



## Supporting Online Material for

### **Genome-Wide Mapping of in Vivo Protein-DNA Interactions**

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Tables S1 to S7  
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**Correction (15 June 2007):** Reference citations on p. 4 are now corrected (copy-editor's error).

## Materials and Methods

### Cell culture and chromatin immunoprecipitation

The Jurkat human T lymphoblast cell line was cultured according to standard protocols. NRSF/REST chromatin immunoprecipitation was performed as previously (S1) with a custom monoclonal antibody (S2). For Experiment 1, 70 separate chromatin immunoprecipitations, corresponding to a single batch of chromatin, were pooled for a single Solexa library preparation. For Experiment 2, four chromatin immunoprecipitations, corresponding to one batch of chromatin, were pooled for a single Solexa library preparation. For both experiments, the controls used chromatin that was reverse cross-linked, phenol extracted, and purified on a QIAQuick PCR cleanup column (Qiagen). The control chromatin matched the chromatin preps of the ChIPs used for each experiment.

### Library preparation for Solexa/Illumina sequencing

The Solexa library was prepared as per instructions ([www.illumina.com](http://www.illumina.com)). The size selection of this library was performed by gel electrophoresis and subsequent excision and purification of DNA (QIAex II, Qiagen) in the ~200- to 700-bp range (Fig. S1A, left panel). The control library for Experiment 1 was constructed in an identical manner, using ~2- $\mu$ g input DNA. For Experiment 2, we modified the Solexa library construction protocol to include a PCR preamplification [30 sec at 98°C; (10 sec at 98°C, 30 sec at 65°C, 30 sec at 72°C) x 25 cycles; 5 min at 72°C] following linker ligation and preceding gel electrophoresis. Size selection was performed by gel electrophoresis and subsequent excision and purification of DNA in the ~150- to 300-bp range (Fig. S1A, right panel). The control library for Experiment 2 was prepared in an identical manner, using ~50 ng input control DNA. Reducing the size and narrowing the size range of DNAs collected from gel purification is intended to improve positional resolution of ChIPSeq. By enriching for smaller pieces of input DNA bound to the factor of interest, it is expected that site location will gain resolution. Tighter size selection, as used in the second experiment, also improved the size uniformity of molecular colonies produced on the Solexa/Illumina platform. Such colony size uniformity also increased the effective read number obtained. Shorter input DNA size also apparently produces more robust colonies on the Solexa/Illumina platform, and this may mean that shorter DNA pieces within any given input sample distribution will be represented more efficiently in the final sequence output than are longer input pieces from the same distribution. We have not titrated an optimal size cut.

We used QPCR (S1) to estimate the enrichment of five loci in these two libraries (Fig. S1B). QPCR loci are (in genome build hg17, NCBI v35): chr1:151353339-15153415 (QPCR1), chr1:158498975-158499043 (QPCR2), chr16:88520383-88520482 (QPCR3), chr17:3247959-3248037 (QPCR4), and chr2:165920458-165920534 (QPCR5). To calculate fold enrichment, each primer pair was normalized against two putative "negative" primer pairs, chr7:115817618-115817717 (NEG1), and chr7:115712789-115712882 (NEG2).

### Enriched region identification

Solexa ChIP and Control reads were analyzed jointly for each experiment to identify regions that have an over-representation of reads in the ChIP sample versus the control

sample using a set of python scripts (available at <http://woldlab.caltech.edu/ChIPSeq>). Candidate enriched regions were identified as aggregations of 13 or more ChIP reads not separated by more than 100 bp and were assigned the number of reads as a score. The threshold of 13 reads was selected on the basis of the ROC analysis described in the text and in Fig. 2; this threshold will need to be selected in future studies based on the structure of each data set, and with consideration of the false-discovery rate that will be tolerated in a given study. Regions that were (a) with at least 20% or more control reads within the same boundaries (these regions corresponded typically either to satellite repeats or to the mitochondrial genome) or (b) with peaks having less than five partly overlapping reads were filtered out and did not participate in subsequent analyses. Criterion (a) resulted in the elimination of 254 regions from Experiment 1 and 108 regions from Experiment 2, all of which occurred in repeat regions of the human genome.

Regions found to be enriched in both experiments comprise the “intersect” or shared set of NRSF ChIPSeq-positive regions, which was used for the gene analysis and site identification.

### **Site analysis**

We performed all motif-oriented analyses by using Cistematic (S1). The NRSE2 PSFM (position specific frequency matrix) derived in that work was used to identify and local canonical NRSE sites (match score thresholds specified in the text and Figure Legends), across human genome hg17 (NCBI v35). These site locations were then used to compare and call the distances from peaks of ChIPSeq read-tag distributions at each location. The analysis of NRSE2 locations relative to called peak site locations was done on the shared set of NRSF ChIPSeq positive regions.

We merged enriched shared regions within 500 bp of one another and combined Experiment 1 reads within these regions. We then applied a triangular 5-point smooth to Experiment 1 reads within these consolidated regions to identify the coordinate(s) with the greatest number of overlapping reads as the peak(s). If there was more than one coordinate with the maximum score in the region, we selected the first one as the peak.

For the initial analysis in Fig. 2D, canonical sites with scores ranging from 70% to 100% were collected, and revealed the existence of regions with high read counts but without canonical sites.

### **Whole-genome gene expression microarrays and analysis**

To assess whole-genome expression patterns in Jurkat cells, we first purified total RNA from three separate growths of cells. Briefly, cells were homogenized in TRIZOL (Invitrogen) with a QIAshredder (Qiagen). We then isolated total RNA from the homogenate by using RNeasy Mini Kits (Qiagen), and labeled and amplified this material (Illumina TotalPrep RNA amplification kit, Ambion). The labeled cRNA was then hybridized to Illumina Sentrix RefSeq8 whole-genome gene expression microarrays according to standard procedures. We then extracted and normalized the data with the rank-invariant method (Illumina BeadStudio software). A database of transcription start sites from SwitchGear Genomics ([www.switchdb.com](http://www.switchdb.com)) was used to obtain high-confidence (score >20; ~65% positive predictive value, D.S. Johnson, E. Anton, C. Medina, R.M. Myers, unpublished results) promoter predictions. We then parsed out predicted promoters and their corresponding RefSeq genes that occur near ChIPSeq

peaks. The 230 transcripts occurring near ChIPSeq peaks had a median expression intensity of 6.8, while the full set of 20,589 transcripts had a median expression intensity of 23.6 (Fig. S5). The difference of medians was significant ( $P = 1 \times 10^{-11}$ ) by the Mann-Whitney test (`wilcox.test` in R).

### **Motif searches by MEME & NRSE half-sites**

Enriched shared regions with >500 reads (a subset that was selected to keep compute resources modest but to focus on quantitatively robust signals) were analyzed with MEME (S3) from within Cistematic using the zoops model for 10 motifs of 8-28 bp in length. We repeated the same analysis with enriched shared regions with 300 or more reads but no 70% NRSE2 match within them to identify non-canonical motifs.

Following the results of the MEME analysis of the strongly enriched non-canonical regions, we divided NRSE2 into two half-sites, i.e. NRSE2-left (position 1 through 10) and NRSE2-right (position 12-21). Position 11 serves as motif-center, allowing us to compare distances between motifs in an orientation-independent manner. We also defined the distance between positions 5 of NRSE2-left and NRSE2-right (corresponding to position 16 of NRSE2). This gives a canonical distance of 11 bp between the two half-sites within NRSE2 and allowed us to consider shorter as well as longer distances. We tabulated the occurrences in Experiment 1 enriched regions of half-sites with distances of 1 up to 25 bp in various orientations, in addition to the canonical orientation (NRSE2-left followed by NRSE2-right) and compare their observed occurrences to their expected occurrences based on their genome-wide occurrences adjusted for the fractional size of the enriched regions (0.06% of the genome, for Experiment 1). We also analyzed other motif arrangements, such as right-left (opposite of canonical), left-left and right-right.

### **P-value estimation for NRSEs**

P-values for sites were estimated by counting the number of 25-nt sequence reads in a 400-bp window centered on the motif and comparing them to the observed frequency of that window count in the control. The P-values presented are from an extremely conservative calculation, in which the entire control dataset was used, unfiltered for sequence read pileups in repeat DNA sequences. We know the latter to be artifactual because they also occur at the same location in the ChIP experiments. Using instead a control from which these reads have been filtered, eliminates any and all 400-bp windows with more than 11 reads. This results in effective P-values of 0 for all ChIPSeq positive sites reported in table S2 and in the text.

### **Final site analysis**

Based on the enrichment of particular distances in the canonical arrangement, we used the following procedure to identify NRSEs in each region of the common enriched region set:

1. analyze each region with NRSE2left and NRSE2right PSFMs using a threshold of 70%.
2. accept any canonical half-sites with distances of 10, 11, 16, 17, 18, 19.
3. accept any 70% or higher canonical NRSE2 site that has not already been picked up by 2.

4. if there are still no site assigned, pick the nearest half-site to the peak of the region.
5. sites were filtered to only retain those with P-values lower than  $10^{-4}$ .

We returned a solo half-site for 260 of the 1,946 common regions.

### **Associated gene and gene ontology analysis**

We used Cistematic to identify the nearest RefSeq gene model in the human genome (UCSC hg17, NCBI v. 35) within 20 kb of each enriched regions in the shared set of ChIPSeq positive regions. We then analyzed this gene cohort for Gene Ontology enrichment using Cistematic, as previously described (S1). Briefly, we tabulate the count of each GO term in our gene cohort, calculated a P-value for that occurrence by chance in a gene cohort of that size, and applied a Bonferroni correction for multiple hypotheses testing. The full set of 6,038 human GO terms were used in the analysis.

### **Supplementary Table Legends**

**Table S1.** Summary table of reads used in the analysis for Experiment 1, Experiment 2, and of their corresponding controls.

**Table S2.** Enriched regions from Experiment 1 that are common with Experiment 2 with NRSE sites with P-value  $< 10^{-4}$ . 1,908 regions in common between both experiments that have a predicted NRSE ordered by number of hits in that region. A half-site distance of 11 corresponds to the canonical 21 bp NRSE, whereas a half-site distance of 0 corresponds to a single half-site only.

**Table S3.** Enriched regions from Experiment 1 that are in common with Experiment 2 without NRSE sites with P-value  $< 10^{-4}$ . Several of these regions have an NRSE, but not enough reads to pass our P-value threshold.

**Table S4.** Motif consensus sequences returned by MEME on 198 Experiment 1 enriched regions with 500 or more ChIPSeq reads. The top four motifs returned all correspond to the NRSE.

**Table S5.** Motif consensus sequences returned by MEME on 22 regions enriched in Experiment 1 with 300 or more ChIPSeq reads and no canonical NRSEs. The top two motifs correspond to the left and right half-sites of the canonical NRSE.

**Table S6.** Distribution of NRSE with respect to gene annotations. Only NRSEs that are within or less than 10 kb from a refseq gene model boundary were associated with a gene part or as “Upstream” or “Downstream”.

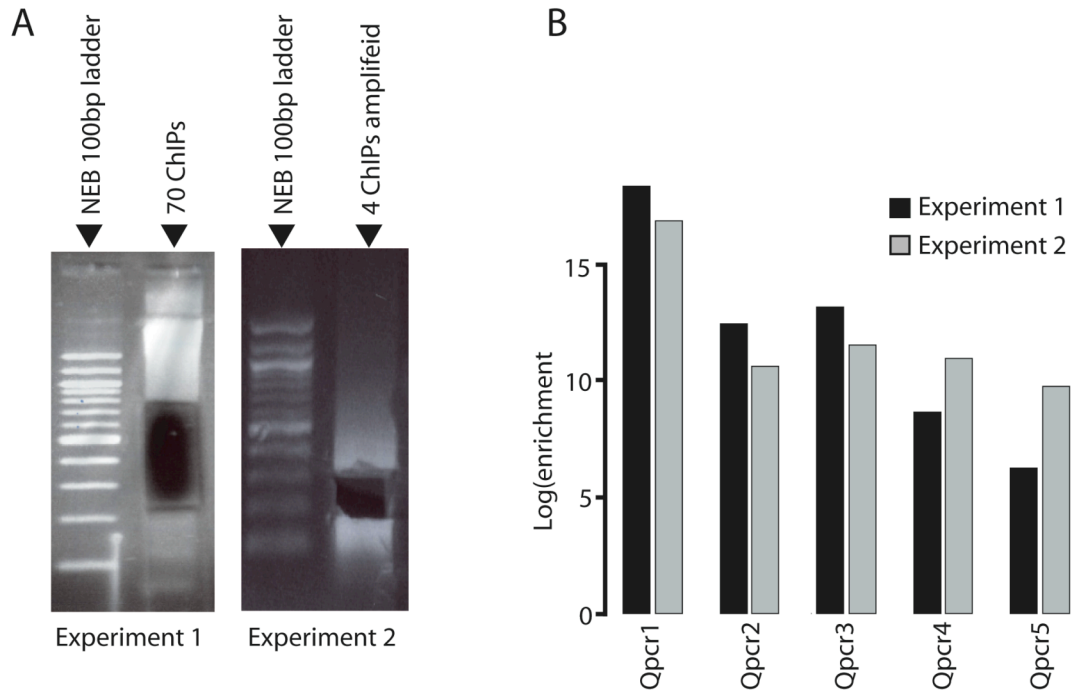
**Table S7.** Distribution of type of gene-associated NRSEs.

### **References**

- S1. A. Mortazavi, E. C. Thompson, S. T. Garcia, R. M. Myers, B. Wold, *Genome Res.* **16**, 1208 (2006).
- S2. Z. F. Chen, A. J. Paquette, D. J. Anderson, *Nat. Genet.* **20**, 136 (1998).
- S3. T. L. Bailey, C. Elkan, *Mach. Learn.* **21**, 51 (1995).

## Supplementary Figures

### Figure S1



### Figure S2

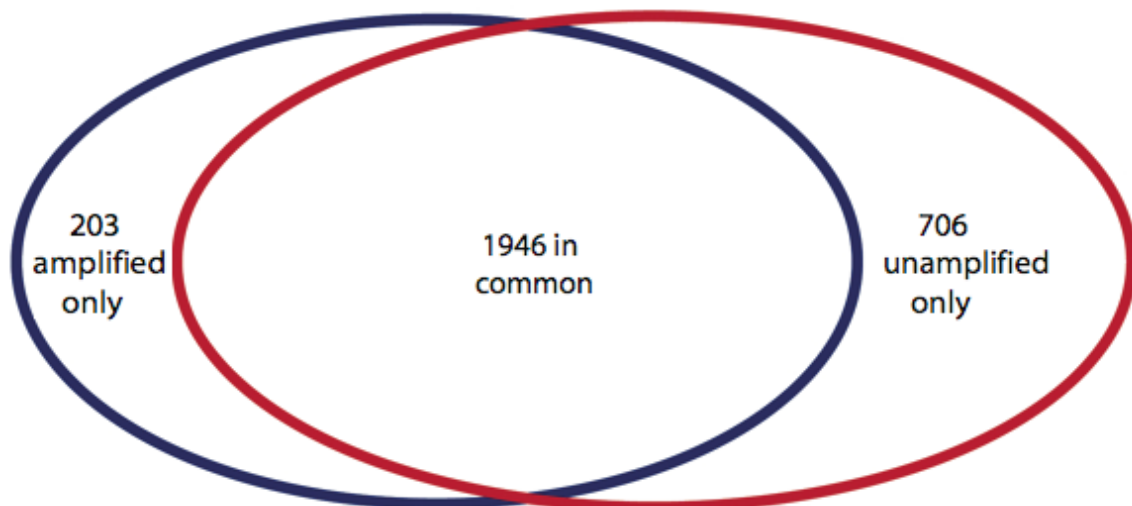


Figure S3

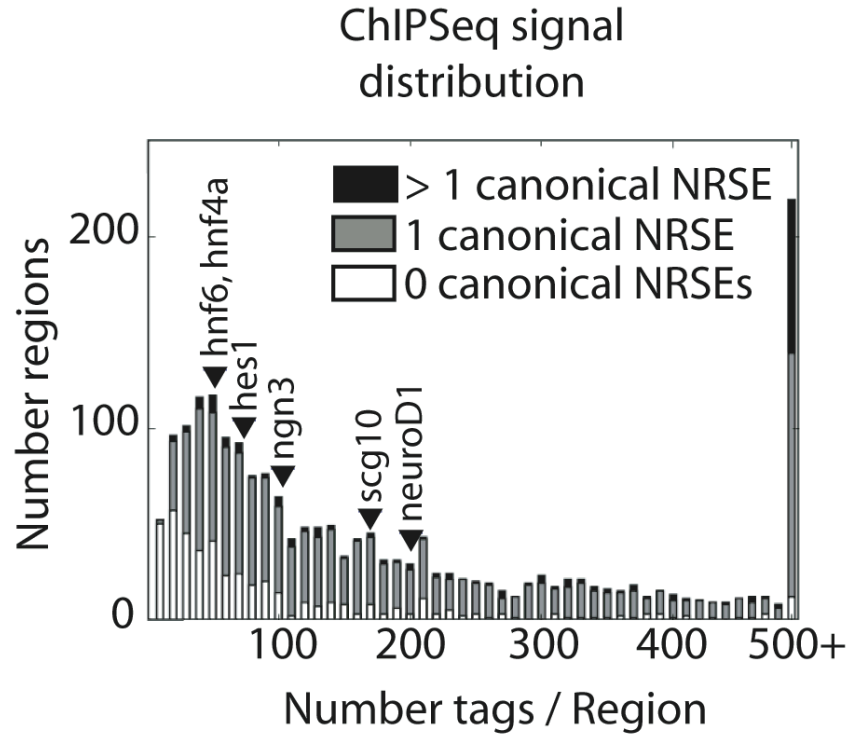
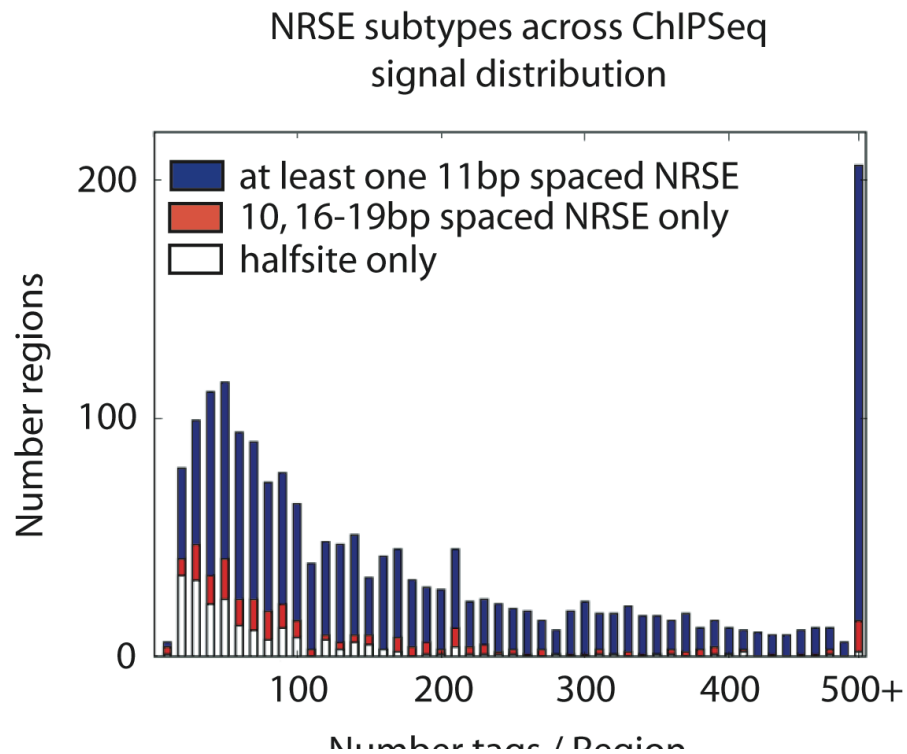


Figure S4



**Figure S5**

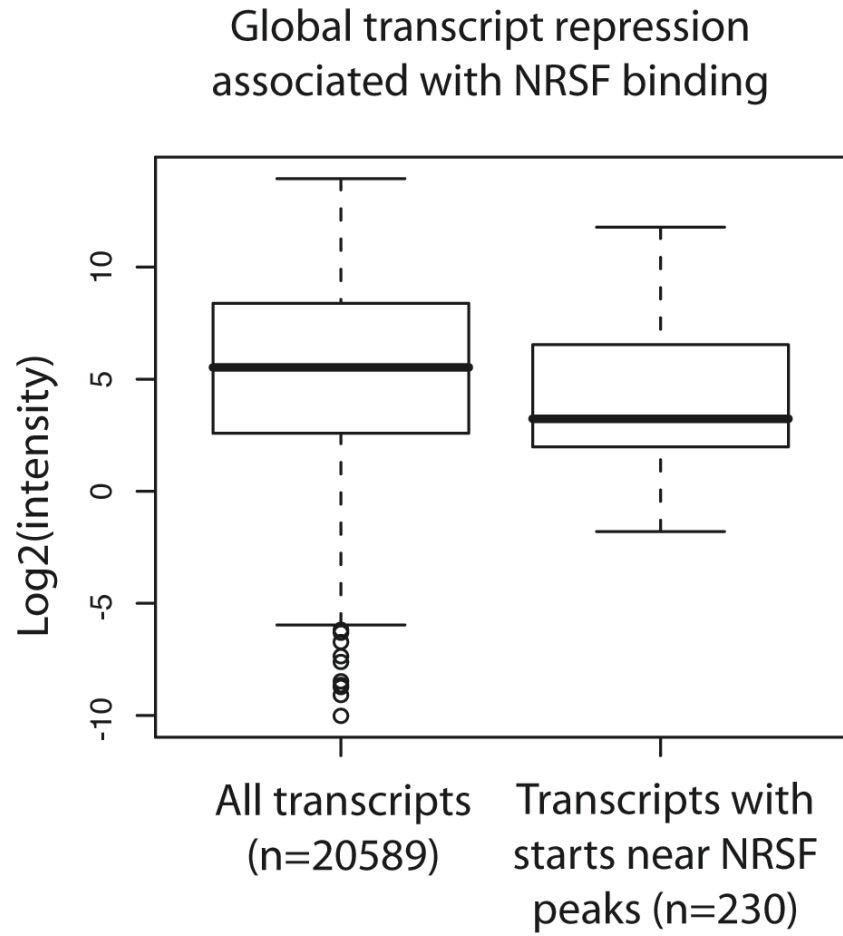
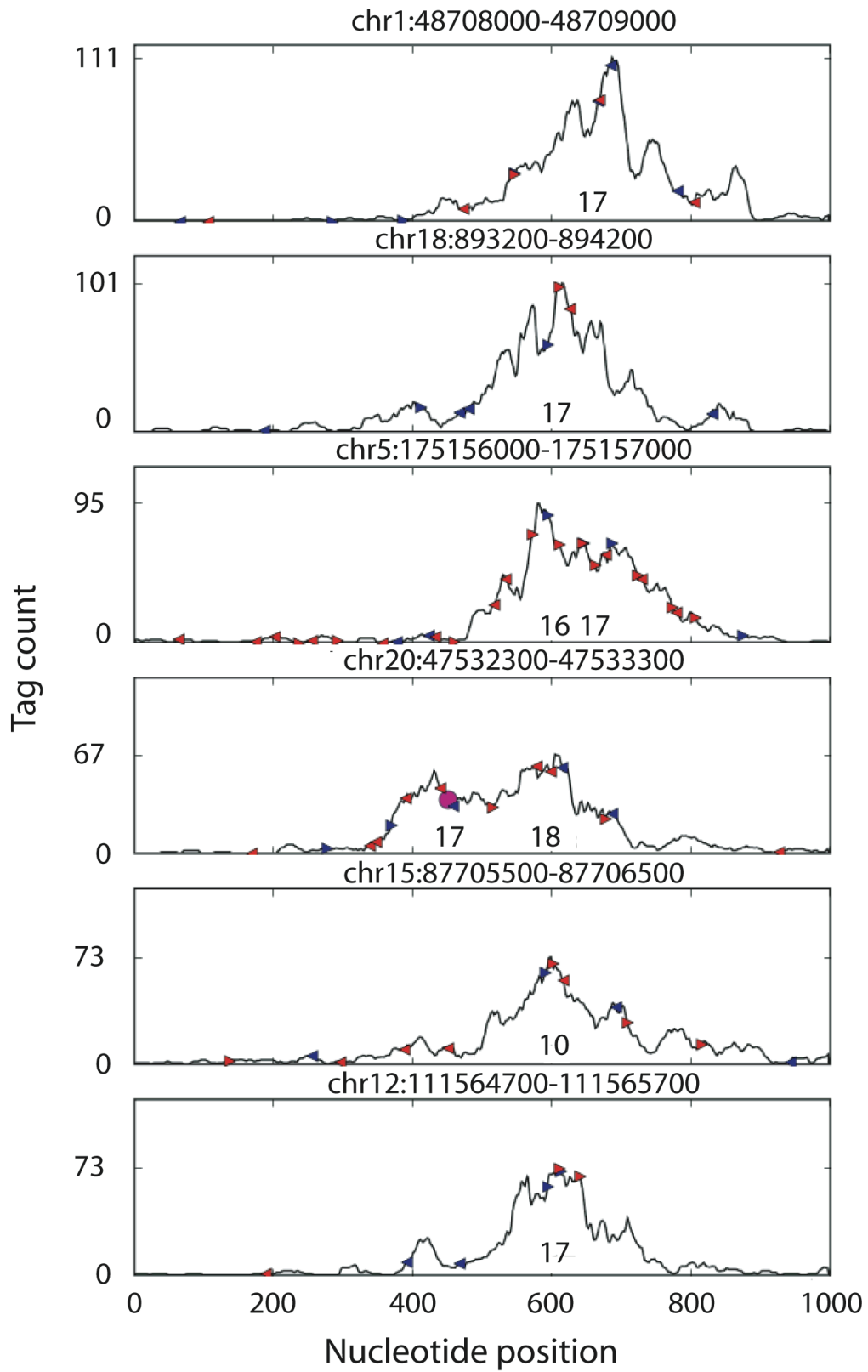




Figure S6



**Table S1.** Summary table of reads used in the analysis for Experiment 1, Experiment 2, and of their corresponding controls.

	Exp 1 ChIPSeq	Exp 1 Control	Exp 2 ChIPSeq	Exp 2 Control
<b>Total reads</b>	4,756,090	5,108,543	2,126,823	3,100,468
<b>Unique location reads</b>	3,661,543	3,834,288	1,697,893	2,319,582
<b>Reads used in analysis</b>	3,661,543	3,661,543	1,697,893	1,697,893
<b>Reads excluded because of control</b>	24,167	-	4,699	-
<b># ChIPSeq enriched regions</b>	2,674	2,674*	2,171	2,171*
<b>Reads in ChIPSeq regions</b>	465,256	5,037	343,234	2,677
<b>Reads in “common” ChIPSeq regions (1,946 regions)</b>	442,797	4,171	336,146	2,505

**Table S2.** Enriched regions from experiment 1 that are common with experiment 2 with NRSE Sites with P-value < 10<sup>-4</sup>

Gene Name	Gene ID	Enriched Region	NRSE	PSFM Score	ChIP:Control reads	Distance to peak	Half-site distance	NRSE P-value*
NXF	266743	chr11:65944803-65948566	chr11:65946197-65946224	53	6718:17	306	18	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945913-65945933	85	6718:17	18	11	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945875-65945895	85	6718:17	-20	11	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945837-65945857	90	6718:17	-58	11	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945797-65945817	88	6718:17	-98	11	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945754-65945774	85	6718:17	-141	11	3.11E-06
NXF	266743	chr11:65944803-65948566	chr11:65945569-65945589	72	6718:17	-326	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182571-55182591	73	5544:9	230	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182564-55182591	50	5544:9	227	18	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182462-55182482	80	5544:9	121	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182406-55182426	81	5544:9	65	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182349-55182369	89	5544:9	8	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55182299-55182319	88	5544:9	-42	11	3.11E-06
VRK3	51231	chr19:55181470-55182863	chr19:55181569-55181589	72	5544:9	-772	11	4.71E-05
C19orf30	284424	chr19:4719510-4720939	chr19:4720743-4720763	79	4153:8	46	11	3.11E-06
C19orf30	284424	chr19:4719510-4720939	chr19:4720697-4720723	69	4153:8	3	17	3.11E-06
C19orf30	284424	chr19:4719510-4720939	chr19:4720636-4720662	67	4153:8	-58	17	3.11E-06
C19orf30	284424	chr19:4719510-4720939	chr19:4720584-4720604	85	4153:8	-113	11	3.11E-06
SYT7	9066	chr11:61090862-61091926	chr11:61091437-61091457	83	2690:12	50	11	3.11E-06
SYT7	9066	chr11:61090862-61091926	chr11:61091397-61091417	86	2690:12	10	11	3.11E-06
SYT7	9066	chr11:61090862-61091926	chr11:61091041-61091061	71	2690:12	-346	11	3.11E-06
HTR5A	3361	chr7:154298661-154300008	chr7:154299552-154299572	82	2399:12	161	11	3.11E-06

HTR5A	3361	chr7:154298661-154300008	chr7:154299487-154299507	82	2399:12	96	11	3.11E-06
HTR5A	3361	chr7:154298661-154300008	chr7:154299437-154299457	84	2399:12	46	11	3.11E-06
LOC343702	343702	chr20:30019540-30021032	chr20:30020053-30020073	94	2318:4	23	11	3.11E-06
LOC343702	343702	chr20:30019540-30021032	chr20:30020017-30020037	86	2318:4	-13	11	3.11E-06
BRUNOL4	56853	chr18:33103451-33105116	chr18:33104199-33104219	83	2278:5	-6	11	3.11E-06
BRUNOL4	56853	chr18:33103451-33105116	chr18:33104182-33104202	81	2278:5	-23	11	3.11E-06
BRUNOL4	56853	chr18:33103451-33105116	chr18:33104165-33104185	80	2278:5	-40	11	3.11E-06
ATP2B2	491	chr3:10476204-10478079	chr3:10477279-10477306	50	2203:9	277	18	3.11E-06
ATP2B2	491	chr3:10476204-10478079	chr3:10477071-10477098	44	2203:9	69	18	3.11E-06
ATP2B2	491	chr3:10476204-10478079	chr3:10476784-10476812	73	2203:9	-218	19	3.11E-06
SCN10A	6336	chr3:38821632-38823084	chr3:38822574-38822594	74	2113:7	134	11	3.11E-06
SCN10A	6336	chr3:38821632-38823084	chr3:38822489-38822509	82	2113:7	49	11	3.11E-06
SCN10A	6336	chr3:38821632-38823084	chr3:38822441-38822461	85	2113:7	1	11	3.11E-06
SCN10A	6336	chr3:38821632-38823084	chr3:38821811-38821831	71	2113:7	-629	11	6.28E-05
-	-	chr9:123951735-123953508	chr9:123952345-123952371	76	2030:8	23	17	3.11E-06
-	-	chr9:123951735-123953508	chr9:123952310-123952330	83	2030:8	-15	11	3.11E-06
CELSR3	1951	chr3:48673868-48675059	chr3:48674313-48674333	81	1988:5	-19	11	3.11E-06
LIN28	79727	chr1:26419021-26420632	chr1:26419359-26419379	73	1941:4	17	11	3.11E-06
LIN28	79727	chr1:26419021-26420632	chr1:26419329-26419349	88	1941:4	-13	11	3.11E-06
-	-	chr5:176196614-176198408	chr5:176197437-176197457	90	1907:4	72	11	3.11E-06
-	-	chr5:176196614-176198408	chr5:176197400-176197425	50	1907:4	38	16	3.11E-06
-	-	chr5:176196614-176198408	chr5:176197378-176197398	90	1907:4	13	11	3.11E-06
-	-	chr5:176196614-176198408	chr5:176197340-176197360	77	1907:4	-25	11	3.11E-06
-	-	chr5:176196614-176198408	chr5:176197133-176197153	75	1907:4	-232	11	3.11E-06
-	-	chr20:34445723-34446793	chr20:34446076-34446096	76	1870:0	97	11	3.11E-06
-	-	chr20:34445723-34446793	chr20:34446014-34446034	90	1870:0	35	11	3.11E-06
-	-	chr20:34445723-34446793	chr20:34445987-34446007	82	1870:0	8	11	3.11E-06
-	-	chr8:10884674-10886584	chr8:10886171-10886191	70	1779:5	890	11	7.75E-06
-	-	chr8:10884674-10886584	chr8:10885387-10885407	78	1779:5	106	11	3.11E-06
-	-	chr8:10884674-10886584	chr8:10885241-10885261	88	1779:5	-40	11	3.11E-06
-	-	chr9:125924083-125925450	chr9:125924713-125924733	76	1727:2	8	11	3.11E-06
-	-	chr9:125924083-125925450	chr9:125924690-125924710	80	1727:2	-15	11	3.11E-06
-	-	chr8:10884674-10885816	chr8:10885387-10885407	78	1668:5	106	11	3.11E-06
-	-	chr8:10884674-10885816	chr8:10885241-10885261	88	1668:5	-40	11	3.11E-06
IGSF4B	57863	chr1:155959897-155960856	chr1:155960361-155960381	72	1644:4	42	11	3.11E-06
IGSF4B	57863	chr1:155959897-155960856	chr1:155960311-155960331	72	1644:4	-8	11	3.11E-06
FAM24A	118670	chr10:124660974-124662225	chr10:124661595-124661615	82	1570:5	40	11	3.11E-06
FAM24A	118670	chr10:124660974-124662225	chr10:124661566-124661586	87	1570:5	11	11	3.11E-06

FAM24A	118670	chr10:124660974-124662225	chr10:124661538-124661558	73	1570:5	-17	11	3.11E-06
C6orf159	134701	chr6:84625345-84626672	chr6:84625915-84625942	70	1496:9	0	18	3.11E-06
KIAA1337	57540	chr1:11544535-11545713	chr1:11545209-11545229	91	1424:2	57	11	3.11E-06
KIAA1337	57540	chr1:11544535-11545713	chr1:11545147-11545167	80	1424:2	-5	11	3.11E-06
KIAA1337	57540	chr1:11544535-11545713	chr1:11544941-11544961	73	1424:2	-211	11	3.11E-06
-	-	chr15:72370320-72371788	chr15:72371043-72371063	90	1337:8	-5	11	3.11E-06
-	-	chr15:72370320-72371788	chr15:72370931-72370959	52	1337:8	-113	19	3.11E-06
KIAA0494	9813	chr1:46913036-46914153	chr1:46913585-46913605	83	1335:3	37	11	3.11E-06
KCNH7	90134	chr2:163522266-163523580	chr2:163522824-163522844	85	1296:5	46	11	3.11E-06
KCNH7	90134	chr2:163522266-163523580	chr2:163522798-163522818	80	1296:5	20	11	3.11E-06
ADCY5	111	chr3:124487255-124488685	chr3:124488242-124488262	73	1285:5	244	11	3.11E-06
ADCY5	111	chr3:124487255-124488685	chr3:124488019-124488039	79	1285:5	21	11	3.11E-06
SLCO2B1	11309	chr11:74602784-74603793	chr11:74603240-74603260	89	1242:4	5	11	3.11E-06
RTBDN	83546	chr19:12803567-12805067	chr19:12804391-12804411	83	1233:11	33	11	3.11E-06
RTBDN	83546	chr19:12803567-12805067	chr19:12804363-12804383	85	1233:11	5	11	3.11E-06
-	-	chr3:67246552-67247542	chr3:67247092-67247112	85	1230:6	-80	11	3.11E-06
GLRA1	2741	chr5:151283451-151285063	chr5:151284507-151284527	93	1226:7	-3	11	3.11E-06
GLRA1	2741	chr5:151283451-151285063	chr5:151283838-151283864	66	1226:7	-669	17	3.29E-05
LOC388617	388617	chr1:35058765-35060185	chr1:35059712-35059732	83	1225:3	43	11	3.11E-06
LOC388617	388617	chr1:35058765-35060185	chr1:35059664-35059684	84	1225:3	-5	11	3.11E-06
-	-	chr3:56503487-56504361	chr3:56503908-56503927	58	1215:7	23	10	3.11E-06
-	-	chr20:35688139-35689654	chr20:35688985-35689005	97	1165:5	38	11	3.11E-06
-	-	chr20:35688139-35689654	chr20:35688957-35688977	79	1165:5	10	11	3.11E-06
LOC283440	283440	chr12:2731696-2732971	chr12:2732485-2732510	70	1160:3	181	16	3.11E-06
LOC283440	283440	chr12:2731696-2732971	chr12:2732262-2732282	84	1160:3	-45	11	3.11E-06
LOC283440	283440	chr12:2731696-2732971	chr12:2732202-2732222	90	1160:3	-105	11	3.11E-06
SORCS3	22986	chr10:106573990-106575069	chr10:106574365-106574385	85	1150:0	11	11	3.11E-06
SORCS3	22986	chr10:106573990-106575069	chr10:106574337-106574357	80	1150:0	-17	11	3.11E-06
CRHR2	1395	chr7:30484640-30485885	chr7:30484928-30484948	74	1149:9	51	11	3.11E-06
CRHR2	1395	chr7:30484640-30485885	chr7:30484875-30484895	88	1149:9	-2	11	3.11E-06
-	-	chr16:47748968-47750171	chr16:47749866-47749891	52	1108:3	225	16	3.11E-06
-	-	chr16:47748968-47750171	chr16:47749665-47749685	73	1108:3	21	11	3.11E-06
-	-	chr16:47748968-47750171	chr16:47749628-47749648	86	1108:3	-16	11	3.11E-06
ZNF19	7567	chr16:70058579-70059506	chr16:70059390-70059416	76	1052:4	55	17	3.11E-06
ZNF19	7567	chr16:70058579-70059506	chr16:70059332-70059352	74	1052:4	-6	11	3.11E-06
QTRT1	81890	chr19:10667175-10668096	chr19:10667632-10667652	89	1029:2	-10	11	3.11E-06
LOC131973	131973	chr3:14614361-14615477	chr3:14614937-14614957	83	1019:13	-1	11	3.11E-06
-	-	chr4:6665806-6667028	chr4:6666566-6666586	89	976:6	21	11	3.11E-06

