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Original Article

Genome-wide ChIP-seq analysis of TCF4 binding regions in colorectal cancer cells

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Abstract: Objective: TCF4 (transcriptional factor 4) forms a complex with its transcriptional coactivator β-catenin and the coactivator carries the final signal output from the canonical Wnt signaling pathway, which is essential for the growth of normal epithelium and also plays important roles in carcinogenesis of colon epithelium. We aimed to gain a better understanding of the genes bound by TCF4 in colorectal cancer cells. Methods: SW620 human colorectal cancer cells were cultured. The TCF4 antibody of this study was confirmed in SW620 cells by Western Blot. A ChIP-seq based genome-wide analysis of TCF4 chromatin occupancy in colorectal cancer cells was conducted and 1506 high confidence TCF4 binding sites wereidentified. Results: Sequence analysis revealed that the binding sites harbor a consensus sequence of C-G/C-A-G-C-T/C-C-T-T-C. Gene ontology and pathway analysis showed that TCF4 regulated 18 genes in Wnt signaling pathway and 97 other transcription factors. Conclusion: Our results suggest TCF4 binding regions were enriched with a motif of C-G/C-A-G-C-T/C-C-T-T-C. The gene regulation of TCF4 may be conserved in colorectal cancer and glioma cells. TCF4 may be involved in a series of important biological processes such as regulation of metabolic and biosynthetic (GO: 0010604, GO: 0031328, GO: 0009891, GO: 0051173, GO: 0010557, GO: 0045935), adhesion (GO: 0007155, GO: 0022610), apoptosis (GO: 0042981, GO: 0043067, GO: 0010941), and important signaling pathways (Wnt, Chemokine, Calciu, GnRH).

Keywords: TCF4, ChIP-seq, colorectal cancer, Wnt signaling pathway

Introduction

TCF4 (also known as Tcf7L2), which is expressed in the colon epithelium, is an important transcription factor of the Tcf/Lef family [1]. It plays a significant role in Wnt signaling pathway with the N-terminal beta-catenin binding domain and the C-terminal DNA binding domain (HMG box) [2]. Beta-catenin/TCF4 complexes accumulate in the nucleus and promote a series of target genes when the Wnt signaling pathway is activated [3, 4]. The lack of Wnt signaling causes TCF4 to bind several transcription repressors, thus, displaying the opposite function [5].

Many previous studies have shown that TCF4 is related to the occurrence and development of colorectal cancer [6-8]. Different kinds of oncogenes, including proliferation promoters (c-Myc, c-Jun, cyclinD1), apoptosis regulator (survivin), migration factor (uPA, MMPs, CD-44), and cell differentiation associated genes (FGF2, PPAR-d, BMP-4, c-Ret), were directly regulated by TCF4 [6, 9-12]. A systematic and genome-wide identification of all TCF4 regulated genes would be necessary to understand the role of TCF4 in cancers. Zhang et al. recently identified 1250 overlapping putative target genes that were co-regulated by TCF4 and STAT3 in gliomas using the ChIP-seq (chromatin immunoprecipitation-sequencing) approach [13]. However, global analysis of TCF4 regulated genes in colorectal cancers has not been conducted to date. Therefore, we conducted a ChIP-seq analysis of TCF4 bound genes in colorectal cancers and reported our dataset in this paper.

Materials and methods

Cell culture

SW620 human colorectal cancer cells (ATCC number CCL-227) were provided by the Second Affiliated Hospital, Zhejiang University School of

Table 1. Primers for validation of ChIP-target genes

Gene	Forward primer	Reverse primer
H2AFY	GAGTGCCAGGTTGTTTGGTT	ATGCCTGAGTAGCCCTAGCA
PLD1	CATTCGAGCTGAGGAGGAAC	CATCCCCAGGAAGTCACTGT
FLJ20294	CCCAGGAAATGCTCAACAAT	TGATGGCACACTCTCAAAGG
ZBTB16	CTATGGGCGAGAGGAGAGTG	TCAATACAGCGTCAGCCTTG
HIPK2	CACTGTGCAGTCTCCCTCAA	TGAGGCCTGGACTAAGCTGT
BRE	AAGTGGCCTTGAACCGAATA	GGGTTTCTGTGGCAGTCAAT
BCL2	TGATGTGAGTCTGGGCTGAG	GAACGCTTTGTCCAGAGGAG
PTEN	TTCTCTCCTCTCGGAAGCTG	AGAGGCTGCACGGTTAGAAA
AIFM1	TCATGCCCACTGTCCTGTAA	TCGGGGAAGAGTTGAATCAC
PAX7	GTTTGCCCCACAGACAAGAT	CTGGTGTGGTCAAGGAAGGT

Medicine, Hangzhou, China. Cells were maintained in L-15 medium (Invitrogen, Grand Island, NY) with 10% fetal bovine serum and penicillin/streptomycin (100 μg/ml) and cultured at 37°C and 5% CO$_2$.

Western blotting analysis

SW620 cells were lysed in RIPA cell lysis buffer (25 mmol/L Tris-HCl (pH 7.6), 150 mmol/L NaCl, 0.01 g/ml NP-40, 0.01 g/ml sodium deoxycholate, 1 g/L sodium dodecyl sulfate (SDS)) containing protease inhibitor cocktail kit (Pierce, Rockford, IL, USA). Protein concentrations were estimated using Pierce BCA protein Assay Kit (Thermo SCIENTIFIC). Approximately 20 mg of protein was denatured at 95°C with loading buffer for 5 min and separated by electrophoresis in 12% SDS-PAGE gels. The proteins were transferred onto a PVDF membrane and blocked for 2 hours in 5% skim milk in TBST buffer. Primary antibodies were diluted and incubated with the PVDF membrane for 3 hours at 37°C. The TCF4 (#2569) antibody was purchased from Cell Signaling Technology.

ChIP-seq analysis

The above-mentioned anti-TCF4 antibody and normal IgG were applied for immunoprecipitation. 10 million SW620 cells were fixed with 1% fresh formaldehyde and then were broken down in lysis buffer according to the ChIP-seq protocol [14]. The cell nucleus was re-suspended and sonicated on ice to DNA fragments of 200-500 bp. A total of 50 μl of Dynal protein G beads, 5 μg of antibody, and the sonicated DNA were incubated at 4°C overnight with rotation. Then, the precipitated immunocomplex was treated with proteinase K at 65°C for 2 h, and ChIP DNA were purified with QIAquick polymerase chain reaction (PCR) purification kit (Qiagen, USA). The DNA fragments were amplified by PCR, ligated with adaptors, and repaired at the double-strand end. The 150 bp ChIP DNA fragments were isolated by agarose gel electrophoresis and sequenced by Illumina Genome Analyzer II System.

Identification of binding sites

The Solexa pipeline analysis was performed as indicated by the operation manual [15]. The 36 nucleotide sequence tags were mapped to the human genome with two mismatches allowed with the SOAP program [16, 17]. The enriched peaks of the TCF4 binding sites were identified by CisGenome program with an IgG-ChIP group as control [18]. The program was executed with the default parameters (window 100, step 25, P0=0.599).

The CisGenome program was also applied to annotate the datasets with the UCSC human genome HG18 database. The annotation regions of these peaks covered 50 kb upstream of the transcription start site to 50 kb downstream the transcription termination site.

ChIP-PCR validation

10 genes of the binding targets were selected randomly to validate the TCF4 ChIP sequencing data by PCR. The genes and PCR primers are listed in **Table 1**. Each PCR reaction was performed in a total volume of 25 ul containing 10 ng DNA template, 5 U/ul TaKaRa Ex Taq, 1 X TAKARA Ex Taq Buffer (Mg2+Plus), 1 ul of dNTP Mixture (2.5 mM), and 1 ul of each primer (20 uM). The PCR results were analyzed by 1.5% agarose gel electrophoresis. Furthermore, 18 genes in the TCF4 binding region that associated with Wnt signaling pathways were confirmed by PCR. The genes and PCR primers are listed in Table S1.

Analysis of distance to transcription start site

The annotations of HG18 database was used to calculate the distance from the binding sites to the transcription start sites (TSSs). The distance number was negative when the binding site was located upstream of the TSS, and it

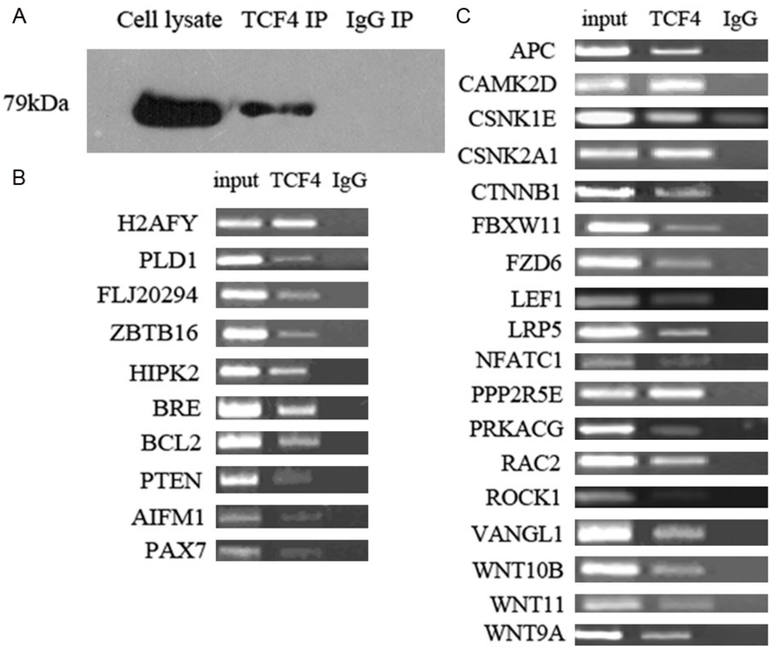

Figure 1. Confirmation of western blot and PCR analysis. A. Western blot validation with TCF4 antibodies and IP products (cell lysate, TCF4IP product, and IgGIP product); B. PCR confirmation of ChIP-seq peaks. The input, TCF4, and IgG DNA samples were extracted from cells, TCF4 IP product, and IgG IP product, respectively; C. PCR confirmation of genes associated with Wnt signaling pathways.

was positive when the binding site was located downstream of the TSS.

Motif searching and identification

We extended the observed TCF4 binding sites to 100 bp at the end of both the 3' and 5' to identify any novel motifs and retrieved the sequences in the FASTA format. We applied the MEME-ChIP program to mark all human repeats in these sequences and searched the up-regulation motifs (default parameters were applied) [19].

Gene ontology analysis

The program named DAVIDwas applied to statistically research the Gene Ontology (GO) terms (*P*-value < 0.01) and KEGG annotations (*P*-value < 0.05) of all evidence levels and categories [13].

Results

Specificity verification of the ChIP antibody

The ChIP antibody's specificity is the premise of ChIP-seq experiments; thus we verified its accuracy. The TCF4 antibody of this study was confirmed in SW620 cells by Western Blot and showed high specificity (**Figure 1A**).

Scanning and locating the TCF4 binding regions in colorectal cancer cells

Using sequence analysis, we mapped a total of 281,261 and 167,452 sequence tags uniquely to the human genome (allowing for two mismatches) for TCF4 and IgG, respectively. We used CisGenome program to analyze the binding regions of TCF4 protein in the entire genome. 1506 TCF4 binding regions were identified in the human genome with IgG ChIP-seq as a negative control (*P*-value < 0.01). In these binding regions, 1013 peaks with a cutoff-value of 50 kb distance contained 940 known gene annotations (Table S2). These results suggested that on average there were about 1.1 enriched regions per gene. 10 genes were selected randomly to verify using PCR analysis whether their DNA binding regions existed specially in the TCF4's ChIP compound rather than the IgG's (**Figure 1B**). The results of gel electrophoresis showed that the false positive level of our dataset was ignorable.

To evaluate the distribution of the TCF4-binding sites along the genome, the distance from the binding region to these genes' TSSs were counted. We found that 117 (12.4%) and 272 (28.9%) of 940 binding sites mapped within 2 kb and 10 kb distances, respectively (**Figure 2A**).

Identification of DNA binding consensus sequences

The MEME-ChIP program was utilized to mark the enriched and unique consensus sequences in the binding regions of TCF4 in human colorectal cancer cells. A consensus sequence of C-G/C-A-G-C-T/C-C-T-T-C was identified with a very high score. The sequence's letter-probability matrix is shown in Table S3. The 598 instances of this motif in 1506 TCF4 binding regions are listed in Table S4. The logo of this motif is shown in **Figure 2B**.

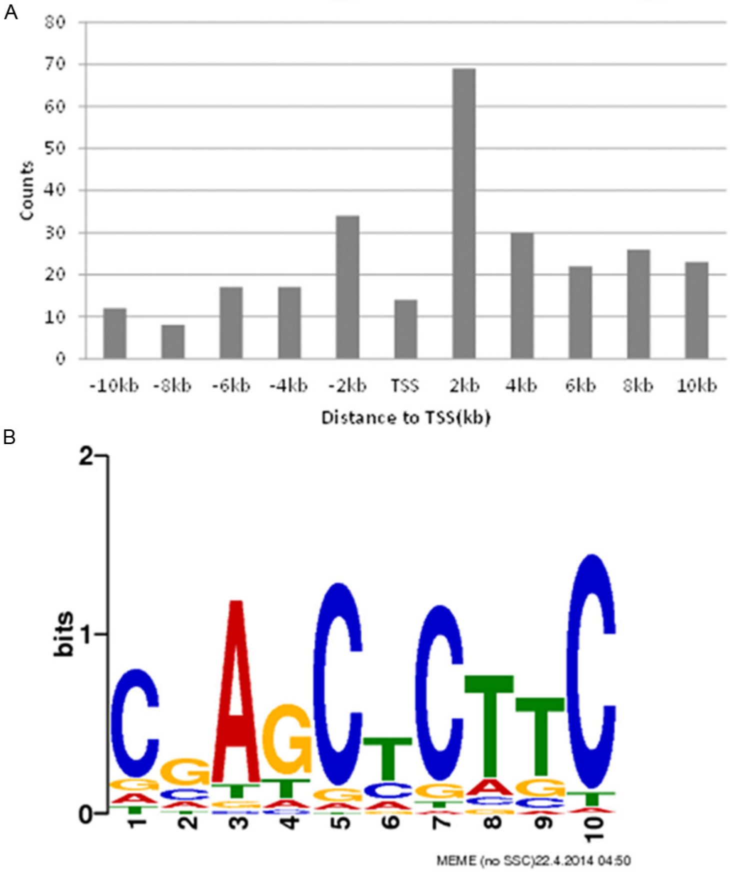

Figure 2. A. Histogram of TCF4 binding sites around annotated TSSs; B. The logo of the motif C-G/C-A-G-C-T/C-C-T-T-C.

Annotation of TCF4-associated biological processes and molecular function

The biological processes and metabolic pathways of TCF4 binding genes were annotated by GO and KEGG terms with the DAVID program (**Table 2**). The top enriched GO terms included intracellular signaling cascade (GO: 0007242), positive regulation of macromolecule metabolic process (GO: 0010604), cell adhesion (GO: 0007155), biological adhesion (GO: 0022610). KEGG terms included Axon guidance (hsa-04360), Chemokine signaling pathway (hsa-04062), Melanogenesis (hsa04916), and Wnt signaling pathway (hsa04310). Having observed that TCF4 regulated 18 genes in Wnt signaling pathway, we verified their TCF4 binding regions' specificity with PCR test as previously mentioned (**Figure 1C**). The results show that most of the gene was verified.

Furthermore, we searched for other known potential TFs (transcription factors) that were regulated by TCF4 and controlled corresponding downstream gene expression. 97 TFs were identified as potential TCF4 cooperators in GO transcription regulator activity terms (GO 0030528) and another 34 TFs were found in transcription activator activity terms (GO 0016563) (Table S5).

Discussion

ChIP analysis is one of the most common approaches to study the binding sites of TFs and the mechanisms of genes' functions. With the help of next generation sequencing technologies, ChIP-seq could efficiently provide a whole-genome view of protein-DNA interactions with high quantity gene detection [20-22]. As an important transcription factor of the Wnt signaling pathway, TCF4 plays diverse functions in the carcinogenesis and progression of several cancers. Identification of TCF4's binding sites on the genome is important for understanding its role in cancer.

