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ARTICLES

Alternative isoform regulation in human tissue transcriptomes

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Through alternative processing of pre-messenger RNAs, individual mammalian genes often produce multiple mRNA and protein isoforms that may have related, distinct or even opposing functions. Here we report an in-depth analysis of 15 diverse human tissue and cell line transcriptomes on the basis of deep sequencing of complementary DNA fragments, yielding a digital inventory of gene and mRNA isoform expression. Analyses in which sequence reads are mapped to exon–exon junctions indicated that 92–94% of human genes undergo alternative splicing, ~86% with a minor isoform frequency of 15% or more. Differences in isoform-specific read densities indicated that most alternative splicing and alternative cleavage and polyadenylation events vary between tissues, whereas variation between individuals was approximately twofold to threefold less common. Extreme or 'switch-like' regulation of splicing between tissues was associated with increased sequence conservation in regulatory regions and with generation of full-length open reading frames. Patterns of alternative splicing and alternative cleavage and polyadenylation were strongly correlated across tissues, suggesting coordinated regulation of these processes, and sequence conservation of a subset of known regulatory motifs in both alternative introns and 3′ untranslated regions suggested common involvement of specific factors in tissue-level regulation of both splicing and polyadenylation.

The mRNA and protein isoforms produced by alternative processing of primary RNA transcripts may differ in structure, function, localization or other properties[1,2]. Alternative splicing in particular is known to affect more than half of all human genes, and has been proposed as a primary driver of the evolution of phenotypic complexity in mammals[3,4]. However, assessment of the extent of differences in mRNA isoform expression between tissues has presented substantial technical challenges[5]. Studies using expressed sequence tags have yielded relatively low estimates of tissue specificity, but have limited statistical power to detect differences in isoform levels[6–8]. Microarray analyses have achieved more consistent coverage of tissues[9], but are constrained in their ability to distinguish closely related mRNA isoforms. High-throughput sequencing technologies have the potential to circumvent these limitations by generating high average coverage of mRNAs across tissues while using direct sequencing rather than hybridization to distinguish and quantify mRNA isoforms[10,11].

Tissue-specific alternative splicing is usually regulated by a combination of tissue-specific and ubiquitously expressed RNA-binding factors that interact with *cis*-acting RNA elements to influence spliceosome assembly at nearby splice sites[1,2]. Many factors can both activate and repress splicing in different contexts, with activity often summarizable by an 'RNA map' describing dependence on the location of binding relative to that of core spliceosomal components[12,13].

A digital inventory of mRNA isoforms

To assess gene and alternative mRNA isoform expression, the mRNA-Seq protocol (Supplementary Methods) was used to amplify and sequence between 12 million and 29 million 32-base-pair (bp) cDNA fragments from ten diverse human tissues and five mammary epithelial or breast cancer cell lines, generating over 400 million reads in total (Supplementary Fig. 1a). Tissue samples were derived from single anonymous unrelated individuals of both sexes; for one tissue, cerebellar cortex, samples from six unrelated men were analysed to assess variation between individuals (Supplementary Table 1). In total, ~60% of reads mapped uniquely to the genome, allowing up to 2 mismatches, and an additional 4% mapped uniquely to splice junctions. Thus, about two-thirds of reads could be assigned unambiguously to individual genes; the frequency of mapping to incorrect genomic locations was estimated to be ~0.1% (Supplementary Table 2).

Read density (coverage) was over 100-fold higher in exons than in introns or intergenic regions (Supplementary Fig. 1c), and only ~3% of reads mapped to ribosomal RNA genes, indicating that most reads derived from mature mRNA. Comparison of relative mRNA-Seq read densities to published quantitative polymerase chain reaction with reverse transcription (RT–PCR) measurements for 787 genes in two reference RNA samples[14] yielded a nearly linear relationship across ~5 orders of magnitude (Supplementary Fig. 1d), indicating that mRNA-Seq read counts give accurate relative gene expression measurements across a very broad dynamic range[10].

Alternative splicing is nearly universal

The mRNA-Seq data were used to assess the expression of alternative transcript isoforms in human genes, as illustrated for the mitochondrial phosphate transporter gene *SLC25A3* in Fig. 1a. Exons 3A and 3B of this gene are 'mutually exclusive exons' (MXEs), meaning that transcripts from this gene contain one or the other of these exons, but not both. Much greater read coverage of exon 3A was seen in heart and skeletal muscle, with almost exclusive coverage of exon 3B in

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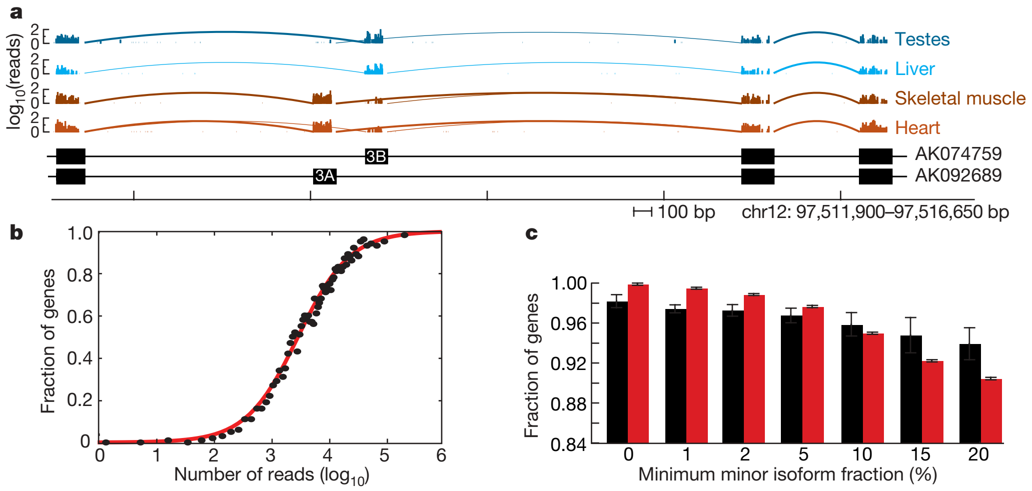


Figure 1 | Frequency and relative abundance of alternative splicing isoforms in human genes. a, mRNA-Seq reads mapping to a portion of the *SLC25A3* gene locus. The number of mapped reads starting at each nucleotide position is displayed ($\log_{10}$) for the tissues listed at the right. Arcs represent junctions detected by splice junction reads. Bottom: exon/intron structures of representative transcripts containing mutually exclusive exons 3A and 3B (GenBank accession numbers shown at the right). **b**, Mean fraction of multi-exon genes with detected alternative splicing in bins of 500 genes, grouped by total read count per gene. A gene was considered as alternatively spliced if splice junction reads joining the same 5′ splice site (5′SS) to different 3′ splice sites (3′SS) (with at least two independently mapping reads supporting each junction), or joining the same 3′SS to different 5′SS, were observed. The true extent of alternative splicing was estimated from the upper asymptote of the best-fit sigmoid curve (red curve). Circles show the fraction of alternatively spliced genes. **c**, Frequency of alternative splicing in the top bin (black bars) and after estimation (as in **b**, red bars), considering only events with relative expression of less abundant (minor) splice variant exceeding a given threshold. Error bars, s.e.m.

testes and liver (as well as in other tissues studied), consistent with the predominant heart and muscle symptoms of exon 3A mutation[15].

The genome-wide extent of alternative splicing was assessed by searching against known and putative splicing junctions using stringent criteria that required each alternative isoform to be supported by multiple independent splice junction reads with different alignment start positions. Binning the multi-exon genes in the RefSeq database (94% of all RefSeq genes) by read coverage and fitting to a sigmoid curve enabled estimation of the asymptotic fraction of alternatively spliced genes in this set as ~98% when excluding cell line data (Supplementary Fig. 2) and ~100% when using all samples (Fig. 1b). This analysis indicated that alternative splicing is essentially universal in human multi-exon genes, which comprise 94% of genes overall, with the important qualification that a portion of detected alternative splicing events may represent allele-specific splicing[16,17].

Some of these events may involve exclusively low frequency alternatively spliced isoforms. However, 92% of multi-exon genes were estimated to undergo alternative splicing when considering only events for which the relative frequency of the minor (less abundant) isoform exceeded 15% in one or more samples (Fig. 1c). Thus, 0.92 × 0.94 or ~86% of human genes were estimated to produce appreciable levels of two or more distinct populations of mRNA isoforms. Conversely, no evidence of alternative splicing was detected in the 6% of RefSeq genes annotated as consisting of a single exon, even when searching against junctions between predicted exons in these genes.

New exons and splice junctions not previously seen in transcript databases were identified by mapping the reads against predicted exons and junctions. This approach yielded a set of 1,413 high-confidence new exons (Supplementary Table 3), with an estimated false discovery rate (FDR) of <1.5% (Supplementary Information), and thousands of putative new splice junctions (not shown). Thus, mRNA-Seq has strong potential for discovery of new exons, although very substantial read depth is required to efficiently detect low-abundance isoforms (Supplementary Fig. 3).

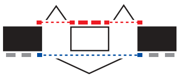
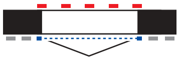
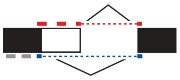
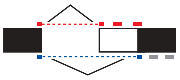
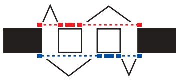
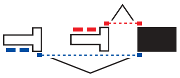
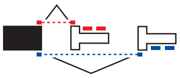
Tissue-specific isoform expression

To explore the extent of tissue regulation of alternative transcripts, we examined eight common types of 'alternative transcript events'[1,2], each capable of producing multiple mRNA isoforms from human genes through alternative splicing, alternative cleavage and polyadenylation (APA) and/or alternative promoter usage (Fig. 2). Event types considered included skipped exons and retained introns, in which a single exon or intron is alternatively included or spliced out of the mature message, and MXEs, described previously. Also included were alternative 5′ splice site (A5SS) and alternative 3′ splice site (A3SS) events, which are particularly difficult to interrogate by microarray analysis because the variably included region is often quite small. Tandem 3′ untranslated regions (UTRs) and alternative last exons (ALEs), in which alternative use of a pair of polyadenylation sites results in shorter or longer 3′ UTR isoforms or in distinct terminal exons, respectively, were also considered. Finally, we considered alternative first exons (AFEs), in which alternative promoter use results in mRNA isoforms with distinct 5′ UTRs.

For each of these event types, reads deriving from specific regions can support the expression of one alternative isoform or the other (Fig. 2). The 'inclusion ratio', defined as the ratio of the number of 'inclusion' (blue) reads to inclusion plus 'exclusion' (red) reads, can be used to detect changes in the proportions of the corresponding mRNA isoforms. The fraction of mRNAs that contain an exon—the 'per cent spliced in' (PSI or Ψ) value—can be estimated as the ratio of the density of inclusion reads (that is, reads per position in regions supporting the inclusion isoform) to the sum of the densities of inclusion and exclusion reads.

To assess tissue-regulated alternative splicing, a comprehensive set of ~105,000 events of these eight types was derived on the basis of available human cDNA and expressed sequence tag data. Reads supporting both alternative isoforms were observed for more than one-third of these events (Fig. 2), and the extent of tissue-specific regulation of these events was assessed by comparison of the inclusion ratio in each tissue relative to the other tissues, requiring a minimum of a 10% absolute change in inclusion ratio (Supplementary Fig. 4). Naturally, transcripts or isoforms identified as being differentially expressed between tissues will reflect the combined effects of cell-type-specific differences in transcript levels, variation in the relative abundances of cell types between tissues, and variations between the individuals from whom the tissues derived.

Notably, a high frequency of tissue-specific regulation was observed for each of the eight event types, including over 60% of the analysed skipped exon, A5SS, A3SS and tandem 3′ UTR events

Alternative transcript events		Total events (×10^3)	Number detected (×10^3)	Both isoforms detected	Number tissue-regulated	% Tissue-regulated (observed)	% Tissue-regulated (estimated)
Skipped exon		37	35	10,436	6,822	65	72
Retained intron		1	1	167	96	57	71
Alternative 5′ splice site (A5SS)		15	15	2,168	1,386	64	72
Alternative 3′ splice site (A3SS)		17	16	4,181	2,655	64	74
Mutually exclusive exon (MXE)		4	4	167	95	57	66
Alternative first exon (AFE)		14	13	10,281	5,311	52	63
Alternative last exon (ALE)		9	8	5,246	2,491	47	52
Tandem 3′ UTRs		7	7	5,136	3,801	74	80
Total		105	100	37,782	22,657	60	68

■ Constitutive exon or region ▬ Body read ▪┅┅▪ Junction read pA Polyadenylation site

□ Alternative exon or extension Inclusive/extended isoform Exclusive isoform Both isoforms

Figure 2 | Pervasive tissue-specific regulation of alternative mRNA isoforms. Rows represent the eight different alternative transcript event types diagrammed. Mapped reads supporting expression of upper isoform, lower isoform or both isoforms are shown in blue, red and grey, respectively. Columns 1–4 show the numbers of events of each type: (1) supported by cDNA and/or EST data; (2) with ≥1 isoform supported by mRNA-Seq reads; (3) with both isoforms supported by reads; and (4) events detected as tissue-regulated (Fisher's exact test) at an FDR of 5% (assuming negligible technical variation[10]). Columns 5 and 6 show: (5) the observed percentage of events with both isoforms detected that were observed to be tissue-regulated; and (6) the estimated true percentage of tissue-regulated isoforms after correction for power to detect tissue bias (Supplementary Fig. 6) and for the FDR. For some event types, 'common reads' (grey bars) were used in lieu of (for tandem 3′ UTR events) or in addition to 'exclusion' reads for detection of changes in isoform levels between tissues.

(Fig. 2 and Supplementary Table 4). In all, a set of over 22,000 tissue-specific alternative transcript events was identified, far exceeding previous sets of tissue-specific alternative splicing events that have typically numbered in the hundreds to low thousands[6–9,18,19]. Tissue-regulated skipped exon and MXE events are listed in Supplementary Tables 5 and 6, respectively. Binning events by expression level commonly yielded sigmoid curves for the fraction of tissue-regulated events of each type, enabling estimation of the true frequency of tissue regulation for each event type (Supplementary Figs 5 and 6). These estimates, ranging from 52% to 80% (Fig. 2), indicated that most alternative splicing events are regulated between tissues, providing an important element of support for the hypothesis that alternative splicing is a principal contributor to the evolution of phenotypic complexity in mammals.

Individual-specific isoform expression

To assess the extent of alternative splicing isoform variation between individuals in comparison to tissue-regulated alternative splicing, the correlations among the vectors of inclusion ratios for all expressed skipped exons between pairs of samples were determined (Fig. 3); this was performed similarly for other event types (not shown). In this analysis, strong clustering of the six cerebellar cortex samples was observed, with generally higher correlations among these samples than between pairs representing distinct tissues. Strong clustering of the five cell lines was also observed. This probably results from a combination of factors, including the common mammary epithelial origin of the cell lines studied, similar adaptations to culture conditions, and the high diversity of the tissues chosen.

The extent of variation in alternative isoform expression between individuals was also addressed by determining the number of differentially expressed exons among the six cerebellar cortex samples. Using the same approach as in Fig. 2, between ~10% and 30% of alternative transcript events showed individual-specific variation, depending on the event type (Supplementary Fig. 7), providing updated estimates of the scope of mRNA isoform variation between individuals[16]. These numbers are higher than estimates based on microarray analyses[20], but are in general agreement with an integrated analysis of multiple data types that estimated that ~21% of alternatively spliced genes are affected by polymorphisms that alter the relative abundances of alternative isoforms[17]. However, these frequencies are still below the 47–74% of events that showed variation among the ten tissues (Fig. 2), and approximately twofold to threefold less than the frequencies observed in comparisons among subsets of six tissues (Supplementary Fig. 7), indicating that, although inter-individual variation is fairly common, it is still substantially less frequent than variation between tissues. Thus, most of the differences observed between tissue samples are likely to represent tissue-specific rather than individual-specific variation.

Switch-like alternatively spliced exons

The quantitative nature of the mRNA-Seq approach allowed assessment of both subtle and switch-like alternative splicing events. By

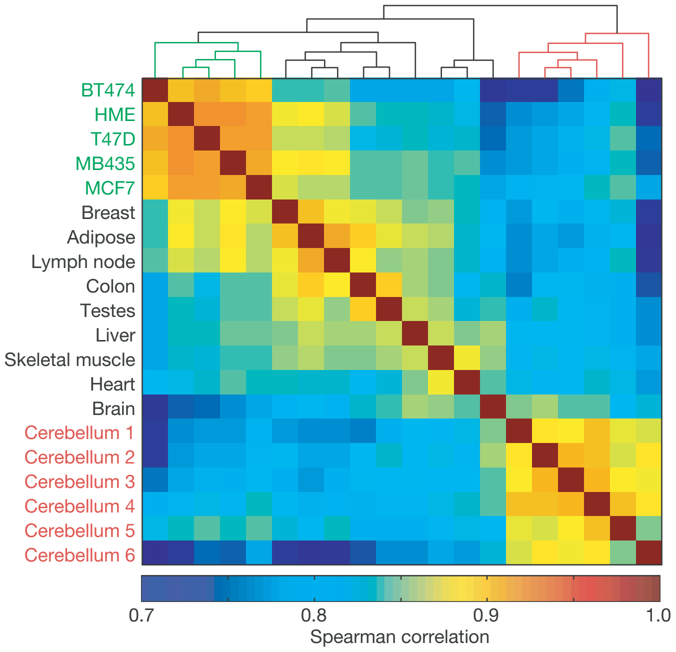


Figure 3 | The extent of individual-specific differences in alternative isoform expression. Spearman correlations of inclusion ratios for skipped exons in human tissues and cell lines (see Methods Summary). Correlations were computed separately for each pair of tissues and cell lines, and clustered according to similarity using average linkage hierarchical clustering.

comparing inclusion levels of skipped exons between tissues, a class of 'switch-like' exons was observed that had markedly different inclusion levels between different tissues (shown for heart versus nine other tissues in Fig. 4a). The examples shown in colour in Fig. 4a (for example, *TPM1* exon 2, with Ψ of 2% in heart and 95% in skeletal muscle, and the *SLC25A3* MXE pair shown in Fig. 1a) underscore the flexibility of the splicing regulatory machinery, with a sizeable number of exons being recognized predominantly as exons in one tissue and predominantly as introns in another tissue, even for developmentally related pairs of tissues such as heart and skeletal muscle.