-	-	chr20:10147330-10148957	chr20:10148319-10148339	86	974:7	42	11	3.11E-06
-	-	chr20:10147330-10148957	chr20:10148268-10148288	77	974:7	-9	11	3.11E-06
RAB37	326624	chr17:70178328-70179703	chr17:70179091-70179111	88	969:0	-88	11	3.11E-06
AP3B2	8120	chr15:81127980-81130020	chr15:81129124-81129144	89	937:3	31	11	3.11E-06
AP3B2	8120	chr15:81127980-81130020	chr15:81128758-81128778	72	937:3	-335	11	1.20E-05
MGC52010	91582	chr22:38265810-38267378	chr22:38266463-38266483	91	923:5	-7	11	3.11E-06
FLJ22374	84182	chr7:30927232-30928732	chr7:30928031-30928051	83	921:4	47	11	3.11E-06
FLJ22374	84182	chr7:30927232-30928732	chr7:30927996-30928016	78	921:4	12	11	3.11E-06
FLJ22374	84182	chr7:30927232-30928732	chr7:30927965-30927985	70	921:4	-19	11	3.11E-06
-	-	chr3:10611464-10612335	chr3:10611751-10611771	77	919:5	2	11	3.11E-06
FLJ33655	284656	chr1:37898794-37899725	chr1:37899245-37899265	81	907:1	1	11	3.11E-06
FLJ33655	284656	chr1:37898794-37899725	chr1:37899221-37899241	85	907:1	-23	11	3.11E-06
NXF	266743	chr11:65941893-65944099	chr11:65942914-65942934	92	900:9	4	11	3.11E-06
-	-	chr12:11544364-11545759	chr12:11545009-11545029	85	898:4	59	11	3.11E-06
-	-	chr12:11544364-11545759	chr12:11544949-11544969	91	898:4	-1	11	3.11E-06
-	-	chr11:115981276-115982074	chr11:115981636-115981656	87	895:1	-11	11	3.11E-06
FLJ34443	285464	chr4:1393354-1395569	chr4:1394744-1394764	71	891:3	536	11	2.91E-05
FLJ34443	285464	chr4:1393354-1395569	chr4:1394265-1394285	96	891:3	57	11	3.11E-06
FLJ34443	285464	chr4:1393354-1395569	chr4:1394205-1394225	82	891:3	-3	11	3.11E-06
FLJ34443	285464	chr4:1393354-1395569	chr4:1394187-1394207	86	891:3	-21	11	3.11E-06
VGF	7425	chr7:100400999-100403160	chr7:100402274-100402294	88	880:4	7	11	3.11E-06
VGF	7425	chr7:100400999-100403160	chr7:100401999-100402027	44	880:4	-264	19	4.00E-06
VGF	7425	chr7:100400999-100403160	chr7:100401299-100401319	82	880:4	-968	11	3.05E-05
KCNH2	3757	chr7:150117654-150119613	chr7:150118844-150118872	44	879:4	52	19	3.11E-06
KCNH2	3757	chr7:150117654-150119613	chr7:150118807-150118827	87	879:4	11	11	3.11E-06
SLIT1	6585	chr10:98831027-98832095	chr10:98831568-98831588	91	871:5	18	11	3.11E-06
SLIT1	6585	chr10:98831027-98832095	chr10:98831556-98831576	71	871:5	6	11	3.11E-06
-	-	chr22:43691470-43692642	chr22:43692142-43692162	92	869:2	1	11	3.11E-06
SIGLEC5	8778	chr19:56802519-56803741	chr19:56803219-56803239	87	853:7	-22	11	3.11E-06
-	-	chr20:56056186-56057192	chr20:56057050-56057070	71	852:4	281	11	6.63E-06
-	-	chr20:56056186-56057192	chr20:56056759-56056779	74	852:4	-10	11	3.11E-06
SIGLEC10	89790	chr19:56616898-56617460	chr19:56617221-56617241	83	850:5	-5	11	3.11E-06
ZDHHC22	283576	chr14:76669494-76670789	chr14:76670322-76670342	75	847:2	294	11	4.32E-06
ZDHHC22	283576	chr14:76669494-76670789	chr14:76670024-76670044	86	847:2	-4	11	3.11E-06
-	-	chr12:51421149-51422049	chr12:51421610-51421630	92	845:2	-4	11	3.11E-06
-	-	chr3:44549058-44549933	chr3:44549511-44549531	86	840:8	5	11	3.11E-06
C6orf165	154313	chr6:88202816-88203364	chr6:88203030-88203050	80	839:4	-9	11	3.11E-06
BARHL1	56751	chr9:132486718-132487721	chr9:132487282-132487302	74	835:1	172	11	3.11E-06

BARHL1	56751	chr9:132486718-132487721	chr9:132487213-132487233	85	835:1	103	11	3.11E-06
BARHL1	56751	chr9:132486718-132487721	chr9:132487115-132487135	90	835:1	5	11	3.11E-06
-	-	chr1:199393673-199394561	chr1:199394134-199394162	64	833:3	217	19	3.11E-06
-	-	chr1:199393673-199394561	chr1:199393928-199393948	92	833:3	7	11	3.11E-06
LOC442399	442399	chr8:142795027-142796052	chr8:142795480-142795500	82	832:2	37	11	3.11E-06
LOC442399	442399	chr8:142795027-142796052	chr8:142795452-142795472	78	832:2	9	11	3.11E-06
BAI3	577	chr6:69999098-70000135	chr6:69999673-69999682	32	828:2	3	0	3.11E-06
TPH2	121278	chr12:70618510-70619395	chr12:70618900-70618920	72	823:4	-16	11	3.11E-06
-	-	chr14:105337962-105338903	chr14:105338758-105338778	79	800:1	24	11	3.11E-06
-	-	chr14:105337962-105338903	chr14:105338714-105338734	71	800:1	-20	11	3.11E-06
LOC441209	441209	chr7:32240263-32241495	chr7:32240726-32240746	90	798:6	-2	11	3.11E-06
-	-	chr22:33135182-33136055	chr22:33135593-33135613	79	792:4	-21	11	3.11E-06
LOC343578	343578	chr20:36747610-36748782	chr20:36748090-36748110	83	786:6	-1	11	3.11E-06
T1	83696	chr8:140801159-140802324	chr8:140801790-140801810	90	785:3	-22	11	3.11E-06
T1	83696	chr8:140801159-140802324	chr8:140801421-140801446	57	785:3	-388	16	7.60E-06
GRM8	2918	chr7:126341469-126342386	chr7:126341922-126341942	89	783:2	13	11	3.11E-06
LOC388496	388496	chr19:5355026-5355968	chr19:5355233-5355253	90	772:0	51	11	3.11E-06
-	-	chr12:117961485-117962609	chr12:117961925-117961945	93	771:3	37	11	3.11E-06
-	-	chr10:125364052-125364994	chr10:125364593-125364613	89	768:4	-3	11	3.11E-06
L1CAM	3897	chrX:152661222-152662299	chrX:152661845-152661865	81	760:1	47	11	3.11E-06
L1CAM	3897	chrX:152661222-152662299	chrX:152661803-152661823	89	760:1	5	11	3.11E-06
RIMS4	140730	chr20:42841757-42843051	chr20:42842417-42842437	73	748:3	20	11	3.11E-06
RIMS4	140730	chr20:42841757-42843051	chr20:42842397-42842417	89	748:3	0	11	3.11E-06
NPPB	4879	chr1:11853361-11854212	chr1:11853793-11853813	91	741:2	-39	11	3.11E-06
PRDM11	56981	chr11:45075708-45076858	chr11:45076203-45076223	95	740:3	-3	11	3.11E-06
-	-	chr17:30054322-30055645	chr17:30054924-30054944	85	737:3	-10	11	3.11E-06
GRM4	2914	chr6:34207514-34209038	chr6:34208471-34208491	91	735:9	4	11	3.11E-06
LOC400369	400369	chr15:46269871-46271092	chr15:46270516-46270536	94	728:5	-16	11	3.11E-06
PCSK1	5122	chr5:95795105-95796600	chr5:95795770-95795795	75	726:1	-12	16	3.11E-06
LOC441968	441968	chr21:45889168-45891065	chr21:45890359-45890379	89	726:9	5	11	3.11E-06
LOC441968	441968	chr21:45889168-45891065	chr21:45889774-45889794	74	726:9	-580	11	5.42E-05
-	-	chr17:6113165-6114649	chr17:6113749-6113769	90	726:2	59	11	3.11E-06
PTPRN	5798	chr2:219997897-219999140	chr2:219998545-219998565	96	721:1	40	11	3.11E-06
PTPRN	5798	chr2:219997897-219999140	chr2:219998526-219998553	48	721:1	25	18	3.11E-06
CAMTA1	23261	chr1:7069181-7070078	chr1:7069836-7069856	90	719:0	4	11	3.11E-06
-	-	chr1:48708226-48709231	chr1:48708663-48708689	50	719:3	-11	17	3.11E-06
-	-	chr9:131703878-131704814	chr9:131704312-131704332	96	711:4	-37	11	3.11E-06
CRH	1392	chr8:67251764-67252923	chr8:67252431-67252451	96	709:1	-6	11	3.11E-06

OR4D1	26689	chr17:53551930-53553148	chr17:53552754-53552774	82	700:5	36	11	3.11E-06
-	-	chr10:99805096-99806210	chr10:99805811-99805831	92	698:3	67	11	3.11E-06
BRUNOL5	60680	chr19:3194778-3195830	chr19:3195190-3195210	93	697:5	-16	11	3.11E-06
HCN4	10021	chr15:71425865-71426887	chr15:71426296-71426316	100	696:2	11	11	3.11E-06
-	-	chr5:141093802-141095444	chr5:141094768-141094788	80	695:7	-1	11	3.11E-06
-	-	chr1:111000922-111001987	chr1:111001520-111001540	92	690:4	-1	11	3.11E-06
KIRREL3	84623	chr11:125936079-125937167	chr11:125936578-125936598	92	689:8	-13	11	3.11E-06
ADCYAP1	116	chr18:893226-894275	chr18:893789-893815	62	681:5	-13	17	3.11E-06
-	-	chr5:175155982-175157259	chr5:175156640-175156666	56	681:1	72	17	3.11E-06
-	-	chr5:175155982-175157259	chr5:175156590-175156615	59	681:1	22	16	3.11E-06
-	-	chr20:1934080-1935756	chr20:1934646-1934666	92	675:7	18	11	3.11E-06
SCAMP5	192683	chr15:73074006-73075187	chr15:73074779-73074799	77	673:5	-2	11	3.11E-06
NPTXR	23467	chr22:37544780-37545830	chr22:37545188-37545208	87	673:6	-41	11	3.11E-06
LOC441798	441798	chr17:55571754-55572756	chr17:55572101-55572121	77	671:5	6	11	3.11E-06
LOC441798	441798	chr17:55571754-55572756	chr17:55572096-55572121	54	671:5	4	16	3.11E-06
-	-	chr2:79649674-79651041	chr2:79650297-79650317	88	671:5	-22	11	3.11E-06
HTR1A	3350	chr5:63294061-63295193	chr5:63294851-63294871	84	669:3	-11	11	3.11E-06
LOC440711	440711	chr1:201537599-201538885	chr1:201538447-201538467	79	668:3	3	11	3.11E-06
LOC440711	440711	chr1:201537599-201538885	chr1:201538407-201538427	70	668:3	-37	11	3.11E-06
CDH23	64072	chr10:73224694-73225730	chr10:73225169-73225189	77	668:3	-46	11	3.11E-06
-	-	chr14:75668828-75669940	chr14:75669300-75669327	54	667:5	8	18	3.11E-06
-	-	chr14:75668828-75669940	chr14:75669288-75669308	77	667:5	-8	11	3.11E-06
-	-	chr3:54196656-54198261	chr3:54197410-54197430	94	664:6	20	11	3.11E-06
-	-	chr3:54196656-54198261	chr3:54197095-54197115	73	664:6	-295	11	8.36E-06
SLC12A5	57468	chr20:44102298-44104368	chr20:44103119-44103139	86	663:3	-10	11	3.11E-06
-	-	chr20:36754246-36755500	chr20:36754618-36754638	90	659:3	29	11	3.11E-06
-	-	chr5:170040450-170041603	chr5:170040933-170040953	90	657:9	-20	11	3.11E-06
-	-	chr5:170040450-170041603	chr5:170040618-170040646	53	657:9	-331	19	3.58E-06
TOR1B	27348	chr9:129632131-129632691	chr9:129632455-129632475	87	656:5	-26	11	3.11E-06
TOR1B	27348	chr9:129632131-129632691	chr9:129632385-129632404	52	656:5	-96	10	3.11E-06
FLJ35220	284131	chr17:76028927-76030200	chr17:76029662-76029682	94	656:2	-14	11	3.11E-06
NPHS1	4868	chr19:41011305-41012082	chr19:41011595-41011615	89	651:2	-3	11	3.11E-06
SLC18A3	6572	chr10:50484538-50485942	chr10:50485333-50485353	70	647:7	149	11	3.11E-06
SLC18A3	6572	chr10:50484538-50485942	chr10:50485177-50485197	80	647:7	-7	11	3.11E-06
-	-	chr3:133236098-133237166	chr3:133236689-133236709	82	643:8	-27	11	3.11E-06
-	-	chr17:2599745-2600441	chr17:2599972-2599992	92	639:3	-67	11	3.11E-06
KCNB1	3745	chr20:47532337-47533421	chr20:47532892-47532919	60	638:2	0	18	3.11E-06
KCNB1	3745	chr20:47532337-47533421	chr20:47532741-47532761	75	638:2	-155	11	3.11E-06

KCNB1	3745	chr20:47532337-47533421	chr20:47532735-47532761	62	638:2	-158	17	3.11E-06
LAIR2	3904	chr19:59720358-59720963	chr19:59720683-59720703	88	635:5	16	11	3.11E-06
DKFZP566A1524	81553	chr2:16648758-16649827	chr2:16649221-16649241	83	635:2	9	11	3.11E-06
-	-	chr1:41944735-41946218	chr1:41945410-41945430	78	631:8	-10	11	3.11E-06
TUBB4	10381	chr16:88520002-88520664	chr16:88520412-88520432	94	629:3	4	11	3.11E-06
TUBB4	10381	chr16:88520002-88520664	chr16:88520008-88520035	48	629:3	-396	18	6.74E-06
CACNG3	10368	chr16:24174361-24175535	chr16:24174913-24174933	82	626:2	12	11	3.11E-06
-	-	chr22:35364484-35365536	chr22:35364968-35364988	83	619:2	2	11	3.11E-06
LOXHD1	125336	chr18:42331013-42332106	chr18:42331281-42331301	87	618:2	-56	11	3.11E-06
NOVA2	4858	chr19:51147215-51148566	chr19:51147828-51147848	94	616:3	-1	11	3.11E-06
CX62	84694	chr6:90661400-90662468	chr6:90661944-90661964	77	616:9	37	11	3.11E-06
CX62	84694	chr6:90661400-90662468	chr6:90661914-90661942	59	616:9	11	19	3.11E-06
CX62	84694	chr6:90661400-90662468	chr6:90661884-90661904	77	616:9	-23	11	3.11E-06
C9orf25	203259	chr9:34402828-34404357	chr9:34403416-34403436	97	616:8	2	11	3.11E-06
-	-	chr3:13157906-13159340	chr3:13158631-13158651	93	616:5	-16	11	3.11E-06
LOC390992	390992	chr1:6239319-6240229	chr1:6239572-6239592	88	613:2	-33	11	3.11E-06
-	-	chr1:150207600-150208549	chr1:150208191-150208211	92	609:0	7	11	3.11E-06
-	-	chr15:64083673-64084927	chr15:64084235-64084255	91	604:4	3	11	3.11E-06
MGC4645	79446	chr14:100022097-100023389	chr14:100022762-100022782	94	600:5	-1	11	3.11E-06
-	-	chr5:141102660-141103904	chr5:141103315-141103335	85	600:4	1	11	3.11E-06
-	-	chr5:141102660-141103904	chr5:141103132-141103152	71	600:4	-182	11	3.11E-06
-	-	chr14:78398912-78400082	chr14:78399433-78399453	86	600:3	45	11	3.11E-06
FLJ11127	54491	chr5:14681179-14682260	chr5:14681656-14681676	90	598:3	8	11	3.11E-06
MYO5B	4645	chr18:45678564-45679691	chr18:45679019-45679039	91	595:4	-10	11	3.11E-06
SLC5A11	115584	chr16:24776770-24778055	chr16:24777456-24777476	86	590:5	-10	11	3.11E-06
PF20	79582	chr2:215100928-215102154	chr2:215101341-215101361	95	589:5	18	11	3.11E-06
C14orf171	57156	chr14:76744176-76745950	chr14:76744970-76744990	89	588:7	-13	11	3.11E-06
C14orf171	57156	chr14:76744176-76745950	chr14:76744571-76744591	80	588:7	-412	11	2.36E-05
LOC390944	390944	chr19:51412901-51413776	chr19:51413448-51413468	97	587:0	0	11	3.11E-06
SHANK2	22941	chr11:70173502-70174846	chr11:70174263-70174283	85	586:3	49	11	3.11E-06
SHANK2	22941	chr11:70173502-70174846	chr11:70174227-70174247	84	586:3	13	11	3.11E-06
SHANK2	22941	chr11:70173502-70174846	chr11:70174191-70174211	83	586:3	-23	11	3.11E-06
-	-	chr11:119149789-119150973	chr11:119150280-119150300	91	586:4	-30	11	3.11E-06
-	-	chr20:46572799-46573711	chr20:46573291-46573311	87	582:4	9	11	3.11E-06
SLC6A3	6531	chr5:1461911-1463023	chr5:1462622-1462641	54	578:5	12	10	3.11E-06
-	-	chr22:24979814-24980653	chr22:24980233-24980253	87	576:1	-5	11	3.11E-06
-	-	chr1:37058499-37059743	chr1:37059093-37059113	83	575:4	8	11	3.11E-06
-	-	chr15:87705498-87706783	chr15:87706086-87706105	53	574:3	-2	10	3.11E-06



EPHA8	2046	chr1:22682680-22684152	chr1:22683455-22683475	91	570:8	-10	11	3.11E-06
SST	6750	chr3:188869863-188870922	chr3:188870728-188870748	74	569:1	416	11	4.42E-05
SST	6750	chr3:188869863-188870922	chr3:188870333-188870353	78	569:1	21	11	3.11E-06
SST	6750	chr3:188869863-188870922	chr3:188870305-188870325	85	569:1	-7	11	3.11E-06
RAB11-FIP4	84440	chr17:26745154-26746144	chr17:26745911-26745931	80	567:7	5	11	3.11E-06
SLC5A1	6523	chr22:30826917-30828620	chr22:30827668-30827688	84	565:4	-40	11	3.11E-06
SLC5A1	6523	chr22:30826917-30828620	chr22:30827368-30827388	71	565:4	-340	11	4.69E-06
PSK-1	26470	chr16:29818307-29819636	chr16:29818899-29818927	61	564:6	0	19	3.11E-06
HAPIP	8997	chr3:125418544-125419948	chr3:125419250-125419270	89	561:5	22	11	3.11E-06
LOC390259	390259	chr11:122357435-122358480	chr11:122357876-122357896	92	559:7	-2	11	3.11E-06
ONECUT2	9480	chr18:53264670-53266214	chr18:53265508-53265528	94	558:5	-4	11	3.11E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841567-61841587	72	558:1	263	11	4.75E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841459-61841479	85	558:1	155	11	3.11E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841396-61841416	91	558:1	92	11	3.11E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841345-61841365	83	558:1	41	11	3.11E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841300-61841320	95	558:1	-4	11	3.11E-06
LOC147670	147670	chr19:61840850-61842086	chr19:61841268-61841288	73	558:1	-36	11	3.11E-06
-	-	chr14:90030777-90031947	chr14:90031545-90031565	86	557:2	5	11	3.11E-06
HTR6	3362	chr1:19747618-19748934	chr1:19748383-19748403	82	555:3	3	11	3.11E-06
RUTBC2	129049	chr22:23596199-23597195	chr22:23596600-23596620	84	553:8	-18	11	3.11E-06
CHGA	1113	chr14:92449842-92450735	chr14:92450340-92450360	86	552:5	-7	11	3.11E-06
INA	9118	chr10:105015054-105016052	chr10:105015656-105015676	83	548:7	-25	11	3.11E-06
GPR158	57512	chr10:25502783-25504072	chr10:25503555-25503564	54	548:3	6	0	3.11E-06
NPDC1	56654	chr9:137216686-137217870	chr9:137217034-137217054	75	535:4	6	11	3.11E-06
LOC343184	343184	chr1:50486150-50487402	chr1:50486722-50486742	85	534:1	32	11	3.11E-06
PRKCG	5582	chr19:59097858-59098834	chr19:59098325-59098345	89	533:1	19	11	3.11E-06
HS3ST2	9956	chr16:22731591-22732539	chr16:22731835-22731855	70	533:1	-252	11	5.25E-06
MPN	83886	chr16:2705120-2706243	chr16:2705680-2705706	65	531:4	17	17	3.11E-06
MPN	83886	chr16:2705120-2706243	chr16:2705639-2705659	94	531:4	-27	11	3.11E-06
-	-	chr20:58597387-58598662	chr20:58598273-58598293	76	530:3	10	11	3.11E-06
-	-	chr20:58597387-58598662	chr20:58598246-58598266	82	530:3	-17	11	3.11E-06
-	-	chr18:43034486-43035812	chr18:43035119-43035139	85	529:5	-13	11	3.11E-06
-	-	chr16:22559632-22560620	chr16:22560059-22560079	76	529:4	7	11	3.11E-06
-	-	chr12:111564249-111566000	chr12:111565289-111565315	66	529:4	-8	17	3.11E-06
OGDHL	55753	chr10:50639914-50641451	chr10:50640472-50640492	84	527:3	1	11	3.11E-06
KIAA1030	22997	chr11:133321795-133323210	chr11:133322552-133322572	76	525:6	-2	11	3.11E-06
-	-	chr1:21730932-21732119	chr1:21731110-21731130	87	522:4	-3	11	3.11E-06
-	-	chr8:31772186-31772963	chr8:31772543-31772563	82	520:0	-37	11	3.11E-06

COL22A1	169044	chr8:139870037-139871258	chr8:139870644-139870664	95	519:1	37	11	3.11E-06
-	-	chr8:142646176-142647198	chr8:142646413-142646433	89	519:1	48	11	3.11E-06
-	-	chr12:3471211-3472623	chr12:3471801-3471821	93	519:8	11	11	3.11E-06
DNAH5	1767	chr5:13919562-13920517	chr5:13920102-13920122	94	518:0	-10	11	3.11E-06
LOC389095	389095	chr3:10770409-10771249	chr3:10770846-10770866	78	516:2	6	11	3.11E-06
FLJ11151	55313	chr16:12662652-12663700	chr16:12663257-12663277	86	516:2	1	11	3.11E-06
FLJ11151	55313	chr16:12662652-12663700	chr16:12663007-12663035	51	516:2	-245	19	3.24E-06
-	-	chr19:38923113-38924412	chr19:38923733-38923753	91	513:2	-6	11	3.11E-06
-	-	chr19:38923113-38924412	chr19:38923629-38923649	70	513:2	-110	11	3.11E-06
-	-	chr19:38923113-38924412	chr19:38923560-38923580	83	513:2	-179	11	3.11E-06
DDC	1644	chr7:50394480-50395370	chr7:50395072-50395092	76	511:3	-29	11	3.11E-06
-	-	chr1:21719208-21720625	chr1:21719885-21719905	79	511:2	2	11	3.11E-06
-	-	chr1:21719208-21720625	chr1:21719395-21719415	70	511:2	-488	11	2.65E-05
-	-	chr5:109363-110761	chr5:110290-110310	78	510:4	13	11	3.11E-06
-	-	chr5:109363-110761	chr5:109825-109844	48	510:4	-452	10	6.28E-05
CNTNAP2	26047	chr7:145250032-145251551	chr7:145250670-145250690	88	509:4	5	11	3.11E-06
-	-	chr2:137118676-137119549	chr2:137119058-137119078	81	509:1	19	11	3.11E-06
-	-	chr17:6147275-6148295	chr17:6147908-6147928	89	509:7	-15	11	3.11E-06
-	-	chr17:6147275-6148295	chr17:6147433-6147461	46	509:7	-486	19	3.05E-05
-	-	chr15:68055403-68056668	chr15:68055958-68055978	85	509:4	9	11	3.11E-06
NEFH	4744	chr22:28198105-28200019	chr22:28199217-28199237	92	508:7	46	11	3.11E-06
MHC2TA	4261	chr16:10896290-10897325	chr16:10896881-10896901	91	507:0	-12	11	3.11E-06
-	-	chr5:141113403-141115373	chr5:141114042-141114062	82	507:3	5	11	3.11E-06
CACNA2D2	9254	chr3:50416338-50418430	chr3:50417871-50417891	87	505:6	16	11	3.11E-06
-	-	chr15:71930986-71931993	chr15:71931279-71931299	93	505:2	1	11	3.11E-06
SULT4A1	25830	chr22:42588357-42589236	chr22:42588795-42588815	92	502:0	-8	11	3.11E-06
GDAP1	54332	chr8:75425018-75425841	chr8:75425409-75425428	55	501:7	-1	10	3.11E-06
LOC283989	283989	chr17:71023372-71024183	chr17:71023656-71023684	64	500:10	-5	19	3.11E-06
FBXL15	79176	chr10:104168604-104170077	chr10:104169419-104169439	76	499:6	-11	11	3.11E-06
SLC12A5	57468	chr20:44089065-44090919	chr20:44089483-44089503	82	497:2	-18	11	3.11E-06
LOC285484	285484	chr4:6344601-6346101	chr4:6345610-6345630	71	495:6	259	11	6.20E-06
LOC285484	285484	chr4:6344601-6346101	chr4:6345360-6345380	89	495:6	9	11	3.11E-06
GDAP1L1	78997	chr20:42309950-42311073	chr20:42310594-42310613	53	494:1	192	10	3.61E-06
GDAP1L1	78997	chr20:42309950-42311073	chr20:42310397-42310417	90	494:1	-5	11	3.11E-06
-	-	chr8:10987088-10988005	chr8:10987521-10987541	74	494:3	-13	11	3.11E-06
-	-	chr8:10987088-10988005	chr8:10987464-10987484	69	494:3	-70	11	3.11E-06
SRPK2	6733	chr7:103786187-103787352	chr7:103786693-103786713	85	491:0	2	11	3.11E-06
SRPK2	6733	chr7:103786187-103787352	chr7:103786269-103786289	71	491:0	-422	11	4.42E-05

SITPEC	51295	chr19:11500219-11501146	chr19:11500908-11500927	42	489:9	472	10	3.29E-05
SITPEC	51295	chr19:11500219-11501146	chr19:11500437-11500457	91	489:9	1	11	3.11E-06
-	-	chr3:171784384-171785789	chr3:171785196-171785216	96	489:5	-30	11	3.11E-06
BAI2	576	chr1:31857824-31859993	chr1:31858634-31858654	85	483:4	-15	11	3.11E-06
-	-	chr8:142968296-142969267	chr8:142968778-142968798	89	483:2	13	11	3.11E-06
-	-	chr9:119211802-119213473	chr9:119212837-119212857	88	482:2	40	11	3.11E-06
KIAA1045	23349	chr9:34973316-34974622	chr9:34974242-34974262	81	481:10	-14	11	3.11E-06
NTE	10908	chr19:7533582-7534334	chr19:7533901-7533921	76	479:2	12	11	3.11E-06
NTE	10908	chr19:7533582-7534334	chr19:7533880-7533900	83	479:2	-9	11	3.11E-06
AOAH	313	chr7:36864871-36866146	chr7:36865694-36865714	92	478:6	-2	11	3.11E-06
-	-	chr8:140327074-140328286	chr8:140327701-140327721	89	477:3	57	11	3.11E-06
-	-	chr14:81611397-81612403	chr14:81611856-81611876	85	477:3	-28	11	3.11E-06
-	-	chr11:84102727-84103236	chr11:84103125-84103151	52	476:1	26	17	3.11E-06
SPR	6697	chr2:73021905-73022833	chr2:73022313-73022322	53	475:4	-30	0	3.11E-06
MGC16703	113691	chr22:19688218-19689216	chr22:19688613-19688633	86	475:1	-10	11	3.11E-06
LOC283177	283177	chr11:133850454-133852408	chr11:133851711-133851738	41	474:2	8	18	3.11E-06
-	-	chr14:78065396-78066820	chr14:78066341-78066361	87	473:2	12	11	3.11E-06
NETO1	81832	chr18:68647968-68648991	chr18:68648533-68648553	85	472:3	-16	11	3.11E-06
MGC33835	222662	chr6:35880506-35881747	chr6:35881049-35881069	91	472:3	32	11	3.11E-06
MGAT5B	146664	chr17:72417383-72418712	chr17:72418000-72418020	75	471:4	231	11	8.04E-06
MGAT5B	146664	chr17:72417383-72418712	chr17:72417758-72417785	54	471:4	-7	18	3.11E-06
DKFZp761B0514	84249	chr5:139168087-139169079	chr5:139168521-139168541	84	469:2	5	11	3.11E-06
-	-	chr4:3830163-3831438	chr4:3830823-3830851	57	468:2	-10	19	3.11E-06
FLJ12650	79570	chr1:31323459-31324909	chr1:31324403-31324423	86	466:6	0	11	3.11E-06
PHACTR1	221692	chr6:12859714-12860548	chr6:12860112-12860132	70	465:3	5	11	3.11E-06
CACNA1A	773	chr19:13413516-13414696	chr19:13413874-13413894	90	464:5	1	11	3.11E-06
-	-	chr14:77693766-77694866	chr14:77694360-77694380	88	464:7	12	11	3.11E-06
-	-	chr14:77693766-77694866	chr14:77694303-77694323	78	464:7	-45	11	3.11E-06
SLC6A5	9152	chr11:20577540-20578450	chr11:20578038-20578058	93	462:5	-2	11	3.11E-06
FBXO2	26232	chr1:11630258-11631062	chr1:11630336-11630356	91	462:4	-1	11	3.11E-06
KCNC3	3748	chr19:55520123-55521585	chr19:55520818-55520838	78	461:3	0	11	3.11E-06
KCNC3	3748	chr19:55520123-55521585	chr19:55520586-55520606	70	461:3	-232	11	8.36E-06
F13A1	2162	chr6:6136523-6137478	chr6:6136904-6136924	78	460:1	13	11	3.11E-06
F13A1	2162	chr6:6136523-6137478	chr6:6136872-6136892	70	460:1	-19	11	3.11E-06
CHGB	1114	chr20:5839612-5840841	chr20:5840349-5840369	92	460:3	-15	11	3.11E-06
CACNA1H	8912	chr16:1177335-1179507	chr16:1178874-1178894	89	460:3	4	11	3.11E-06
-	-	chr1:207288028-207289137	chr1:207288521-207288541	86	459:1	-25	11	3.11E-06
R29124_1	90273	chr19:46786444-46787327	chr19:46786891-46786911	88	458:1	5	11	3.11E-06

-	-	chr11:116972690-116973399	chr11:116973198-116973218	89	458:1	-7	11	3.11E-06
MGC34646	157807	chr8:62570705-62571975	chr8:62571441-62571461	80	457:3	3	11	3.11E-06
KIAA1337	57540	chr1:11467757-11469016	chr1:11468141-11468161	86	457:2	2	11	3.11E-06
ACSL6	23305	chr5:131375646-131376915	chr5:131376300-131376320	87	457:4	7	11	3.11E-06
APLP1	333	chr19:41062299-41063146	chr19:41062716-41062736	92	456:1	0	11	3.11E-06
APLP1	333	chr19:41062299-41063146	chr19:41062705-41062724	42	456:1	-11	10	3.11E-06
BASE	317716	chr20:31260879-31261834	chr20:31261384-31261404	87	454:4	-22	11	3.11E-06
-	-	chr15:25510697-25512042	chr15:25511750-25511769	49	452:7	458	10	9.11E-05
SLC8A3	6547	chr14:69589358-69590374	chr14:69589659-69589684	59	451:3	6	16	3.11E-06
SLC8A3	6547	chr14:69589358-69590374	chr14:69589647-69589667	86	451:3	-9	11	3.11E-06
-	-	chr4:171119309-171120081	chr4:171119784-171119804	71	450:1	-13	11	3.11E-06
-	-	chr17:43217552-43218689	chr17:43218256-43218276	84	449:3	4	11	3.11E-06
-	-	chr3:10980886-10981970	chr3:10981454-10981474	81	447:1	38	11	3.11E-06
PHACTR3	116154	chr20:57773665-57774651	chr20:57774190-57774210	93	445:1	-4	11	3.11E-06
-	-	chr11:115754955-115756317	chr11:115755542-115755562	80	444:4	-3	11	3.11E-06
LOXHD1	125336	chr18:42335676-42337270	chr18:42336576-42336596	86	442:4	-4	11	3.11E-06
LOXHD1	125336	chr18:42335676-42337270	chr18:42336510-42336530	73	442:4	-70	11	3.11E-06
-	-	chr17:30056758-30057768	chr17:30057344-30057364	85	442:1	1	11	3.11E-06
FLJ22222	79701	chr17:77965570-77966706	chr17:77966061-77966081	87	441:2	1	11	3.11E-06
CREB3L3	84699	chr19:4123755-4124804	chr19:4124202-4124222	87	441:1	-11	11	3.11E-06
-	-	chr15:51151289-51152261	chr15:51151846-51151866	80	440:2	9	11	3.11E-06
NPHP4	261734	chr1:5841160-5842259	chr1:5841802-5841822	86	438:3	26	11	3.11E-06
-	-	chr14:88513689-88514564	chr14:88514056-88514076	82	438:4	-9	11	3.11E-06
RPL11	6135	chr1:23744684-23745691	chr1:23745061-23745081	92	434:1	3	11	3.11E-06
LOC388563	388563	chr19:60419544-60420642	chr19:60420313-60420333	94	434:7	-10	11	3.11E-06
FLJ35409	400765	chr1:98225407-98226333	chr1:98225963-98225990	65	434:6	-72	18	3.11E-06
-	-	chr2:119579607-119580886	chr2:119580285-119580305	100	434:0	-23	11	3.11E-06
SELP	6403	chr1:166296525-166297232	chr1:166296837-166296857	75	432:4	-14	11	3.11E-06
KCNAB2	8514	chr1:6046576-6047788	chr1:6046931-6046951	92	432:2	5	11	3.11E-06
INA	9118	chr10:105028146-105029294	chr10:105028754-105028774	90	430:3	-6	11	3.11E-06
-	-	chr1:237812651-237813652	chr1:237813046-237813066	79	429:3	8	11	3.11E-06
JPH3	57338	chr16:86252230-86253115	chr16:86252817-86252837	82	428:1	-2	11	3.11E-06
JPH3	57338	chr16:86252230-86253115	chr16:86252657-86252685	52	428:1	-158	19	3.11E-06
-	-	chr3:50538172-50539803	chr3:50538644-50538664	85	428:4	-33	11	3.11E-06
-	-	chr2:2302809-2303570	chr2:2303116-2303136	71	426:0	-16	11	3.11E-06
FLJ43860	389690	chr8:142595614-142596620	chr8:142596069-142596089	90	425:4	-23	11	3.11E-06
-	-	chr1:202159393-202160315	chr1:202159912-202159932	93	424:1	-27	11	3.11E-06
SYNJ1	8867	chr21:33021986-33023227	chr21:33022627-33022647	75	423:9	9	11	3.11E-06

