2	-6.34	0.000266	0.00348	0	0	9	7
SLC16A10	-1.704	0.000267	0.00349	9	28	74	47
RP11-713M6.2	-1.232	0.000269	0.00352	21	27	53	60
CD101	-1.309	0.000277	0.0036	18	19	45	47
HOXB13	-3.108	0.000277	0.00361	0	4	11	25
RP1-127B20.4	-2.397	0.000277	0.00361	4	4	30	13
ANXA1	-1.24	0.000279	0.00363	19	30	61	55
RP11-734K21.5	-2.033	0.000299	0.00384	13	2	38	24

RP11-267A15.1	-2.893	0.000308	0.00393	2	2	21	10
TMEM40	-1.007	0.000312	0.00398	38	44	91	74
RP11-309H21.3	-2.257	0.000322	0.00409	3	5	24	15
SHC3	-2.369	0.000322	0.00409	5	2	23	14
DIO3	-1.137	0.000338	0.00428	29	25	66	53
RSL24D1P3	-1.649	0.000342	0.00431	12	7	35	25
CASQ2	-3.459	0.000371	0.00462	2	0	16	8
AC073063.10	-1.513	0.000372	0.00463	11	12	38	28
TMEM139	-1.173	0.000384	0.00476	32	22	73	49
SCIN	-1.702	0.000384	0.00476	8	10	24	35
ABCB4	-1.398	0.000396	0.00489	20	11	48	34
PCDH8	-1.155	0.000411	0.00505	32	55	112	82
SOAT2	-6.34	0.000412	0.00505	0	0	6	10
CTD-2210P24.4	-1.838	0.000425	0.0052	5	8	25	22
RP11-45P15.4	-1.825	0.000457	0.00553	7	16	55	27
RP11-364B14.3	-2.695	0.000461	0.00556	2	2	16	11
XKR7	-3.399	0.000461	0.00556	2	0	9	14
TMEM171	-1.373	0.000469	0.00565	14	16	42	36
AC074289.1	-1.845	0.000471	0.00565	4	12	29	29
GSTA1	-1.948	0.000478	0.00573	4	7	24	19
SOX6	-1.838	0.000486	0.00581	7	6	28	19
AP001136.2	-6.426	0.000492	0.00586	0	0	5	12
GLP2R	-2.377	0.000517	0.00611	5	1	18	14
SORCS1	-2.016	0.00054	0.00633	4	5	19	18
CHGA	-1.793	0.000546	0.00638	9	5	29	20
KMO	-1.068	0.00056	0.00653	38	32	89	58
OR2B6	-1.104	0.000562	0.00654	32	20	58	54
PP13439	-1.619	0.000578	0.00671	11	11	45	23
FAM133A	-1.412	0.000584	0.00677	20	43	67	101
RP11-47P18.1	-2.798	0.000584	0.00677	1	3	19	10
HAR1A	-1.857	0.000588	0.0068	7	5	19	25
RP11-91H12.2	-2.29	0.000599	0.00692	3	4	22	13
SLITRK1	-1.181	0.0006	0.00693	21	23	56	44
ATP5G1P4	-1.446	0.000609	0.00702	12	11	33	30
RP11-642P15.1	-1.354	0.000623	0.00715	23	16	65	35
FRY	-1.147	0.000627	0.00718	30	39	95	58
F5	-4.143	0.000665	0.00756	0	1	6	15
RP11-707O23.5	-1.672	0.000678	0.00768	15	4	32	29
KLK7	-2.919	0.00069	0.00779	2	1	15	9
COL17A1	-1.529	0.000695	0.00782	13	8	36	25
PDE3B	-1.6	0.000695	0.00783	8	11	35	23

ABCB1	-2.919	0.000701	0.00788	0	3	12	12
PKDCC	-1.519	0.000708	0.00795	8	17	39	33
ACOX2	-1.335	0.000717	0.00802	18	12	35	41
NXPH1	-2.695	0.00072	0.00805	0	4	14	13
CYS1	-1.288	0.000722	0.00807	16	15	37	39
BPIFB1	-1.218	0.000723	0.00807	20	19	43	48
EREG	-1.275	0.00073	0.00813	18	17	37	48
RP11-412D9.4	-1.549	0.000746	0.00827	8	11	30	26
MEF2C	-3.399	0.000758	0.00837	0	2	16	7
TRIM46	-1.976	0.000779	0.00858	4	5	18	18
USP26	-6.15	0.000799	0.00876	0	0	8	6
PTH	-2.919	0.0008	0.00877	0	3	14	10
AC068580.7	-2.284	0.000809	0.00886	2	4	15	15
AC114812.5	-6.34	0.000811	0.00887	0	0	12	4
IGSF9B	-1.008	0.000855	0.00928	34	42	89	64
PABPC1P7	-6.15	0.000882	0.00951	0	0	6	8
LAG3	-3.335	0.00089	0.00959	0	2	8	14
PPARGC1A	-2.585	0.000896	0.00964	2	2	12	13
ZNF716	4.925	1.13E-129	6.01E-126	2314	2371	97	57
APOD	4.635	6.27E-116	1.85E-112	4366	4335	219	131
RP11-402M4.1	12.105	1.10E-109	2.65E-106	441	440	0	0
SLC17A9	3.893	5.97E-98	1.22E-94	2161	2493	163	150
RP11-313J2.1	3.15	2.42E-90	4.02E-87	2648	2589	313	277
ZNF844	4.061	1.90E-77	2.65E-74	906	1083	65	54
CTD-3006G17.2	3.027	6.13E-77	8.13E-74	1479	1350	179	168
ZNF788	4.857	6.71E-76	8.10E-73	391	368	16	10
RP11-10A2.1	11.308	3.31E-72	3.82E-69	238	269	0	0
ZNF69	3.192	1.69E-71	1.79E-68	1456	1506	187	137
LINC00645	3.591	2.14E-69	2.19E-66	587	572	49	47
RMST	2.716	1.23E-68	1.21E-65	2418	2460	396	346
RP11-101E13.1	3.19	1.11E-66	1.05E-63	856	734	98	76
SPAM1	4.686	5.55E-66	5.08E-63	341	359	17	10
ZNF729	7.557	6.11E-65	5.41E-62	208	206	2	0
NEB	2.603	2.40E-62	2.05E-59	1878	1812	332	275
VCAN	4	3.36E-62	2.79E-59	474	425	38	18
CTC-260E6.2	2.811	2.11E-60	1.65E-57	1200	1209	193	150
POTEF	2.842	6.25E-60	4.74E-57	852	791	116	113
INSL4	7.448	1.24E-57	8.87E-55	182	202	2	0
IGFBP5	2.411	5.97E-56	4.17E-53	38584	37530	8015	6300
ZNF98	2.378	6.04E-54	4.01E-51	1671	1532	334	282
ZNF486	2.324	2.09E-53	1.32E-50	4458	4628	975	840



AC104135.3	2.351	2.11E-52	1.27E-49	15518	16041	3422	2762
FAM123A	2.661	8.11E-49	4.22E-46	803	862	142	121
RNF217	3.724	2.01E-48	9.91E-46	316	347	31	19
CXCL14	2.921	6.96E-46	3.13E-43	1105	1130	187	108
AKAP6	4.155	4.07E-45	1.69E-42	203	210	15	8
RP11-384J4.2	4.185	1.08E-44	4.41E-42	241	290	12	17
ZNF676	4.408	4.07E-44	1.59E-41	220	251	17	5
RP11-867G2.6	4.184	4.33E-44	1.67E-41	190	177	9	11
RP11-553A10.1	3.619	4.61E-44	1.75E-41	246	260	19	22
BX571672.5	2.585	2.29E-43	8.45E-41	533	464	90	76
RAB34	5.559	5.35E-43	1.95E-40	139	153	2	4
RAG1	4.094	6.98E-43	2.50E-40	202	228	12	13
PI15	2.879	1.01E-41	3.47E-39	365	372	50	50
PABPC4L	2.076	1.16E-41	3.95E-39	2478	2487	667	510
ZNF415	3.562	6.79E-41	2.23E-38	238	272	22	21
hsa-mir-3171	3.487	7.17E-40	2.29E-37	229	188	18	19
PSG9	3.363	1.01E-39	3.18E-37	349	414	47	27
RP11-14K3.6	6.612	8.08E-39	2.44E-36	118	97	0	2
FAM201B	2.354	9.88E-39	2.95E-36	582	513	119	95
NT5E	2.098	8.13E-38	2.37E-35	1446	1475	388	294
CTB-33O18.1	1.986	8.70E-38	2.51E-35	2413	2677	658	627
RP11-423O2.2	2.04	1.82E-37	5.13E-35	2125	1662	440	481
ZNF355P	3.468	1.47E-36	3.97E-34	231	280	21	25
COL5A2	2.135	8.47E-36	2.21E-33	724	744	178	156
RP11-95P9.1	3.297	5.34E-35	1.31E-32	193	192	24	15
ATRNL1	1.838	3.51E-34	8.41E-32	3733	4020	1153	1016
INHBA	1.929	8.21E-34	1.93E-31	3270	3348	1000	738
TMEM229A	4.634	8.85E-34	2.06E-31	144	109	2	8
COL12A1	1.761	1.98E-33	4.57E-31	8698	8440	2792	2265
SHISA2	1.695	6.05E-33	1.37E-30	2806	2779	929	796
GATM	2.815	9.65E-33	2.15E-30	247	268	36	37
ZNF962P	3.288	1.17E-32	2.59E-30	178	195	17	21
RNF32	1.808	1.23E-32	2.71E-30	1457	1450	451	379
ANXA9	1.795	1.34E-32	2.92E-30	4124	4474	1315	1163
ART4	2.045	1.38E-32	2.99E-30	977	1103	269	235
ZNF441	2.048	2.88E-32	6.13E-30	948	1067	264	223
SSFA2	1.756	4.24E-31	8.66E-29	39101	41426	13123	10721
ABCA12	1.692	5.00E-31	1.01E-28	6975	6937	2367	1938
PHLDA1	1.715	1.40E-30	2.81E-28	11662	11176	3918	3038
PTGER4	2.022	1.06E-29	2.09E-27	1322	1424	401	275
RP11-192P9.1	2.327	5.60E-29	1.07E-26	297	281	56	59

LRP2	2.043	6.44E-29	1.21E-26	440	434	111	101
ITM2A	4.637	1.43E-28	2.65E-26	92	87	2	5
SLC5A12	4.107	1.98E-28	3.62E-26	103	107	8	4
TACC1	1.707	3.45E-28	6.23E-26	3959	4101	1403	1066
ZNF679	3.715	3.53E-28	6.34E-26	125	127	15	4
CABP4	4.602	4.17E-28	7.43E-26	91	108	4	4
AC018865.8	2.033	4.29E-28	7.60E-26	565	520	121	144
SLC4A10	1.636	6.17E-28	1.08E-25	2064	2190	739	630
ZNF492	1.656	6.85E-28	1.20E-25	1336	1358	449	406
KRT8P4	1.777	7.07E-28	1.23E-25	744	658	222	187
MKX	2.288	2.00E-27	3.39E-25	301	325	65	63
RP11-80F22.5	6.827	2.34E-27	3.94E-25	68	68	1	0
AC093375.1	1.713	3.58E-27	5.99E-25	821	756	241	240
AC108142.1	2.365	3.69E-27	6.13E-25	447	522	83	105
C7orf13	1.576	4.44E-27	7.29E-25	3592	3662	1327	1106
HAPLN1	6.024	9.31E-27	1.50E-24	69	74	0	2
CADM1	1.608	1.20E-26	1.89E-24	4409	4670	1640	1338
ZNF626	4.954	1.62E-26	2.53E-24	83	109	4	2
CXorf61	1.98	2.09E-26	3.23E-24	537	560	160	118
RP11-366L5.1	2.282	2.45E-26	3.75E-24	252	240	50	51
ZNF208	9.484	6.47E-26	9.75E-24	60	83	0	0
KIAA0087	4.745	1.43E-25	2.11E-23	77	89	4	2
BCAS1	1.572	2.59E-25	3.76E-23	4737	5070	1818	1480
EIF3FP1	2.329	3.88E-25	5.50E-23	360	339	89	50
SERPINA1	1.588	6.76E-25	9.39E-23	3189	3426	1227	973
RP11-46C20.1	1.974	7.96E-25	1.10E-22	414	396	120	86
ZNF733P	5.453	1.09E-24	1.50E-22	81	59	2	1
FHL1	1.455	3.58E-24	4.77E-22	2438	2363	970	781
FAM84A	1.431	4.61E-24	6.12E-22	2606	2661	1040	913
SGCG	1.559	6.99E-24	9.06E-22	1689	1761	659	512
FOS	1.51	9.49E-24	1.22E-21	3476	3813	1354	1205
POTEE	1.724	1.86E-23	2.36E-21	569	535	161	173
LDHD	1.532	2.54E-23	3.18E-21	1323	1424	504	446
RNA5SP18	2.139	2.95E-23	3.65E-21	271	298	63	66
ZNF264	1.703	2.99E-23	3.69E-21	1019	1069	373	268
RAB37	1.695	3.41E-23	4.15E-21	1129	1338	399	363
CYP24A1	1.804	4.82E-23	5.85E-21	900	958	317	215
STC1	1.47	4.90E-23	5.91E-21	22122	22435	8995	7091
SPATA17	1.825	5.41E-23	6.49E-21	411	429	127	110
DNALI1	2.468	6.34E-23	7.59E-21	236	307	52	46
RP11-476K15.1	4.304	1.57E-22	1.83E-20	71	71	3	4

AC018890.6	1.981	3.66E-22	4.21E-20	290	283	68	77
ZNF734P	4.636	3.99E-22	4.55E-20	94	60	4	2
GDNF	2.806	4.14E-22	4.70E-20	135	167	22	21
AC104135.2	1.976	4.92E-22	5.54E-20	306	277	68	80
HPN	2.974	5.12E-22	5.73E-20	114	131	15	16
ZNF257	1.357	6.51E-22	7.26E-20	2229	2242	929	816
GEM	1.706	1.26E-21	1.38E-19	570	628	200	167
MAST4	1.432	1.66E-21	1.81E-19	6050	6499	2558	2093
DNAAF1	1.704	2.48E-21	2.69E-19	613	681	221	176
WIPF1	1.405	4.15E-21	4.46E-19	1586	1623	666	546
BNIP1	1.596	4.58E-21	4.89E-19	955	995	373	272
ZNF442	1.53	1.21E-20	1.27E-18	1308	1523	530	450
HMG11P16	1.565	1.26E-20	1.30E-18	563	523	181	186
FOXP2	2.87	1.81E-20	1.87E-18	106	100	18	10
BRWD3	1.47	2.11E-20	2.18E-18	1105	1144	456	356
LINC00491	2.124	2.62E-20	2.67E-18	192	166	45	37
TENM3	1.398	3.26E-20	3.32E-18	1043	1031	428	359
VWDE	2.048	3.51E-20	3.55E-18	193	184	49	42
RP11-282E4.1	2.965	6.20E-20	6.26E-18	138	207	21	23
RP11-561N12.2	8.752	1.60E-19	1.59E-17	43	43	0	0
KIAA1467	1.354	2.34E-19	2.30E-17	3168	3193	1410	1079
SYCP2	1.282	2.90E-19	2.82E-17	2299	2334	1040	865
SAMD13	1.755	4.56E-19	4.38E-17	291	253	80	81
TDRD1	1.405	5.37E-19	5.13E-17	984	1000	418	331
AP000462.2	1.887	8.04E-19	7.57E-17	341	303	74	100
RP11-460N11.2	3.441	1.39E-18	1.30E-16	72	82	5	9
PLA2G16	1.385	1.49E-18	1.38E-16	1614	1797	725	581
ZNF334	3.087	2.09E-18	1.92E-16	79	84	9	10
UNC13D	1.476	3.09E-18	2.82E-16	729	773	260	280
RP11-8L2.1	1.832	3.09E-18	2.82E-16	215	202	61	56
MUC16	1.642	3.10E-18	2.82E-16	583	416	173	147
RP11-730G20.1	2.304	4.50E-18	4.07E-16	178	124	32	29
FAM13C	2.712	4.66E-18	4.19E-16	91	87	14	13
RNU5F-1	1.853	5.34E-18	4.78E-16	217	188	62	50
AC005534.6	1.813	5.82E-18	5.18E-16	342	379	122	83
TGFB1	1.248	7.76E-18	6.83E-16	2130	2258	992	856
SV2B	2.374	9.10E-18	7.97E-16	124	105	26	18
DCDC2	1.356	1.25E-17	1.08E-15	4365	4479	2012	1442
RP11-80F22.6	5.435	1.66E-17	1.43E-15	43	52	2	0
GJB7	1.597	2.50E-17	2.12E-15	391	417	151	116
RP11-6N13.1	2.682	3.42E-17	2.88E-15	91	109	16	15