In this study, we applied ChIP-seq approach to search and identify physical interactions between TCF4 proteins and DNA in SW620 colorectal cancercell line. Subsequently, we found that TCF4 binding regions were enriched with a motif of C-G/C-A-G-C-T/C-C-T-T-C, which was undiscovered previously. In earlier studies, similar experiments were carried out by Bottomly et al. in HCT116 cells [23]. They found a core TCF4 motif (T/A-T/A-C-A-A-A-G). However, the antibodies we used (Cell Signaling Technology, #2569) and the ones Bottomly et al. used (Millipore, 05-511) were different. This would affect the protein binding sites. Meanwhile, it is worth noting the cell lines were different and from patients who had different genotypes. Our cell lines (SW620) were separated from a 51 years male (Dukes' type C), and HCT116 cell lines were separated from anadult male (no age data). These unique protocols suggest that the difference between the results derived from different antibodies and cell types. In addition, it reveals that the TCF4 protein may have a different mechanism of action in differ-

Table 2. Annotation of TCF4 binding genes by GO and KEGG terms

Category	Term	Number of genes	Fold Enrichment	lgP
GO	GO: 0007242_intracellular signaling cascade	80	1.370	-2.517
	GO: 0010604_positive regulation of macromolecule metabolic process	65	1.631	-3.994
	GO: 0007155_cell adhesion	63	1.936	-6.195
	GO: 0022610_biological adhesion	63	1.933	-6.173
	GO: 0006357_regulation of transcription from RNA polymerase II promoter	60	1.775	-4.735
	GO: 0006811_ion transport	59	1.652	-3.796
	GO: 0042981_regulation of apoptosis	59	1.578	-3.280
	GO: 0043067_regulation of programmed cell death	59	1.563	-3.183
	GO: 0010941_regulation of cell death	59	1.557	-3.138
	GO: 0031328_positive regulation of cellular biosynthetic process	55	1.727	-4.036
	GO: 0009891_positive regulation of biosynthetic process	55	1.702	-3.875
	GO: 0016310_phosphorylation	55	1.479	-2.465
	GO: 0042127_regulation of cell proliferation	54	1.476	-2.404
	GO: 0051173_positive regulation of nitrogen compound metabolic process	53	1.770	-4.175
	GO: 0010557_positive regulation of macromolecule biosynthetic process	53	1.743	-3.998
	GO: 0006468_protein amino acid phosphorylation	53	1.709	-3.791
	GO: 0045935_positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	51	1.758	-3.950
	GO: 0042592_homeostatic process	50	1.432	-2.007
KEGG	hsa04360_Axon guidance	20	2.953	-4.478
	hsa04062_Chemokine signaling pathway	20	2.037	-2.416
	hsa04916_Melanogenesis	18	3.463	-4.950
	hsa04310_Wnt signaling pathway	18	2.270	-2.677
	hsa04270_Vascular smooth muscle contraction	17	2.891	-3.694
	hsa04020_Calcium signaling pathway	16	1.731	-1.386
	hsa05414_Dilated cardiomyopathy	13	2.691	-2.554
	hsa04912_GnRH signaling pathway	13	2.526	-2.325
	hsa04114_Oocyte meiosis	12	2.078	-1.554
	hsa05412_Arrhythmogenic right ventricular cardiomyopathy (ARVC)	10	2.506	-1.774

ent cell environments. This requires more clinical samples for further study.

Apart from the motif difference, Bottomly et al. found 2168 TCF4 enriched regions in HCT116 cells. 241 binding sites overlapped with the 1506 binding sites in this study [23]. Despite the differences between cell samples and antibodies, our results can be verified.

Identification of TCF4 binding sites in glioblastoma has been done with ChIP-seq technology [24]. Zhang et al. identified 3812 TCF4 putative target genes in U87 human glioblastoma cell lines [24]. We found that 128 of those genes overlapped with our data in the present study. This may suggest that the gene regulation of TCF4 is conserved in colorectal cancer and glioma cells.

Further, we investigated the enriched analysis of GO and KEGG terms. The results show that TCF4 may be involved in a series of important biological processes such as regulation of metabolic and biosynthetic (GO: 0010604, GO: 0031328, GO: 0009891, GO: 0051173, GO: 0010557, GO: 0045935), adhesion (GO: 0007155, GO: 0022610), apoptosis (GO: 0042981, GO: 0043067, GO: 0010941), and important signaling pathways (Wnt, Chemokine, Calciu, GnRH). Some of these important interactions have not been studied in depth.

In conclusion, our study provides a genome-wide binding profile of TCF4, the major transcription factor of Wnt signaling in colorectal cancer. This work may provide new ideas to clarify the mechanism of colorectal carcinogenesis.

Disclosure of conflict of interest

None.

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Table S1. Primers for validation of ChIP-target sequence associated with Wnt signaling pathways

Gene	Forward primer	Reverse primer
APC	CCCTAGAACCAAATCCAGCA	AACATGAGTGGGGTCTCCTG
CAMK2D	CCCTCCCCTCTGCTTCTACT	CGCTTCCTTCTTCTCCACTG
CSNK1E	TGTGTTTCCCAAGACAGCAG	CTCCATGGATTCTGCCCTAA
CSNK2A1	AGGCCCCCATTTTATACACC	ACTTTTTCCATCCCCAATCC
CTNNB1	GGTGGGCTGGTATCTCAGAA	CAAGCAAGGCTAGGGTTTGA
FBXW11	ATTGCGTGTGTGTGGTTTGT	GCCACGACTGCACAGAATAA
FZD6	GTTGGCCTTTATGACCTGGA	CACAAGATACAAGCCGCTGA
LEF1	CCCTTCCAACTCTCCTTTCC	TTGAAGGGGATCATCTCGTC
LRP5	CGTGTGTGACAGCGACTACA	TTACAGGGGCACAGAGAAGC
NFATC1	CCCACTCCTAGTTGCCACAT	CCTGCTTTCCTTCTTGTTGG
PPP2R5E	GGGATGGGAAAGGGATGTAT	GTCTGGTGCCACCTTTTTGT
PRKACG	TGGTCCCTCTGTGCTTCTCT	CAGGATTACGCCAAAGGGTA
RAC2	GGCCAGCTGCTCTAATATCG	CAGATATCCCCAGAGGCGTA
ROCK1	ATGTCTGCACACTGCCTCAG	GGTGCATGGGCTAACTCAAT
VANGL1	ATGTCACAGTCCGTGTTCCA	CCAGAAGTGCCGAATCATTT
WNT10B	TGGGATGTGTAGCCTTCTCC	CCCAGCCAAAAGGAGTATGA
WNT11	ACAAGACATCCAACGGAAGC	TGAGGGTCCTTGAGCAGAGT
WNT9A	GCATGCAGTATGAGGGGTCT	CTCAGAAAGCATTGGTGCAA

Table S2. Annotations of the TCF4 binding regions

annotation	gene	distance to TSS	chr	start	end	strand
FLJ20294	NM_017749	140881	chr11	46428410	46428608	+
H2AFY	NM_138609	72989	chr5	134689639	134689837	+
SGCZ	NM_139167	161667	chr8	14978297	14978495	+
TLE3	NM_005078	9121	chr15	68166892	68167090	+
METTL6	NM_152396	22168	chr3	15421648	15421846	+
PLD1	NM_002662	148495	chr3	172789872	172790070	+
APOL3	NM_014349	29546	chr22	34857178	34857376	+
FRMD6	NM_001042481	12131	chr14	51037735	51037933	+
FLJ35740	NM_147195	5938	chr9	38561067	38561265	0
TNFSF18	NM_005092	-28434	chr1	171315112	171315310	+
DLG5	NM_004747	85549	chr10	79270606	79270804	+
LMO2	NM_005574	-1419	chr11	33871830	33872028	+
SLIT3	NM_003062	602112	chr5	168058340	168058441	+
ZBTB16	NM_001018011	66501	chr11	113502998	113503196	+
CDC2L5	NM_003718	-30593	chr7	39925842	39926040	+
NFASC	NM_015090	150735	chr1	203215180	203215378	+
SLC12A2	NM_001046	32237	chr5	127479618	127479816	+
KCNC1	NM_004976	19443	chr11	17733532	17733730	+
ARL13B	NM_144996	29838	chr3	95211509	95211707	+
SYT2	NM_177402	86283	chr1	200859686	200859884	+
HOXC9	NM_006897	4746	chr12	52684889	52685087	+
KCNMA1	NM_002247	392336	chr10	78675048	78675246	+
PCGF3	NM_006315	61203	chr4	750775	750973	+
LEF1	NM_016269	59532	chr4	109249296	109249494	+
ATP9B	NM_198531	3545	chr18	74933929	74934127	+
RASSF8	NM_007211	-30218	chr12	25972819	25973017	+

TSSC1	NM_003310	34578	chr2	3325827	3326026	+
TMEM173	NM_198282	-29712	chr5	138872187	138872385	+
B4GALT1	NM_001497	-33785	chr9	33191015	33191213	+
DNMBP	NM_015221	58514	chr10	101663158	101663356	+
KCTD1	NM_198991	229344	chr18	22244763	22244961	+
SLC1A1	NM_004170	2938	chr9	4483381	4483579	+
DAB2IP	NM_138709	12720	chr9	123557604	123557802	+
RALA	NM_005402	109660	chr7	39739346	39739544	+
LOC440131	NM_001010918	-33797	chr13	29374672	29374870	+
GRM7	NM_181875	328333	chr3	7206259	7206457	+
PITPNM2	NM_020845	82030	chr12	122078699	122078897	+
ELL	NM_006532	14046	chr19	18479673	18479871	+
RARB	NM_000965	157241	chr3	25601998	25602197	+
DSCAML1	NM_020693	71571	chr11	117101416	117101614	+
GPR6	NM_005284	23652	chr6	110430642	110430840	+
FLJ10154	NM_018011	0	chr13	106018470	106018669	+
UBQLN1	NM_013438	-351	chr9	85513123	85513321	+
PKNOX1	NM_004571	66997	chr21	43334708	43334906	+
AZIN1	NM_015878	-32714	chr8	103978286	103978484	+
C1orf19	NM_052965	57597	chr1	182345065	182345263	+
MYH9	NM_002473	-11505	chr22	35125431	35125629	+
WDSUB1	NM_152528	-222	chr2	159851530	159851728	+
LOC387882	NM_207376	20835	chr12	104269604	104269802	+
TMEM132D	NM_133448	631380	chr12	128322587	128322785	+
WDR42B	NM_001017930	-17539	chrX	27927025	27927223	+
NIN	NM_182944	-58	chr14	50367646	50367844	+
ADAMTS14	NM_080722	42421	chr10	72144985	72145183	+
ZNF397	NM_032347	0	chr18	31074894	31075092	+
WBSCR28	NM_182504	26140	chr7	72939564	72939762	+
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AMIGO1	NM_020703	-13119	chr1	109866945	109867143	+
TOMM34	NM_006809	3753	chr20	43018576	43018774	+
VPS37C	NM_017966	23368	chr11	60661925	60662123	+
RFWD2	NM_001001740	-8266	chr1	174451258	174451456	+
GSG1	NM_031289	-31633	chr12	13171584	13171782	+
KCNQ1	NM_181798	378195	chr11	2817454	2817652	+
TNFSF18	NM_005092	36456	chr1	171250024	171250222	+
MAML3	NM_018717	25955	chr4	141268529	141268727	+
B3GALT6	NM_080605	10448	chr1	1167939	1168137	+
CACNA1C	NM_000719	297214	chr12	2329938	2330136	+
GSTA4	NM_001512	47233	chr6	52920667	52920865	+
EFNA5	NM_001962	-2242	chr5	107036736	107036934	+
OXT	NM_000915	-443	chr20	2999624	2999822	+
TTC7A	NM_020458	37731	chr2	47059547	47059745	+
CREB3L1	NM_052854	3058	chr11	46258861	46259059	+
GRB10	NM_001001550	85747	chr7	50654546	50654744	+
AGPS	NM_003659	-43295	chr2	177922237	177922435	+
STK32B	NM_018401	90255	chr4	5194682	5194781	+
NTN1	NM_004822	197110	chr17	9062693	9062891	+
FGD1	NM_004463	12641	chrX	54526484	54526682	+

FAM96B	NM_016062	0	chr16	65525694	65525892	+
NFYB	NM_006166	-49361	chr12	103105530	103105728	+
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HTRA4	NM_153692	-11249	chr8	38939406	38939604	+
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CRSP8	NM_004269	235226	chr9	133709649	133709847	+
C9orf23	NM_148178	177	chr9	34601725	34601923	+
DOCK5	NM_024940	123472	chr8	25221675	25221873	+
SDK1	NM_152744	380930	chr7	3688535	3688733	+
SLC30A3	NM_003459	6126	chr2	27333139	27333337	+
MGC39900	NM_194324	-572	chrX	103103090	103103288	+
ZFP37	NM_003408	-46931	chr9	114905747	114905945	+
ELP3	NM_018091	-25808	chr8	27980638	27980836	+
CRKL	NM_005207	28618	chr22	19630331	19630529	+
KIF13B	NM_015254	144765	chr8	29031596	29031794	+
MMP28	NM_001032278	-5758	chr17	31152510	31152708	+
LUC7L	NM_201412	17044	chr16	202207	202405	+
CLEC4G	NM_198492	7372	chr19	7695435	7695633	+
LONRF3	NM_001031855	68624	chrX	118061364	118061563	+
COL23A1	NM_173465	320454	chr5	177629509	177629707	+
OVCH2	NM_198185	-42969	chr11	7727485	7727683	+
EN2	NM_001427	-45856	chr7	154896121	154896319	+
FLJ10159	NM_018013	150118	chr6	108068127	108068325	+
RPP25	NM_017793	273	chr15	73036356	73036554	+
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CPE	NM_001873	137599	chr4	166657142	166657340	+
ZNF319	NM_020807	-539	chr16	56591801	56591999	+
MYOT	NM_006790	7537	chr5	137239009	137239207	+
FBN2	NM_001999	-29976	chr5	127931609	127931807	+
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C12orf12	NM_152638	898	chr12	89871987	89872185	+
RXRA	NM_002957	17203	chr9	136375433	136375631	+
LONRF2	NM_198461	-12347	chr2	100304745	100304943	+
WNT9A	NM_003395	-1790	chr1	226204011	226204209	+
NFIA	NM_005595	89785	chr1	61410667	61410865	+
OLFM1	NM_014279	45602	chr9	137152593	137152791	+
DMBT1	NM_004406	74619	chr10	124384789	124384987	+
OBSCN	NM_052843	106609	chr1	226569092	226569290	+
STXBP5	NM_139244	-29041	chr6	147537328	147537526	+

COMMD4	NM_017828	1136	chr15	73416562	73416760	+
PRDM16	NM_022114	325031	chr1	3300634	3300832	+
PRPF8	NM_006445	33977	chr17	1500749	1500948	+
ASMTL	NM_004192	7203	chrX	1524442	1524640	+
SLC23A2	NM_005116	105507	chr20	4824439	4824637	+
MBIP	NM_016586	34778	chr14	35824619	35824817	+
CUTL2	NM_015267	207016	chr12	110163227	110163425	+
IGF2	NM_000612	49615	chr11	2066966	2067164	+
NEURL	NM_004210	48407	chr10	105292444	105292642	+
C7orf26	NM_024067	14279	chr7	6610718	6610916	+
SDK1	NM_152744	955403	chr7	4263008	4263206	+
COMMD8	NM_017845	2780	chr4	47157454	47157652	+
PIGG	NM_017733	533	chr4	483542	483740	+
ACCN1	NM_183377	184714	chr17	28459206	28459404	+
NOM1	NM_138400	-9034	chr7	156425945	156426143	+
WFS1	NM_006005	36972	chr4	6359449	6359647	+
C21orf13	NM_152505	27508	chr21	39710291	39710489	+
PUM2	NM_015317	85231	chr2	20305195	20305393	+
C18orf1	NM_181482	312743	chr18	13521537	13521735	+
XPO4	NM_022459	-33454	chr13	20374293	20374491	+
TNFRSF21	NM_014452	74975	chr6	47310465	47310663	+
MGAT5B	NM_198955	61064	chr17	72441387	72441587	+
NTF3	NM_002527	-15231	chr12	5458095	5458295	+
PLK4	NM_014264	1099	chr4	129022649	129022847	+
MGLL	NM_007283	34924	chr3	128989268	128989466	+
LTBP3	NM_021070	1955	chr11	65079852	65080050	+
LDHA	NM_005566	583	chr11	18373269	18373467	+
INPP5A	NM_005539	100366	chr10	134301708	134301906	+
NHS	NM_198270	149461	chrX	17452924	17453122	+
C7orf41	NM_152793	148	chr7	30141224	30141422	+
KIAA1984	NM_001039374	-115	chr9	138810309	138810507	+
NPAL2	NM_024759	73441	chr8	99302157	99302355	+
DZIP1L	NM_173543	61480	chr3	139255462	139255660	+
FLJ21839	NM_001035507	-1476	chr2	27126350	27126548	+
TMEM132D	NM_133448	479900	chr12	128474067	128474265	+
RYR2	NM_001035	667010	chr1	235939334	235939532	+
CDC7	NM_003503	67298	chr1	91806329	91806527	+
LOC116236	NM_198147	5100	chr17	24912874	24913073	+
UBE2R2	NM_017811	89763	chr9	33896944	33897142	+
ADCY8	NM_001115	257917	chr8	131865738	131865936	+
C6orf117	NM_138409	0	chr6	84800067	84800265	+
EML4	NM_019063	-43191	chr2	42206630	42206828	+
KIAA1370	NM_019600	0	chr15	50758054	50758252	+
XPO4	NM_022459	-15605	chr13	20356444	20356642	+
ABCC8	NM_000352	357	chr11	17454469	17454667	+
NFIA	NM_005595	143907	chr1	61464789	61464987	+
ATP2B2	NM_001001331	-19305	chr3	10485850	10486048	+
MYO3B	NM_138995	328986	chr2	171071886	171072084	+
JARID2	NM_004973	-31236	chr6	15323170	15323269	+