To characterize functional features of such switch-like exons, skipped exons and MXEs were divided into groups depending on their 'switch score', defined as the maximum pairwise Ψ difference between tissues. Switch scores for pairs of MXEs were shifted towards higher values relative to skipped exons ($P = 3.7 \times 10^{-5}$, Kolmogorov–Smirnov test; Fig. 4b), suggesting that MXEs are more often involved in regulating highly tissue-specific functions. Preservation of the reading frame in both isoforms was observed more commonly for exons with higher switch scores both for skipped exons, consistent with ref. 19, and to an even greater extent for MXEs (Fig. 4c). Thus, switch-like regulation seems to be used preferentially to express distinct 'full-length' protein isoforms in different tissues rather than as a means to switch off genes through production of truncated proteins or of messages subject to nonsense-mediated mRNA decay[21]. Indeed, genes containing skipped exons with high switch scores were enriched for Gene Ontology functional categories including 'developmental processes', 'cell communication', 'signal transduction' and 'regulation of metabolism' that are likely to contribute to fundamental differences in the biology of different human tissues (Supplementary Table 7).

Notably, skipped exons with switch scores exceeding 0.5 showed higher sequence conservation in the regulated exon itself[19] and in portions of the flanking introns than exons with lower switch scores (Fig. 4d). This observation suggested that such exons are of unusual biological importance and that switch-like regulation between tissues requires the presence of additional splicing regulatory sequence information, particularly in adjacent intronic regions.

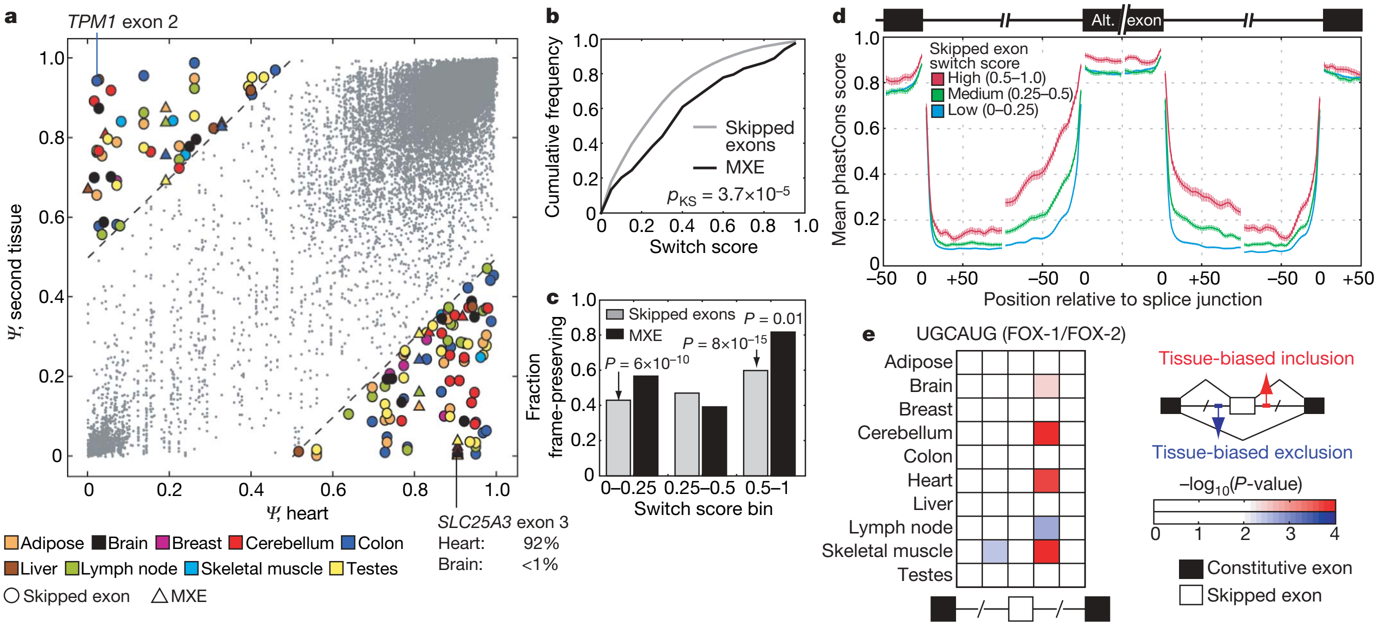


Figure 4 | Conservation and function of switch-like alternative splicing exons. **a**, Scatter plot showing Ψ values of skipped exons and MXEs for which switch score was determined on the basis of comparison of heart (*x*-axis) with a second tissue (*y*-axis). Exons with a switch score >0.5 are shown as filled symbols; others are shown as small grey dots. **b**, Cumulative distribution functions of switch scores for skipped exons and MXE pairs (*P*-value based on Kolmogorov–Smirnov test). **c**, Reading frame preservation of skipped exons and MXEs grouped by switch score. Skipped exons with lengths divisible by 3 and MXE pairs with lengths differing by 0 or a multiple of 3 were considered to preserve the reading frame. *P*-values are based on Fisher's exact test. **d**, Conservation in skipped exon and flanking intron regions grouped by skipped exon switch score. The mean per-position phastCons score (from alignment of four mammalian genomes) and s.e.m. are shown. **e**, Enrichment of UGCAUG motifs near tissue-regulated skipped exons. Coloured squares represent $-\log_{10}(P\text{-value})$ for the enrichment of UGCAUG counts relative to cohorts of control hexanucleotides in regions surrounding skipped exons with significantly increased (red) or decreased (blue) inclusion in each tissue with respect to other tissues.

FOX-1 and FOX-2 activity map

Among the best-characterized tissue-specific splicing factors are the FOX-1 (also known as A2BP1) and FOX-2 (RBM9) proteins, which bind RNA *cis*-elements that contain UGCAUG hexanucleotides or closely related sequences[22–24]. Analysis of UGCAUG frequencies revealed substantial enrichment in the intron immediately downstream of exons with increased inclusion in heart, skeletal muscle, brain and cerebellar cortex (Fig. 4e)—tissues where FOX proteins are highly expressed, suggesting common splicing activation activity in this location[22–24]. Enrichment of UGCAUG hexanucleotides was also noted upstream of exons that had reduced inclusion in skeletal muscle, suggesting possible repressive activity in this context. This example illustrates the power of these expanded tissue-specific exon sets for inference of 'tissue RNA maps', summarizing both the location-dependent activity and tissue specificity of splicing regulatory elements.

Applying a similar approach to analyse enrichment of all hexanucleotides in regions adjacent to tissue-specific exons identified 362 motif/tissue enrichment patterns (at an estimated 17% FDR), representing hexanucleotides that showed significant enrichment adjacent to exons with increased or decreased inclusion in specific cell lines or tissues (Supplementary Table 8). Enrichment of UGCAUG downstream of exons with high inclusion in skeletal muscle appears as the third most significant motif/tissue pair, after enrichment of UCUCUC and CUCUCU (resembling the binding motifs of PTBP1 (also known as PTB) and PTBP2 (nPTB)[25]) upstream of exons with increased inclusion in cerebellar cortex. The remaining motif/tissue pairs contained a variety of known regulatory elements, including ACUAAC (see later), as well as putative new regulatory motifs.

Coordination of splicing and polyadenylation

Tandem 3′ UTR events showed an even higher frequency of tissue-regulated expression than skipped exons or other alternative splicing events studied (Fig. 2), yet little is known about how tissue regulation of tandem UTRs is accomplished (for example, whether through APA or through the differential stability of alternative UTR isoforms). By grouping tandem 3′ UTRs by switch score, the most switch-like events showed increased sequence conservation relative to events with lower switch scores in the vicinity of and upstream of the proximal (5′) polyadenylation signal (PAS), and also upstream of the distal (3′) PAS (Fig. 5a). Whereas *cis*-regulatory elements contributing to differential stability should be located predominantly in the region unique to the long UTR isoform, APA could be regulated by elements located near to either or both PASs. The observation of increased conservation around and upstream of the proximal PAS in switch-like tandem UTRs therefore supports a primary role for regulation at the level of APA.

In assessing the spectrum of *cis*-elements that may drive tissue regulation of tandem 3′ UTRs, a set of heptanucleotides was identified that showed high conservation in the extension region of tandem 3′ UTRs (Fig. 5a, inset), with signal:background ratios in four mammals[26] exceeding 2:1. As expected, this set included the extended (seven-base) seed matches to a number of conserved mammalian microRNAs (miRNAs)[26–28]. Surprisingly, it also included all eight of the heptanucleotides that contain the FOX-1/FOX-2 consensus binding motif, UGCAUG: all such heptanucleotides had signal/background ratios above 2.5:1, exceeding the signal/background ratio observed for seed matches to important miRNAs such as miR-7 and miR-181 (inset, Supplementary Table 9). Strong conservation of UGCAUG motifs in this location (>1 kilobase on average from the nearest splice site) would not be expected on the basis of the canonical splicing regulatory activity of FOX-1/FOX-2 proteins. Instead, the high conservation observed in extended 3′ UTR regions suggests that these factors (or others with identical RNA-binding specificity) have additional 3′ UTR-related roles, for example, in APA or in mRNA localization and/or translation.

To investigate possible connections between tissue-specific regulation of alternative splicing and APA further, global patterns of tissue-specific alternative isoform expression were compared. By applying singular value decomposition (SVD) (Supplementary Methods) to the vectors of inclusion ratios across samples for each alternative splicing and APA event type separately, a strong and consistent separation of the breast cell lines (four cancer-derived and one immortalized cell line) from all tissue samples was observed (Fig. 5c,

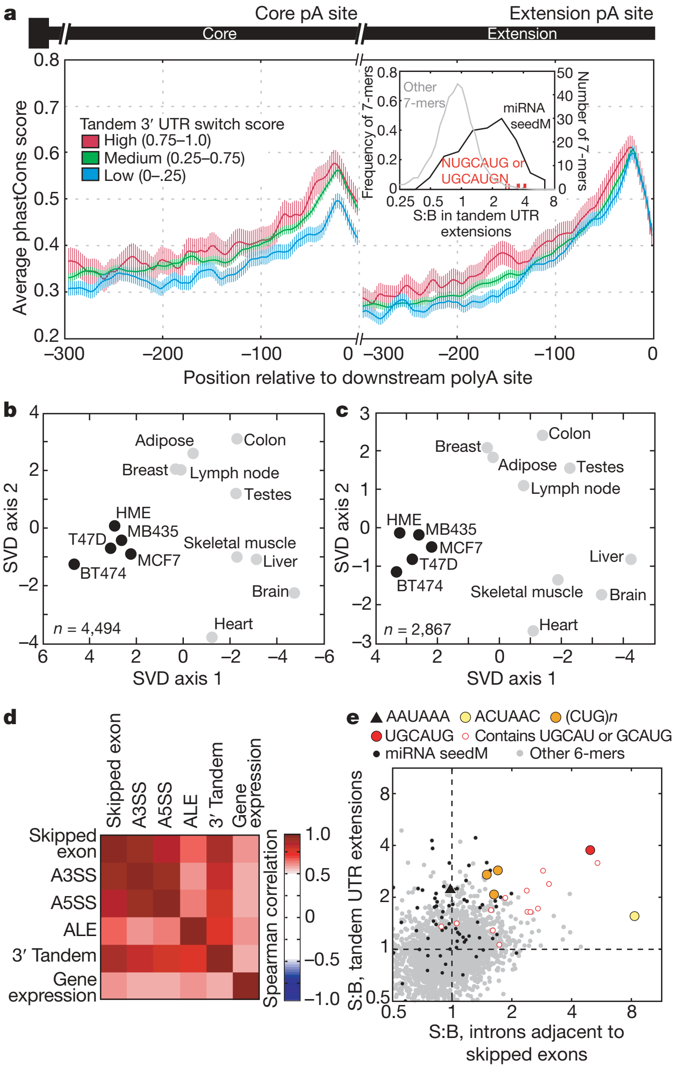


Figure 5 | Evidence for coordination between splicing and polyadenylation. **a**, Mean and s.e.m. of per-position phastCons score in the region 300 bp upstream of proximal and distal cleavage sites for tandem 3′ UTRs grouped by switch score. Inset, increased conservation of FOX-1/FOX-2 motifs in tandem 3′ UTR extension regions. All non-CpG-containing heptanucleotides (grey line), miRNA seed matches (black), and 7-mers containing UGCAUG (red) are shown. **b**, SVD analysis of skipped exon inclusion ratio values across tissues and cell lines for skipped exons meeting minimum read coverage criteria in each of the 14 samples. Projections are shown in the dimensions corresponding to the two leading eigenvalues, which accounted for 25% of the variance. **c**, SVD analysis of tandem UTR inclusion ratio values (as in **b**). **d**, SVD analysis was conducted for the 14 samples on the basis of inclusion ratio values for the five indicated alternative transcript event types or on the basis of gene expression values. Spearman correlations between corresponding pairwise distances in projections of the sort shown in **b** and **c** are shown. **e**, Signal:background (S:B) ratios of non-CpG-containing hexanucleotides in introns flanking skipped exons (*x*-axis) and in extended 3′ UTR regions (*y*-axis). The canonical PAS hexanucleotide AAUAAA (black triangle), hexanucleotides corresponding to seed matches to conserved mammalian miRNAs (black dots), hexanucleotides corresponding to binding motifs for the indicated splicing or 3′ UTR-binding factors (coloured), and other hexanucleotides (small gray dots) are shown.

d). This separation implied the existence of a systematic difference in RNA processing regulation between cell lines and tissues that held for all types of alternative events studied. For most alternative splicing and APA events, SVD analysis yielded similar groupings of tissues, for example, with heart, skeletal muscle, brain and liver consistently clustered (Supplementary Fig. 8). Consistent with this observation, pairwise distances between SVD projections for different types of alternative splicing events, for example, skipped exons, A5SS and A3SS events, were all highly correlated (Fig. 5e), suggesting similarities in the regulatory control of these types of events[1,2,13]. More surprisingly, distances between SVD projections for tandem 3′ UTR events also correlated highly with distances for events controlled purely at the level of splicing such as skipped exons (Fig. 5e). This observation raised the possibility that splicing and polyadenylation may be coordinately regulated across human tissues.

To explore possible regulatory connections between splicing and polyadenylation regulation (for example, refs 29–32), the conservation of hexanucleotides adjacent to conserved alternative splicing and APA events was compared. Whereas canonical 3′ UTR regulatory motifs such as the consensus PAS hexanucleotide AAUAAA and various miRNA seed matches showed high signal:background ratios, often 1.5:1 or higher, in extended 3′ UTR regions, these motifs generally had signal/background ratios close to 1:1 in alternatively spliced introns. However, a distinct subset of motifs with high signal:background ratios in both UTRs and introns was also observed, several of which corresponded to well-known splicing-related motifs (Fig. 5h and Supplementary Table 9). This set included not only the FOX-1/FOX-2 motif UGCAUG and variations, consistent with the heptanucleotide analysis of Fig. 5a, but also permutations of $(CUG)_n$, which represent putative substrates of the bruno-like (BRUNOL, also known as CELF) and muscleblind-like (MBNL) families of muscle- and brain-specific splicing factors[33]. The highly significant signal:background ratio in both 3′ UTRs and introns suggested that these well-known splicing-related motifs also commonly have 3′ UTR-related roles—for example, control of APA or of mRNA stability, localization or translation—as recently demonstrated for the NOVA family of splicing factors[34].

The hexanucleotide ACUAAC, an excellent match to the consensus binding motifs of STAR family RNA-binding factors, in particular quaking homologue (QKI)[35], was also notable. Not only did ACUAAC have significant signal:background ratio in 3′ UTRs, as expected from the known role of QKI in control of mRNA stability[36], but it also showed an extremely high signal:background ratio in introns, exceeding 7:1. This extreme conservation suggested a common and important function in splicing regulation—a role that has been suggested but not yet directly demonstrated[9,37]. Motif enrichment analyses also suggested a possible role in brain-specific APA regulation (Supplementary Fig. 9).