STC2	1.238	4.36E-17	3.66E-15	39442	40407	18886	14978
LONRF2	1.184	5.27E-17	4.40E-15	11175	11223	5315	4542
ABCG2	1.312	9.40E-17	7.71E-15	1449	1548	685	522
CNGB3	1.355	1.30E-16	1.05E-14	596	576	252	206
CASP10	1.565	1.33E-16	1.07E-14	325	341	120	105
SPARCL1	2.23	1.43E-16	1.15E-14	116	110	23	25
LIMCH1	1.57	1.46E-16	1.17E-14	383	431	139	135
MAT1A	2.158	2.50E-16	1.96E-14	132	123	35	22
RP11-321E8.1	3.251	5.00E-16	3.87E-14	62	73	6	8
ZNF439	2.867	5.02E-16	3.87E-14	126	167	30	10
COL21A1	1.28	8.33E-16	6.32E-14	1020	1010	478	358
XCL1	2.733	1.07E-15	7.97E-14	84	70	10	13
ZNF479	4.849	1.09E-15	8.10E-14	56	36	2	1
POTEI	1.225	1.38E-15	1.02E-13	1391	1507	680	560
MAP2	1.245	1.49E-15	1.09E-13	765	672	333	273
ZNF91	1.171	1.55E-15	1.13E-13	21403	22675	10744	8829
KRT24	2.432	1.82E-15	1.32E-13	92	87	15	18
RP11-395N3.1	1.106	1.92E-15	1.39E-13	15985	15278	7899	6628
FAM63A	1.313	2.47E-15	1.77E-13	3377	3877	1681	1238
ADIPOR2	1.145	2.53E-15	1.81E-13	11648	12308	5833	5003
RP11-68L18.1	1.365	3.30E-15	2.36E-13	1143	1199	541	368
RP11-662G23.1	1.261	3.46E-15	2.45E-13	1752	2085	854	747
PAPLN	1.575	4.03E-15	2.84E-13	242	247	87	77
ZNF506	1.161	5.00E-15	3.48E-13	3460	3618	1766	1399
ZDHC15	5.076	1.11E-14	7.65E-13	38	36	0	2
PTGER3	1.468	1.18E-14	8.09E-13	364	397	133	142
AC002075.3	1.087	1.39E-14	9.44E-13	2011	2047	1030	880
WNT2B	1.58	1.43E-14	9.65E-13	240	197	79	67
PCDHB5	1.522	1.62E-14	1.09E-12	304	288	94	112
TP53TG3B	2.151	2.03E-14	1.36E-12	100	105	26	20
MPV17L	1.233	2.09E-14	1.40E-12	1226	1372	619	486
SPINK5	1.493	2.16E-14	1.44E-12	286	311	109	103
RP11-6N13.4	1.041	3.21E-14	2.12E-12	2362	2224	1115	1113
GAPDHP21	2.306	3.46E-14	2.29E-12	84	80	17	16
CTD-2015H3.1	4.291	4.21E-14	2.74E-12	45	37	4	0
CD74	1.861	4.56E-14	2.95E-12	154	119	40	35
MIR1305	2.002	4.95E-14	3.18E-12	125	148	32	36
NEK9	1.271	5.15E-14	3.30E-12	946	1050	473	354
ZNF347	1.229	5.17E-14	3.31E-12	538	482	237	198
LMCD1	1.19	5.80E-14	3.68E-12	1015	1094	516	408
CYP4F30P	2.188	6.54E-14	4.13E-12	91	92	19	21

BAG3	1.1	7.31E-14	4.59E-12	6739	7228	3564	2950
GALM	1.291	9.75E-14	6.09E-12	804	907	399	300
CLMP	1.411	1.00E-13	6.23E-12	327	354	140	116
NECAB1	1.091	1.13E-13	6.97E-12	12337	12897	6573	5276
PROS1	1.244	1.31E-13	8.06E-12	477	409	202	172
CXCR7	1.13	1.34E-13	8.21E-12	6441	6820	3443	2615
MIR4652	1.142	1.36E-13	8.33E-12	770	693	365	298
MATN3	1.294	1.65E-13	1.01E-11	395	400	177	147
MC4R	2.344	2.19E-13	1.32E-11	90	124	21	21
RP11-248C1.2	1.705	2.31E-13	1.39E-11	226	270	91	61
UCN3	2.705	3.00E-13	1.80E-11	70	55	11	8
SLC7A2	1.063	3.22E-13	1.93E-11	72915	74398	39393	31132
DLC1	1.114	3.41E-13	2.03E-11	2132	2207	1154	851
ZNF853	1.472	3.53E-13	2.10E-11	249	259	104	79
ZNF737	1.071	3.71E-13	2.20E-11	3180	3270	1721	1350
FAM46A	1.068	4.16E-13	2.46E-11	8709	9025	4730	3727
FRK	1.137	7.21E-13	4.18E-11	1344	1354	712	515
CYP4F43P	1.53	7.33E-13	4.23E-11	194	179	74	55
MCEE	1.069	8.23E-13	4.74E-11	803	722	376	351
C12orf69	1.424	8.92E-13	5.12E-11	225	202	85	74
FGF18	1.537	9.86E-13	5.62E-11	269	332	114	93
FCGRT	1.777	1.04E-12	5.89E-11	140	145	51	32
COL9A3	1.092	1.29E-12	7.24E-11	852	894	434	385
LINC00534	1.064	1.31E-12	7.36E-11	923	902	435	438
LMBR1	1.007	1.62E-12	8.99E-11	22528	22653	12408	10080
CLEC3A	1.053	1.94E-12	1.06E-10	1771	1919	981	797
MXRA7	1.114	2.78E-12	1.52E-10	1064	1220	549	506
SPATA9	1.351	3.05E-12	1.66E-10	250	230	93	95
ATP8A2	1.557	3.24E-12	1.76E-10	310	379	141	93
SNCAIP	2.585	4.39E-12	2.37E-10	83	146	19	19
GPR158	1.429	4.77E-12	2.57E-10	360	386	169	108
NR3C1	1.068	4.88E-12	2.62E-10	4382	4707	2477	1858
TRIM54	2.515	5.03E-12	2.69E-10	60	61	12	9
AC139666.1	1.378	5.08E-12	2.71E-10	239	237	104	79
RCN1	1.079	7.95E-12	4.18E-10	768	793	408	331
BCAM	1.055	8.83E-12	4.60E-10	1261	1414	693	594
MYT1	1.807	9.18E-12	4.77E-10	120	150	40	37
GNA15	1.663	1.51E-11	7.73E-10	211	277	70	84
GS1-179L18.1	3.29	1.54E-11	7.86E-10	41	39	3	5
AP000462.1	1.678	1.59E-11	8.06E-10	160	122	39	49
C21orf88	1.615	1.64E-11	8.30E-10	182	192	77	45

NAV2	1.165	1.66E-11	8.43E-10	705	659	361	247
CLDN9	1.115	1.67E-11	8.44E-10	828	842	447	324
AC005534.8	1.826	1.74E-11	8.80E-10	96	96	30	24
CSGALNACT1	1.253	1.87E-11	9.37E-10	294	257	113	118
GIMAP2	2.02	2.47E-11	1.22E-09	82	89	26	16
HTR2C	1.679	3.23E-11	1.57E-09	112	119	36	36
HEBP1	1.044	3.24E-11	1.57E-09	865	810	464	348
RP11-742B18.1	1.684	3.33E-11	1.61E-09	132	148	53	34
RP11-293M10.6	1.384	3.35E-11	1.62E-09	179	171	70	64
CTD-3199J23.4	1.674	3.79E-11	1.81E-09	152	193	63	45
RTKN	1.056	4.12E-11	1.96E-09	708	748	385	315
ZNF702P	1.996	5.41E-11	2.54E-09	87	105	30	18
KIF5C	1.033	6.38E-11	2.99E-09	1344	1457	780	589
PSG4	2.768	6.45E-11	3.02E-09	48	69	8	9
B3GALT5	1.084	7.97E-11	3.67E-09	409	384	197	177
ZNF563	1.103	8.98E-11	4.08E-09	540	601	271	260
DSCAM	1.361	1.07E-10	4.84E-09	179	181	69	71
HTR7P1	1.08	1.82E-10	8.10E-09	831	951	476	367
MIR548Y	1.726	1.87E-10	8.31E-09	94	105	32	28
BX571672.8	1.678	2.75E-10	1.20E-08	306	168	76	72
AC004947.2	3.178	4.21E-10	1.81E-08	36	38	2	6
DSPP	2.448	4.55E-10	1.95E-08	66	44	10	10
DUSP5P1	2.385	4.90E-10	2.09E-08	52	69	13	10
SMPDL3A	1.052	5.25E-10	2.23E-08	511	561	278	239
RGL3	1.128	6.07E-10	2.56E-08	515	604	249	263
GJB3	1.073	7.17E-10	3.02E-08	725	851	421	328
BTN3A1	1.849	7.30E-10	3.06E-08	84	111	29	25
ZNF99	2.254	7.41E-10	3.10E-08	71	49	16	9
ZSCAN30	1.099	7.56E-10	3.16E-08	309	274	146	126
C20orf144	1.037	8.21E-10	3.42E-08	587	661	331	277
RNU5A-8P	1.132	9.09E-10	3.76E-08	276	248	132	107
RP11-61G23.1	3.118	9.13E-10	3.77E-08	38	33	2	6
SEC14L4	1.923	9.92E-10	4.07E-08	77	79	16	25
CTD-2134A5.3	2.714	1.00E-09	4.10E-08	51	42	12	2
LAMB1	1.495	1.17E-09	4.76E-08	112	111	41	38
RNU5A-1	1.059	1.47E-09	5.87E-08	461	431	249	179
RFTN2	1.233	1.58E-09	6.32E-08	192	168	83	70
POTEJ	1.066	2.50E-09	9.75E-08	299	298	146	139
RP11-798K3.2	4.867	2.55E-09	9.93E-08	46	18	2	0
INHBA-AS1	2.092	2.87E-09	1.11E-07	55	65	15	13
HRH1	2.555	3.28E-09	1.25E-07	53	42	4	12

CST9	3.533	3.39E-09	1.29E-07	32	28	5	0
TP53TG3	1.98	4.26E-09	1.59E-07	58	57	17	12
DMP1	1.65	5.53E-09	2.04E-07	102	140	41	36
TRIM9	1.749	5.66E-09	2.09E-07	76	69	26	17
WNT5B	2.055	6.09E-09	2.23E-07	67	50	12	16
C14ORF57	1.573	6.31E-09	2.31E-07	151	132	64	31
PCDH15	3.768	7.19E-09	2.61E-07	25	32	0	4
ALDH1A2	2.36	7.58E-09	2.75E-07	47	77	14	10
ENG	1.425	8.43E-09	3.04E-07	126	151	59	44
RNY3P4	1.696	9.54E-09	3.40E-07	78	65	24	20
PHACTR3	1.364	9.89E-09	3.52E-07	144	124	63	41
ANKRD6	1.028	1.00E-08	3.55E-07	414	469	237	196
RP11-124L5.7	1.018	1.06E-08	3.76E-07	376	410	194	194
OVGP1	1.38	1.12E-08	3.94E-07	114	105	45	39
DRAXIN	2.643	1.17E-08	4.11E-07	40	36	10	2
NEUROD1	1.377	1.47E-08	5.08E-07	113	121	51	39
BTN3A2	1.506	1.53E-08	5.25E-07	93	92	38	27
CYP4F31P	2.858	1.68E-08	5.75E-07	42	68	3	12
RP11-21K20.1	1.278	1.83E-08	6.22E-07	132	123	59	46
RP11-451B8.1	5.358	1.94E-08	6.58E-07	16	33	0	1
LSM3P4	1.325	2.35E-08	7.89E-07	170	191	62	82
RP11-42I10.1	2.475	2.46E-08	8.25E-07	64	37	6	12
RNU5B-1	1.008	2.50E-08	8.38E-07	533	638	325	257
RP11-430C1.1	3.18	3.10E-08	1.02E-06	26	30	4	2
SLCO6A1	7.788	3.66E-08	1.20E-06	33	11	0	0
CTD-2280E9.1	1.633	3.79E-08	1.24E-06	78	62	24	21
CPQ	1.094	3.84E-08	1.25E-06	224	199	114	84
AC005682.5	1.275	3.88E-08	1.27E-06	187	244	87	91
CCDC148	1.463	4.32E-08	1.39E-06	93	92	40	27
RNA5SP93	1.571	5.00E-08	1.59E-06	83	66	27	23
C12orf60	1.017	5.36E-08	1.69E-06	276	299	144	140
VWA5A	1.638	5.65E-08	1.78E-06	101	80	39	19
CTD-2154I11.2	1.488	5.83E-08	1.83E-06	83	80	33	25
FRAS1	1.288	6.36E-08	1.99E-06	141	145	51	66
TRDN	3.608	7.43E-08	2.29E-06	22	29	4	0
BCL2L10	2.734	8.37E-08	2.56E-06	29	32	5	4
SCNN1G	1.781	1.04E-07	3.14E-06	54	53	17	14
ZNF72P	2.99	1.05E-07	3.17E-06	34	23	3	4
GPR63	2.073	1.11E-07	3.32E-06	43	46	14	7
FAM135A	1.864	1.19E-07	3.54E-06	52	65	15	17
STK31	1.086	1.19E-07	3.54E-06	170	155	79	74

HAP1	1.133	1.41E-07	4.14E-06	152	164	74	70
ARL11	1.062	1.49E-07	4.35E-06	262	308	154	119
CTB-33O18.3	1.327	1.70E-07	4.92E-06	110	106	53	33
AC008069.2	2.44	1.97E-07	5.64E-06	32	34	6	6
DIRC3	1.297	2.24E-07	6.34E-06	101	113	47	40
SLC25A5P5	1.919	2.28E-07	6.44E-06	69	45	20	10
PVRL3-AS1	1.436	2.43E-07	6.83E-06	90	97	43	26
ZNF883	1.537	2.45E-07	6.88E-06	86	74	36	19
TCEA3	1.154	2.64E-07	7.40E-06	130	135	65	54
NLRC5	2.121	2.73E-07	7.63E-06	39	53	11	10
TM4SF20	1.011	2.82E-07	7.89E-06	191	192	103	87
CACNA2D4	1.451	3.02E-07	8.37E-06	78	70	31	23
CYP1A1	1.031	3.47E-07	9.46E-06	198	217	101	102
TMPRSS6	1.785	3.90E-07	1.05E-05	49	48	17	11
SLC30A8	3.788	4.27E-07	1.14E-05	28	16	3	0
RP11-384L8.1	1.815	4.32E-07	1.15E-05	54	45	12	16
RP11-216M21.7	1.295	4.35E-07	1.16E-05	94	83	39	33
RP11-439E19.10	1.443	5.12E-07	1.35E-05	167	146	40	75
RP11-1281K21.7	1.861	5.41E-07	1.42E-05	49	46	18	8
C1orf168	1.708	5.53E-07	1.45E-05	58	47	16	16
AB015752.4	1.035	5.54E-07	1.45E-05	162	166	82	78
GRPR	1.957	5.62E-07	1.47E-05	49	37	10	12
RBM11	1.099	6.03E-07	1.56E-05	152	131	63	69
FAM78B	2.725	6.64E-07	1.70E-05	29	25	6	2
TSPAN10	1.604	9.02E-07	2.26E-05	57	62	18	21
RP11-341G5.3	7.087	9.20E-07	2.29E-05	16	11	0	0
AC018865.9	1.528	9.60E-07	2.38E-05	62	71	28	18
RHBDL2	1.469	1.09E-06	2.68E-05	134	168	75	34
RP11-443N24.3	3.522	1.19E-06	2.89E-05	55	16	4	2
RP11-30J20.1	7.14	1.21E-06	2.93E-05	11	17	0	0
HDX	1.581	1.21E-06	2.93E-05	61	86	23	26
CTD-2147F2.1	1.049	1.24E-06	2.99E-05	165	191	96	76
SRPX	1.918	1.33E-06	3.19E-05	41	54	10	15
AC144521.1	2.532	1.33E-06	3.19E-05	26	27	5	4
AC005537.2	2.636	1.34E-06	3.20E-05	33	24	2	7
ZNF491	1.302	1.55E-06	3.65E-05	93	75	31	37
PLS3	1.346	1.74E-06	4.09E-05	93	70	38	26
CYP4B1	1.058	1.75E-06	4.09E-05	125	123	63	56
COLEC12	1.569	1.85E-06	4.31E-05	59	69	28	15
RP11-37L2.1	1.519	1.90E-06	4.42E-05	60	55	19	21
SKAP1	1.628	2.21E-06	5.09E-05	53	68	17	22