GNA13	NM_006572	-8309	chr17	60491524	60491722	+
LOC388910	NM_001012986	-24152	chr22	43319532	43319730	+
TASP1	NM_017714	255130	chr20	13312254	13312452	+
FIBCD1	NM_032843	25348	chr9	132778511	132778709	+
C9orf165	NM_198573	0	chr9	34512992	34513190	+
INSIG1	NM_198337	14373	chr7	154734848	154735046	+
IRF5	NM_002200	-35239	chr7	128329792	128329990	+
SORCS2	NM_020777	274106	chr4	7519478	7519676	+
SST	NM_001048	20791	chr3	188849905	188850103	+
ATRN	NM_139322	91291	chr20	3490966	3491164	+
CNTNAP5	NM_130773	556789	chr2	125056122	125056320	+
PGAM5	NM_138575	9219	chr12	131806727	131806925	+
DNAJC6	NM_014787	120894	chr1	65623911	65624109	+
ARFGEF2	NM_006420	108401	chr20	47080234	47080432	+
PHYH	NM_001037537	27275	chr10	13354278	13354476	+
ABLIM3	NM_014945	106158	chr5	148607483	148607681	+
LRRN6A	NM_032808	-41716	chr15	75753479	75753677	+
ANKRD13A	NM_033121	11878	chr12	108933495	108933693	+
ADAMTSL3	NM_207517	301084	chr15	82414925	82415123	+
PTEN	NM_000314	2645	chr10	89615819	89616017	+
GPR123	NM_032422	30822	chr10	134765244	134765442	+
CSMD3	NM_052900	23046	chr8	114495173	114495371	+
TAF1A	NM_139352	34653	chr1	220795026	220795224	+
HEATR2	NM_017802	29986	chr7	762852	763050	+
PSMF1	NM_178579	125	chr20	1047369	1047567	+
DENND1A	NM_024820	197467	chr9	125534572	125534770	+
VPS53	NM_018289	43892	chr17	520667	520865	+
NUPL1	NM_001008565	28631	chr13	24802296	24802494	+
STK10	NM_005990	3125	chr5	171544541	171544739	+
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SH3BP2	NM_003023	-748	chr4	2789392	2789590	+
TMPRSS6	NM_153609	7600	chr22	35821840	35822038	+
C20orf102	NM_080607	36696	chr20	36001615	36001813	+
PASK	NM_015148	8715	chr2	241728637	241728835	+
C18orf1	NM_181482	-41204	chr18	13167392	13167590	+
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CCR7	NM_001838	11049	chr17	35964002	35964200	+
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PCID1	NM_006360	3371	chr11	32565337	32565535	+
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RCOR1	NM_015156	102338	chr14	102231323	102231522	+
FLJ22374	NM_032222	-4063	chr7	30773296	30773494	+
PACRG	NM_152410	25623	chr6	163093776	163093974	+
FAM86A	NM_201400	-42472	chr16	5130253	5130451	+
GLIS2	NM_032575	-18193	chr16	4303834	4304032	+
KIAA1333	NM_017769	-29636	chr14	30068293	30068491	+
C12orf30	NM_024953	218	chr12	111030563	111030761	+
MYOM3	NM_152372	-3465	chr1	24297544	24297742	+
LRP8	NM_001018054	51262	chr1	53514852	53515051	+

TTLL11	NM_194252	129890	chr9	123765617	123765815	+
UBAP2	NM_018449	76796	chr9	33961952	33962150	+
TRPS1	NM_014112	-49038	chr8	116799439	116799637	+
IL7	NM_000880	33287	chr8	79846827	79847025	+
FSTL4	NM_015082	173528	chr5	132802395	132802593	+
PISD	NM_014338	10068	chr22	30346543	30346741	+
BRWD1	NM_033656	116860	chr21	39490367	39490565	+
PARD3B	NM_057177	-4834	chr2	205113728	205113926	+
FBXL16	NM_153350	2064	chr16	693546	693744	+
CHSY1	NM_014918	103694	chr15	99505756	99505954	+
FOXB1	NM_012182	108	chr15	58083820	58084018	+
SLC2A13	NM_052885	2598	chr12	38783131	38783329	+
TSPAN9	NM_006675	8254	chr12	3065071	3065269	+
LRRC18	NM_001006939	-24643	chr10	49816925	49817123	+
CACNA2D1	NM_000722	51097	chr7	81859671	81859869	+
FOXP4	NM_001012426	-23524	chr6	41598419	41598617	+
ICOSLG	NM_015259	43635	chr21	44441428	44441626	+
FLJ45964	NM_207483	-13434	chr2	240151299	240151497	+
BCL2	NM_000633	153350	chr18	58984044	58984242	+
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NFKBIA	NM_020529	7032	chr14	34936464	34936662	+
PHGDHL1	NM_177967	115448	chr13	98766611	98766809	+
LARP4	NM_052879	-34989	chr12	49045729	49045927	+
FAM60A	NM_021238	23912	chr12	31346229	31346427	+
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C11orf11	NM_006133	49158	chr11	61253643	61253841	+
AK5	NM_012093	122359	chr1	77643233	77643431	+
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HSF2BP	NM_007031	142140	chr21	43761463	43761661	+
C20orf79	NM_178483	14968	chr20	18757337	18757535	+
HCN2	NM_001194	9840	chr19	550732	550930	+
CALM1	NM_006888	-28157	chr14	89904770	89904968	+
ZC3H10	NM_032786	3665	chr12	54801961	54802159	+
FAM53B	NM_014661	47549	chr10	126375172	126375370	+
C9orf93	NM_173550	-77	chr9	15542821	15543019	+
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FASTK	NM_006712	2441	chr7	150406244	150406442	+
ELMO1	NM_001039459	740	chr7	36990251	36990449	+
CELSR3	NM_001407	20511	chr3	48654642	48654840	+
ZCWPW2	NM_001040432	174593	chr3	28581583	28581781	+
PLTP	NM_006227	-7761	chr20	43981953	43982151	+
C20orf26	NM_015585	15843	chr20	19997038	19997236	+
GLI2	NM_005270	240597	chr2	121506923	121507121	+
CAPN13	NM_144575	-29958	chr2	30913772	30913970	+
RAB27B	NM_004163	-480	chr18	50646159	50646357	+
CDRT15	NM_001007530	12157	chr17	14068519	14068717	+

SMPD3	NM_018667	-30375	chr16	67070279	67070477	+
CRYM	NM_001014444	5495	chr16	21216224	21216422	+
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C11orf52	NM_080659	1232	chr11	111296078	111296276	+
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GNB1	NM_002074	68149	chr1	1744007	1744205	+
ENTPD6	NM_001247	9069	chr20	25133440	25133543	+
NYD-SP18	NM_032599	9522	chr7	128152200	128152398	+
TNS3	NM_022748	298997	chr7	47246528	47246726	+
SORCS2	NM_020777	383405	chr4	7628777	7628975	+
CSDC2	NM_014460	15557	chr22	40302571	40302769	+
DSCAM	NM_001389	-3964	chr21	41144872	41145070	+
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LOC284274	NM_001037331	36694	chr18	71231684	71231882	+
NDRG4	NM_022910	18073	chr16	57097233	57097431	+
SPG3A	NM_015915	31637	chr14	50128136	50128334	+
SLC15A1	NM_005073	89008	chr13	98113702	98113900	+
FAM124A	NM_145019	69051	chr13	50763558	50763756	+
KIAA0774	NM_001033602	75495	chr13	28572242	28572440	+
VEZT	NM_017599	6032	chr12	94175883	94176081	+
C12orf36	NM_182558	-41391	chr12	13462302	13462500	+
FLJ45337	NM_207465	103569	chr1	55922866	55923064	+
TMCO4	NM_181719	92995	chr1	19905803	19906001	+
PAX7	NM_002584	-26978	chr1	18802910	18803108	+
NIBP	NM_031466	9087	chr8	141528669	141528772	+
GRIN2A	NM_000833	23972	chr16	10159941	10160139	+
OR4D1	NM_012374	-26101	chr17	53561213	53561412	+
MOSC1	NM_022746	19127	chr1	219046020	219046218	+
MST150	NM_032947	17182	chr5	150155241	150155439	+
KIAA1622	NM_020958	-10818	chr14	93699385	93699583	+
KIAA0133	NM_014777	38269	chr1	227866872	227867070	+
C16orf68	NM_024109	22828	chr16	8645855	8646053	+
TBC1D22A	NM_014346	298250	chr22	45835462	45835660	+
BRE	NM_199192	196472	chr2	28163532	28163730	+
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ABLIM2	NM_032432	199363	chr4	8011876	8012074	+
GNAL	NM_002071	25517	chr18	11767702	11767900	+
PKNOX2	NM_022062	251937	chr11	124791705	124791808	+
BOC	NM_033254	10487	chr3	114424551	114424749	+
AQP2	NM_000486	-4404	chr12	48626190	48626391	+
ZNF277P	NM_021994	160992	chr7	111794870	111795069	+
GSH2	NM_133267	-1875	chr4	54658881	54659079	+
POU3F4	NM_000307	-18445	chrX	82631297	82631495	+
LAS1L	NM_031206	2229	chrX	64668964	64669162	+
DLG2	NM_001364	848439	chr11	83463574	83463673	+
CAMKK2	NM_172226	55931	chr12	120162758	120162956	+
SLC26A7	NM_134266	76212	chr8	92406903	92407101	+
CDK10	NM_003674	8951	chr16	88289529	88289727	+
C20orf133	NM_001033086	803923	chr20	14728191	14728389	+

CDH10	NM_006727	153857	chr5	24526612	24526810	+
LEMD1	NM_001001552	-3314	chr1	203661117	203661316	+
ANKRD18B	NM_001013728	48906	chr9	33563118	33563316	+
FAM107B	NM_031453	175667	chr10	14681036	14681234	+
NFATC1	NM_172390	58168	chr18	75314927	75315125	+
C21orf63	NM_058187	25046	chr21	32731668	32731866	+
RABGAP1L	NM_014857	-46882	chr1	172348176	172348374	+
POMC	NM_000939	27303	chr2	25217560	25217759	+
USF2	NM_003367	2923	chr19	40454658	40454857	+
FAF1	NM_007051	539104	chr1	50659221	50659419	+
HECW1	NM_015052	266706	chr7	43385428	43385626	+
ITPK1	NM_014216	146915	chr14	92504866	92505064	+
SLC35C2	NM_015945	11520	chr20	44414752	44414950	+
ARAF	NM_001654	6094	chrX	47311544	47311742	+
NCOA2	NM_006540	171777	chr8	71306598	71306796	+
GRK5	NM_005308	234118	chr10	121191304	121191502	+
SLC9A10	NM_183061	-13968	chr3	113509731	113509929	+
ASB14	NM_130387	6301	chr3	57281520	57281718	+
CREB3L1	NM_052854	-39664	chr11	46215941	46216139	+
C10orf92	NM_017609	-33855	chr10	134555080	134555278	+
ATP10A	NM_024490	70325	chr15	23589439	23589637	+
WNT11	NM_004626	32461	chr11	75562562	75562760	+
PARD3B	NM_057177	900632	chr2	206019392	206019590	+
ITGAL	NM_002209	40814	chr16	30432385	30432583	+
KCND3	NM_004980	177439	chr1	112155662	112155860	+
ERC2	NM_015576	735346	chr3	55741886	55742084	+
GRB10	NM_001001549	4467	chr7	50762878	50763076	+
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ZUBR1	NM_020765	122517	chr1	19286617	19286815	+
RSU1	NM_152724	118002	chr10	16781357	16781456	+
LRP1B	NM_018557	987174	chr2	141618367	141618565	+
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CAPZB	NM_004930	-15145	chr1	19699723	19699921	+
ITGB1BP1	NM_004763	7322	chr2	9473573	9473771	+
CLEC4M	NM_214677	35232	chr19	7769312	7769510	+
RHOJ	NM_020663	19934	chr14	62760831	62761029	+
SAMD4A	NM_015589	200445	chr14	54304831	54305029	+
EXTL3	NM_001440	3623	chr8	28618694	28618892	+
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MAGI1	NM_004742	482687	chr3	65516663	65516861	+
WDR64	NM_144625	16209	chr1	239929713	239929911	+
ZMIZ2	NM_031449	449	chr7	44755503	44755701	+
NUDT12	NM_031438	57270	chr5	102869015	102869118	+
NIBP	NM_031466	350569	chr8	141187092	141187290	+
SOX21	NM_007084	-3773	chr13	94166162	94166360	+
SMAF1	NM_001018082	38981	chr20	36682232	36682430	+
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PABPC1	NM_002568	12466	chr8	101790826	101791024	+
SEC24B	NM_001042734	29285	chr4	110603704	110603902	+
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KIAA1324	NM_020775	-3618	chr1	109454239	109454437	+
FFAR2	NM_005306	-3980	chr19	40628278	40628476	+
SUPT3H	NM_003599	450166	chr6	45003188	45003386	+
Tenr	NM_139243	-28929	chr4	123490490	123490688	+
OXT	NM_000915	413	chr20	3000678	3000876	+
ABCC1	NM_019862	74579	chr16	16025513	16025711	+
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PRKAR1B	NM_002735	41604	chr7	676855	677054	+
SYT9	NM_175733	163323	chr11	7393079	7393277	+
LOH12CR1	NM_058169	1407	chr12	12402728	12402926	+
KHDRBS2	NM_152688	629405	chr6	62424487	62424685	+
TIAM2	NM_012454	10025	chr6	155463139	155463337	+
SKAP1	NM_003726	226668	chr17	43635726	43635924	+
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KIAA0427	NM_014772	203040	chr18	44522464	44522662	+
SLC5A11	NM_052944	29218	chr16	24794270	24794468	+
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CFDP1	NM_006324	-859	chr16	74025746	74025944	+
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MYO1E	NM_004998	201650	chr15	57250613	57250712	+
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APC	NM_000038	72086	chr5	112173568	112173766	+
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SH3KBP1	NM_001024666	24298	chrX	19703293	19703491	+
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NEK1	NM_012224	63016	chr4	170706974	170707172	+
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OSBPL11	NM_022776	1126	chr3	126795299	126795497	+
WDR4	NM_033661	60324	chr21	43112224	43112422	+
COX10	NM_001303	55745	chr17	13969188	13969386	+
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TLL2	NM_012465	101330	chr10	98162129	98162327	+
NEUROG3	NM_020999	-17626	chr10	71020753	71020951	+
ABCD3	NM_002858	17648	chr1	94674246	94674444	+
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FSTL4	NM_015082	354694	chr5	132621224	132621427	+

ENPP3	NM_005021	23267	chr6	132023401	132023599	+
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NDRG1	NM_006096	8975	chr8	134369506	134369704	+
SDC2	NM_002998	42962	chr8	97618019	97618217	+
THEX1	NM_153332	38338	chr8	8936197	8936395	+
HIPK2	NM_022740	18534	chr7	138948281	138948479	+
HERPUD2	NM_022373	38656	chr7	35662399	35662597	+
EPHA7	NM_004440	143242	chr6	94042552	94042750	+
TREM1	NM_018643	620	chr6	41361616	41361814	+
WRNIP1	NM_020135	-674	chr6	2709792	2709990	+
SCOC	NM_032547	102475	chr4	141500364	141500562	+
SLCO2A1	NM_005630	62027	chr3	135169192	135169390	+
CD96	NM_005816	103636	chr3	112847251	112847449	+
PTPRT	NM_007050	921396	chr20	40330376	40330574	+
TPX2	NM_012112	47011	chr20	29837575	29837773	+
NR1H2	NM_007121	883	chr19	55572397	55572595	+
PRDX2	NM_181738	211	chr19	12773284	12773482	+
METRNL	NM_001004431	5956	chr17	78636811	78637009	+
KRT33B	NM_002279	6132	chr17	36773242	36773440	+
CNTNAP4	NM_033401	268785	chr16	75137461	75137659	+
CRTC3	NM_001042574	-388	chr15	88873615	88873813	+
HS6ST3	NM_153456	56731	chr13	95597824	95598022	+
SERPINH1	NM_001235	12426	chr11	74963243	74963441	+
PRDX5	NM_012094	9211	chr11	63851355	63851553	+
CREB3L1	NM_052854	11829	chr11	46267632	46267830	+
PNLIPRP1	NM_006229	16516	chr10	118356995	118357193	+
C1orf21	NM_030806	129787	chr1	182752559	182752757	+
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DLC1	NM_182643	335503	chr8	13081066	13081262	+
CPA6	NM_020361	-37124	chr8	68858257	68858455	+
SPARC	NM_003118	59697	chr5	150986814	150987012	+
TADA2L	NM_133439	33462	chr17	32874886	32875084	+
TBX5	NM_181486	60895	chr12	113267178	113267376	+
KIAA0999	NM_025164	14948	chr11	116459056	116459254	+
CAMTA1	NM_015215	725709	chr1	7493679	7493877	+
DPYSL2	NM_001386	91022	chr8	26582359	26582557	+
AKAP7	NM_016377	17563	chr6	131525716	131525914	+
MEA1	NM_014623	1247	chr6	43088150	43088348	+
ZNF193	NM_006299	-2169	chr6	28298684	28298882	+
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UBE2L3	NM_198157	46006	chr22	20297962	20298160	+
NOVA2	NM_002516	-2900	chr19	51171396	51171594	+
NARF	NM_012336	32240	chr17	78042100	78042298	+
BCAS3	NM_017679	667064	chr17	56777078	56777276	+
SNIP	NM_025248	123137	chr17	33892373	33892571	+

ZNF207	NM_003457	43409	chr17	27744680	27744878	+
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ADCY7	NM_001114	-13335	chr16	48865790	48865988	+
CCPG1	NM_004748	18401	chr15	53469234	53469432	+
RGS6	NM_004296	647504	chr14	72117089	72117287	+
LUZP2	NM_001009909	176612	chr11	24651743	24651941	+
MRPL23	NM_021134	6652	chr11	1931765	1931963	+
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SMYD3	NM_022743	186189	chr1	244460946	244461144	+
C1orf21	NM_030806	262301	chr1	182885073	182885271	+
DAB1	NM_021080	368326	chr1	58120274	58120472	+
PRDM16	NM_022114	283818	chr1	3259421	3259619	+
TNPO2	NM_013433	18398	chr19	12675577	12675679	+
MTX2	NM_006554	-5	chr2	176842276	176842377	+
LASS3	NM_178842	110245	chr15	98792103	98792202	+
C9orf23	NM_148178	7167	chr9	34594735	34594933	+
TRPM1	NM_002420	-9941	chr15	29191156	29191354	+
HSPB1	NM_001540	0	chr7	75769796	75769994	+
AUTS2	NM_015570	884984	chr7	69587238	69587436	+
XAB2	NM_020196	16501	chr19	7583739	7583937	+
AZI1	NM_014984	23354	chr17	76787793	76787991	+
FUT8	NM_178157	114160	chr14	65320045	65320243	+
PCF11	NM_015885	-27715	chr11	82517947	82518145	+
NFASC	NM_015090	149136	chr1	203213581	203213779	+
ENG	NM_000118	17001	chr9	129639605	129639803	+
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XKR6	NM_173683	131907	chr8	10964179	10964377	+
AARSL	NM_020745	-14557	chr6	44403597	44403795	+
KIF6	NM_145027	284034	chr6	39516926	39517124	+
EDIL3	NM_005711	341	chr5	83715827	83716025	+
HERC3	NM_014606	-244	chr4	89732227	89732425	+
PCBP4	NM_033008	201	chr3	51976109	51976307	+
SLC25A18	NM_031481	21119	chr22	16444301	16444499	+
MARCO	NM_006770	-38857	chr2	119377159	119377357	+
C14orf49	NM_152592	88174	chr14	94923553	94923751	+
CLMN	NM_024734	-435	chr14	94856389	94856587	+
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NEU3	NM_006656	30314	chr11	74407911	74408109	+
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C10orf71	NM_199459	9540	chr10	50186732	50186930	+
GRHL3	NM_021180	19825	chr1	24541941	24542139	+
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SETD3	NM_032233	119194	chr14	98897684	98897784	+
PACRG	NM_152410	454750	chr6	163522903	163523101	+
PDSS2	NM_020381	209588	chr6	107677661	107677859	+
CXCL14	NM_004887	0	chr5	134942864	134943062	+
MBP	NM_001025100	88586	chr18	72884977	72885175	+
WWOX	NM_016373	885354	chr16	77576405	77576603	+