Discussion

We conclude that the coordination between tissue-specific alternative splicing and APA events implied by the correlated patterns of tissue bias observed in Fig. 5 may be mediated at least in part by tissue-specific RNA-binding factors that have roles in regulation of both of these RNA processing steps. Such factors may include both canonical tissue-specific splicing factors (for example, of the FOX-1/FOX-2 and CELF families), moonlighting in 3′ UTR-related roles, and also canonical UTR-binding factors such as QKI. Such functional duality has the potential to enable tightly coordinated regulation of polyadenylation and splicing, ensuring that the appropriate UTR regulatory sequences are expressed in conjunction with the coding regions for the relevant tissue-specific protein isoforms.

METHODS SUMMARY

Tissues and cell lines. Tissue samples from individual unrelated anonymous donors (Supplementary Table 1) were obtained from Ambion for the following tissue types: adipose, whole brain, breast, colon, heart, liver, lymph node, skeletal muscle and testes. Cerebellar cortex samples were obtained from six anonymous unrelated donors, according to NIH guidelines for confidentiality and privacy using protocols described previously[38]. HME is a human mammary epithelial cell line immortalized with human TERT[39]. The other cell lines are all breast cancer cell lines derived from invasive ductal carcinomas (ATCC). MCF-7, BT474 and T47D are oestrogen-receptor- and progesterone-receptor-positive; MDA-MD435 is negative for both.

Library preparation for Illumina sequencing. Poly-T capture beads were used to isolate mRNA from 10 μg of total RNA. First-strand cDNA was generated using random hexamer-primed reverse transcription, and subsequently used to generate second-strand cDNA using RNase H and DNA polymerase. Sequencing adaptors were ligated using the Illumina Genomic DNA sample prep kit. Fragments ~200 bp long were isolated by gel electrophoresis, amplified by 16 cycles of PCR, and sequenced on the Illumina Genome Analyser, as described[40,41].

Computational analyses of mRNA-Seq read data. Computational and statistical methods used in analysis of the read data are described in the Supplementary Methods. High-confidence new exons were required to be supported by at least one splice juction read involving each splice site, and at least one exon body read; putative new splice junctions required splice junction read support only[42].

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Author Information The reported sequence read data have been deposited to the Short Read Archive section of GEO at NCBI under accession numbers GSE12946 and SRA002355.1. The authors declare competing financial interests: details accompany the full-text HTML version of the paper at www.nature.com/nature. Reprints and permissions information is available at www.nature.com/reprints. Correspondence and requests for materials should be addressed to C.B.B. (cburge@mit.edu).

Methods

Mapping of mRNA-Seq reads to genome and transcriptome

mRNA-Seq reads were mapped to the human genome (hg18)[1] and a collection of splice junctions (see below), allowing up to two mismatches, using the ELAND (Efficient Alignment of Nucleotide Databases) module within the Illumina Genome Analyzer Pipeline software. Mapping statistics are shown in Fig. S1a. Mean read density values for exons, introns, and intergenic regions were computed in units of reads per kilobase of exon [intron/intergenic] model per million mapped reads (RPKM)[2] and are displayed in Fig. S1c. Reads were mapped to the annotated transcribed strand of the genome, since the sequencing protocol used does not distinguish strand. All sequence read data have been submitted to the Short Read Archive section of the GEO database at NCBI under accession numbers GSE12946 and SRA002355.1.

Sequencing error rate estimation

The sequencing error rate of our mRNA-Seq dataset was estimated by assessing the frequency of reads mapping to the genome with 0, 1, and 2 mismatches. These counts closely followed a Poisson distribution with mean $\lambda = 0.4$ errors per 32-bp read. Considering all 32 bp segments from Ensembl annotated exons, ~91% occurred uniquely in the genome, and most differed at multiple positions from the closest 32 bp sequence in the genome. Thus, a sequencing error rate with mean λ = 0.4 / read, that produces mainly reads with 0 or 1 incorrect bases out of 32, is expected to produce a majority of reads that can be mapped uniquely to the genome. The mismatch frequency had a U-shaped distribution as a function read position (Fig. S1b). The increase in error rate toward the end of a read is an intrinsic property of the Solexa sequencing technology used, while the lesser increase in mismatch frequency at the first few positions likely results from biases related to the random hexamer priming, with the necessity of perfect base pairing increasing toward the 3' end (corresponding to base 6) of the primer.

Estimation of rate of mis-mapping

The frequency of mis-mapping of reads to the genome and splice junction dataset (see below) was estimated by using all uniquely mapped reads for the low-coverage UHR sample (5M reads). We first corrected all mismatches to match reference sequence to generate 5M perfectly mapping reads. Then we generated a set of mock reads, introducing errors at a frequency of 0.4 errors/read, that were then mapped to the genome and junctions using ELAND, also allowing for two mismatches. The fraction of mock reads mapping to a unique genomic location or junction was 98.7%. Of those uniquely mapping reads, 99.9% were correctly remapped to their location of origin.

Generation of splice junction database

A comprehensive list of known exons was compiled from UCSC knowngenes, Refseq and Ensembl transcripts, together with predicted exons from GENSCAN[3], and EXONIPHY[4] . All possible splice junctions between any two known or predicted exons located within Ensembl gene boundaries or within the full intergenic region flanking those gene boundaries were considered. Each generated splice junction sequence was 56 bp in length, containing the last 28 bases of the upstream exon and the first 28 bp of the downstream exon, yielding 13.8 million junctions in total. Use of 28 bp on each side effectively ensured that each junction-mapped read must match a minimum of 4 bases on each side of the junction, a requirement we have found is sufficient to ensure unique mapping in the vast majority of cases. This comprehensive database of potential splice junctions, as well as the database of known splice junctions used in assessment of tissue-specific AS will be posted at http://genes.mit.edu/burgelab/mRNA-Seq.

Estimation of transcript abundance and comparison to real time RT-PCR data

Reads in the low coverage UHR sample (derived from Stratagene Universal Human Reference RNA) and the low coverage brain sample (derived from Ambion Human Brain Reference RNA) were mapped to all Refseq exons and splice junctions to obtain read counts for each transcript. Taqman data from the MAQC project were downloaded from NCBI Gene Expression Omnibus (GEO), specifically for four replicates each of Stratagene UHR RNA (tables GSM129638, GSM129639, GSM129640, GSM129641) and the Ambion brain RNA (GSM129643, GSM129644, and GSM129645). The ΔCt values with respect to *POLR2A* (endogenous control gene) were averaged across the four replicates, using only data points for which expression was detectable ($\leq$ 35 cycles). The difference in average ΔCt value between brain and UHR (ΔΔCt) for each Refseq transcript was compared with the log of the ratio of read counts in brain over UHR for each Refseq transcript interrogated by Taqman assay, where mRNA-Seq read counts were normalized by read counts for *POLR2A* (Fig. S1d). The slope of the best fit line determined by linear regression (MATLAB). The Pearson correlation coefficient value is also reported.

While read counts varied substantially between different positions in exons (e.g., Fig. 1A), summing these counts across a gene provided highly quantitative estimates of gene expression (Fig. S1d). Using typical values of ~100 mappable positions per exon and ~2500 per gene, percent spliced in (Ψ) values based on exonic read densities are expected to have a sampling error ~√25 = 5-fold higher than expression values based on read density across the gene, but ~√100 = 10-fold lower than for expression estimates based on read density at individual read positions. Comparison of Ψ values estimated from mRNA-Seq data in 293T cells to exon inclusion levels measured by qRT-PCR yielded correlations in the range of between 0.8 and 0.9 with mRNA-Seq Ψ values (X. Xiao, R. Nutiu, G. S. and C. B. B., unpublished data).

Estimation of extent of alternative splicing in human genes

We first identified all single-exon transcripts using Refseq annotations (n=1330, 5% of total number of transcripts). Since we frequently observed single-exon transcripts to be mapping to genes with other annotated multi-exon transcripts, we filtered for gene loci with exclusively annotated single-exon transcripts to create our set of 'single-exon genes' and the remaining loci were designated 'multi-exon genes'. For both single- and multi-exon genes we grouped the overlapping transcripts for each gene locus to generate a set of non-redundant gene boundary annotations by selecting the most upstream genomic start and downstream end coordinates for each locus. This procedure generated a set of 1056 single-exon genes and 16,810 multi-exon genes. For the 6% of single-exon genes (1056 out of 17,866) we saw no evidence for alternative splicing. The remaining non-redundant set of multi-exon genes was sorted and binned based on read coverage, i.e. the number of reads that mapped between the genomic start and end coordinates. The fraction of alternatively spliced genes was determined for each bin, where a gene was defined to be alternatively spliced if there was evidence of a 5'SS spliced to multiple 3'SS or of a 3'SS spliced to multiple 5'SS. Both termini of a junction were required to be located within the annotated gene boundaries, and each splice junction was required to be supported by at least two reads with different alignment positions within the splice junction. Junctions involving annotated alternative first exons (which are typically generated by alternative promoters) were not considered to represent alternative splicing in this analysis.

One limitation of the analysis is that the read coverage of some genes may be insufficient to detect all mRNA isoforms. Therefore, to estimate the true extent of alternative splicing (essentially, the extent of alternative splicing that would be observed given saturating coverage), a sigmoid curve of the form $F(x) = \frac{\alpha}{1+e^{-(x-a)*b}}$ was fitted to the fraction of alternatively spliced genes ($F(x)$) in each bin as a function of read coverage (x), where α, the upper asymptote, represents the true extent of alternative splicing (Fig. S2a). Estimates were robust to the bin size used, as similar results were obtained when using a range of different bin sizes (Fig. S2b).

To assess whether the genes with highest read coverage (genes in the top bin) exhibited a frequency of alternative splicing different than that for genes with lower coverage (genes in lower bins), a sub-sampling approach was used (Fig S1a). In this approach, reads were sampled from the topmost bin to simulate levels of read coverage in the other bins, and the fraction of genes alternatively spliced was evaluated in each sub-sampled bin. This procedure was repeated 100 times to obtain stable means.

To assess the contribution of the cell lines to estimates of the frequency of alternative splicing, the analysis described above was performed using 9 tissues (excluding the 6 cerebellar cortex and 5 cell line samples), and compared to the analysis using random subsets of 9 samples from the set consisting of the union of the 9 tissues and 5 cell lines (Fig. S2c). Both analyses yielded similar fractions of alternative splicing, indicating that the estimates of the fraction of alternative splicing were robust to the choice of samples and that the cell lines did not appear to contribute disproportionately to estimates of the total fraction of alternative splicing.

While we found that essentially 100% of multi-exon genes (94% of all genes) undergo alternative splicing, no evidence of alternative splicing was detected in the set of single-exon genes (the remaining 6% of genes) in our data using the above criteria, even though predicted exon-exon junctions were searched against.

Estimation of alternative splicing frequency with a minimum minor isoform threshold

To investigate the relative expression of the two splice junctions used to infer the alternative splicing event, we compared the splice junction read counts for each alternative 3' (or 5') splice site, designating the splice site with lower read count as 'minor'. The fraction of splice junction reads that supported the minor splice site was then compared to a given threshold. For example, if 12 splice junctions reads mapped to a splice junction joining a 5'SS to a 3'SS, and 4 splice junction reads mapped to a splice junction joining the same 5'SS to a different 3'SS, the second 3'SS would be considered minor, with a “minor isoform frequency” of 4 / (12+4) = 25%. The fractions of genes with detected alternative splicing passing different minimum minor isoform frequency thresholds are shown in Fig 1c. The lowest minor isoform frequency that can be detected depends on the read coverage (i.e. expression level) of the gene. The statistical power available to detect minor isoforms with different frequencies as a function of the read coverage (RPKM) was estimated by simulation (Fig. S3), where power was defined as the percentage of time that the minor isoform can be detected, given predefined minor isoform frequency and read coverage values. For example, these results indicate that sequencing of 15M mappable reads yields for the 1000 genes with highest expression level (RPKM > 100), power of 99%, 44% and 4% to detect both junctions (with 2 or more reads each) at minor isoform frequencies of 20%, 5% and 1%, respectively.

Estimation of false positive rate in discovery of high confidence novel exons

To estimate the fraction of novel exons which are potential false positives, we generated a set of "modified" splice junctions, where 5 nucleotides were removed from the upstream exon (positions -10 to -6 relative to the junction) and 5 nucleotides were removed from the downstream exon (positions +6 to +10 relative to the junction). All reads from adipose and brain samples were mapped using ELAND to the genome and to either (i) the set of authentic splice junctions, or (ii) the set of "modified" splice junctions. Using authentic junctions, 1.4M adipose reads were mapped, and 600K brain reads were mapped; using "modified" junctions, 771 adipose reads were mapped, and 370 brain reads were mapped, yielding an overall FDR of 0.056%. When counting the number of junctions with two or more reads mapping to distinct positions, using authentic junctions yielded 38,265 adipose junctions and 54,602 brain junctions, while using "modified" junctions yielded 33 adipose reads and 11 brain junctions (for an estimated FDR < 0.047%). When counting the number of exons with both upstream and downstream junctions supported by two or more reads mapping to different positions, the authentic junctions yielded 46,581 exons (including 158 novel junctions) in adipose and brain combined, and "modified" junctions yielded 0 exons (FDR<0.002%).

Since it is possible that a number of misannotated or (incorrectly) predicted junctions in combination with real junctions may result in false discovery of novel exons, we considered addition of the “false” junctions identified for the “modified junctions” to the large set of real junctions in adipose and brain. Twenty-one additional exons were identified, out of which 2 were supported by GENSCAN and/or EXONIPHY predictions alone. Therefore, we infer a FDR for detection of novel exons of ~2/158, or ~1.3%.

Identification of tissue-regulated alternative transcript events

Eight different types of alternative mRNA processing events were analyzed: skipped exons (SE), retained introns (RI), alternative 3' splice sites (A3SS), alternative 5' splice sites (A5SS), mutually exclusive exons (MXE), alternative last exons (ALE), alternative first exons (AFE), and tandem 3' UTR events. The set of events evaluated for tissue-regulation was derived from a combination of EST evidence, UCSC known gene annotations, and a database of cleavage and polyadenylation sites constructed based on EST alignments in a manner similar to that used in PolyA_DB[5]. For each event, mRNA-Seq reads were categorized as “common”, “inclusion”, or “exclusion” reads, as illustrated in Fig. 2. To assess possible tissue-specific expression for each event, a Fisher’s exact test was performed to evaluate the significance of the 2x2 table in which reads were divided by: 1) tissue of origin (e.g., brain versus all others); and 2) read type (i.e. inclusion versus exclusion). Tissue-specific expression was assessed by comparing read data in each tissue sample to that in the other 14. The tissues/cell lines used in this analysis were adipose, brain, breast, cerebellum (Cerebellum #4), colon, heart, liver, lymph node, skeletal muscle, testes, BT474, HME, MB435, MCF7, and T47D. For this analysis, inclusion ratio was defined as the ratio of the number of inclusion reads to the sum of inclusion plus exclusion plus "common" reads, i.e. those in regions (generally in adjacent exons) corresponding to gray reads in Fig. 2, to increase power to detect tissue regulation. Those events which were significant at a

P-value cutoff corresponding to a false discovery rate cutoff of 5% (in the Benjamini-Hochberg sense), and which exhibited an inclusion ratio difference of at least 0.10 between at least one pair of tissues were considered tissue-regulated. For this analysis, a minimum of 20 inclusion, exclusion and common reads (in total) were required in each tissue for determination of an inclusion ratio. The latter criterion was imposed based on the observation that SE events with inclusion ratio difference at least 0.10 exhibited significantly increased sequence conservation in the vicinity of the regulated exon relative to control events whose inclusion ratios differed less. No such difference was observed at lower difference threshold (Fig. S4, see below), suggesting that an inclusion ratio difference of 0.10 may represent a minimum difference that is commonly associated with additional conserved biological function. While technical variation in sample preparation and sequencing may yield false positives, analysis of technical replicates of mouse liver and muscle sequence data[2] suggested a false positive rate of <2% in determination of differentially regulated alternative mRNA processing events.

Determination of minimum functional inclusion ratio difference

Phylogenetic conservation was examined for exons with different degrees of evidence for tissue-specific regulation. Defining ΔIR_{max} as the maximum difference in inclusion ratio between any pair of tissues (same set of tissues used in analysis shown in Fig. 2), phastCons scores were obtained for regions containing and flanking each skipped exon (the same regions used in motif analysis), using the UCSC 17-way alignments of 17 vertebrate genomes. Subsequently, all skipped exons were grouped into *n* bins based on ΔIR_{max} values divided evenly from 0 to 1. The CDF of phastCons scores for all skipped exons in each switch score bin was computed, and compared to the CDFs of phastCons scores in every other bin, using a two-tailed Kolmogorov-

Smirnov test. In order of ascending switch score, the first bin to contain significantly greater conservation than in the previous bin was used to define the ΔIR_{max} cutoff; that is, events designated as significantly tissue-regulated were required to pass not only the FDR <5% criterion imposed on the Fisher's exact test P-value, but also to exhibit a ΔIR_{max} value greater than or equal to the cutoff value of 0.1. For all events types, ΔIR_{max} values were computed using the same read count values used in the Fisher's exact test for tissue regulation. A summary of the method and results are shown in Fig. S4.