ADA	1.096	2.33E-06	5.35E-05	154	152	89	54
DLX3	1.017	2.45E-06	5.59E-05	216	191	124	77
ADAMTS20	1.371	2.76E-06	6.23E-05	91	137	46	42
ALS2CR11	1.757	3.21E-06	7.17E-05	45	40	11	14
SLC22A18AS	1.362	3.27E-06	7.26E-05	76	58	26	26
C12orf56	2.031	3.44E-06	7.62E-05	33	33	8	8
ADPRH	1.014	3.49E-06	7.71E-05	148	137	83	58
TAC4	6.977	4.02E-06	8.79E-05	16	9	0	0
VCX	1.934	4.07E-06	8.90E-05	42	35	15	5
GDNF-AS1	3.222	4.23E-06	9.19E-05	20	19	4	0
WTAPP1	2.131	4.32E-06	9.35E-05	29	33	7	7
RP13-15E13.1	1.764	4.41E-06	9.51E-05	40	42	13	11
EDIL3	2.585	5.10E-06	0.000109	26	23	2	6
HSPD1P10	1.348	5.26E-06	0.000112	69	56	26	23
LINC00578	2.951	5.32E-06	0.000113	18	22	3	2
SLC44A5	1.877	7.61E-06	0.000157	34	40	12	8
RP11-408B11.2	1.214	7.84E-06	0.000161	83	68	35	30
KCNV2	1.402	9.50E-06	0.000191	62	52	20	23
RP11-174O3.3	1.347	1.01E-05	0.000202	77	53	25	26
RP11-562F9.1	3.021	1.03E-05	0.000205	18	24	5	0
RP13-192B19.2	1.578	1.04E-05	0.000207	45	39	16	12
XXbac-B135H6.1	1.036	1.06E-05	0.000211	135	138	58	75
RP11-439E19.8	2.355	1.08E-05	0.000214	28	70	11	8
RP11-638F5.1	2.877	1.13E-05	0.000223	19	19	3	2
RP11-1281K21.6	1.944	1.16E-05	0.000229	70	46	7	23
AC121251.1	1.753	1.17E-05	0.00023	36	42	13	10
CYB5R2	1.215	1.20E-05	0.000235	76	96	39	35
GSTM2	1.319	1.24E-05	0.000241	70	90	39	25
INPP1	1.03	1.26E-05	0.000245	168	212	111	75
RP11-63P12.6	1.652	1.31E-05	0.000254	40	39	16	9
HTR7	1.629	1.32E-05	0.000255	50	37	14	14
TMEM106A	1.071	1.37E-05	0.000263	96	108	52	45
AC010886.2	2.353	1.57E-05	0.000297	22	35	7	4
RP1-234P15.4	1.217	1.61E-05	0.000303	121	121	71	33
RP11-510J16.3	1.163	1.63E-05	0.000306	89	68	36	34
RP11-439E19.6	1.156	1.81E-05	0.000338	103	71	41	37
RP11-443N24.2	2.389	1.95E-05	0.00036	24	24	7	2
RP11-161I6.2	4.392	1.96E-05	0.000362	14	11	1	0
C20orf195	2.801	2.06E-05	0.000378	24	19	0	6
BATF2	1.614	2.11E-05	0.000387	45	35	13	13
AP001053.11	1.06	2.45E-05	0.000438	140	173	93	57

RP11-182N22.7	1.636	2.46E-05	0.00044	39	36	12	12
SECTM1	1.134	2.57E-05	0.000458	190	146	103	50
AC012501.2	1.109	2.62E-05	0.000464	143	101	71	42
COL4A4	1.518	2.69E-05	0.000477	45	47	13	19
PDCL3P3	2.661	2.94E-05	0.000514	18	21	4	2
PDZD7	1.216	3.10E-05	0.00054	104	161	68	46
DCAF12L2	1.55	3.24E-05	0.000559	51	46	11	22
SDR9C7	2.248	3.25E-05	0.000561	26	27	2	9
ACTL8	1.057	3.50E-05	0.000599	103	97	60	36
PKHD1	4.448	3.51E-05	0.000602	9	17	1	0
AL450307.1	3.68	3.66E-05	0.000624	17	11	2	0
RP11-80F22.9	6.728	3.67E-05	0.000625	8	13	0	0
RP11-439E19.3	1.381	3.78E-05	0.000641	58	83	34	20
AC002076.9	1.292	4.03E-05	0.000681	73	62	37	18
ANKRD36BP2	1.119	4.05E-05	0.000683	93	68	42	32
NBEAP3	1.346	4.57E-05	0.000761	55	47	18	22
POU6F2-AS2	6.794	4.91E-05	0.00081	7	15	0	0
ZNF849P	1.269	4.95E-05	0.000816	68	60	35	18
DACH2	3.628	5.08E-05	0.000836	16	11	0	2
KB-1184D12.1	3.238	5.35E-05	0.000875	13	17	1	2
RP11-178L8.3	1.764	5.58E-05	0.00091	31	51	11	13
RP11-180K7.1	6.585	5.59E-05	0.000911	9	10	0	0
GNPATP	6.585	5.73E-05	0.000929	11	8	0	0
AGGF1P1	1.616	5.92E-05	0.000954	43	31	12	12
RP11-178A10.1	3.826	6.07E-05	0.000974	9	22	1	1
RP11-973N13.3	1.399	6.19E-05	0.00099	41	49	18	16
KRTAP4-1	1.235	6.39E-05	0.00102	67	98	33	37
CMTM8	1.027	6.97E-05	0.0011	94	108	60	39
ACVR1C	1.549	7.28E-05	0.00114	38	56	14	18
AC104297.1	1.557	7.63E-05	0.00119	39	32	13	11
RP11-358L22.2	1.19	8.05E-05	0.00125	57	71	28	28
CRISP3	1.449	8.23E-05	0.00127	49	36	16	15
VWA2	1.54	8.35E-05	0.00129	43	33	12	14
IBSP	1.453	8.99E-05	0.00137	61	79	37	14
AC017002.1	1.362	9.58E-05	0.00144	60	38	20	18
C3orf55	1.597	9.64E-05	0.00145	32	41	12	12
GSG1	1.796	9.70E-05	0.00146	38	25	7	11
SDAD1P4	1.367	9.71E-05	0.00146	41	47	20	14
RP11-973N13.2	1.309	9.85E-05	0.00148	64	75	20	36
ATP10D	1.498	0.000102	0.00152	37	34	16	9
CYP4Z2P	2.041	0.000103	0.00153	23	27	9	3

RP11-204K16.1	6.508	0.000106	0.00157	8	10	0	0
RARRES3	1.597	0.000111	0.00164	34	39	9	15
RP11-13P5.1	4.334	0.000121	0.00177	17	7	1	0
OTOGL	1.22	0.000132	0.0019	55	78	28	29
CTD-2036A18.2	1.834	0.000132	0.00191	24	30	9	6
C14orf183	2.63	0.000138	0.00198	16	16	2	3
AC010890.1	1.462	0.00014	0.00199	36	47	19	11
TAS2R63P	1.952	0.000142	0.00202	26	21	6	6
SPINK6	2.43	0.000144	0.00205	18	26	1	7
FAM49A	1.079	0.000146	0.00208	94	109	63	33
BFSP2	1.748	0.000147	0.00208	27	44	14	7
NRSN1	6.426	0.000147	0.00209	9	8	0	0
ANKRD2	1.668	0.000153	0.00216	28	36	12	8
COL4A3	1.415	0.000167	0.00233	49	34	15	16
TEX15	1.228	0.000169	0.00235	63	45	21	25
CTD-2554C21.3	2.329	0.000196	0.00268	15	26	4	4
CPA6	1.229	0.000211	0.00285	54	40	23	17
AC074093.1	4.073	0.000228	0.00304	10	10	0	1
RP11-328J2.1	1.868	0.000235	0.00313	22	26	5	8
AC018804.3	1.677	0.000242	0.00321	27	31	12	6
RP11-776H12.1	1.41	0.000242	0.00321	40	56	14	22
IL34	2.29	0.000247	0.00327	19	16	3	4
PRKAA2	1.423	0.000276	0.00359	60	69	37	11
ANKRD1	1.1	0.000329	0.00418	81	65	46	22
CTD-2591A6.2	1.648	0.00033	0.00419	56	51	7	27
BOLL	1.779	0.000338	0.00428	26	50	8	14
RP11-360I20.2	3.087	0.000344	0.00433	10	17	3	0
LA16c-60H5.7	1.093	0.000353	0.00443	63	46	26	25
RP11-885L14.1	1.554	0.000355	0.00444	54	55	30	7
DNAH6	1.326	0.000355	0.00445	41	37	13	18
MDGA2	1.868	0.000361	0.00451	30	18	7	6
RPL26P3	4	0.000363	0.00453	10	9	0	1
CTC-281F24.1	1.01	0.000393	0.00486	61	60	30	30
ZNF280A	1.229	0.000411	0.00505	46	41	16	21
RP1-30E17.2	6.248	0.000414	0.00507	8	7	0	0
RP11-80F22.10	2.421	0.000422	0.00516	21	12	4	2
RP4-647C14.2	1.317	0.000423	0.00517	36	44	16	16
UBBP2	1.78	0.000436	0.00531	23	29	11	4
RP11-321E8.2	1.244	0.000468	0.00564	54	86	38	21
SPAG17	1.174	0.00048	0.00575	49	37	21	17
RP11-754I20.3	2.717	0.000486	0.00582	25	9	3	2

AC098973.2	6.426	0.000495	0.0059	5	12	0	0
RP11-82I10.1	1.229	0.000505	0.006	58	36	23	17
PLSCR4	1.25	0.000528	0.00622	37	37	18	13
C10orf11	1.334	0.000533	0.00627	42	39	23	9
SPDYC	2.377	0.000534	0.00628	20	12	4	2
MAST4-IT1	3.033	0.000554	0.00646	18	8	2	1
PRDM9	1.283	0.000583	0.00677	37	46	15	19
RP11-439E19.7	2.801	0.000589	0.00682	12	31	6	0
MIR4778	1.855	0.000617	0.00709	43	19	12	5
PSG8	3.399	0.000692	0.00781	8	15	2	0
OR4F29	3.268	0.000714	0.008	12	9	0	2
OR4F3	3.268	0.000714	0.008	12	9	0	2
OR4F16	3.268	0.000714	0.008	12	9	0	2
RP11-479O17.8	2.377	0.00072	0.00805	21	11	4	2
IL15	1.744	0.000723	0.00807	23	21	8	5
CDH17	2.205	0.00073	0.00814	14	19	2	5
RP11-495P10.7	2.182	0.000753	0.00833	21	16	1	7
RAD21L1	1.506	0.000769	0.00847	37	23	11	10
RSL24D1P8	6.15	0.000775	0.00854	8	6	0	0
MAP6	1.347	0.00078	0.00858	30	39	17	10
RP11-522L3.4	6.248	0.000836	0.0091	5	10	0	0
CIDEC	3.268	0.000868	0.00938	13	8	2	0

**Table S5: Functional annotation of TRIM28 regulated genes**

Functional annotation (GO) analysis of TRIM28 activated genes				
Identifier	GO Term	Genes in the list	Total genes	PValue
GO:0030030	cell projection organization	31	368	1.70E-06
GO:0048812	neuron projection morphogenesis	22	213	3.49E-06
GO:0031175	neuron projection development	24	256	5.87E-06
GO:0048666	neuron development	28	339	8.76E-06
GO:0048858	cell projection morphogenesis	23	245	9.38E-06
GO:0032990	cell part morphogenesis	23	256	1.89E-05
GO:0000902	cell morphogenesis	28	356	2.13E-05
GO:0042475	odontogenesis of dentine-containing tooth	9	39	2.28E-05
GO:0000904	cell morphogenesis involved in differentiation	22	244	2.83E-05
GO:0040012	regulation of locomotion	19	192	3.43E-05
GO:0007409	axonogenesis	19	193	3.67E-05
GO:0006928	cell motion	33	475	3.96E-05
GO:0030182	neuron differentiation	31	438	5.13E-05
GO:0007398	ectoderm development	19	199	5.50E-05
GO:0042127	regulation of cell proliferation	46	787	6.67E-05
GO:0048667	cell morphogenesis involved in neuron differentiation	19	209	1.04E-04
GO:0043627	response to estrogen stimulus	13	105	1.08E-04
GO:0044057	regulation of system process	24	309	1.15E-04
GO:0007411	axon guidance	13	107	1.29E-04
GO:0032989	cellular component morphogenesis	28	397	1.37E-04
GO:0042476	odontogenesis	9	54	2.56E-04
GO:0043616	keratinocyte proliferation	5	11	2.64E-04
GO:0030334	regulation of cell migration	16	169	2.79E-04
GO:0048545	response to steroid hormone stimulus	17	192	3.61E-04
GO:0051270	regulation of cell motion	17	193	3.83E-04
GO:0001501	skeletal system development	23	319	4.65E-04
GO:0007586	digestion	11	91	5.48E-04
GO:0008544	epidermis development	16	184	6.88E-04
GO:0040017	positive regulation of locomotion	11	98	9.84E-04
GO:0048732	gland development	13	135	0.0010981

GO:0009725	response to hormone stimulus	24	367	0.0012912
GO:0048871	multicellular organismal homeostasis	10	85	0.001343
GO:0007584	response to nutrient	13	140	0.0015047
GO:0009991	response to extracellular stimulus	17	220	0.0015639
GO:0031328	positive regulation of cellular biosynthetic process	37	685	0.0016621
GO:0030335	positive regulation of cell migration	10	89	0.0018581
GO:0009891	positive regulation of biosynthetic process	37	695	0.0021269
GO:0009719	response to endogenous stimulus	25	405	0.0021568
GO:0050927	positive regulation of positive chemotaxis	5	19	0.0025365
GO:0050926	regulation of positive chemotaxis	5	19	0.0025365
GO:0016477	cell migration	19	276	0.0027573
GO:0008283	cell proliferation	26	436	0.0027621
GO:0042060	wound healing	15	191	0.0027989
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	23	371	0.0032269
GO:0045596	negative regulation of cell differentiation	16	216	0.0033727
GO:0051272	positive regulation of cell motion	10	98	0.0035967
GO:0031667	response to nutrient levels	15	197	0.0037015
GO:0051674	localization of cell	20	307	0.003828
GO:0048870	cell motility	20	307	0.003828
GO:0051173	positive regulation of nitrogen compound metabolic process	34	644	0.0038327
GO:0035108	limb morphogenesis	10	99	0.0038498
GO:0035107	appendage morphogenesis	10	99	0.0038498
GO:0010033	response to organic substance	37	721	0.0038934
GO:0008593	regulation of Notch signaling pathway	4	11	0.004181
GO:0030850	prostate gland development	4	11	0.004181
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	33	624	0.0043262
GO:0007242	intracellular signaling cascade	57	1256	0.0043475
GO:0045893	positive regulation of transcription, DNA-dependent	27	477	0.004457
GO:0007267	cell-cell signaling	32	600	0.0044625
GO:0050817	coagulation	10	102	0.0046937
GO:0007596	blood coagulation	10	102	0.0046937
GO:0010557	positive regulation of macromolecule biosynthetic process	34	654	0.0048228