ZFYVE26	NM_015346	30308	chr14	67322548	67322746	+
KIAA1522	NM_020888	-22841	chr1	32957059	32957257	+
IL28RA	NM_170743	8788	chr1	24377351	24377549	+
PRKG1	NM_006258	186	chr10	52504484	52504600	+
EGFR	NM_005228	163368	chr7	55217586	55217685	+
TCHP	NM_032300	4760	chr12	108827465	108827564	+
GLRA2	NM_002063	210944	chrX	14668514	14668712	+
COL22A1	NM_152888	108415	chr8	139886804	139887002	+
CHRNB3	NM_000749	-42154	chr8	42629366	42629564	+
RARRES2	NM_002889	926	chr7	149668514	149668712	+
GRM8	NM_000845	-18901	chr7	126689446	126689644	+
LPA	NM_005577	107588	chr6	160899610	160899808	+
UNC5A	NM_133369	-41514	chr5	176128453	176128651	+
NEUROG1	NM_006161	0	chr5	134899420	134899618	+
SLC12A2	NM_001046	93861	chr5	127541242	127541440	+
KCNH8	NM_144633	409968	chr3	19574988	19575186	+
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NCK2	NM_001004722	561	chr2	105728346	105728544	+
KCMF1	NM_020122	-3910	chr2	85047649	85047847	+
FALZ	NM_004459	5293	chr17	63257534	63257732	+
CACNG1	NM_000727	9819	chr17	62480986	62481184	+
TRAP1	NM_016292	3997	chr16	3703318	3703516	+
CHRNA3	NM_000743	979	chr15	76699199	76699397	+
TDRD3	NM_030794	200318	chr13	60069440	60069638	+
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VANGL1	NM_138959	4390	chr1	115990486	115990683	+
ITPK1	NM_014216	155884	chr14	92495897	92496095	+
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CYFIP2	NM_014376	83968	chr5	156712907	156713105	+
TAOK1	NM_020791	-20326	chr17	24721641	24721742	+
SLC25A32	NM_030780	13373	chr8	104482875	104483073	+
ROR2	NM_004560	163138	chr9	93588928	93589126	+
CABIN1	NM_012295	130948	chr22	22868712	22868910	+
SGK2	NM_016276	19680	chr20	41647830	41648028	+
LDLRAP1	NM_015627	29711	chr1	25772463	25772661	+
RABL4	NM_006860	-6977	chr22	35509036	35509234	+
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KIAA1128	NM_018999	232171	chr10	86310560	86310758	+
DHRS7	NM_016029	-33229	chr14	59735085	59735283	+
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CUTL1	NM_181552	331980	chr7	101579581	101579779	+
FZD6	NM_003506	42903	chr8	104423178	104423376	+
STEAP3	NM_182915	-5721	chr2	119691934	119692132	+
HIPK2	NM_022740	23196	chr7	138943619	138943817	+

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SYK	NM_003177	119871	chr9	92723761	92723959	+
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SERPINB3	NM_006919	2481	chr18	59477414	59477612	+
CCBE1	NM_133459	212209	chr18	55303162	55303360	+
TMEM105	NM_178520	-32829	chr17	76951897	76952095	+
KREMEN2	NM_024507	3462	chr16	2957679	2957877	+
ADAM10	NM_001110	0	chr15	56829436	56829634	+
GTF2A1	NM_015859	50553	chr14	80706295	80706493	+
C13orf30	NM_182508	-30496	chr13	42223056	42223254	+
HNT	NM_001048209	391301	chr11	131136881	131137079	+
NRP1	NM_001024629	39132	chr10	33624125	33624323	+
GPR158	NM_020752	115208	chr10	25619503	25619701	+

RTCD1	NM_003729	610	chr1	100504960	100505158	+
BARHL2	NM_020063	-12424	chr1	90967805	90968003	+
PGM1	NM_002633	568	chr1	63832102	63832300	+
PHC2	NM_198040	-4013	chr1	33617793	33617991	+
PDIK1L	NM_152835	623	chr1	26311540	26311738	+
BAT1	NM_004640	395	chr6	31617611	31617808	+
FLJ45187	NM_207371	846	chr10	21853611	21853770	+
TRPC5	NM_012471	79109	chrX	111133352	111133550	+
GYG2	NM_003918	3358	chrX	2760220	2760418	+
PNPLA7	NM_152286	84511	chr9	139479947	139480145	+
PLAA	NM_004253	15790	chr9	26909218	26909416	+
VLDLR	NM_001018056	22996	chr9	2634788	2634986	+
UST	NM_005715	289734	chr6	149399890	149400088	+
AIM1	NM_001624	28083	chr6	107094505	107094703	+
C6orf145	NM_183373	-33266	chr6	3730200	3730398	+
TRPC7	NM_020389	129900	chr5	135590873	135591071	+
CLSTN2	NM_022131	93017	chr3	141229913	141230111	+
LMOD3	NM_198271	-47204	chr3	69301610	69301808	+
CNTN4	NM_175607	84806	chr3	2202052	2202250	+
MKL1	NM_020831	41872	chr22	39320565	39320763	+
PEX26	NM_017929	-14789	chr22	16925717	16925915	+
RIPK4	NM_020639	25760	chr21	42034359	42034557	+
OSBPL2	NM_014835	5951	chr20	60252925	60253123	+
NKX2-2	NM_002509	-3966	chr20	21446629	21446827	+
PARD3B	NM_057177	756988	chr2	205875748	205875946	+
SMC6	NM_024624	36	chr2	17798306	17798504	+
CKM	NM_001824	15918	chr19	50501857	50502055	+
FBL	NM_001436	439	chr19	45028175	45028373	+
CHST9	NM_031422	20221	chr18	22998859	22999057	+
PDK2	NM_002611	3686	chr17	45531380	45531578	+
C16orf75	NM_152308	15221	chr16	11362032	11362230	+
MAPK6	NM_002748	10936	chr15	50109674	50109872	+
OCA2	NM_000275	346487	chr15	25671375	25671573	+
PPP2R5E	NM_006246	102078	chr14	62977555	62977753	+
GJB6	NM_006783	-6597	chr13	19709663	19709861	+
LRP1	NM_002332	67585	chr12	55876133	55876331	+
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CHKA	NM_001277	68929	chr11	67576306	67576504	+
TSPAN15	NM_012339	28071	chr10	70909302	70909500	+
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CRNN	NM_016190	-35571	chr1	150688922	150689120	+
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AIFM1	NM_004208	33148	chrX	129094142	129094340	+
SP8	NM_198956	10162	chr7	20782669	20782867	+
EMCN	NM_016242	68031	chr4	101589972	101590170	+
C1orf198	NM_032800	-3420	chr1	229074319	229074419	+

EFHA1	NM_152726	126665	chr13	20949542	20949641	+
DKFZp761B107	NM_173463	80267	chr4	24510458	24510656	+
ACCN1	NM_001094	180127	chr17	29327612	29327810	+
C20orf94	NM_001009608	43494	chr20	10407444	10407642	+
EIF2AK3	NM_004836	-30440	chr2	88738513	88738711	+
ZIC3	NM_003413	-19900	chrX	136455913	136456111	+
TMEM28	NM_015686	19962	chrX	68661764	68661962	+
ENG	NM_000118	13429	chr9	129643177	129643375	+
TSNARE1	NM_145003	191353	chr8	143290892	143291090	+
ASPH	NM_020164	6059	chr8	62758582	62758780	+
RP1L1	NM_178857	81545	chr8	10468283	10468481	+
SMOC2	NM_022138	78614	chr6	168663493	168663691	+
IRF4	NM_002460	1113	chr6	337872	338070	+
GCNT4	NM_016591	-28250	chr5	74390729	74390927	+
BFSP2	NM_003571	-1196	chr3	134600085	134600283	+
ADCY5	NM_183357	16011	chr3	124633872	124634070	+
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COL18A1	NM_030582	24183	chr21	45724034	45724232	+
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PDYN	NM_024411	1043	chr20	1921460	1921658	+
CSNK2A1	NM_177560	143	chr20	472140	472338	+
PSMD14	NM_005805	97855	chr2	161971040	161971238	+
TEKT4	NM_144705	14146	chr2	94915104	94915302	+
ADD2	NM_017482	21313	chr2	70827325	70827523	+
CCDC128	NM_152994	239	chr2	48521650	48521848	+
SIX2	NM_016932	-1119	chr2	45091144	45091342	+
ZNF579	NM_152600	30922	chr19	60752902	60753100	+
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NUAK1	NM_014840	69716	chr12	104988026	104988224	+
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CACNA1C	NM_000719	258949	chr12	2291673	2291871	+
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HMX2	NM_005519	2292	chr10	124899919	124900117	+
VANGL1	NM_138959	3267	chr1	115989363	115989561	+
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PAK3	NM_002578	24116	chrX	110250371	110250568	+
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ADCY1	NM_021116	115528	chr7	45696173	45696366	+
IRF2	NM_002199	78183	chr4	185554332	185554513	+

ATP8B1	NM_005603	21154	chr18	53528764	53528882	+
USP25	NM_013396	41127	chr21	16065493	16065691	+
C1orf121	NM_016076	15104	chr1	242898078	242898240	+
NANP	NM_152667	-5438	chr20	25558051	25558249	+
STX7	NM_003569	12838	chr6	132862827	132863020	+
SPTBN1	NM_178313	102536	chr2	54741570	54741673	+
PASD1	NM_173493	75904	chrX	150558653	150558851	+
PAG1	NM_018440	117584	chr8	82069075	82069273	+
OPRK1	NM_000912	9154	chr8	54317394	54317592	+
ZFAND2A	NM_182491	-9099	chr7	1175422	1175620	+
LPP	NM_005578	493168	chr3	189906582	189906780	+
TEX101	NM_031451	18414	chr19	48603016	48603214	+
USMG5	NM_032747	6185	chr10	105139829	105140027	+
WWOX	NM_130844	-5703	chr16	76685249	76685348	+
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ESX1	NM_153448	-48660	chrX	103434903	103435101	+
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SARDH	NM_007101	48098	chr9	135546566	135546764	+
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CAGE1	NM_205864	48717	chr6	7286025	7286223	+
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MBNL1	NM_021038	-10814	chr3	153457506	153457704	+
ACAD11	NM_032169	105210	chr3	133756207	133756405	+
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DAG1	NM_004393	-2871	chr3	49479525	49479723	+
UBE2E2	NM_152653	71027	chr3	23290838	23291036	+
MYH9	NM_002473	98594	chr22	35015134	35015332	+
R3HDM1	NM_015361	78207	chr2	136083759	136083957	+
SLC8A1	NM_021097	274001	chr2	40236748	40236946	+
MEGF8	NM_001410	-2976	chr19	47529623	47529821	+
GRIK5	NM_002088	49010	chr19	47212588	47212786	+
GATA6	NM_005257	-192	chr18	18003023	18003221	+
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DLGAP1	NM_001003809	295550	chr18	3539547	3539745	+
TMC8	NM_152468	5742	chr17	73644205	73644403	+
ICAM2	NM_000873	1294	chr17	59436346	59436544	+
MYH1	NM_005963	20860	chr17	10341525	10341723	+

CDH1	NM_004360	79951	chr16	67408646	67408844	+
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RPGRIP1	NM_020366	46653	chr14	20872628	20872826	+
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STX2	NM_001980	42660	chr12	129846905	129847103	+
PLXNC1	NM_005761	250	chr12	93066879	93067077	+
ABCD2	NM_005164	40524	chr12	38259514	38259712	+
RNF26	NM_032015	98	chr11	118710544	118710742	+
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SLC13A5	NM_177550	10764	chr17	6546426	6546623	+
PAX6	NM_001604	-36945	chr11	31826399	31826596	+
PDE4DIP	NM_022359	58989	chr1	143728193	143728390	+
ARPP-21	NM_016300	197122	chr3	35855974	35856170	+
DEFB115	NM_001037730	-39192	chr20	29269739	29269935	+
FLJ46300	NM_001001677	40437	chr10	133431892	133432087	+
STK10	NM_005990	9139	chr5	171538532	171538725	+
ISG15	NM_005101	2656	chr1	941397	941590	+
NOL4	NM_003787	7834	chr18	30049495	30049678	+
PCBD2	NM_032151	20063	chr5	134288771	134288953	+
GLYCTK	NM_145262	-8965	chr3	52287771	52287946	+
STRN	NM_003162	115321	chr2	36931644	36931797	+
ADCK2	NM_052853	15474	chr7	140034895	140035023	+
SURF4	NM_033161	1316	chr9	135231349	135231474	+
SFT2D1	NM_145169	11691	chr6	166664186	166664289	+
POLS	NM_006999	47824	chr5	6815541	6815640	+
SSH2	NM_033389	295428	chr17	24985517	24985715	+
WARS2	NM_015836	13698	chr1	119470913	119471111	+
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OVCH1	NM_183378	59984	chr12	29481703	29481901	+
IFIT1	NM_001548	10151	chr10	91152452	91152650	+
HIPK2	NM_022740	44029	chr7	138922786	138922984	+
C14orf145	NM_152446	405553	chr14	80069885	80070083	+
DHRS3	NM_004753	-293	chr1	12600699	12600897	+
GDF9	NM_005260	2675	chr5	132225502	132225700	+
UCK2	NM_012474	16464	chr1	164079977	164080175	+
CLPX	NM_006660	-360	chr15	63264975	63265173	+
C1orf175	NM_001039464	32999	chr1	54913030	54913228	+
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NXF3	NM_022052	8871	chrX	102225608	102225806	+

SVIL	NM_021738	153258	chr10	29810450	29810648	+
ROCK1	NM_005406	173593	chr18	16772019	16772216	+
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NRG1	NM_013962	227398	chr8	31844207	31844404	+
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LZTR2	NM_033127	71600	chr1	176133874	176134072	+
ACY1	NM_000666	3885	chr3	51996487	51996685	+
FLJ21986	NM_024913	290756	chr7	120706787	120706985	+
FLJ42133	NM_001001690	-40182	chr20	35698389	35698543	+
CD24	NM_013230	20519	chrY	19593375	19593573	+
MAGEC3	NM_138702	-22406	chrX	140731163	140731361	+
NXT2	NM_018698	47543	chrX	108713208	108713406	+
FAM125B	NM_001011703	981	chr9	128129929	128130127	+
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PAPPA	NM_002581	60045	chr9	118015936	118016134	+
CA8	NM_004056	88313	chr8	61267996	61268194	+
TTC26	NM_024926	57533	chr7	138526596	138526794	+
CALN1	NM_001017440	1080	chr7	71438617	71438815	+
UTRN	NM_007124	224912	chr6	144879477	144879675	+
KHDRBS2	NM_152688	419728	chr6	62634164	62634362	+
FBXW11	NM_012300	172464	chr5	171193819	171194017	+
HMHB1	NM_021182	-42780	chr5	143128940	143129138	+
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RAB6B	NM_016577	23879	chr3	135073303	135073501	+
LIMD1	NM_014240	-4834	chr3	45606294	45606492	+
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RUTBC2	NM_133454	18115	chr22	23550369	23550567	+
C21orf29	NM_144991	198893	chr21	44756831	44757029	+
SOX12	NM_006943	1885	chr20	256123	256321	+
SGPP2	NM_152386	38176	chr2	223035741	223035939	+
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STEAP3	NM_182915	2347	chr2	119700200	119700398	+
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PRKG1	NM_006258	984110	chr10	53488408	53488606	+
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GOLPH3L	NM_018178	10067	chr1	148925991	148926189	+
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GJB4	NM_153212	8769	chr1	35008133	35008331	+
RUNX3	NM_004350	517	chr1	25128641	25128839	+
NECAP2	NM_018090	817	chr1	16640636	16640834	+
ZFPM2	NM_012082	158774	chr8	106559096	106559293	+
CBX3	NM_016587	630	chr7	26208478	26208675	+
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DRD3	NM_000796	68431	chr3	115311960	115312157	+
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TMSB10	NM_021103	30699	chr2	85016972	85017169	+
SOX9	NM_000346	-28957	chr17	67599601	67599798	+
CDK5R1	NM_003885	0	chr17	27838072	27838269	+
SERPINA12	NM_173850	12621	chr14	94041115	94041312	+
FBXW8	NM_012174	78888	chr12	115912031	115912228	+
ETV6	NM_001987	69915	chr12	11763969	11764166	+
DHDDS	NM_024887	39006	chr1	26670394	26670591	+
SKI	NM_003036	79019	chr1	2229012	2229209	+
AMELY	NM_001143	24276	chrY	6777595	6777791	+
WDR31	NM_001006615	0	chr9	115142278	115142473	+
CSMD1	NM_033225	112399	chr8	4727141	4727336	+
ADAMTS18	NM_139054	39778	chr16	75986539	75986733	+
OLFM4	NM_006418	-21662	chr13	52479116	52479310	+
ADAMTSL2	NM_014694	51163	chr9	135440958	135441151	+
CCDC51	NM_024661	10569	chr3	48445770	48445963	+
CAPN13	NM_144575	84975	chr2	30798646	30798839	+
OR4K2	NM_001005501	-7721	chr14	19406352	19406545	+
KCNAB2	NM_003636	34567	chr1	6043533	6043726	+
PTER	NM_001001484	54389	chr10	16573361	16573543	+
TSHZ1	NM_005786	25234	chr18	71076952	71077131	+
LAMA3	NM_000227	70955	chr18	19777958	19778134	+
CITED2	NM_006079	-13925	chr6	139751402	139751577	+
HRBL	NM_006076	417	chr7	99975186	99975359	+
ABCA7	NM_019112	428	chr19	992672	992845	+
RAB17	NM_022449	-40123	chr2	238204597	238204765	+
LOC649159	NM_001040069	-768	chr16	33870771	33870934	+
NME3	NM_002513	927	chr16	1760625	1760783	+
MDS1	NM_004991	450746	chr3	170413265	170413421	+
ATXN7L2	NM_153340	6025	chr1	109834108	109834255	+
SHB	NM_003028	75877	chr9	37983187	37983332	+
C20orf4	NM_015511	38631	chr20	34326491	34326636	+
NAB1	NM_005966	55324	chr2	191277416	191277561	+
AP2A1	NM_014203	-76	chr19	54961775	54961915	+
PAX5	NM_016734	6194	chr9	37018149	37018281	+