Assessment of power to detect tissue regulation

The ability to detect tissue-regulation of an alternative mRNA processing event depends fundamentally on read coverage, which is related to both the expression level of the transcript isoforms and the size of the variably included regions. The statistical power to detect a given degree of tissue-specific difference in inclusion level was assessed as a function of increasing transcript expression level by simulation for each of the 8 alternative processing events analyzed (Fig. S5). For each event, we first determined the median length of the regions used to determine tissue regulation (i.e. core region of A3SS and A5SS, core region of tandem 3' UTR, skipped exon and associated flanking exons, etc.). We used these values to specify the probability that a read for a given gene containing an alternative event would map to one of these regions. Then, given an underlying difference in inclusion ratio between two different tissues (we used 0.6 in tissue 1 versus 0.4 in tissue 2, based on typical inclusion ratio values observed across events), reads were randomly sampled at a level of read coverage corresponding to transcripts containing the event of interest. For each level of read coverage, we determined the fraction of events detected as tissue-regulated (at $P<0.001$), over many random sampling trials, which we define as the statistical power. In our simulation, the ability to detect tissue regulation in one sample relative to 13 other samples was considered, i.e. we used reads in 1 tissue as compared to the sum of reads in 13 other tissues, each with expression levels matching the first. For reference, the cumulative frequency of the number of reads per gene is shown for two representative tissues, skeletal muscle and liver, in Fig. S5b. From this plot, one can infer that essentially 100% of tandem 3' UTR events, ~95% of ALE events, ~45% of RI events, and so on can be detected for genes with coverage above the median, i.e. genes with > 100 reads per gene.

Estimation of true fraction of tissue-regulated alternative mRNA processing events

In a manner similar to the procedure used to estimate the extent of AS in human genes, events for each of the 8 alternative mRNA processing events were binned by read coverage (Fig. S6a). Here, instead of sorting by the number of reads which map to each gene, we sorted by the maximum number of reads available to detect tissue regulation across all tissues, i.e. the maximum power to detect tissue regulation. We found that this value is correlated with the power available to detect tissue bias, but possesses the additional advantage of being able to distinguish events with saturating power values, i.e. when power is close to 1.0. To estimate the true extent of tissue-regulated alternative splicing (essentially, the extent of tissue-regulated alternative splicing that would be observed given saturating coverage), a sigmoid curve of the form $F(x) = \frac{\alpha}{1+e^{-(x-a)*b}}$ was fitted to the fraction of tissue-biased events (*F(x)*) in each bin as a function of maximum read coverage per event across tissues (x), where α, the upper asymptote, represents the true extent of tissue-biased events (Fig. S6b). To obtain estimates robust to the size of each bin, α values were obtained for sigmoid curves fitted using different sized bins, from 10 to 50 total bins (Fig. S6a, bar plot).

Assessment of tissue-specific versus individual-specific differences in alternative isoform regulation

To assess the degree of similarity between different tissue/cell line samples, we performed pairwise comparisons between every sample pair, correlating the inclusion ratios of skipped exons for which sufficient read coverage (>=20 reads) was present in both samples, restricting analysis to the set of skipped exons determined to be tissue-regulated as shown in Fig. 2. Spearman correlation coefficients were computed for each pairwise comparison, and the resulting correlation matrix was clustered using average linkage hierarchical clustering to generate a dendrogram (MATLAB) as shown in Fig. 3.

To quantify the extent to which tissue regulation and inter-individual variation each contribute to differences in alternative isoform expression, analyses analogous to that performed for Fig. 2 were performed using only the 6 cerebellum samples, and 100 random subsets of 6 tissues (from adipose, brain, breast, colon, heart, liver, lymph node, skeletal muscle, and testes). Sigmoid fitting to estimate the true fraction of alternative isoform regulation was performed for the cerebellum samples and the 100 random subsets of tissues (Fig. S7).

Estimation of switch score for skipped exons, MXEs, and tandem 3' UTRs

The switch score was defined as the maximal difference in “Percent Spliced In” (PSI or Ψ) of an alternative region across all pairwise comparisons of tissues and cell lines. For skipped exons, Ψ was defined as (inclusion density / inclusion density + exclusion density), where inclusion density was computed as the density of reads mapping to the alternative exon and to both inclusion junctions (density = no. reads spanning inclusion junctions and alternative exon / total number of genomically unique positions in the region), and exclusion density was computed as the read density of the exclusion junction. For MXEs, inclusion density was defined as the read density of the first MXE and its supporting junctions; exclusion density was defined by the read density of the second MXE and its supporting junctions. For tandem 3' UTRs, the estimated inclusion level was computed using a Bayesian approach, which computes the expected density of the extension region, given a uniform prior on the relative fraction of transcripts terminating at each of the two alternative polyA sites, the observed read counts, and the number of uniquely mappable positions in the core and extension regions. Specifically, we computed the posterior probability of the ***Ψ*** as $p(\psi|N_e, d_c) = \frac{p(N_e|\psi, d_c)\cdot p(\psi)}{\int p(N_e|\psi, d_c)\cdot p(\psi = x)\cdot \partial x}$, where N_e = number extension reads, d_c = density of core region, and the prior $p(\Psi)$ is uniform on [0,1]. The number of extension reads was modeled as Poisson-distributed, where

$p(N_e|\psi, d_c) = \frac{e^{-L_e\cdot\psi\cdot d_c}\cdot(L_e\cdot\psi\cdot d_c)^{N_e}}{N_e!}$, in which L_e = length of the extension region.

Conservation analysis of switch events

PhastCons scores were downloaded from the UCSC Genome Browser for regions in and around all skipped exons and tandem 3' UTRs. In Figs. 4d and 5a, the per-position average phastCons score was plotted for skipped exons or tandem 3' UTRs grouped by switch score, showing means at all base pair positions and standard errors every 2 bp for skipped exons and every 5 bp for tandem 3' UTRs.

Identification of UGCAUG occurrences enriched near skipped exons

The total number of UGCAUG occurrences was counted in five different regions in and around SEs. These regions included the intronic region from +10 to +150 relative to the upstream 5' splice site, the intronic region from -150 to -30 relative to the upstream 3'SS, the skipped exon itself, the intronic region +10 to +150 downstream of the downstream 5'SS, and the intronic region -150 to -30 relative to the downstream 3'SS. A binomial test was performed to determine whether increased occurrences of the hexamer was associated with increased inclusion or exclusion of significantly tissue-regulated skipped exons in each tissue, where the number of UGCAUG occurrences was compared to the occurrence frequency of control 6-mers derived by permuting the bases of the UGCAUG 6-mer, requiring also that the number of CpG dinucleotides - 0 in this case - be preserved in the controls. This analysis was also performed to identify all non-CpG-containing 6-mers enriched in regions upstream and downstream of skipped exons exhibiting increased inclusion or exclusion in different tissues (Table S8).

Signal to Background (S:B) motif analysis

MAF alignment files for tandem 3' UTR extension regions and skipped exon regions were downloaded from the UCSC Genome Browser. The number of conserved (across the human, mouse, rat, and dog genomes) and total occurrences of each k-mer were counted. The number of conserved occurrences in each region was tested for significance using a binomial test, where controls were chosen by matching GC content and total number of occurrences (~40-80 control motifs per tested k-mer).

Singular value decomposition (SVD) analysis

RNA processing events for which there was sufficient read coverage in every sample (≥10 reads/event) were chosen for SVD analysis. A matrix of inclusion ratios was computed for each event type (tissues x events) and column means were subtracted. The first and second principal components were computed from the mean-centered matrices, as described[6] and the data were projected onto these axes for visualization (Fig. S8). For each event type, the pairwise Euclidean distances between tissues (as projected onto 2-dimensional principal component space) were computed between every pair of samples. This vector of pairwise distances was correlated with analogous vectors derived from the other event types to yield Spearman correlation coefficients. For analysis of gene expression, the procedure was identical, except that the analysis was restricted to the set of genes possessing non-zero read density in all tissues, and the log of the estimated expression was used as input, instead of the inclusion ratio value.

The consistent separation of cell lines from tissues on the basis of alternative splicing and gene expression seen in Fig. S8 might be attributable to the effects of cell culture conditions per se or to the effects of selection for high in vitro proliferation rate. Whatever its source, the existence of this difference strongly suggests that studies seeking to profile cancer-specific transcriptomes that make use of cell lines will need to contend with and control for a very strong cell line expression signature affecting both transcription and RNA processing in order to identify authentic cancer-specific differences.

References

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3. Burge, C. & Karlin, S. Prediction of complete gene structures in human genomic DNA. J Mol Biol 268, 78-94 (1997).
4. Siepel, A. & Haussler, D. Combining phylogenetic and hidden Markov models in biosequence analysis. J Comput Biol 11, 413-28 (2004).
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7. Yeo, G. & Burge, C. B. Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. J Comput Biol 11, 377-94 (2004).

Figure S1

a

Samples	No. Reads	Genomic Reads unique	Genomic Reads non-unique	Junction Reads unique
Adipose	27,752,231	17.6 M	4.8 M	1.4 M
Brain	17,246,957	11.0 M	3.2 M	0.6 M
Breast	16,120,746	10.6 M	2.9 M	0.8 M
Colon	28,435,996	17.7 M	5.5 M	1.3 M
Heart	20,169,301	11.3 M	5.1 M	0.7 M
Liver	18,517,121	11.5 M	3.6 M	1.0 M
Lymph node	27,492,254	15.8 M	6.6 M	1.4 M
Skeletal muscle	22,640,454	14.4 M	4.0 M	1.3 M
Testes	27,303,938	18.6 M	4.1 M	1.6 M
BT474	18,424,533	11.5 M	3.2 M	0.8 M
HME	19,657,452	12.4 M	3.7 M	1.2 M
MB435	18,610,758	12.5 M	3.2 M	1.1 M
MCF7	16,059,515	10.2 M	3.2 M	0.9 M
T47D	16,719,597	9.9 M	2.8 M	0.8 M
Cerebellum 1	12,890,252	6.6 M	1.6 M	0.4 M
Cerebellum 2	12,180,619	5.8 M	1.5 M	0.3 M
Cerebellum 3	25,402,905	16.4 M	3.7 M	1.0 M
Cerebellum 4	24,486,091	15.9 M	3.6 M	0.9 M
Cerebellum 5	24,347,196	17.5 M	3.5 M	1.0 M
Cerebellum 6	24,016,465	17.4 M	3.9 M	0.9 M
Brain (low cov.)	8,762,894	5.7 M	1.6 M	0.3 M
UHR (low cov.)	7,970,336	4.9 M	1.7 M	0.4 M
Total	435M	275 M	77 M	20 M
Fractions (%)	100%	60%	17 %	4%

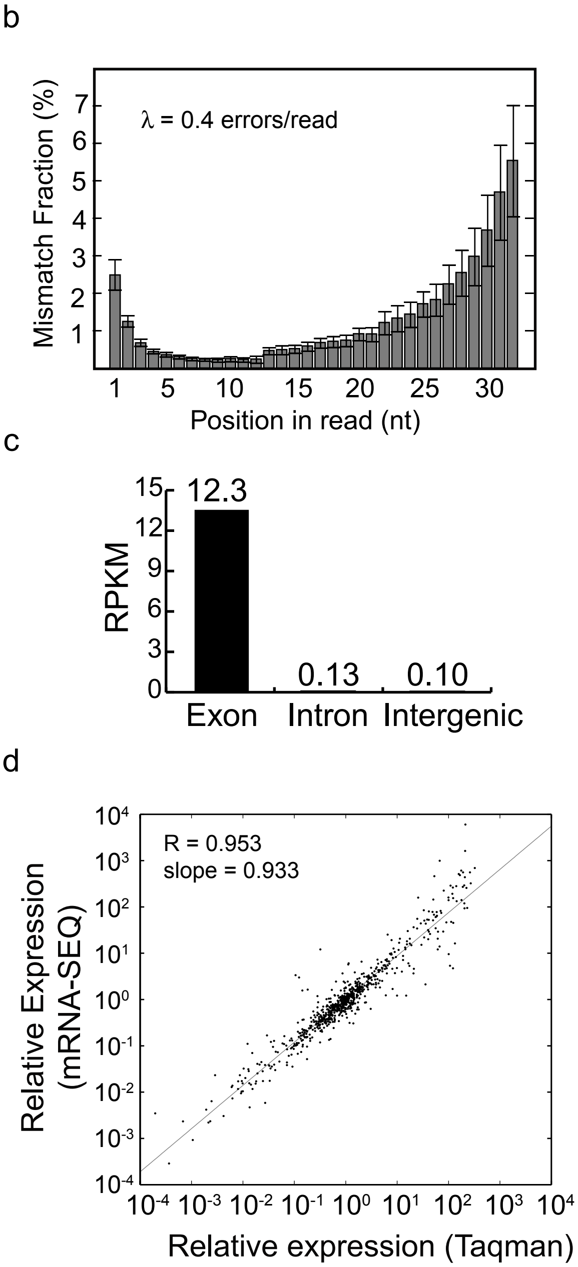
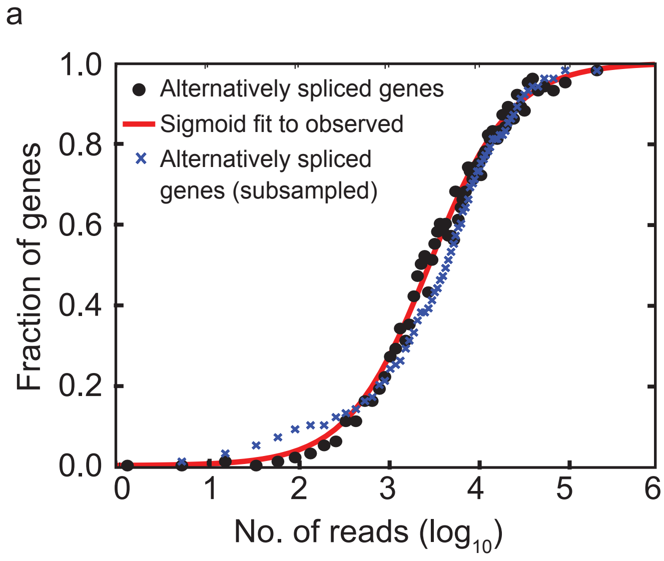


Figure S1. Mapping of Illumina reads to transcriptomes.

a, Summary of mRNA-SEQ read counts and mapping statistics. **b,** Mismatch frequency at each read position using all uniquely mapped reads from all tissues. The barplot displays the mean and standard deviation (across all tissues and cell lines) of the fraction of reads mismatched at each read position. **c,** RPKM of exons, introns, and intergenic regions. **d,** Scatter plot shows relative expression of 787 Refseq transcripts between brain and UHR samples as measured by Taqman Gene Expression Assays and by mRNA-SEQ read counts. Expression in the two samples was normalized to that of POLR2A, the control used in the Taqman assays. The Pearson correlation coefficient and slope of the best fit linear regression line are shown.

Figure S2



b

Bin size (genes/bin)	Fraction Alt. splicing (top bin)	Fraction Alt. splicing (estimated)
50	0.98	1.0
100	0.99	1.0
150	0.99	1.0
200	0.98	1.0
250	0.98	1.0
300	0.98	1.0
350	0.98	1.0
400	0.97	1.0
450	0.97	1.0
500	0.97	1.0
Mean:	0.98	1.0
Std:	0.01	0

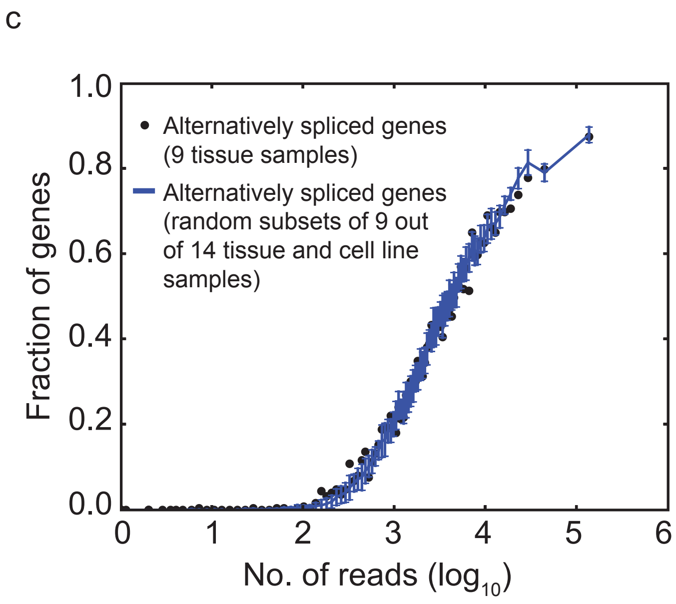
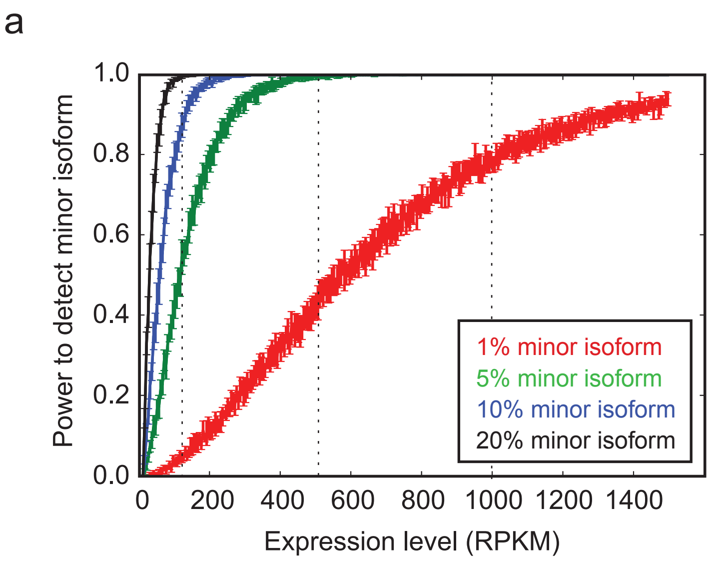


Figure S2. Assessment of frequency of alternative splicing in human genes. **a,** Fraction of alternatively spliced genes binned by read coverage using a bin size of 250 genes per bin. The upper asymptote of the sigmoid curve which best fits the observed data was used to infer the true fraction of alternative spliced genes (1.0 using bin size of 250). To assess whether high coverage genes exhibit a different fraction of alternative splicing, a subsampling approach was implemented (blue x's). **b,** Results from curve fitting using different sized bins. The fraction of alternatively spliced genes was estimated using bin sizes ranging from 50 to 500. The mean and standard deviation of results from each bin size are displayed. **c,** The fraction of alternatively spliced genes using only 9 tissue samples (black) or random subsets of 9 out of all 14 samples (blue). Mean and standard deviations after 100 randomizations are shown.