GO:0050878 regulation of body fluid levels

12

141 0.0048235

### Functional annotation (GO) analysis of TRIM28 repressed genes

Identifier	GO Term	Genes in the list	Total genes	PValue
GO:0030198	extracellular matrix organization	10	104	3.39E-05
GO:0043062	extracellular structure organization	12	163	4.72E-05
GO:0051046	regulation of secretion	11	202	0.0012235
GO:0007155	cell adhesion	23	700	0.0013039
GO:0022610	biological adhesion	23	701	0.0013279
GO:0007565	female pregnancy	8	110	0.0016214
GO:0001503	ossification	8	115	0.0020922
GO:0009743	response to carbohydrate stimulus	6	60	0.0023481
GO:0007267	cell-cell signaling	20	600	0.0025594
GO:0060348	bone development	8	123	0.0030576
GO:0009749	response to glucose stimulus	5	45	0.005112
GO:0034284	response to monosaccharide stimulus	5	47	0.0059744
GO:0009746	response to hexose stimulus	5	47	0.0059744
GO:0007584	response to nutrient	8	140	0.0062067
GO:0051047	positive regulation of secretion	7	109	0.00702
GO:0009991	response to extracellular stimulus	10	220	0.0074629
GO:0008037	cell recognition	5	55	0.0103797
GO:0001501	skeletal system development	12	319	0.0109996
GO:0031667	response to nutrient levels	9	197	0.0117288
GO:0045619	regulation of lymphocyte differentiation	5	63	0.0164786
GO:0001654	eye development	7	132	0.0169731
GO:0006355	regulation of transcription, DNA-dependent	39	1773	0.0233437
GO:0043010	camera-type eye development	6	107	0.0255579
GO:0010817	regulation of hormone levels	7	151	0.03041
GO:0051252	regulation of RNA metabolic process	39	1813	0.0317557
GO:0046879	hormone secretion	4	45	0.0324678
GO:0009566	fertilization	5	79	0.0343882
GO:0060341	regulation of cellular localization	9	248	0.03985
GO:0009914	hormone transport	4	49	0.0403151
GO:0007188	G-protein signaling, coupled to cAMP nucleotide second messenger	5	85	0.043182



GO:0003001	generation of a signal involved in cell-cell signaling	5	85	0.043182
GO:0045580	regulation of T cell differentiation	4	51	0.0445656
GO:0046085	adenosine metabolic process	2	3	0.0458542
GO:0070244	negative regulation of thymocyte apoptosis	2	3	0.0458542
GO:0007517	muscle organ development	8	211	0.046655
GO:0007200	activation of phosphoinositase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	4	52	0.0467712
GO:0001889	liver development	4	53	0.0490298

### KEGG pathway analysis s of TRIM28 activated genes

Identifier	GO Term	Genes in the list	Total g	PValue
hsa00534	Heparan sulfate biosynthesis	5	26	0.0116458
hsa05200	Pathways in cancer	20	328	0.0187532
hsa00860	Porphyrin and chlorophyll metabolism	5	33	0.0264152
hsa04012	ErbB signaling pathway	8	87	0.030989
hsa04540	Gap junction	8	89	0.034505
hsa04360	Axon guidance	10	129	0.0349984

### KEGG pathway analysis s of TRIM28 repressed genes

Identifier	GO Term	Genes in the list	Total g	PValue
hsa04512	ECM-receptor interaction	5	84	0.0149469
hsa04080	Neuroactive ligand-receptor interaction	8	256	0.0252555
hsa04020	Calcium signaling pathway	6	176	0.049122

**Table S6. List of genes co-regulated by EZH2 and TRIM28**

<b>Genes co-activated (77)</b>	<b>Genes co-repressed (8)</b>	<b>TRIM28-activated EZH2-repressed (9)</b>	<b>TRIM28- repressed EZH2-activated (40)</b>
HS3ST5	BAG3	ANXA1	BTN3A2
RP11-347E10.1	ANKRD1	ETV4	ACVR1C
ONECUT1/HNF6	RNU5A-8P	ATP5G1P4	GAPDHP21
RNASE4	RP13-15E13.1	ARSB	TEX15
EGFR	INHBA	BCYRN1	VCAN
SLC2A12	RNU5B-1	SGK1	RP11-63P12.6
CD36	COL12A1	PRSS23	RP11-46C20.1
BCL11B	RNU5A-1	RP11-145G20.1	RP11-192P9.1
FAM81A		RP11-109N23.1	GDNF-AS1
OLFM2			RAB37
CNTNAP2			SNCAIP
FST			RP11-42I10.1
KREMEN2			TP53TG3B
FBLN2			SLC5A12
TPTEP1			WTAPP1
GPRC5B			HTR2C
IKZF2			MYT1
MIR375			RP11-124L5.7
Z83851.1			FAM123A
RP11-830F9.7			FRK
NTNG1			DIRC3

GCNT2  
RP11-317J10.2  
PPARGC1A  
SULF1  
TMCC3  
PALMD  
SLCO4C1  
FAM129A  
BMP5  
RP11-284F21.7  
CXCR4  
C3  
TRPM6  
RP11-1C8.4  
SPOCD1  
MIR148A  
  
SLITRK6  
  
PCDH8  
JAKMIP1  
C1QL4  
MYEOV  
SLITRK1  
STRA6  
SYNPO2  
KIAA0226L  
GAS6  
*PADI2*  
LAMP3  
ABCB4  
RP11-61L23.2

CTC-281F24.1  
COL9A3  
COL5A2  
BATF2  
COL4A4  
COL4A3  
IGFBP5  
RP11-293M10.6  
LRP2  
PLSCR4  
RNA5SP93  
DNAH6  
RP11-174O3.3  
EDIL3  
SECTM1  
SRPX  
  
RAG1  
  
COL21A1  
STC1

AC104655.3  
FRY  
CXCL12  
KCNJ3  
KRT6A  
BAI2  
CA2  
INPP5D  
CCM2L  
CCBL1  
NPY1R  
CCDC110  
KIT  
PRODH  
SOWAHA  
FREM1  
CREB3L1  
SNCB  
GPNMB  
MAF  
HES2  
KIAA1217  
RP11-129B22.6  
SLC1A1  
HPGD  
SCIN

### Functional annotation (GO) analysis of co-activated genes

Identifier	GO Term	Genes in the list	Total genes	PValue
GO:0048858	cell projection morphogenesis	8	245	3.44E-05
GO:0032990	cell part morphogenesis	8	256	4.55E-05
GO:0048812	neuron projection morphogenesis	7	213	1.42E-04
GO:0048666	neuron development	8	339	2.62E-04
GO:0000902	cell morphogenesis	8	356	3.52E-04
GO:0031175	neuron projection development	7	256	3.82E-04
GO:0030030	cell projection organization	8	368	4.30E-04
GO:0032989	cellular component morphogenesis	8	397	6.75E-04
GO:0040012	regulation of locomotion	6	192	7.56E-04
GO:0007409	axonogenesis	6	193	7.74E-04
GO:0008354	germ cell migration	3	12	8.98E-04
GO:0048667	cell morphogenesis involved in neuron differentiat	6	209	0.00110643
GO:0030182	neuron differentiation	8	438	0.001200885
GO:0000904	cell morphogenesis involved in differentiation	6	244	0.002189057
GO:0030334	regulation of cell migration	5	169	0.003719836
GO:0051094	positive regulation of developmental process	6	278	0.003838002
GO:0030335	positive regulation of cell migration	4	89	0.004564017
GO:0008283	cell proliferation	7	436	0.005718038
GO:0051270	regulation of cell motion	5	193	0.005949164

GO:0040017	positive regulation of locomotion	4	98	0.005969317
GO:0051272	positive regulation of cell motion	4	98	0.005969317
GO:0045639	positive regulation of myeloid cell differentiation	3	33	0.006828209
GO:0045597	positive regulation of cell differentiation	5	229	0.010734299
GO:0010810	regulation of cell-substrate adhesion	3	46	0.012974437
GO:0007389	pattern specification process	5	267	0.017943965
GO:0001775	cell activation	5	287	0.022717395
GO:0045637	regulation of myeloid cell differentiation	3	70	0.028590174
GO:0048609	reproductive process in a multicellular organism	6	487	0.035787186
GO:0032504	multicellular organism reproduction	6	487	0.035787186
GO:0046649	lymphocyte activation	4	199	0.038989126
GO:0007155	cell adhesion	7	700	0.046869382
GO:0022610	biological adhesion	7	701	0.047140442
GO:0008045	motor axon guidance	2	13	0.047936847

### KEGG pathway analysis s of co-activated genes

Identifier	GO Term	Genes in the list	Total genes	PValue
hsa04060	Cytokine-cytokine receptor interaction	4	262	0.071156664
hsa04360	Axon guidance	3	129	0.082470642

**Functional annotation (GO) analysis of TRIM28-repressed EZH2-activated genes**

<b>Identifier</b>	<b>GO Term</b>	<b>Genes in the list</b>	<b>Total genes</b>	<b>PValue</b>
GO:0031099	regeneration	3	69	0.005545
GO:0001503	ossification	3	115	0.0148105
GO:0060348	bone development	3	123	0.0168203
GO:0050804	regulation of synaptic transmission	3	136	0.02032
GO:0051969	regulation of transmission of nerve impulse	3	147	0.0234993
GO:0007155	cell adhesion	5	700	0.0246981
GO:0022610	biological adhesion	5	701	0.0248132
GO:0031644	regulation of neurological system process	3	153	0.025315
GO:0046928	regulation of neurotransmitter secretion	2	21	0.0336261
GO:0051588	regulation of neurotransmitter transport	2	26	0.0414718
GO:0031100	organ regeneration	2	26	0.0414718
GO:0051046	regulation of secretion	3	202	0.0421375

## **Supplementary Table S7.**

### **Top Five Categories (by P Value) of EZH2 and TRIM28co-activated genes:**

**Cell projection morphogenesis:** EGFR, SLITRK1, ONECUT1, CXCR4, BCL11B, NTNG1, SLITRK6, CXCL12

**Cell part morphogenesis:** EGFR, SLITRK1, ONECUT1, CXCR4, BCL11B, NTNG1, SLITRK6, CXCL12

**Neuron projection morphogenesis:** EGFR, SLITRK1, CXCR4, BCL11B, NTNG1, SLITRK6, CXCL12

**Neuron development:** EGFR, SLITRK1, CXCR4, BCL11B, NTNG1, CNTNAP2, SLITRK6, CXCL12

**Cell morphogenesis:** EGFR, SLITRK1, ONECUT1, CXCR4, BCL11B, NTNG1, SLITRK6, CXCL12



<b>chr</b>	<b>start</b>	<b>end</b>	<b>Average Peak Intensity</b>
chrY	10043293	10044379	5.72
chrY	13448262	13451988	6.73
chrY	13454256	13455599	5.38
chrY	13457705	13459215	9.75
chrY	13680559	13681164	6.73
chrY	13704141	13704530	9.08
chrY	13810653	13811330	4.04
chrY	13869169	13870011	6.39
chrY	58974475	58975871	6.73
chrY	58976093	58984162	8.07
chrY	58988022	58989319	4.71
chrY	59001468	59002451	5.05
chrX	9430607	9431583	4.04
chrX	16240985	16242276	4.04
chrX	16543791	16544836	4.04
chrX	16599332	16600577	6.39
chrX	23483894	23484878	1.35
chrX	26796343	26797089	2.35
chrX	33864134	33865247	0.67
chrX	46358526	46362807	7.06
chrX	47271343	47273555	9.75
chrX	47275779	47276656	3.36
chrX	47306360	47308834	4.71
chrX	47774602	47775844	4.37
chrX	47833881	47837475	7.4
chrX	47917883	47919766	5.05
chrX	52963892	52964735	1.68
chrX	54685803	54686441	4.37
chrX	55608338	55609745	1.35
chrX	56571461	56572653	3.03
chrX	57990522	57992290	8.75
chrX	58324092	58325168	4.04
chrX	58336366	58337947	6.05
chrX	58338849	58339739	3.7
chrX	58341344	58343250	4.04
chrX	58343791	58345565	4.71
chrX	58354079	58355667	4.37
chrX	58359961	58366364	5.38
chrX	58367278	58368402	3.7
chrX	58377830	58380809	4.37
chrX	58381125	58384202	5.38

chrX	58384583	58385772	3.7
chrX	58386624	58387648	3.7
chrX	58387957	58388927	4.04
chrX	58406528	58407336	4.04
chrX	58414258	58416317	4.71
chrX	58416896	58418732	4.71
chrX	58419954	58421107	3.7
chrX	58428258	58429118	3.03
chrX	58429967	58431136	3.7
chrX	58434160	58436805	4.37
chrX	58438133	58439994	4.04
chrX	58440535	58442360	3.36
chrX	58449774	58450610	3.36
chrX	58451488	58453110	4.04
chrX	58460774	58461734	3.36
chrX	58462023	58464272	4.04
chrX	58469454	58470471	4.04
chrX	58497327	58498521	3.7
chrX	58559376	58561899	7.06
chrX	58562719	58564246	7.4
chrX	61683041	61683838	12.11
chrX	61685172	61687824	6.39
chrX	61691636	61692022	11.77
chrX	61693518	61695285	6.39
chrX	61695677	61696794	9.75
chrX	61714917	61715882	6.05
chrX	61717094	61718619	26.57
chrX	61719904	61721241	5.72
chrX	61721894	61722725	3.7
chrX	61723064	61724778	4.71
chrX	61726195	61727004	4.37
chrX	61727770	61729873	3.7
chrX	61730335	61734685	9.08
chrX	61757160	61757939	3.36
chrX	61851138	61852097	5.72
chrX	61875131	61875905	6.39
chrX	61919674	61921143	4.04
chrX	61931867	61932693	2.35
chrX	61946082	61948271	5.38
chrX	61951823	61953168	4.71
chrX	61957470	61958405	4.04
chrX	61968335	61969645	4.71
chrX	61971803	61973207	4.04

chrX	61979932	61982802	4.04
chrX	61985264	61991694	5.38
chrX	61992355	61995832	4.71
chrX	61996527	61997313	2.69
chrX	62003311	62004121	1.35
chrX	62027959	62028856	2.69
chrX	62093714	62095005	1.35
chrX	62694562	62695907	7.06
chrX	67113299	67114485	8.41
chrX	67937861	67938725	0.34
chrX	68344933	68346014	1.35
chrX	71216031	71217458	1.68
chrX	71217797	71218618	1.01
chrX	71409055	71409862	1.01
chrX	71524952	71526144	1.35
chrX	72631697	72632547	1.35
chrX	72996575	72997662	1.68
chrX	73080454	73081595	1.68
chrX	73098688	73099604	1.68
chrX	73163911	73164770	5.38
chrX	73309453	73310738	5.38
chrX	73339860	73341147	2.02
chrX	73358614	73359363	2.02
chrX	73378907	73379713	1.01
chrX	73974980	73975878	1.35
chrX	74070741	74071584	2.35
chrX	77358858	77360421	4.37
chrX	78598620	78599502	1.35
chrX	79748000	79749157	1.35
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C5ORF66	ZSCAN30	ZNF286B	ZNF572	LOC100507217	SNX31	MIR4648
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NCBP1	DYNLL1	ZFP64	C1orf106	PCDHGC3	ACOT7	CMBL
HSPA5	DYNLL2	ZCCHC10	ZNF577	IQCG	USP32	DLX4
RNF13	RAD9A	PPAP2A	ZNF578	COL23A1	SP6	MON2
FOXA1	ERGIC1	SUMO3	RRM2B	MUC17	ZAN	SMARCD2
HIST1H4H	ZNF321P	AP1M1	NUP210	REXO1L2P	ADCY5	SMARCD1
TYW1B	RBM4B	SMIM6	SETDB1	RNU5E-1	STMN3	ABLIM2
MPZL3	MALRD1	MOCS3	IFRD1	CNDP1	TOR1AIP1	ZNF880
ARFRP1	POLR3C	CCDC146	LUC7L2	C14ORF37	ADCY1	GATA3
CCDC129	ZNF805	LOC100505921	CTSH	COL15A1	ZFYVE9	F5
ZNF791	HSDL2	CCDC149	ERBB3	GALNT10	KIF25	FAM172A
SQLE	CPPED1	POLG	ZNF205	TC2N	PHB	SNAP25
MIR6080	UHRF1BP1	DLG1	ZNF200	ZNF174	ST20	LINC00630
C1ORF112	CMC2	GRAMD3	SHC3	ZNF175	ADCY8	LOC284395
ZNF709	CALM2	SNORA72	IDH2	DDX43	ADCY9	LINC00637
ZNF708	CALM1	DLG2	IDH1	MBTD1	KIF23	DUSP6
ZNF879	LINC00423	DLG5	FPR3	LOC401320	RSRC1	LITAF
NCBP2	CACNA1B	SAMD10	RNF216P1	LMLN	SNHG7	GRB14
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SLC28A1	THRB	TPM4	SH3GLB2	POP1	PNPO	C11orf49
ZNF707	CACNA1E	COMMD1	PPP1R37	CEP70	DLST	SCNM1
ZNF706	FAM46C	C11orf30	RPL15	ENC1	RNF217	PRR14
RNF114	DLGAP1	PTGER2	CTSZ	ZNF778	ZBTB21	LACTB
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MIR554	MBNL1	METTL18	RPL13	ZNF776	HHIPL1	IPCEF1
NET1	ATP6V0D1	LINC00323	SETD3	KLC1	FAM208B	PRR19
KDM2A	SYCP1	ZNF585B	SETD2	KLC2	DOCK2	SUCLA2
ZNF781	MGC70870	PTPN4	FGFR2	ZNF772	GRIA3	FAM102B
SLC12A2	WSB2	LMBRD2	MIR5694	SNRK	ADORA3	ZNF630
CBLB	TRIM24	C15ORF32	SOS2	LGR5	SKAP1	HMGN1
ZNF45	SLC25A2	METTL15	PCYT1A	ZNF197	ZNF75D	XRRA1
ZNF44	LOC102724596	B3GALT5	INPP5B	MMP16	ARL13A	MX2
ZNF43	PRMT7	IGF1R	NME7	ZNF195	DOCK4	ATP6V1H
GCC1	CDH26	SLC38A1	DZIP3	MIR548F1	KLLN	LOC100128398
ZNF41	LOC101927053	RGMA	SYK	DSTYK	CC2D1A	MX1
XPC	SLC15A2	PTDSS1	NKAIN3	LSM14B	CDYL2	PUM2
SP2	FAM84B	PTGR1	DSCAM-IT1	FKBP3		4-Sep LOC646813
CRB1	LOC101927058	SLC45A3	SURF4	UBE2D3	FAM184A	RAD1
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OPA1	PTPN13	STK3	B4GALT7	ZNF219	SMURF2	SPAG17
IREB2	MIR152	MACROD2	RALGPS1	TPK1	SLC9A1	SPTSSA
CEP83	MIR4515	CEP112	PRSS23	BAZ2A	SUPT7L	SERPINE1
RAB40B	LOC101927459	OSBPL2	CHURC1-FNTB	TSTD2	TNRC18	SPTSSB
MEG8	NKAP	TMEM184A	ZNF37A	RALYL	SLC9A8	PANK1