SCEL	NM_003843	61572	chr13	77069431	77069563	+
GPX7	NM_015696	4321	chr1	52844952	52845081	+
ARL16	NM_001040025	0	chr17	77261288	77261411	+
RAB33A	NM_004794	5630	chrX	129139083	129139205	+
TMEM117	NM_032256	393845	chr12	42910073	42910187	+
PHF17	NM_024900	40375	chr4	129990603	129990711	+
SRC	NM_198291	44578	chr20	35452548	35452655	+
IBTK	NM_015525	10676	chr6	83003385	83003490	+
MBNL2	NM_144778	-33909	chr13	96638562	96638665	+
TLE1	NM_005077	28837	chr9	83464476	83464578	+
TBC1D22A	NM_014346	14215	chr22	45551427	45551527	+
RAC2	NM_002872	16626	chr22	35953524	35953624	+
TPO	NM_000547	150268	chr2	1546509	1546609	+
NID2	NM_007361	276	chr14	51605319	51605419	+
GLB1	NM_000404	90505	chr3	33022928	33023126	+
PCMTD2	NM_018257	68924	chr20	62426488	62426686	+
BRCC2	NM_001001786	44294	chr11	121447640	121447838	+
LYN	NM_002350	-2810	chr8	56951917	56952115	+
BRD1	NM_014577	39582	chr22	48564675	48564873	+
SHKBP1	NM_138392	304	chr19	45774933	45775131	+
SLC39A11	NM_139177	416129	chr17	68184099	68184297	+
APC	NM_000038	16183	chr5	112117665	112117862	+
HFM1	NM_001017975	13650	chr1	91625489	91625603	+
C3orf56	NM_001007534	-48286	chr3	128346179	128346377	+
PRPF38B	NM_018061	287	chr1	109036947	109037145	+
MEIS2	NM_172315	928	chr15	35176669	35176866	+
NELL1	NM_006157	93852	chr11	20741563	20741712	+
SLIT2	NM_004787	178982	chr4	20043314	20043417	+
ENTHD1	NM_152512	55092	chr22	38564548	38564647	+
VWA2	NM_198496	46521	chr10	116035528	116035726	+
OPLAH	NM_017570	9416	chr8	145177345	145177542	+
EPHB4	NM_004444	20037	chr7	100242843	100243041	+
SUPT3H	NM_003599	481120	chr6	44972234	44972432	+
NRSN1	NM_080723	-45826	chr6	24188304	24188502	+
SLC30A9	NM_006345	51173	chr4	41738452	41738650	+
RNF157	NM_052916	26300	chr17	71721486	71721684	+
OPCML	NM_002545	103681	chr11	132214367	132214565	+
HSPA14	NM_016299	7084	chr10	14927350	14927548	+
AMY2B	NM_020978	9881	chr1	103908725	103908923	+
GABRG3	NM_033223	110928	chr15	24910190	24910387	+
BTBD3	NM_181443	4092	chr20	11823568	11823667	+
MDM1	NM_017440	-1529	chr12	67013907	67014105	+
TCERG1	NM_001040006	60913	chr5	145867978	145868176	+
TRIM24	NM_003852	-22559	chr7	137772960	137773059	+
LRRC62	NM_052906	-18690	chr22	36120214	36120412	+
KIDINS220	NM_020738	55942	chr2	8839040	8839238	+
GNGT2	NM_031498	9170	chr17	44632373	44632571	+
CCDC64	NM_207311	90646	chr12	119002676	119002874	+
CUTL2	NM_015267	74864	chr12	110031075	110031273	+
PRKACG	NM_002732	-6252	chr9	70825079	70825182	+

NCOA1	NM_147223	149981	chr2	24810830	24810929	+
C6orf145	NM_183373	-34166	chr6	3731100	3731298	+
COX6A1	NM_004373	-8323	chr12	119351765	119351963	+
IKBKE	NM_014002	-257	chr1	204709963	204710161	+
SPATA5	NM_145207	113607	chr4	124177285	124177478	+
TSPAN33	NM_178562	13086	chr7	128585033	128585198	+
KCNK12	NM_022055	50130	chr2	47600744	47600843	+
TMC1	NM_138691	198560	chr9	74525096	74525294	+
GLIS3	NM_001042413	-5156	chr9	4295190	4295388	+
PDE1C	NM_005020	306064	chr7	31771253	31771451	+
APC	NM_000038	25479	chr5	112126961	112127159	+
ATOH8	NM_032827	6920	chr2	85841452	85841650	+
CRIM1	NM_016441	192858	chr2	36629758	36629956	+
C18orf1	NM_181482	205893	chr18	13414687	13414885	+
ST8SIA2	NM_006011	38638	chr15	90776781	90776979	+
ANKRD19	NM_001010925	5446	chr9	94617116	94617313	+
DDB1	NM_001923	22705	chr11	60834222	60834419	+
PKNOX2	NM_022062	186909	chr11	124726677	124726870	+
LOC399744	NM_001013665	51345	chr10	38828622	38828809	+
ST6GAL1	NM_173216	53053	chr3	188184262	188184398	+
ELK3	NM_005230	47240	chr12	95159577	95159687	+
SOX8	NM_014587	288	chr16	972096	972199	+
IL1RAPL1	NM_014271	821360	chrX	29336839	29337037	+
LY96	NM_015364	81355	chr8	75147498	75147696	+
SHFM1	NM_006304	-45820	chr7	96222958	96223156	+
OPN5	NM_001030051	62988	chr6	47925808	47926006	+
CAV3	NM_001234	-17933	chr3	8732364	8732562	+
MCM10	NM_018518	50322	chr10	13293908	13294106	+
HMCN1	NM_031935	320085	chr1	184290390	184290588	+
SH3RF2	NM_152550	2234	chr5	145298568	145298765	+
GNAO1	NM_138736	65601	chr16	54849249	54849446	+
STT3A	NM_152713	-337	chr11	124967436	124967629	+
CTNNB1	NM_001904	44799	chr3	41260814	41261005	+
ARID2	NM_152641	-2646	chr12	44407098	44407240	+
KIAA0350	NM_015226	239939	chr16	11185881	11186013	+
RASSF8	NM_007211	-39315	chr12	25963808	25963920	+

Table S3. Motif letter-probability matrix

site	A	C	G	T
1	8.19%	75.59%	9.20%	7.02%
2	14.05%	22.91%	54.01%	9.03%
3	85.62%	2.68%	4.35%	7.36%
4	8.53%	5.35%	66.89%	19.23%
5	3.68%	87.79%	7.02%	1.51%
6	12.21%	23.58%	6.19%	58.03%
7	2.68%	84.95%	8.36%	4.01%
8	13.04%	7.19%	5.69%	74.08%
9	4.18%	10.03%	17.39%	68.39%
10	2.51%	90.97%	0.50%	6.02%

w=10; sites=598; E=4.4e-201; Consensus=C-G/C-A-G-C-T/C-C-T-T-C.

Table S4. The 598 instances of the motif

Gene	Chr	start	end	Sites	Num	Strand	Start	*P*-value
SLC35F1	chr6	118588151	118588250	CGAGCTCTTC	548	+	6	8.31E-07
NID2	chr14	51605319	51605419	CGAGCTCTTC	1373	-	33	8.31E-07
INPP5B	chr1	38121850	38122048	CGAGCTCTTC	312	-	56	8.31E-07
CLPX	chr15	63264975	63265173	CGAGCTCTTC	1209	+	56	8.31E-07
SLC4A1	chr17	39695144	39695342	CGAGCTCTTC	165	-	56	8.31E-07
LEF1	chr4	109249296	109249494	CGAGCTCTTC	35	+	56	8.31E-07
NUPL1	chr13	24802296	24802494	CGAGCTCTTC	289	-	56	8.31E-07
STK32B	chr4	5194682	5194781	CGAGCTCTTC	107	+	6	8.31E-07
FCRL3	chr1	155919181	155919280	CGAGCTCTTC	1229	+	11	8.31E-07
MAPK6	chr15	50109674	50109872	CGAGCTCTTC	956	+	56	8.31E-07
USP25	chr21	16065493	16065691	CGAGCTCTTC	1069	-	56	8.31E-07
C14orf49	chr14	94923553	94923751	CGAGCTCTTC	722	-	56	8.31E-07
TNFRSF21	chr6	47310465	47310663	CGAGCTCTTC	209	+	56	8.31E-07
KCNMB2	chr3	179755458	179755656	CGAGCTCTTC	874	-	56	8.31E-07
KCNK10	chr14	87831997	87832194	CGAGCCCTTC	975	-	55	1.57E-06
LONRF3	chrX	118061364	118061563	CGAGCCCTTC	133	-	55	1.57E-06
DMBT1	chr10	124384789	124384987	CGAGCCCTTC	178	+	56	1.57E-06
EFNA5	chr5	107036736	107036934	CGAGCCCTTC	99	+	56	1.57E-06
BRE	chr2	28163532	28163730	CCAGCTCTTC	435	-	56	2.40E-06
MELK	chr9	36557023	36557221	CCAGCTCTTC	607	+	56	2.40E-06
RAB6B	chr3	135073303	135073501	CCAGCTCTTC	1261	+	56	2.40E-06
LRRC16	chr6	25437384	25437582	CCAGCTCTTC	1107	-	56	2.40E-06
GALNT17	chr4	173589934	173590132	CCAGCTCTTC	845	-	51	2.40E-06
SST	chr3	188849905	188850103	CCAGCTCTTC	265	+	56	2.40E-06
MBNL1	chr3	153457506	153457704	CCAGCTCTTC	1116	+	56	2.40E-06
VPS33A	chr12	121301766	121301964	CCAGCTCTTC	393	+	56	2.40E-06
CABIN1	chr22	22868712	22868910	CCAGCTCTTC	800	-	56	2.40E-06
CSDC2	chr22	40302571	40302769	CCAGCTCTTC	404	+	61	2.40E-06
UBE2L3	chr22	20297962	20298160	CCAGCTCTTC	666	-	56	2.40E-06
DZIP1L	chr3	139255462	139255660	CCAGCTCTTC	228	-	56	2.40E-06
OXT	chr20	3000678	3000876	CCAGCTCTTC	536	-	56	2.40E-06
VPS53	chr17	520667	520865	CCAGCTCTTC	288	-	55	2.40E-06

THEG	chr19	316160	316358	CGAGCTCTGC	1277	+	56	3.13E-06
CFDP1	chr16	74025746	74025944	CGAGCTCTGC	556	+	56	3.13E-06
ARVP6125	chr3	131283353	131283551	CGAGCTCTGC	1119	-	56	3.13E-06
TSSC1	chr2	3325827	3326026	CGAGCTCTGC	38	+	56	3.13E-06
LRRN6A	chr15	75753479	75753677	CGAGCTCTGC	275	+	56	3.13E-06
C21orf63	chr21	32731668	32731866	CGAGCTCTGC	469	+	56	3.13E-06
BRWD1	chr21	39490367	39490565	CGATCTCTTC	332	+	56	4.07E-06
SVIL	chr10	29810450	29810648	CGATCTCTTC	1213	+	56	4.07E-06
ZNF208	chr19	21931946	21932144	CGATCTCTTC	885	-	56	4.07E-06
ELMO1	chr7	36990251	36990449	CAAGCTCTTC	381	+	56	5.01E-06
CRNN	chr1	150688922	150689120	CAAGCTCTTC	971	-	56	5.01E-06
DKFZP564J102	chr4	187336929	187337127	CAAGCTCTTC	366	+	57	5.01E-06
ZNF277P	chr7	111794870	111795069	CAAGCTCTTC	449	-	56	5.01E-06
C1orf21	chr1	182885073	182885271	CAAGCTCTTC	686	+	56	5.01E-06
ADAMTSL2	chr9	135440958	135441151	CGAGCACTTC	1328	-	53	5.84E-06
DENND1A	chr9	125534572	125534770	CGAGCACTTC	287	-	56	5.84E-06
SORCS2	chr4	7613055	7613253	CGAGCACTTC	849	-	51	5.84E-06
SKI	chr1	2229012	2229209	CGAGCACTTC	1321	-	55	5.84E-06
CUTL1	chr7	101579581	101579779	CCAGCCCTTC	815	+	61	6.57E-06
TMSB10	chr2	85016972	85017169	CCAGCCCTTC	1313	-	50	6.57E-06
LRRC8B	chr1	89829936	89830134	CCAGCCCTTC	1299	+	56	6.57E-06
KIAA1333	chr14	30068293	30068491	CCAGCCCTTC	320	-	51	6.57E-06
KIAA0284	chr14	104419396	104419594	CCAGCCCTTC	1040	-	51	6.57E-06
SUB1	chr5	32617421	32617619	CGAGCTCTCC	1112	-	55	8.14E-06
ZUBR1	chr1	19286617	19286815	CGAGCTCATC	496	-	56	8.14E-06
C7orf41	chr7	30141224	30141422	CGAGCTCATC	224	+	61	8.14E-06
SLIT3	chr5	168058340	168058441	CGAGCTCTCC	19	+	7	8.14E-06
PRKAR1B	chr7	676855	677054	CGAGCTCTCC	539	+	61	8.14E-06
ITPK1	chr14	92504866	92505064	CGAGCTCATC	476	-	56	8.14E-06
NEK1	chr4	170706974	170707172	CTAGCTCTTC	578	+	56	9.08E-06
RTCD1	chr1	100504960	100505158	CTAGCTCTTC	904	-	3	9.08E-06
ALDH1A1	chr9	74735523	74735721	CTAGCTCTTC	508	+	56	9.08E-06
CLMN	chr14	94856389	94856587	CGAGCCCTGC	724	+	56	9.73E-06
NIBP	chr8	141528669	141528772	CCAGCTCTGC	421	+	36	1.29E-05
PSMD14	chr2	161971040	161971238	GGAGCTCTTC	1028	-	56	1.29E-05
ZNF579	chr19	60752902	60753100	CCAGCTCTGC	1036	-	56	1.29E-05
LDLRAP1	chr1	25772463	25772661	CCAGCTCTGC	806	-	19	1.29E-05
DPYSL2	chr8	26582359	26582557	CCAGCTCTGC	653	+	56	1.29E-05
BFSP2	chr3	134600085	134600283	CCAGCTCTGC	1019	+	73	1.29E-05
AIM1	chr6	107094505	107094703	CCAGCTCTGC	931	+	56	1.29E-05
SOX8	chr16	972096	972199	CGAGCGCTTC	1480	+	8	1.29E-05
KCNC1	chr11	17733532	17733730	GGAGCTCTTC	24	-	56	1.29E-05
KIAA1370	chr15	50758054	50758252	CGAACTCTTC	242	+	56	1.38E-05
SGK2	chr20	41647830	41648028	CGAACTCTTC	803	+	56	1.38E-05
C20orf4	chr20	34326491	34326636	CGAGCTCCTC	1346	+	30	1.63E-05
PCMTD2	chr20	62426488	62426686	CCATCTCTTC	1378	+	70	1.63E-05
KIAA0427	chr18	44522464	44522662	CGAGCTCCTC	550	+	61	1.63E-05
SLC5A11	chr16	24794270	24794468	CAAGCCCTTC	551	-	56	1.63E-05
LUC7L	chr16	202207	202405	CGAGCTCCTC	131	-	54	1.63E-05
NME3	chr16	1760625	1760783	CGAGCTCCTC	1342	-	36	1.63E-05