-	-	chr6:105441815-105442343	chr6:105442105-105442125	78	421:1	35	11	3.11E-06
-	-	chr15:87763190-87764414	chr15:87763789-87763809	77	421:3	8	11	3.11E-06
-	-	chr15:87763190-87764414	chr15:87763784-87763809	56	421:3	6	16	3.11E-06
-	-	chr12:76029367-76030435	chr12:76029988-76030008	83	421:2	-35	11	3.11E-06
LOC286333	286333	chr9:112973405-112974430	chr9:112974226-112974246	73	419:5	393	11	5.03E-05
LOC286333	286333	chr9:112973405-112974430	chr9:112973838-112973858	82	419:5	5	11	3.11E-06
HMP19	51617	chr5:173405024-173405817	chr5:173405351-173405360	67	418:7	9	0	3.11E-06
-	-	chr5:176163428-176164873	chr5:176163722-176163742	84	417:1	-10	11	3.11E-06
-	-	chr3:128659218-128660841	chr3:128660397-128660417	88	417:2	13	11	3.11E-06
-	-	chr10:94136696-94137540	chr10:94137240-94137260	82	415:1	3	11	3.11E-06
-	-	chr16:13037678-13038610	chr16:13038137-13038157	90	414:1	-69	11	3.11E-06
LOC441617	441617	chr11:74621880-74623087	chr11:74622548-74622568	88	413:1	4	11	3.11E-06
-	-	chr20:61183319-61184881	chr20:61184252-61184278	78	412:4	8	17	3.11E-06
-	-	chr1:198295059-198296375	chr1:198295598-198295607	51	412:4	5	0	3.11E-06
-	-	chr22:29522904-29524076	chr22:29523466-29523486	92	411:4	31	11	3.11E-06
SLC6A18	348932	chr5:1299881-1301214	chr5:1300158-1300178	94	410:5	-31	11	3.11E-06
SATB2	23314	chr2:200005455-200006373	chr2:200005746-200005766	82	409:0	-24	11	3.11E-06
ANGPT4	51378	chr20:807000-808073	chr20:807572-807592	92	409:1	-6	11	3.11E-06
MGC18079	146395	chr16:27714133-27715814	chr16:27715007-27715027	91	408:3	-12	11	3.11E-06
-	-	chr1:7610314-7612008	chr1:7610854-7610874	85	406:3	-8	11	3.11E-06
GRID1	2894	chr10:87952998-87953863	chr10:87953422-87953442	78	405:3	16	11	3.11E-06
-	-	chr20:4491808-4492752	chr20:4492346-4492366	88	405:3	7	11	3.11E-06
LOC388459	388459	chr18:5858143-5859023	chr18:5858469-5858478	56	403:4	2	0	3.11E-06
FLJ32915	219844	chr11:125277933-125279370	chr11:125278747-125278767	87	403:6	17	11	3.11E-06
LOC391370	391370	chr2:41975523-41976371	chr2:41975947-41975967	70	401:2	29	11	3.11E-06
LOC391370	391370	chr2:41975523-41976371	chr2:41975906-41975926	81	401:2	-12	11	3.11E-06
-	-	chr16:54605039-54606273	chr16:54605545-54605565	90	401:0	6	11	3.11E-06
-	-	chr10:26696415-26697348	chr10:26696931-26696951	92	401:4	-3	11	3.11E-06
NPPA	4878	chr1:11839695-11840622	chr1:11840035-11840055	83	400:2	8	11	3.11E-06
-	-	chr10:121880590-121881312	chr10:121880841-121880868	72	399:4	-8	18	3.11E-06
SLC5A5	6528	chr19:17861355-17861885	chr19:17861601-17861621	94	398:1	8	11	3.11E-06
-	-	chr15:75832246-75833497	chr15:75832841-75832861	92	398:2	-23	11	3.11E-06
LHX5	64211	chr12:112380254-112381413	chr12:112380788-112380808	92	396:5	-24	11	3.11E-06
DRD3	1814	chr3:115380208-115381068	chr3:115380498-115380518	92	396:2	12	11	3.11E-06
PAX5	5079	chr9:37017096-37018237	chr9:37017678-37017706	48	395:4	-17	19	3.11E-06
LOC388494	388494	chr19:3827997-3828422	chr19:3828091-3828111	83	394:0	30	11	3.11E-06
PLXNA4	57671	chr7:130887349-130888386	chr7:130887825-130887845	92	393:5	22	11	3.11E-06
-	-	chr20:44354664-44355736	chr20:44355306-44355315	38	393:5	40	0	3.11E-06

SYT5	6861	chr19:60381709-60383858	chr19:60383798-60383817	54	392:9	409	10	9.11E-05
SYT5	6861	chr19:60381709-60383858	chr19:60383379-60383399	89	392:9	-10	11	3.11E-06
DNAI1	27019	chr9:34483729-34484736	chr9:34484135-34484155	87	392:3	-3	11	3.11E-06
-	-	chr6:39212832-39213611	chr6:39213202-39213222	87	392:1	5	11	3.11E-06
PDE4C	5143	chr19:18204734-18206474	chr19:18205508-18205536	48	390:3	398	19	4.10E-06
PDE4C	5143	chr19:18204734-18206474	chr19:18205437-18205462	57	390:3	326	16	4.15E-06
PDE4C	5143	chr19:18204734-18206474	chr19:18205186-18205214	47	390:3	76	19	3.11E-06
PDE4C	5143	chr19:18204734-18206474	chr19:18205115-18205141	61	390:3	4	17	3.11E-06
LGALS13	29124	chr19:44781032-44782221	chr19:44781792-44781812	91	390:2	-8	11	3.11E-06
-	-	chr5:7147468-7148533	chr5:7147933-7147953	87	390:3	21	11	3.11E-06
-	-	chr17:74699503-74701072	chr17:74700649-74700675	56	389:9	334	17	1.87E-05
-	-	chr17:74699503-74701072	chr17:74700352-74700372	89	389:9	34	11	3.11E-06
-	-	chr14:78055677-78057238	chr14:78056136-78056156	89	389:1	6	11	3.11E-06
ALK	238	chr2:29428103-29429136	chr2:29428529-29428555	54	387:2	-28	17	3.11E-06
JPH3	57338	chr16:86198780-86200038	chr16:86199695-86199715	88	385:3	59	11	3.11E-06
SCG2	7857	chr2:224292135-224293030	chr2:224292581-224292600	54	384:1	4	10	3.11E-06
SLC39A3	29985	chr19:2690973-2691745	chr19:2691268-2691296	50	383:0	4	19	3.11E-06
CDH22	64405	chr20:44292265-44293854	chr20:44293179-44293199	81	383:5	-3	11	3.11E-06
CDH22	64405	chr20:44292265-44293854	chr20:44292888-44292908	88	383:5	-294	11	4.21E-06
GRM4	2914	chr6:34190720-34191731	chr6:34191683-34191702	43	382:0	404	10	3.66E-05
GRM4	2914	chr6:34190720-34191731	chr6:34191281-34191301	80	382:0	2	11	3.11E-06
-	-	chr8:104582814-104583858	chr8:104583305-104583325	77	380:7	5	11	3.11E-06
-	-	chr8:104582814-104583858	chr8:104583068-104583094	53	380:7	-229	17	3.11E-06
-	-	chr17:29850485-29851432	chr17:29850866-29850886	83	380:2	3	11	3.11E-06
-	-	chr13:26001170-26002197	chr13:26001752-26001772	82	380:3	-1	11	3.11E-06
-	-	chr12:111691575-111692815	chr12:111692072-111692092	91	380:2	-32	11	3.11E-06
KIAA0789	9671	chr12:107110152-107111375	chr12:107110920-107110940	84	379:5	41	11	3.11E-06
FLJ44674	400535	chr16:47936984-47937856	chr16:47937418-47937438	89	379:2	-7	11	3.11E-06
CHRN2	1141	chr1:151352688-151354138	chr1:151353502-151353522	100	379:2	4	11	3.11E-06
-	-	chr1:112118979-112120216	chr1:112119729-112119749	81	378:7	-40	11	3.11E-06
-	-	chr1:112118979-112120216	chr1:112119314-112119334	71	378:7	-455	11	2.75E-05
SLC8A2	6543	chr19:52639250-52640263	chr19:52639553-52639573	89	377:5	-9	11	3.11E-06
-	-	chr9:132018714-132019645	chr9:132019218-132019238	93	377:2	10	11	3.11E-06
MGC8407	79012	chr3:49879860-49881547	chr3:49880519-49880544	64	375:7	135	16	3.11E-06
MGC8407	79012	chr3:49879860-49881547	chr3:49880382-49880402	75	375:7	-5	11	3.11E-06
-	-	chr13:26339146-26340437	chr13:26339782-26339802	86	375:8	19	11	3.11E-06
LRFN3	79414	chr19:41145907-41146959	chr19:41146481-41146501	83	374:5	-13	11	3.11E-06
-	-	chr2:137173451-137174734	chr2:137174100-137174127	65	374:6	-27	18	3.11E-06

PSMB2	5690	chr1:35795150-35795899	chr1:35795850-35795870	82	373:1	29	11	3.11E-06
PSMB2	5690	chr1:35795150-35795899	chr1:35795749-35795769	72	373:1	-72	11	3.11E-06
-	-	chr9:131680819-131681938	chr9:131681603-131681623	79	373:2	0	11	3.11E-06
-	-	chr9:131680819-131681938	chr9:131681346-131681366	79	373:2	-257	11	5.67E-06
LOC389204	389204	chr4:26956137-26957512	chr4:26956701-26956721	83	372:7	5	11	3.11E-06
LOC339568	339568	chr20:37257380-37258521	chr20:37257980-37257999	60	372:4	4	10	3.11E-06
LOC339568	339568	chr20:37257380-37258521	chr20:37257798-37257818	71	372:4	-178	11	3.11E-06
CHS1	1130	chr1:232137612-232138909	chr1:232138408-232138434	70	372:7	8	17	3.11E-06
-	-	chr6:110682793-110683882	chr6:110683450-110683470	81	372:5	-10	11	3.11E-06
-	-	chr6:110682793-110683882	chr6:110683375-110683403	52	372:5	-81	19	3.11E-06
-	-	chr15:75781321-75782595	chr15:75782068-75782088	87	372:5	29	11	3.11E-06
EPHB1	2047	chr3:136307736-136308721	chr3:136308256-136308276	81	371:2	40	11	3.11E-06
CYP4F8	11283	chr19:15603315-15604079	chr19:15603737-15603757	93	369:0	-66	11	3.11E-06
-	-	chr1:50457282-50458350	chr1:50457845-50457865	86	369:3	15	11	3.11E-06
TNNI3K	51086	chr1:74679730-74680731	chr1:74680300-74680320	76	368:2	20	11	3.11E-06
TNNI3K	51086	chr1:74679730-74680731	chr1:74679963-74679983	72	368:2	-317	11	3.52E-05
LOC170425	170425	chr10:86040992-86041756	chr10:86041350-86041375	51	368:4	12	16	3.11E-06
LOC170425	170425	chr10:86040992-86041756	chr10:86041292-86041312	78	368:4	-49	11	3.11E-06
-	-	chr2:94846816-94847762	chr2:94847057-94847082	68	368:4	-17	16	3.11E-06
-	-	chr2:94846816-94847762	chr2:94846836-94846856	70	368:4	-241	11	3.54E-06
YIF1	10897	chr11:65813051-65814285	chr11:65813757-65813782	70	367:11	18	16	3.11E-06
-	-	chr10:102430219-102431232	chr10:102430660-102430680	83	367:2	77	11	3.11E-06
CHST8	64377	chr19:38950549-38951074	chr19:38950793-38950813	80	366:2	0	11	3.11E-06
USP7	7874	chr16:8932809-8934197	chr16:8933388-8933408	97	365:3	1	11	3.11E-06
-	-	chr8:129226193-129226986	chr8:129226502-129226522	86	365:3	-1	11	3.11E-06
-	-	chr17:30148482-30149318	chr17:30149007-30149027	87	363:4	5	11	3.11E-06
MAPK8IP2	23542	chr22:49328460-49329050	chr22:49328851-49328876	56	362:0	18	16	3.11E-06
RIMS4	140730	chr20:42838548-42840197	chr20:42839236-42839256	94	361:5	-7	11	3.11E-06
-	-	chr7:75475721-75476224	chr7:75475873-75475882	49	361:0	1	0	3.11E-06
-	-	chr8:136401352-136402450	chr8:136401974-136401994	89	360:2	0	11	3.11E-06
PPAPDC1	196051	chr10:122262965-122264212	chr10:122263709-122263729	90	359:3	-7	11	3.11E-06
ASTN2	23245	chr9:116839943-116840755	chr9:116840297-116840317	81	358:4	21	11	3.11E-06
SALPR	51289	chr5:33970537-33972430	chr5:33971946-33971966	92	357:8	-5	11	3.11E-06
-	-	chr14:48840045-48841078	chr14:48840598-48840618	70	357:2	-9	11	3.11E-06
-	-	chr14:48840045-48841078	chr14:48840592-48840618	52	357:2	-12	17	3.11E-06
-	-	chr1:29878184-29879619	chr1:29878719-29878739	95	357:2	8	11	3.11E-06
-	-	chr8:68935205-68936205	chr8:68935610-68935630	80	355:5	-8	11	3.11E-06
-	-	chr7:103861766-103862561	chr7:103862125-103862145	88	355:3	-15	11	3.11E-06

MGC35338	130619	chr2:219735969-219736844	chr2:219736368-219736388	86	354:3	-4	11	3.11E-06
GPR78	27201	chr4:8699671-8700868	chr4:8700836-8700862	56	354:2	321	17	3.66E-05
GPR78	27201	chr4:8699671-8700868	chr4:8700821-8700841	73	354:2	303	11	2.75E-05
GPR78	27201	chr4:8699671-8700868	chr4:8700511-8700531	89	354:2	-7	11	3.11E-06
GPR78	27201	chr4:8699671-8700868	chr4:8700473-8700492	50	354:2	-45	10	3.11E-06
-	-	chr5:71394416-71395415	chr5:71394985-71395005	93	354:2	7	11	3.11E-06
FLJ14627	84900	chr12:115758572-115759424	chr12:115758770-115758779	27	353:1	10	0	3.11E-06
-	-	chr17:32133428-32135114	chr17:32134527-32134547	90	352:2	-9	11	3.11E-06
-	-	chr1:50445829-50446479	chr1:50445941-50445961	84	352:3	24	11	3.11E-06
SEC14L3	266629	chr22:29179597-29180701	chr22:29180035-29180055	83	350:7	-3	11	3.11E-06
LILRB4	11006	chr19:59887360-59888021	chr19:59887785-598887804	55	350:0	66	10	3.11E-06
LILRB4	11006	chr19:59887360-59888021	chr19:59887757-598887777	70	350:0	38	11	3.11E-06
LILRB4	11006	chr19:59887360-59888021	chr19:59887712-598887732	86	350:0	-7	11	3.11E-06
HTR3A	3359	chr11:113366777-113367922	chr11:113367278-113367298	91	350:7	6	11	3.11E-06
-	-	chr16:22945359-22946344	chr16:22945778-22945798	82	350:0	12	11	3.11E-06
-	-	chr17:47301386-47302602	chr17:47301926-47301946	86	349:2	48	11	3.11E-06
SHOX2	6474	chr3:159298438-159299274	chr3:159299056-159299083	48	348:5	294	18	2.36E-05
MFNG	4242	chr22:36182887-36184275	chr22:36183623-36183643	94	348:4	35	11	3.11E-06
GRIK3	2899	chr1:37154753-37156392	chr1:37155553-37155573	89	348:1	-11	11	3.11E-06
-	-	chr3:128434600-128435709	chr3:128435083-128435103	85	348:4	-15	11	3.11E-06
SI00A7	6278	chr1:150237814-150238234	chr1:150238148-150238168	87	347:1	37	11	3.11E-06
-	-	chr1:95561865-95562730	chr1:95562332-95562352	89	346:2	-14	11	3.11E-06
LOC441351	441351	chr8:65454618-65455965	chr8:65455193-65455213	92	345:2	23	11	3.11E-06
LOC389777	389777	chr9:97228732-97229578	chr9:97229160-97229180	72	345:4	-29	11	3.11E-06
LOC343578	343578	chr20:36742035-36743323	chr20:36742761-36742781	76	345:3	18	11	3.11E-06
-	-	chr17:28679026-28680020	chr17:28679446-28679466	84	345:0	3	11	3.11E-06
LOC440000	440000	chr10:102829866-102831315	chr10:102830876-102830896	85	344:0	-12	11	3.11E-06
LOC440000	440000	chr10:102829866-102831315	chr10:102830706-102830726	70	344:0	-182	11	3.11E-06
LOC440000	440000	chr10:102829866-102831315	chr10:102830672-102830692	72	344:0	-216	11	3.50E-06
-	-	chr15:72344000-72345136	chr15:72344618-72344638	89	343:1	-32	11	3.11E-06
-	-	chr11:45521695-45522589	chr11:45522150-45522170	87	342:1	-9	11	3.11E-06
CADPS	8618	chr3:62489882-62490469	chr3:62490133-62490153	75	341:0	-7	11	3.11E-06
-	-	chr20:62263370-62264209	chr20:62263901-62263921	73	341:0	47	11	3.11E-06
-	-	chr20:62263370-62264209	chr20:62263854-62263874	82	341:0	0	11	3.11E-06
RYR1	6261	chr19:43637316-43638362	chr19:43637716-43637736	82	340:2	-9	11	3.11E-06
UNC13A	23025	chr19:17653192-17653756	chr19:17653561-17653581	94	339:0	6	11	3.11E-06
NOS2A	4843	chr17:23113835-23114709	chr17:23114276-23114296	91	339:3	-5	11	3.11E-06
GBF1	8729	chr10:104111022-104111802	chr10:104111646-104111666	81	339:4	3	11	3.11E-06



CDK5R2	8941	chr2:219651841-219653858	chr2:219653243-219653263	91	338:5	-17	11	3.24E-06
CDK5R2	8941	chr2:219651841-219653858	chr2:219652279-219652299	71	338:5	-981	11	1.83E-05
CDK5R2	8941	chr2:219651841-219653858	chr2:219652203-219652223	85	338:5	-1057	11	1.83E-05
-	-	chr3:63028339-63029326	chr3:63028921-63028941	92	338:3	1	11	3.11E-06
TU3A	11170	chr3:58548557-58549413	chr3:58548972-58548992	79	337:2	-1	11	3.11E-06
KIAA1423	57583	chr6:158926982-158928024	chr6:158927637-158927657	92	337:3	-2	11	3.11E-06
-	-	chr9:131678719-131680172	chr9:131679012-131679032	84	337:2	-20	11	3.11E-06
-	-	chr9:23819167-23820127	chr9:23819769-23819789	81	336:2	13	11	3.11E-06
MLN	4295	chr6:33888234-33888859	chr6:33888621-33888641	91	335:1	3	11	3.11E-06
MAD2L1BP	9587	chr6:43710876-43711918	chr6:43711252-43711272	87	335:11	20	11	3.11E-06
SYN1	6853	chrX:47235291-47236140	chrX:47235722-47235742	94	333:1	-76	11	3.11E-06
ZNF579	163033	chr19:60784062-60785315	chr19:60784700-60784720	89	332:7	-9	11	3.11E-06
MEGF11	84465	chr15:64031527-64032821	chr15:64032022-64032042	85	332:3	23	11	3.11E-06
IREM2	342510	chr17:70117563-70118395	chr17:70118033-70118053	91	332:2	16	11	3.11E-06
-	-	chr16:67039320-67040478	chr16:67039904-67039931	66	332:7	29	18	3.11E-06
-	-	chr1:93233437-93234315	chr1:93233987-93234007	77	332:2	-48	11	3.11E-06
SLC8A2	6543	chr19:52666877-52667536	chr19:52667192-52667219	77	331:2	15	18	3.11E-06
CEACAM5	1048	chr19:46900865-46902008	chr19:46901401-46901421	84	331:2	5	11	3.11E-06
-	-	chr1:111054432-111055358	chr1:111054958-111054978	77	331:2	27	11	3.11E-06
LOC442435	442435	chr9:136089442-136090203	chr9:136089957-136089977	85	330:2	56	11	3.11E-06
LOC442435	442435	chr9:136089442-136090203	chr9:136089880-136089900	85	330:2	-21	11	3.11E-06
SYCN	342898	chr19:44406084-44406795	chr19:44406357-44406377	83	328:3	-9	11	3.11E-06
PDE2A	5138	chr11:72065081-72066287	chr11:72065649-72065669	84	328:2	-5	11	3.11E-06
LOC400600	400600	chr17:39741052-39742312	chr17:39741501-39741521	85	328:3	5	11	3.11E-06
LOC390278	390278	chr11:134402060-134402936	chr11:134402771-134402780	56	328:2	1	0	3.11E-06
-	-	chr1:58468191-58469025	chr1:58468552-58468572	80	327:6	34	11	3.11E-06
-	-	chr3:140999057-141000037	chr3:140999466-140999486	95	326:1	0	11	3.11E-06
-	-	chr12:107364089-107364925	chr12:107364746-107364766	86	326:2	9	11	3.11E-06
LOC90113	90113	chr3:185440275-185441689	chr3:185441034-185441054	79	325:2	-20	11	3.11E-06
STK32C	282974	chr10:133957797-133958883	chr10:133958241-133958261	80	324:14	6	11	3.11E-06
NP220	27332	chr2:71485978-71487706	chr2:71487275-71487295	86	324:1	821	11	6.84E-06
NP220	27332	chr2:71485978-71487706	chr2:71486458-71486478	80	324:1	4	11	4.32E-06
-	-	chr9:34420711-34421536	chr9:34420931-34420951	82	324:7	30	11	3.11E-06
-	-	chr5:146184720-146185289	chr5:146184986-146185006	80	323:2	7	11	3.11E-06
-	-	chr1:112426647-112427610	chr1:112427179-112427199	84	323:1	33	11	3.11E-06
VMP	140767	chr6:24234712-24235780	chr6:24235163-24235183	82	322:6	-7	11	3.11E-06
IRS1	3667	chr2:227500845-227501648	chr2:227501435-227501455	88	322:0	16	11	3.11E-06
-	-	chr16:87603229-87604110	chr16:87603528-87603548	87	322:5	-4	11	3.11E-06

KIAA0408	9729	chr6:127878411-127880128	chr6:127879077-127879097	72	320:13	-14	11	3.11E-06
-	-	chr5:75435267-75436362	chr5:75435819-75435839	80	320:0	86	11	3.11E-06
-	-	chr13:99246256-99247222	chr13:99246648-99246668	89	319:4	9	11	3.11E-06
-	-	chr12:112501809-112502979	chr12:112502396-112502416	92	318:6	-3	11	3.11E-06
-	-	chr1:37100571-37101556	chr1:37101149-37101169	89	318:0	-7	11	3.11E-06
-	-	chr1:37100571-37101556	chr1:37101112-37101139	47	318:0	-40	18	3.11E-06
NTNG1	22854	chr1:107389926-107390837	chr1:107390305-107390325	87	317:1	11	11	3.11E-06
LOC146713	146713	chr17:74801586-74802794	chr17:74802456-74802484	48	317:2	117	19	3.11E-06
LOC146713	146713	chr17:74801586-74802794	chr17:74802332-74802352	95	317:2	-11	11	3.11E-06
-	-	chr19:41158121-41158795	chr19:41158550-41158570	76	317:1	-20	11	3.11E-06
SEZ6	124925	chr17:24356562-24357574	chr17:24357166-24357186	90	316:0	7	11	3.11E-06
HSGP25L2G	54732	chr5:176940947-176941570	chr5:176941369-176941389	88	314:0	5	11	3.11E-06
-	-	chr3:42316244-42317103	chr3:42316659-42316685	61	313:2	-10	17	3.11E-06
-	-	chr1:172426090-172427345	chr1:172426640-172426660	89	313:1	-20	11	3.11E-06
STK29	9024	chr11:1379226-1380279	chr11:1379634-1379654	70	312:0	114	11	3.11E-06
LOC388617	388617	chr1:35041752-35043034	chr1:35042365-35042385	87	312:1	8	11	3.11E-06
-	-	chr19:45318558-45319393	chr19:45318813-45318833	85	312:1	-12	11	3.11E-06
-	-	chr15:57972297-57973210	chr15:57972627-57972647	81	312:3	-41	11	3.11E-06
LOC441850	441850	chr19:44827934-44829105	chr19:44828486-44828506	91	311:3	7	11	3.11E-06
GPR26	2849	chr10:125408982-125409496	chr10:125409052-125409078	60	310:0	-34	17	3.11E-06
-	-	chr15:68052106-68053374	chr15:68052738-68052747	61	310:5	-7	0	3.11E-06
-	-	chr1:172443392-172444840	chr1:172444469-172444497	50	310:3	542	19	1.87E-05
-	-	chr1:172443392-172444840	chr1:172444321-172444349	41	310:3	394	19	1.74E-05
-	-	chr1:172443392-172444840	chr1:172443952-172443972	85	310:3	21	11	3.11E-06
-	-	chr1:172443392-172444840	chr1:172443525-172443545	71	310:3	-406	11	7.34E-05
PDE4C	5143	chr19:18210917-18211802	chr19:18211353-18211373	84	309:1	5	11	3.11E-06
NR1H4	9971	chr12:99435239-99436201	chr12:99435638-99435658	86	309:1	-15	11	3.11E-06
FLJ45530	400555	chr16:87154591-87155354	chr16:87154828-87154848	71	309:0	44	11	3.11E-06
FLJ45530	400555	chr16:87154591-87155354	chr16:87154823-87154848	56	309:0	42	16	3.11E-06
FLJ45530	400555	chr16:87154591-87155354	chr16:87154799-87154819	89	309:0	15	11	3.11E-06
EGR4	1961	chr2:73428908-73430386	chr2:73430053-73430079	75	309:7	-7	17	3.11E-06
NXPH1	30010	chr7:8536581-8537562	chr7:8537121-8537141	82	308:10	-7	11	3.11E-06
BRUNOL4	56853	chr18:33317227-33318314	chr18:33317719-33317739	85	308:1	20	11	3.11E-06
-	-	chr12:65873334-65874333	chr12:65873937-65873957	77	308:3	10	11	3.11E-06
KIAA0450	9651	chr1:2430942-2432300	chr1:2431794-2431814	86	307:0	-7	11	3.11E-06
LOC388394	388394	chr17:42396448-42397400	chr17:42396844-42396864	91	306:1	-4	11	3.11E-06
SCNN1G	6340	chr16:23093217-23094199	chr16:23093649-23093669	78	305:2	54	11	3.11E-06
-	-	chr12:99722357-99723500	chr12:99722767-99722787	83	305:1	-21	11	3.11E-06

TRAF1	7185	chr9:120755271-120756284	chr9:120755802-120755822	83	304:4	-3	11	3.11E-06
TRAF1	7185	chr9:120755271-120756284	chr9:120755433-120755453	70	304:4	-372	11	2.43E-05
LOC440599	440599	chr1:110410236-110411220	chr1:110410756-110410776	83	304:4	-1	11	3.11E-06
GPR51	9568	chr9:98551839-98552806	chr9:98552403-98552423	73	304:0	-20	11	3.11E-06
-	-	chr11:112849850-112850725	chr11:112850430-112850450	89	304:2	44	11	3.11E-06
-	-	chr11:112849850-112850725	chr11:112850217-112850237	71	304:2	-169	11	3.96E-06
SORBS1	10580	chr10:97141610-97142276	chr10:97141906-97141926	84	303:6	-37	11	3.11E-06
SORBS1	10580	chr10:97141610-97142276	chr10:97141787-97141807	71	303:6	-156	11	3.11E-06
NEUROD2	4761	chr17:35001841-35003112	chr17:35002298-35002318	93	303:1	12	11	3.11E-06
HSPC056	25852	chr3:139398445-139399173	chr3:139398828-139398848	75	302:3	2	11	3.11E-06
CACNA1B	774	chr9:138054073-138055448	chr9:138055024-138055044	93	302:5	-12	11	3.11E-06
CACNA1B	774	chr9:138054073-138055448	chr9:138054919-138054938	43	302:5	-117	10	3.11E-06
LOC149297	149297	chr1:162770132-162770892	chr1:162770489-162770509	83	301:1	-5	11	3.11E-06
E1F2C1	26523	chr1:36011607-36012352	chr1:36011861-36011881	84	301:1	-8	11	3.11E-06
FLJ46361	375940	chr10:124535551-124536493	chr10:124535973-124535993	78	300:5	1	11	3.11E-06
CSPG3	1463	chr19:19186329-19187638	chr19:19186935-19186955	93	300:4	-4	11	3.11E-06
PSMF1	9491	chr20:1099662-1100744	chr20:1100305-1100325	89	299:4	22	11	3.11E-06
POU2F2	5452	chr19:47335970-47336938	chr19:47336173-47336193	71	299:5	-154	11	3.11E-06
MGC39827	160777	chr12:118413027-118414320	chr12:118413949-118413977	40	298:1	390	19	2.75E-05
MGC39827	160777	chr12:118413027-118414320	chr12:118413592-118413612	86	298:1	29	11	3.11E-06
LOC124976	124976	chr17:4342994-4343750	chr17:4343487-4343507	82	298:4	11	11	3.11E-06
-	-	chr9:123133393-123134581	chr9:123133779-123133799	82	298:2	17	11	3.11E-06
-	-	chr1:37544997-37546041	chr1:37545611-37545631	87	298:1	-9	11	3.11E-06
CEACAM8	1088	chr19:47797734-47798545	chr19:47798001-47798021	80	297:1	1	11	3.11E-06
-	-	chr1:206694237-206695076	chr1:206694520-206694540	82	297:1	9	11	3.11E-06
FSTL4	23105	chr5:132929331-132930152	chr5:132929758-132929778	84	296:1	-8	11	3.11E-06
-	-	chr17:31893716-31894916	chr17:31894108-31894133	72	296:2	-19	16	3.11E-06
POU4F2	5458	chr4:147922382-147923120	chr4:147922774-147922794	78	295:3	30	11	3.11E-06
OLFM3	118427	chr1:102174044-102175109	chr1:102174643-102174663	91	294:5	-26	11	3.11E-06
SLC17A6	57084	chr11:22315365-22316143	chr11:22315871-22315891	89	293:1	-18	11	3.11E-06
KIAA1173	57467	chr3:42717683-42718556	chr3:42718110-42718130	80	293:3	-6	11	3.11E-06
-	-	chr8:135490453-135491601	chr8:135491187-135491207	82	293:4	-26	11	3.11E-06
-	-	chr11:118894529-118895462	chr11:118894960-118894980	70	292:7	64	11	3.11E-06
-	-	chr11:118894529-118895462	chr11:118894876-118894896	79	292:7	-20	11	3.11E-06
KREMEN2	79412	chr16:2958473-2959327	chr16:2958931-2958951	81	291:3	-4	11	3.11E-06
HABP2	3026	chr10:115326414-115327555	chr10:115326774-115326794	83	291:3	11	11	3.11E-06
IPO13	9670	chr1:44102527-44103701	chr1:44103278-44103298	89	290:1	3	11	3.11E-06
-	-	chr7:75499150-75500248	chr7:75500047-75500067	69	288:2	522	11	5.42E-05

-	-	chr7:75499150-75500248	chr7:75499518-75499538	90	288:2	-7	11	3.11E-06
MAPK11	5600	chr22:49011302-49012694	chr22:49011820-49011840	83	287:5	4	11	3.11E-06
KCNH8	131096	chr3:19165609-19166621	chr3:19166072-19166092	83	287:1	-21	11	3.11E-06
HPCA	3208	chr1:33021162-33022237	chr1:33021458-33021477	53	286:4	-9	10	3.11E-06
HPCA	3208	chr1:33021162-33022237	chr1:33021364-33021384	77	286:4	-103	11	3.11E-06
-	-	chr1:37389569-37390740	chr1:37390291-37390311	95	286:4	-13	11	3.11E-06
DPP6	1804	chr7:153190071-153190860	chr7:153190428-153190448	86	283:0	19	11	3.11E-06
-	-	chr20:40086419-40087304	chr20:40086889-40086909	79	283:0	4	11	3.11E-06
-	-	chr16:67035233-67036174	chr16:67035648-67035668	76	282:3	-25	11	3.11E-06
FLJ25555	124930	chr17:24944858-24945770	chr17:24945470-24945496	58	281:5	24	17	3.11E-06
FLJ25555	124930	chr17:24944858-24945770	chr17:24945449-24945468	54	281:5	0	10	3.11E-06
FLJ25555	124930	chr17:24944858-24945770	chr17:24945448-24945468	73	281:5	-1	11	3.11E-06
-	-	chr3:68438207-68439163	chr3:68438590-68438610	85	281:1	26	11	3.11E-06
RYR3	6263	chr15:31627258-31628096	chr15:31627594-31627603	25	280:2	11	0	3.11E-06
RSU1	6251	chr10:16694078-16694686	chr10:16694443-16694463	86	279:3	11	11	3.11E-06
-	-	chr8:41872212-41873199	chr8:41872735-41872755	90	278:2	0	11	3.11E-06
-	-	chr2:26972490-26973622	chr2:26973178-26973204	61	277:4	-5	17	3.11E-06
LOC442144	442144	chr5:174681409-174682095	chr5:174681721-174681741	93	276:2	-10	11	3.11E-06
LOC441790	441790	chr17:23359392-23360152	chr17:23359892-23359912	76	276:1	89	11	3.11E-06
LOC441790	441790	chr17:23359392-23360152	chr17:23359827-23359853	69	276:1	27	17	3.11E-06
GRIK2	2898	chr6:101950812-101952114	chr6:101951403-101951423	72	276:3	62	11	3.24E-06
GRIK2	2898	chr6:101950812-101952114	chr6:101951337-101951357	91	276:3	-4	11	3.11E-06
-	-	chr12:106900248-106901281	chr12:106900842-106900862	79	276:2	-46	11	3.11E-06
-	-	chr5:95845250-95845973	chr5:95845512-95845532	86	275:5	-5	11	3.11E-06
-	-	chr3:2320009-2320721	chr3:2320418-2320444	63	274:2	-43	17	3.11E-06
TRPM8	79054	chr2:234603137-234604271	chr2:234603645-234603665	86	273:2	-22	11	3.11E-06
TRPM8	79054	chr2:234603137-234604271	chr2:234603633-234603653	76	273:2	-34	11	3.11E-06
-	-	chr9:36738072-36738922	chr9:36738499-36738519	81	273:2	13	11	3.11E-06
-	-	chr9:36738072-36738922	chr9:36738312-36738332	73	273:2	-174	11	3.59E-06
LOC283849	283849	chr16:65776216-65777266	chr16:65776916-65776936	81	272:4	8	11	3.11E-06
-	-	chr1:112337771-112338744	chr1:112338352-112338372	81	271:0	4	11	3.11E-06
-	-	chr1:18327887-18328692	chr1:18328640-18328660	71	271:2	363	11	3.80E-05
-	-	chr1:18327887-18328692	chr1:18328293-18328313	88	271:2	16	11	3.11E-06
CYP4F8	11283	chr19:15595294-15596209	chr19:15595709-15595735	58	270:1	-8	17	3.11E-06
CABP7	164633	chr22:28437030-28438143	chr22:28437472-28437492	91	269:2	2	11	3.11E-06
ACCN3	9311	chr7:150185627-150186328	chr7:150186185-150186205	71	268:1	269	11	8.04E-06
ACCN3	9311	chr7:150185627-150186328	chr7:150185970-150185990	82	268:1	54	11	3.11E-06
-	-	chr14:98115718-98117170	chr14:98116546-98116566	87	268:1	-20	11	3.11E-06