TRAPPC9	RP9P	DEPDC1B	GLDN	PKHD1L1	C8ORF44-SG	PANK3
ZNF676	GLT1D1	RSU1	ZNF483	LMTK2	SYT12	VPS13B
ZNF675	LOC101927901	R3HCC1L	HELQ	CYP11A1	TFRC	ETAA1
ZNF674	CMTR2	LOC729683	ZGPAT	TANK	ZNF669	SOX13
MYL12A	LINC00663	LINC01082	ERF	CHCHD4	RBM33	CCT5
ZNF671	NTSR2	C7orf55	HELZ	KCNH6	SYT15	EPPK1
AP5S1	DNAJC22	AKAP6	LOC100506639	LOC101928272	PRPF6	LINC00524
PARP15	HIF1A	AKAP1	PAIP1	FBXO34	ZFAS1	LINC00520
ERI2	NTSR1	SOX4	RBAK	APOH	RBM38	CALHM2
GOLGA6L17	LARGE	GTF2F2	KIAA0195	FKBP9	PLCB1	LINC01036
ZNF679	LINC00938	LZTS2	RASSF5	ZNF519	HOXB1	SNX33
ZNF678	ZNF853	ZNF833P	PCNXL4	NF2	MIR6760	SNX32
LOC441666	ZNF852	AKAP9	NFE2L2	NFIL3	MYO9A	LINC01033
ANP32E	ZFP90	TEX2	PDE4DIP	ZNF510	EPHB4	LINC01031
EYS	ZNF850	ZSCAN18	NEAT1	ZNF514	DNAJC5B	LINC01030
SPPL2A	ARHGAP5	ARHGAP12	AFF4	ZNF221	TOM1L1	KMT2A
MTX3	CMIP	LINC01317	AFF3	ZNF222	SEC13	ERVV-1
ITGA9	ZSCAN1	CADPS2	LOC101929412	ZNF223	EHBP1	ERVV-2
LOC1001295	SUCO	RAPGEF1	PDPR	ZNF224	BTNL8	ZFP28
MYO3B	LINC00936	PHPT1	PNPLA7	ZNF225	PCDHGA8	FTX
EVL	THEM6	PA2G4P4	C15ORF59	ZNF226	ESPNP	MC3R
LOC1005057	PPM1E	INTS2	NMB	CCDC57	TP53INP1	LOC101927406
HACL1	PPM1D	RRP1B	NKAIN4	FAM133B	PAPD4	ANHX
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DENND4A	C4BPA	CELF2	KIAA0196	KCNQ3	PCDHGA3	RAP1GDS1
DENND4B	TMOD3	C3ORF20	VGf	KCNQ1	PCDHGA1	RPRD2
IQSEC1	PPM1L	TANGO6	UNC5A	BLM	PCDHGA6	CDIP1
PHLDA1	SLC35B1	FAM133DP	TUBB3	SLC39A9	LOC1027238	ARNT2
DUSP22	USP43	KRR1	LINC00592	HOXC13	PCDHGA4	TNK2
PHLDA3	PPM1H	C1orf21	ATG14	KRTAP10-11	GPHN	CIZ1
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MIR5093	HSPA4	TMEM132B	MIR4505	SAMD12	ESR2	LRR1
CSDE1	KIF7	MIR5047	FRMD6	LINC01429	CUX1	ZDHHC7
ZNF454	TMEM71	BMS1	PSMB5	C7orf26	AAMDC	MIR345
BACH2	ANXA13	ZBTB40	ABCA10	LOC221946	MRPS23	FAM207A
LOC1001321	CA2	AHSA2	C21ORF91	LOC102577426	MRPS21	ZC3H6
ZNF37BP	TMEM75	H3F3B	ABCA12	PFN2	ITSN1	SLC22A5
FBXL13	PRKAB2	RNF103-CHMP3	ZNF133	CNGA1	MIR326	PRDM6
FBXL15	LINC01090	ARPC2	FBXW11	DNAJB12	RPSAP58	PRDM7
HRH3	TSHZ2	GRM6	DSCR8	NAPSB	OAZ3	ANPEP
TMEM260	KCNQ2	GRM7	GNAS	ZNF426	PHF2	LOC101927539
HRH1	SMEK2	DPY19L4	DSCR4	LOC101928306	PPP2R5C	FLNA
FBXL18	MKLN1-AS	NR1H3	CDHR3	ZNF350	C12ORF56	WDPCP
KSR2	MRC2	TBC1D2B	ST8SIA2	ZNF398	STPG2	C8orf37
FAM169B	ZNF581	ALPK3	ST8SIA1	FLOT2	C2CD4D	EFCAB3
LARP6	ZNF580	MAPK1IP1L	UBE2Z	FBXO33	SMIM14	KRT18

KCNIP1	ZNF583	ATP1A1	NRROS	EMC3	ZFP1	KLHL24
SDK1	C14ORF159	RNF43	DPF3	ATXN7	LAX1	ABHD17B
XPOT	ZNF584	SENP5	PTGFR	ZNF429	TBX3	DNMT1
THSD4	ZNF587	LOC100631378	SGK223	ZNF836	ZNF34	KLHL20
FAM212B	ZNF586	PPP1R3E	SEC14L1	C17orf67	ZNF35	NBPF8
PPIG	SCRN2	PPARG	SIX1	SRGAP1	ZNF32	TLE3
EPS15L1	PTPN1	CUX2	ALS2CR12	CDH13	CTNND2	CROT
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HMCN2	MRPL9	PPARA	LOC283335	SMG8	C9ORF84	NAPEPLD
C2ORF47	ZNF611	ING5	SNED1	SDR42E1	ASTN2	NBPF1
TACR1	ZNF610	FLJ32255	LOC100506023	MBOAT2	SH3GL1	TAF13
CHST6	ZNF613	BRF1	HARS	CDH12	SH3GL3	XIAP
LOC1019296	ZNF615	FSIP2	PWP1	AKAP13	ZNF668	DDX42
KCNH7	ZNF614	DCDC2	ZNF383	CCDC181	SUV420H1	LOC101927244
KIAA1217	ZNF616	CENPBD1	THSD7B	FOXP2	TMEM38B	SLC26A9
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ATAD1	PSD	DNAJC5	LOC148709	CCDC186	ZHX2	MIR6785
KCNH8	LRCH1	CAMSAP1	ESRP2	NEURL1B	ZHX3	CROCCP2
TOP1	VAT1L	DNAJC1	ZNF33BP1	NEDD9	GOLGA2P10	TM9SF4
ATAD2	FSTL4	ERMP1	MTG2	SCLT1	ZHX1	SAP30BP
FTCD	BAG3	CTAGE10P	TMCC1	UNC79	PYGB	PCDHB15
TMEM198B	AGBL5	BHLHE40	GSDMC	BIRC8	OPTC	PSMD4
RTFDC1	AGBL1	CD14	RAB22A	LOC100506499	SPAM1	PCDHB18
LOC1019287	YBEY	ZNF701	TSEN2	N6AMT2	DDX55	TPRA1
FAM134B	HAVCR1P1	TTC34	LINC00111	GARNL3	LOC1001330	BEND6
ZNF292	MSRB2	GOSR2	NMNAT2	CDH18	MIR6165	LAMA5
ZNF7	C15orf39	LOC728485	LFNG	BRWD1	PUS10	PSMC6
METTL2A	PTK2	EFHB	LOC101926941	SLCO4A1	ERN1	OSGIN1
ZNF700	PLCE1	LINC00359	ZIM2	AREL1	RPS26	RXRA
TRERF1	ADAMTS17	RRP15	ZNF587B	FBXO31	ZNF248	CDK18
SMAD5	ARRB1	CEP85L	PPCDC	LONRF2	ITPRIPL2	TAF4
SMAD6	ADAMTS19	ACP6	EPB41L2	C15orf27	RPS20	ATP6V0D2
GOLPH3L	VDAC1	CCDC97	LOC102724163	JARID2	RPS21	UBE2V1
SMAD1	NTRK3	MRPL40	UBE2H	PGK1	CCDC33	ZNF732
SMAD3	CD79B	ACP2	ACSS3	B3GALT1	ANKRD33B	TAF1B
MUS81	HMCN1	SLC2A13	ACSS1	LOC100288798	CCDC36	ZNF730
NPHP1	LOC553103	RAP1B	RABEPK	TMSB10	MIR3687-1	WDR61
NDUF6F6	DENND3	SLC2A10	TFF1	LOC101927811	PTBP3	ZNF736
NDUF6F2	DEF6	ZNF831	SALL4	FBXO32	MTERF4	ZNF737
ZNF704	CBLN4	ANKRD35	VPS4A	KIAA1598	UGT1A10	POC1B-GALNT4
MIR4713	SF3B4	DYRK3	ADAM22	ARID5B	MVB12B	ZNF883
MIR4712	GMFB	MKRN2	GMEB2	BMPR1A	PAWR	ZNF738
LOC440311	TOMM20L	ANKRD32	BCL11B	NTN1	ZNF354C	GPR158
LINC01107	BNIP1	C1ORF158	PRKRIP1	MICALL2	CHSY1	ATP6V1E1
NT5DC1	ARPP19	LINC00917	IL19	NAA30	RAD51B	SLC37A1

ARF1	PSMA7	GADD45G	HDGF	LINC01350	SIKE1	LINC00862
SNTB1	PSMA5	PCBP2	LOC101927495	BANF1	CSNK1A1	ABCA6
ARF6	OCLN	UBE2Q1	LOC101927497	RNVU1-8	TFAP4	KRTCAP3
LOC1019290	SLC6A11	LHFPL3	GSTM3	RPS10P7	PRRT3	ABCA5
CRBN	SLC6A17	ITPR1	LRRN2	LINC01194	RARRES1	TRERNA1
LOC400558	C6	FAM91A1	IL16	ATAD2B	LOC1024672	RADIL
ELMSAN1	KIF16B	FLJ10038	LINC00578	LINC01197	ZNF404	TMEM170A
ERICH6	NEMF	TMEM19	CNTNAP2	IL23R	MIR5095	ZNF493
ERICH5	GALNTL6	NT5C3A	LINC01331	PLCG1	COL21A1	STXBP3
ZIK1	KIAA1324	SLC22A25	ODF1	LOC727751	SLC35D2	TUBGCP3
TUG1	ZNF320	NR2F2	LOC101927124	B4GALNT2	GATAD2A	CCBL1
MIR3620	FBXO43	ARL8B	LOC101927123	LAPTM4B	CCDC85C	NBEAL1
DBNDD1	ZNF322	LINC00924	UBE2B	ANKH	CCDC85B	NBEAL2
MYEOV	FAM214A	LIMD2	SNORA43	LOC101927780	PPIA	ABCA9
IL5RA	LOC101927845	RNF150	LOC647323	ARL8A	SARS	CAPS2
TCEA2	ZNF329	ANKRD28	AAGAB	MIR301A	SPDEF	GCH1
CALB1	SORD	KIF21A	BIRC7	ZNF813	LOC1005059	EPS8
NACAP1	C1orf56	RIMS2	LOC102724467	WDR87	C20orf195	C2CD2L
COX4I1	GUCD1	MST1P2	HOXC13-AS	TTC7B	IL1RAPL2	IGSF5
SH2B2	ATXN10	ZNF83	EIF5	MAN2C1	DIP2B	PSMD7
PRKAR1A	RMND5B	ZNF81	HIST2H2BC	WDR89	DIP2C	DDX46
PRKAR1B	MYL12B	TMEM65	OXR1	PGF	EBAG9	PSMD1
C19orf18	SNORD12	ZNF85	RUNX1T1	ACER3	NGFR	IGSF3
LINC00674	EIF2AK1	SUGCT	LINC00970	TRIM25	SLCO3A1	ANKRD46
MOB4	EIF2AK4	TMEM64	CMAHP	ZNF559	DNAJC2	SGMS2
SRPK2	LOC101928736	LOC643711	GNN	TMEM212	MOXD1	BAALC
BDKRB2	UBE2G2	SLC27A2	SPTBN2	PDE1C	FAM19A2	CPSF6
PFKP	AGPAT3	CYP2C9	FLJ26850	PDE1A	MID2	ZNF14
FAM20A	BAGE	IL2RA	LOC100289333	SSUH2	DCLRE1C	VAV3
ADARB2	KIAA1211	ERO1L	KLF10	ATP13A4	YES1	ZNF16
CCDC113	MYO10	ZFYVE20	TFAP2A	ESYT2	THUMPD3	ZNF17
ADARB1	DRG2	ACPP	TFAP2C	ZNF816	KYNU	ZNF10
LEO1	CEMIP	TPCN1	PCDHGA10	RAI1	WASF1	MYOF
LOC340512	MCM3AP	IL21R	PCDHGA11	LOC284344	FAM171B	ZNF12
LINC01213	ATG101	SPAG16	PCDHGA12	COL28A1	WASF3	ANKRD40
METTL25	CMYA5	GEMIN5	DPP8	CXCR5	CFAP44	EPS15
ZNF3	LOC101929196	C16orf58	GBE1	CXCR4	NPAS4	PPFIA2
MYL6B	ZNF876P	CDK5RAP3	CENPF	ANKRD11	NPAS3	PPFIA3
MGRN1	KIAA1524	C20orf197	DPP3	IVNS1ABP	NPAS2	RASGRP3
CTHRC1	NIP7	CDK5RAP1	DPP4	NUP210P1	RNU6ATAC	MAD1L1
LOC284581	PEX13	PRKD1	DPP6	APPBP2	LOC1019291	PLEKHG4B
LOC1019276	PSMD12	CHMP4C	SLC44A1	TLDC1	WDR36	MYBPHL
CUEDC1	ALDH1A3	WRNIP1	SLC44A2	MEF2D	COPG2	HINT3
C2CD2	AP3B1	CCDC7	SNORD115-3	COA1	HNRNPA2B1	TM4SF4
CPEB4	SEL1L2	ERG	ZBTB7B	SLC38A8	PHOSPHO1	MAB21L3
EEF1A2	GCNT7	BHMT2	TPST1	KDM3B	NBAS	LOC440704
CPEB1	AP3B2	CBLL1	ANXA9	DCSTAMP	ZCCHC6	WNK2