C9orf19	chr9	36154339	36154537	CCATCTCTTC	1097	+	56	1.63E-05
ARHGEF2	chr1	154227265	154227463	CCATCTCTTC	1296	+	81	1.63E-05
PCGF3	chr4	750775	750973	CGAGCTCCTC	32	-	56	1.63E-05
ZNF236	chr18	72766111	72766309	CAAGCCCTTC	888	+	61	1.63E-05
HIBADH	chr7	27580367	27580565	AGAGCTCTTC	868	+	56	1.81E-05
C16orf75	chr16	11362032	11362230	AGAGCTCTTC	955	+	57	1.81E-05
PDE2A	chr11	71926877	71927076	AGAGCTCTTC	811	+	56	1.81E-05
PASD1	chrX	150558653	150558851	AGAGCTCTTC	1075	+	58	1.81E-05
NEFM	chr8	24828558	24828756	AGAGCTCTTC	847	-	56	1.81E-05
MDM1	chr12	67013907	67014105	AGAGCTCTTC	1422	-	54	1.81E-05
ZMIZ2	chr7	44755503	44755701	AGAGCTCTTC	515	+	58	1.81E-05
KCNT1	chr9	137739227	137739425	CGTGCTCTTC	149	-	56	2.21E-05
LPA	chr6	160899610	160899808	CGACCTCTTC	757	-	56	2.21E-05
B4GALT1	chr9	33191015	33191213	CGAGGTCTTC	41	+	61	2.21E-05
PSMD14	chr2	161971040	161971238	CGTGCTCTTC	1029	-	56	2.21E-05
OSBPL3	chr7	24911740	24911938	TGAGCTCTTC	1103	+	54	2.45E-05
B3GALT6	chr1	1167939	1168137	CGAGCCCTCC	93	+	56	2.45E-05
TLL2	chr10	98162129	98162327	TGAGCTCTTC	592	-	51	2.45E-05
FRMD6	chr14	51041258	51041456	TGAGCTCTTC	826	+	56	2.45E-05
TP73L	chr3	191094892	191095090	TGAGCTCTTC	161	+	56	2.45E-05
NR6A1	chr9	126525447	126525645	TGAGCTCTTC	151	+	56	2.45E-05
HERPUD2	chr7	35662399	35662597	TGAGCTCTTC	613	-	56	2.45E-05
SGIP1	chr1	66876501	66876600	CGATCTCTGC	979	+	6	2.53E-05
GRB10	chr7	50762878	50763076	CCAGCTCATC	494	+	56	2.69E-05
ABCC8	chr11	17454469	17454667	CCAGCTCATC	244	-	56	2.69E-05
CRYM	chr16	21216224	21216422	CAAGCTCTGC	392	-	56	2.85E-05
RIPK4	chr21	42034359	42034557	CGAGCACTGC	944	-	56	3.11E-05
C20orf79	chr20	18757337	18757535	CGAGCTCTAC	370	-	56	3.11E-05
CAPN13	chr2	30798646	30798839	CGAGCACTGC	1330	+	68	3.11E-05
MELK	chr9	36557023	36557221	CGAGCTCTAC	606	+	56	3.11E-05
PEX26	chr22	16925717	16925915	CGAGCACTGC	942	-	46	3.11E-05
SMOC2	chr6	168663493	168663691	CAATCTCTTC	1009	+	71	3.11E-05
ANKRD13A	chr12	108960564	108960762	CGGGCTCTTC	726	-	56	3.28E-05
NRG1	chr8	31844207	31844404	CGAGCTCTTT	1218	+	55	3.28E-05
RPGRIP1	chr14	20872628	20872826	CGAGCTCTTT	1143	+	66	3.28E-05
RGS6	chr14	72117089	72117287	CGGGCTCTTC	679	+	57	3.28E-05
ATOH8	chr2	85841452	85841650	CGAGCTCTTT	1467	+	56	3.28E-05
CFDP1	chr16	74025746	74025944	CGAGCTCTTT	555	+	56	3.28E-05
ZMIZ2	chr7	44755503	44755701	CGATCACTTC	514	+	65	3.51E-05
MPHOSPH6	chr16	80753450	80753648	GGAGCCCTTC	676	-	56	3.51E-05
GRB10	chr7	50654546	50654744	GGAGCCCTTC	103	+	56	3.51E-05
CRTC3	chr15	88873615	88873813	CCAGCCCTGC	633	-	56	3.51E-05
FGD1	chrX	54526484	54526682	CCAGCCCTGC	109	+	90	3.51E-05
PNPLA7	chr9	139479947	139480145	CGAACCCTTC	922	+	56	3.60E-05
SGCZ	chr8	14978297	14978495	CCATCCCTTC	4	+	56	4.07E-05
LOC375449	chr5	66048493	66048691	CCAGCGCTTC	1221	+	56	4.07E-05
MOSC1	chr1	219046020	219046218	CAAGCACTTC	425	+	56	4.07E-05
SPOCK3	chr4	167861593	167861791	CAAGCACTTC	1113	+	56	4.07E-05
STK10	chr5	171538532	171538725	CCAGCGCTTC	1177	-	53	4.07E-05
AZIN1	chr8	103978286	103978484	GCAGCTCTTC	63	+	56	4.07E-05

KCNMB2	chr3	179755458	179755656	CCAGCTCCTC	875	-	56	4.49E-05
ADCY5	chr3	124633872	124634070	CCAGCTGTTC	1015	+	56	5.07E-05
ARAF	chrX	47311544	47311742	CGAGCCCGTC	479	-	57	5.07E-05
C6orf145	chr6	3730200	3730398	CGAGCCCGTC	934	-	56	5.07E-05
VANGL1	chr1	115990486	115990683	CAAGCTCATC	784	+	56	5.07E-05
LAMA3	chr18	19777958	19778134	CAAGCTCTCC	1336	-	45	5.07E-05
USF2	chr19	40454658	40454857	CGAGGCCTTC	472	-	56	5.59E-05
SGK2	chr20	41647830	41648028	CTATCTCTTC	802	+	56	5.59E-05
MAGEC3	chrX	140731163	140731361	CTATCTCTTC	1238	+	7	5.59E-05
LOC441956	chr21	13999062	13999260	CGAGGCCTTC	879	+	20	5.59E-05
PDSS2	chr6	107677661	107677859	CTATCTCTTC	737	-	56	5.59E-05
POLS	chr5	6815541	6815640	CGAGGCCTTC	1191	+	7	5.59E-05
CNTNAP5	chr2	125056122	125056320	CGAGGCCTTC	267	-	56	5.59E-05
COX6A1	chr12	119351765	119351963	CTATCTCTTC	1446	+	56	5.59E-05
TRPM1	chr15	29191156	29191354	CGAGATCTTC	694	-	56	5.59E-05
HIBADH	chr7	27580367	27580565	CTATCTCTTC	869	-	11	5.59E-05
SH3RF2	chr5	145298568	145298765	CGTGCCCTTC	1492	-	51	5.59E-05
KCNC1	chr11	17733532	17733730	TGAGCCCTTC	26	-	56	5.90E-05
NECAP2	chr1	16640636	16640834	CGAGCACTCC	1304	-	56	5.90E-05
FLJ46300	chr10	133431892	133432087	CCAGCTCGTC	1176	+	54	5.90E-05
LOC283331	chr12	48470680	48470878	CCAGCTCGTC	558	+	58	5.90E-05
HNT	chr11	131136881	131137079	CGCGCTCTTC	901	-	51	6.43E-05
RABGAP1L	chr1	172348176	172348374	CCACCTCTTC	470	+	57	6.43E-05
CDK10	chr16	88289529	88289727	CCAGGTCTTC	457	+	56	6.43E-05
SGK2	chr20	41647830	41648028	GGAGCTCTGC	801	+	56	6.43E-05
FBXL16	chr16	693546	693744	GGAGCTCTGC	334	-	53	6.43E-05
PEX26	chr22	16925717	16925915	CGAGCGCTGC	943	-	56	6.43E-05
SH3RF2	chr5	145298568	145298765	GGAGCTCTGC	1493	+	56	6.43E-05
IPMK	chr10	59589954	59590152	CCACCTCTTC	780	+	59	6.43E-05
TNPO2	chr19	12675577	12675679	GGAGCTCTGC	690	+	8	6.43E-05
TADA2L	chr17	32874886	32875084	GGAGCTCTGC	647	-	56	6.43E-05
C1orf198	chr1	229074319	229074419	GGAGCTCTGC	988	+	56	6.43E-05
WBSCR28	chr7	72939564	72939762	CCAGCCCATC	79	-	56	6.75E-05
DOCK5	chr8	25221675	25221873	CCAGCCCATC	118	+	61	6.75E-05
LTBP3	chr11	65079852	65080050	CCAGCCCATC	220	+	61	6.75E-05
SGK2	chr20	41647830	41648028	CCAGCCCATC	804	+	61	6.75E-05
MGC39900	chrX	103103090	103103288	CGAACTCTGC	122	+	56	6.75E-05
NTN1	chr17	9062693	9062891	TCAGCTCTTC	108	-	56	6.75E-05
MGAT5B	chr17	72441387	72441587	CCAGCCCTCC	211	-	55	6.75E-05
GATA6	chr18	18003023	18003221	CGAACTCTGC	1133	-	56	6.75E-05
CAMK2D	chr4	114680006	114680204	CAAGCCCTGC	1257	-	56	7.24E-05
PTPRM	chr18	8212425	8212623	GGATCTCTTC	1135	+	56	7.24E-05
C20orf133	chr20	14728191	14728389	GGATCTCTTC	459	+	56	7.24E-05
FLJ90680	chr22	35561944	35562142	CTAGCACTTC	144	+	8	7.24E-05
LOC387882	chr12	104269604	104269802	CGAGCTATTC	69	-	56	7.91E-05
ZFPM1	chr16	87039465	87039663	CGAGCTGTGC	495	-	56	7.91E-05
SH3BP2	chr4	2785563	2785761	CGAGCTGTGC	581	+	56	7.91E-05
KIAA0350	chr16	11056570	11056768	GAAGCTCTTC	524	-	56	7.91E-05
CD24	chrY	19593375	19593573	CAATCCCTTC	1235	+	61	7.91E-05

CNTNAP4	chr16	75137461	75137659	CAATCCCTTC	632	-	51	7.91E-05
KIF6	chr6	39516926	39517124	GAAGCTCTTC	714	+	57	7.91E-05
OSBPL2	chr20	60252925	60253123	CAAGCGCTTC	945	-	56	7.91E-05
ENPP3	chr6	132023401	132023599	AGAGCTCTGC	600	-	56	8.25E-05
FLNC	chr7	128276698	128276896	AGAGCTCTGC	1099	+	56	8.25E-05
FLJ22374	chr7	30773296	30773494	CAAACTCTTC	315	-	87	8.25E-05
FRMD6	chr14	51041258	51041456	CAAACTCTTC	825	-	56	8.25E-05
C7orf26	chr7	6610718	6610916	AGAGCTCTGC	195	-	56	8.25E-05
GCNT4	chr5	74390729	74390927	CCAGCTCTAC	1014	-	56	9.00E-05
SLC25A32	chr8	104482875	104483073	CGAGCTCTTA	797	+	56	9.00E-05
LPA	chr6	160899610	160899808	CCAGCTCTAC	756	+	56	9.00E-05
LAS1L	chrX	64668964	64669162	CTAGCTCATC	453	-	56	9.00E-05
R3HDM1	chr2	136083759	136083957	GGAGCACTTC	1124	-	56	9.00E-05
COL23A1	chr5	177629509	177629707	CTAGCTCTCC	135	+	57	9.00E-05
GTF2A1	chr14	80706295	80706493	GGAGCACTTC	897	+	56	9.00E-05
ADAMTS14	chr10	72144985	72145183	CGATCTGTTC	75	-	56	9.00E-05
CXorf48	chrX	134127561	134127759	CGAACACTTC	567	+	56	9.59E-05
PRPF38B	chr1	109036947	109037145	CGTGCTCTGC	1394	+	56	9.59E-05
IHPK3	chr6	33797838	33798036	AGATCTCTTC	575	+	58	9.59E-05
TREM1	chr6	41361616	41361814	CCAGCTCTTT	617	-	88	9.59E-05
WNT11	chr11	75562562	75562760	CCAGCTCTTT	488	+	61	9.59E-05
AMIGO1	chr1	109866945	109867143	AGATCTCTTC	81	-	56	9.59E-05
DKFZp761B107	chr4	24510458	24510656	CGAGGTCTGC	993	+	56	9.59E-05
KCNT1	chr9	137750017	137750215	TGAGCTCTGC	147	+	59	1.02E-04
CACNG1	chr17	62480986	62481184	TGAGCTCTGC	773	-	56	1.02E-04
FBN2	chr5	127931609	127931807	TGAGCTCTGC	158	+	56	1.02E-04
IRF5	chr7	128329792	128329990	TGAGCTCTGC	262	+	56	1.02E-04
PITPNM2	chr12	122078699	122078897	CGAGCCCAGC	51	+	56	1.02E-04
CPE	chr4	166657142	166657340	CGTTCTCTTC	155	+	61	1.05E-04
CACNA1S	chr1	199309149	199309347	AAAGCTCTTC	1160	-	56	1.05E-04
SOX12	chr20	256123	256321	CCAACCCTTC	1269	-	56	1.05E-04
DAG1	chr3	49479525	49479723	CAAGCTCGTC	1120	-	56	1.14E-04
ENTHD1	chr22	38564548	38564647	CGAGCAGTTC	1404	+	6	1.14E-04
C10orf92	chr10	134555080	134555278	GGAGCTCTCC	485	+	56	1.14E-04
KCNMB2	chr3	179755458	179755656	CGAGCGCTCC	872	+	56	1.14E-04
COL23A1	chr5	177629509	177629707	CGATCCCATC	134	+	61	1.14E-04
ADAMTSL3	chr15	82414925	82415123	GGAGCTCTCC	278	+	57	1.14E-04
COMMD8	chr4	47157454	47157652	CCAGCTCAGC	198	+	71	1.14E-04
SCOC	chr4	141500364	141500562	CATGCTCTTC	621	+	61	1.21E-04
KIAA1984	chr9	138810309	138810507	CGAACTCATC	225	-	51	1.21E-04
ZNF596	chr8	230055	230253	CGAGCCTTTC	867	-	56	1.21E-04
C9orf93	chr9	15542821	15543019	AGAGCACTTC	376	+	56	1.21E-04
NLGN4Y	chrY	15203407	15203605	CAACCTCTTC	565	-	56	1.21E-04
ROR2	chr9	93588928	93589126	CAACCTCTTC	799	-	56	1.21E-04
PHC2	chr1	33617793	33617991	CGAGCACGTC	908	+	56	1.28E-04
AARSL	chr6	44403597	44403795	CAAGCCCTCC	710	-	55	1.28E-04
RPL39L	chr3	188366387	188366585	CCATCTCATC	368	-	38	1.28E-04
GSG1	chr12	13171584	13171782	CCATCTCATC	85	+	61	1.28E-04
PAX5	chr9	36956257	36956455	CAAGCCCTCC	1096	+	56	1.28E-04
SOX8	chr16	972096	972199	CGAGCTCCCC	1479	+	13	1.28E-04

CDC42EP1	chr22	36287988	36288186	CAAGCCCTCC	1263	+	57	1.28E-04
CXCL14	chr5	134942864	134943062	CCAGCTTTTC	738	+	56	1.36E-04
ZP1	chr11	60397320	60397518	CGAGACCTTC	1292	+	56	1.36E-04
RAB6B	chr3	135073303	135073501	CAATCTCTGC	1260	-	56	1.36E-04
MGC39715	chr8	101699482	101699680	CAATCTCTGC	864	-	46	1.36E-04
WNK2	chr9	95120125	95120323	CCAGCTTTTC	824	+	56	1.36E-04
LMO2	chr11	33871830	33872028	CGGGCTCTGC	18	+	56	1.42E-04
ZNF579	chr19	60752902	60753100	TGAGCACTTC	1034	+	56	1.42E-04
CALN1	chr7	71438617	71438815	CCAGCCCGTC	1248	+	89	1.42E-04
CDH10	chr5	24526612	24526810	TGAGCACTTC	462	-	56	1.42E-04
KCNK12	chr2	47600744	47600843	GGAGCCCTGC	1458	-	52	1.52E-04
ERC2	chr3	55741886	55742084	AGAGCTCATC	493	-	56	1.52E-04
FZD6	chr8	104423178	104423376	CTAGCTCCTC	816	+	56	1.52E-04
LPP	chr3	189906582	189906780	AGAGCTCATC	1080	-	51	1.52E-04
LRRC18	chr10	49816925	49817123	CGAGTTCTTC	340	+	56	1.52E-04
MAML3	chr4	141268529	141268727	CCAGCACATC	90	+	61	1.57E-04
KHDRBS2	chr6	62424487	62424685	CCAGCACATC	545	+	78	1.57E-04
INPP5A	chr10	134301708	134301906	CCAGCACATC	222	-	56	1.57E-04
TRPC5	chrX	111133352	111133550	CCAGCACTCC	917	-	56	1.57E-04
COX6A1	chr12	119351765	119351963	CGTGCTCATC	1447	-	51	1.70E-04
C18orf1	chr18	13167392	13167590	CGAGCCCCGC	304	-	56	1.70E-04
ENG	chr9	129643177	129643375	CGACCTCATC	1001	-	56	1.70E-04
SDC2	chr8	97618019	97618217	CAAGCTCTAC	609	-	56	1.70E-04
CACNA2D1	chr7	81859671	81859869	GGAACTCTTC	344	-	56	1.78E-04
ACCN1	chr17	29327612	29327810	TGAGCTCATC	994	+	56	1.78E-04
PDE7B	chr6	136171797	136171995	CCAACTCTGC	1105	-	56	1.78E-04
ADCY3	chr2	24940022	24940220	GGAACTCTTC	854	+	56	1.78E-04
PACRG	chr6	163522903	163523101	CAATCACTTC	736	+	56	1.88E-04
SDK1	chr7	3688535	3688733	CGAGCGCCTC	119	-	56	1.88E-04
ITPK1	chr14	92504866	92505064	CTAGCTCGTC	475	+	56	1.88E-04
PRDM16	chr1	3300634	3300832	CGAGCGCCTC	183	-	56	1.88E-04
C20orf133	chr20	14728191	14728389	CGAGCACTAC	460	+	56	1.88E-04
MYO3B	chr2	171071886	171072084	CCATCGCTTC	251	+	56	1.88E-04
EDN1	chr6	12389189	12389387	CTAGGTCTTC	112	+	56	1.97E-04
FALZ	chr17	63257534	63257732	AGAGCCCTGC	771	+	77	1.97E-04
SRC	chr20	35452548	35452655	CCAGCTCACC	1361	-	78	1.97E-04
UST	chr6	149399890	149400088	CTAGGTCTTC	928	+	56	1.97E-04
NIBP	chr8	141187092	141187290	CTTGCTCTTC	521	-	56	1.97E-04
MRPL23	chr11	1931765	1931963	CGGGCACTTC	683	+	9	1.97E-04
KIAA0350	chr16	11185881	11186013	TTAGCTCTTC	1500	-	89	2.08E-04
FLJ90680	chr22	35561944	35562142	CCAGCCCTAC	143	-	56	2.08E-04
CCDC51	chr3	48445770	48445963	CGAGCCCGGC	1329	-	53	2.08E-04
ZMIZ2	chr7	44755503	44755701	GGAGCTGTTC	518	+	56	2.08E-04
EPHA7	chr6	94042552	94042750	CGAGCCCTTA	616	+	56	2.08E-04
MYO3B	chr2	171071886	171072084	CTAGCCCTCC	252	+	56	2.08E-04
SLC25A32	chr8	104482875	104483073	CGAGCGGTTC	795	-	56	2.08E-04
ENPP3	chr6	132023401	132023599	GGAGCTGTTC	598	+	56	2.08E-04
TBC1D22A	chr22	45835462	45835660	CGAGCGGTTC	433	-	56	2.08E-04
NANP	chr20	25558051	25558249	TTAGCTCTTC	1072	+	56	2.08E-04
RAB6B	chr3	135073303	135073501	CCAGCCCTAC	1258	-	56	2.08E-04