TNRC4	11189	chr1:148502312-148503572	chr1:148502648-148502668	85	267:6	-14	11	3.61E-06
BEX1	55859	chrX:102123734-102124697	chrX:102124398-102124418	84	267:4	-2	11	3.11E-06
LOC391345	391345	chr2:2692939-2693713	chr2:2693241-2693261	81	266:1	-36	11	3.11E-06
LOC391345	391345	chr2:2692939-2693713	chr2:2693062-2693087	45	266:1	-212	16	3.59E-06
DOCK5	80005	chr8:25249265-25250145	chr8:25249671-25249691	76	266:1	-42	11	3.11E-06
LOC387765	387765	chr11:46370530-46371388	chr11:46370840-46370860	89	265:1	23	11	3.11E-06
FLJ33360	401172	chr5:6380978-6381938	chr5:6381430-6381456	61	265:8	15	17	3.11E-06
-	-	chr9:77419961-77421122	chr9:77420454-77420474	90	265:2	-2	11	3.11E-06
-	-	chr5:136816685-136817629	chr5:136817255-136817275	89	265:1	-5	11	3.11E-06
-	-	chr2:58972678-58973893	chr2:58973376-58973396	80	265:0	2	11	3.11E-06
-	-	chr17:29907134-29908506	chr17:29907692-29907712	82	265:4	25	11	3.11E-06
-	-	chr18:69726184-69727282	chr18:69726703-69726723	76	262:2	-3	11	3.11E-06
-	-	chr18:69726184-69727282	chr18:69726302-69726328	53	262:2	-401	17	3.39E-05
PRRXL1	117065	chr10:50275748-50276669	chr10:50276175-50276195	79	261:2	21	11	3.11E-06
C20orf39	79953	chr20:24505721-24506808	chr20:24506327-24506347	80	261:7	16	11	3.11E-06
-	-	chr4:180393491-180394667	chr4:180394234-180394254	87	261:3	21	11	3.11E-06
-	-	chr2:44154784-44155740	chr2:44155259-44155279	85	261:0	1	11	3.11E-06
PPP2R2C	5522	chr4:6482322-6483110	chr4:6482903-6482923	90	260:3	29	11	3.11E-06
TREM2	54209	chr6:41242398-41243546	chr6:41243037-41243057	81	259:4	-15	11	3.39E-06
TREM2	54209	chr6:41242398-41243546	chr6:41243008-41243028	73	259:4	-44	11	3.31E-06
LOC387762	387762	chr11:43554586-43555726	chr11:43555274-43555302	55	259:3	-10	19	3.11E-06
CPLX2	10814	chr5:175231083-175231846	chr5:175231496-175231516	93	259:3	-8	11	3.11E-06
LOC441779	441779	chr16:87631076-87632238	chr16:87631652-87631672	91	258:4	-5	11	3.11E-06
-	-	chr16:46561499-46562470	chr16:46561911-46561931	80	258:2	-5	11	3.11E-06
-	-	chr12:107920903-107921846	chr12:107921465-107921491	69	257:0	-5	17	3.11E-06
AOX1	316	chr2:201282778-201283714	chr2:201283157-201283177	83	256:5	-7	11	3.11E-06
-	-	chr6:38305294-38305976	chr6:38305695-38305715	87	256:3	47	11	3.11E-06
PAK7	57144	chr20:9588661-9589565	chr20:9589060-9589080	90	255:1	19	11	3.11E-06
FGF14	2259	chr13:101855863-101856679	chr13:101856242-101856262	76	255:3	-3	11	3.11E-06
-	-	chr14:73973881-73974708	chr14:73974302-73974322	77	255:3	-14	11	3.11E-06
SH3GL2	6456	chr9:17734503-17735422	chr9:17734971-17734991	87	254:4	-3	11	3.11E-06
ASTN2	23245	chr9:116876432-116877151	chr9:116876881-116876901	87	254:2	-20	11	3.11E-06
-	-	chr16:6183529-6184492	chr16:6183922-6183942	73	254:1	55	11	3.11E-06
KIF13A	63971	chr6:17876312-17877019	chr6:17876734-17876754	74	253:4	-39	11	3.11E-06
GNAO1	2775	chr16:54785254-54786324	chr16:54785898-54785907	38	253:1	-6	0	3.11E-06
-	-	chr7:130007373-130008252	chr7:130007654-130007674	90	252:3	1	11	3.11E-06
-	-	chr5:138026135-138026803	chr5:138026367-138026387	89	251:2	7	11	3.11E-06
LOC390638	390638	chr15:89531249-89531930	chr15:89531677-89531697	82	250:0	-18	11	3.11E-06

BCAN	63827	chr1:153434516-153435436	chr1:153435072-153435092	93	250:1	-1	11	3.11E-06
SARM1	23098	chr17:23724485-23725151	chr17:23725060-23725080	87	249:4	16	11	3.22E-06
-	-	chr5:86248375-86249301	chr5:86248775-86248795	81	249:1	-2	11	3.11E-06
SLC6A11	6538	chr3:10883799-10884652	chr3:10884236-10884256	76	248:1	23	11	3.11E-06
-	-	chr17:32208474-32209065	chr17:32208615-32208635	79	248:2	9	11	3.11E-06
OR4D2	124538	chr17:53608404-53609468	chr17:53608794-53608814	87	247:4	-14	11	3.11E-06
ATP6V0A1	535	chr17:37864772-37865905	chr17:37865540-37865560	85	247:9	-8	11	3.53E-06
-	-	chr4:83295823-83296440	chr4:83296218-83296238	87	247:2	-32	11	3.11E-06
-	-	chr6:130724619-130725613	chr6:130725210-130725230	82	246:2	31	11	3.11E-06
-	-	chr6:130724619-130725613	chr6:130724934-130724960	49	246:2	-242	17	9.10E-06
KIAA1399	57574	chr2:217062172-217063089	chr2:217062558-217062586	65	245:0	-9	19	3.11E-06
-	-	chr9:117901161-117902245	chr9:117901553-117901573	96	245:4	19	11	3.13E-06
-	-	chr5:75372897-75374024	chr5:75373652-75373672	81	245:5	-61	11	3.11E-06
EXTL3	2137	chr8:28650669-28651581	chr8:28651056-28651076	85	244:1	-8	11	3.11E-06
SLC24A2	25769	chr9:19771679-19772498	chr9:19772144-19772164	74	243:1	-92	11	3.11E-06
KBTD9	114818	chr2:23808569-23809438	chr2:23808994-23809014	84	243:5	14	11	3.11E-06
ESR1	2099	chr6:152260065-152260634	chr6:152260500-152260520	81	243:3	-6	11	3.11E-06
-	-	chr19:56748158-56748898	chr19:56748430-56748450	98	243:0	-1	11	3.11E-06
-	-	chr10:6795166-6796224	chr10:6795850-6795870	77	243:7	10	11	3.31E-06
-	-	chr10:6795166-6796224	chr10:6795272-6795292	74	243:7	-568	11	2.43E-05
-	-	chr1:17991249-17991977	chr1:17991422-17991442	89	242:0	11	11	3.11E-06
C9orf65	158471	chr9:76750606-76751320	chr9:76750854-76750863	38	241:0	1	0	3.11E-06
GAR17	246176	chr17:31094726-31095655	chr17:31095129-31095149	88	240:2	9	11	3.11E-06
EPHB1	2047	chr3:136326389-136327361	chr3:136326922-136326942	79	240:1	27	11	3.11E-06
-	-	chr10:95815789-95816647	chr10:95816325-95816345	82	240:0	-4	11	3.11E-06
RTN2	6253	chr19:50690534-50691993	chr19:50691572-50691599	67	239:5	-10	18	3.75E-06
RTN2	6253	chr19:50690534-50691993	chr19:50691110-50691138	52	239:5	-472	19	3.29E-05
LPPR2	64748	chr19:11341050-11341676	chr19:11341495-11341515	82	239:0	23	11	3.11E-06
LPPR2	64748	chr19:11341050-11341676	chr19:11341458-11341478	94	239:0	-14	11	3.11E-06
CEACAM4	1089	chr19:46814745-46816007	chr19:46815330-46815350	88	239:1	4	11	3.55E-06
-	-	chr11:109017324-109017958	chr11:109017675-109017684	52	239:2	15	0	3.11E-06
SHC3	53358	chr9:89029979-89031044	chr9:89030725-89030750	65	237:2	55	16	3.59E-06
SHC3	53358	chr9:89029979-89031044	chr9:89030647-89030667	90	237:2	-26	11	3.22E-06
MAPK8IP1	9479	chr11:45862802-45863833	chr11:45863659-45863679	94	237:3	22	11	4.32E-06
-	-	chr20:34406137-34407021	chr20:34406517-34406537	85	237:1	9	11	3.22E-06
-	-	chr14:95489026-95489909	chr14:95489595-95489615	72	237:3	133	11	4.39E-06
-	-	chr14:95489026-95489909	chr14:95489443-95489463	85	237:3	-19	11	3.24E-06
-	-	chr14:95471030-95471774	chr14:95471502-95471522	87	237:1	-15	11	3.11E-06

STK33	65975	chr11:8381000-8382026	chr11:8381609-8381635	69	235:1	-45	17	3.13E-06
RPH3A	22895	chr12:111768738-111769545	chr12:111769142-111769162	84	235:2	40	11	3.11E-06
LOC392395	392395	chr9:130140332-130141062	chr9:130140650-130140670	89	235:1	-17	11	3.11E-06
-	-	chr8:35409096-35409922	chr8:35409506-35409526	89	235:3	-3	11	3.20E-06
MGC20579	348013	chr13:113632630-113633947	chr13:113633342-113633362	86	234:1	-23	11	3.73E-06
-	-	chr20:5328332-5329381	chr20:5329007-5329033	61	234:5	2	17	3.20E-06
-	-	chr14:77935412-77936083	chr14:77935586-77935606	84	233:3	1	11	3.11E-06
TUWD12	282809	chr12:88429313-88430116	chr12:88429667-88429687	85	232:4	-29	11	3.11E-06
CA10	56934	chr17:47592806-47593753	chr17:47593306-47593326	85	232:2	28	11	3.22E-06
-	-	chr4:180391549-180392989	chr4:180392321-180392341	87	232:4	24	11	4.10E-06
-	-	chr19:6515190-6516003	chr19:6515613-6515633	82	232:4	-4	11	3.24E-06
-	-	chr11:118869430-118870366	chr11:118869827-118869847	81	232:1	31	11	3.17E-06
-	-	chr11:118869430-118870366	chr11:118869815-118869835	71	232:1	19	11	3.11E-06
LRRC22	340745	chr10:85974193-85975009	chr10:85974592-85974612	80	231:6	-18	11	3.11E-06
-	-	chr1:20510739-20511739	chr1:20511233-20511253	78	231:2	29	11	3.22E-06
-	-	chr1:112087691-112088954	chr1:112088271-112088296	44	230:2	-22	16	3.64E-06
OR1B1	347169	chr9:122483733-122484723	chr9:122484238-122484258	83	229:2	-41	11	3.24E-06
CACNG7	59284	chr19:59122915-59123241	chr19:59122963-59122983	82	229:1	-12	11	3.11E-06
-	-	chr1:226868811-226869926	chr1:226869195-226869221	62	229:4	3	17	3.24E-06
UNC13A	23025	chr19:17659926-17660821	chr19:17660148-17660174	72	228:3	-18	17	3.20E-06
NPTX2	4885	chr7:97887309-97888219	chr7:97887760-97887780	89	228:3	0	11	3.31E-06
-	-	chr15:27528299-27529242	chr15:27528830-27528850	84	228:2	-5	11	3.39E-06
GLRA2	2742	chrX:14306559-14307550	chrX:14307265-14307284	60	227:3	-20	10	3.24E-06
-	-	chr16:69907108-69907946	chr16:69907750-69907770	81	227:2	3	11	3.11E-06
GLRA3	8001	chr4:176124437-176125175	chr4:176124816-176124836	84	225:0	-4	11	3.24E-06
-	-	chr1:30116861-30117638	chr1:30117214-30117234	86	225:0	6	11	3.27E-06
DGKG	1608	chr3:187507890-187508738	chr3:187508288-187508308	96	224:1	-7	11	3.79E-06
-	-	chr15:89682739-89683775	chr15:89683205-89683214	41	224:2	6	0	3.24E-06
GAD2	2572	chr10:26544285-26545545	chr10:26545225-26545245	79	223:4	44	11	3.96E-06
GAD2	2572	chr10:26544285-26545545	chr10:26545048-26545074	50	223:4	-130	17	3.97E-06
-	-	chr3:116526976-116527727	chr3:116527281-116527301	82	223:1	22	11	3.27E-06
-	-	chr19:34511903-34512895	chr19:34512414-34512434	87	223:6	4	11	3.35E-06
-	-	chr1:199357676-199358619	chr1:199358195-199358215	73	223:2	11	11	3.53E-06
LOC113386	113386	chr19:63520669-63521255	chr19:63520821-63520841	84	221:0	-10	11	3.27E-06
GABRG2	2566	chr5:161427714-161428676	chr5:161428259-161428279	86	221:1	51	11	3.11E-06
CMA1	1215	chr14:24051684-24052767	chr14:24052234-24052254	81	221:1	-19	11	3.64E-06
-	-	chr12:93775653-93776361	chr12:93775999-93776019	89	221:0	-4	11	3.53E-06
-	-	chr10:88056206-88057148	chr10:88056588-88056608	86	221:1	-2	11	3.27E-06

-	-	chr1:205711731-205712370	chr1:205712041-205712061	83	221:0	26	11	3.39E-06
SNCB	6620	chr5:175970804-175971702	chr5:175971124-175971144	90	220:1	25	11	3.50E-06
MGC33600	202500	chr6:44361215-44361823	chr6:44361425-44361445	93	219:2	23	11	3.11E-06
-	-	chr16:25665750-25666836	chr16:25666159-25666186	68	219:1	-27	18	3.31E-06
-	-	chr13:107314622-107315684	chr13:107315075-107315095	93	219:1	5	11	3.73E-06
-	-	chr10:99823681-99824721	chr10:99824242-99824262	80	219:4	7	11	3.55E-06
MGC10233	219899	chr11:120458344-120459015	chr11:120458770-120458790	84	218:2	4	11	3.11E-06
LOC440035	440035	chr11:45558438-45559371	chr11:45558721-45558741	83	218:4	21	11	3.11E-06
-	-	chr13:93139994-93141208	chr13:93140623-93140643	78	218:5	-24	11	4.00E-06
-	-	chr12:12728523-12729461	chr12:12729183-12729203	87	218:2	22	11	3.50E-06
RALY	22913	chr20:32110192-32111131	chr20:32110565-32110585	76	217:3	7	11	3.71E-06
LOC92017	92017	chr16:12536826-12537661	chr16:12537025-12537044	49	217:2	-187	10	5.20E-06
LOC390732	390732	chr16:54301489-54302445	chr16:54302081-54302101	82	217:2	0	11	3.67E-06
GRIK5	2901	chr19:47192449-47193822	chr19:47193335-47193344	42	217:3	31	0	4.00E-06
NMNAT2	23057	chr1:180117206-180118256	chr1:180117720-180117747	65	216:4	19	18	3.58E-06
LOC440764	440764	chr20:44585885-44586460	chr20:44586192-44586219	49	216:1	3	18	3.22E-06
-	-	chr7:152196274-152197281	chr7:152196815-152196840	58	216:2	3	16	3.53E-06
-	-	chr5:168926384-168927235	chr5:168926835-168926855	83	216:2	-4	11	3.64E-06
-	-	chr5:13606786-13607581	chr5:13607389-13607414	45	216:4	191	16	1.35E-05
-	-	chr5:13606786-13607581	chr5:13607189-13607209	83	216:4	-12	11	3.58E-06
-	-	chr5:13606786-13607581	chr5:13607178-13607197	53	216:4	-23	10	3.45E-06
VIP	7432	chr6:153163619-153164558	chr6:153164141-153164161	86	215:2	32	11	3.24E-06
T1	83696	chr8:140977789-140978877	chr8:140978252-140978272	88	215:4	-3	11	3.60E-06
SCHIP1	29970	chr3:160473802-160474767	chr3:160474302-160474322	89	215:0	21	11	3.71E-06
RELN	5649	chr7:103085731-103086435	chr7:103085950-103085970	83	215:2	5	11	3.24E-06
HCN3	57657	chr1:152060488-152061766	chr1:152061248-152061268	88	215:6	5	11	4.12E-06
CACNG2	10369	chr22:35423760-35424696	chr22:35424046-35424055	41	215:3	1	0	3.20E-06
-	-	chr20:59538974-59539649	chr20:59539325-59539351	64	215:2	5	17	3.31E-06
-	-	chr17:62255713-62256990	chr17:62256293-62256312	43	215:3	6	10	3.79E-06
DAO	1610	chr12:107786211-107787066	chr12:107786643-107786663	82	214:2	-49	11	3.55E-06
CDH4	1002	chr20:59960209-59961044	chr20:59960607-59960627	79	214:2	20	11	3.59E-06
CADPS	8618	chr3:62836591-62837429	chr3:62837004-62837024	80	214:1	1	11	3.24E-06
-	-	chr2:27128126-27129007	chr2:27128540-27128549	48	214:1	10	0	3.59E-06
SLC22A6	9356	chr11:62503954-62504837	chr11:62504371-62504391	77	213:1	-23	11	3.39E-06
MGC20410	116071	chr11:64501395-64502074	chr11:64501886-64501906	78	213:1	21	11	3.73E-06
DPYSL4	10570	chr10:133857438-133858383	chr10:133857939-133857959	80	213:3	36	11	3.50E-06
DPYSL4	10570	chr10:133857438-133858383	chr10:133857768-133857787	50	213:3	-135	10	4.18E-06
CUTL2	23316	chr12:110112490-110113541	chr12:110112885-110112905	87	213:1	22	11	3.73E-06



CHD5	26038	chr1:6155437-6156504	chr1:6156139-6156159	92	213:3	34	11	3.64E-06
-	-	chr2:207892842-207893731	chr2:207893102-207893122	83	213:2	-34	11	3.54E-06
-	-	chr16:82011001-82011778	chr16:82011506-82011526	90	213:0	-11	11	3.60E-06
-	-	chr14:95319995-95321008	chr14:95320413-95320433	85	213:2	11	11	4.06E-06
CEACAM7	1087	chr19:46891994-46892777	chr19:46892259-46892279	79	212:5	6	11	3.54E-06
-	-	chr6:20096476-20097385	chr6:20096969-20096989	81	212:3	5	11	3.60E-06
-	-	chr13:34384951-34385777	chr13:34385410-34385430	73	212:4	16	11	3.53E-06
-	-	chr11:133343007-133344245	chr11:133343810-133343830	77	211:7	218	11	1.14E-05
-	-	chr11:133343007-133344245	chr11:133343597-133343617	89	211:7	5	11	3.76E-06
-	-	chr9:36762203-36763205	chr9:36762626-36762635	42	210:5	-1	0	3.73E-06
-	-	chr14:77982594-77983575	chr14:77983084-77983104	81	210:0	5	11	3.73E-06
-	-	chr11:127739729-127740680	chr11:127740395-127740415	78	210:3	-16	11	3.75E-06
-	-	chr11:10356707-10357721	chr11:10357311-10357337	54	210:2	-15	17	3.76E-06
POU2F2	5452	chr19:47339250-47339952	chr19:47339537-47339557	74	209:4	-12	11	3.27E-06
KIAA1671	85379	chr22:23913812-23914662	chr22:23914250-23914270	89	209:4	-4	11	3.58E-06
GLP1R	2740	chr6:39163759-39165070	chr6:39164336-39164356	75	209:2	-3	11	3.91E-06
GLP1R	2740	chr6:39163759-39165070	chr6:39164232-39164259	57	209:2	-103	18	3.97E-06
-	-	chr18:31609811-31610335	chr18:31610039-31610059	76	209:5	-25	11	3.22E-06
PEX5R	51555	chr3:181236680-181237609	chr3:181237270-181237297	54	208:3	-24	18	3.87E-06
-	-	chr8:102325211-102325939	chr8:102325273-102325293	77	208:1	4	11	3.24E-06
-	-	chr2:98156796-98157376	chr2:98157071-98157091	80	208:7	-7	11	3.11E-06
-	-	chr17:10719189-10720358	chr17:10719533-10719553	82	208:3	-8	11	4.00E-06
ASTN2	23245	chr9:116647829-116648486	chr9:116648093-116648113	79	207:4	3	11	3.55E-06
ARC	23237	chr8:143710133-143711005	chr8:143710775-143710803	49	207:0	190	19	1.23E-05
ARC	23237	chr8:143710133-143711005	chr8:143710596-143710616	88	207:0	7	11	3.73E-06
-	-	chr19:33559587-33560292	chr19:33559960-33559980	88	207:2	3	11	3.73E-06
NEUROD1	4760	chr2:182368153-182368760	chr2:182368481-182368500	46	206:1	105	10	3.73E-06
NEUROD1	4760	chr2:182368153-182368760	chr2:182368382-182368402	78	206:1	6	11	3.27E-06
CHPF	79586	chr2:220233805-220234757	chr2:220234280-220234300	70	206:4	22	11	3.79E-06
-	-	chr17:29082717-29083719	chr17:29083456-29083476	95	206:1	1	11	3.79E-06
-	-	chr8:11500251-11501107	chr8:11500840-11500860	76	205:2	-9	11	3.64E-06
-	-	chr16:7236302-7237308	chr16:7236742-7236762	94	205:3	-3	11	3.87E-06
ICA1	3382	chr7:8255251-8256344	chr7:8255843-8255863	95	204:0	18	11	4.08E-06
TBX15	6913	chr1:119183254-119184243	chr1:119183807-119183827	83	203:4	-6	11	3.73E-06
LOC390616	390616	chr15:77362609-77363587	chr15:77363152-77363172	93	203:2	-7	11	4.00E-06
FLJ31568	150244	chr22:22071188-22071964	chr22:22071620-22071640	71	202:6	35	11	3.64E-06
FLJ31568	150244	chr22:22071188-22071964	chr22:22071582-22071602	84	202:6	-3	11	3.58E-06
-	-	chr6:99212207-99213034	chr6:99212553-99212573	78	202:2	-1	11	3.69E-06

-	-	chr1:201348108-201348762	chr1:201348549-201348558	51	202:0	11	0	3.24E-06
PRG3	10394	chr11:56903198-56904183	chr11:56903901-56903921	85	201:4	-19	11	3.82E-06
MGC47816	284716	chr1:42514446-42515254	chr1:42514718-42514738	74	201:4	15	11	3.69E-06
FNDC1	84624	chr6:159658230-159659242	chr6:159658802-159658822	84	201:5	-11	11	3.76E-06
CACNA1E	777	chr1:178186255-178187134	chr1:178187004-178187024	80	200:3	276	11	4.00E-05
CACNA1E	777	chr1:178186255-178187134	chr1:178186864-178186884	72	200:3	136	11	6.05E-06
CACNA1E	777	chr1:178186255-178187134	chr1:178186767-178186787	72	200:3	39	11	3.79E-06
CACNA1E	777	chr1:178186255-178187134	chr1:178186705-178186725	80	200:3	-23	11	3.73E-06
-	-	chr4:80419655-80420523	chr4:80420073-80420093	70	200:6	-3	11	3.73E-06
-	-	chr4:80419655-80420523	chr4:80420059-80420079	78	200:6	-17	11	3.75E-06
-	-	chr12:97192658-97193673	chr12:97193101-97193127	57	200:0	6	17	4.02E-06
-	-	chr12:97192658-97193673	chr12:97192881-97192906	46	200:0	-214	16	6.20E-06
SIGLECL1	89858	chr19:56675279-56676305	chr19:56675867-56675887	78	199:3	19	11	3.82E-06
DDX18	8886	chr2:118306698-118307642	chr2:118307270-118307290	75	199:0	62	11	3.71E-06
DDX18	8886	chr2:118306698-118307642	chr2:118307216-118307236	71	199:0	8	11	3.67E-06
-	-	chr8:92761894-92762836	chr8:92762223-92762243	90	199:1	-14	11	3.79E-06
SCN3B	55800	chr11:123029608-123030363	chr11:123029985-123030005	84	198:1	20	11	3.61E-06
LOC149329	149329	chr16:59634046-59634775	chr16:59634349-59634375	51	198:4	-11	17	3.67E-06
-	-	chr8:4134115-4135039	chr8:4134570-4134590	80	198:2	20	11	3.97E-06
-	-	chr7:45037446-45038564	chr7:45037892-45037912	74	198:1	24	11	3.82E-06
TFAP2BL1	83741	chr6:50796050-50796859	chr6:50796453-50796473	73	197:2	-13	11	3.73E-06
UNQ644	374918	chr19:51420435-51421410	chr19:51420812-51420838	53	196:4	10	17	4.06E-06
IMP5	162540	chr17:41290963-41291828	chr17:41291357-41291377	81	196:2	5	11	4.08E-06
CXorf20	139105	chrX:17924618-17925242	chrX:17924959-17924979	79	196:3	64	11	3.39E-06
DIABLO	56616	chr12:121235188-121237158	chr12:121235959-121235985	53	195:9	112	17	6.75E-06
CYP11B1	1584	chr8:143952580-143953324	chr8:143952896-143952916	84	194:1	16	11	3.64E-06
TRPC7	57113	chr5:135728511-135729487	chr5:135728939-135728959	89	193:1	-20	11	3.98E-06
-	-	chr7:131412202-131413387	chr7:131412727-131412754	45	193:0	2	18	4.39E-06
-	-	chr6:88885960-88886948	chr6:88886373-88886393	84	193:1	-15	11	4.08E-06
LOC390226	390226	chr11:76112521-76113305	chr11:76113047-76113067	86	192:1	5	11	3.71E-06
LOC390226	390226	chr11:76112521-76113305	chr11:76112852-76112878	47	192:1	-187	17	4.66E-06
LOC388924	388924	chr2:10930124-10931178	chr2:10930733-10930753	91	192:5	9	11	4.10E-06
DAXX	1616	chr6:33398596-33400115	chr6:33399284-33399304	71	192:11	-10	11	4.48E-06
AIP1	9863	chr7:77894623-77895288	chr7:77895062-77895082	82	192:4	-15	11	3.64E-06
-	-	chr12:50273309-50274124	chr12:50273656-50273676	75	192:3	-15	11	4.08E-06
KCNH6	81033	chr17:58954111-58954464	chr17:58954408-58954436	42	191:0	202	19	6.99E-06
KCNH6	81033	chr17:58954111-58954464	chr17:58954217-58954242	76	191:0	10	16	3.24E-06
CACNA1A	773	chr19:13434940-13435552	chr19:13435313-13435333	90	191:1	32	11	3.73E-06

CIQA	712	chr1:22696951-22698068	chr1:22697497-22697517	77	191:3	19	11	4.42E-06
-	-	chr6:167199349-167200186	chr6:167199710-167199730	81	191:1	-23	11	3.91E-06
-	-	chr12:117822721-117823591	chr12:117823118-117823138	85	191:0	-18	11	3.96E-06
SPTBN4	57731	chr19:45727499-45729161	chr19:45728510-45728530	82	190:7	0	11	4.32E-06
-	-	chr6:89304232-89305208	chr6:89304811-89304820	57	190:2	26	0	4.10E-06
-	-	chr5:153456563-153457506	chr5:153456982-153457002	77	190:2	-31	11	3.91E-06
LIR9	353514	chr19:59507226-59507842	chr19:59507757-59507777	86	189:3	-2	11	4.02E-06
INSM2	84684	chr14:35073904-35074682	chr14:35074335-35074354	58	189:1	25	10	3.96E-06
-	-	chr6:37601098-37601925	chr6:37601699-37601725	55	189:3	-62	17	3.79E-06
-	-	chr2:108213935-108215257	chr2:108214688-108214708	84	189:3	71	11	4.12E-06
-	-	chr2:71994974-71996085	chr2:71995651-71995671	89	189:3	-13	11	4.00E-06
-	-	chr13:52726368-52727217	chr13:52726840-52726860	79	189:0	-1	11	3.75E-06
TRH	7200	chr3:131185399-131186312	chr3:131185855-131185875	84	188:1	65	11	4.08E-06
TRH	7200	chr3:131185399-131186312	chr3:131185706-131185726	70	188:1	-84	11	4.31E-06
KIAA1627	57721	chr4:119948080-119948352	chr4:119948119-119948139	84	188:0	3	11	3.35E-06
KIAA1486	57624	chr2:226089766-226090674	chr2:226090381-226090401	73	188:1	3	11	3.97E-06
hIAN7	168537	chr7:149179398-149180071	chr7:149179695-149179715	81	187:3	-11	11	3.98E-06
SIAT7E	81849	chr1:77214106-77215091	chr1:77214466-77214486	97	187:2	-3	11	4.10E-06
LOC284612	284612	chr1:109733244-109734083	chr1:109733645-109733665	75	187:3	133	11	4.18E-06
LOC284612	284612	chr1:109733244-109734083	chr1:109733428-109733447	50	187:3	-84	10	6.48E-06
-	-	chr4:8794639-8795774	chr4:8795347-8795367	86	187:2	19	11	4.18E-06
-	-	chr6:88986778-88987492	chr6:88987135-88987155	80	186:0	32	11	3.98E-06
LOC441348	441348	chr8:56076298-56077150	chr8:56076609-56076629	91	185:3	8	11	3.91E-06
PTK2B	2185	chr8:27361301-27362027	chr8:27361359-27361379	91	184:4	-7	11	3.87E-06
-	-	chr3:193714217-193714958	chr3:193714628-193714648	84	184:0	38	11	3.98E-06
CDH22	64405	chr20:44291087-44292101	chr20:44291771-44291791	72	183:2	105	11	4.48E-06
CDH22	64405	chr20:44291087-44292101	chr20:44291663-44291683	91	183:2	-3	11	4.12E-06
CDH22	64405	chr20:44291087-44292101	chr20:44291467-44291486	48	183:2	-199	10	6.20E-06
STXBP5L	9515	chr3:122109349-122110306	chr3:122109750-122109770	78	182:6	-25	11	4.31E-06
POU4F3	5459	chr5:145700175-145700841	chr5:145700444-145700464	92	182:1	-10	11	3.91E-06
LOC375323	375323	chr3:9568660-9569362	chr3:9569046-9569066	82	182:0	-56	11	3.79E-06
-	-	chr14:40823903-40824852	chr14:40824325-40824351	70	182:0	-44	17	4.32E-06
-	-	chr1:58638001-58638883	chr1:58638360-58638380	81	182:1	-20	11	4.15E-06
RPH3A	22895	chr12:111712725-111714275	chr12:111713313-111713333	81	181:7	-11	11	5.37E-06
FLJ35784	374877	chr19:7480206-7481255	chr19:7480690-7480710	79	181:3	-50	11	4.10E-06
FLJ35784	374877	chr19:7480206-7481255	chr19:7480656-7480681	49	181:3	-81	16	4.21E-06
-	-	chr10:78758027-78758561	chr10:78758342-78758362	88	181:1	61	11	3.82E-06
-	-	chr1:202188745-202189372	chr1:202189009-202189029	80	181:6	-33	11	4.00E-06

-	-	chr1:30753725-30754440	chr1:30754048-30754068	80	181:1	6	11	4.02E-06
XYLT1	64131	chr16:17150957-17151791	chr16:17151421-17151441	84	180:3	2	11	4.32E-06
LOC81569	81569	chr1:17903175-17903951	chr1:17903566-17903593	54	180:1	-7	18	3.97E-06
FLJ40365	126402	chr19:14986395-14988120	chr19:14987962-14987982	92	180:1	-8	11	1.31E-05
FLJ40365	126402	chr19:14986395-14988120	chr19:14986562-14986582	92	180:1	-1408	11	1.25E-05
-	-	chr8:142899670-142900571	chr8:142900102-142900122	86	180:1	-6	11	4.19E-06
VIPR2	7434	chr7:157654911-157655851	chr7:157655296-157655316	79	179:2	16	11	4.18E-06
LGALS9	3965	chr17:23008433-23009542	chr17:23008996-23009016	87	179:3	-19	11	4.68E-06
-	-	chr8:140152137-140152998	chr8:140152711-140152731	82	179:0	40	11	4.15E-06
-	-	chr8:137199027-137199728	chr8:137199421-137199440	57	179:2	3	10	4.08E-06
-	-	chr6:80607943-80608681	chr6:80608203-80608223	73	179:3	39	11	3.97E-06
-	-	chr2:135621809-135622825	chr2:135622366-135622386	85	179:2	-17	11	4.32E-06
-	-	chr16:8336247-8336919	chr16:8336493-8336520	43	179:1	-26	18	3.97E-06
-	-	chr16:5668199-5668816	chr16:5668552-5668572	81	179:5	-32	11	4.02E-06
-	-	chr1:29893916-29894482	chr1:29894232-29894252	87	179:0	20	11	4.06E-06
RHCG	51458	chr15:87817054-87817853	chr15:87817282-87817302	88	178:2	-21	11	4.06E-06
MUC17	140453	chr7:100294910-100295710	chr7:100295290-100295310	93	178:2	3	11	4.10E-06
ICA1	3382	chr7:8246550-8247385	chr7:8246938-8246958	88	178:1	-6	11	4.26E-06
FAM13C1	220965	chr10:60694768-60695516	chr10:60695110-60695130	86	178:1	4	11	4.02E-06
ACSL6	23305	chr5:131331903-131332735	chr5:131332342-131332362	72	178:1	15	11	4.48E-06
-	-	chr9:71290629-71291404	chr9:71291041-71291061	88	178:1	26	11	4.08E-06
-	-	chr8:143462377-143463487	chr8:143462751-143462771	95	178:3	-15	11	4.29E-06
-	-	chr4:3906887-3907630	chr4:3907239-3907259	80	178:3	13	11	4.18E-06
-	-	chr2:239452161-239452983	chr2:239452647-239452672	48	178:1	62	16	4.06E-06
-	-	chr1:98297135-98297969	chr1:98297569-98297589	78	178:1	-52	11	4.09E-06
ODZ2	57451	chr5:167220677-167221312	chr5:167220892-167220912	84	177:1	-22	11	4.18E-06
KCNH4	23415	chr17:37585241-37586264	chr17:37585826-37585846	85	177:2	-12	11	4.42E-06
GPR6	2830	chr6:110406122-110406950	chr6:110406584-110406604	92	177:1	22	11	4.18E-06
-	-	chr8:20363816-20364642	chr8:20364187-20364207	80	176:2	11	11	4.15E-06
-	-	chr3:128522027-128522832	chr3:128522254-128522274	83	176:0	19	11	4.09E-06
-	-	chr10:1675449-1676085	chr10:1675835-1675855	86	176:0	-27	11	4.09E-06
LOC345630	345630	chr5:167887965-167888738	chr5:167888416-167888436	76	175:0	130	11	4.99E-06
LOC345630	345630	chr5:167887965-167888738	chr5:167888296-167888316	89	175:0	10	11	4.19E-06
DPP6	1804	chr7:153544236-153545034	chr7:153544630-153544650	77	175:4	14	11	4.31E-06
-	-	chrX:73933859-73934771	chrX:73934220-73934240	72	175:4	10	11	4.15E-06
-	-	chr18:73397796-73398372	chr18:73398153-73398173	82	175:0	-3	11	3.87E-06
EHMT1	79813	chr9:137998738-137999362	chr9:137999124-137999144	83	174:2	40	11	4.12E-06
-	-	chr2:139732931-139734110	chr2:139733724-139733744	92	174:5	8	11	4.48E-06