Figure S3



b

Minor isoform frequency	RPKM 100	RPKM 500	RPKM 1000
1%	0.04	0.42	0.78
5%	0.44	0.99	1.0
10%	0.79	1.0	1.0
20%	0.99	1.0	1.0

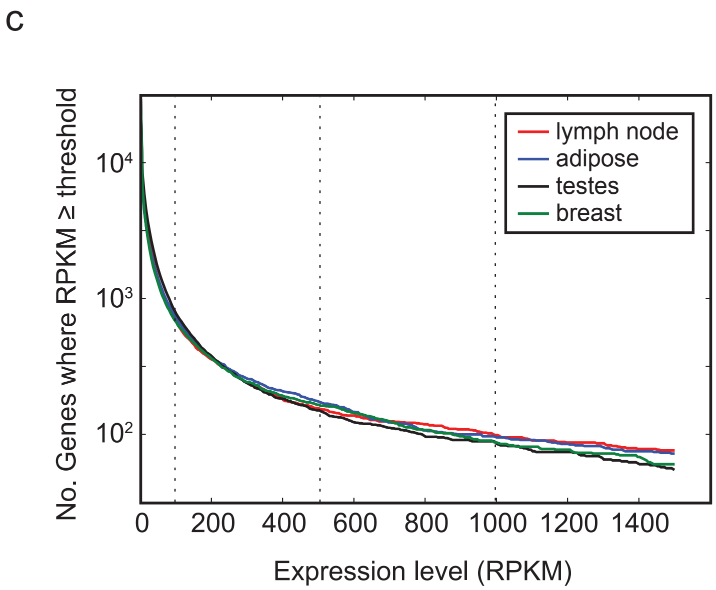


Figure S3. Power to detect minor isoforms.

a, Estimated statistical power to detect minor isoforms as a function of expression level (RPKM). A simulation was implemented to estimate the read coverage required to detect minor isoforms at various minor isoform frequencies. At least two reads mapping to at least two junction alignment positions were required for detection of both major and minor isoform junctions. The simulation was performed using minor isoform frequencies of 1%, 5%, 10%, and 20%, a sequence depth of 15M uniquely mapping reads, and an average number of 20 unique positions within splicing junctions. **b,** Estimated power to detect minor isoform of genes at varying expression levels and varying minor isoform frequencies. **c,** Number of genes expressed above different RPKM thresholds for lymph node, adipose, testes, and breast samples.

Figure S4

a

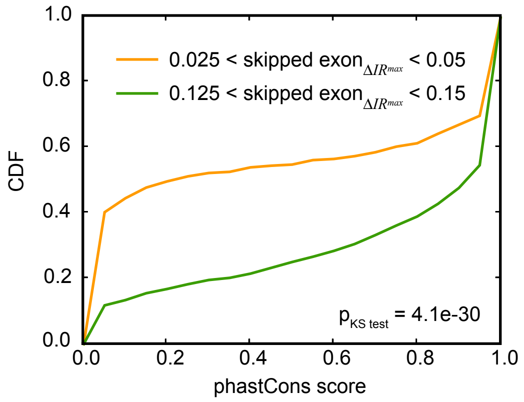
1) Skipped exons were divided into 40 ΔIR_{max} bins.

2) phastCons scores were obtained for regions surrounding skipped exons

3) For each region, pairwise comparisons were performed between the skipped exons in each ΔIR_{max} bin, measuring the difference in overall phastCons score by using a Kolmogorov-Smirnov test. P values for each KS test were recorded.

4) For each region, the pairwise comparisons between each ΔIR_{max} bin are illustrated as heatmaps, in which color represents an increase in conservation with higher ΔIR_{max} (red) or a decrease in conservation with higher ΔIR_{max} (blue), and intensity of color represents -log$_{10}$(p value).

b



Illustrated above is an example comparison between skipped exons found in the 0.025-0.05 ΔIR_{max} bin and skipped exons found in the 0.125-0.15 ΔIR_{max} bin. The cumulative distribution function of phastCons scores in the skipped exon region is plotted for each group of skipped exons. There is increased conservation in the skipped exons with higher ΔIR_{max} values, as indicated by the shift of the CDF to the right and the significant p value.

c

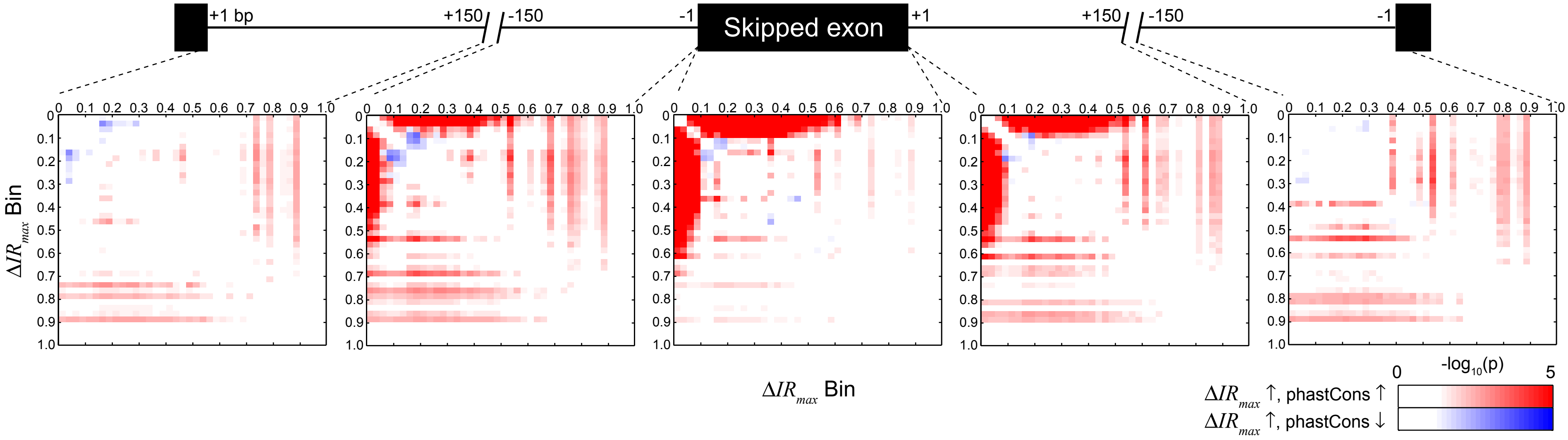


Figure S4. Determination of a threshold for change in inclusion ratio indicative of tissue-biased function.
a, Outlined is the procedure by which we determined the threshold for the change in inclusion ratio as indicative of function. Essentially, skipped exons were grouped by their maximum dynamic range in inclusion ratio (ΔIR_{max}), and queried for conservation in regions within and surrounding the skipped exons. **b,** A Kolmogorov Smirnov test was used to evaluate whether conservation of skipped exons in one ΔIR_{max} bin was significantly greater or less than conservation of skipped exons in another ΔIR_{max} bin. **c,** Results of the KS tests are displayed in the form of heat maps, where color denotes direction of the change (increased conservation = red, decreased = blue), and intensity of color denotes significance. Clearly visible is the increased conservation in events having ΔIR_{max} > 0.10 vs. events having ΔIR_{max} < 0.10, particularly in the intronic region directly upstream of the skipped exon, the intronic region directly downstream of the skipped exon, and in the exonic region of the skipped exon itself.

Figure S5

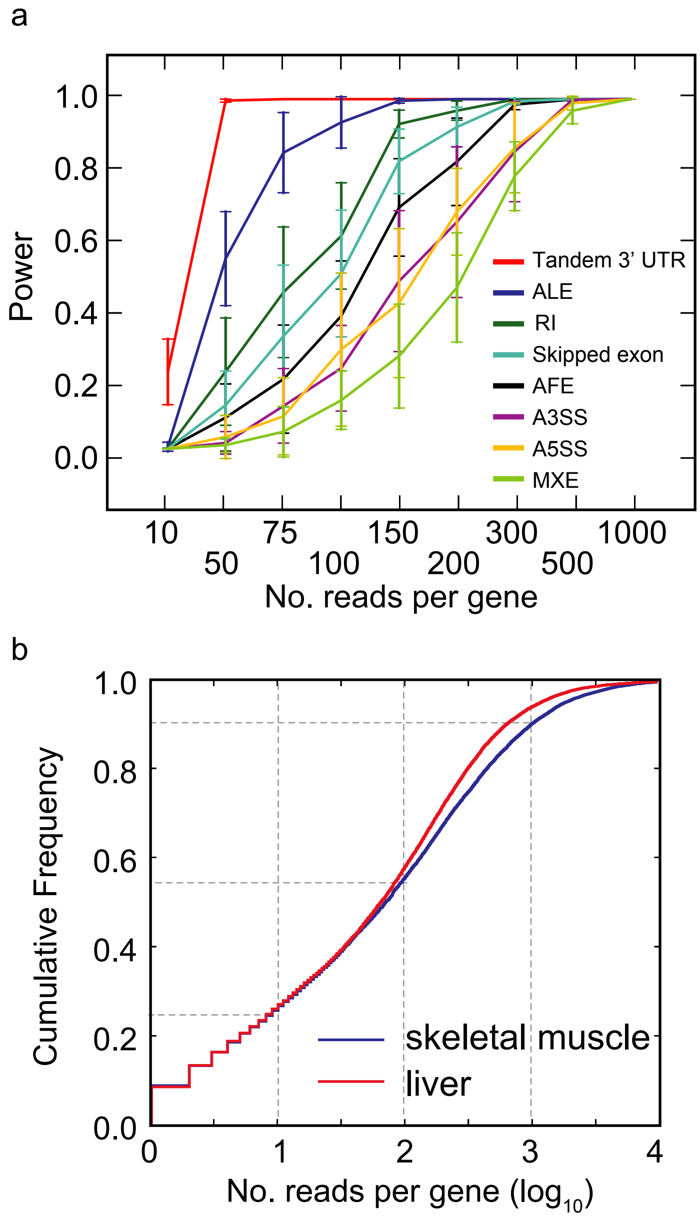


Figure S5. The power available to detect alternative mRNA processing.
a, Estimated statistical power to identify tissue-biased alternative events as a function of increased read coverage. **b,** Cumulative frequency of read coverage per gene locus in skeletal muscle and liver samples.

Figure S6

a

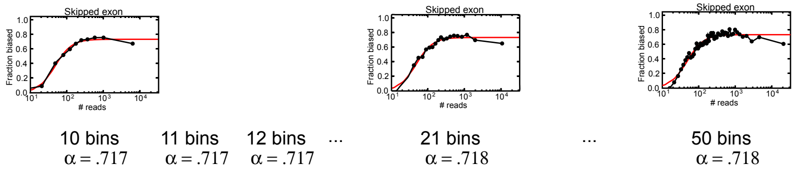
1) Events were binned by coverage, ie the maximum number of reads mapping to the event across tissues.

2) A sigmoid curve was fitted to the fraction of tissue-biased events in each bin using the function:

$$F(x) = \frac{\alpha}{1 + e^{-(x - a) * b}}$$

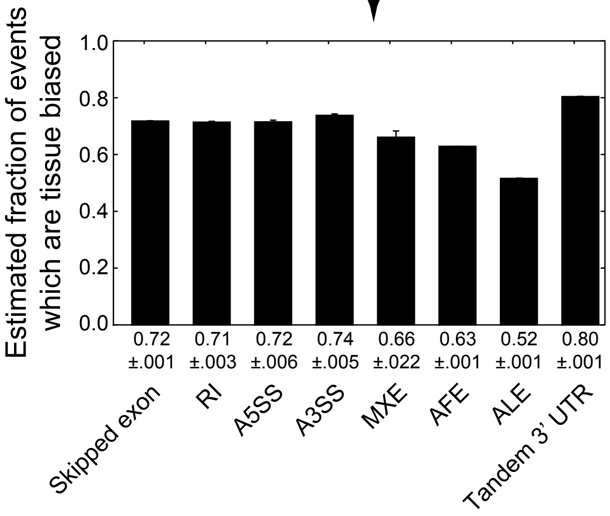
where F is the fraction of tissue-biased events, and α is the estimated "true" fraction of events which are tissue-biased.

3) The procedure was repeated such that a curve is fit for every bin size yielding 10, 11, 12 ... 50 total bins.



– Increasing # of bins (decreasing bin size) ⟶

4) The α values derived from all curve fittings across all bin sizes were averaged.



b

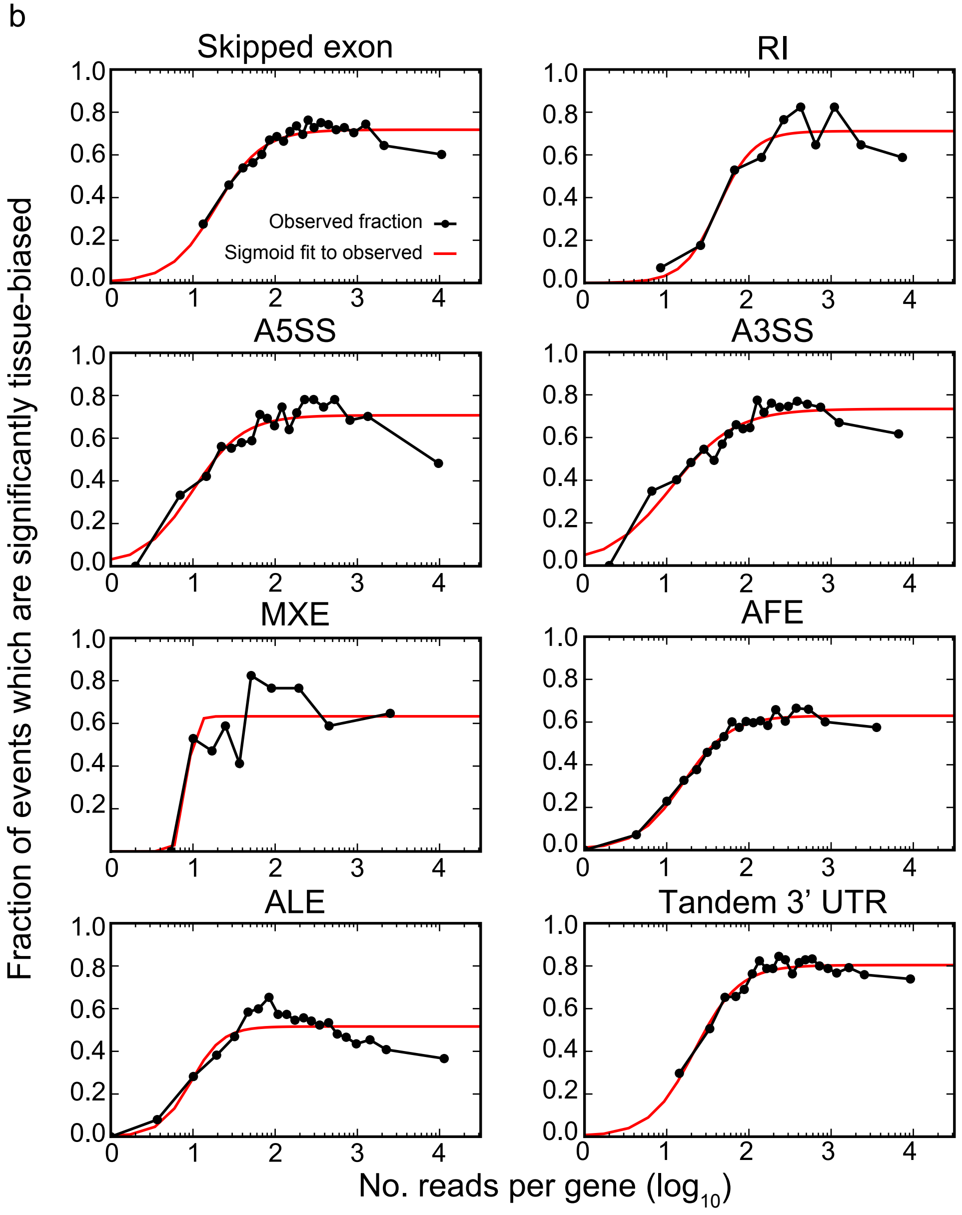


Figure S6. Estimation of the extent of tissue-bias in alternative transcript events.
a, The procedure for obtaining a robust estimate of the "true" fraction of tissue-biased events is outlined. The α values, or upper asymptotes of the sigmoid curves, are displayed in a boxplot, along with means and standard deviations across 41 independent bin sizes. **b,** Examples of the analysis described in (A). The fraction of events which are tissue-biased are plotted (black dots), along with their best fit sigmoid curves (red lines). Events are grouped by read coverage into approximately 20 bins for all event types, except for RIs and MXEs, in which events are grouped into 10 bins.