NADSYN1	GCNT1	ZNF491	MSI2	MIR645	PDZK1	CNOT8
RAB2A	NAP1L1	ZNF490	LOC100507501	TTBK1	ZNF663P	CPSF1
SRBD1	CALCOCO2	NAA20	MCM7	CCDC174	TRIP11	ZNF649
ABAT	AMHR2	NOXRED1	PCNP	LOC255654	LOC1005066	DYNLRB2
ZNF780A	PARPBP	PRR15L	ZDHHC20	MIR643	SPOP	CNOT2
ZNF780B	C14orf132	COBLL1	PCNX	DMXL2	KIAA0247	SIPA1L3
TLN2	CATSPER3	DCAF13	ZDHHC22	E2F6	TBL1X	HSD17B3
NFX1	RGS6	CDK19	LCA5L	ARSG	OSR2	HSD17B4
WDR45B	RGS7	GFI1B	SQSTM1	EXOC6	AP4E1	CNOT6
MIR4532	SLC16A10	ERBB4	GRHL2	EXOC5	LOC441455	KCP
TP53TG1	LPCAT1	ZNF121	PCAT6	HEXA	PPP6R1	TTLL5
DPYS	SCAND2P	LPIN1	PCP4	ZNFX1	ZNF2	MIR5188
CLIP2	LOC100133669	CDK10	RPA3	HEXB	TMBIM4	ITGB2
YLPM1	RGS9	FMO5	ANKFN1	LOC101927967	IPPK	ITGB5
POU5F1B	EYA2	LOC101928137	TENC1	SHISA9	ZNF804B	LTBP2
ETNK2	MIR548W	SULF2	HSPB11	COX16	PCDHA2	LTBP1
CDCA4	NFKBIA	GJB7	GSTCD	MGAT4C	CASP7	ITGB8
HOMER2	MIR548Q	GPR126	RINT1	PPP1R13L	ARID3B	KPNB1
ISM1	LOXL1	KLF6	SECISBP2	FUT9	MLKL	SCN8A
DHRS7B	PIEZO2	NEO1	PRPF18	FUT8	LINC01170	RTN1
C14orf2	PIEZO1	MIR548AI	COQ4	ZDBF2	BCL9	LOC101928295
LINC01476	PIGK	MTRNR2L3	LOC728730	LINC00959	CFDP1	ZNF124
SP4	PIGL	RBM22	CRIM1	GHR	C14orf142	ACTR6
CD47	ZNF891	CBX1	BLZF1	EVA1A	HECTD2	LOC729296
CA14	MIR548G	N4BP1	JAGN1	RAD18	YWHAQ	MIR548AZ
PRICKLE2	C9ORF153	MIR548AC	APCDD1L	LINS	HECTD4	LCP1
RSF1	EMC2	N4BP3	USH2A	ZNF334	UBE2QL1	LOC220729
CA10	MIR548N	HECW1	ZNF75A	GDF6	NPEPL1	COPS7B
ATG4B	KIAA1143	HEATR6	NRCAM	NUDCD1	SETD1A	IPO4
POGK	CATSPERB	HEATR4	ISL2	USP29	AKT1	LPIN3
POLR3GL	TAX1BP1	HEATR2	MRGBP	LOC100128233	LYRM1	CERS2
EIF1AD	SRCAP	RGS22	MCF2L2	CXCL13	D2HGDH	AKR1C8P
ZNF48	MINPP1	ZNF304	PCDHGB3	FBLN5	SPG7	BACE2
RAB21	RHPN1	MIR548A2	PCDHGB2	ZNF333	LOC146880	BTBD6
NIPAL2	LINC01278	SLC24A3	PCDHGB1	ADAMTS7	LRFN5	MGC39584
CLK3	CSNK1G3	ZNF300	PCDHGB7	LOC648987	WBP4	NCK1
THAP4	CCDC170	SFSWAP	PCDHGB6	ZNF239	S100A11	IER5
THAP5	SRRM2	ZNF208	ATP9A	ADAMTS2	GPR75-ASB3	ZKSCAN2
CFH	LINC01271	MIR4533	ZNF300P1	NDUFC2-KCTD14	LOC1005075	MYO6
THAP9	CCDC175	MEX3B	MROH7	CCSER1	S100A16	SPIRE2
ANKFY1	LINC01273	DEDD	ZNF141	ADAMTS9	LINC00620	MBD5
PXDNL	C9orf116	PHF21A	DENND2C	COTL1	TRMT12	TMEM41A
CDKAL1	PDK2	ZC3H13	ABCA11P	OSBPL7	CACNA2D1	CMTM8
SYBU	KANK2	ZNF137P	ZNF142	TSPEAR	LINC00624	RABGGTA
WDR70	RDH12	PPP1R35	LOC101928443	MKLN1	PKD1L2	FAM228B
WDR73	KANK1	LOC100422737	ZNF146	CDH3	PKD1L3	KDM7A
IGDCC3	LNPEP	ZNF544	LOC283575	IL36B	GRK6	ZNF391

WDR74	ATXN1	ZNF547	CCDC88C	CDH4	GRK4	ZNF460
ZNF724P	FAM178B	ZNF546	INPP4B	DPY19L1P1	LOC285593	ZNF461
AAAS	COL6A6	ZNF540	INPP4A	LINC00824	TDP1	ZNF394
PCK1	TBC1D31	ZNF543	GSE1	CENPN	CAPN7	PSKH2
LOC1019277	TM2D3	SLC1A5	ZNF782	HPCAL1	CAPN5	ZNF397
SYTL2	MTBP	SLC1A6	LOC153684	RAB5A	14-Sep	AVPR1A
PABPC1	ZFAND6	ZNF549	PHC3	NPTX2	MYC	IL1RL2
UVRAG	FAM71D	ZNF548	SUSD1	HSPB1	NECAB2	MGC32805
NUF2	MAFK	SLC1A2	LYN	STRA6	NECAB1	ZFPM2
PPP2R3A	FBP1	TCAIM	ZNF788	REV3L	AURKA	GNPAT
SIDT1	AMN1	PPP1R15B	RNF126P1	SSH3	ZNF847P	HCN4
NQO1	PHKB	IMMP2L	WHAMM	TMEM229B	COG8	SULF1
SFMBT2	PLIN1	LRRC42	C20orf27	LINC00636	SPAG9	SLC25A19
C16orf95	LOC100507412	LRRC49	VWA9	CENPT	FRA10AC1	COIL
CDC42SE1	CEP128	ZNF702P	MIR5087	PAFAH1B3	COG5	C2orf88
PRPF3	MIR4513	LINC01411	LSG1	RNF19A	SPAG1	LLGL2
LINC00992	SLC39A11	C2ORF69	MGMT	SLC41A1	HTR7	KIAA1429
ASB2	PPP2R3C	EIF3H	PMS2	C10orf126	IGHMBP2	RASAL2
ASB3	MIR4514	RARB	BRINP3	SLC41A3	RAE1	SLC25A12
TMBIM6	NPDC1	RARG	BRINP2	GH2	SNAPC5	HECTD1
ASB7	NTRK2	EHHADH	RASEF	CNBP	TRMT1L	SMAGP
NAB2	RSBN1	LOC100507065	OTUD6B	ATP5G1	DIO2	TMEM55A
SIX5	SLC34A1	FNBP4	SNRPA1	SCARB1	NFAT5	CFAP61
PLEKHH2	ZSCAN29	CLIP1	ROBO1	UCKL1	ZNF132	EPX
MUC12	PTP4A2	MAN1A1	ZNF335	LOC102723354	KRTAP10-9	ATP5J2-PTCD1
C7ORF55	CREBRF	SETD5	HPS3	DBF4	SLC4A7	USP3
LOC1005065	ZSCAN25	ATP5S	H2AFX	PLEKHA6	GSK3B	ROPN1L
ESRP1	AMDHD2	SKA2	PKIA	PLEKHA7	LINC00535	FAIM3
CNPY4	ZSCAN20	PWWP2B	PKIB	C16orf92	CCDC83	ZNF264
C7ORF50	ZSCAN22	GMPR	CCDC84	MRPL46	LINC00536	SLC12A4
ZFP69	CD8A	TEX22	TLR2	C16orf91	EXD3	ZNF266
LOC1019275	MLYCD	RABIF	DDX5	MEF2A	EXD2	ZNF267
ANKRD30BL	TDRD9	WWP1	DDX6	TRIP4	LOC1019271	ZNF260
ZFP62	TDRD3	MTMR4	FAM179B	MRPL48	TRIM59	CCDC12
ATG7	VPS45	NOL11	ZNF569	WNT7A	STC2	ZNF263
CRISPLD2	RIIAD1	MYT1	ZNF568	ZNF699	LINC01006	SPIN1
MRPL30	VAPB	CCNL1	GRIP1	ERAP1	RNF40	SLC12A8
PTRH2	MIR3175	JAKMIP1	ZNF566	STARD13	HIRIP3	IMP3
RGS3	ABHD2	SMG7	C1orf116	UBE2E1	ANKRD52	MIR320B1
PTH2R	UBR2	LOC101929089	LINCR-0002	PEAK1	LOC1027244	HSP90AB1
C3orf70	UBR7	EPHA3	SLC19A2	EMR3	ZNF837	EXT1
UFSP1	PA2G4	TSC22D2	ZNF562	ZNF695	POU2F1	RNU5D-1
FAM92B	UBR5	C9ORF171	ZNF561	SEC63	MAMDC4	KIAA0226L
ARRDC1	BMP7	PSRC1	ZNF560	MALAT1	FSBP	LPP
ZFP82	BMP6	BAZ1A	CCDC64	CNTN1	ST3GAL1	LPO
PDE8A	BMP5	CCDC150	NCAPG2	HDC	MIR548H4	TMEM222
SYPL1	GIN1	SNAI3	ZNF211	TRIB1	ZNF839	TNFRSF21

LOC653602	ACYP2		CCDC158	CCDC60	CNTN4	SPRYD3	APOL6
LOC643623	MBTPS1		SNAI1	C10ORF107	ARFGAP1	FAXDC2	PLA2G4C
SH3BP5	CCNY		SNORD127	DPY19L1	LAMB1	MANEA	TESK2
RFX4	TERF2		TUFT1	SYS1-DBNDD2	CRADD	URAFP	LOC100506747
RFX5	C8ORF88		RPUSD3	SVOPL	NEK6	KLHDC2	ZNF841
RFX7	CCNC		LOC100505938	DCLK1	NEK7	PTGFRN	LINC01151
NRXN3	C8ORF87		OSBPL10	PRC1	ZNF169	LOC1019271	TSEN15
CSAD	CCNJ		LINC01525	ZNF845	NEK5	KBTBD4	ADCY3
ZNF846	VPS72		PTGES3	NFKBIZ	KMT2E	KBTBD2	PSMC5
ELK4		11-Mar	SYT1	LRRC69	HRNR	MIR4325	GNG4
TMEM44		10-Mar	SYT2	NOX5	U2AF1	PHYH	LINC01482
LOC1001302	PRKCH		FA2H	RABGAP1L	ZNF160	HDDC3	LINC01483
PAK1	TRIM33		SYT6	CLTC	B3GNTL1	LANCL2	VIT
PAK2	RASSF3		SYT7	CLTB	ZNF165	PCTP	LIMA1
HAAO	FKTN		UBTD2	ARID4A	NEK9	HTR2A	LOC100288866
RECQL5	TRIM37		PLAGL2	DNAAF2	PRR11	PCBP3	YIPF2
RECQL4	HOXC4		PLAGL1	TMEM116	FAM129A	GFRA1	DDAH1
ZNF177	LOC283692		MESDC1	TMEM117	CDC42BPA	LINC00910	CYB5R4
TIGD7	NHP2		NFATC2	LOC101928069	CDC42BPB	RNF224	SNX5
MSL2	NCKAP5		NFATC4	KRT8	FAM129B	TECPR2	ALDH3B2
ZNF57	THAP11		LOC644189	PLAC4	ZNF765	ZBTB37	ALG3
FALEC	FAM200A		METRNL	UBE3A	ZNF766	DDX1	RBBP6
KCNG1	TERC		COLQ	MRPL41	ZNF761	KLHL36	LINC00665
KCNG2	IL1R1		TBC1D3P1-DHX4	UBE3D	ZNF763	TMEM170B	MIR4471
LOC284837	NFS1		RAI14	MED12L	TXNRD1	RAB7A	SLC29A3
ZNHIT1	JMY		VANGL1	GRB2	ZNF184	KLHL35	RBBP5
NUBPL	LRRK1		MTDH	PRSS36	ZNF180	SPATA17	LINC00664
NME1	CHD6		EXOSC4	SSR4P1	STAG1	DKKL1	RNGTT
YTHDF3	CHD9		LOC100507477	UBXN4	ZNF182	SIRT5	FUK
YTHDF1	MIR634		ADAMTSL3	PRSS38	ZNF189	PVT1	ITGB4
ZNF596	ABHD12		MADD	DRAM1	UBE2E2	MED30	MIR4674
ZNF597	ZNF585A		TMEM167B	EDN3	ZNF25	NUCKS1	S100A10
ZNF594	SUPT16H		ST20-MTHFS	FLG2	CCDC3	ZNF567	ARIH1
ZNF595	SPO11		LOC101927822	FAM219B	MIR4736	LINC00847	YPEL3
FLJ41278	TMEM245		DISC1	FAF2	ZNF20	RNA45S5	YPEL2
ZNF599	LOC101927932		LINC01322	ZSCAN2	ZNF23	PLEC	CCNE2
CEP95	IL22RA2		COA4	LMX1B	HYKK	LINC00842	HAR1B
ZNF600	FN3K		BLACAT1	SLC26A5	SHH	SEZ6L2	HAR1A
ZNF606	TSC1		RRBP1	SLC26A7	LOC400867	ZNF227	TIMELESS
ZNF607	MFSD3		ANGPT1	FGF7	ZNF28	C10ORF11	TREML3P
ZNF605	MRPL10		PPP1R14C	MTFR1	PLA2G16	ZNF564	MKL2
CBX3	MRPL11		KPNA2	COL6A4P1	CSRP2	CXXC5	SREK1
ZNF609	MRPL13		PRSS22	GET4	DNAH6	PEX7	RAB11A
AXDND1	RAB3GAP2		ENG	ACTB	MAPK8IP1	MGAT1	DERL1
PLCH1	IL4R		C9orf43	CMSS1	DNAH5	ZNF563	SRMS
VEZF1	MRPL16		GTF2IRD1	SLC25A40	HS6ST1	NWD1	C8ORF34
POP7	RAB3GAP1		TNFAIP8L2-SCN1	LINC01503	HS6ST2	LAD1	PRR29

PPP1R9B	TANC1	F12	SLC25A45	ZNF501	RBM25	CDK14
KIF14	ATP8B4	C3ORF14	SDC2	ZNF502	C9ORF3	LMBR1
TARS2	TTC9	EXOG	VAV2	ZNF506	SPOCK1	PKM
CEP72	MFSD4	MIR3193	SDC4	TMEM131	HECW2	ITPK1
NUDT3	TMPRSS13	ZNF382	PRPH	LOC440461	SLC19A1	ZNF844
PMEP1A	LINC00928	FZD6	STRADA	TMEM134	RBM28	CSK
LOC101929	CIB1	LINGO1	NUP153	CCDC47	FNBP1	SNORA70G
LOC339166	ITPR2	TBC1D30	ECI1	LOC101929224	RFWD2	CNOT11
C14orf80	WFDC3	CACNB3	ESD	ZNF235	ACE	PPDPF
PHLDB1	ZNF829	TBC1D32	STON2	ZNF234	ACD	MLLT10
LRR37A11F	LINC00927	LINC00693	FAM105A	ZNF233	EPHA7	ZNF302
STK32C	ANKRD29	PCDH15	BAIAP2	ZNF232	EPHA6	DAP3
STK32B	LINC00925	VPS51	ZNF592	ZNF230	MIR1256	EIF4H
ZSWIM6	ABCG1	RTEL1-TNFRSF6E	RNU6-2	GPBP1	C6ORF165	SMYD3
SMEK1	ABCG2	RALA	CLUAP1	HMGNA4	ME3	BFSP1
PPP5C	PRDM15	VPS54	LINC01298	CDKL3	TENM4	BCAR1
DHX40	DEPTOR	ZNF627	SORCS2	SPRY4	LSMEM1	NTNG1
CALML5	TLK2	LOC101927557	DMRT2	SAMD4A	ZNF229	MIR4792
GAS8	MPO	SCYL3	RHOD	SAMD4B	VASP	PAAF1
CIPC	FIS1	GPR149	FYTTD1	MIR646HG	ATP5E	CEP170
NXPH3	USP50	STXBP4	MIR6773	GAS2L3	TBC1D8	RNASEH2B
ZNF117	TMEM68	SMPD2	CCAT1	LOC100128885	KATNBL1	CD96
ZNF114	MTSS1	BRIP1	LRR37A11F	ABHD17C	TBK1	LINC01021
KDM3A	CASKIN2	ZNF623	HYDIN	TMEM63B	ZNF740	LINC01023
ZNF112	FLJ46284	INF2	CNR2	CDKL1	MRPS31	ISY1
ISLR2	AIFM1	ZFPM1	FOXP4	LOC100499484	TBC1D5	LOC101927746
GAS7	IL17RC	PRKXP1	MIR4790	BAGE2	ZNF749	CLK4
NUTF2	LRR37A11F	GSG1L	LINC01340	SLC39A1	IPO5P1	SNX27
ZNF337	DSCAML1	CYP1B1	SCPEP1	AZI2	ZNF101	LINC00993
PDGFRA	MIR323B	MIR1207	MAPK6	FBXO22	FGF12	HDAC4
TMC7	FJX1	ABCA8	BCO1	ZNF341	FAM209B	HDAC9
APIP	HTR5A	DNAJB2	GTDC1	ZNF436	ABHD16B	ONCUT1
TMC1	CRNN	OR4D2	COL26A1	ZNF431	SLC7A5	TMEM161A
HIST1H4C	MAPK14	SDR9C7	FOXN3	ZNF430	UGCG	AHI1
ZNF331	KRIT1	LINC00342	DUSP1	ZNF345	LOC441242	ZFH3
TEX14	FOXH1	LOC101927487	SGPP1	ZNF432	MTHFS	XRCC4
AMPD1	MIR1273H	RNU6-83P	LINC01184	ZNF347	SNUPN	KIF15
EIF2B5	FAM217B	HNRNPAB	GABPB2	ZNF439	COL9A3	FANCD2
EIF2B3	NCOR2	HAS2	ACTN3	VGLL4	UNC13B	ST6GALNAC6
LOC100129	NCOR1	F13B	GABPB1	ZNF346	UNC13C	RGS19
PI4KB	KRTAP5-11	PHIP	ATP8A2	FGD5	SYNE1	MESP1
CSMD3	FZD1	LOC81691	MARK3	PUS1	MNAT1	MESP2
LGR6	SCAPER	ELMOD3	PAQR5	SERPINA13P	POMK	PARP4
MPHOSPH6	BTG2	DMXL1	SNAR-A3	MACC1	MAD2L1BP	C15ORF38-AP35
LOC102659	AKR1B15	ZNF808	TOMM70A	ZNF433	YTHDC2	ATXN7L1
TXNIP	ZNF624	CITED2	TGS1	FGD3	TRPS1	AKR1C3
LOC101929	ZNF626	LOC101927311	RAD54B	FGD2	ZNF527	NLRP7