-	-	chr1:240463575-240464405	chr1:240464214-240464223	67	174:0	3	0	4.06E-06
OPRM1	4988	chr6:154452104-154453036	chr6:154452784-154452804	79	173:1	-20	11	4.15E-06
NTSR1	4923	chr20:60842607-60843908	chr20:60843369-60843389	85	173:4	-2	11	5.11E-06
ADCY8	114	chr8:132118256-132118835	chr8:132118546-132118571	67	173:5	57	16	3.98E-06
-	-	chr9:121898191-121899002	chr9:121898522-121898542	82	173:7	58	11	4.12E-06
-	-	chr1:38210543-38211500	chr1:38211001-38211021	90	173:2	-7	11	4.32E-06
STMN2	11075	chr8:80684103-80684973	chr8:80684340-80684360	94	172:5	6	11	4.33E-06
-	-	chr6:91460952-91462342	chr6:91461439-91461459	70	172:5	10	11	5.20E-06
SLC8A2	6543	chr19:52632374-52633322	chr19:52632782-52632802	82	171:3	13	11	4.32E-06
-	-	chr11:57409278-57410011	chr11:57409528-57409555	45	171:3	9	18	4.18E-06
RNF20	56254	chr9:101378452-101379244	chr9:101378967-101378993	44	170:5	-20	17	4.29E-06
CACNA2D4	93589	chr12:1810275-1811142	chr12:1810675-1810695	77	170:3	2	11	4.55E-06
C6orf168	84553	chr6:99907448-99908318	chr6:99907956-99907965	35	170:1	-31	0	4.18E-06
BRUNOL5	60680	chr19:3258282-3258751	chr19:3258669-3258689	72	170:0	137	11	6.15E-06
BRUNOL5	60680	chr19:3258282-3258751	chr19:3258502-3258529	72	170:0	-26	18	4.08E-06
TLL2	7093	chr10:98245775-98246568	chr10:98246156-98246176	83	169:3	-2	11	4.48E-06
MGC34646	157807	chr8:62362860-62363985	chr8:62363335-62363362	66	169:3	-7	18	4.42E-06
MGC34646	157807	chr8:62362860-62363985	chr8:62363189-62363209	77	169:3	-157	11	4.32E-06
MGC33962	148014	chr19:45415802-45416446	chr19:45416096-45416116	86	169:1	11	11	3.96E-06
KCNN4	3783	chr19:48984861-48985422	chr19:48985245-48985265	88	169:0	-9	11	4.12E-06
KCNN4	3783	chr19:48984861-48985422	chr19:48985212-48985232	76	169:0	-42	11	4.09E-06
GRIN2A	2903	chr16:98371117-9838255	chr16:9837669-9837689	84	169:4	0	11	4.19E-06
C6orf213	134829	chr6:123385660-123386327	chr6:123386004-123386024	78	169:0	24	11	4.10E-06
-	-	chr6:11643881-11644581	chr6:11644133-11644153	86	169:2	7	11	4.32E-06
-	-	chr10:43099775-43100431	chr10:43099979-43099999	78	169:2	39	11	4.21E-06
SYT14	255928	chr1:206498988-206499698	chr1:206499519-206499539	78	168:0	-20	11	4.15E-06
SLIT2	9353	chr4:20151862-20152681	chr4:20152201-20152221	81	168:2	2	11	4.39E-06
PDE2A	5138	chr11:72001009-72001980	chr11:72001499-72001519	85	167:7	53	11	4.32E-06
LOC400748	400748	chr1:31000405-31001276	chr1:31000970-31000990	77	167:3	-13	11	4.15E-06
LOC284296	284296	chr19:60640228-60641075	chr19:60640703-60640723	82	167:2	-6	11	4.48E-06
ITGA9	3680	chr3:37636506-37637487	chr3:37637140-37637160	69	167:5	189	11	9.58E-06
ITGA9	3680	chr3:37636506-37637487	chr3:37636952-37636972	77	167:5	1	11	4.48E-06
CHRNA4	1137	chr20:61480363-61481082	chr20:61480618-61480638	78	167:2	-12	11	4.21E-06
-	-	chr3:117086893-117087922	chr3:117087339-117087359	78	167:2	-26	11	4.66E-06
-	-	chr1:239336441-239337384	chr1:239336923-239336932	22	167:1	0	0	4.66E-06
-	-	chr1:93947769-93948870	chr1:93948394-93948414	81	167:2	55	11	4.29E-06
XYLB	9942	chr3:38413827-38414303	chr3:38414060-38414080	79	166:0	34	11	4.09E-06
SP140	11262	chr2:230979598-230979815	chr2:230979695-230979715	86	166:0	21	11	3.79E-06

-	-	chr7:64741289-64741786	chr7:64741552-64741572	81	166:0	43	11	3.91E-06
PAX7	5081	chr1:18724946-18725902	chr1:18725473-18725493	83	165:5	25	11	4.39E-06
FBXL16	146330	chr16:689863-691582	chr16:690784-690804	83	165:4	0	11	6.67E-06
-	-	chrX:11842771-11843575	chrX:11843208-11843228	84	165:1	-58	11	4.32E-06
-	-	chr5:152635703-152636485	chr5:152636091-152636111	84	165:0	-7	11	4.48E-06
-	-	chr16:9040543-9041009	chr16:9040760-9040780	82	165:1	-5	11	3.98E-06
LMX1A	4009	chr1:161929145-161930231	chr1:161929680-161929700	82	164:1	-19	11	4.78E-06
C20orf166	128826	chr20:60595174-60596265	chr20:60595597-60595617	88	164:1	-13	11	4.42E-06
-	-	chr9:133504018-133504936	chr9:133504154-133504174	89	164:2	7	11	4.55E-06
LOC441830	441830	chr18:74573872-74574895	chr18:74574264-74574284	79	163:4	-28	11	4.39E-06
-	-	chr20:54337003-54337827	chr20:54337519-54337539	71	163:1	14	11	4.29E-06
-	-	chr20:54337003-54337827	chr20:54337513-54337539	52	163:1	11	17	4.29E-06
-	-	chr13:52440122-52440711	chr13:52440369-52440378	42	163:3	11	0	4.19E-06
-	-	chr11:132680863-132681931	chr11:132681264-132681284	79	163:1	0	11	4.48E-06
C14orf120	25983	chr14:23020254-23021259	chr14:23020585-23020605	85	162:2	-23	11	4.68E-06
-	-	chr11:78703745-78704467	chr11:78704207-78704227	83	162:2	-49	11	4.33E-06
-	-	chr6:96247516-96248193	chr6:96247882-96247902	88	161:1	-5	11	4.58E-06
-	-	chr16:82292524-82293176	chr16:82292824-82292844	91	161:2	-11	11	4.32E-06
-	-	chr12:128059175-128060075	chr12:128059526-128059546	83	161:0	2	11	4.39E-06
-	-	chr1:166815663-166816563	chr1:166816419-166816447	47	161:5	449	19	8.03E-05
-	-	chr1:166815663-166816563	chr1:166815903-166815923	84	161:5	-71	11	4.78E-06
LOC343629	343629	chr20:57142457-57143314	chr20:57142816-57142836	87	160:2	17	11	4.55E-06
HMG2	3151	chr1:26481923-26483160	chr1:26482429-26482438	44	160:5	-1	0	6.33E-06
-	-	chr11:131552111-131552825	chr11:131552392-131552412	89	160:2	10	11	4.66E-06
KIAA1576	57687	chr16:76566229-76566776	chr16:76566514-76566540	61	159:2	-19	17	4.18E-06
-	-	chr9:119531455-119532154	chr9:119531905-119531925	86	159:2	35	11	4.29E-06
-	-	chr10:24155195-24155980	chr10:24155519-24155539	77	159:0	-48	11	4.32E-06
C1QL2	165257	chr2:119640660-119641484	chr2:119641062-119641082	85	157:2	7	11	4.53E-06
-	-	chr8:21502893-21503720	chr8:21503308-21503328	72	157:3	15	11	4.75E-06
-	-	chr5:94163726-94164743	chr5:94164116-94164136	83	157:3	24	11	5.20E-06
-	-	chr18:52924954-52925959	chr18:52925526-52925546	76	157:1	29	11	4.82E-06
-	-	chr12:97792812-97793776	chr12:97793407-97793434	73	157:0	-16	18	4.69E-06
FLJ33360	401172	chr5:6355634-6356626	chr5:6356001-6356021	84	156:1	-45	11	5.67E-06
CHIT1	1118	chr1:199920577-199921194	chr1:199920914-199920934	87	156:2	-32	11	4.26E-06
CHIT1	1118	chr1:199920577-199921194	chr1:199920664-199920684	70	156:2	-282	11	1.79E-05
CHIT1	1118	chr1:199920577-199921194	chr1:199920622-199920649	43	156:2	-320	18	3.05E-05
CHIT1	1118	chr1:199920577-199921194	chr1:199920605-199920630	52	156:2	-338	16	4.15E-05
-	-	chr17:32128302-32129061	chr17:32128642-32128662	85	156:3	36	11	4.32E-06

-	-	chr15:51272503-51273395	chr15:51272857-51272877	82	155:0	12	11	4.55E-06
HT021	57415	chr3:62279919-62280593	chr3:62280177-62280197	84	154:2	-9	11	4.66E-06
FLJ10842	55750	chr7:140250441-140250775	chr7:140250595-140250615	86	154:0	16	11	4.09E-06
-	-	chr16:54009637-54010780	chr16:54010203-54010212	58	154:0	3	0	4.78E-06
-	-	chr10:16752490-16752850	chr10:16752748-16752768	89	154:1	30	11	4.48E-06
SLC12A5	57468	chr20:44091006-44092224	chr20:44091668-44091693	51	153:0	60	16	4.84E-06
SLC12A5	57468	chr20:44091006-44092224	chr20:44091607-44091627	88	153:0	-4	11	4.84E-06
LOC389656	389656	chr8:50986478-50987290	chr8:50986807-50986834	64	153:0	-3	18	4.71E-06
LOC389172	389172	chr3:161954729-161955707	chr3:161954948-161954957	54	153:5	5	0	5.37E-06
KCNQ2	3785	chr20:61562853-61563545	chr20:61563346-61563366	79	153:3	41	11	4.53E-06
KCNQ2	3785	chr20:61562853-61563545	chr20:61563335-61563354	53	153:3	30	10	4.48E-06
ATP6V1B2	526	chr8:20098561-20099147	chr8:20098987-20099007	70	153:6	9	11	4.66E-06
-	-	chr8:53327100-53327949	chr8:53327499-53327508	35	153:1	-1	0	4.99E-06
-	-	chr5:151902443-151903076	chr5:151902671-151902691	76	153:0	46	11	4.32E-06
-	-	chr16:8016088-8017022	chr16:8016632-8016658	68	153:4	-5	17	4.58E-06
TSAP6	55240	chr2:119708303-119709216	chr2:119708644-119708664	82	152:0	-5	11	4.58E-06
RANBP3	8498	chr19:5923052-5923987	chr19:5923564-5923573	46	152:5	28	0	5.25E-06
FLJ38377	205147	chr2:131347148-131348025	chr2:131347601-131347621	86	152:1	3	11	4.75E-06
-	-	chr21:35515880-35517031	chr21:35516378-35516387	37	152:8	-26	0	5.20E-06
SYP	6855	chrX:48812398-48813540	chrX:48812951-48812971	86	151:6	-64	11	4.66E-06
GDAP1L1	78997	chr20:42326192-42327174	chr20:42326548-42326568	81	151:0	-10	11	5.20E-06
-	-	chr12:107278138-107278972	chr12:107278538-107278558	90	151:4	8	11	4.68E-06
LOC440505	440505	chr19:5307189-5308000	chr19:5307550-5307570	86	150:2	30	11	5.11E-06
-	-	chr20:61217934-61219138	chr20:61218404-61218424	90	150:4	11	11	4.99E-06
UNQ9366	125931	chr19:49708627-49709236	chr19:49708981-49709001	80	149:0	-11	11	4.55E-06
PRKCB1	5579	chr16:24097279-24097813	chr16:24097504-24097524	90	149:2	-14	11	4.66E-06
LOC90668	90668	chr14:23590942-23592311	chr14:23591620-23591640	79	149:6	-9	11	5.94E-06
LOC388503	388503	chr19:10033293-10034198	chr19:10033800-10033820	77	149:1	33	11	5.20E-06
LOC388503	388503	chr19:10033293-10034198	chr19:10033758-10033778	90	149:1	-9	11	5.25E-06
LOC388503	388503	chr19:10033293-10034198	chr19:10033689-10033709	71	149:1	-78	11	6.48E-06
CHGA	1113	chr14:92459335-92460201	chr14:92459620-92459640	96	149:0	1	11	4.32E-06
-	-	chr5:151606172-151606811	chr5:151606357-151606377	86	149:2	-18	11	4.32E-06
LOC441651	441651	chr12:130768853-130769827	chr12:130769221-130769241	89	148:2	-58	11	4.71E-06
LOC388514	388514	chr19:15741185-15741884	chr19:15741562-15741587	69	148:2	-2	16	5.06E-06
LOC388514	388514	chr19:15741185-15741884	chr19:15741484-15741504	71	148:2	-83	11	5.78E-06
LOC146713	146713	chr17:74832999-74833981	chr17:74833581-74833590	25	148:2	0	0	4.84E-06
LMAN1L	79748	chr15:72905577-72906563	chr15:72906001-72906028	62	148:1	-6	18	6.48E-06
GPS2	2874	chr17:7158263-7159217	chr17:7159044-7159064	71	148:0	260	11	3.66E-05

FLJ31340	222223	chr7:86182887-86183515	chr7:86183103-86183123	83	148:1	-6	11	4.39E-06
-	-	chr3:12066070-12066490	chr3:12066359-12066379	75	148:0	-24	11	4.42E-06
-	-	chr20:12776294-12776992	chr20:12776593-12776613	82	148:1	18	11	4.55E-06
RWDD1	51389	chr6:117024316-117025140	chr6:117024867-117024887	81	147:1	6	11	4.91E-06
RWDD1	51389	chr6:117024316-117025140	chr6:117024847-117024875	41	147:1	-10	19	4.91E-06
LOC391025	391025	chr1:29612569-29613265	chr1:29613087-29613107	84	147:1	-9	11	4.68E-06
LOC388563	388563	chr19:60423594-60424358	chr19:60423924-60423944	84	147:3	7	11	4.55E-06
GPR149	344758	chr3:155621429-155622319	chr3:155621757-155621766	54	147:0	5	0	4.84E-06
-	-	chr18:38008635-38009609	chr18:38009092-38009101	25	147:0	15	0	5.67E-06
-	-	chr12:117766623-117767335	chr12:117767063-117767083	81	147:3	-1	11	4.82E-06
SIX6	4990	chr14:60045081-60045786	chr14:60045490-60045518	57	146:4	-23	19	4.68E-06
LGALS13	29124	chr19:44772463-44773383	chr19:44772931-44772951	81	146:2	7	11	5.20E-06
-	-	chrX:31915012-31915960	chrX:31915510-31915530	88	146:2	15	11	5.11E-06
EBF	1879	chr5:158076141-158076814	chr5:158076461-158076481	81	145:0	19	11	4.84E-06
-	-	chr5:139334384-139334909	chr5:139334531-139334557	68	145:1	-10	17	4.32E-06
-	-	chr16:67485508-67486114	chr16:67485899-67485919	77	145:1	-22	11	4.48E-06
-	-	chr1:228527294-228528011	chr1:228527545-228527565	72	145:2	37	11	4.68E-06
-	-	chr1:58144559-58145089	chr1:58144870-58144890	79	145:1	20	11	4.33E-06
-	-	chr1:58144559-58145089	chr1:58144789-58144808	68	145:1	-61	10	4.39E-06
AP3D1	8943	chr19:2096520-2097329	chr19:2097150-2097170	76	144:4	2	11	5.11E-06
-	-	chr2:77097344-77098021	chr2:77097741-77097761	92	144:1	15	11	4.48E-06
-	-	chr10:59578671-59579416	chr10:59578903-59578923	77	144:0	-7	11	4.71E-06
LOC388228	388228	chr16:28222666-28223401	chr16:28223150-28223170	72	143:0	-4	11	5.06E-06
LOC388228	388228	chr16:28222666-28223401	chr16:28223144-28223170	60	143:0	-7	17	5.06E-06
HBXAP	51773	chr11:77168360-77169258	chr11:77168828-77168848	88	143:2	-5	11	6.74E-06
-	-	chr21:43567119-43567717	chr21:43567308-43567328	82	143:2	8	11	4.53E-06
MGC39827	160777	chr12:118428537-118429389	chr12:118428951-118428971	80	142:2	-17	11	5.67E-06
MGAT3	4248	chr22:38198435-38199433	chr22:38199104-38199124	84	142:4	13	11	5.20E-06
LOC402665	402665	chr19:56513709-56514354	chr19:56513929-56513949	75	142:1	5	11	4.68E-06
FERD3L	222894	chr7:18959404-18960260	chr7:18959774-18959794	75	142:2	-60	11	4.99E-06
CGRRF1	10668	chr14:54086089-54086983	chr14:54086518-54086538	80	142:2	7	11	5.37E-06
-	-	chrX:12326336-12326937	chrX:12326721-12326741	79	142:1	27	11	4.91E-06
-	-	chr16:47311470-47312238	chr16:47311867-47311887	81	142:0	-12	11	4.91E-06
CUTL1	1523	chr7:101526256-101526894	chr7:101526610-101526619	34	141:4	-16	0	4.53E-06
-	-	chr9:69929604-69930294	chr9:69929902-69929922	76	141:1	-9	11	5.37E-06
-	-	chr22:48449629-48450588	chr22:48450011-48450031	91	141:2	-22	11	5.94E-06
SH2D3C	10044	chr9:127592966-127594055	chr9:127593463-127593472	43	140:1	3	0	6.67E-06
PCDHB1	29930	chr5:140400658-140401283	chr5:140401032-140401052	81	140:1	-6	11	4.84E-06



PCDHB1	29930	chr5:140400658-140401283	chr5:140401026-140401052	70	140:1	-9	17	4.84E-06
FLJ46354	374977	chr1:54882797-54883396	chr1:54883040-54883060	82	140:1	-178	11	5.06E-06
-	-	chr2:77193541-77194176	chr2:77193922-77193931	61	140:1	3	0	4.48E-06
-	-	chr17:28493723-28494459	chr17:28494035-28494055	86	140:0	-8	11	5.06E-06
-	-	chr16:59536425-59537183	chr16:59536812-59536832	81	140:1	5	11	5.25E-06
-	-	chr16:47718189-47719232	chr16:47718686-47718706	86	140:1	-11	11	7.60E-06
PHYHIPL	84457	chr10:60606820-60607622	chr10:60607280-60607300	88	139:1	9	11	5.25E-06
PHYHIPL	84457	chr10:60606820-60607622	chr10:60606914-60606934	73	139:1	-357	11	6.78E-05
-	-	chr20:22733740-22734457	chr20:22734086-22734106	77	139:1	1	11	4.71E-06
ANKHD1	54882	chr5:139761816-139762730	chr5:139762367-139762387	78	138:6	4	11	5.37E-06
-	-	chr16:69453092-69454054	chr16:69453594-69453614	79	138:2	14	11	6.15E-06
-	-	chr16:7003865-7004727	chr16:7004146-7004166	84	138:2	1	11	5.54E-06
TLP19	51060	chr1:52180023-52180428	chr1:52180206-52180226	73	137:3	-16	11	4.42E-06
PPM1E	22843	chr17:54187858-54188670	chr17:54188209-54188236	55	137:1	-5	18	5.78E-06
LOC391542	391542	chr3:63714076-63714994	chr3:63714467-63714487	75	137:3	-45	11	6.15E-06
FLJ40452	115708	chr14:103066488-103067125	chr14:103066859-103066885	57	137:3	227	17	1.28E-05
FLJ40452	115708	chr14:103066488-103067125	chr14:103066689-103066709	85	137:3	54	11	4.71E-06
-	-	chr7:134477668-134478444	chr7:134477956-134477976	81	137:3	37	11	4.91E-06
-	-	chr7:134477668-134478444	chr7:134477789-134477815	68	137:3	-127	17	5.25E-06
-	-	chr10:110719446-110720392	chr10:110719945-110719965	86	137:2	-8	11	5.20E-06
SCGB1D4	404552	chr11:61819473-61820064	chr11:61819808-61819817	30	136:2	10	0	4.99E-06
PITPNM3	83394	chr17:6370304-6371111	chr17:6370593-6370613	75	136:2	-6	11	6.67E-06
OSBPL7	114881	chr17:43230109-43230783	chr17:43230366-43230386	79	136:0	2	11	4.91E-06
LOC400852	400852	chr20:61277677-61278559	chr20:61277902-61277922	84	136:0	4	11	5.25E-06
LOC388104	388104	chr15:28965085-28965824	chr15:28965470-28965490	75	136:4	42	11	5.54E-06
C21orf54	339629	chr21:33451400-33451905	chr21:33451737-33451757	86	136:4	-9	11	4.69E-06
-	-	chr2:137121297-137121864	chr2:137121642-137121662	76	136:0	-1	11	4.78E-06
DNER	92737	chr2:230405052-230405857	chr2:230405378-230405398	82	135:0	2	11	6.70E-06
DKFZp76102018	92293	chr12:127619034-127619828	chr12:127619468-127619488	84	135:1	11	11	5.94E-06
-	-	chr5:155567742-155568921	chr5:155568061-155568081	83	135:2	5	11	6.48E-06
-	-	chr5:155085877-155086502	chr5:155086221-155086247	54	135:1	-26	17	4.99E-06
-	-	chr12:117545579-117546347	chr12:117545935-117545955	86	135:3	8	11	4.91E-06
-	-	chr1:34844221-34844689	chr1:34844424-34844444	73	135:1	12	11	4.68E-06
-	-	chr1:34844221-34844689	chr1:34844412-34844432	72	135:1	0	11	4.68E-06
ODZ4	26011	chr11:78249654-78250143	chr11:78249882-78249902	80	134:0	5	11	4.78E-06
MGC20410	116071	chr11:64527171-64527900	chr11:64527553-64527573	76	134:2	0	11	4.82E-06
MGC20410	116071	chr11:64527171-64527900	chr11:64527541-64527561	81	134:2	-12	11	4.91E-06
KIAA0789	9671	chr12:107090510-107091720	chr12:107091033-107091053	87	134:2	22	11	6.74E-06

COP1	64326	chr1:172802890-172803430	chr1:172803225-172803245	76	134:0	10	11	5.20E-06
-	-	chr18:43040348-43041152	chr18:43040894-43040921	60	134:0	7	18	6.15E-06
LOC442400	442400	chr8:144254498-144255395	chr8:144254752-144254772	82	133:1	-23	11	6.41E-06
FLJ14721	84915	chr12:108637074-108637970	chr12:108637344-108637364	86	133:3	5	11	6.70E-06
FLJ14721	84915	chr12:108637074-108637970	chr12:108637170-108637190	72	133:3	-169	11	8.55E-06
-	-	chr5:176165717-176166584	chr5:176166102-176166127	44	132:3	117	16	7.31E-06
-	-	chr5:176165717-176166584	chr5:176165980-176166000	77	132:3	-8	11	6.70E-06
-	-	chr21:17637175-17637828	chr21:17637429-17637449	79	132:0	-35	11	5.94E-06
-	-	chr20:35634552-35634998	chr20:35634868-35634888	79	132:0	-35	11	4.91E-06
-	-	chr11:111041808-111042335	chr11:111041900-111041920	75	132:3	-38	11	4.99E-06
-	-	chr1:207300919-207302032	chr1:207301543-207301563	82	132:1	-39	11	6.75E-06
-	-	chr1:198314748-198315606	chr1:198315120-198315140	80	132:2	0	11	6.74E-06
LOC339505	339505	chr1:20442944-20444014	chr1:20443411-20443431	91	131:2	24	11	6.74E-06
FLJ39501	126410	chr19:15510597-15511157	chr19:15510777-15510797	82	131:2	-3	11	4.84E-06
-	-	chr11:112109981-112110764	chr11:112110327-112110347	77	131:2	18	11	6.70E-06
SYT6	148281	chr1:114409292-114410486	chr1:114410215-114410235	74	130:1	340	11	7.34E-05
SYT6	148281	chr1:114409292-114410486	chr1:114410134-114410153	46	130:1	259	10	3.66E-05
SYT6	148281	chr1:114409292-114410486	chr1:114409881-114409901	92	130:1	6	11	6.88E-06
LOC402280	402280	chr7:65803516-65804226	chr7:65803841-65803861	81	130:1	42	11	6.05E-06
LOC342357	342357	chr16:25183179-25183851	chr16:25183615-25183635	82	130:1	14	11	6.41E-06
HCRTR2	3062	chr6:55149631-55150392	chr6:55149914-55149923	54	130:1	3	0	6.20E-06
GAD1	2571	chr2:171495959-171496619	chr2:171496372-171496392	94	130:0	2	11	5.20E-06
-	-	chr15:71902286-71902940	chr15:71902586-71902606	81	130:2	8	11	4.82E-06
-	-	chr1:174299934-174300284	chr1:174300018-174300027	59	130:0	-1	0	4.82E-06
LOC440343	440343	chr16:20517653-20518686	chr16:20518028-20518048	81	129:0	-10	11	5.78E-06
KCNC1	3746	chr11:17712724-17713569	chr11:17713240-17713260	76	129:6	19	11	6.33E-06
HRASLS3	11145	chr11:63116706-63117562	chr11:63117157-63117177	86	129:3	-5	11	6.70E-06
-	-	chr2:165920098-165921089	chr2:165920500-165920520	85	129:0	26	11	6.67E-06
-	-	chr13:24965727-24966703	chr13:24966269-24966278	59	129:5	-6	0	6.20E-06
SPIRE2	84501	chr16:88422406-88423004	chr16:88422524-88422544	73	128:0	18	11	4.84E-06
SPIRE2	84501	chr16:88422406-88423004	chr16:88422518-88422544	68	128:0	15	17	4.84E-06
RPS15	6209	chr19:1397529-1398544	chr19:1398016-1398036	88	128:0	15	11	8.08E-06
RPL38	6169	chr17:69698283-69699194	chr17:69698709-69698729	92	128:7	-36	11	6.99E-06
LOC92017	92017	chr16:12269847-12270436	chr16:12270087-12270096	55	128:0	-34	0	5.20E-06
-	-	chr2:25476887-25477413	chr2:25477138-25477147	36	128:1	9	0	5.06E-06
-	-	chr15:75788350-75788954	chr15:75788705-75788725	70	128:0	27	11	6.05E-06
-	-	chr1:34634868-34635832	chr1:34635320-34635340	82	128:2	-10	11	6.70E-06
SNIP	80725	chr17:33970314-33971115	chr17:33970836-33970855	50	127:0	-16	10	6.48E-06

SLC5A11	115584	chr16:24818819-24819466	chr16:24819236-24819256	85	127:1	8	11	5.67E-06
-	-	chr1:162650066-162650879	chr1:162650426-162650446	75	127:3	-1	11	6.33E-06
SH3KBP1	30011	chrX:19528654-19529672	chrX:19529036-19529056	80	126:2	50	11	6.88E-06
HRH3	11255	chr20:60228796-60229311	chr20:60228831-60228851	90	126:0	6	11	6.70E-06
-	-	chr6:96671210-96671898	chr6:96671454-96671474	93	126:1	-26	11	6.33E-06
CNTN4	152330	chr3:2827113-2827824	chr3:2827596-2827616	82	125:0	-6	11	5.20E-06
BASE	317716	chr20:31244173-31245136	chr20:31244593-31244602	37	125:4	16	0	6.48E-06
BARHL2	343472	chr1:90884686-90885356	chr1:90885094-90885114	75	125:1	-7	11	6.67E-06
-	-	chr2:79592442-79593275	chr2:79592902-79592922	84	125:0	-24	11	6.74E-06
-	-	chr12:117533238-117534094	chr12:117533790-117533810	90	125:1	16	11	6.79E-06
PTPRT	11122	chr20:40241650-40242437	chr20:40242023-40242043	88	124:2	-4	11	7.31E-06
LOC92979	92979	chr12:56440259-56441157	chr12:56440624-56440644	79	124:4	-7	11	6.63E-06
LOC441284	441284	chr7:140373688-140374800	chr7:140374199-140374219	76	124:4	8	11	6.88E-06
LOC441284	441284	chr7:140373688-140374800	chr7:140374193-140374219	62	124:4	5	17	6.88E-06
GRIPAP1	56850	chrX:48609296-48610398	chrX:48609787-48609807	94	124:1	-17	11	8.97E-06
-	-	chr9:120093874-120094526	chr9:120094263-120094283	84	124:1	9	11	6.63E-06
-	-	chr9:119481280-119481826	chr9:119481594-119481614	80	124:0	35	11	6.33E-06
-	-	chr8:140290457-140291278	chr8:140290876-140290896	90	124:2	-4	11	6.79E-06
-	-	chr3:136954179-136954934	chr3:136954581-136954601	76	124:0	0	11	6.48E-06
-	-	chr3:136954179-136954934	chr3:136954488-136954508	70	124:0	-93	11	7.60E-06
-	-	chr3:136954179-136954934	chr3:136954476-136954496	71	124:0	-105	11	7.60E-06
-	-	chr19:8944926-8945809	chr19:8945371-8945391	85	124:2	2	11	6.79E-06
-	-	chr19:8944926-8945809	chr19:8945297-8945317	75	124:2	-72	11	7.89E-06
-	-	chr9:123769373-123770480	chr9:123770039-123770048	36	123:3	-3	0	1.17E-05
-	-	chr15:73067370-73067868	chr15:73067574-73067583	44	123:3	19	0	4.99E-06
-	-	chr10:2996435-2997234	chr10:2996902-2996922	77	123:1	-11	11	6.99E-06
NPAS3	64067	chr14:32749199-32749904	chr14:32749457-32749477	77	122:1	-14	11	6.67E-06
LOC200726	200726	chr2:207332827-207333306	chr2:207333067-207333087	82	122:1	23	11	5.67E-06
ELAVL3	1995	chr19:11453396-11454166	chr19:11453779-11453799	82	122:4	17	11	6.79E-06
COL25A1	84570	chr4:110140002-110140726	chr4:110140331-110140340	35	122:0	5	0	6.99E-06
ANKRD6	22881	chr6:90325571-90326398	chr6:90326127-90326153	64	122:2	-8	17	6.79E-06
-	-	chr3:69050706-69051363	chr3:69051016-69051036	81	122:3	0	11	5.94E-06
CECR6	27439	chr22:15975707-15976558	chr22:15975948-15975968	90	121:4	-19	11	5.94E-06
CECR6	27439	chr22:15975707-15976558	chr22:15975858-15975877	52	121:4	-109	10	6.05E-06
AP3B2	8120	chr15:81174657-81175845	chr15:81175319-81175339	77	121:7	-8	11	1.52E-05
-	-	chr20:59616515-59617210	chr20:59616921-59616941	74	121:3	2	11	6.41E-06
-	-	chr20:7536729-7537309	chr20:7537074-7537094	86	121:1	1	11	6.70E-06
CRMP1	1400	chr4:5994837-5995683	chr4:5995517-5995537	87	120:1	-50	11	6.84E-06

-	-	chr2:41930274-41930909	chr2:41930502-41930522	84	120:1	-12	11	5.94E-06
-	-	chr12:117881965-117883202	chr12:117882357-117882377	88	120:1	22	11	6.84E-06
PPP2R2B	5521	chr5:145983878-145984459	chr5:145984131-145984151	80	119:2	-4	11	6.15E-06
KIAA0408	9729	chr6:127882688-127883580	chr6:127883091-127883111	77	119:0	-43	11	6.99E-06
FLJ20366	55638	chr8:110767169-110768065	chr8:110767607-110767627	86	119:1	28	11	6.84E-06
-	-	chr8:9844593-9845259	chr8:9844984-9845010	53	119:1	20	17	6.63E-06
-	-	chr15:59663663-59664535	chr15:59664111-59664131	88	119:1	1	11	6.99E-06
-	-	chr10:92101992-92102676	chr10:92102208-92102228	75	119:2	12	11	7.45E-06
TUBB4	10381	chr16:88517909-88518910	chr16:88518393-88518413	78	118:5	-21	11	6.99E-06
LOC339903	339903	chr3:42976746-42977416	chr3:42976983-42977003	82	118:0	11	11	6.33E-06
-	-	chr6:98757845-98758477	chr6:98758201-98758221	83	118:0	8	11	7.75E-06
-	-	chr2:64435006-64436200	chr2:64435741-64435761	70	118:2	20	11	1.04E-05
-	-	chr2:64435006-64436200	chr2:64435691-64435711	87	118:2	-30	11	8.36E-06
-	-	chr1:38815503-38816184	chr1:38815794-38815814	78	118:2	-28	11	6.74E-06
-	-	chr3:128364360-128365015	chr3:128364555-128364575	76	116:0	26	11	6.20E-06
-	-	chr3:128364360-128365015	chr3:128364550-128364575	55	116:0	24	16	6.20E-06
-	-	chr2:13350785-13351890	chr2:13351328-13351348	83	116:2	4	11	8.04E-06
-	-	chr16:57755826-57756492	chr16:57756056-57756076	87	116:0	-7	11	6.74E-06
PRSS22	64063	chr16:2850801-2851792	chr16:2851365-2851385	90	115:2	2	11	9.19E-06
NTRK3	4916	chr15:86510517-86511237	chr15:86510776-86510796	90	115:1	-9	11	6.99E-06
GRIK4	2900	chr11:120028640-120029352	chr11:120029064-120029084	91	115:1	1	11	7.45E-06
FLJ90805	284339	chr19:47509068-47510105	chr19:47509836-47509855	56	115:1	58	10	7.45E-06
CALB1	793	chr8:91163897-91164501	chr8:91164231-91164251	86	115:0	-21	11	6.48E-06
-	-	chr4:7701064-7701891	chr4:7701463-7701483	91	115:1	-5	11	6.75E-06
GPR139	124274	chr16:19941999-19942700	chr16:19942223-19942243	83	114:1	-4	11	6.70E-06
LOC440581	440581	chr1:37929632-37930708	chr1:37930310-37930336	74	113:0	-57	17	9.19E-06
AP3D1	8943	chr19:2074155-2075339	chr19:2074907-2074927	88	113:1	8	11	8.08E-06
AP3D1	8943	chr19:2074155-2075339	chr19:2074895-2074915	86	113:1	-4	11	8.36E-06
-	-	chr3:128360111-128360961	chr3:128360539-128360559	83	113:4	0	11	8.04E-06
-	-	chr16:7172378-7172922	chr16:7172705-7172725	80	113:0	16	11	6.20E-06
-	-	chr14:78697552-78698079	chr14:78697866-78697886	85	113:3	47	11	6.48E-06
-	-	chr1:37278354-37278952	chr1:37278699-37278719	86	113:1	53	11	7.45E-06
SCN10A	6336	chr3:38771378-38772348	chr3:38771808-38771828	84	112:0	-16	11	9.19E-06
OR4D2	124538	chr17:53598273-53599015	chr17:53598536-53598556	79	112:3	-24	11	6.75E-06
XYLT1	64131	chr16:17140101-17140817	chr16:17140385-17140405	80	111:0	9	11	6.99E-06
TFAP2BL1	83741	chr6:50774707-50775541	chr6:50775360-50775387	54	111:1	178	18	5.42E-05
TFAP2BL1	83741	chr6:50774707-50775541	chr6:50775117-50775137	72	111:1	-69	11	7.31E-06
OVCA2	124641	chr17:1899969-1901044	chr17:1900203-1900223	87	111:0	-13	11	9.58E-06