Figure S7

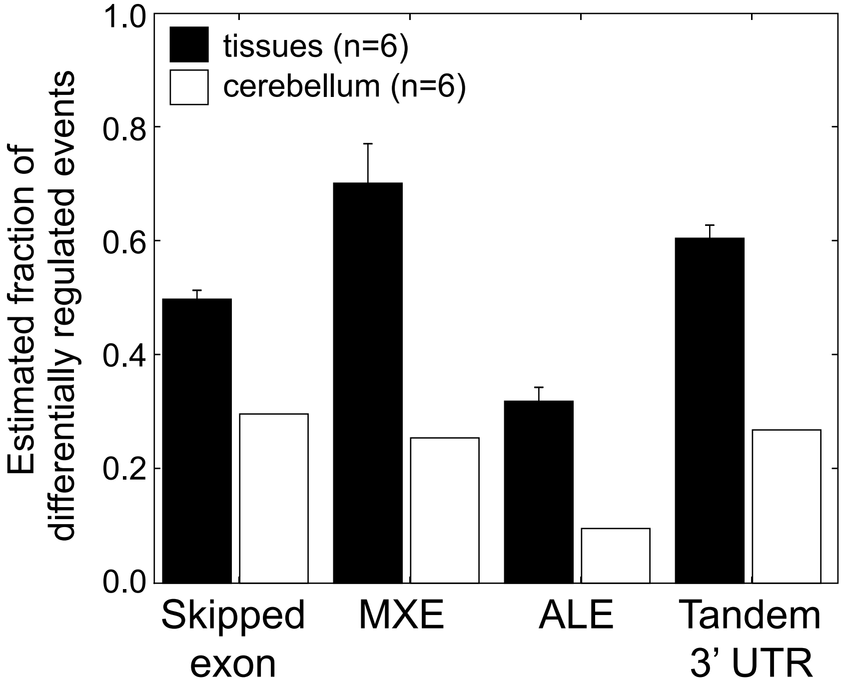
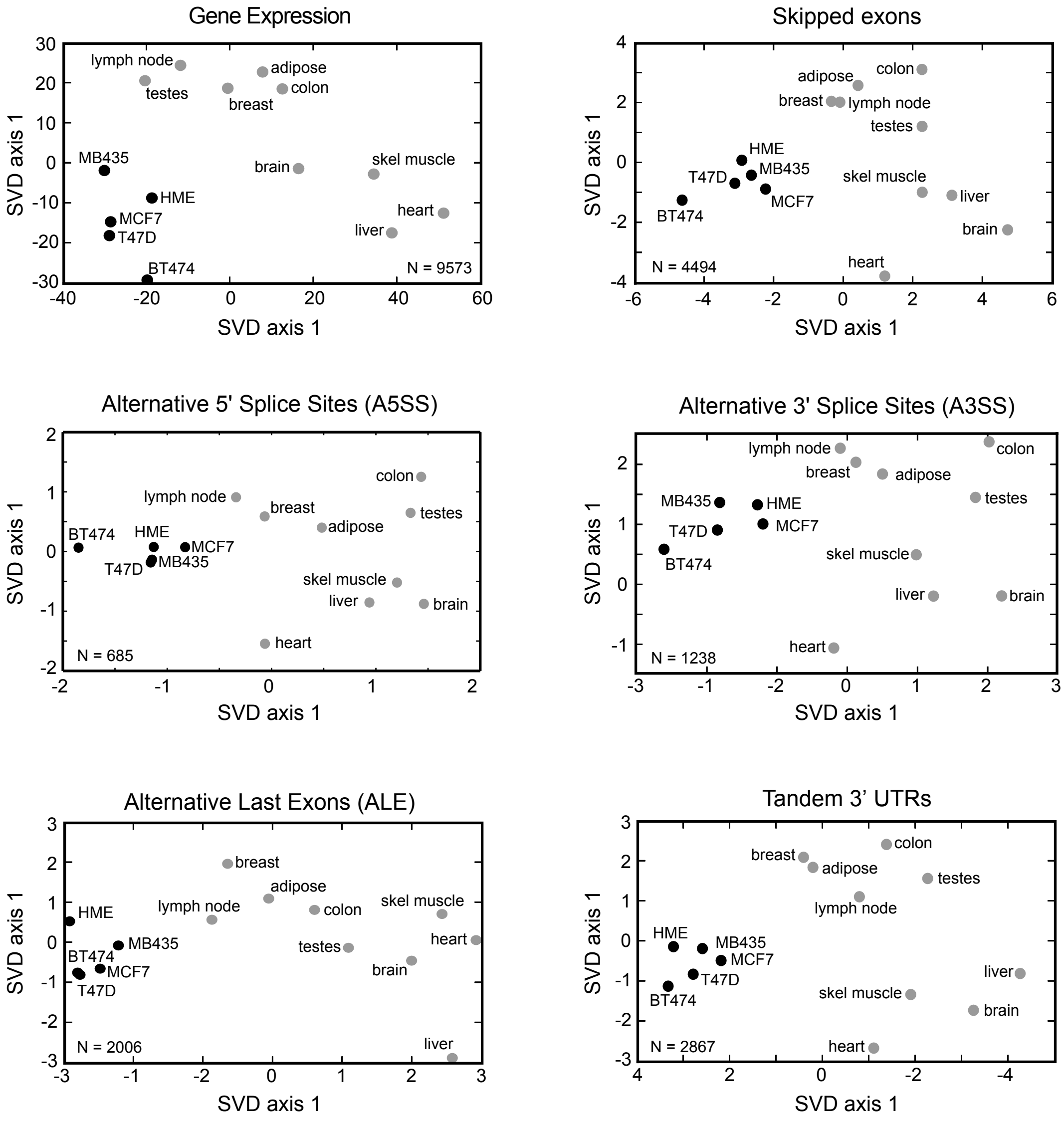


Figure S7. The extent of individual-specific differences in alternative isoform expression.

Differential expression of alternative transcript events among anatomically distinct tissues relative to cerebellar cortex samples from different individuals. The fractions of differentially regulated skipped exon, MXE, ALE, and Tandem 3' UTR events were estimated among 6 cerebellum samples (white bars), and compared to the fractions estimated using 6 randomly selected tissues (out of 10). The mean and standard deviation over 100 random trials are shown (black bars). The ratio of tissue-specific vs. individual-specific regulation was observed to be lower for event types not shown.

Figure S8


Gene Expression

Skipped exons

Alternative 5' Splice Sites (A5SS)

Alternative 3' Splice Sites (A3SS)

Alternative Last Exons (ALE)

Tandem 3' UTRs

Figure S8. SVD Analysis.

SVD analysis of vectors of inclusion ratios for five different mRNA processing events and vector of expression levels for gene expression across nine human tissues and five cell lines. Only events exhibiting sufficient read coverage across all tissues and cell lines were used in the analysis. Projections are shown in the dimensions corresponding to the two leading eigenvalues. Cell lines are displayed as black circles and tissue samples are gray.

Figure S9

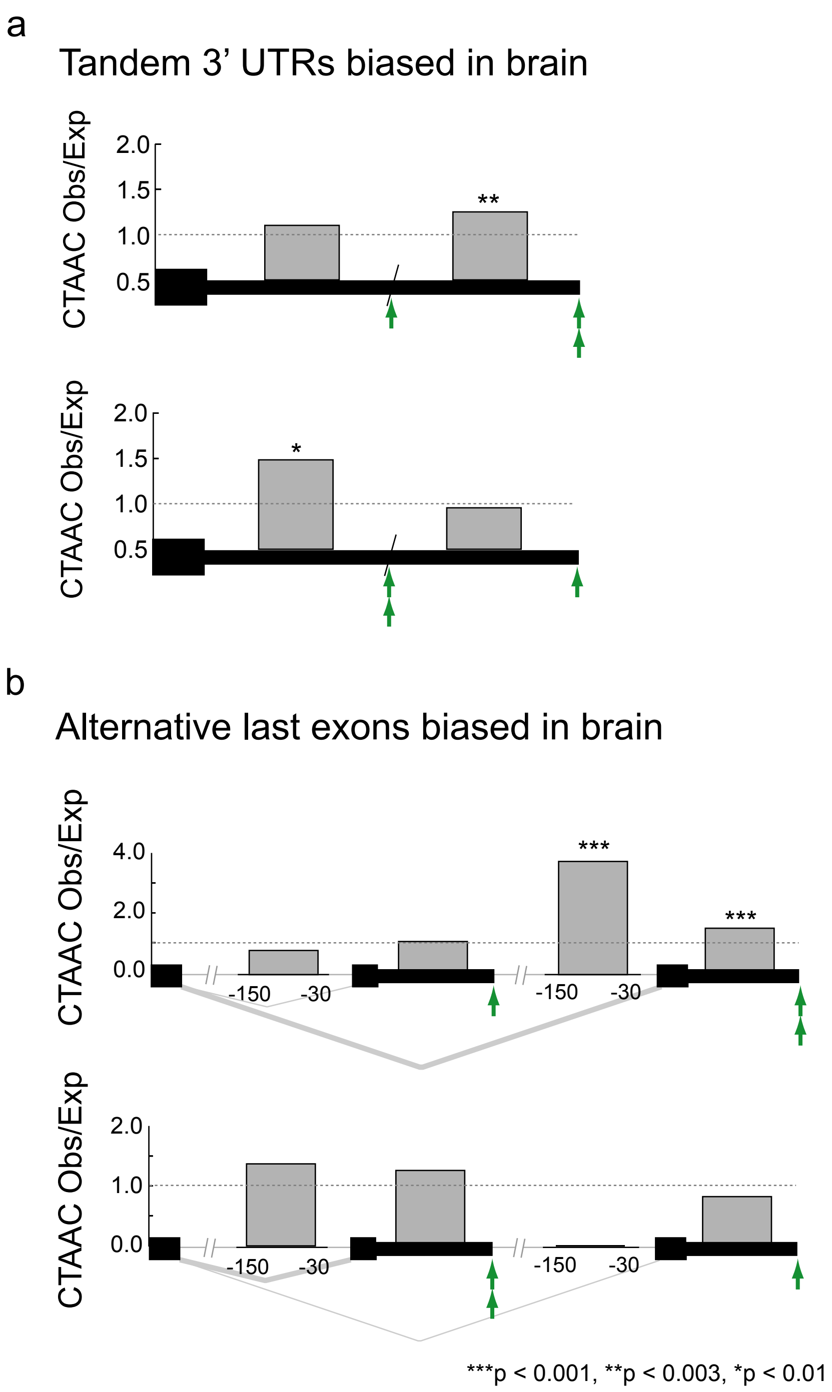


Figure S9. Enrichment of CTAAC motifs in 3' UTRs differentially processed in brain. **a,** Shown is the enrichment of CTAAC occurrences (observed/expected) relative to motif controls in the core and extension regions of tandem 3’ UTRs that are tissue-biased in brain. Double green arrows and a single green arrow denote the more commonly and less commonly used cleavage and polyadenylation site used in the set of UTRs analyzed, respectively. CTAAC is significantly enriched in the extension region of tandem 3‘ UTRs biased towards distal pA site usage in brain, and in the core region of tandem 3’ UTRs biased towards proximal pA site usage in brain. **b,** CTAAC is significantly enriched in the upstream intron and UTR region of alternative last exons biased towards distal pA usage in brain.

Table S1. Origin of tissue samples.

Tissue	Sex	Age (y)	Race
Adipose	Female	73	Caucasian
Brain	Male	23	Caucasian
Breast	Female	29	Caucasian
Colon	Female	68	Caucasian
Heart	Male	77	Caucasian
Liver	Male	37	Caucasian
Lymph node	Female	86	Caucasian
Skeletal muscle	Male	77	Caucasian
Testes	Male	19	Caucasian
Cerebellum 1	Male	48	Caucasian
Cerebellum 2	Male	50	Caucasian
Cerebellum 3	Male	33	African American
Cerebellum 4	Male	43	Caucasian
Cerebellum 5	Male	47	Caucasian
Cerebellum 6	Male	27	African

Table S2. Estimation of read mis-mapping frequency.[1]

General summary	**No. reads**	**% reads**
No. simulated reads generated	5057532	100.00%
No. of uniquely mapping simulated reads	4992854	98.72%
No. of non-uniquely mapping simulated reads	27694	0.55%
No. unmapped reads allowing for 2 mismatches	36984	0.73%

Statistics for unique mapping of simulated reads to genome or splice junctions allowing for 0, 1 or 2 mismatches	**No. of mismatches (simulated vs. reference)**			
	0	**1**	**2**	**Total**
Correct	3380064	1347875	260541	4988480
Incorrect	2788	1299	287	4374
% Correct	**99.92%**	**99.90%**	**99.89%**	**99.91%**
% Incorrect	**0.08%**	**0.10%**	**0.11%**	**0.09%**

Statistics for unique mapping of simulated reads to genome allowing for 0, 1 or 2 mismatches	**No. of mismatches (simulated vs. reference)**			
	0	**1**	**2**	**Total**
Correct	3145118	1255080	242746	4642944
Incorrect	2483	1151	259	3893
% Correct	**99.92%**	**99.91%**	**99.89%**	**99.92%**
% Incorrect	**0.08%**	**0.09%**	**0.11%**	**0.08%**

Statistics for unique mapping of simulated reads to splice junctions allowing for 0, 1 or 2 mismatches	**No. of mismatches (simulated vs. reference)**			
	0	**1**	**2**	**Total**
Correct	234946	92795	17795	345536
Incorrect	305	148	28	481
% Correct	**99.87%**	**99.84%**	**99.84%**	**99.86%**
% Incorrect	**0.13%**	**0.16%**	**0.16%**	**0.14%**

[1] Protocol described in Supplementary Information.

Table S3. High confidence novel exons identified using mRNA-SEQ[1]