TOR3A	TEC	SYCP2	METTL8	GNB5	ZNF525	LOC102724084
LOC1019296	ZNF620	TAOK3	SIL1	AMBRA1	LOC1019285	BLVRA
MIR6871	ZNF621	FAM65C	WWTR1	LOC100287944	GM140	P2RY6
NOTCH2NL	CACNB4	LIME1	LEP	TMEM9	ZNF529	PSEN1
CFLAR	MIR454	SLC22A15	TBC1D19	NUDT17	ZNF528	PCDHA1
MECOM	NBN	GRIK4	MORF4L1	SATB1	RIN3	ADAP1
RSPH1	TMEM30B	CRTC3	TPTE2P5	ZNF253	MET	WDR27
CSF1R	ZFP14	TTLL3	TBC1D16	BTD	EMP2	PDZD2
PRPF40B	RAP2B	CA3	TBC1D17	C11orf80	WVOX	TRAPPC10
TPM1	SIAH2	MDM2	TBC1D15	TMEM5	GLT6D1	TRAPPC12
CIB3	LMNB1	MIR296	KCTD3	CNNM3	ZNF420	RAB13
TNFSF8	KCNQ1OT1	NSMCE2	KCTD2	C1orf27	RPS6KB1	LYST
PLEKHA3	ZFP36L1	PNP	DHX30	PIP5K1A	STEAP4	SEMA3C
MYT1L	TRIM36	COBL	ADAM12	STX6	GLP2R	PPP1R12A
PRELP	MLXIP	POLR3E	UST	BASP1	CLPX	LYSMD2
UTP18	LYZL1	MIR298	AMZ2P1	GDPD1	RPS14	KLHL12
FAM117A	ZER1	CA1	FAM83B	PARD3B	ZNF251	MED22
ETFA	PHLPP2	ZNF793	FAM83A	POLR1D	ZNF250	PPP1R12B
TRIO	C10orf91	RNF139	CPNE9	SLC4A10	LEKR1	GOLT1A
DPAGT1	C15orf40	OBSCN	C12orf73	TGFB2	SLC25A32	RRS1
PHACTR3	ADK	AMOTL2	SERPINA6	TGFB3	RUNDC3B	GAB2
PHACTR2	RASGRF1	PLEKHF2	EXOC6B	TDRKH	ZNF254	LOC102724710
TET3	B3GALNT1	PTK6	PLOD2	MTERF1	ZNF257	SPATA33
LOC1019279	ZNF480	RABGAP1	PLOD3	LOC389831	ZNF256	ASCL5
CELSR2	MEIG1	SF3B1	TPRXL	FBRSL1	LOC1019295	COL5A1
IER5L	TACC3	MSH6	RNU6-81P	LETMD1	DCAF11	PEX2
ENY2	ZNF484	SPECC1	C5orf24	GTF2A1	LOC1019295	IGF2BP1
LOC1019268	ZNF485	CYP17A1	VKORC1L1	SLC5A7	RIPK4	TOB1
PTCHD2	ZNF486	AFG3L1P	RFTN2	FLJ36000	DSCAM	UNK
TSEN54	ZNF487	ADORA1	RFTN1	LOC100506175	LOC1005070	CD101
SLMO2	ZNF138	GAL3ST2	DGKI	NBPF18P	UBASH3A	MAPK9
DDX19B	PIAS3	SEMA6C	PXN	IQGAP1	AVL9	NELFCD
FSD1L	DEK	SEMA6A	DGKB	UIMC1	ZNF818P	SLC31A1
LINC01440	PRKACB	MUC3A	PCF11	YWHAZ	LOC1024672	LINC00534
LINC01441	MIR1208	NSMCE4A	DGKE	ARHGAP44	TMEM183A	GTPBP10
TMED10P1	DECR1	DDHD1	LOC104054148	HDGFRP3	TMEM183B	ZFP37
RAB15	PSMB4	ADCK4	SNORA76C	MTMR11	C1GALT1	HKR1
LRRC34	ZNF134	SUN1	RAD21	CASQ2	COPZ2	CNBD1
YOD1	ZNF135	NAA16	DDX58	TGOLN2	ZNF419	
ZNF33B	ZNF136	SUPT3H	PTGIS	GNRHR2	ZNF418	ACSBG1
FANCI	RPS3	C3orf33	ZNF324B	MIR3194	ZNF417	USP8
LOC400548	ZNF317	CCDC71L	LINC00964	ICA1	DCAF7	RPP25
ZNF33A	KALRN	DNAJC14	DDX59	ETS2	ZNF415	ERCC1
SH3PXD2B	LOC100506470	DNAJC15	LINC00963	ARNT	C12ORF42	USP2
RMST	TEX36	NARFL	USP15	RPE	ZMIZ1	ACN9
FAM117B	TFF3	LOC101928135	MIR7851	LINC01164	DAPK1	RPRD1A
LOC1019280	LOC285692	NANP	ZNF878	SENP6	ULK2	SPATS2

9-Sep



LOC400541	LOC285696	C16orf47	MIR7853	PCMTD2	NR3C2	NDRG1
FER1L6	NOTCH3	XPR1	SSBP2	ZBTB1	NR3C1	HIP1
VMP1	RMI2	FEM1B	PACS1	PDP1	LOC729911	ZNF721
SNORA11B	CORO7	FEM1C	PACS2	RP9	DCAF5	ZNF720
KTN1	CIART	PPP1R13B	LINC00969	CARD11	KCNJ15	SERTAD2
PCBD2	DIDO1	MATN2	FAM63A	HRASLS5	AP5M1	ZNF727
PRDX6	KCNK9	FUT1	USPL1	MGAT2	TARS	ZNF726
LINC01270	SNORD26	PRKCA	RBM17	LOC101927588	MYNN	ZNF729
AP3S2	NEK10	PRKCE	ATF1	DYNC1H1	NMD3	ZNF728
TSNAX-DISC	TCFL5	FLJ16171	RNF169	LINC00494	TNN	ZNF468
BMPER	CRY1	TANC2	TXNDC16	CASC8	GPATCH2	PRR7
LINC00645	KCNK2	PRKCZ	UNC45A	CALD1	HM13	ABCB1
SYNJ2BP-CO	ZNF556	METTL21B	RLTPR	TBKBP1	LOC1005071	MED13
SMOC1	ZNF557	LMAN2	TMEM25	SNAR-B2	C20orf85	LOC100130987
LINC01272	ZNF554	MCL1	C8orf76	CTU2	ACTN1	MIR570
RBBP9	ZNF555	HIST2H2AC	ZBTB43	CHST15	PTPRT	LOC100128164
MIR4638	ATP13A1	ENDOU	ZBTB45	VAMP4	CFAP58	AEN
NBPF13P	RSAD1	BDH1	ZBTB46	FBXL6	ACTN4	DSCR3
CCDC169	ZNF550	SEC11A	GORASP2	CSTF1	PRPF38B	SMURF1
CFAP43	ZNF551	WDR72	AHNAK2	FIBP	PTPRG	KCND3
NPTN	NACC2	ZNF157	SNHG21	COL20A1	KCNT2	TMEM249
AXIN2	ZNF90	ZNF154	PRKAG2	TSHB	PTPRB	INTS5
CTCFL	ACOT13	DDX24	SCG3	C14ORF182	PTPRO	INTS4
MMRN2	ADRM1	LINC01535	RIC1	RIPK2	RNLS	ANKRD34A
POR	ZNF558	MAP1LC3B	JPH3	PITPNC1	PTPRK	DIRC3
CCDC166	TRAF3	SAE1	HIPK1	GLCCI1	PTPRJ	INTS8
ZNF8	TRAF4	ZNF790	SMARCC1	BPTF	DTWD1	LOC100507377
ZNF252P	LOC101243545	ZNF91	ANP32B	BCL2L1	UBL3	THEM5
ARL1	RPA3OS	ZNF792	SLC39A13	SLC6A6	CPO	TMEM243
ZNF559-ZNF	RMDN1	ZNF93	ANP32A	NDUFB9	ZNF814	ZNF69
SYNDIG1	HOOK2	DTNB	SYNPR	NCR3LG1	STK10	THEM4
LINC00861	TMPRSS2	ATP6V1C1	SEMA4B	PCCB	POLG2	TNFRSF11B
OGFR	TMPRSS3	ZNF98	SEMA4C	GPR39	CPE	CYB561D1
CDC5L	TMPRSS4	ZNF799	LEMD3	CHN2	MFAP3	FAM227B
VASN	MIR4729	FLVCR2	NOS3	CTSS	FKBP2	LOC101928516
RAC1	MAPKAP1	LOC100506457	OTUD7B	IL24	RPTN	CTNNA1
RUFY1	KAT6B	RAB3IP	NCAN	LOC730202	CPQ	CTNNA3
VCL	CACNG4	VPS37C	AMZ1	LOC643339	LOC153910	TAMM41
NBPF15	LINC01461	C12orf10	AMZ2	NAALADL2	GAPVD1	LOC643770
SKIL	DENND1A	TACO1	ZFYVE16	PDE4A	LOC1019293	IST1
NBPF10	LINC01465	ATF7IP	ALMS1	PECAM1	CASS4	CHRNA5
CHCHD6	FOXN2	GPER1	ATRNL1	DCAF10	LOC1005067	AZIN1
CADPS	NEBL	PPIL6	MKRN2OS	ZRANB3	CYP46A1	NOTCH2
NPSR1	SPATA2L	ACHE	MRPL50	TPD52	NBEA	STXBPSL
LYPLAL1	RPL38	RALGPS2	SCN4A	FMNL3	APBB2	CACNG1
CYP7B1	RPL37	KCNB1	SCN4B	IL12RB2	STARD10	MLPH
TUFM	RPL32	TMED10	CDS1	CBFA2T3	NOB1	CCDC58

AGR2	RPL30	MIR6839	MIR1206	STAP1	KCTD5	CACNG5
LOC1019275	C1ORF185	PRPF39	ARHGEF11	CTDSP2	IRAK2	ZNF652
SLC16A6	MIR635	PPP1R3D	MIR1204	ENSA	SV2B	MIR663AHG
MAN2A2	GNA14	MAP3K3	MIR1205	UMAD1	LOC1019295	LMAN1L
BCKDHB	GNA12	CNGB3	MIR1203	PLEKHO1	DEGS2	HSF5
ABRA	GNA13	MAP3K1	TRIQQ	MC1R	NR5A2	MLEC
WIPF3	MIR142	BCLAF1	CYP1A1	AQP5	TATDN1	EPB41L4B
ARHGAP39	ZSCAN12P1	MAP3K5	ZNF682	LINC00689	FAIM2	SESTD1
WIPF1	ATF7	ZNF570	ZNF677	VRK3	MYO15B	RAPGEF4
PTCH1	ZNF286A	ZNF571	ZNF680	CRYL1	WRB	FIRRE
ZSCAN32	SLC4A1AP	ZNF681	ZNF687	LOC101927421	DYSF	SLC30A8
ZSCAN31	SHARPIN	SYNE2	ZNF684	IRF2BPL	LOC1019277	ATP2C2
FNDC3B	SLC30A6	MIPOL1	LINC01005	MRPL3	SGK3	KMT2C
TRPM7	RANBP17	FLJ22447	LOC101928973	LOC101929106	ZNF670-ZNF	ESRRG
NINL	FURIN	MDM4	LOC100506730	WDYHV1	LRP4	PDSS2
TRPM2	LINGO4	ROR2	SUMF1	MRPL1	GALNT11	LOC63930
TRPM3	ZNF354A	MAN1A2	NCALD	EIF3E	ZNF268	COL18A1
ROMO1	CERS3	GMPS	ZBP1	OLFM1	MIR3134	MIR6723
XRN2	POC1B	RSPO2	PPP4R1L	HIST1H4B	ESR1	SERPINA3
KAT2B	TSNARE1	ULK3	LINC01126	ZFP30	ASNS	RHOBTB3
GID8	SELENBP1	SNRPD3	PCDHB5	RHOT2	PLXNA4	NUMB
ACSF3	EML1	MIR181A1HG	CLSTN1	RNU6-72P	TBC1D9B	ALDOA
MAL2	RORC	MYLK	MKS1	ARHGEF1	OR4K17	INO80D
SGOL1	MPP5	ZNF273	PC	PSTPIP1	TMTC2	ATP1B1
SGOL2	EML5	WDR93	DNASE2	FAM173A	LINC00479	INO80B
TUBB1	MIR4692	MPHOSPH10	RYR1	RAF1	PSCA	MIR3680-1
MB21D2	NXPE3	6-Mar	SNORD116-4	BCAS3	PDE4D	C1ORF101
CORO2A	MAGI3	BOLA1	TCHHL1	BCAS1	HARS2	FMN1
CASC19	MAMLD1	ZNF276	WNT8B	EHMT1	MAP4K3	ZNF718
CR1	MAGI1	KPNA1	ZFP2	APH1A	STKLD1	FAM43A
GALK1	ZNF471	SCAND1	ZFP3	STAT4	MAP4K5	ZNF714
IMPG1	ZNF470	MYO5C	NAV1	SEC23A	LINC00879	ZNF716
FAM174B	ZNF473	MYO5A	KIAA0825	SNX11	CDH17	ZNF710
LINC00854	LINGO2	KCNV1	ZNF660	CD55	LOC1019272	FCHSD2
CYP19A1	HES1	IFT43	RPIA	CCAT2	LINC00877	ZNF860
PTPN9	GUSB	SYNM	ZNF662	NBPF20	JUNB	ZNF713
FAM168A	SPEF1	IFT46	ZNF665	PCDHGA7	LINC00871	COMMD10
C17orf58	ZNF271P	PKP1	ZNF667	LINC01056	MAP2K3	CPNE3
PCDHGA9	ZNF542P	PLGRKT	MIR3150A	STOX1	TMEM43	IPP
POLE3	FAM210A	MIR3916	SCAMP5	ICAM2	MAP2K5	LOC100630923
POLE2	SNTG1	FRS2	SCAMP2	CPAMD8	ZMYND11	SERPINA9
DHRS7	SNTG2	NBPF25P	FNIP1	FGFBP3	AACS	HAO1
STK39	BZRAP1	ITGA10	ABCC5	PCDHGA5	BCL9L	HTR1F
TMLHE	SLC25A21	LOC101928979	TMED3	BCL7C	LOC1019270	ZNF625-ZNF20
SYN2	SLC25A24	LOC101928977	MBLAC1	DPM1	ZNF204P	ABCC1
SYN3	CFAP70	TSHR	SMIM5	CKB	MICU1	ZNF512B
TFDP1	RPLP0	CRH	CGN	LOC101927391	PTPN22	DNAH14