COL5A3	50509	chr19:9980736-9981771	chr19:9981243-9981263	87	111:2	-30	11	9.25E-06
-	-	chr10:100049079-100049603	chr10:100049252-100049272	77	111:1	-10	11	6.63E-06
XPO7	23039	chr8:21916370-21917110	chr8:21916674-21916694	86	110:1	-1	11	7.45E-06
FGF14	2259	chr13:101369534-101370292	chr13:101369968-101369988	86	110:1	22	11	7.60E-06
CEACAM3	1084	chr19:47009334-47010150	chr19:47009501-47009521	83	110:1	-9	11	6.75E-06
-	-	chr19:37498708-37499140	chr19:37498935-37498955	81	110:4	68	11	6.41E-06
-	-	chr10:23500006-23500673	chr10:23500405-23500425	90	110:1	57	11	6.75E-06
STK29	9024	chr11:1428702-1429421	chr11:1428953-1428979	75	109:0	-6	17	7.89E-06
NELL1	4745	chr11:20951683-20952529	chr11:20952256-20952276	74	109:0	-22	11	8.08E-06
LOC343629	343629	chr20:57150461-57151347	chr20:57150825-57150845	86	109:3	13	11	8.36E-06
KIAA1765	85443	chr3:36772440-36773561	chr3:36772945-36772965	70	109:6	-5	11	9.19E-06
HLXB9	3110	chr7:155678034-155678842	chr7:155678410-155678436	61	109:3	1	17	7.66E-06
C22orf1	758	chr22:42169518-42170173	chr22:42169795-42169815	97	109:3	3	11	8.08E-06
-	-	chr9:119588386-119588957	chr9:119588808-119588828	82	109:1	36	11	6.88E-06
-	-	chr9:73192824-73193444	chr9:73193161-73193181	71	109:2	6	11	7.89E-06
-	-	chr4:163442463-163442972	chr4:163442703-163442723	73	109:2	-3	11	6.67E-06
-	-	chr15:96247861-96248609	chr15:96248266-96248286	74	109:2	2	11	7.75E-06
-	-	chr13:58909813-58910644	chr13:58910233-58910242	30	109:2	-12	0	9.58E-06
-	-	chr11:91928829-91929717	chr11:91929429-91929449	80	109:1	7	11	9.19E-06
-	-	chr10:19150838-19151550	chr10:19151253-19151279	66	109:0	-25	17	7.89E-06
-	-	chr1:3939262-3939820	chr1:3939467-3939493	52	109:1	38	17	7.31E-06
RFPL2	10739	chr22:30897766-30898527	chr22:30898136-30898156	71	108:0	59	11	7.31E-06
PTCH	5727	chr9:95335575-95336738	chr9:95336371-95336380	67	108:19	4	0	1.41E-05
OTP	23440	chr5:76967207-76967813	chr5:76967382-76967402	82	108:2	2	11	7.66E-06
KCNK12	56660	chr2:47709829-47710645	chr2:47710255-47710275	88	108:2	-22	11	8.08E-06
DEPDC2	80243	chr8:69246850-69247474	chr8:69247172-69247192	79	108:0	-41	11	7.66E-06
-	-	chr6:12549112-12549621	chr6:12549372-12549392	77	108:0	-77	11	6.84E-06
-	-	chr4:153445251-153446149	chr4:153445513-153445533	83	108:2	-12	11	9.19E-06
-	-	chr10:92371134-92371728	chr10:92371499-92371519	76	108:1	1	11	7.31E-06
LOC388010	388010	chr14:96475968-96476722	chr14:96476326-96476354	52	107:0	81	19	1.14E-05
LOC388010	388010	chr14:96475968-96476722	chr14:96476290-96476310	86	107:0	41	11	9.25E-06
KIAA1345	57545	chr4:15241700-15242106	chr4:15241944-15241964	77	107:0	-43	11	6.63E-06
FCGBP	8857	chr19:45114314-45115040	chr19:45114776-45114796	87	107:4	-33	11	8.36E-06
-	-	chr10:99709729-99710786	chr10:99710393-99710413	76	107:2	-14	11	1.04E-05
-	-	chr1:162893738-162894395	chr1:162894136-162894156	80	107:3	44	11	8.36E-06
ACTA1	58	chr1:225873134-225873693	chr1:225873390-225873410	83	106:0	2	11	6.99E-06
-	-	chr7:157846365-157846865	chr7:157846491-157846511	79	106:0	10	11	6.79E-06
-	-	chr6:81538249-81538910	chr6:81538565-81538585	71	106:2	-26	11	7.66E-06

-	-	chr12:124390519-124391339	chr12:124391019-124391045	56	106:2	-27	17	7.75E-06
PCSK1	5122	chr5:95789042-95789862	chr5:95789485-95789505	78	105:0	-53	11	7.75E-06
MAPK8IP1	9479	chr11:45877070-45877897	chr11:45877651-45877660	49	105:2	-2	0	9.19E-06
LOC388906	388906	chr22:41014646-41015705	chr22:41015067-41015087	75	105:4	5	11	9.25E-06
LOC388170	388170	chr15:86207229-86207870	chr15:86207604-86207624	85	105:1	1	11	7.89E-06
LOC338328	338328	chr8:144380741-144381419	chr8:144381123-144381143	92	105:1	23	11	7.45E-06
LOC338328	338328	chr8:144380741-144381419	chr8:144381041-144381061	71	105:1	-59	11	7.60E-06
-	-	chr3:53979703-53980419	chr3:53979908-53979934	52	105:1	-22	17	7.75E-06
-	-	chr10:83727868-83728428	chr10:83728153-83728173	80	105:1	-33	11	7.66E-06
PTPRT	11122	chr20:41249848-41250358	chr20:41250018-41250027	44	104:1	3	0	7.45E-06
KIAA1337	57540	chr1:11474211-11475258	chr1:11474578-11474598	92	104:5	4	11	9.25E-06
KIAA1337	57540	chr1:11474211-11475258	chr1:11474493-11474513	74	104:5	-81	11	1.09E-05
FLJ31164	203062	chr8:143296636-143297104	chr8:143296717-143296737	85	104:0	9	11	7.75E-06
BAI1	575	chr8:143574331-143575400	chr8:143574896-143574905	58	104:3	19	0	1.04E-05
-	-	chr18:10726876-10727590	chr18:10727388-10727408	70	104:0	194	11	3.15E-05
-	-	chr18:10726876-10727590	chr18:10727175-10727195	82	104:0	-19	11	9.10E-06
-	-	chr18:10726876-10727590	chr18:10727077-10727105	44	104:0	-113	19	1.04E-05
SCRT1	83482	chr8:145530716-145531563	chr8:145531207-145531227	81	103:0	7	11	8.36E-06
SCRT1	83482	chr8:145530716-145531563	chr8:145531180-145531200	91	103:0	-20	11	8.36E-06
NELL1	4745	chr11:20832256-20832737	chr11:20832532-20832552	81	103:0	10	11	6.75E-06
LOC441991	441991	chr22:22275137-22275884	chr22:22275472-22275492	80	103:1	11	11	8.08E-06
-	-	chr7:9589603-9590449	chr7:9589974-9590000	49	103:1	-45	17	9.25E-06
SRD5A1	6715	chr5:6739750-6740430	chr5:6740085-6740105	87	102:3	-3	11	8.55E-06
PHF15	23338	chr5:133904984-133905733	chr5:133905485-133905505	78	102:3	14	11	8.36E-06
NEUROG3	50674	chr10:70997224-70998247	chr10:70997777-70997797	86	102:5	-4	11	1.25E-05
EPS8L1	54869	chr19:60269111-60269704	chr19:60269452-60269472	85	102:1	-19	11	8.55E-06
CRMP1	1400	chr4:6010754-6011621	chr4:6011048-6011068	85	102:1	2	11	8.55E-06
-	-	chr4:5481648-5482448	chr4:5481955-5481975	91	102:2	3	11	1.04E-05
-	-	chr22:31796826-31797527	chr22:31797113-31797133	87	102:1	4	11	8.97E-06
SRM	6723	chr1:11047950-11048764	chr1:11048313-11048333	81	101:2	-10	11	8.55E-06
SRM	6723	chr1:11047950-11048764	chr1:11048213-11048233	71	101:2	-110	11	1.20E-05
LOC389075	389075	chr2:220021486-220022475	chr2:220021969-220021989	95	101:3	13	11	1.29E-05
FIBL-6	83872	chr1:182618253-182618905	chr1:182618636-182618656	76	101:0	-9	11	8.08E-06
DOCK1	1793	chr10:128805361-128805824	chr10:128805577-128805597	71	101:0	-24	11	6.88E-06
DOCK1	1793	chr10:128805361-128805824	chr10:128805571-128805597	60	101:0	-27	17	6.88E-06
-	-	chr21:38208249-38208954	chr21:38208531-38208551	91	101:0	9	11	9.19E-06
-	-	chr21:38208249-38208954	chr21:38208296-38208324	42	101:0	-222	19	1.65E-05
KCNS2	3788	chr8:99508003-99508543	chr8:99508354-99508363	65	100:0	7	0	6.88E-06

GABRA1	2554	chr5:161206210-161206985	chr5:161206529-161206538	59	100:0	0	0	8.36E-06
FLJ25328	148231	chr19:16023062-16023738	chr19:16023506-16023531	47	100:5	278	16	6.28E-05
FLJ25328	148231	chr19:16023062-16023738	chr19:16023231-16023251	75	100:5	0	11	7.60E-06
-	-	chr18:55335795-55336413	chr18:55336177-55336197	88	100:2	-11	11	9.25E-06
-	-	chr10:92876911-92877487	chr10:92877274-92877283	30	100:6	-9	0	8.04E-06
PTPRR	5801	chr12:69599291-69600066	chr12:69599764-69599784	81	99:0	2	11	1.09E-05
PTPRR	5801	chr12:69599291-69600066	chr12:69599665-69599685	70	99:0	-97	11	1.17E-05
LOC284898	284898	chr22:25795676-25796387	chr22:25795978-25795998	86	99:0	-22	11	8.04E-06
C22orf1	758	chr22:42127695-42128057	chr22:42127793-42127813	71	99:0	-18	11	6.84E-06
-	-	chr5:141818833-141819427	chr5:141819139-141819159	74	99:3	-26	11	8.04E-06
-	-	chr3:179885357-179885992	chr3:179885538-179885565	54	99:2	-11	18	9.58E-06
-	-	chr10:59605606-59606122	chr10:59605953-59605973	86	99:1	-26	11	8.55E-06
MYT1	4661	chr20:62294111-62294809	chr20:62294369-62294395	71	98:0	3	17	8.04E-06
-	-	chr5:38246771-38247465	chr5:38247033-38247053	83	98:0	-16	11	9.19E-06
-	-	chr22:24799408-24799997	chr22:24799713-24799733	74	98:1	38	11	8.97E-06
-	-	chr17:29802364-29803006	chr17:29802638-29802658	79	98:0	5	11	8.55E-06
-	-	chr17:29802364-29803006	chr17:29802575-29802600	40	98:0	-55	16	8.04E-06
-	-	chr16:27841200-27841713	chr16:27841453-27841462	34	98:3	10	0	7.45E-06
-	-	chr13:86948846-86949727	chr13:86949124-86949144	79	98:2	-2	11	1.04E-05
SCGB1D2	10647	chr11:61769091-61769909	chr11:61769449-61769458	33	97:2	0	0	1.17E-05
PHF12	57649	chr17:24304164-24305101	chr17:24304756-24304765	35	97:7	2	0	1.14E-05
LOC442081	442081	chr3:71841743-71842528	chr3:71842144-71842164	72	97:10	-11	11	1.25E-05
IPO13	9670	chr1:44080777-44081670	chr1:44081060-44081069	24	97:4	-5	0	1.48E-05
-	-	chr8:28570663-28571270	chr8:28570832-28570852	74	97:1	-13	11	8.08E-06
-	-	chr3:61276408-61277048	chr3:61276754-61276781	52	97:2	58	18	8.08E-06
-	-	chr13:64397329-64397957	chr13:64397342-64397362	72	97:1	-271	11	5.03E-05
-	-	chr13:64397329-64397957	chr13:64397335-64397362	66	97:1	-274	18	5.03E-05
XYLT1	64131	chr16:17179333-17180106	chr16:17179747-17179767	74	96:1	44	11	9.58E-06
NTSR2	23620	chr2:11760548-11761090	chr2:11760677-11760703	72	96:1	-13	17	8.97E-06
FLJ13842	79698	chr8:40805431-40806117	chr8:40805697-40805723	62	96:0	31	17	1.04E-05
FLJ13842	79698	chr8:40805431-40806117	chr8:40805661-40805681	77	96:0	-8	11	1.23E-05
-	-	chr8:143046044-143046976	chr8:143046562-143046582	82	96:4	7	11	1.25E-05
-	-	chr8:36354899-36355509	chr8:36355237-36355257	86	96:2	-10	11	9.58E-06
-	-	chr5:136958140-136958786	chr5:136958491-136958511	80	96:2	-47	11	9.58E-06
SEZ6L	23544	chr22:24891095-24891714	chr22:24891503-24891512	45	95:1	2	0	8.55E-06
NOVA1	4857	chr14:25983729-25984203	chr14:25983953-25983962	63	95:5	3	0	8.08E-06
MGC2731	79035	chr12:54904994-54905603	chr12:54905212-54905232	83	95:1	-6	11	9.58E-06
IGSF10	285313	chr3:152643666-152644501	chr3:152644268-152644288	81	95:2	21	11	1.41E-05

CNOT4	4850	chr7:134583533-134584249	chr7:134583925-134583945	73	95:1	-17	11	1.09E-05
-	-	chr5:169971222-169971843	chr5:169971518-169971538	88	95:1	-7	11	1.17E-05
-	-	chr3:192040466-192041255	chr3:192040822-192040842	82	95:2	-1	11	9.19E-06
SEC8L1	60412	chr7:132281206-132281788	chr7:132281518-132281527	41	94:3	2	0	1.04E-05
RIC3	79608	chr11:8145876-8146413	chr11:8146124-8146133	53	94:2	12	0	8.55E-06
OR1E2	8388	chr17:3283406-3283722	chr17:3283415-3283442	41	94:0	-1	18	7.66E-06
NDUFS4	4724	chr5:52948540-52949239	chr5:52948711-52948737	54	94:2	57	17	8.55E-06
NALP1	22861	chr17:5437517-5438005	chr17:5437777-5437797	75	94:3	-48	11	8.97E-06
LOC388787	388787	chr20:5438698-5439406	chr20:5439293-5439313	83	94:1	-8	11	9.10E-06
DKFZP434I2117	83723	chr16:29947228-29948081	chr16:29947639-29947659	92	94:0	18	11	1.56E-05
-	-	chr6:29937197-29937901	chr6:29937346-29937355	49	94:1	-37	0	1.20E-05
-	-	chr5:125161803-125162704	chr5:125162075-125162095	96	94:0	-7	11	1.31E-05
-	-	chr4:191070184-191070799	chr4:191070373-191070393	74	94:3	-7	11	9.19E-06
-	-	chr4:191070184-191070799	chr4:191070362-191070382	70	94:3	-18	11	8.55E-06
-	-	chr22:25643349-25644173	chr22:25643571-25643591	84	94:2	-6	11	1.29E-05
-	-	chr17:60680701-60681243	chr17:60680927-60680947	75	94:1	-35	11	9.58E-06
LOC442011	442011	chr2:26282953-26283595	chr2:26283209-26283229	86	93:1	5	11	1.09E-05
KIAA1110	23280	chr12:46257-46901	chr12:46649-46669	91	93:0	-66	11	1.34E-05
KIAA1110	23280	chr12:46257-46901	chr12:46589-46609	84	93:0	-126	11	1.65E-05
DNAJA3	9093	chr16:4444625-4445321	chr16:4444814-4444834	80	93:0	-12	11	9.19E-06
CYP4F12	66002	chr19:15656472-15657074	chr19:15656896-15656916	71	93:1	50	11	1.29E-05
CYP4F12	66002	chr19:15656472-15657074	chr19:15656825-15656850	64	93:1	-18	16	1.09E-05
-	-	chr8:133487088-133487794	chr8:133487306-133487315	48	93:6	7	0	9.10E-06
-	-	chr3:182516922-182517509	chr3:182517163-182517183	93	93:0	1	11	8.04E-06
SMPX	23676	chrX:21500858-21501425	chrX:21501128-21501148	80	92:0	-7	11	9.10E-06
OR10H4	126541	chr19:15933998-15934677	chr19:15934330-15934350	93	92:0	47	11	9.10E-06
LOC440763	440763	chr20:39716791-39717492	chr20:39717150-39717159	46	92:3	9	0	1.31E-05
LOC389421	389421	chr6:105498258-105499007	chr6:105498556-105498576	80	92:0	-43	11	1.31E-05
LOC149830	149830	chr20:4659351-4660023	chr20:4659736-4659756	86	92:0	-26	11	9.10E-06
CX36	57369	chr15:32832670-32833238	chr15:32832972-32833000	52	92:4	58	19	8.55E-06
AUH	549	chr9:91075874-91077136	chr9:91076514-91076534	93	92:2	-32	11	1.56E-05
-	-	chr9:123991661-123992492	chr9:123992010-123992030	87	92:1	-20	11	1.04E-05
-	-	chr21:30989998-30990812	chr21:30990356-30990365	48	92:0	7	0	1.09E-05
-	-	chr2:114916210-114916954	chr2:114916562-114916582	82	92:3	6	11	1.20E-05
XYLT1	64131	chr16:17373589-17374384	chr16:17373927-17373947	82	91:5	53	11	1.25E-05
RNU3IP2	9136	chr3:51938325-51938959	chr3:51938676-51938701	68	91:3	-11	16	1.14E-05
EAF1	85403	chr3:15451146-15451833	chr3:15451446-15451466	84	91:0	-7	11	1.20E-05
-	-	chr1:240433597-240434213	chr1:240433854-240433874	86	91:1	9	11	9.10E-06



-	-	chr1:240392751-240393689	chr1:240393406-240393426	78	91:0	-4	11	1.28E-05
TMIE	259236	chr3:46721618-46722262	chr3:46721921-46721941	78	90:5	17	11	1.45E-05
SEMA5B	54437	chr3:124120437-124121098	chr3:124120686-124120706	74	90:2	4	11	1.04E-05
PDE2A	5138	chr11:72062009-72063023	chr11:72062434-72062453	46	90:0	-37	10	1.48E-05
MGC13053	84796	chr11:117810217-117811419	chr11:117810993-117811012	54	90:11	107	10	2.31E-05
LOC392159	392159	chr7:156785224-156786041	chr7:156785405-156785425	74	90:1	-13	11	9.58E-06
LOC392159	392159	chr7:156785224-156786041	chr7:156785400-156785425	45	90:1	-15	16	9.58E-06
GALNT14	79623	chr2:31241952-31242699	chr2:31242329-31242349	85	90:3	46	11	1.09E-05
-	-	chr3:63324998-63325920	chr3:63325368-63325388	82	90:0	4	11	1.58E-05
-	-	chr20:41102312-41102865	chr20:41102652-41102672	85	90:3	-46	11	8.97E-06
-	-	chr20:17012227-17012773	chr20:17012562-17012582	86	90:0	47	11	1.17E-05
-	-	chr2:103731145-103732108	chr2:103731734-103731754	78	90:4	-26	11	1.37E-05
-	-	chr2:94850106-94850603	chr2:94850370-94850390	77	90:1	1	11	9.58E-06
-	-	chr15:51407575-51408444	chr15:51408016-51408036	73	90:0	22	11	1.23E-05
LOC440113	440113	chr12:119541687-119542675	chr12:119542050-119542059	65	89:3	4	0	1.34E-05
-	-	chr5:165525091-165525774	chr5:165525355-165525375	75	89:3	-5	11	1.28E-05
-	-	chr15:61949763-61950351	chr15:61949962-61949981	47	89:3	-62	10	9.58E-06
-	-	chr11:126473728-126474365	chr11:126473952-126473961	49	89:1	6	0	1.14E-05
-	-	chr11:8330089-8330899	chr11:8330335-8330344	42	89:0	-9	0	1.31E-05
RUTBC2	129049	chr22:23563403-23564259	chr22:23563757-23563783	65	88:1	34	17	1.23E-05
GRIA2	2891	chr4:158498825-158499405	chr4:158499144-158499164	96	88:0	11	11	1.28E-05
FLJ32786	136332	chr7:132783326-132784076	chr7:132783654-132783674	77	88:2	108	11	1.17E-05
CRMP1	1400	chr4:6001042-6001498	chr4:6001334-6001354	70	88:2	6	11	1.23E-05
-	-	chr6:30453877-30454529	chr6:30454266-30454286	83	88:3	-4	11	1.20E-05
-	-	chr2:154545859-154546407	chr2:154546225-154546245	84	88:1	20	11	1.29E-05
LOC441284	441284	chr7:140226185-140226715	chr7:140226272-140226292	82	87:0	-45	11	1.20E-05
CRTAC1	55118	chr10:99741575-99742066	chr10:99741799-99741825	59	87:1	52	17	1.14E-05
-	-	chr15:77287371-77287971	chr15:77287788-77287808	71	87:2	106	11	1.20E-05
OR10H2	26538	chr19:15689318-15690124	chr19:15689791-15689811	90	86:2	-57	11	1.35E-05
NR2E1	7101	chr6:108615819-108616413	chr6:108616178-108616205	46	86:3	-41	18	9.58E-06
LOC113174	113174	chr11:18088782-18089753	chr11:18089349-18089369	76	86:6	-5	11	1.74E-05
HCN1	348980	chr5:45730092-45730585	chr5:45730310-45730330	80	86:1	10	11	1.09E-05
CYP11B2	1585	chr8:143990287-143990939	chr8:143990647-143990672	54	86:0	156	16	1.28E-05
CYP11B2	1585	chr8:143990287-143990939	chr8:143990503-143990523	88	86:0	9	11	1.23E-05
-	-	chr14:73961836-73962659	chr14:73962516-73962536	92	86:0	1	11	1.83E-05
LOC92017	92017	chr16:12200692-12201457	chr16:12200998-12201017	53	85:2	-17	10	1.35E-05
CNTNAP5	129684	chr2:124498765-124499660	chr2:124499069-124499095	57	85:3	10	17	1.29E-05
CDH22	64405	chr20:44323675-44324519	chr20:44324079-44324099	80	85:1	-1	11	1.52E-05

-	-	chr17:16656066-16656555	chr17:16656343-16656363	87	85:0	-16	11	1.31E-05
-	-	chr13:106968543-106969014	chr13:106968804-106968813	67	85:3	-35	0	9.10E-06
-	-	chr13:43257924-43258760	chr13:43258424-43258444	75	85:2	-22	11	1.34E-05
-	-	chr11:33478921-33479430	chr11:33479156-33479176	88	85:2	-11	11	1.20E-05
PCSK2	5126	chr20:17154728-17155503	chr20:17155402-17155422	72	84:1	-26	11	1.41E-05
KCNN3	3782	chr1:151488728-151489232	chr1:151488952-151488972	72	84:1	13	11	1.34E-05
GPR4	2828	chr19:50789491-50789813	chr19:50789699-50789719	75	84:1	17	11	9.19E-06
DPP6	1804	chr7:153366403-153366979	chr7:153366664-153366684	82	84:4	-8	11	1.25E-05
DKFZp761B0514	84249	chr5:139195029-139196167	chr5:139195673-139195692	46	84:3	26	10	2.00E-05
DKFZp761B0514	84249	chr5:139195029-139196167	chr5:139195616-139195636	80	84:3	-31	11	2.00E-05
-	-	chr22:25669438-25670210	chr22:25669924-25669944	85	84:1	16	11	1.35E-05
-	-	chr16:22807580-22808169	chr16:22807803-22807823	87	84:1	-8	11	1.28E-05
-	-	chr11:88077240-88077828	chr11:88077513-88077533	87	84:0	-23	11	1.20E-05
WFDC6	140870	chr20:43577031-43577711	chr20:43577392-43577412	88	83:0	-192	11	1.29E-05
TNXB	7148	chr6:32181189-32181787	chr6:32181383-32181403	72	83:2	-54	11	1.29E-05
TNXB	7148	chr6:32181189-32181787	chr6:32181365-32181385	73	83:2	-72	11	1.20E-05
PLA2G4C	8605	chr19:53305383-53305953	chr19:53305611-53305620	31	83:1	3	0	1.35E-05
-	-	chr5:7063546-7064292	chr5:7063890-7063910	90	83:4	-10	11	1.87E-05
-	-	chr22:25572387-25573141	chr22:25572844-25572864	76	83:3	-10	11	1.35E-05
-	-	chr15:78859687-78860571	chr15:78860169-78860189	73	83:0	-32	11	1.31E-05
SCEL	8796	chr13:77035062-77035815	chr13:77035482-77035502	84	82:0	13	11	1.56E-05
ORC4L	5000	chr2:148536943-148537529	chr2:148537155-148537175	81	82:0	9	11	1.29E-05
ORC4L	5000	chr2:148536943-148537529	chr2:148537093-148537119	50	82:0	-50	17	1.28E-05
LOC391738	391738	chr5:13701855-13702444	chr5:13702111-13702131	89	82:2	-11	11	1.35E-05
CNTNAP5	129684	chr2:124911507-124912169	chr2:124911801-124911821	86	82:0	-1	11	1.37E-05
CLECSF1	10143	chr16:76637247-76637782	chr16:76637531-76637559	60	82:0	19	19	1.14E-05
-	-	chr7:158267960-158268505	chr7:158268181-158268201	73	82:2	16	11	1.31E-05
-	-	chr5:123910226-123910775	chr5:123910436-123910456	88	82:1	21	11	1.28E-05
-	-	chr20:61171372-61172339	chr20:61171825-61171845	84	82:3	37	11	1.69E-05
-	-	chr20:61171372-61172339	chr20:61171574-61171599	52	82:3	-211	16	3.05E-05
-	-	chr17:30246454-30247028	chr17:30246735-30246755	75	82:2	39	11	1.23E-05
-	-	chr11:133793280-133794105	chr11:133793733-133793753	87	82:0	-2	11	1.56E-05
-	-	chr11:93590863-93591727	chr11:93591380-93591400	88	82:1	-15	11	1.58E-05
P2RY4	5030	chrX:69267451-69268140	chrX:69267851-69267871	87	81:2	-70	11	1.60E-05
LOC130940	130940	chr2:158869808-158870388	chr2:158870107-158870127	72	81:3	32	11	1.29E-05
GUCY1A2	2977	chr11:106394794-106395385	chr11:106395138-106395147	29	81:1	13	0	1.25E-05
FRMD3	257019	chr9:83140552-83141033	chr9:83140789-83140809	74	81:0	-37	11	1.17E-05
FLJ11286	55337	chr19:10064683-10065334	chr19:10065040-10065060	84	81:1	-16	11	1.37E-05

CXorf9	54440	chrX:128641155-128641943	chrX:128641646-128641666	70	81:2	42	11	1.60E-05
CENTB5	116983	chr1:1274159-1274970	chr1:1274541-1274561	90	81:1	1	11	1.48E-05
BCNP1	199786	chr19:17510618-17511776	chr19:17511154-17511174	83	81:8	6	11	2.08E-05
-	-	chr5:131388057-131388812	chr5:131388556-131388582	50	81:2	36	17	1.37E-05
-	-	chr2:53093653-53094361	chr2:53094058-53094078	70	81:0	47	11	1.41E-05
-	-	chr18:1082208-1082651	chr18:1082442-1082462	85	81:3	3	11	1.28E-05
PHF14	9678	chr7:10787291-10787808	chr7:10787529-10787538	56	80:12	-3	0	1.37E-05
LOC388171	388171	chr15:86949662-86950603	chr15:86950045-86950070	72	80:1	-9	16	1.74E-05
CROC4	10485	chr1:153197294-153197739	chr1:153197524-153197544	90	80:1	-7	11	1.35E-05
-	-	chr5:30844812-30845350	chr5:30845056-30845076	74	80:0	22	11	1.25E-05
-	-	chr3:44153019-44153711	chr3:44153116-44153142	47	80:0	39	17	1.37E-05
-	-	chr17:53187769-53188297	chr17:53188036-53188063	45	80:2	61	18	1.37E-05
-	-	chr15:100168418-100169098	chr15:100168839-100168859	85	80:2	-2	11	1.52E-05
-	-	chr13:98870444-98871181	chr13:98870696-98870715	45	80:10	-10	10	1.45E-05
-	-	chr11:18814411-18815251	chr11:18814752-18814772	91	80:3	-17	11	1.45E-05
-	-	chr1:24008455-24008985	chr1:24008730-24008750	81	80:2	46	11	1.28E-05
SND1	27044	chr7:126708471-126708891	chr7:126708655-126708675	76	79:0	0	11	1.20E-05
LOC390930	390930	chr19:44748442-44749292	chr19:44748753-44748773	90	79:2	-19	11	1.48E-05
KIAA0789	9671	chr12:107094077-107094729	chr12:107094467-107094487	85	79:0	-5	11	1.48E-05
C20orf102	128434	chr20:35963162-35964031	chr20:35963735-35963755	80	79:0	0	11	2.04E-05
C20orf102	128434	chr20:35963162-35964031	chr20:35963729-35963755	60	79:0	-3	17	2.04E-05
C20orf102	128434	chr20:35963162-35964031	chr20:35963662-35963682	79	79:0	-73	11	2.12E-05
C20orf102	128434	chr20:35963162-35964031	chr20:35963268-35963288	84	79:0	-467	11	7.34E-05
-	-	chr9:97587121-97587616	chr9:97587358-97587383	56	79:3	-16	16	1.20E-05
-	-	chr5:29999684-30000175	chr5:30000013-30000022	45	79:0	-2	0	1.35E-05
-	-	chr22:37636923-37637556	chr22:37637497-37637517	84	79:1	-5	11	1.45E-05
-	-	chr16:26235704-26236500	chr16:26236076-26236096	76	79:1	2	11	1.52E-05
STMN3	50861	chr20:61754908-61755344	chr20:61755130-61755150	79	78:1	-22	11	1.23E-05
SDS3	64426	chr12:117332460-117333009	chr12:117332828-117332848	70	78:0	5	11	1.25E-05
PRKCB1	5579	chr16:23892858-23893448	chr16:23893223-23893243	88	78:1	7	11	1.48E-05
NR3C2	4306	chr4:149485694-149486300	chr4:149486021-149486041	79	78:1	1	11	1.65E-05
-	-	chr6:103738500-103738968	chr6:103738725-103738745	79	78:3	15	11	1.23E-05
-	-	chr22:25698050-25698885	chr22:25698451-25698471	83	78:2	-24	11	1.65E-05
-	-	chr20:40102841-40103679	chr20:40103200-40103228	44	78:2	-13	19	1.48E-05
-	-	chr10:103789923-103790603	chr10:103790218-103790238	74	78:2	-1	11	1.48E-05
LTBP2	4053	chr14:74083807-74084561	chr14:74084179-74084199	80	77:5	-11	11	1.58E-05
LOC390896	390896	chr19:15548862-15549595	chr19:15549260-15549280	71	77:0	88	11	2.00E-05
LOC390896	390896	chr19:15548862-15549595	chr19:15549177-15549202	54	77:0	8	16	1.65E-05

LOC284434	284434	chr19:16711274-16711771	chr19:16711536-16711562	69	77:6	-8	17	1.31E-05
KIAA1889	114786	chr8:56177885-56178519	chr8:56178112-56178132	96	77:1	11	11	1.35E-05
HD	3064	chr4:3235521-3236151	chr4:3235885-3235894	58	77:4	13	0	1.37E-05
FLJ30296	139411	chrX:23104859-23105581	chrX:23105063-23105083	88	77:0	32	11	1.37E-05
ADCY8	114	chr8:131889948-131890549	chr8:131890280-131890300	80	77:2	-16	11	1.58E-05
-	-	chr8:5969467-5969962	chr8:5969613-5969633	74	77:2	-28	11	1.31E-05
-	-	chr6:126987464-126988271	chr6:126988034-126988054	76	77:4	22	11	1.52E-05
-	-	chr2:234800831-234801326	chr2:234801050-234801070	88	77:0	76	11	1.31E-05
-	-	chr2:22051372-22052111	chr2:22051666-22051675	45	77:4	1	0	1.37E-05
-	-	chr14:95398181-95398807	chr14:95398528-95398548	79	77:3	5	11	1.48E-05
-	-	chr13:43216432-43217385	chr13:43216963-43216983	90	77:1	33	11	1.69E-05
MAP3K9	4293	chr14:70340926-70341581	chr14:70341210-70341219	30	76:0	3	0	1.56E-05
CDT6	10218	chr1:11188702-11189278	chr1:11188921-11188941	87	76:0	6	11	1.35E-05
-	-	chr12:46214508-46215193	chr12:46214755-46214775	73	76:1	-197	11	1.79E-05
PBEF1	10135	chr7:104889343-104889837	chr7:104889559-104889579	74	75:3	51	11	1.48E-05
MYO1A	4640	chr12:55729786-55730278	chr12:55730053-55730073	73	75:1	19	11	1.31E-05
KIAA1399	57574	chr2:217057353-217057770	chr2:217057469-217057478	31	75:1	7	0	1.35E-05
FLJ30681	147372	chr18:55264019-55264623	chr18:55264385-55264405	70	75:2	-38	11	1.37E-05
CALU	813	chr7:127402349-127403181	chr7:127402803-127402828	72	75:1	-5	16	1.58E-05
C20orf166	128826	chr20:60584367-60584866	chr20:60584644-60584670	54	75:0	-30	17	1.41E-05
ALPL	249	chr1:21606352-21607104	chr1:21606846-21606866	85	75:4	76	11	1.45E-05
-	-	chr4:45859182-45859715	chr4:45859441-45859461	87	75:0	10	11	1.45E-05
-	-	chr3:171804092-171804783	chr3:171804451-171804471	85	75:1	-6	11	1.74E-05
-	-	chr3:118524156-118524768	chr3:118524596-118524616	83	75:0	40	11	1.60E-05
-	-	chr16:7829502-7830089	chr16:7829716-7829736	84	75:2	58	11	1.48E-05
-	-	chr16:7829502-7830089	chr16:7829669-7829689	73	75:2	11	11	1.56E-05
LOC442724	442724	chr7:130353932-130354517	chr7:130354311-130354331	70	74:0	-30	11	1.41E-05
KCNC4	3749	chr1:110473306-110473878	chr1:110473590-110473610	76	74:0	33	11	1.56E-05
DRB1	129831	chr2:178802404-178803104	chr2:178802771-178802791	70	74:8	120	11	1.91E-05
DISP2	85455	chr15:38437763-38438249	chr15:38437775-38437800	72	74:2	-6	16	1.56E-05
CHST8	64377	chr19:38860428-38861211	chr19:38860727-38860753	64	74:0	-21	17	1.79E-05
C6orf60	79632	chr6:119452903-119453610	chr6:119453305-119453314	41	74:2	-3	0	1.79E-05
-	-	chr8:111229957-111230496	chr8:111230245-111230265	80	74:0	26	11	1.65E-05
-	-	chr22:17330099-17330923	chr22:17330414-17330434	71	74:0	43	11	1.87E-05
-	-	chr22:17330099-17330923	chr22:17330402-17330422	84	74:0	31	11	1.60E-05
-	-	chr2:133654941-133655546	chr2:133655267-133655287	86	74:1	18	11	1.60E-05
-	-	chr15:57500685-57501198	chr15:57500946-57500966	82	74:0	-32	11	1.52E-05
-	-	chr10:99836966-99837491	chr10:99837249-99837258	21	74:1	5	0	1.29E-05