Exon coordinates	No. reads in exon body	No. reads spanning upstream junction	No. reads spanning downstream junction	Relationship to annotated exons	Name of closest gene(s)	Gene description(s)
chr1:109040422-109040496	48	21	2	bounded	PRPF38B;RP11-293A10.1	Novel protein (FLJ10330).;PRP38 pre-mRNA processing factor 38 (yeast)
chr1:113038894-113039167	537	108	3	extending	MOV10	Mov10, Moloney leukemia virus 10, homolog (Mouse).;Mov10, Moloney leukemia viru
chr1:115071163-115071234	1324	13	332	bounded	CSDE1;KIAA0885	Homo sapiens mRNA for KIAA0885 protein, partial cds.;upstream of NRAS isoform 1;
chr1:11509353-11509479	20	3	15	bounded	RP1-69M21.1;KIAA1337	Novel protein (Fragment).;Homo sapiens mRNA for KIAA1337 protein, partial cds.
chr1:120079441-120079775	1729	389	2	extending	PHGDH	phosphoglycerate dehydrogenase
chr1:1229925-1230018	467	31	5	bounded	KIAA1716;CENTB5	CDNA FLJ36635 fis, clone TRACH2018835, moderately similar to Homo sapiens cen
chr1:1232269-1232399	777	6	4	extending	KIAA1716;CENTB5	CDNA FLJ36635 fis, clone TRACH2018835, moderately similar to Homo sapiens cen
chr1:1233012-1233060	102	89	3	bounded	KIAA1716;CENTB5	CDNA FLJ36635 fis, clone TRACH2018835, moderately similar to Homo sapiens cen
chr1:1280946-1280995	89	17	340	bounded	MXRA8	matrix-remodelling associated 8
chr1:1323858-1323914	269	6	35	bounded	CCNL2	cyclin L2 isoform A;cyclin L2 isoform B;Cyclin-L2 (Paneth cell-enhanced expression p
chr1:143592099-143592215	271	163	45	bounded	PDE4DIP;NBPF14;KIAA1245;I	hypothetical protein LOC400818;NBPF8 protein.;phosphodiesterase 4D interacting pr
chr1:149212733-149212785	1	2	2	isolated	LASS2	LAG1 longevity assurance homolog 2
chr1:149505408-149505522	647	62	3	bounded	PSMD4	proteasome 26S non-ATPase subunit 4 isoform 2;proteasome 26S non-ATPase subu
chr1:149522288-149522418	33	6	11	isolated	ZNF687	zinc finger protein 687
chr1:149666923-149667114	485	185	5	bounded	POGZ	pogo transposable element with ZNF domain
chr1:150134153-150134294	85	5	56	bounded	CTMP;THEM4	thioesterase superfamily member 4;Homo sapiens full length insert cDNA ZD26E01.
chr1:151926113-151926187	58	3	17	extending	NPR1	natriuretic peptide receptor A/guanylate cyclase
chr1:152494799-152494855	188	4	349	bounded	UBAP2L	ubiquitin associated protein 2-like
chr1:152500066-152500209	2195	23	144	bounded	UBAP2L	ubiquitin associated protein 2-like
chr1:153205262-153205319	40	708	24	bounded	SHC1	SHC (Src homology 2 domain containing)
chr1:153254266-153254914	3109	5	323	bounded	ZBTB7B	kruppel-related zinc finger protein hcKrox
chr1:153496952-153497008	381	167	4	bounded	SCAMP3	secretory carrier membrane protein 3 isoform 2;Homo sapiens secretory carrier mem
chr1:153520366-153520550	198	3	3	extending	HCN3	hyperpolarization activated cyclic
chr1:153559817-153560142	466	5	3	extending	RUSC1;C1orf104	RUN and SH3 domain containing 1.;hypothetical protein LOC284618
chr1:153559817-153560227	592	5	10	extending	RUSC1;C1orf104	RUN and SH3 domain containing 1.;hypothetical protein LOC284618
chr1:153974572-153974657	417	91	2	bounded	DAP3	death-associated protein 3
chr1:154116915-154117035	604	104	36	bounded	SYT11	synaptotagmin 12
chr1:154705196-154705254	253	131	6	bounded	MEF2D	MADS box transcription enhancer factor 2,
chr1:1552080-1552272	1446	549	12	extending	MIB2;DKFZp434A0311	mindbomb homolog 2;CDNA FLJ25919 fis, clone CBR04994.;Homo sapiens mRNA f
chr1:1554667-1554809	437	3	162	bounded	MIB2;DKFZp434A0311	Homo sapiens mRNA for skeletrophin, complete cds.;mindbomb homolog 2;CDNA FL
chr1:158330124-158330576	6422	58	8	bounded	IGSF8	immunoglobulin superfamily, member 8
chr1:158570013-158570093	140	3	242	extending	COPA	coatomer protein complex, subunit alpha
chr1:15924464-15924627	1058	2	285	bounded	PLEKHM2	Pleckstrin homology domain containing, family M (With RUN domain) member 2.
chr1:159274965-159275048	119	42	31	bounded	F11R;KAT	F11 receptor isoform a precursor;Putative thiosulfate sulfurtransferase KAT (EC 2.8.1
chr1:159400948-159401356	626	77	56	bounded	USP21	ubiquitin-specific protease 21
chr1:159412222-159412475	1288	88	2	bounded	PPOX;B4GALT3	Homo sapiens cDNA FLJ37536 fis, clone BRCAN2022472, highly similar to PROTOP
chr1:160099615-160099726	154	3	82	bounded	ATF6	activating transcription factor 6
chr1:166340339-166340748	396	13	2	bounded	GPR161	G protein-coupled receptor 161 isoform 1;G protein-coupled receptor 161 isoform 2
chr1:16689700-16690008	273	81	16	extending	KIAA1922	Homo sapiens mRNA for KIAA1922 protein, partial cds.
chr1:167363086-167363144	609	452	8	bounded	ATP1B1	Homo sapiens Na,K-ATPase beta 1 subunit mRNA, complete cds.;Na+/K+ -ATPase b
chr1:16824990-16825087	314	6	51	bounded	FLJ00313	Homo sapiens mRNA for FLJ00313 protein.
chr1:16827550-16827708	603	70	3	bounded	FLJ00313	Homo sapiens mRNA for FLJ00313 protein.
chr1:169825143-169825367	332	18	64	bounded	BAT2D1;KIAA1096	Homo sapiens mRNA for KIAA1096 protein, partial cds.;HBxAg transactivated protein
chr1:169825195-169825367	197	3	64	bounded	BAT2D1;KIAA1096	Homo sapiens mRNA for KIAA1096 protein, partial cds.;HBxAg transactivated protein
chr1:17818421-17818548	320	173	4	extending	ARHGEF10L	Rho guanine nucleotide exchange factor (GEF)
chr1:181468445-181468615	302	8	32	bounded	LAMC2	laminin, gamma 2 isoform b precursor;laminin, gamma 2 isoform a precursor
chr1:182946151-182946307	118	188	6	extending	EDEM3	ER degradation enhancer, mannosidase alpha-like
chr1:1844284-1844414	35	10	3	bounded	LOC339457	hypothetical protein LOC339457

chr1:1848906-1849045	51	3	22	bounded	LOC339457	hypothetical protein LOC339457
chr1:1850083-1850181	34	22	22	isolated	NA	NA
chr1:1863327-1863455	25	4	10	bounded	NA	NA
chr1:19078306-19078454	103	2	31	extending	ALDH4A1	aldehyde dehydrogenase 4A1 precursor
chr1:19344874-19345011	750	20	12	bounded	RP5-1126H10.1;ZUBR1	retinoblastoma-associated factor 600;Retinoblastoma-associated factor 600 (RBAF60
chr1:199594961-199595006	502	3	1127	bounded	TNNT2	troponin T type 2, cardiac isoform 1;troponin T type 2, cardiac isoform 3;troponin T typ
chr1:201002677-201002802	431	58	8	bounded	JARID1B	Jumonji, AT rich interactive domain 1B
chr1:201719129-201719908	15256	6	280	bounded	PRELP	proline arginine-rich end leucine-rich repeat
chr1:202085462-202085771	1529	247	5	bounded	ZC3H11A	zinc finger CCCH-type containing 11A
chr1:202478865-202479014	88	11	25	isolated	PLEKHA6	phosphoinositol 3-phosphate-binding protein-3
chr1:206129129-206129171	46	55	3	bounded	CD34	CD34 antigen isoform a;CD34 antigen.;CD34 antigen isoform b
chr1:207863473-207863968	1856	547	17	extending	LAMB3	laminin subunit beta 3 precursor
chr1:20836922-20837043	5731	447	4	bounded	PINK1	PTEN induced putative kinase 1 precursor
chr1:20848119-20848311	1718	10	213	bounded	PINK1	PTEN induced putative kinase 1 precursor
chr1:21419039-21419211	1809	3	773	bounded	ECE1	endothelin converting enzyme 1
chr1:21809200-21809349	580	42	4	bounded	RAP1GAP	RAP1, GTPase activating protein 1
chr1:219978899-219979716	650	19	2	bounded	DUSP10	dual specificity phosphatase 10 isoform b;dual specificity phosphatase 10 isoform a
chr1:22022696-22022762	649	397	6	bounded	LDLRAD2;HSPG2	heparan sulfate proteoglycan 2;Homo sapiens mRNA for Basement membrane-specif
chr1:22023386-22023444	2091	1015	10	bounded	LDLRAD2;HSPG2	heparan sulfate proteoglycan 2;Homo sapiens mRNA for Basement membrane-specif
chr1:22035882-22036050	734	333	3	bounded	HSPG2	heparan sulfate proteoglycan 2
chr1:22043228-22043373	130	25	8	bounded	HSPG2	heparan sulfate proteoglycan 2
chr1:226351915-226351973	3911	2105	11	bounded	ARF1	ADP-ribosylation factor 1;Homo sapiens clone 24537 ADP-ribosylation factor 1 mRNA
chr1:226526249-226526545	647	8	13	extending	OBSCN	obscurin, cytoskeletal calmodulin and
chr1:226559447-226559710	1886	135	77	extending	OBSCN	obscurin, cytoskeletal calmodulin and
chr1:226572219-226572497	1272	64	60	bounded	OBSCN	obscurin, cytoskeletal calmodulin and
chr1:226591328-226591707	1882	26	69	extending	OBSCN;KIAA1639	Homo sapiens mRNA for KIAA1639 protein, partial cds.;obscurin, cytoskeletal calmod
chr1:2306242-2306364	310	7	82	extending	MORN1	MORN repeat containing 1
chr1:232650849-232650945	42	85	3	bounded	TARBP1	TAR RNA binding protein 1
chr1:23632505-23632773	403	60	135	extending	DDEFL1;UPLC1	development and differentiation enhancing;Homo sapiens UPLC1 mRNA for up-regul
chr1:239730360-239730455	584	710	3	bounded	FH	fumarate hydratase precursor
chr1:239734019-239734168	194	5	94	bounded	FH	fumarate hydratase precursor
chr1:241415704-241416347	245	24	22	extending	CEP170	centrosomal protein 170kDa isoform gamma;centrosomal protein 170kDa isoform bet
chr1:243085349-243085505	5437	1542	15	bounded	HNRPU;SAF-A	Homo sapiens scaffold attachment factor A (SAF-A) mRNA, complete cds.;heterogen
chr1:243093542-243093923	23169	324	7	bounded	HNRPU	heterogeneous nuclear ribonucleoprotein U
chr1:243093599-243093716	3189	645	64	bounded	HNRPU	heterogeneous nuclear ribonucleoprotein U
chr1:2527532-2527665	32	4	29	extending	MMEL1	membrane metallo-endopeptidase-like 1
chr1:25431182-25431229	154	376	12	bounded	SYF2	SYF2 protein (Fragment).;SYF2 homolog, RNA splicing factor isoform 1;SYF2 homolo
chr1:27141991-27142143	4703	6	1227	bounded	NUDC	nuclear distribution gene C homolog
chr1:27193543-27193690	331	5	65	bounded	LOC388610	hypothetical protein LOC388610
chr1:27505264-27505440	2173	206	2	bounded	KIAA1037;WDTC1	Homo sapiens mRNA for KIAA1037 protein, partial cds.;WD and tetratricopeptide rep
chr1:27548736-27548843	862	2	88	bounded	SYTL1	Synaptotagmin-like 1.;synaptotagmin-like 1
chr1:27746402-27749857	17233	3	5	bounded	AHDC1	AT hook, DNA binding motif, containing 1
chr1:31674385-31674502	1365	2	799	extending	SERINC2	tumor differentially expressed 2-like
chr1:31678483-31678619	1185	2	209	bounded	SERINC2	tumor differentially expressed 2-like
chr1:32599918-32600000	310	108	9	bounded	BC111382	Homo sapiens cDNA FLJ36415 fis, clone THYMU2010917.
chr1:3501544-3501871	10	7	5	extending	MEGF6	EGF-like-domain, multiple 3
chr1:35713033-35713094	166	4	73	bounded	KIAA0319L	polycystic kidney disease 1-like isoform a;polycystic kidney disease 1-like isoform b
chr1:35797265-35797435	1886	53	287	extending	NCDN	neurochondrin isoform 2;neurochondrin isoform 1
chr1:36409159-36409226	1554	574	160	bounded	MAP7D1	arginine/proline rich coiled-coil 1
chr1:36409230-36409503	4088	163	132	bounded	MAP7D1	arginine/proline rich coiled-coil 1
chr1:36544786-36544943	48	15	7	bounded	NA	NA
chr1:3799307-3799413	407	75	2	bounded	C1orf174	hypothetical protein LOC339448
chr1:38046051-38046281	658	23	10	bounded	RP11-109P14.5;YRDC;C1orf1	ischemia/reperfusion inducible protein;Novel protein.;Homo sapiens cDNA FLJ45459
chr1:40652424-40652499	202	3	77	bounded	SMAP1L	stromal membrane-associated protein 1-like

chr1:41751872-41752008	180	8	51	bounded	KIAA1555;HIVEP3	Homo sapiens mRNA for KIAA1555 protein, partial cds.;human immunodeficiency viru
chr1:43664626-43664796	122	7	14	extending	C1orf84;KIAA0467	RP11-506B15.1 protein isoform 1;hypothetical protein LOC23334
chr1:43841875-43842447	5868	6	116	bounded	PTPRF	protein tyrosine phosphatase, receptor type, F
chr1:44882957-44883079	1038	527	2	extending	RP4-678E16.2;C1orf164	CDNA FLJ10597 fis, clone NT2RP2004802.;Novel DUF829 domain-containing protei
chr1:45579332-45579602	214	46	77	extending	TOE1	target of EGR1, member 1 (nuclear);Homo sapiens cDNA FLJ13949 fis, clone Y79AA
chr1:46906316-46906371	135	206	2	bounded	ATPAF1	ATP synthase mitochondrial F1 complex assembly
chr1:53514952-53515162	50	7	32	bounded	LRP8	low density lipoprotein receptor-related protein
chr1:54481496-54481584	177	21	31	extending	SSBP3	single stranded DNA binding protein 3 isoform c;single stranded DNA binding protein
chr1:55416228-55416390	101	6	4	bounded	NA	NA
chr1:555637-555812	2915	252	1562	isolated	NA	NA
chr1:57144928-57145041	142	39	2	bounded	C8A	complement component 8, alpha polypeptide
chr1:61642364-61642527	339	90	4	bounded	KIAA1439;NFIA	nuclear factor I/A;Homo sapiens mRNA for KIAA1439 protein, partial cds.;Nuclear fac
chr1:6437081-6438442	88	7	2	isolated	ESPN	espin
chr1:6444641-6444740	898	252	6	bounded	DR3;TNFRSF25	Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.;tumor necrosis fact
chr1:6448716-6448816	305	28	8	bounded	DR3;TNFRSF25;PLEKHG5	pleckstrin homology domain containing family G;Homo sapiens death receptor 3 beta
chr1:6451689-6451739	595	350	31	bounded	KIAA0720;PLEKHG5	pleckstrin homology domain containing family G;Homo sapiens mRNA for KIAA0720
chr1:6454372-6454455	357	3	301	extending	PLEKHG5	pleckstrin homology domain containing family G
chr1:78041550-78041679	15	12	4	bounded	FAM73A;DKFZp686K12247	Hypothetical protein DKFZp686K12247 (Fragment).;hypothetical protein LOC374986
chr1:78111284-78111393	55	2	8	bounded	FAM73A	hypothetical protein LOC374986
chr1:89022910-89023047	98	14	2	bounded	PKN2	protein kinase N2
chr1:89207680-89207735	38	56	2	bounded	KAT3;CCBL2	KAT3 protein.;kynurenine aminotransferase III isoform 2;kynurenine aminotransferase
chr1:93830410-93830529	529	45	7	bounded	BC084562;BCAR3	Homo sapiens cDNA clone IMAGE:6285657.;breast cancer antiestrogen resistance 3
chr1:9718019-9718260	9387	5	536	extending	CLSTN1	calsyntenin 1 isoform 1;calsyntenin 1 isoform 2
chr10:101118365-101118427	5	8	3	isolated	CNNM1	cyclin M1
chr10:101284732-101285216	222	5	13	bounded	NKX2-3	NK2 transcription factor related, locus 3
chr10:105199134-105199760	2283	116	6	bounded	FAM26B	Protein FAM26B.;hypothetical protein LOC51063
chr10:105782986-105783118	3258	487	4	bounded	COL17A1	alpha 1 type XVII collagen
chr10:105783693-105784029	6187	1182	4	bounded	COL17A1	alpha 1 type XVII collagen
chr10:112530549-112531632	540	15	6	extending	NA	NA
chr10:112533114-112533175	4	6	3	extending	NA	NA
chr10:112571023-112571683	610	28	14	extending	BX648563	Homo sapiens mRNA; cDNA DKFZp313A2231 (from clone DKFZp313A2231).
chr10:120799303-120799557	5751	804	5	extending	EIF3S10	eukaryotic translation initiation factor 3,
chr10:120907373-120907564	123	15	40	extending	SFXN4	sideroflexin 4 isoform 3;sideroflexin 4 isoform 2;Sideroflexin-4 (Breast cancer resistan
chr10:134580043-134580176	23	7	3	isolated	NA	NA
chr10:15175320-15175499	10	104	5	isolated	NA	NA
chr10:27539749-27539868	1298	167	2	bounded	DKFZp434A2417;ACBD5	Acyl-Coenzyme A binding domain containing 5.;acyl-Coenzyme A binding domain con
chr10:29836672-29836749	17	5	38	isolated	SVIL	supervillin isoform 2;supervillin isoform 1
chr10:29851345-29851564	2711	174	5	bounded	SVIL	supervillin isoform 2;supervillin isoform 1
chr10:44792846-44792897	1009	5	8	bounded	C10orf10;RASSF4;DKFZp667	Ras association domain family 4;Ras association domain family 4 isoform a variant (F
chr10:5975946-5976021	33	15	3	bounded	FBXO18	F-box only protein, helicase, 18 isoform 2
chr10:60682565-60682761	99	4	4	bounded	FAM13C1	hypothetical protein LOC220965 isoform 2;hypothetical protein LOC220965 isoform 1
chr10:61481239-61481325	25	8	7	isolated	ANK3	ankyrin 3 isoform 1;ankyrin 3 isoform 2
chr10:61489104-61489770	984	161	17	extending	ANK3	ankyrin 3 isoform 1;ankyrin 3 isoform 2
chr10:73248380-73248477	5405	2045	27	bounded	PSAP	prosaposin isoform a preproprotein
chr10:73249228-73249365	6318	529	9	bounded	PSAP	prosaposin isoform a preproprotein
chr10:75193697-75193747	24	7	31	bounded	SEC24C	SEC24-related protein C
chr10:86249611-86249743	69	8	5	extending	KIAA1128	granule cell antiserum positive 14;Homo sapiens mRNA for KIAA1128 protein, partial
chr10:87362793-87362883	10	2	7	bounded	GRID1	glutamate receptor, ionotropic, delta 1
chr10:88720714-88720998	140	4	3	bounded	KIAA1975	KIAA1975 protein (Fragment).
chr10:89564175-89564336	631	42	3	bounded	ATAD1	ATPase family, AAA domain containing 1
chr10:95122677-95122826	859	54	3	bounded	FER1L3	myoferlin isoform b;myoferlin isoform a
chr10:97040567-97040669	773	333	11	bounded	CLP-36;PDLIM1	Homo sapiens mRNA for CLP-36 protein.;PDZ and LIM domain 1 (elfin)
chr10:97071710-97071900	536	102	38	extending	SORBS1;KIAA1296	Homo sapiens mRNA for KIAA1296 protein, partial cds.;sorbin and SH3 domain conta
chr10:97105374-97106852	390	5	4	bounded	SORBS1;KIAA1296	Homo sapiens mRNA for KIAA1296 protein, partial cds.;sorbin and SH3 domain conta