FNTB	TCHH	TMEM182	BAIAP2L1	NDUFA13	LOC1005007	FAM160A1
KIAA1244	ZKSCAN5	PIK3R5	SMIM8	EFNA1	C7orf49	DNAH10
BOLL	ZKSCAN7	PVRL4	SHANK2	MIR589	PTPN21	LOC100379224
PRPF4B	LOC79160	PIK3R1	HNRNPK	ANG	RHBDF1	TMOD2
ENPP1	ZKSCAN8	LOC646736	REEP1	TPD52L2	CHIT1	NME1-NME2
TSPAN2	RBBP8NL	ZNF287	TCF25	TPD52L1	PPL	ZNF79
UMODL1	KDM5B	IFT122	ARMC1	EFCAB11	GAN	LDLRAD4
CT62	PLS1	ZNF282	HNRNPD	TYW5	EHD1	YY1
ATP2B2	ZNF280D	ZNF283	HNRNPF	SLC33A1	DAAM1	ZNF77
ATP2B4	AFAP1L1	PTPRN2	LOC101927657	TMEM87B	ACY3	SPINT2
FAM193B	GLIS3	MIR124-3	TSKU	GALNT14	FANK1	IL10RA
ZNF445	ZNF19	LNX2	SREK1IP1	LOC101928048	ATP5G2	SNORD116-8
CABLES2	CHMP3	MIR4257	PRUNE	RCOR1	LRP10	PLEKHG4
ZNF440	MUC20	TMEM189	APRT	LOC644554	LRP12	SLC7A14
ZNF441	DNM2	TLE1	SLC13A1	RNF168	LINC00885	CD160
ZNF442	EED	LINC01481	HDLBP	KCNK12	CLASP2	BBS4
ZNF443	MAPKAPK2	LIX1L	CHRNA4	C7ORF60	LINC00886	SLC7A13
KRTAP10-5	ICT1	DSTN	LINC01336	CHGA	KIAA1755	COX6C
MIR548H2	PREX1	HSF2BP	ERP44	CD58	RNU6-71P	SIGLEC9
MEGF11	TUBA1C	C14orf166	CHRNA7	HMGCS2	ORC5	INSL4
CD2AP	CPA3	CEACAM21	RMDN3	TMEM26	LOC1019272	SELT
ZKSCAN1	FKBP1AP1	TAF7	CHD2	PDE9A	ACAP2	SPATA2
SUPT4H1	LINC01484	TAF6	PCDHB19P	UGT1A8	ABCC3	SERPINH1
PDXK	LOC101929164	TUBAL3	PLEKHA8P1	CIT	SLC11A2	LINC00316
SS18L1	DOK5	TAF3	ZNF107	ACBD6	LINC00313	CYB561
LOC400706	LDHD	LINC01136	RGS16	MIS18BP1	OR1F1	LOC100996348
C9ORF129	MIR3614	AP1G1	STAU1	ZNF354B	C10ORF53	SLC2A4RG
ABL1	MTA1	USP10	ZNF767P	CST6	BBS9	SF3A3
TNFAIP8L3	MTA2	BCAS4	FAAH	TATDN2	SEC22B	C4ORF36
NCAM2	MTA3	DCAF4L2	C7	ADNP	SEC22A	ZNF100
MIR5707	POGZ	BTBD1	XKR9	LRP1B	ZNF274	EHD4
CASC11	ISG20	LINC00301	EXOSC8	GLI1	ADAMTSL4	EHD2
LINC00265	HSP90AA1	CASC15	RGS18	TTLL11	LINC00403	

<b>TRIM28 direct repressed target genes</b>	<b>TRIM28 direct activated target genes</b>
C12ORF56	CDH13
BAG3	TMC7
ZNF334	C10ORF107
SLC4A10	UBE2QL1
SKAP1	GLIS3
ZNF257	TEX14
ZNF853	EPHA3
SLC30A8	CPE
LINC00645	CHGA
DSCAM	AFF3
LAMB1	BMPER
CPQ	LRFN5
BCAS1	ADAMTS19
LMBR1	GABBR2
ATRNL1	KIAA1217
ZNF486	PKHD1L1
RNF217	SEMA6A
ZNF729	CASQ2
ZNF626	RUNDC3B
NEK9	CBLN4
ZNF264	ADAMTS9
RFTN2	SULF1
SDR9C7	LRP1B
RMST	PLCH1
HRH1	FAM129A
ABCG2	SLC16A10
ZNF415	CCDC33
SV2B	REEP1
B3GALT5	CNTNAP2
NR3C1	NCAM2
SPATA17	S100A16
COL9A3	UST
C10ORF11	PPP1R14C
ATP8A2	DAPK1
DIRC3	GBE1
PLA2G16	PTPRN2
ZNF208	CBLB
FAM84A	JAKMIP1
HTR7	TSKU
INHBA-AS1	LTBP1
SPAM1	HAR1A

DCDC2	STRA6
ZNF676	BMP5
AKAP6	TMPRSS4
DNAH6	KIAA0226L
ZNF737	STON2
ZNF883	NMNAT2
ZNF716	ZNF583
GPR158	TNFRSF11B
ZNF679	DENND1A
LINC00578	PLEKHO1
CMTM8	ARNT2
ZNF91	ZNF804B
PCDH15	BMP7
COL21A1	CD101
WIPF1	PLAGL1
ZSCAN30	F5
BOLL	ROBO1
ZNF506	NTN1
FOXP2	STEAP4
CDH17	ZFP37
ZNF491	SPOCK1
ZNF702P	HS6ST2
PHLDA1	LIMA1
INSL4	PDE4D
CNGB3	WDR72
PCDHB5	CCBL1
ZNF347	SYN3
C20ORF195	GLP2R
LDHD	PRSS23
ZNF788	BCL11B
ZNF439	ONECUT1
NECAB1	DNAJC22
MYT1	TFF3
LONRF2	SLC2A10
PHACTR3	ANKRD35
ENG	OLFM1
ANXA9	RUNX1T1
ZNF69	PKP1
SYCP2	TPK1
FAM63A	C3ORF70
CYP1A1	SERPINE1
ABCA12	PTPN22
ZNF441	NTNG1

ZNF442	HRNR
ZNF563	HAR1B
ZNF844	NAALADL2
SPAG17	FAM178B
LINC00534	TTLL11
STC2	DIO2
ZNF98	CXCR4
	ATP6V0D2
	RIMS2
	PDZK1
	HMGCS2
	TMPRSS3
	MYEOV
	SHC3
	VGFB
	SLC12A2
	LARGE
	LINC00665
	TFF1
	CT62
	ZFP82
	SHH
	ZNF256
	MAPK8IP1
	AXIN2
	GPR39
	CSRFP2
	ZNF880
	POC1B
	FAM43A
	CA2
	VAV3
	SPDEF
	NTSR1
	CALML5
	LRRC10B
	ELOVL2-AS1
	FBXO32
	SYBU
	PSCA
	CTHRC1
	MYO10

## Supplementary Table S11: hTRIM28 Deletion Mutants Primers

hTRIM28	
delRING-F	gccgaggcgctggagttctccaaagacatc
delRING-R	gatgtctttggagaactccagcgcctcggc
del-CC-antisense	5'-gccttcctgcacctcctggactggtggtc-3'
del-CC	5'-gaccaccagtaccaggaggtgcaggaaggc-3'
del-RBB	5'-ggcgctggagctgctgttcttagaggatgcag-3'
del-RBB-antisense	5'-ctgcatcctctaagaacagcagctccagcgcc-3'
del-RB-antisense	5'-cagcactggttcgcctccagcagctcca-3'
del-RB	5'-tggagctgctggaggcgaaccagtgctg-3'
del-B-Box	5'-caccgacgcccaggatttagaggatgcagtga-3'
del-B-Box -antisense	5'-tcaactgcatcctctaaatcctgggcgtcggtg-3'
delLinker-antisense	5'-ggcagacacggcacatgggctggctg-3'
delLinker	5'-cagccagcccattgtgccgtgctgcc-3'
del-PB	5'-ggatgacagtgccaccattaccaagtctctgct-3'
del-PB-antisense	5'-agcagagaactggtaatggtggcactgtcatcc-3'
shTRIM28-resistant <i>TRIM28</i>	5'-cctgtcctcagtaactgttaaactgttaaacatccggccc acatcctgggcaaact-3'
shTRIM28-resistant <i>TRIM28</i> -antisense	5'-agtttcccaggatgtggccggatgttaaacagtttaac aagttaactgaggacaagg-3'
shEZH2-resistant <i>EZH2</i>	5'-cggcagccttgtgacagttcgtgtccatgagtaatcgccca aaatttgtgaaaagtttg-3'
shEZH2-resistant <i>EZH2</i> -antisense	5'-caaaactttcacaaaaatgtggcgattactcatggacac gaactgtcacaaggctgccg-3'

**Table S12.1: Oligonucleotide sequences for Real Time qPCR analysis**

hTRIM28-RT-F1	TTTCATGCGTGATAGTGGCAG
hTRIM28-RT-R1	GCCTCTACACAGGTCTCACAC
hTRIM28-RT-F2	CGGGATGGTGAACGTA CTGTC
hTRIM28-RT-R2	GTCTCGGCAGGTGAGAGTATC
EZH2-RT-F2	GAGACTGGCGAAGAGCTGTTT
EZH2-RT-R2	GGCATCAGCCTGGCTGTATC
EZH2-RT-F3	CCCTGACCTCTGTCTTACTTGTGGA
EZH2-RT-R3	ACGTCAGATGGTGCCAGCAATA
$\beta$ -Actin-RT-F	TCATGAAGTGTGACGTTGACATCCGT
$\beta$ -Actin-RT-R	CCTAGAAGCACTTGCGGTGCACGATGGAG
hCXCR4-RT-F1	ACTACACCGAGGAAATGGGCT
hCXCR4-RT-R1	CCCACAATGCCAGTTAAGAAGA
hCXCR4-RT-F2	ACGCCACCAACAGTCAGAG
hCXCR4-RT-R2	AGTCGGGAATAGTCAGCAGGA
hCA2-RT-F1	GGGTACGGCAAACACAACG
hCA2-RT-R1	GGCTGTATGAGTGTGCGATGTC
SULF1-RT-F1	GATCCCCGAGGTTTCAGAGGA
SULF1-RT-R1	GGTGTAGTCACAAAGGCATTGA
JAKMIP1-RT-F1	GACGAGCGAGATGTGAGGC
JAKMIP1-RT-R1	GCCAACAGCGTATTTCTGTCTT
BCL11B-RT-F1	GGTGCCTGCTATGACAAGG
BCL11B-RT-R1	GGCTCGGACACTTTCCTGAG
BAI2-RT-F1	TGGGCAAGGGACATAGGATGA
BAI2-RT-R1	CGAGGCGATGGTAGGAAAGA
hONECUT1-RT-F1	GAACATGGGAAGGATAGAGGCA
hONECUT1-RT-R1	GTAGAGTTCGACGCTGGACAT
hSTRA6-RT-F1	CCACAGAGGACTACTCCTATGG
hSTRA6-RT-R1	CAGCACAAGGATTGACAGCG
hMYEOV-RT-F1	TGAGCAGGCCATTAGCTCG
hMYEOV-RT-R1	CATCCATTCGCGCCACATA
hCNTNAP2-RT-F1	CTTTGGCAATCGGAAGCAGAT
hCNTNAP2-RT-R1	GAGCATCCGGTATTGGGTAC
hCCBL1-RT-F1	CCAGTGGATGGTCTACGACG
hCCBL1-RT-R1	CTCCCGTTCAAAGCTCTCG
hKIAA1217-RT-F1	GTGAGGTCAACCAACCAGACG
hKIAA1217-RT-R1	TGATTTTCATTTCGGCATCCTGAG
hNTNG1-RT-F1	AAGTTTGGGATTACATGGCCTG
hNTNG1-RT-R1	CGGAGGATCGAGTTTCACTTTC
hFAM129A-RT-F1	AGACCGGCTTATGAATCTTCCG
hFAM129A-RT-R1	GCTCGTGAAGCAGGTTGAC
hBMP5-RT-F1	GCTGCTGGGTTCTAGTGGG



hBMP5-RT-R1

TTCGTGGTTCGTTAGTCTTCTA

**Table S12.2: Oligonucleotide sequences for Real Time qPCR analysis after ChIP**

CXCR4-ChIP-F1	CAGCCCATTCAGGAGGTAAA
CXCR4-ChIP-R1	TGCACCTGACCCTAGTGATG
CXCR4-ChIP-F2	CTTCCTTCGGAGGATGTAGC
CXCR4-ChIP-R2	TGCACCTGACCCTAGTGATG
CXCR4-Distal-F	CAAGGCAGGTGCCATTACTT
CXCR4-Distal-R	GACTGGGTGCAGATCCTCAT
KIAA1217-ChIP-F1	TCCAACTTTGGGGAAAGAGA
KIAA1217-ChIP-R1	CAGGGAAGCAGAGTTTGGAG
KIAA1217-ChIP-F2	CCCATTTACCTAGGCCGTTT
KIAA1217-ChIP-R2	ACATCCAACCACAGGCTACC
MYEOV-ChIP-F1	CAACGCCATCATTATCACCA
MYEOV-ChIP-R1	CCAGCCCACCTGTAAATCA
SULF1-ChIP-F1	CTCAGCCTCCAATCCGTAAG
SULF1-ChIP-R1	TTGAAACACGTCCTCAAGCA
SULF1-ChIP-F2	TGTCCCGAAATTCACCCTTA
SULF1-ChIP-R2	ACACACCCCATAGAACCAA
CCBL1-ChIP-F1	AGTGTCCGAGCGAGAATCAG
CCBL1-ChIP-R1	TATAACGGAGTGGCTGCACA
FAM129A-ChIP-F1	TGTTTGTTTTGCAGCCTCAC
FAM129A-ChIP-R1	GCTTTGTAAGTGGCCGAAAG
CA2-ChIP-F1	GCCTACGAGGAAATGCAATC
CA2-ChIP-R1	GCCGTGGAATAAACGAGAC
CA2-ChIP-F1	CAATGGTCATGCTTTCAACG
CA2-ChIP-R1	GCTCGGAAAACAGCTACTGG

**Supplementary Figure 3.** A) Distribution of genomic sites of TRIM28 chromatin occupancy in MCF7 cells. Peaks are categorized as TSS (+/-3Kb), 5'UTR, 3'UTR, genic (coding exon + intron), , or intergenic. B) UCSC genome browser screenshot of tracks representing normalized sequence tags for expression of CXCR4 in shControl, shEZH2, and shTRIM28 RNA-seq, and enrichment of EZH2 (ChIP-seq in HMEC cells), and TRIM28 (ChIP-Seq in MCF7 cells) (<http://genome.ucsc.edu/>). C) UCSC genome browser screenshot of tracks representing enrichment of EZH2 (ChIP-seq in HMEC cells), and TRIM28 (ChIP-Seq in MCF7 cells) (<http://genome.ucsc.edu/>) on MYEOV and CA2 genes.

**Supplementary Figure 4.** Co-immunoprecipitation. Endogenous EZH2 was immunoprecipitated from whole cell lysates of T47D cells, followed by western blotting with antibodies for TRIM28, and SWI/SNF complex members as indicated.

**Supplementary Figure 5.** A) Brightfield images showing that mammosphere formation ability of MCF7 cells is reduced after depletion of TRIM28. Bars of graph shows the average sphere numbers  $\pm$  SEM per  $2 \times 10^3$  plated cells (\* $P < 0.05$ ). The sphere size that is more than 60  $\mu$ m was counted. Error bars represent SEM from three independent experiments (\*  $P < 0.05$ ). B) CD44<sup>+</sup>/CD24<sup>-</sup> populations analyzed by flow-cytometry analysis of control and TRIM28 depleted T47D cells with quantified results shown in the graph. Error bars represent SEM from three independent experiments (\*  $P < 0.05$ ). C) TRIM28 and CXCR4 expression analyzed by RT-qPCR in TRIM28 depleted T47D cells. Error bars represent SEM from three independent experiments (\*  $P < 0.05$ ).