IKBKE	chr1	204709963	204710161	CTATCTCTGC	1449	+	56	2.18E-04
APC	chr5	112173568	112173766	CGATCTTTTC	564	-	44	2.18E-04
CHRNB3	chr8	42629366	42629564	CCGGCCCTTC	752	-	56	2.18E-04
CHRNA3	chr15	76699199	76699397	CGAGGCCTGC	775	-	84	2.18E-04
MAGI1	chr3	65516663	65516861	CAATCTCTCC	512	-	56	2.30E-04
NR4A1	chr12	50717697	50717895	GGAGCTCGTC	779	+	58	2.30E-04
PSMF1	chr20	1047369	1047567	CGAGCGCGTC	285	-	56	2.30E-04
TASP1	chr20	13312254	13312452	CCAGCTCGGC	256	+	56	2.30E-04
GSTA4	chr6	52920667	52920865	CGAGCGCGTC	98	-	56	2.30E-04
TCERG1	chr5	145867978	145868176	CCATCTGTTC	1424	+	6	2.30E-04
FAM60A	chr12	31346229	31346427	CAATCTCATC	358	+	61	2.30E-04
PDK2	chr17	45531380	45531578	CCAACACTTC	954	+	56	2.49E-04
SLC25A32	chr8	104482875	104483073	CGATGCCTTC	796	-	56	2.49E-04
PRKG1	chr10	52504484	52504600	CGCGCTCTGC	745	-	50	2.49E-04
ATP2B2	chr3	10485850	10486048	TCAGCTCTGC	248	+	56	2.60E-04
FASTK	chr7	150406244	150406442	CGAAGTCTTC	380	-	36	2.60E-04
HNT	chr11	131713221	131713419	GGAGCCCTCC	1291	+	56	2.60E-04
WNT10B	chr12	47651609	47651807	CGATCACTCC	1047	-	46	2.60E-04
CAMTA1	chr1	7493679	7493877	CGAGCATTTC	652	+	56	2.76E-04
APC	chr5	112117665	112117862	CAAGGCCTTC	1386	+	17	2.76E-04
FLJ45187	chr10	21853611	21853770	CCTTCTCTTC	913	-	61	2.76E-04
C6orf145	chr6	3730200	3730398	CTAGCTCTAC	933	-	56	2.76E-04
TMEM105	chr17	76951897	76952095	CTAGCACTGC	891	+	56	2.76E-04
LOH12CR1	chr12	12402728	12402926	CGAGCATTTC	543	+	56	2.76E-04
C18orf1	chr18	13167392	13167590	CAACCCCTTC	302	+	56	2.76E-04
KIAA1324	chr1	109454239	109454437	CGCTCTCTTC	530	+	56	2.76E-04
CHSY1	chr15	99505756	99505954	CTAGCACTGC	335	-	56	2.76E-04
OBSCN	chr1	226569092	226569290	TGAGCTCCTC	179	+	58	2.89E-04
HOXC9	chr12	52684889	52685087	CCAGCGCTCC	30	-	56	2.89E-04
SHKBP1	chr19	45774933	45775131	CCATCCCTCC	1383	-	81	2.89E-04
FLJ23356	chr8	43115184	43115381	CGAGCCCCCC	1059	-	55	2.89E-04
CA8	chr8	61267996	61268194	CTAGCTCTTT	1245	+	56	2.89E-04
HOXD13	chr2	176657912	176658109	CTAGCTCTTT	1169	-	55	2.89E-04
VLDLR	chr9	2634788	2634986	CTAGCTCTTT	925	+	62	2.89E-04
ITGB1BP1	chr2	9473573	9473771	CCATCCCATC	503	+	61	2.89E-04
HECW1	chr7	43385428	43385626	CCATCCCATC	474	+	61	2.89E-04
PLD1	chr3	172789872	172790070	CCATCCCATC	8	+	61	2.89E-04
TSPAN9	chr12	3065071	3065269	CCAACTCATC	339	-	56	3.04E-04
TRIM24	chr7	137772960	137773059	CGAGGTGTTC	1428	+	6	3.04E-04
EN2	chr7	154896121	154896319	CGTGCTGTTC	139	-	56	3.04E-04
POLS	chr5	6815541	6815640	CGAGAACTTC	1190	+	6	3.04E-04
ADAM22	chr7	87576277	87576376	CGAGGTGTTC	1222	-	56	3.04E-04
LASS3	chr15	98792103	98792202	CGTGCTGTTC	692	+	10	3.04E-04
EMCN	chr4	101589972	101590170	CGACCTGTTC	984	-	56	3.04E-04
APC	chr5	112117665	112117862	CGAGAACTTC	1385	+	56	3.04E-04
THEX1	chr8	8936197	8936395	CACGCTCTTC	611	+	56	3.04E-04
RAB6B	chr3	135073303	135073501	CCAGCACGTC	1259	-	56	3.14E-04
LEMD1	chr1	203661117	203661316	TGAGCTGTTC	463	+	56	3.14E-04
SIX2	chr2	45091144	45091342	CGAGCCGATC	1033	-	51	3.14E-04
ZIC3	chrX	136455913	136456111	CCAGCACGTC	998	-	31	3.14E-04

GNA13	chr17	60491524	60491722	CGATCCCTAC	254	-	51	3.35E-04
UBE2E2	chr3	23290838	23291036	CTAGCTCAGC	1121	+	56	3.35E-04
FBXW11	chr5	171193819	171194017	CCAGCTCTGT	1251	+	48	3.51E-04
PDE1C	chr7	31771253	31771451	CGACGTCTTC	1462	-	56	3.51E-04
NRP1	chr10	33663297	33663495	GGGGCTCTTC	684	-	55	3.51E-04
SOX12	chr20	256123	256321	GGGGCTCTTC	1266	-	56	3.51E-04
CACNA1S	chr1	199309149	199309347	GGGGCTCTTC	1161	-	56	3.51E-04
SUPT3H	chr6	45003188	45003386	CGAGGCCATC	532	-	51	3.78E-04
C18orf1	chr18	13414687	13414885	CCATCACTGC	1469	-	46	3.78E-04
KCNMA1	chr10	78675048	78675246	ACAGCTCTCC	31	+	73	3.78E-04
LOC284274	chr18	71231684	71231882	TGAGGTCTTC	409	-	56	3.78E-04
DNAJC6	chr1	65623911	65624109	CAAGCCCTAC	271	+	56	3.78E-04
GYG2	chrX	2760220	2760418	CCAACCCTGC	919	-	56	3.92E-04
SETD3	chr14	98897684	98897784	CTAGCTTTTC	733	+	87	3.92E-04
INSIG1	chr7	154734848	154735046	TGAGCCCTCC	260	-	55	3.92E-04
BAT1	chr6	31617611	31617808	CGCGCTCTCC	911	-	54	4.12E-04
TEKT4	chr2	94915104	94915302	CGAGCAATTC	1030	+	56	4.12E-04
LRP8	chr1	53514852	53515051	CCAGCCCCGC	323	-	20	4.12E-04
SAMD13	chr1	84537615	84537813	CAAACACTTC	973	-	56	4.31E-04
PAX5	chr9	37018149	37018281	CTAGATCTTC	1351	+	88	4.31E-04
RPP25	chr15	73036356	73036554	CTAGCACATC	141	+	56	4.52E-04
KCNK10	chr14	87831997	87832194	CCATCCCCTC	976	+	55	4.52E-04
KIAA1199	chr15	78866319	78866517	CCAGCCATTC	1284	+	75	4.52E-04
OPN5	chr6	47925808	47926006	AGAGCTCTTT	1487	-	56	4.52E-04
PCBP4	chr3	51976109	51976307	CCAGCGCCTC	719	+	56	4.52E-04
WDR42B	chrX	27927025	27927223	CGTGCACTGC	72	+	56	4.73E-04
SLC23A2	chr20	4824439	4824637	CCAACTCCTC	187	-	76	4.73E-04
C9orf23	chr9	34594735	34594933	CCAGCACTTT	693	-	56	4.73E-04
KIDINS220	chr2	8839040	8839238	CAATGTCTTC	1433	+	56	4.73E-04
ARL16	chr17	77261288	77261411	CGGGGTCTTC	1355	-	54	4.99E-04
PGM1	chr1	63832102	63832300	CCAGCCCGGC	907	-	20	4.99E-04
TSPAN15	chr10	70909302	70909500	CAATCCCATC	967	-	56	4.99E-04
FZD6	chr8	104423178	104423376	CGACCTCTTT	817	-	56	4.99E-04
POU3F4	chrX	82631297	82631495	CGGGGTCTTC	452	-	56	4.99E-04
XPO4	chr13	20374293	20374491	CAATCCCTCC	208	+	57	4.99E-04
KIAA0020	chr9	2807888	2807991	CAAACTCATC	977	+	23	5.28E-04
DDB1	chr11	60834222	60834419	TGAGCTCTTT	1472	-	55	5.28E-04
MRPL23	chr11	1931765	1931963	CAAACTCATC	682	-	51	5.28E-04
B4GALT1	chr9	33191015	33191213	ACATCCCTTC	42	-	56	5.28E-04
HCN2	chr19	550732	550930	GGACCCCTTC	371	-	56	5.28E-04
SPARC	chr5	150986814	150987012	CAAACTCATC	646	+	56	5.28E-04
C1orf21	chr1	182752559	182752757	TGAGCTCTTT	640	+	56	5.28E-04
NFKBIA	chr14	34936464	34936662	CGAGCTCATA	355	-	51	5.47E-04
IPMK	chr10	59589954	59590152	CCAGCTCAAC	781	-	56	5.47E-04
TRPC5	chrX	111133352	111133550	CGATCTCTGT	915	+	6	5.47E-04
AARSL	chr6	44403597	44403795	GGAGCACTCC	711	+	56	5.47E-04
DLGAP1	chr18	3539547	3539745	CATGCACTTC	1136	+	56	5.83E-04
CA8	chr8	61267996	61268194	TGAACCCTTC	1246	+	56	5.83E-04
CCR9	chr3	45901753	45901951	CTAGCTGTGC	821	-	56	5.83E-04
CSNK1E	chr22	37062373	37062570	CGAGGCCCTC	1060	-	50	5.83E-04

SAMD13	chr1	84537615	84537813	CAAGACCTTC	974	-	56	5.83E-04
YWHAE	chr17	1228022	1228220	CCCGCTCTGC	1280	+	64	5.83E-04
UBE2R2	chr9	33896944	33897142	CGAGATCCTC	235	-	55	5.83E-04
TBC1D22A	chr22	45551427	45551527	CGATTTCTTC	1368	+	7	5.83E-04
TMEM105	chr17	76951897	76952095	CGACCCCCTC	892	-	56	5.83E-04
ST6GAL1	chr3	188184262	188184398	AGAGCTTTTC	1476	-	86	6.04E-04
C12orf12	chr12	89871987	89872185	CGAGCGCCGC	167	-	56	6.35E-04
ASB14	chr3	57281520	57281718	CTAGCTCTTA	483	-	56	6.35E-04
FUT8	chr14	65320045	65320243	CCAACCCATC	701	+	61	6.35E-04
COX6A1	chr12	119351765	119351963	CCATCGCTGC	1448	-	56	6.35E-04
BUB3	chr10	124909946	124910144	CGAGATGTTC	834	+	56	6.35E-04
SLC40A1	chr2	190106914	190107111	CGAGCTTGTC	1312	-	54	6.35E-04
AK5	chr1	77643233	77643431	TGATCTCTCC	361	-	56	6.63E-04
RFWD2	chr1	174451258	174451456	AGAGATCTTC	84	+	56	6.63E-04
ZFYVE26	chr14	67322548	67322746	CGAGGTTTTC	742	-	56	6.63E-04
HS6ST3	chr13	95597824	95598022	CGATCCCACC	634	-	51	6.63E-04
DNAJC6	chr1	65623911	65624109	CTAACACTTC	270	+	56	6.63E-04
KIAA1370	chr15	50758054	50758252	GGAGCTGTGC	241	-	56	6.99E-04
C18orf1	chr18	13521537	13521735	CAACCTCTCC	206	-	55	6.99E-04
TMEM63C	chr14	76721217	76721415	CGACCCCGTC	1141	+	56	6.99E-04
ULK1	chr12	130967702	130967897	CGTGGCCTTC	1062	+	86	7.28E-04
GSTA4	chr6	52920667	52920865	CCGGCCCTGC	95	-	56	7.28E-04
OCA2	chr15	25671375	25671573	CGTGGCCTTC	957	-	51	7.28E-04
C20orf94	chr20	10407444	10407642	CCATCTCACC	995	-	56	7.28E-04
PTPRE	chr10	129601296	129601494	CGATCACTTT	602	-	46	7.28E-04
WDR8	chr1	3546472	3546670	CGTGCACATC	1167	+	56	7.76E-04
CRKL	chr22	19630331	19630529	CAATCTCAGC	126	+	56	7.76E-04
LTBP3	chr11	65079852	65080050	AGAACTCTGC	217	+	35	7.76E-04
SLC4A1	chr17	39695144	39695342	CCATCTGTGC	166	-	56	7.76E-04
HIPK2	chr7	138943619	138943817	CTATCCCATC	819	-	44	7.76E-04
KIAA0427	chr18	44522464	44522662	GGATCTGTTC	549	-	56	7.76E-04
ECE1	chr1	21473582	21473780	CTAGCAGTTC	553	+	56	7.76E-04
SLC30A9	chr4	41738452	41738650	GGATCTGTTC	1413	-	56	7.76E-04
MTDH	chr8	98704155	98704353	CCAGTCCTTC	865	+	57	7.76E-04
NEURL	chr10	105296673	105296871	TGAGGCCTTC	842	+	48	7.76E-04
CDC7	chr1	91806329	91806527	CAAGCACTTT	233	-	8	8.14E-04
NEDD4L	chr18	54147159	54147357	CCGGCGCTTC	354	+	56	8.14E-04
RUTBC2	chr22	23550369	23550567	CCACCCCATC	1264	+	28	8.49E-04
FLJ45187	chr10	21853611	21853770	CAATCCGTTC	912	-	70	8.49E-04
NR1I3	chr1	159467756	159467954	CCAGATCTCC	160	-	56	8.49E-04
TMSB10	chr2	85016972	85017169	CGATCACAGC	1314	-	55	8.49E-04
CAV3	chr3	8732364	8732562	CCGACTCTTC	1488	-	56	8.49E-04
ADAMTS14	chr10	72144985	72145183	CGAACACCTC	74	+	56	8.87E-04
NRSN1	chr6	24188304	24188502	AGAGCCCTAC	1412	-	51	8.87E-04
WDR64	chr1	239929713	239929911	CGATGGCTTC	513	-	56	8.87E-04
PCF11	chr11	82517947	82518145	TCAGCCCATC	703	+	61	8.87E-04
TMEM39B	chr1	32304936	32305134	AGATCTCCTC	1056	-	56	8.87E-04
DRD3	chr3	115311960	115312157	CGGGCTTTTC	1309	-	55	9.21E-04
WWOX	chr16	76685249	76685348	AAAACTCTTC	1087	-	36	9.21E-04
CLSTN2	chr3	141229913	141230111	CGGGCTTTTC	936	+	56	9.21E-04