-	-	chr10:4173505-4174151	chr10:4173842-4173862	77	74:0	-29	11	1.58E-05
-	-	chr1:110797497-110798008	chr1:110797552-110797572	88	74:2	-1	11	1.45E-05
TAS1R3	83756	chr1:1310134-1310806	chr1:1310394-1310414	73	73:1	122	11	1.65E-05
TAS1R3	83756	chr1:1310134-1310806	chr1:1310355-1310375	85	73:1	83	11	1.60E-05
TAS1R3	83756	chr1:1310134-1310806	chr1:1310314-1310334	80	73:1	42	11	1.77E-05
SLC35F1	222553	chr6:118334381-118335026	chr6:118334779-118334806	53	73:1	-21	18	1.56E-05
LOC147670	147670	chr19:61842506-61842979	chr19:61842587-61842607	91	73:1	7	11	1.52E-05
GSH1	219409	chr13:27264322-27264829	chr13:27264707-27264727	71	73:3	132	11	2.00E-05
CGI-85	51111	chr11:67733022-67733878	chr11:67733333-67733353	87	73:6	-2	11	1.65E-05
-	-	chr3:162831205-162831705	chr3:162831463-162831483	79	73:1	2	11	1.45E-05
-	-	chr2:240345897-240346608	chr2:240346305-240346314	47	73:2	5	0	1.56E-05
-	-	chr2:58566228-58566987	chr2:58566463-58566489	67	73:1	6	17	1.65E-05
-	-	chr14:97116958-97117614	chr14:97117170-97117190	85	73:2	-4	11	1.58E-05
-	-	chr14:51316919-51317544	chr14:51317403-51317412	64	73:2	3	0	1.87E-05
-	-	chr11:18996864-18997463	chr11:18997224-18997244	81	73:1	54	11	1.52E-05
PGM2L1	283209	chr11:73806173-73807000	chr11:73806638-73806666	58	72:6	-11	19	1.91E-05
LOC286144	286144	chr8:94047129-94047717	chr8:94047460-94047480	71	72:8	12	11	1.69E-05
LOC129521	129521	chr2:100545815-100546374	chr2:100546071-100546091	83	72:1	12	11	1.48E-05
GRIN3A	116443	chr9:101578506-101579233	chr9:101578769-101578789	79	72:1	29	11	1.69E-05
FLJ32682	220081	chr13:45068208-45068572	chr13:45068291-45068311	79	72:1	-36	11	1.34E-05
DKFZP564D172	83989	chr5:92974023-92974387	chr5:92974140-92974160	88	72:1	8	11	1.31E-05
-	-	chrX:7352051-7352594	chrX:7352307-7352327	80	72:0	-42	11	1.60E-05
-	-	chr8:140642657-140643269	chr8:140642925-140642934	38	72:0	5	0	1.56E-05
-	-	chr8:24974155-24974769	chr8:24974333-24974359	67	72:3	11	17	1.48E-05
-	-	chr3:117781297-117781805	chr3:117781519-117781539	89	72:1	8	11	1.45E-05
-	-	chr22:48426346-48427330	chr22:48426868-48426888	88	72:0	14	11	2.17E-05
-	-	chr2:153632029-153632598	chr2:153632357-153632377	81	72:1	-1	11	1.56E-05
-	-	chr10:23845526-23845898	chr10:23845664-23845684	79	72:2	15	11	1.29E-05
MYO18B	84700	chr22:24720459-24720961	chr22:24720570-24720590	78	71:0	-12	11	1.60E-05
-	-	chr4:13873767-13874464	chr4:13874209-13874229	78	71:0	18	11	1.56E-05
-	-	chr4:13873767-13874464	chr4:13874197-13874217	86	71:0	6	11	1.56E-05
-	-	chr2:240301943-240302365	chr2:240302220-240302229	49	71:1	-1	0	1.35E-05
-	-	chr16:5166331-5167053	chr16:5166682-5166701	63	71:0	-23	10	1.60E-05
-	-	chr16:5166331-5167053	chr16:5166469-5166494	47	71:0	-233	16	2.91E-05
LOC157697	157697	chr8:667039-667714	chr8:667379-667406	34	70:3	24	18	1.77E-05
LOC157697	157697	chr8:667039-667714	chr8:667335-667355	84	70:3	-24	11	1.69E-05
HNRPUL1	11100	chr19:46503783-46504302	chr19:46503870-46503890	81	70:2	-3	11	1.65E-05
E1F3S5	8665	chr11:7986289-7986998	chr11:7986583-7986609	49	70:1	-46	17	1.60E-05

-	-	chr7:95179088-95179589	chr7:95179319-95179339	76	70:1	3	11	1.41E-05
-	-	chr16:46379237-46379669	chr16:46379304-46379324	87	70:2	-22	11	1.45E-05
-	-	chr1:36737990-36738751	chr1:36738335-36738355	77	70:3	-26	11	1.87E-05
PRLH	51052	chr2:238254336-238254912	chr2:238254648-238254668	82	69:2	-25	11	1.52E-05
MGC70857	414919	chr8:145723063-145723571	chr8:145723377-145723397	89	69:0	-9	11	1.41E-05
KIAA0420	9717	chr16:4947899-4948877	chr16:4948373-4948400	57	69:5	35	18	2.27E-05
KIAA0420	9717	chr16:4947899-4948877	chr16:4948307-4948327	75	69:5	-35	11	2.17E-05
FLJ00133	25992	chr2:241726165-241727008	chr2:241726585-241726605	70	69:2	18	11	1.69E-05
FLJ00133	25992	chr2:241726165-241727008	chr2:241726578-241726605	56	69:2	15	18	1.69E-05
EPHA8	2046	chr1:22678967-22679480	chr1:22679091-22679111	79	69:1	40	11	1.56E-05
ADCY2	108	chr5:7583002-7583519	chr5:7583243-7583263	81	69:1	-69	11	1.79E-05
-	-	chr8:20535603-20536039	chr8:20535812-20535832	87	69:2	13	11	1.37E-05
-	-	chr5:148025859-148026710	chr5:148026289-148026309	85	69:5	40	11	2.04E-05
-	-	chr3:187711984-187712593	chr3:187712468-187712495	44	69:3	44	18	2.04E-05
-	-	chr3:187711984-187712593	chr3:187712372-187712392	87	69:3	-56	11	1.91E-05
-	-	chr3:187711984-187712593	chr3:187712218-187712246	55	69:3	-206	19	2.04E-05
-	-	chr3:187711984-187712593	chr3:187712147-187712167	78	69:3	-281	11	3.29E-05
-	-	chr17:74845933-74846311	chr17:74846019-74846039	79	69:0	3	11	1.52E-05
-	-	chr16:5699894-5700450	chr16:5700058-5700078	90	69:1	-3	11	1.48E-05
-	-	chr15:85034660-85035539	chr15:85035028-85035055	51	69:2	19	18	2.00E-05
-	-	chr12:128128913-128129482	chr12:128129149-128129169	88	69:1	8	11	1.56E-05
-	-	chr12:128128913-128129482	chr12:128129057-128129077	72	69:1	-84	11	1.83E-05
-	-	chr1:66200726-66201179	chr1:66200794-66200803	41	69:3	11	0	1.56E-05
LOC285307	285307	chr3:34436296-34436768	chr3:34436500-34436520	82	68:4	-26	11	1.65E-05
NEUROD4	58158	chr12:53699825-53700308	chr12:53700074-53700102	61	67:3	102	19	1.52E-05
NEUROD4	58158	chr12:53699825-53700308	chr12:53700032-53700060	54	67:3	60	19	1.56E-05
NALP14	338323	chr11:7054867-7055391	chr11:7055102-7055122	79	67:1	46	11	1.52E-05
LPAAT-e	55326	chr8:6553504-6554023	chr8:6553599-6553619	78	67:5	22	11	1.77E-05
Dlc2	140735	chr17:53516701-53517346	chr17:53516944-53516953	22	67:3	9	0	1.83E-05
C10orf11	83938	chr10:77446997-77447782	chr10:77447297-77447317	83	67:1	27	11	1.91E-05
-	-	chrX:6591448-6592050	chrX:6591797-6591817	86	67:0	4	11	1.74E-05
-	-	chr7:64729336-64730066	chr7:64729593-64729613	81	67:0	-32	11	2.04E-05
-	-	chr7:52196936-52197602	chr7:52197161-52197181	86	67:2	-12	11	1.69E-05
-	-	chr16:11651465-11651887	chr16:11651718-11651738	89	67:0	-4	11	1.58E-05
-	-	chr12:124204388-124204823	chr12:124204619-124204639	83	67:1	-29	11	1.48E-05
-	-	chr12:124204388-124204823	chr12:124204516-124204536	70	67:1	-132	11	1.65E-05
-	-	chr1:29795322-29795822	chr1:29795576-29795596	72	67:1	62	11	1.79E-05
HES1	3280	chr3:195336299-195336899	chr3:195336684-195336704	76	66:4	39	11	1.87E-05

CRIP2	1397	chr14:105011286-105011814	chr14:105011571-105011591	84	66:1	-6	11	1.79E-05
CPLX1	10815	chr4:809122-809732	chr4:809311-809337	70	66:0	2	17	1.65E-05
CHST8	64377	chr19:38866807-38867389	chr19:38867130-38867150	81	66:2	-27	11	1.69E-05
-	-	chr7:51689612-51690095	chr7:51689817-51689837	78	66:1	70	11	1.52E-05
-	-	chr20:58357663-58358258	chr20:58358051-58358071	75	66:2	-53	11	2.12E-05
-	-	chr20:58357663-58358258	chr20:58357778-58357804	57	66:2	-323	17	4.15E-05
-	-	chr2:226820393-226820824	chr2:226820605-226820614	60	66:0	17	0	1.52E-05
MADD	8567	chr11:47250763-47251437	chr11:47251018-47251038	88	65:2	11	11	1.79E-05
IL31RA	133396	chr5:55197251-55197845	chr5:55197625-55197645	72	65:1	26	11	1.60E-05
FLJ21477	80225	chr5:159976192-159977058	chr5:159976466-159976486	80	65:1	-3	11	2.17E-05
CRYBA2	1412	chr2:219681818-219682509	chr2:219682108-219682128	86	65:0	13	11	1.87E-05
CDC42BPA	8476	chr1:223767902-223768381	chr1:223768154-223768174	82	65:4	1	11	1.52E-05
BRUNOL4	56853	chr18:33398640-33399142	chr18:33398895-33398921	80	65:0	31	17	1.69E-05
-	-	chr8:9819880-9820442	chr8:9820070-9820090	85	65:1	-5	11	1.60E-05
-	-	chr2:48250168-48250933	chr2:48250601-48250621	71	65:3	4	11	1.77E-05
ZNRF1	84937	chr16:73688592-73689014	chr16:73688773-73688793	83	64:3	-3	11	1.58E-05
MYH14	79784	chr19:55387550-55388157	chr19:55387722-55387742	74	64:2	10	11	1.87E-05
LOC338825	338825	chr12:125690820-125691595	chr12:125691276-125691296	93	64:3	-62	11	2.12E-05
LOC338825	338825	chr12:125690820-125691595	chr12:125691090-125691110	73	64:3	-248	11	4.71E-05
KIAA1786	84462	chr12:124527393-124527911	chr12:124527698-124527707	34	64:1	-59	0	1.69E-05
KCNC2	3747	chr12:73889281-73889990	chr12:73889723-73889732	62	64:1	2	0	2.08E-05
GNAO1	2775	chr16:54784334-54784988	chr16:54784734-54784754	70	64:1	188	11	4.71E-05
FSTL4	23105	chr5:132610699-132611455	chr5:132611067-132611076	48	64:4	-14	0	1.94E-05
DFNA5	1687	chr7:24528614-24529119	chr7:24528874-24528894	70	64:4	63	11	1.94E-05
BRE	9577	chr2:28148161-28148686	chr2:28148302-28148322	74	64:2	17	11	1.77E-05
ANKHD1	54882	chr5:139760227-139761138	chr5:139760574-139760583	57	64:6	5	0	2.65E-05
-	-	chr2:23464458-23465146	chr2:23464848-23464874	66	64:0	-7	17	1.77E-05
-	-	chr12:15479595-15480169	chr12:15479959-15479979	77	64:0	-9	11	1.94E-05
PSMB7	5695	chr9:124257031-124258034	chr9:124257471-124257480	56	63:6	-10	0	2.27E-05
KCNB2	9312	chr8:73993560-73994150	chr8:73994005-73994031	64	63:5	-6	17	2.00E-05
GHRHR	2692	chr7:30783684-30784085	chr7:30783823-30783843	70	63:0	9	11	1.58E-05
COX7C	1350	chr5:85957576-85958213	chr5:85958100-85958119	51	63:0	147	10	3.15E-05
COX7C	1350	chr5:85957576-85958213	chr5:85957904-85957932	49	63:0	-45	19	1.87E-05
-	-	chr8:143330036-143330630	chr8:143330279-143330299	84	63:1	5	11	1.77E-05
-	-	chr8:103257108-103257496	chr8:103257283-103257303	71	63:1	-10	11	1.56E-05
-	-	chr2:226627780-226628260	chr2:226628047-226628067	92	63:0	20	11	1.74E-05
-	-	chr15:87708860-87709463	chr15:87709201-87709221	86	63:2	20	11	1.91E-05
-	-	chr15:85269441-85269923	chr15:85269851-85269877	45	63:2	104	17	1.83E-05

-	-	chr13:50608425-50608853	chr13:50608537-50608546	50	63:1	-32	0	1.69E-05
ZNF444	55311	chr19:61370381-61370673	chr19:61370624-61370652	53	62:1	112	19	1.79E-05
ZNF444	55311	chr19:61370381-61370673	chr19:61370551-61370571	85	62:1	35	11	1.58E-05
TRBV12-4	28576	chr7:141321541-141322193	chr7:141321920-141321940	76	62:2	-2	11	1.77E-05
SIAT7E	81849	chr1:77240655-77241287	chr1:77241036-77241045	33	62:3	-5	0	1.91E-05
SCGB1D1	10648	chr11:61717850-61718416	chr11:61718176-61718185	33	62:1	5	0	1.83E-05
PSK-1	26470	chr16:29816802-29817340	chr16:29817061-29817081	78	62:0	-25	11	1.91E-05
LOC388406	388406	chr17:56018444-56019099	chr17:56018967-56018987	72	62:2	-15	11	3.05E-05
LOC196463	196463	chr12:112258877-112259426	chr12:112259187-112259207	83	62:3	-25	11	1.87E-05
CNGB1	1258	chr16:56466736-56467366	chr16:56466934-56466954	74	62:0	65	11	2.00E-05
BSN	8927	chr3:49567094-49567906	chr3:49567149-49567177	56	62:1	24	19	2.31E-05
-	-	chr9:16101945-16102635	chr9:16102305-16102325	76	62:1	-34	11	1.94E-05
-	-	chr5:165868615-165869254	chr5:165868875-165868895	84	62:1	-66	11	1.94E-05
-	-	chr12:130399641-130400421	chr12:130400044-130400064	80	62:1	38	11	2.27E-05
-	-	chr11:134061537-134062127	chr11:134061721-134061730	54	62:2	9	0	1.77E-05
-	-	chr1:18133759-18134302	chr1:18134179-18134199	88	62:0	37	11	2.08E-05
SLITRK1	114798	chr13:83353928-83354476	chr13:83354289-83354314	39	61:1	10	16	1.87E-05
SLITRK1	114798	chr13:83353928-83354476	chr13:83354247-83354267	70	61:1	-35	11	1.77E-05
SLITRK1	114798	chr13:83353928-83354476	chr13:83354240-83354267	48	61:1	-38	18	1.77E-05
PPP2R2B	5521	chr5:146005024-146005578	chr5:146005328-146005337	69	61:2	35	0	1.91E-05
PKD2L1	9033	chr10:102074671-102075343	chr10:102075099-102075119	72	61:1	13	11	1.87E-05
PDYN	5173	chr20:1907843-1908512	chr20:1908226-1908246	71	61:0	22	11	2.08E-05
KIAA0984	23329	chr12:63506240-63506811	chr12:63506548-63506574	64	61:2	-13	17	1.83E-05
-	-	chr7:107581854-107582313	chr7:107582196-107582216	83	61:1	4	11	1.79E-05
-	-	chr2:21046549-21047276	chr2:21046843-21046863	83	61:1	8	11	1.91E-05
-	-	chr2:21046549-21047276	chr2:21046816-21046842	54	61:1	-16	17	1.87E-05
-	-	chr1:22261482-22262029	chr1:22261624-22261644	73	61:0	-2	11	1.83E-05
SYT6	148281	chr1:114411316-114411659	chr1:114411380-114411400	71	60:3	30	11	1.60E-05
Rgr	266747	chr22:22358944-22359893	chr22:22359560-22359580	77	60:4	5	11	2.31E-05
Rgr	266747	chr22:22358944-22359893	chr22:22359542-22359562	89	60:4	-13	11	2.31E-05
PTPRT	11122	chr20:40750627-40751111	chr20:40750818-40750838	80	60:0	-4	11	1.91E-05
E46L	25814	chr22:44563265-44563858	chr22:44563561-44563581	80	60:1	-3	11	2.08E-05
-	-	chr9:19710309-19710813	chr9:19710578-19710598	84	60:1	0	11	1.79E-05
-	-	chr4:37092445-37092915	chr4:37092693-37092713	85	60:1	-16	11	1.77E-05
-	-	chr20:58247699-58248179	chr20:58247926-58247946	86	60:3	16	11	1.79E-05
-	-	chr15:79260555-79261309	chr15:79260805-79260831	55	60:8	-18	17	2.36E-05
-	-	chr10:111473000-111473871	chr10:111473247-111473267	79	60:2	7	11	2.12E-05
SHANK1	50944	chr19:55890203-55890549	chr19:55890388-55890408	92	59:0	-52	11	1.74E-05



SHANK1	50944	chr19:55890203-55890549	chr19:55890364-55890384	71	59:0	-76	11	1.69E-05
SCG3	29106	chr15:49760492-49761226	chr15:49760999-49761025	60	59:1	-2	17	2.27E-05
ODZ4	26011	chr11:78072930-78073566	chr11:78073270-78073290	75	59:3	-11	11	2.31E-05
LOC90701	90701	chr18:54958337-54959006	chr18:54958690-54958699	48	59:3	-14	0	2.27E-05
FSTL4	23105	chr5:132974425-132975030	chr5:132974760-132974769	40	59:6	3	0	1.83E-05
DLG4	1742	chr17:7035577-7036145	chr17:7035829-7035849	80	59:3	-28	11	2.00E-05
COL22A1	169044	chr8:139709992-139710197	chr8:139710060-139710080	91	59:0	-17	11	1.69E-05
-	-	chr8:140739884-140740547	chr8:140740311-140740331	89	59:0	6	11	1.94E-05
-	-	chr5:141792746-141793229	chr5:141792966-141792986	72	59:6	-20	11	1.83E-05
-	-	chr20:32033341-32033834	chr20:32033615-32033624	58	59:2	-50	0	1.77E-05
-	-	chr1:207295346-207296047	chr1:207295788-207295808	75	59:1	-11	11	2.75E-05
PDZK10	9758	chrX:12498767-12499300	chrX:12499032-12499041	27	58:0	-3	0	1.94E-05
MMD2	221938	chr7:4764770-4765642	chr7:4765357-4765366	48	58:1	3	0	2.65E-05
MGAT5B	146664	chr17:72377999-72378460	chr17:72378227-72378247	84	58:0	9	11	1.79E-05
LOC284434	284434	chr19:16730847-16731470	chr19:16730924-16730933	37	58:1	10	0	1.94E-05
LOC149704	149704	chr20:42458457-42458969	chr20:42458683-42458709	55	58:1	42	17	1.91E-05
/HNF4A	/ 3172							
ABLIM3	22885	chr5:148614396-148614733	chr5:148614508-148614517	44	58:0	2	0	1.74E-05
-	-	chr21:23816825-23817446	chr21:23817128-23817148	78	58:0	-11	11	2.36E-05
-	-	chr16:25420435-25420972	chr16:25420556-25420576	72	58:2	-14	11	2.12E-05
-	-	chr13:35529116-35529696	chr13:35529369-35529389	76	58:3	-21	11	2.22E-05
-	-	chr10:129288745-129289525	chr10:129288978-129288998	86	58:0	34	11	2.31E-05
-	-	chr10:129288745-129289525	chr10:129288808-129288828	70	58:0	-136	11	3.05E-05
VSX1	30813	chr20:25009295-25010042	chr20:25009801-25009828	64	57:3	21	18	2.54E-05
SEZ6	124925	chr17:24355179-24356175	chr17:24355409-24355418	59	57:0	5	0	2.91E-05
SEMA5A	9037	chr5:9251463-9252151	chr5:9251713-9251733	82	57:3	-8	11	2.12E-05
PRRXL1	117065	chr10:50245591-50246052	chr10:50245777-50245797	81	57:0	-8	11	1.83E-05
PCBP3	54039	chr21:46130089-46130545	chr21:46130472-46130481	24	57:7	-6	0	2.43E-05
LOC92558	92558	chr12:118890326-118890930	chr12:118890427-118890454	55	57:0	30	18	2.12E-05
LOC402036	402036	chr22:17397545-17398150	chr22:17397594-17397614	81	57:1	-5	11	2.08E-05
LOC150159	150159	chr4:104280984-104281722	chr4:104281495-104281515	78	57:0	24	11	2.12E-05
FER1L3	26509	chr10:95166909-95167500	chr10:95167185-95167211	37	57:1	42	17	2.00E-05
C10orf77	79847	chr10:104211409-104211951	chr10:104211701-104211710	67	57:1	22	0	2.08E-05
-	-	chr17:11350629-11351124	chr17:11350862-11350882	86	57:1	24	11	2.00E-05
-	-	chr16:16798622-16799216	chr16:16798792-16798812	90	57:2	-3	11	1.91E-05
-	-	chr12:106852389-106853058	chr12:106852679-106852699	71	57:1	46	11	2.17E-05
-	-	chr11:126313529-126314384	chr11:126313994-126314020	67	57:2	-17	17	2.36E-05
MMP24	10893	chr20:33278366-33278862	chr20:33278631-33278651	70	56:1	48	11	3.29E-05
MMP24	10893	chr20:33278366-33278862	chr20:33278412-33278432	89	56:1	-171	11	2.12E-05

LOC441579	441579	chr10:133042611-133043183	chr10:133042856-133042876	70	56:0	18	11	2.27E-05	
LOC441579	441579	chr10:133042611-133043183	chr10:133042850-133042876	59	56:0	15	17	2.27E-05	
LOC441579	441579	chr10:133042611-133043183	chr10:133042835-133042855	88	56:0	-3	11	2.17E-05	
GABRB3	2562	chr15:24570061-24570574	chr15:24570362-24570382	78	56:1	-12	11	2.27E-05	
EPC2	26122	chr2:149235363-149236073	chr2:149235418-149235438	73	56:5	49	11	2.27E-05	
BTEB1	687	chr9:70234159-70234738	chr9:70234453-70234473	74	56:4	4	11	2.22E-05	
	24432	65057	chr16:66252410-66252833	chr16:66252712-66252732	70	56:2	22	11	2.08E-05
-	-		chr5:166204612-166204982	chr5:166204809-166204829	82	56:0	-4	11	2.00E-05
-	-		chr16:17785407-17786023	chr16:17785619-17785639	87	56:0	-6	11	2.08E-05
UNQ9433	389658	chr8:53611339-53611618	chr8:53611407-53611427	81	55:0	-29	11	1.83E-05	
RIMS3	9783	chr1:40773206-40773603	chr1:40773388-40773408	86	55:2	42	11	1.87E-05	
PKD1L2	114780	chr16:79761597-79762263	chr16:79762091-79762111	83	55:0	-29	11	2.31E-05	
ONECUT1/HNF6	3175	chr15:50862760-50863665	chr15:50862986-50863006	77	55:10	-11	11	3.05E-05	
NALP5	126206	chr19:61218913-61219383	chr19:61219130-61219150	86	55:0	3	11	2.27E-05	
MEIS3	56917	chr19:52602177-52602781	chr19:52602352-52602372	92	55:1	2	11	2.17E-05	
MAN1C1	57134	chr1:25741298-25741687	chr1:25741462-25741471	47	55:3	-20	0	1.83E-05	
LOC345557	345557	chr5:41553712-41554159	chr5:41553952-41553978	45	55:0	-29	17	2.04E-05	
INSR	3643	chr19:7064241-7064700	chr19:7064446-7064466	81	55:0	-3	11	2.00E-05	
FLJ00060	90011	chr19:59761576-59761898	chr19:59761788-59761813	55	55:0	-42	16	1.87E-05	
CAMK4	814	chr5:110728279-110729186	chr5:110728780-110728800	90	55:2	-21	11	2.65E-05	
CACNA1B	774	chr9:138060843-138061460	chr9:138061251-138061271	86	55:1	-21	11	2.36E-05	
BTBD9	114781	chr6:38423739-38424164	chr6:38423781-38423790	53	55:1	8	0	2.27E-05	
-	-		chr6:90225089-90225545	chr6:90225341-90225361	85	55:0	13	11	2.00E-05
-	-		chr5:87784460-87784932	chr5:87784568-87784588	78	55:2	0	11	2.00E-05
-	-		chr2:114542222-114542867	chr2:114542587-114542607	71	55:0	144	11	3.15E-05
-	-		chr2:114542222-114542867	chr2:114542451-114542477	44	55:0	11	17	2.27E-05
-	-		chr16:48014234-48014833	chr16:48014498-48014518	72	55:0	18	11	2.17E-05
-	-		chr14:92967280-92967807	chr14:92967569-92967589	77	55:2	251	11	5.42E-05
-	-		chr14:92967280-92967807	chr14:92967330-92967350	94	55:2	12	11	2.31E-05
RASGRF1	5923	chr15:77179042-77179567	chr15:77179278-77179287	43	54:0	-6	0	2.08E-05	
NEF3	4741	chr8:24825917-24826477	chr8:24826244-24826264	89	54:0	-7	11	2.08E-05	
LOC442399	442399	chr8:142755663-142756133	chr8:142755876-142755902	63	54:0	-9	17	2.00E-05	
KIAA1751	85452	chr1:1907314-1907983	chr1:1907711-1907730	57	54:2	38	10	2.91E-05	
FGD2	221472	chr6:37082782-37083318	chr6:37083126-37083146	86	54:1	13	11	2.22E-05	
-	-		chr9:117175717-117176517	chr9:117176125-117176145	71	54:5	32	11	2.36E-05
-	-		chr18:25813920-25814268	chr18:25814013-25814033	87	54:0	20	11	1.94E-05
TRIM44	54765	chr11:35701974-35702452	chr11:35702167-35702187	87	53:1	-2	11	2.12E-05	
SF1	7536	chr11:64301396-64301829	chr11:64301585-64301605	71	53:2	26	11	1.94E-05	

SEMA5B	54437	chr3:124117811-124118613	chr3:124118299-124118308	38	53:1	9	0	3.52E-05
PPAP2C	8612	chr19:228490-229059	chr19:228744-228753	35	53:1	-8	0	2.17E-05
OSMR	9180	chr5:38957143-38957455	chr5:38957206-38957226	85	53:1	-8	11	1.91E-05
NCF4	4689	chr22:35585903-35586405	chr22:35586159-35586179	73	53:1	-9	11	2.17E-05
MC3R	4159	chr20:54252680-54253156	chr20:54252916-54252942	54	53:2	13	17	2.00E-05
KIAA0450	9651	chr1:2446315-2446682	chr1:2446397-2446417	79	53:1	6	11	2.08E-05
DNM3	26052	chr1:168612379-168612881	chr1:168612494-168612514	80	53:0	-56	11	2.12E-05
DAPK3	1613	chr19:3922150-3922579	chr19:3922363-3922383	78	53:4	146	11	2.00E-05
AMPH	273	chr7:38325074-38325924	chr7:38325727-38325747	73	53:1	-41	11	2.65E-05
-	-	chr18:11494952-11495424	chr18:11495151-11495171	71	53:0	-37	11	2.12E-05
-	-	chr18:11494952-11495424	chr18:11494974-11494994	77	53:0	-214	11	2.91E-05
-	-	chr17:29440286-29440800	chr17:29440366-29440386	86	53:0	8	11	2.27E-05
-	-	chr16:8669033-8669562	chr16:8669071-8669097	63	53:0	-7	17	2.27E-05
-	-	chr14:31740044-31740774	chr14:31740634-31740654	72	53:4	319	11	7.34E-05
-	-	chr14:31740044-31740774	chr14:31740472-31740498	48	53:4	160	17	3.66E-05
-	-	chr14:31740044-31740774	chr14:31740295-31740315	72	53:4	-20	11	2.91E-05
-	-	chr1:207417089-207417677	chr1:207417359-207417379	71	53:3	21	11	2.36E-05
ZZEF1	23140	chr17:3899577-3899968	chr17:3899768-3899788	77	52:0	-27	11	2.00E-05
ST18	9705	chr8:53290184-53290706	chr8:53290435-53290455	76	52:2	-62	11	2.54E-05
POLN	353497	chr4:2146622-2147031	chr4:2146795-2146814	49	52:1	-14	10	1.94E-05
LOC401721	401721	chr12:50895952-50896899	chr12:50896350-50896370	82	52:3	-8	11	2.91E-05
LOC283432	283432	chr12:101720639-101721228	chr12:101720886-101720906	81	52:1	-4	11	2.27E-05
LOC283432	283432	chr12:101720639-101721228	chr12:101720706-101720732	45	52:1	-181	17	4.00E-05
KIAA1393	57570	chr14:60517488-60518035	chr14:60517800-60517809	55	52:3	-13	0	2.12E-05
FLJ32770	157376	chr8:125162160-125162613	chr8:125162387-125162396	31	52:0	17	0	2.00E-05
-	-	chr9:118535400-118535894	chr9:118535656-118535676	84	52:0	28	11	2.12E-05
-	-	chr5:162063456-162063935	chr5:162063693-162063720	43	52:0	34	18	2.17E-05
-	-	chr13:94368044-94368490	chr13:94368259-94368268	66	52:1	2	0	2.08E-05
SLC12A5	57468	chr20:44119231-44119649	chr20:44119447-44119467	84	51:0	37	11	2.08E-05
SLC12A5	57468	chr20:44119231-44119649	chr20:44119402-44119422	70	51:0	-8	11	2.04E-05
ROBO3	64221	chr11:124238763-124239484	chr11:124239064-124239073	38	51:1	10	0	2.75E-05
LRP11	84918	chr6:150277401-150277972	chr6:150277583-150277611	54	51:1	-3	19	2.31E-05
IRTA1	83417	chr1:154368673-154369265	chr1:154369044-154369069	72	51:3	-4	16	2.54E-05
FLJ00133	25992	chr2:241709149-241709763	chr2:241709369-241709389	86	51:0	9	11	2.31E-05
CCL11	6356	chr17:29642815-29643265	chr17:29643029-29643049	74	51:3	-13	11	2.31E-05
-	-	chr4:26795267-26795626	chr4:26795544-26795553	28	51:1	-2	0	3.15E-05
-	-	chr3:138021280-138022240	chr3:138021834-138021854	87	51:4	8	11	3.05E-05
-	-	chr21:38827543-38828135	chr21:38827908-38827917	44	51:2	-40	0	2.36E-05

-	-	chr20:48467616-48468050	chr20:48467852-48467872	90	51:0	-19	11	2.17E-05
-	-	chr18:73043823-73044335	chr18:73044134-73044143	54	51:0	-3	0	2.31E-05
-	-	chr15:24250041-24250549	chr15:24250322-24250342	83	51:0	7	11	2.22E-05
-	-	chr13:76104648-76105157	chr13:76104991-76105011	74	51:1	31	11	2.31E-05
-	-	chr10:88303361-88303745	chr10:88303562-88303571	53	51:1	-21	0	2.08E-05
-	-	chr1:18082564-18083054	chr1:18082950-18082970	86	51:0	-18	11	2.75E-05
PUNC	9543	chr15:63410294-63411027	chr15:63410589-63410616	50	50:2	42	18	2.91E-05
PUNC	9543	chr15:63410294-63411027	chr15:63410540-63410559	53	50:2	-11	10	2.75E-05
OTOA	146183	chr16:21603920-21604384	chr16:21603976-21603996	84	50:1	-3	11	2.31E-05
NBEA	26960	chr13:34398724-34399226	chr13:34398826-34398846	83	50:0	-19	11	2.17E-05
LOC285018	285018	chr2:413330-413836	chr2:413619-413628	68	50:4	4	0	2.12E-05
EGFL3	1953	chr1:3441685-3442413	chr1:3442006-3442026	77	50:0	26	11	2.54E-05
EGFL3	1953	chr1:3441685-3442413	chr1:3441832-3441859	47	50:0	-144	18	3.39E-05
-	-	chr6:5762974-5763574	chr6:5763284-5763304	80	50:2	-10	11	2.27E-05
POU4F2	5458	chr4:147915582-147916059	chr4:147915815-147915835	85	49:1	6	11	2.17E-05
MAPK7	5598	chr17:19222032-19222434	chr17:19222247-19222256	36	49:2	7	0	2.17E-05
LOC400505	400505	chr16:19226420-19226859	chr16:19226618-19226638	83	49:2	-21	11	2.17E-05
LOC126435	126435	chr19:1685764-1686423	chr19:1686157-1686177	90	49:0	12	11	2.75E-05
LHX4	89884	chr1:176942755-176943180	chr1:176942970-176942979	40	49:3	12	0	2.27E-05
CYP4F3	4051	chr19:15624363-15624874	chr19:15624651-15624671	71	49:2	90	11	2.31E-05
CYP4F3	4051	chr19:15624363-15624874	chr19:15624568-15624593	45	49:2	10	16	2.36E-05
CBFA2T2	9139	chr20:31698387-31698837	chr20:31698616-31698636	83	49:2	57	11	2.27E-05
CBFA2T2	9139	chr20:31698387-31698837	chr20:31698579-31698599	76	49:2	20	11	2.31E-05
-	-	chrX:106373977-106374433	chrX:106374194-106374214	78	49:0	-7	11	2.22E-05
-	-	chr5:56718611-56718971	chr5:56718727-56718747	70	49:0	-45	11	2.08E-05
-	-	chr20:21031282-21032105	chr20:21031547-21031567	74	49:6	-208	11	4.71E-05
-	-	chr20:21031282-21032105	chr20:21031539-21031567	43	49:6	-212	19	4.71E-05
-	-	chr16:74709683-74710194	chr16:74709930-74709950	76	49:0	40	11	2.36E-05
-	-	chr10:133717837-133718371	chr10:133718233-133718253	86	49:2	-10	11	3.39E-05
-	-	chr10:2264735-2265048	chr10:2264858-2264878	73	49:0	1	11	2.08E-05
-	-	chr1:58422668-58422896	chr1:58422765-58422785	79	49:1	-11	11	2.00E-05
ZC3HAV1	56829	chr7:138186467-138187106	chr7:138186703-138186712	33	48:3	31	0	3.05E-05
TMEM28	27112	chrX:68506540-68507082	chrX:68506737-68506757	76	48:0	34	11	2.54E-05
TMEM14A	28978	chr6:52636826-52637366	chr6:52636996-52637022	69	48:5	23	17	2.54E-05
TLL1	7092	chr4:167357701-167358165	chr4:167357905-167357925	74	48:0	5	11	2.31E-05
OTOP3	347741	chr17:70445102-70445676	chr17:70445334-70445360	62	48:1	-22	17	2.65E-05
FRMD3	257019	chr9:83199321-83199956	chr9:83199566-83199586	77	48:2	-15	11	2.31E-05
BDNF	627	chr11:27698472-27699060	chr11:27698798-27698818	91	48:0	2	11	2.65E-05

-	-	chr6:31368995-31369600	chr6:31369258-31369278	85	48:1	11	11	2.65E-05
-	-	chr18:72985643-72986166	chr18:72985880-72985900	72	48:1	26	11	2.43E-05
-	-	chr15:77197032-77197722	chr15:77197406-77197415	38	48:2	3	0	2.65E-05
-	-	chr10:132612343-132612889	chr10:132612557-132612577	81	48:0	-10	11	2.31E-05
PROM2	150696	chr2:95372719-95373114	chr2:95372967-95372987	79	47:2	-84	11	2.36E-05
POU4F1	5457	chr13:78061251-78061801	chr13:78061540-78061560	88	47:0	193	11	3.29E-05
MARK2	2011	chr11:63416017-63416696	chr11:63416486-63416495	48	47:2	-18	0	2.65E-05
LOC441023	441023	chr4:73045129-73045643	chr4:73045386-73045406	79	47:0	-14	11	2.65E-05
LOC440403	440403	chr17:16379704-16380242	chr17:16379939-16379948	56	47:4	-6	0	2.75E-05
LOC387787	387787	chr11:73895528-73896042	chr11:73895746-73895766	70	47:0	17	11	2.54E-05
ABLM2	84448	chr4:8280426-8280846	chr4:8280559-8280579	71	47:0	52	11	2.22E-05
-	-	chr3:65833692-65834089	chr3:65833872-65833898	59	47:2	-6	17	2.22E-05
-	-	chr12:129562003-129562313	chr12:129562211-129562231	83	47:0	1	11	2.31E-05
TRIM9	114088	chr14:50631121-50631786	chr14:50631484-50631504	79	46:6	62	11	3.05E-05
OR4D2	124538	chr17:53604532-53605236	chr17:53604851-53604860	54	46:3	-4	0	3.52E-05
MRPS22	56945	chr3:140530736-140531358	chr3:140531105-140531125	73	46:1	-36	11	2.91E-05
GPR10	2834	chr10:120345520-120346195	chr10:120346027-120346047	74	46:1	267	11	9.11E-05
GPR10	2834	chr10:120345520-120346195	chr10:120345765-120345785	87	46:1	5	11	3.15E-05
FLJ31121	153527	chr5:140070949-140071521	chr5:140071169-140071197	51	46:4	43	19	2.54E-05
-	-	chr8:129550780-129551608	chr8:129551247-129551267	83	46:0	41	11	3.80E-05
-	-	chr17:1173367-1173648	chr17:1173546-1173566	87	46:0	-35	11	2.22E-05
-	-	chr13:90508361-90508781	chr13:90508486-90508506	83	46:2	-30	11	2.36E-05
-	-	chr10:122438395-122438743	chr10:122438562-122438571	23	46:1	-13	0	2.22E-05
ZSIG11	51368	chr3:51715783-51716063	chr3:51715920-51715945	71	45:0	-9	16	2.27E-05
TIEG2	8462	chr2:10124000-10124520	chr2:10124305-10124325	77	45:2	-68	11	2.75E-05
STMN2	11075	chr8:80685226-80685932	chr8:80685405-80685425	76	45:0	36	11	3.29E-05
PCDH1	5097	chr5:141243096-141243680	chr5:141243383-141243392	52	45:0	0	0	3.15E-05
PAH	5053	chr12:101730448-101730808	chr12:101730497-101730517	87	45:1	4	11	2.54E-05
LOC441386	441386	chr9:9081383-9081831	chr9:9081579-9081599	86	45:1	5	11	2.65E-05
LOC283677	283677	chr15:71470664-71471408	chr15:71471053-71471073	70	45:1	150	11	4.71E-05
KCNQ2	3785	chr20:61576796-61577460	chr20:61577191-61577200	61	45:2	7	0	3.29E-05
CHKA	1119	chr11:67645748-67646601	chr11:67646120-67646140	80	45:2	-43	11	4.71E-05
-	-	chr4:181531029-181531536	chr4:181531209-181531234	45	45:0	36	16	2.43E-05
-	-	chr19:8937538-8938190	chr19:8937744-8937764	79	45:0	13	11	2.75E-05
-	-	chr1:11892986-11893925	chr1:11893363-11893383	87	45:3	76	11	4.00E-05
RHBDL4	162494	chr17:27628221-27628869	chr17:27628582-27628602	82	44:0	-39	11	3.05E-05
NR4A1	3164	chr12:50721663-50722167	chr12:50721860-50721880	70	44:4	-45	11	2.65E-05
LOC441061	441061	chr5:16231854-16232269	chr5:16232066-16232086	96	44:0	16	11	2.65E-05

FUS	2521	chr16:31098630-31099423	chr16:31098988-31098997	28	44:7	17	0	4.15E-05
CNTN2	6900	chr1:201745355-201745969	chr1:201745715-201745735	81	44:3	-49	11	2.91E-05
CLECSF14	10462	chr17:6925650-6925981	chr17:6925852-6925861	53	44:0	-21	0	2.43E-05
ATP2B2	491	chr3:10467129-10467712	chr3:10467377-10467397	83	44:2	16	11	3.39E-05
ABCC8	6833	chr11:17456036-17456650	chr11:17456393-17456413	82	44:0	-12	11	3.80E-05
-	-	chr3:121264066-121264583	chr3:121264205-121264225	76	44:4	-101	11	2.75E-05
-	-	chr20:58929468-58929978	chr20:58929674-58929694	87	44:0	10	11	2.65E-05
RIMS3	9783	chr1:40788483-40788959	chr1:40788838-40788858	80	43:2	17	11	3.66E-05
PTPRN2	5799	chr7:157879887-157880156	chr7:157879915-157879924	42	43:0	-24	0	2.43E-05
PRKCG	5582	chr19:59091827-59092148	chr19:59091934-59091954	77	43:2	-55	11	2.36E-05
OR1E1	8387	chr17:3248001-3248258	chr17:3248011-3248038	41	43:1	-3	18	2.04E-05
NEDL2	57520	chr2:197111986-197112540	chr2:197112294-197112314	78	43:0	-10	11	2.75E-05
MYOC	4653	chr1:168336816-168337373	chr1:168337096-168337105	56	43:0	20	0	2.91E-05
LOC441224	441224	chr7:51239613-51239728	chr7:51239714-51239723	81	43:0	14	0	2.08E-05
LOC402273	402273	chr7:63079491-63079805	chr7:63079660-63079680	82	43:0	-17	11	2.36E-05
LOC150577	150577	chr2:100277566-100278206	chr2:100277756-100277776	88	43:0	-32	11	3.29E-05
COL9A1	1297	chr6:71066019-71066306	chr6:71066061-71066088	63	43:0	8	18	2.31E-05
-	-	chr8:80311843-80312442	chr8:80312211-80312231	78	43:1	17	11	3.52E-05
-	-	chr2:133080292-133080774	chr2:133080631-133080651	74	43:0	23	11	5.42E-05
-	-	chr2:133080292-133080774	chr2:133080601-133080621	90	43:0	-7	11	4.00E-05
-	-	chr2:98421510-98421908	chr2:98421661-98421681	76	43:0	-26	11	2.43E-05
-	-	chr2:98421510-98421908	chr2:98421654-98421681	60	43:0	-29	18	2.43E-05
-	-	chr16:17039549-17040078	chr16:17039853-17039862	47	43:1	-22	0	2.65E-05
-	-	chr12:123705332-123705714	chr12:123705483-123705492	64	43:1	-3	0	2.36E-05
-	-	chr1:167469721-167470193	chr1:167469922-167469942	75	43:2	19	11	2.75E-05
SDK1	221935	chr7:4283090-4283400	chr7:4283319-4283339	93	42:0	-48	11	3.05E-05
SCRT2	85508	chr20:604189-604419	chr20:604325-604334	38	42:0	-3	0	2.36E-05
LOC124220	124220	chr16:2817816-2818554	chr16:2818195-2818215	88	42:1	4	11	3.29E-05
KIAA0318	23504	chr12:129536248-129536624	chr12:129536429-129536449	75	42:0	0	11	2.54E-05
CAM-KIIN	94032	chr3:185460360-185460552	chr3:185460462-185460482	78	42:0	-17	11	2.31E-05
-	-	chr8:131830597-131831471	chr8:131831158-131831178	76	42:6	-93	11	3.66E-05
-	-	chr8:131830597-131831471	chr8:131831146-131831166	73	42:6	-105	11	3.66E-05
-	-	chr6:119105000-119105459	chr6:119105224-119105244	82	42:0	10	11	2.65E-05
-	-	chr4:116990428-116990960	chr4:116990488-116990508	73	42:1	44	11	3.52E-05
-	-	chr10:43098122-43098972	chr10:43098515-43098535	83	42:1	8	11	6.28E-05
MLPH	79083	chr2:238238438-238238720	chr2:238238586-238238595	30	41:0	11	0	2.54E-05
LRRC20	55222	chr10:71745114-71745877	chr10:71745795-71745815	76	41:1	9	11	7.34E-05
LOC399947	399947	chr11:108800734-108801288	chr11:108801022-108801050	54	41:1	41	19	3.05E-05

KIAA1727	85462	chr4:154261825-154262426	chr4:154262160-154262180	78	41:3	-2	11	3.15E-05
FLJ20225	54546	chr1:19880607-19881295	chr1:19881033-19881060	63	41:2	28	18	3.66E-05
FGF18	8817	chr5:170778139-170778616	chr5:170778296-170778305	31	41:3	-26	0	3.80E-05
FARS1	10667	chr6:5367637-5368015	chr6:5367759-5367786	45	41:6	-53	18	2.75E-05
DNAJC12	56521	chr10:69211005-69211247	chr10:69211175-69211184	32	41:2	31	0	2.36E-05
-	-	chr3:100763607-100764106	chr3:100763884-100763904	74	41:0	-45	11	3.15E-05
-	-	chr3:100763607-100764106	chr3:100763878-100763904	72	41:0	-48	17	3.15E-05
-	-	chr20:59340111-59340681	chr20:59340454-59340474	72	41:3	157	11	4.15E-05
-	-	chr20:59340111-59340681	chr20:59340303-59340323	89	41:3	6	11	3.15E-05
-	-	chr15:84788708-84789057	chr15:84788937-84788957	84	41:1	7	11	3.05E-05
-	-	chr11:93654068-93654747	chr11:93654337-93654357	84	41:0	-16	11	4.71E-05
SCGN	10590	chr6:25760450-25760860	chr6:25760601-25760621	84	40:0	-44	11	2.75E-05
PAX5	5079	chr9:36964321-36964742	chr9:36964565-36964585	80	40:1	13	11	3.05E-05
OR2Z1	284383	chr19:8702754-8703210	chr19:8702980-8703006	53	40:1	24	17	3.05E-05
CLYBL	171425	chr13:99351117-99351599	chr13:99351363-99351383	77	40:1	-25	11	3.05E-05
ALG12	79087	chr22:48630107-48630471	chr22:48630258-48630278	87	40:1	32	11	2.65E-05
-	-	chrX:134336970-134337417	chrX:134337245-134337254	69	40:1	6	0	2.91E-05
-	-	chr20:56096569-56097119	chr20:56096799-56096819	87	40:2	1	11	2.91E-05
-	-	chr2:17210846-17211189	chr2:17211134-17211160	63	40:0	132	17	4.71E-05
-	-	chr2:17210846-17211189	chr2:17210958-17210978	70	40:0	-47	11	2.65E-05
-	-	chr18:4220872-4221434	chr18:4220975-4220995	71	40:3	8	11	3.52E-05
XPO6	23214	chr16:28006730-28007223	chr16:28006971-28006980	38	39:1	15	0	3.39E-05
SIAT8C	51046	chr18:53171977-53172544	chr18:53172404-53172431	49	39:0	108	18	3.52E-05
SIAT8C	51046	chr18:53171977-53172544	chr18:53172299-53172319	87	39:0	-1	11	3.29E-05
MAP3K4	4216	chr6:161480374-161480796	chr6:161480552-161480572	81	39:0	16	11	2.75E-05
LIPC	3990	chr15:56513911-56514471	chr15:56514138-56514166	63	39:0	-46	19	3.29E-05
HIST1H1E	3008	chr6:26263991-26264710	chr6:26264471-26264480	29	39:6	39	0	4.42E-05
GTF2I	2969	chr7:73156716-73157081	chr7:73156968-73156988	76	39:1	-39	11	3.39E-05
FLJ20403	284695	chr1:90172270-90172932	chr1:90172560-90172586	71	39:2	51	17	5.42E-05
FLJ12681	64788	chr16:882663-883125	chr16:882727-882747	75	39:1	33	11	3.29E-05
EYA2	2139	chr20:45078163-45078628	chr20:45078294-45078321	64	39:0	-10	18	3.05E-05
CNNM3	26505	chr2:96919411-96919731	chr2:96919489-96919509	83	39:2	-20	11	2.75E-05
ACACB	32	chr12:108159479-108159887	chr12:108159672-108159692	86	39:1	-29	11	2.91E-05
ACACB	32	chr12:108159479-108159887	chr12:108159501-108159521	70	39:1	-200	11	4.00E-05
-	-	chr3:41767951-41768397	chr3:41768274-41768283	28	39:4	26	0	3.15E-05
-	-	chr12:128321403-128321885	chr12:128321668-128321688	84	39:1	6	11	3.29E-05
-	-	chr12:127250139-127250448	chr12:127250352-127250372	72	39:0	44	11	3.05E-05
-	-	chr12:107300203-107300582	chr12:107300382-107300402	83	39:2	17	11	2.75E-05

-	-	chr1:50435551-50436142	chr1:50435782-50435809	46	39:2	49	18	3.52E-05
-	-	chr1:46649720-46650062	chr1:46650005-46650025	76	39:2	35	11	3.15E-05
PGS1	9489	chr17:73889437-73889991	chr17:73889708-73889717	39	38:6	1	0	3.39E-05
OR111	126370	chr19:15051926-15052079	chr19:15052028-15052048	88	38:0	49	11	2.75E-05
OLFM1	10439	chr9:135216131-135216808	chr9:135216354-135216374	71	38:0	13	11	3.66E-05
NR6A1	2649	chr9:124613093-124613507	chr9:124613135-124613144	53	38:2	27	0	4.00E-05
LOC440787	440787	chr22:15913581-15914002	chr22:15913839-15913848	58	38:2	-3	0	3.66E-05
LOC284395	284395	chr19:34598231-34598684	chr19:34598422-34598431	43	38:1	39	0	3.29E-05
GRIN2C	2905	chr17:70360125-70360540	chr17:70360298-70360318	70	38:0	-19	11	2.91E-05
GRIN2C	2905	chr17:70360125-70360540	chr17:70360271-70360291	79	38:0	-46	11	3.05E-05
CBLN1	869	chr16:47871509-47872146	chr16:47871899-47871919	92	38:1	-33	11	3.66E-05
ALB	213	chr4:74648797-74649062	chr4:74648835-74648855	79	38:0	-69	11	2.91E-05
-	-	chr3:179890996-179891412	chr3:179891230-179891250	79	38:1	14	11	3.29E-05
-	-	chr17:72347480-72347857	chr17:72347634-72347643	50	38:2	-12	0	2.91E-05
-	-	chr15:91514430-91515189	chr15:91514866-91514875	36	38:1	18	0	4.42E-05
-	-	chr14:30067020-30067504	chr14:30067241-30067261	82	38:1	6	11	3.29E-05
MOCOS	55034	chr18:32109491-32109838	chr18:32109730-32109750	77	37:0	-27	11	3.39E-05
GPR123	84435	chr10:134782430-134782982	chr10:134782623-134782643	84	37:0	18	11	3.52E-05
-	-	chr3:10563163-10563605	chr3:10563236-10563256	75	37:1	38	11	3.29E-05
-	-	chr20:59354061-59354530	chr20:59354375-59354384	49	37:0	19	0	4.00E-05
-	-	chr16:47441432-47441910	chr16:47441696-47441716	83	37:3	18	11	3.29E-05
UBASH3A	53347	chr21:42722904-42723657	chr21:42723236-42723256	86	36:3	22	11	4.42E-05
UBASH3A	53347	chr21:42722904-42723657	chr21:42723111-42723139	50	36:3	-99	19	5.42E-05
TZFP	27033	chr19:40886884-40887230	chr19:40887133-40887153	74	36:0	-5	11	3.29E-05
TREX2	11219	chrX:152256029-152256623	chrX:152256246-152256255	37	36:2	9	0	4.15E-05
TAS2R4	50832	chr7:140486273-140486894	chr7:140486637-140486657	86	36:1	-6	11	4.00E-05
TAP1	6890	chr6:32929798-32930186	chr6:32930153-32930162	36	36:6	9	0	6.28E-05
MRPS11	64963	chr15:86833511-86834006	chr15:86833715-86833735	85	36:0	-77	11	3.52E-05
KRT10	3858	chr17:36232097-36232610	chr17:36232400-36232409	32	36:2	16	0	3.52E-05
KIF26A	26153	chr14:103669112-103669523	chr14:103669178-103669198	85	36:0	11	11	4.00E-05
KIF26A	26153	chr14:103669112-103669523	chr14:103669167-103669186	45	36:0	0	10	4.15E-05
APBB3	10307	chr5:139917073-139917696	chr5:139917487-139917496	48	36:2	24	0	4.00E-05
-	-	chr16:22933329-22933829	chr16:22933566-22933586	71	36:0	7	11	4.00E-05
-	-	chr1:42073958-42074374	chr1:42074147-42074173	59	36:0	57	17	3.29E-05
MYH11	4629	chr16:15767200-15767641	chr16:15767354-15767363	60	35:2	-15	0	3.39E-05
LOC399818	399818	chr10:126426749-126427145	chr10:126426978-126426987	40	35:0	0	0	3.39E-05
LOC387991	387991	chr14:58333263-58333737	chr14:58333585-58333605	76	35:0	-2	11	4.15E-05
KHDRBS3	10656	chr8:136528545-136529200	chr8:136528758-136528767	57	35:1	-7	0	5.80E-05



FLJ32784	127731	chr1:20396463-20396958	chr1:20396707-20396727	82	35:2	-17	11	3.66E-05
-	-	chr6:79296455-79296960	chr6:79296829-79296838	25	35:3	49	0	3.66E-05
-	-	chr22:47947044-47947400	chr22:47947247-47947273	71	35:0	-15	17	3.52E-05
-	-	chr21:14141071-14141172	chr21:14141109-14141134	68	35:0	-27	16	2.75E-05
-	-	chr11:113403932-113404400	chr11:113404072-113404092	73	35:3	130	11	3.66E-05
SMO	6608	chr7:128452398-128452831	chr7:128452557-128452577	80	34:5	8	11	3.52E-05
LOC343629	343629	chr20:57146543-57147016	chr20:57146774-57146794	81	34:1	29	11	3.52E-05
GRIK3	2899	chr1:37000854-37001322	chr1:37001074-37001083	62	34:0	7	0	4.15E-05
CRHR1	1394	chr17:41210401-41210932	chr17:41210501-41210510	22	34:1	-54	0	5.42E-05
ALK	238	chr2:30054516-30055005	chr2:30054793-30054813	89	34:0	40	11	4.15E-05
LOC440822	440822	chr22:23465233-23465565	chr22:23465337-23465346	59	33:0	53	0	3.52E-05
LOC375323	375323	chr3:9517206-9517596	chr3:9517432-9517441	37	33:1	9	0	3.66E-05
KCNK10	54207	chr14:87871285-87871747	chr14:87871421-87871441	74	33:1	56	11	5.03E-05
EP300	2033	chr22:39868266-39868715	chr22:39868406-39868426	83	33:2	-12	11	3.66E-05
C22orf9	23313	chr22:43933015-43933440	chr22:43933250-43933270	73	33:1	56	11	3.80E-05
-	-	chr8:60419217-60419515	chr8:60419405-60419425	80	33:0	-6	11	3.29E-05
-	-	chr10:117932995-117933783	chr10:117933387-117933407	74	33:1	-9	11	6.28E-05
PHKA2	5256	chrX:18662527-18663190	chrX:18662911-18662931	82	32:1	10	11	5.42E-05
MAD1L1	8379	chr7:2274245-2274786	chr7:2274448-2274468	76	32:3	-36	11	4.42E-05
LOC388394	388394	chr17:42415956-42416515	chr17:42416422-42416450	49	32:2	188	19	6.28E-05
LOC388394	388394	chr17:42415956-42416515	chr17:42416337-42416357	79	32:2	99	11	5.03E-05
IRS2	8660	chr13:109254795-109255284	chr13:109255146-109255166	76	32:2	-6	11	4.71E-05
FSHB	2488	chr11:30206574-30207007	chr11:30206797-30206817	73	32:2	5	11	3.80E-05
-	-	chr18:48799114-48799741	chr18:48799338-48799358	85	32:0	-6	11	6.78E-05
-	-	chr13:109717441-109717861	chr13:109717649-109717675	71	32:1	58	17	4.15E-05
-	-	chr1:7040567-7041034	chr1:7040761-7040788	76	32:3	14	18	4.00E-05
UBASH3A	53347	chr21:42730729-42731454	chr21:42731154-42731174	74	31:0	7	11	5.03E-05
REST	5978	chr4:57615243-57615658	chr4:57615407-57615416	57	31:0	-13	0	4.15E-05
RAB39	54734	chr11:107304252-107304704	chr11:107304436-107304445	37	31:1	-51	0	4.15E-05
PPP1R16B	26051	chr20:36940937-36941414	chr20:36941048-36941057	46	31:0	15	0	4.42E-05
PDE6D	5147	chr2:232470200-232470797	chr2:232470464-232470473	34	31:1	21	0	6.28E-05
NRXN3	9369	chr14:78511737-78512117	chr14:78512021-78512030	68	31:0	-22	0	4.42E-05
LOXHD1	125336	chr18:42376439-42376861	chr18:42376630-42376650	81	31:0	-40	11	4.00E-05
HCN2	610	chr19:542383-542972	chr19:542669-542689	95	31:1	5	11	5.03E-05
GABARAPL2	11345	chr16:74158272-74158735	chr16:74158478-74158506	68	31:1	-35	19	4.42E-05
FLJ35424	285492	chr4:3627387-3627944	chr4:3627699-3627708	48	31:2	-13	0	5.80E-05
FLJ21069	79745	chr2:29239214-29239677	chr2:29239448-29239476	55	31:3	-2	19	5.42E-05
CARM1L	256280	chr9:2913843-2914071	chr9:2913918-2913937	54	31:0	17	10	3.80E-05

C2orf21	285175	chr2:210461709-210462146	chr2:210461995-210462022	59	31:2	26	18	5.42E-05
C20orf103	24141	chr20:9443006-9443371	chr20:9443195-9443204	50	31:0	0	0	3.80E-05
ALK	238	chr2:30036839-30037203	chr2:30037091-30037100	47	31:0	0	0	5.42E-05
-	-	chr2:121578436-121579053	chr2:121578677-121578704	56	31:5	31	18	4.42E-05
LOC441266	441266	chr7:82436563-82437085	chr7:82436773-82436782	34	30:2	16	0	4.71E-05
LOC440073	440073	chr12:101179-101610	chr12:101261-101281	85	30:0	-6	11	4.71E-05
LOC341720	341720	chr13:76426699-76426956	chr13:76426900-76426909	62	30:1	6	0	4.15E-05
KIAA1893	114787	chr5:175969411-175969744	chr5:175969507-175969527	73	30:0	34	11	4.00E-05
GRID1	2894	chr10:88114193-88114758	chr10:88114701-88114721	70	30:3	107	11	8.03E-05
GRID1	2894	chr10:88114193-88114758	chr10:88114584-88114604	77	30:3	-10	11	5.42E-05
COL22A1	169044	chr8:139816903-139817635	chr8:139817361-139817389	48	30:0	-48	19	6.28E-05
-	-	chr9:135274286-135274738	chr9:135274501-135274521	87	30:0	1	11	5.42E-05
-	-	chr1:178811470-178811859	chr1:178811614-178811634	73	30:0	36	11	4.15E-05
LOC390944	390944	chr19:51416825-51417437	chr19:51417178-51417198	73	29:2	-74	11	7.34E-05
CACNA1A	773	chr19:13215841-13216357	chr19:13215971-13215997	73	29:0	14	17	5.03E-05
-	-	chr2:50320001-50320364	chr2:50320185-50320205	76	29:0	6	11	4.42E-05
-	-	chr17:28923741-28924020	chr17:28923915-28923924	67	29:4	-8	0	4.00E-05
-	-	chr15:71912027-71912310	chr15:71912250-71912259	41	29:0	0	0	4.00E-05
-	-	chr15:67193717-67194223	chr15:67194004-67194032	55	29:2	-6	19	5.42E-05
-	-	chr10:131014230-131014602	chr10:131014336-131014356	70	29:1	-35	11	4.71E-05
-	-	chr10:106500051-106500478	chr10:106500239-106500259	81	29:0	7	11	4.71E-05
SERPINA13	388007	chr14:94190233-94190774	chr14:94190493-94190513	80	28:0	-67	11	6.28E-05
PSMB2	5690	chr1:35796054-35796551	chr1:35796147-35796156	30	28:2	11	0	6.28E-05
PAM	5066	chr5:102257518-102257792	chr5:102257741-102257750	30	28:0	10	0	4.15E-05
HPGD	3248	chr4:175770353-175770686	chr4:175770478-175770498	80	28:0	-18	11	4.42E-05
C6orf107	54887	chr6:34947979-34948611	chr6:34948335-34948344	36	28:3	28	0	6.28E-05
C10orf132	401647	chr10:99599763-99600380	chr10:99599989-99600009	79	28:2	68	11	6.78E-05
C10orf132	401647	chr10:99599763-99600380	chr10:99599922-99599942	87	28:2	1	11	8.03E-05
-	-	chr6:42420468-42420929	chr6:42420665-42420685	89	28:0	-2	11	5.80E-05
-	-	chr3:119198056-119198340	chr3:119198246-119198274	74	28:2	19	19	4.71E-05
-	-	chr11:127663483-127663809	chr11:127663600-127663620	70	28:2	-86	11	4.42E-05
-	-	chr11:21601238-21601629	chr11:21601359-21601368	64	28:2	4	0	5.42E-05
PRDM10	56980	chr11:129340395-129340635	chr11:129340537-129340563	51	27:0	1	17	4.00E-05
P2RX5	5026	chr17:3545598-3546125	chr17:3545829-3545838	69	27:3	1	0	5.80E-05
LOC441828	441828	chr18:74462114-74462758	chr18:74462479-74462488	68	27:0	-9	0	7.34E-05
LOC126075	126075	chr19:11320851-11321274	chr19:11320988-11321008	86	27:1	21	11	5.80E-05
KCNIP2	30819	chr10:103590705-103591256	chr10:103591072-103591092	87	27:1	37	11	6.78E-05
FLJ20619	55001	chr1:54981442-54981963	chr1:54981656-54981676	72	27:0	-1	11	5.80E-05

CENPB	1059	chr20:3715492-3715947	chr20:3715772-3715781	35	27:0	21	0	7.34E-05
-	-	chr9:125950210-125950701	chr9:125950300-125950320	81	27:1	12	11	6.28E-05
-	-	chr15:84700082-84700322	chr15:84700212-84700240	60	27:0	-73	19	4.71E-05
PCDH8	5100	chr13:52322641-52323059	chr13:52322919-52322945	53	26:3	-11	17	9.11E-05
LOC441651	441651	chr12:130737484-130737796	chr12:130737731-130737751	71	26:1	28	11	5.80E-05
GRM1	2911	chr6:146391011-146391418	chr6:146391221-146391241	83	26:0	-17	11	5.42E-05
GRB2	2885	chr17:70900995-70901416	chr17:70901322-70901331	55	26:2	9	0	5.42E-05
-	-	chr3:72109481-72109923	chr3:72109530-72109539	24	26:0	31	0	5.80E-05
-	-	chr10:129245051-129245584	chr10:129245376-129245396	78	26:0	19	11	5.80E-05
NRXN1	9378	chr2:51170827-51171298	chr2:51171084-51171104	76	25:0	48	11	6.28E-05
LOC388002	388002	chr14:80971601-80971999	chr14:80971923-80971943	73	25:1	23	11	7.34E-05
FLJ42133	400844	chr20:35743305-35743492	chr20:35743384-35743404	82	25:0	-75	11	5.42E-05
FLJ35784	374877	chr19:7476568-7477125	chr19:7476750-7476759	64	25:0	1	0	6.28E-05
COL1A2	1278	chr7:93668374-93668693	chr7:93668501-93668510	30	25:2	0	0	5.42E-05
CLTCL1	8218	chr22:17563868-17564382	chr22:17564239-17564248	34	25:1	5	0	6.78E-05
CDH16	1014	chr16:65504606-65504784	chr16:65504711-65504731	80	25:1	14	11	4.15E-05
CDH16	1014	chr16:65504606-65504784	chr16:65504608-65504628	70	25:1	-89	11	5.42E-05
-	-	chr7:8442460-8442852	chr7:8442549-8442558	40	25:2	7	0	6.28E-05
-	-	chr5:59225390-59225884	chr5:59225668-59225677	48	25:0	-5	0	6.78E-05
-	-	chr2:601441-601889	chr2:601680-601689	52	25:0	16	0	5.80E-05
-	-	chr13:26345087-26345324	chr13:26345225-26345245	71	25:2	-65	11	4.42E-05
-	-	chr11:132698474-132698775	chr11:132698629-132698649	81	25:1	-16	11	5.42E-05
-	-	chr1:205230700-205231101	chr1:205230923-205230943	75	25:0	31	11	5.80E-05
UCN	7349	chr2:27442900-27443229	chr2:27443117-27443137	84	24:0	-35	11	6.28E-05
RNU3IP2	9136	chr3:51943244-51943525	chr3:51943395-51943415	72	24:0	90	11	5.80E-05
RNU3IP2	9136	chr3:51943244-51943525	chr3:51943325-51943345	81	24:0	20	11	5.80E-05
RGN	9104	chrX:46714396-46714708	chrX:46714447-46714456	38	24:0	-31	0	9.11E-05
LOC440778	440778	chr21:33307904-33308263	chr21:33307976-33307985	47	24:0	6	0	6.78E-05
CRHR1	1394	chr17:41201118-41201413	chr17:41201316-41201325	60	24:0	19	0	5.80E-05
-	-	chr2:177818231-177818392	chr2:177818256-177818276	69	24:0	-45	11	5.80E-05
-	-	chr18:64753808-64754161	chr18:64754112-64754121	36	24:0	-20	0	6.28E-05
-	-	chr17:68992980-68993277	chr17:68993052-68993061	36	24:1	2	0	5.80E-05
-	-	chr16:26870856-26871177	chr16:26870967-26870992	56	24:2	28	16	5.80E-05
-	-	chr1:172391616-172392017	chr1:172391902-172391922	70	24:1	-29	11	6.28E-05
SNTG1	54212	chr8:51638441-51638681	chr8:51638538-51638547	46	23:0	90	0	6.28E-05
NPTX1	4884	chr17:76056752-76057030	chr17:76056774-76056783	59	23:1	4	0	5.42E-05
MESP1	55897	chr15:88104938-88105397	chr15:88105204-88105213	24	23:0	3	0	7.34E-05
KIAA1543	57662	chr19:7582373-7582684	chr19:7582617-7582626	40	23:1	-1	0	9.11E-05

CUL5	8065	chr11:107379622-107379872	chr11:107379745-107379765	71	23:1	-4	11	6.28E-05
C19orf30	284424	chr19:4721140-4721499	chr19:4721465-4721474	44	23:0	25	0	6.28E-05
ADAMTS20	80070	chr12:42224880-42225207	chr12:42224953-42224973	82	23:0	9	11	7.34E-05
-	-	chr3:140051817-140052044	chr3:140051886-140051895	41	23:0	-18	0	6.28E-05
-	-	chr17:62274244-62274549	chr17:62274464-62274484	80	23:0	53	11	8.03E-05
TRPM8	79054	chr2:234668051-234668517	chr2:234668276-234668296	70	21:0	19	11	8.03E-05
TRPM8	79054	chr2:234668051-234668517	chr2:234668270-234668296	51	21:0	16	17	8.03E-05
LOC440586	440586	chr1:43357636-43358008	chr1:43357843-43357863	70	21:1	6	11	8.03E-05
BBC3	27113	chr19:52426635-52426903	chr19:52426721-52426741	76	21:2	-9	11	7.34E-05
ABCA3	21	chr16:2271181-2271607	chr16:2271385-2271394	57	21:0	3	0	9.11E-05
-	-	chr19:41156182-41156558	chr19:41156379-41156399	76	21:1	26	11	9.11E-05
-	-	chr15:29949932-29950205	chr15:29949973-29949993	81	21:0	-10	11	6.78E-05
-	-	chr1:185200555-185200840	chr1:185200675-185200684	59	21:0	-11	0	7.34E-05
PTPRH	5794	chr19:60401825-60402157	chr19:60402025-60402034	38	20:0	0	0	9.11E-05
DOCK2	1794	chr5:169000891-169001105	chr5:169000986-169001006	73	20:1	17	11	6.78E-05
C5orf16	285613	chr5:140997735-140998034	chr5:140997811-140997820	57	20:1	7	0	8.03E-05
C10orf49	221044	chr10:13306831-13307131	chr10:13306863-13306883	89	20:0	6	11	9.11E-05
BRUNOL6	60677	chr15:70399045-70399295	chr15:70399191-70399211	92	20:0	-4	11	8.03E-05
-	-	chr5:68015376-68015688	chr5:68015578-68015587	34	20:2	11	0	9.11E-05
-	-	chr10:2900079-2900302	chr10:2900185-2900194	35	20:2	5	0	7.34E-05
LOC440730	440730	chr1:227604805-227605070	chr1:227604894-227604922	60	19:2	38	19	9.11E-05
KIAA0265	23008	chr7:128756553-128756952	chr7:128756576-128756596	75	19:0	-13	11	8.03E-05
FLJ23436	79724	chr16:30444795-30445039	chr16:30444960-30444986	44	19:0	9	17	9.11E-05
APBB1	322	chr11:6398561-6398774	chr11:6398697-6398717	77	19:0	73	11	7.34E-05
-	-	chr22:48084137-48084408	chr22:48084226-48084253	51	19:2	-60	18	9.11E-05
LOC391783	391783	chr5:54186899-54187148	chr5:54186955-54186964	31	18:1	38	0	9.11E-05

**Table S3.** Enriched regions from Experiment 1 that are common with Experiment 2 without NRSE Sites with P-value < 10<sup>-4</sup>

<b>Enriched Region</b>	<b>ChIP reads</b>
chr22:29526902-29527779	79
chr20:17155636-17156563	62
chr5:1722418-1723211	51
chr19:5296950-5297326	42
chr4:102610601-102611258	41
chr8:26428389-26429016	28
chr13:26741034-26741551	26
chr12:11916074-11916669	25
chr19:55993229-55993843	25
chr4:152939536-152940200	25
chr7:19585567-19586167	25
chr20:62429329-62429374	23
chrX:152618973-152619284	23
chr17:75848329-75848824	22
chr1:240558062-240558387	21
chr14:57401761-57402153	21
chr2:40797628-40798115	21
chr2:218494725-218495130	20
chr22:42850506-42850958	20
chr7:128332424-128332879	20
chr14:102581296-102581847	19
chr2:11706767-11707252	19
chr20:55975805-55976239	19
chr6:11152303-11152645	19
chr7:155330486-155330846	19
chr8:40825384-40825752	19
chr8:4239613-4240247	19
chr1:21666201-21666474	18
chr11:1400249-1400525	18
chr13:18213990-18214191	18
chr13:29492947-29493338	18
chr13:52319205-52319403	18
chr1:3657549-3657996	17
chr1:94795936-94796302	17
chr10:73007934-73008385	17

chr11:11985391-11985748	17
chr11:65537302-65537693	17
chr19:15641302-15641600	17
chr21:39822918-39823104	17
chr3:12895772-12896052	17
chr6:108602156-108602591	17
chr16:21085394-21085719	16
chr5:152224870-152225166	16
chr9:133705311-133705604	16
chr1:153624191-153624523	15
chr10:16906865-16906996	15
chr12:131330415-131330682	15
chr22:47925480-47925714	15
chr4:177362313-177362466	15
chr4:26790609-26790954	15
chr5:169912311-169912637	15
chr9:125574375-125574638	15
chr1:239031755-239032000	14
chr1:65487446-65487795	14
chr12:18827018-18827266	14
chr3:29738402-29738559	14
chr3:72529517-72529716	14
chr2:219654074-219654307	13
chr5:1932869-1933156	13
chr6:10851840-10852057	13

**Table S4.** Motif consensus returned by MEME on 198 Experiment 1 enriched regions with 500 or more ChIPSeq reads

Motif ID	Motif	# matches	Note
1-meme-1	BHDCTSTCCNHGGTSCTGR	209	Matches NRSE (reverse comp)
1-meme-2	DGGWGCTRTCC	268	Matches NRSE right half-site (rev comp)
1-meme-3	CTGYCMNBKGTKSTG	272	Matches NRSE (reverse comp)
1-meme-4	TTCAGCAY	390	Matches NRSE left half-site
1-meme-5	YTSHNYYHYCTHMTSCTDDBSKYYBK	7	
1-meme-6	ANRRVBAGADARVCWGSTS	28	
1-meme-7	WYTTTTTCWNHKKHWG	45	
1-meme-8	YYWBHHVNHBDGRVRHWGSMWDGVVNNG	28	
1-meme-9	AAATAAAACA	73	
1-meme-10	AWKTTMAVRYMACMAGACAWWKVAW	3	

**Table S5.** Motif consensus returned by MEME on 22 Experiment 1-enriched regions with 300 or more ChIPSeq reads and no canonical NRSEs

Motif ID	Motif	# matches	Note
1-meme-1	KGWGCTGTCCD	59	Matches NRSE right half-site (rev comp)
1-meme-2	KTCAGCAC	91	Matches NRSE left half-site
1-meme-3	RNWDVRAMADVRAA	272	OligoA
1-meme-4	RARAMASHNMWRRDDDDRVNW	112	
1-meme-5	AWMYRWRYWWAAWDW	97	
1-meme-6	AAATHTVWWGWKWKVYWK	8	
1-meme-7	RGVSKSNGSVNSRGB	203	
1-meme-8	AGMAWHWKWTDWAARBBVTCT	4	
1-meme-9	ATTTGAAACAA	23	
1-meme-10	AAACAAAACKACTTC	5	

**Table S6.** Distribution of NRSE with respect to gene annotations. Only NRSEs that are within or less than 10kb from a refseq gene model boundary were associated with a gene as “Upstream” or “Downstream”.

<b>Gene Part</b>	<b>Count</b>
<b>Upstream</b>	328
<b>5' UTR</b>	50
<b>CDS</b>	102
<b>Intron</b>	657
<b>3' UTR</b>	19
<b>Downstream</b>	201
<b>Further than 10kb</b>	857

**Table S7.** Distribution of type of gene-associated NRSEs.

<b>Site Type</b>	<b>Count</b>
<b>Canonical</b>	993
<b>Non-canonical (10bp, 16-19bp)</b>	224
<b>Half-site only</b>	140