SUPT3H	chr6	45003188	45003386	CTAGCTCTGT	533	-	56	9.21E-04
MBNL1	chr3	153457506	153457704	CGAGCTTTTT	1115	+	56	9.21E-04
SYT9	chr11	7393079	7393277	CCAGCTCTTG	540	+	56	9.70E-04
PSMD14	chr2	161971040	161971238	AGAGCTCTTA	1027	-	56	9.70E-04
FLNC	chr7	128276698	128276896	CCAGCTCTTG	1100	+	56	9.70E-04
CACNA2D1	chr7	81859671	81859869	CATTCCCTTC	341	-	51	9.70E-04
STK10	chr5	171544541	171544739	GGAACTCATC	292	-	56	9.70E-04
SERPINB3	chr18	59477414	59477612	CAGGCTCATC	889	+	58	9.70E-04
KIAA1706	chr7	36221217	36221415	CGAGCCGAGC	164	+	56	1.01E-03
HSF2BP	chr21	43761463	43761661	CGATCTGGTC	369	-	54	1.01E-03
CTNND2	chr5	11979085	11979283	CCTGCTCTAC	1254	-	56	1.07E-03
C7orf26	chr7	6610718	6610916	CGACCTCTTA	194	+	56	1.07E-03
ATXN7L2	chr1	109834108	109834255	CACTCTCTTC	1344	-	55	1.07E-03
NR1H2	chr19	55572397	55572595	CAAACCCTCC	628	-	56	1.07E-03
GRID1	chr10	87991092	87991290	ACAACCCTTC	395	-	56	1.11E-03
PDE1C	chr7	31771253	31771451	CGATCCGATC	1464	+	61	1.11E-03
SLC8A1	chr2	40236748	40236946	GGAGCTCTGT	1129	-	56	1.11E-03
NEU3	chr11	74407911	74408109	ACAGCCCCTC	727	+	56	1.17E-03
GPR158	chr10	25619503	25619701	CGACCACCTC	903	-	56	1.17E-03
LOC284274	chr18	71231684	71231882	AGATCCCTCC	407	+	67	1.17E-03
ASPH	chr8	62758582	62758780	CGGTCGCTTC	1004	+	56	1.21E-03
FOXP4	chr6	41598419	41598617	CCATCTGATC	346	+	61	1.21E-03
CCDC128	chr2	48521650	48521848	CGAGCGCGCC	1032	+	56	1.21E-03
LOC553158	chr22	43520250	43520448	CCATCTGTCC	1017	+	65	1.21E-03
ARPP-21	chr3	35855974	35856170	CGACCAGTTC	1174	+	57	1.27E-03
JARID2	chr6	15323170	15323269	CGAGGGCTCC	253	+	6	1.27E-03
BTBD14A	chr9	138143615	138143813	CGACCGCTCC	569	-	56	1.27E-03
C1orf198	chr1	229074319	229074419	AGAGCACGTC	987	+	58	1.27E-03
ITGAL	chr16	30432385	30432583	CAATCCCTAC	490	-	37	1.27E-03
MEA1	chr6	43088150	43088348	CGATATCTCC	656	+	56	1.27E-03
GLIS2	chr16	4303834	4304032	CGACCGCATC	319	-	56	1.27E-03
SHB	chr9	37983187	37983332	CGTTCCCATC	1345	-	24	1.27E-03
PKNOX2	chr11	124726677	124726870	TGATCCCATC	1473	-	8	1.32E-03
ASPH	chr8	62758582	62758780	CGTACTCATC	1006	+	56	1.32E-03
WDR4	chr21	43112224	43112422	CATGGTCTTC	583	+	74	1.32E-03
SCOC	chr4	141500364	141500562	AGAGACCTTC	619	+	56	1.32E-03
FLJ35740	chr9	38561067	38561265	CCAGCACCCC	12	-	42	1.32E-03
SMC6	chr2	17798306	17798504	CGAAGTCTCC	950	+	30	1.32E-03
GRIK5	chr19	47212588	47212786	CGAAGTCATC	1132	-	46	1.32E-03
AP2A1	chr19	54961775	54961915	CGAACCCCGC	1350	+	27	1.32E-03
LRRC3	chr21	44705894	44706092	CGTGCACGTC	878	-	54	1.39E-03
GNAL	chr18	11767702	11767900	TGAACTCATC	442	+	61	1.39E-03
ICAM2	chr17	59436346	59436544	CCTTCTCATC	1138	+	56	1.39E-03
ADAMTS18	chr16	75986539	75986733	CAACCCCATC	1326	-	36	1.39E-03
VLDLR	chr9	2634788	2634986	CCAGGTTTTC	926	-	30	1.45E-03
C9orf23	chr9	34601725	34601923	GGATCCGTTC	117	-	56	1.52E-03
ECE1	chr1	21473582	21473780	GCAGCCCTAC	552	-	56	1.52E-03
LMCD1	chr3	8498906	8499104	CAATCACCTC	1016	-	31	1.52E-03
LRP1B	chr2	141618367	141618565	AGTGCTCATC	499	-	54	1.58E-03
ADD2	chr2	70827325	70827523	CCTGGCCTTC	1031	+	70	1.58E-03

RHOJ	chr14	62760831	62761029	CAAGCTGTTT	505	+	10	1.58E-03
LRRC62	chr22	36120214	36120412	GGAGGCCTGC	1429	+	36	1.58E-03
NYD-SP18	chr7	128152200	128152398	CAAGCACTTA	400	+	73	1.64E-03
KIDINS220	chr2	8839040	8839238	TCAGATCTTC	1432	-	48	1.64E-03
ITPK1	chr14	92495897	92496095	CGATCCCAAC	787	+	66	1.64E-03
ATRN	chr20	3490966	3491164	TGATCTCTAC	266	+	56	1.64E-03
SURF4	chr9	135231349	135231474	CCATCGGTTC	1187	-	42	1.64E-03
GLB1	chr3	33022928	33023126	AGAACGCTTC	1377	+	56	1.64E-03
ARHGEF11	chr1	155230127	155230325	CCTGCACATC	538	+	6	1.64E-03
CBX3	chr7	26208478	26208675	CGACCCCCGC	1307	-	45	1.72E-03
IL28RA	chr1	24377351	24377549	CTAGCTATGC	744	-	56	1.72E-03
CYP2R1	chr11	14882363	14882561	CTAGCCCTGT	1051	+	70	1.79E-03
FLJ21839	chr2	27126350	27126548	TGACCTCTCC	229	+	56	1.79E-03
POMC	chr2	25217560	25217759	CGAGCCGGGC	471	+	43	1.79E-03
CTNNB1	chr3	41260814	41261005	GGCTCTCTTC	1498	-	36	1.88E-03
CSNK2A1	chr20	472140	472338	CGCGCTCCGC	1026	+	58	1.88E-03
C7orf26	chr7	6610718	6610916	CTAGTCCTTC	193	-	56	1.88E-03
BAT1	chr6	31617611	31617808	CATACCCTTC	910	+	77	1.95E-03
GLI2	chr2	121506923	121507121	TCAGCTCCGC	387	+	41	1.95E-03
USP25	chr21	16065493	16065691	AGATCTTTTC	1067	-	24	1.95E-03
MYO1E	chr15	57250613	57250712	CGAAGTCCTC	559	-	29	1.95E-03
ISG15	chr1	941397	941590	CCACCTCACC	1178	+	8	1.95E-03
FLJ45964	chr2	240151299	240151497	CGGGCTGTCC	351	-	55	2.04E-03
ZIC2	chr13	99476743	99476941	GGAGGTGTTC	830	+	56	2.04E-03
GRK5	chr10	121191304	121191502	CGAGCTCTCG	481	-	55	2.04E-03
C10orf71	chr10	50186732	50186930	CGAGATCTTA	729	+	56	2.04E-03
NOVA2	chr19	51171396	51171594	CGAGCGATGC	667	-	56	2.04E-03
IKBKE	chr1	204709963	204710161	GGAGCTATGC	1451	-	56	2.04E-03
PGM1	chr1	63832102	63832300	CTACCCCTCC	906	+	57	2.04E-03
SGIP1	chr1	66876501	66876600	GGAGCCCTGT	980	+	7	2.12E-03
PRKACG	chr9	70825079	70825182	AGAGCTCTCT	1440	-	6	2.12E-03
MAPKAP1	chr9	127204345	127204543	GGATCTGTGC	1243	-	56	2.21E-03
FBLN1	chr22	44306710	44306908	TGAGCTCAAC	876	+	56	2.30E-03
DSCAML1	chr11	117101416	117101614	GCAGCTGATC	55	-	67	2.30E-03
APC	chr5	112117665	112117862	TGAGCACAGC	1387	+	39	2.30E-03
SORCS2	chr4	7628777	7628975	CGATGACTCC	403	-	45	2.41E-03
LRP1	chr12	55876133	55876331	CACGCTCGTC	963	-	56	2.61E-03
SPATA5	chr4	124177285	124177478	CATGCACTCC	1452	+	32	2.61E-03
CHRNB3	chr8	42629366	42629564	CTAGCTTCTC	750	+	70	2.71E-03
PHGDHL1	chr13	98766611	98766809	TTGGCTCTTC	356	-	56	2.71E-03
AP2A1	chr19	54961775	54961915	CGATCTTTTT	1349	+	38	2.82E-03
HIPK2	chr7	138948281	138948479	CCCTCTCTCC	612	-	69	2.82E-03
SPTBN1	chr2	54741570	54741673	CAATGGCTTC	1074	-	46	2.94E-03
BAI3	chr6	69930646	69930844	GGTGCTCTTT	573	+	56	3.06E-03
CNTN4	chr3	2202052	2202250	AGTTCTCTGC	939	-	39	3.06E-03
RP1L1	chr8	10468283	10468481	CTAGCTTGTC	1007	-	56	3.19E-03
FLNC	chr7	128276698	128276896	CATGCTGTGC	1098	-	46	3.19E-03
USMG5	chr10	105139829	105140027	AAAGCTCTTA	1082	-	54	3.19E-03
NXT2	chrX	108713208	108713406	CTGGCTCTAC	1240	-	56	3.32E-03
ITPK1	chr14	92495897	92496095	CCATCTGAGC	788	-	8	3.32E-03

HIPK2	chr7	138922786	138922984	GTAGCTCACC	1201	+	86	3.32E-03
HECTD1	chr14	30774368	30774566	GGATCTGTCC	725	-	56	3.32E-03
GLYCTK	chr3	52287771	52287946	CGAGACGTGC	1181	+	37	3.46E-03
HNT	chr11	131136881	131137079	CGAGCCTGGC	900	+	66	3.46E-03
BRE	chr2	28163532	28163730	CGTGCAATTC	434	-	1	3.46E-03
TRIM24	chr7	137772960	137773059	AGAGCGTTTC	1427	-	85	3.57E-03
ZNF428	chr19	48807927	48808125	TCAGGTCATC	1275	+	61	3.57E-03
AKAP7	chr6	131525716	131525914	CACGCTCTTT	655	+	56	3.57E-03
ESX1	chrX	103434903	103435101	CGAAATCCTC	1091	-	41	3.57E-03
ROCK1	chr18	16772019	16772216	CATTGTCTTC	1214	-	27	3.86E-03
LOC399744	chr10	38828622	38828809	CGAGTCCTTT	1475	-	67	3.86E-03
B3GALT1	chr2	168433850	168434048	CGAGTTCTTA	1272	-	54	4.03E-03
EMCN	chr4	101589972	101590170	CGAGTTCTTA	983	+	56	4.03E-03
FBXO34	chr14	54877683	54877881	AGACCCCCTC	1288	-	56	4.19E-03
ENTPD6	chr20	25133440	25133543	TCACCCCTGC	399	-	5	4.34E-03
ATF7IP	chr12	14381001	14381199	GCCGCACTTC	590	-	48	4.34E-03
NFIC	chr19	3385234	3385432	AGAACGCTGC	887	+	87	4.34E-03
ADAM10	chr15	56829436	56829634	CCAAGTCGTC	895	+	56	4.51E-03
GHR	chr5	42695070	42695268	CTACCCCTAC	365	+	56	4.51E-03
LOC375449	chr5	66048493	66048691	GGTACTCTGC	1219	-	15	4.68E-03
FRAS1	chr4	79304320	79304518	CAAACGGTTC	1114	-	15	4.85E-03
PTEN	chr10	89615819	89616017	AAACCTCTCC	279	-	55	4.85E-03
GABRG3	chr15	24910190	24910387	CGTTCCCCGC	1418	-	45	4.85E-03
UTRN	chr6	144879477	144879675	AGGTCACTTC	1249	-	56	5.02E-03
TMEM117	chr12	42910073	42910187	CAAGCCCCTA	1358	+	41	5.02E-03
MBNL2	chr13	96638562	96638665	CGTTCCATTC	1364	+	42	5.24E-03
CD24	chrY	19593375	19593573	CAAACTGCTC	1234	-	55	5.24E-03
PASK	chr2	241728637	241728835	CGGACCCGTC	299	-	56	5.43E-03
MTX2	chr2	176842276	176842377	CGCGCCGTCC	691	-	79	5.43E-03
COX10	chr17	13969188	13969386	CTGTCGCTTC	585	-	56	5.43E-03
WDR31	chr9	115142278	115142473	GAATCACTCC	1323	+	54	5.43E-03
TBC1D22A	chr22	45551427	45551527	CGCGCTCTGA	1369	-	48	5.66E-03
KCNK12	chr2	47600744	47600843	CGACCTGACC	1456	+	75	5.86E-03
WWOX	chr16	76685249	76685348	CATTCCGTTC	1084	+	71	6.08E-03
PCBD2	chr5	134288771	134288953	CCACATCATC	1180	-	49	6.08E-03
PTPRE	chr10	129601296	129601494	CGATCCCCGT	603	-	46	6.28E-03
STT3A	chr11	124967436	124967629	AAATATCTTC	1495	+	16	6.28E-03
SEC24B	chr4	110603704	110603902	CGAGTGCCTC	526	+	56	6.52E-03
GLB1	chr3	33022928	33023126	AGAGCCATCC	1374	-	49	6.52E-03
ABCD3	chr1	94674246	94674444	CTGACACTTC	594	+	56	6.52E-03
STT3A	chr11	124967436	124967629	AGAACACGTC	1496	-	65	6.75E-03
COL18A1	chr21	45724034	45724232	AGTGCTCTTA	1018	-	54	6.75E-03
MBIP	chr14	35824619	35824817	GTATCCCGTC	188	-	52	7.01E-03
RASSF8	chr12	25963808	25963920	CAATCTACTC	1504	+	12	7.01E-03
GLIS3	chr9	4295190	4295388	CGAGACCATT	1455	-	75	7.28E-03
NCOA1	chr2	24810830	24810929	TGAACCTTTC	1441	+	22	7.28E-03
PKP4	chr2	159290667	159290865	CTAGATATTC	766	-	56	7.80E-03
ATP8B1	chr18	53528764	53528882	TTAGCCATTC	1066	-	73	8.06E-03
GLB1	chr3	33022928	33023126	CATTCTATTC	1376	+	61	8.35E-03
RABL4	chr22	35509036	35509234	CATTCTATTC	807	+	26	8.35E-03

IL1RAPL1	chrX	29336839	29337037	CCTGATCCTC	1481	-	28	8.35E-03
OPLAH	chr8	145177345	145177542	CATTCCCTTT	1407	+	83	8.64E-03
RNF157	chr17	71721486	71721684	CTATGCCGTC	1414	-	52	8.96E-03
EFHA1	chr13	20949542	20949641	GCATCATTTC	991	-	46	9.62E-03
ENG	chr9	129639605	129639803	AGAGCAGTTT	705	+	86	9.93E-03
BTBD3	chr20	11823568	11823667	TTATCTCACC	1421	-	34	1.14E-02
SERPINH1	chr11	74963243	74963441	CGATCTGTAT	636	+	56	1.14E-02
AMY2B	chr1	103908725	103908923	AGACCCCTTA	1419	-	12	1.14E-02
STK10	chr5	171544541	171544739	CGAGTCCATT	291	+	45	1.30E-02
METRNL	chr17	78636811	78637009	GGGGCGCGTC	630	-	56	1.30E-02
ADAM22	chr7	87576277	87576376	CAGGCGTTTC	1225	-	59	1.34E-02
MBNL1	chr3	153457506	153457704	CGCACACTAC	1117	-	56	1.62E-02
BARHL2	chr1	90967805	90968003	CGATCGTCGC	905	+	66	1.84E-02
GRIN2A	chr16	9890403	9890601	CCAGCTATAT	1224	-	91	1.84E-02
SLIT2	chr4	20043314	20043417	CCTGCACGAC	1400	+	79	1.90E-02
DEFB115	chr20	29269739	29269935	CTTTCGCGTC	1175	-	55	2.08E-02
EMCN	chr4	101589972	101590170	GAATATATTC	985	+	58	4.59E-02

Table S5. TF binding sites in the TCF4 binding regions

Term	Count	%	*P* Value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
GO: 0030528~transcription regulator activity	97	11.52019002	0.001866848	HMX2, HOXD13, CBX3, CITED2, CTNNB1, HOXC9, GATA6, ZNF397, CREB3L1, RARB, ATOH8, RXRA, BARHL2, SIX2, ZNF193, ZNF236, CAMTA1, TSHZ1, ELL, ELK3, SOX9, SOX8, NR1H2, TCERG1, MEIS2, MAML3, SLC30A9, NKX2-2, RUNX3, SUB1, LMCD1, NR4A1, NEUROG1, SKI, EN2, ESX1, NEUROG3, FOXP4, USF2, ATF6, NR1I3, LASS3, TRPS1, CRYM, TAF1A, SOX21, NR6A1, PAX6, PAX5, GLI2, SKAP1, ZNF207, GTF2A1, PAX7, FOXB1, NRG1, MKL1, ATF7IP, ELP3, SOX12, LEF1, TLE1, ZFP37, BRWD1, NCOA1, TAF12, NCOA2, ZMIZ2, NAB1, HIPK2, ZNF711, KCNH8, ZFPM2, GLIS3, SUPT3H, GLIS2, CDH1, NFYB, ZBTB16, PRDM16, TSC22D1, NR1D1, BCL2, POU3F4, LIMD1, ETV6, NFATC1, JARID2, TBX5, TRIM24, PKNOX2, PKNOX1, IRF5, IRF2, IRF4, NFIC, NFIA	620	1512	12983	1.343393711
GO: 0016563~transcription activator activity	34	4.038004751	0.002291256	SUPT3H, GLIS2, CDH1, PRDM16, SOX9, GLI2, SKAP1, CITED2, CTNNB1, NR1H2, TCERG1, HOXC9, GTF2A1, GATA6, BCL2, MAML3, RARB, MKL1, NFATC1, SUB1, TBX5, RXRA, LEF1, NR4A1, TRIM24, NEUROG3, USF2, ATF6, NCOA1, NR1I3, TAF12, NCOA2, ZMIZ2, IRF4	620	410	12983	1.736514555