chr10:97240789-97240867	477	6	131	bounded	SORBS1	sorbin and SH3 domain containing 1 isoform 2;sorbin and SH3 domain containing 1 is
chr10:97363489-97363908	1585	113	71	extending	ALDH18A1	pyrroline-5-carboxylate synthetase isoform 1;pyrroline-5-carboxylate synthetase isofor
chr11:1005762-1008770	19533	6	19	extending	MUC6	Homo sapiens mucin glycoprotein (MUC6) mRNA, partial cds.;Homo sapiens cDNA F
chr11:1015805-1016141	63	9	6	extending	MUC6	Homo sapiens mucin glycoprotein (MUC6) mRNA, partial cds.
chr11:10786972-10787061	3972	16	7	bounded	EIF4G2	eukaryotic translation initiation factor 4
chr11:113183883-113184068	85	5	49	extending	KIAA1515;USP28	ubiquitin specific protease 28;Homo sapiens mRNA for KIAA1515 protein, partial cds.
chr11:116206743-116206822	626	3	206	bounded	APOC3	apolipoprotein C-III precursor
chr11:116411822-116411940	101	5	5	isolated	KIAA0999	KIAA0999 protein.;KIAA0999 protein
chr11:118275836-118276015	2195	217	6	bounded	BCL9L	B-cell CLL/lymphoma 9-like
chr11:118476550-118476747	472	46	4	bounded	DPAGT1	UDP-N-acetylglucosamine-dolichyl-phosphate;Homo sapiens cDNA FLJ37803 fis, clo
chr11:118569686-118569805	36	18	12	bounded	LOC283152	hypothetical protein LOC283152;Homo sapiens hypothetical protein LOC283152, mR
chr11:11986547-11986731	2761	4	143	bounded	DKK3;dickkopf-3	dickkopf homolog 3 precursor;Homo sapiens dickkopf-3 mRNA, complete cds.
chr11:120538009-120538289	20	6	3	bounded	TECTA	tectorin alpha precursor
chr11:122434550-122434738	6728	2299	5	bounded	HSPA8	heat shock 70kDa protein 8 isoform 1;heat shock 70kDa protein 8 isoform 2
chr11:124050353-124050524	2036	3	126	bounded	SPA17	sperm autoantigenic protein 17
chr11:124297695-124297924	273	10	76	extending	HEPACAM;DKFZp547O159	hepatocyte cell adhesion molecule;CDNA FLJ16002 fis, clone BRAWH2007658, wea
chr11:124452336-124452634	32	10	3	extending	SLC37A2	solute carrier family 37 (glycerol-3-phosphate
chr11:129564844-129565005	591	38	2	extending	ST14	suppression of tumorigenicity 14
chr11:1416112-1416201	200	49	8	extending	PEN11B;BRSK2	Homo sapiens PEN11B mRNA, complete cds.;BR serine/threonine kinase 2;BR serin
chr11:1735130-1735302	56520	1435	21	bounded	HCCA2;CTSD	HCCA2 protein;cathepsin D preproprotein
chr11:17406412-17406594	240	68	3	extending	ABCC8	ATP-binding cassette, sub-family C, member 8
chr11:17749788-17750721	4012	70	206	bounded	KCNC1	Shaw-related voltage-gated potassium channel
chr11:17757579-17757767	1004	206	92	bounded	AK123157	Homo sapiens cDNA FLJ41162 fis, clone BRACE2039600, highly similar to VOLTAG
chr11:310565-310772	17463	10	2	bounded	IFITM3;BC040735	Homo sapiens cDNA clone IMAGE:5200448, partial cds.;interferon-induced transme
chr11:31788952-31789106	281	14	5	bounded	PAX6	paired box gene 6 isoform b;paired box gene 6 isoform a
chr11:33235844-33236011	619	2	111	bounded	HIPK3	homeodomain interacting protein kinase 3 isoform
chr11:3749581-3749734	235	4	46	bounded	NUP98	nucleoporin 98kD isoform 4;nucleoporin 98kD isoform 1;nucleoporin 98kD isoform 3;n
chr11:45202344-45202970	89	7	4	bounded	PRDM11	PR domain containing 11
chr11:45892258-45892595	1020	214	293	extending	PEX16	peroxisomal biogenesis factor 16 isoform 1;peroxisomal biogenesis factor 16 isoform
chr11:45895534-45895620	16	7	49	extending	PEX16	peroxisomal biogenesis factor 16 isoform 1;peroxisomal biogenesis factor 16 isoform
chr11:46345778-46345990	137	546	5	bounded	DGKZ	Homo sapiens mRNA for diacylglycerol kinase, zeta 104kDa isoform 3 variant protein.
chr11:47262502-47262566	938	261	45	bounded	MADD	MAP-kinase activating death domain-containing
chr11:47262573-47262692	2706	6	219	bounded	MADD	MAP-kinase activating death domain-containing
chr11:5210770-5210898	39	6	4	bounded	HBD	delta globin
chr11:547884-548054	308	6	3	bounded	C11orf35;AX748330	Homo sapiens cDNA FLJ36520 fis, clone TRACH2002100.;hypothetical protein LOC2
chr11:56833975-56834606	7850	7	56	bounded	TNKS1BP1	tankyrase 1-binding protein 1
chr11:57130537-57130596	424	3	113	bounded	SERPING1	complement component 1 inhibitor precursor;Serine/cysteine proteinase inhibitor clad
chr11:57265903-57266002	513	5	169	bounded	C11orf31;CTNND1	catenin (cadherin-associated protein), delta 1;selenoprotein H
chr11:59139352-59139520	1058	247	4	bounded	OSBP	oxysterol binding protein
chr11:59319651-59319761	115	10	3	isolated	STX3	syntaxin 3A
chr11:60425547-60425581	194	577	17	bounded	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19
chr11:61066259-61066627	216	42	37	extending	Y19237;SYT7	Homo sapiens partial mRNA for synaptotagmin 7 (SYT7 gene), exons 3d, 3e and 4.;s
chr11:61486303-61487197	698	12	3	bounded	BEST1	Bestrophin-1 (Vitelliform macular dystrophy protein 2) (TU15B).;bestrophin
chr11:61669677-61669776	448	86	3	bounded	INCENP	inner centromere protein antigens 135/155kDa
chr11:61670706-61670825	838	289	3	bounded	INCENP	inner centromere protein antigens 135/155kDa
chr11:62042577-62044481	29719	2	37	bounded	AHNAK	AHNAK nucleoprotein isoform 1;AHNAK nucleoprotein isoform 2
chr11:62095847-62095949	8	77	13	bounded	EEF1G	eukaryotic translation elongation factor 1
chr11:62099178-62100292	4715	16	80	bounded	TUT1;FLJ00132	Homo sapiens cDNA: FLJ22267 fis, clone HRC03120.;RNA binding motif protein 21
chr11:62100034-62100292	322	66	80	bounded	TUT1;FLJ00132	Homo sapiens cDNA: FLJ22267 fis, clone HRC03120.;RNA binding motif protein 21
chr11:62102609-62102955	2045	291	4	bounded	TUT1	RNA binding motif protein 21
chr11:62118564-62118674	521	380	8	bounded	MTA2	metastasis-associated protein 2
chr11:62163675-62163747	2264	938	18	bounded	GANAB	alpha glucosidase II alpha subunit isoform 2;Neutral alpha-glucosidase AB precursor (
chr11:62250667-62251243	19426	2929	5	bounded	HNRPUL2	heterogeneous nuclear ribonucleoprotein U-like

chr11:63289855-63290352	1052	38	21	extending	AB231751	Homo sapiens mRNA for hypothetical protein, partial sequence, clone:Hsa11-digit25-
chr11:63438309-63438381	138	116	2	extending	RCOR2	REST corepressor 2
chr11:63761575-63761703	1451	6	245	bounded	VEGFB	vascular endothelial growth factor B;Vascular endothelial growth factor B precursor (V
chr11:6378795-6378866	549	554	5	bounded	APBB1	amyloid beta A4 precursor protein-binding,;Homo sapiens adaptor protein FE65a2 (A
chr11:63892180-63892284	185	180	5	bounded	RPS6KA4	ribosomal protein S6 kinase, 90kDa, polypeptide
chr11:64146957-64147126	1311	5	281	bounded	NRXN2	neurexin 2 isoform beta precursor;neurexin 2 isoform alpha-1 precursor;neurexin 2 is
chr11:64166587-64166851	3807	346	2	bounded	NRXN2	neurexin 2 isoform beta precursor;neurexin 2 isoform alpha-1 precursor;neurexin 2 is
chr11:64357279-64357438	302	77	2	extending	CDC42BPG	CDC42 binding protein kinase gamma (DMPK-like)
chr11:64611371-64611481	423	4	60	bounded	ZFPL1	zinc finger protein-like 1
chr11:6475930-6476767	335	3	19	bounded	C11orf47	hypothetical protein LOC283294
chr11:65049968-65050087	442	118	5	bounded	SCYL1	SCY1-like 1 isoform A;SCY1-like 1 isoform B;N-terminal kinase-like protein (SCY1-like
chr11:65146253-65146413	494	95	25	extending	PCNXL3	CDNA: FLJ22427 fis, clone HRC09013.
chr11:65153332-65153462	183	3	201	extending	DKFZp686M14190	Hypothetical protein DKFZp686M14190.
chr11:65164883-65165647	2304	4	13	bounded	SIPA1	signal-induced proliferation-associated protein
chr11:65173608-65173912	546	198	44	extending	SIPA1	signal-induced proliferation-associated protein
chr11:65443827-65443932	3391	2392	5	bounded	DRAP1	DR1-associated protein 1
chr11:65579174-65579362	2473	4	626	bounded	SF3B2	Homo sapiens splicing factor 3b, subunit 2, 145kDa, mRNA (cDNA clone IMAGE:282
chr11:65795844-65795920	674	2576	4	bounded	RAB1B;AK125412	Homo sapiens cDNA FLJ43423 fis, clone OCBBF2026981, weakly similar to alpha 1
chr11:65809748-65809803	529	474	24	bounded	YIF1A	Yip1 interacting factor homolog
chr11:66053868-66053999	538	2	75	bounded	BBS1;ZDHHC24	BBS1 protein.;Homo sapiens Bardet-Biedl syndrome 1 (BBS1) mRNA, complete cds.;
chr11:66090054-66090214	3007	2	653	extending	CTSF	cathepsin F
chr11:66381782-66383140	7089	25	478	bounded	PC;LRFN4	pyruvate carboxylase precursor;leucine rich repeat and fibronectin type III
chr11:67135408-67135616	5126	7	1142	extending	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1,
chr11:677911-678049	456	162	3	bounded	DEAF1	deformed epidermal autoregulatory factor 1
chr11:68591550-68591649	143	2	23	bounded	TPCN2	two pore segment channel 2
chr11:690152-690235	815	3	106	bounded	TMEM80	hypothetical protein LOC283232 isoform 2;hypothetical protein LOC283232 isoform 1
chr11:69956918-69957032	1383	4	367	bounded	CTTN	CTTN protein.;cortactin isoform a;cortactin isoform b
chr11:710549-710746	332	3	45	extending	EPS8L2	epidermal growth factor receptor pathway
chr11:74024898-74024968	84	2	43	bounded	POLD3	polymerase (DNA directed), delta 3
chr11:74818442-74819323	78	29	4	extending	FLJ33790	hypothetical protein LOC283212
chr11:76781024-76781213	989	34	30	bounded	PAK1	Serine/threonine-protein kinase PAK 1 (EC 2.7.11.1) (p21-activated kinase 1) (PAK-1)
chr11:77598737-77599438	948	39	15	bounded	KIAA1372	Homo sapiens mRNA for KIAA1372 protein, partial cds.
chr11:782553-782680	353	99	7	bounded	SLC25A22	mitochondrial glutamate carrier 1
chr11:814523-814700	34823	1880	3	bounded	PNPLA2	patatin-like phospholipase domain containing 2
chr11:855513-855629	358	100	2	bounded	TSPAN4	tetraspanin 4 isoform b;tetraspanin 4 isoform a
chr11:8602482-8602674	60	3	6	bounded	KIAA0298	Homo sapiens mRNA for KIAA0298 protein, partial cds.
chr11:8602836-8603351	310	7	3	bounded	KIAA0298	Homo sapiens mRNA for KIAA0298 protein, partial cds.
chr11:8661297-8661388	4261	2	7808	extending	RPL27A	ribosomal protein L27a
chr11:874064-874169	1528	4	582	bounded	CHID1	chitinase domain containing 1
chr11:8981885-8982045	295	35	5	bounded	NRIP3	nuclear receptor interacting protein 3
chr11:9171617-9171693	99	170	2	bounded	RAB6IP1	RAB6 interacting protein 1
chr12:107128028-107128216	1077	39	3	extending	WSCD2	hypothetical protein LOC9671
chr12:108169728-108169891	305	48	38	extending	ACACB	Homo sapiens mRNA for Acetyl-CoA carboxylase 2 variant protein.;acetyl-Coenzyme
chr12:108175149-108175346	651	2	160	extending	ACACB	Homo sapiens mRNA for Acetyl-CoA carboxylase 2 variant protein.;acetyl-Coenzyme
chr12:109203978-109204095	5528	11	259	bounded	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow
chr12:110712690-110712749	727	11	846	bounded	ALDH2	mitochondrial aldehyde dehydrogenase 2
chr12:111169649-111169737	5	8	2	bounded	KIAA0614	KIAA0614 protein (Fragment).
chr12:111170254-111170358	94	3	9	isolated	NA	NA
chr12:111172331-111172564	113	24	10	bounded	C12orf51	hypothetical protein LOC283450
chr12:112122768-112123001	58	10	12	bounded	IQCD	IQ motif containing D;Homo sapiens cDNA FLJ45209 fis, clone BRCAN2015757.
chr12:112745416-112745509	264	7	71	bounded	RBM19	RNA binding motif protein 19
chr12:112760798-112760881	4	4	2	isolated	RBM19	RNA binding motif protein 19
chr12:114913204-114914145	4344	4	39	extending	THRAP2	thyroid hormone receptor associated protein 2
chr12:119119483-119119648	225	64	148	extending	RPLP0	ribosomal protein P0;RPLP0 protein.

chr12:119139027-119139302	339	7	14	bounded	PXN	Homo sapiens mRNA for Paxillin variant protein.;paxillin;CDNA FLJ46879 fis, clone U
chr12:119268321-119268475	114	60	14	bounded	MSI1	musashi 1
chr12:119391608-119391711	3043	302	2	bounded	SFRS9	splicing factor, arginine/serine-rich 9
chr12:120471748-120471926	760	6	20	bounded	FBXL10	FBXL10 protein.;F-box and leucine-rich repeat protein 10 isoform
chr12:120549211-120549339	175	2	46	bounded	TMEM142A	hypothetical protein LOC84876
chr12:120740088-120740193	144	8	3	isolated	NA	NA
chr12:121185736-121185845	358	2	76	bounded	MLXIP	MLX interacting protein
chr12:12155364-12155516	5	6	3	bounded	BCL2L14;ETV6	ets variant gene 6;BCL2-like 14 isoform 3
chr12:122032204-122032379	8592	3	1928	bounded	ARL6IP4	SRp25 nuclear protein (ARL6IP4 protein).;SRp25 nuclear protein isoform 4;SRp25 nu
chr12:122045889-122046034	1039	11	16	bounded	PITPNM2	phosphatidylinositol transfer protein,
chr12:122317685-122317775	521	41	5	bounded	CDK2AP1;doc-1	Homo sapiens doc-1 (alias DORC1) mRNA, complete cds.;CDK2-associated protein
chr12:123387138-123387679	3790	60	386	extending	NCOR2	nuclear receptor co-repressor 2 isoform 2;nuclear receptor co-repressor 2 isoform 1
chr12:123390496-123390623	1920	8	9	extending	NCOR2	nuclear receptor co-repressor 2 isoform 2;nuclear receptor co-repressor 2 isoform 1
chr12:123390505-123390623	1905	336	9	bounded	NCOR2	nuclear receptor co-repressor 2 isoform 2;nuclear receptor co-repressor 2 isoform 1
chr12:123390704-123390942	2766	5	235	extending	NCOR2	nuclear receptor co-repressor 2 isoform 2;nuclear receptor co-repressor 2 isoform 1
chr12:123422745-123423109	1665	2	317	bounded	NCOR2	nuclear receptor co-repressor 2 isoform 2;nuclear receptor co-repressor 2 isoform 1
chr12:123545646-123545732	588	254	3	bounded	SMRTE;NCOR2	Homo sapiens mRNA for nuclear receptor co-repressor 2 variant protein.;nuclear rece
chr12:130969629-130969882	880	2	269	extending	ULK1	unc-51-like kinase 1
chr12:131095823-131096058	623	2	53	bounded	EP400	E1A binding protein p400
chr12:131656794-131656900	201	3	91	bounded	KIAA1545	KIAA1545 protein (Fragment).
chr12:131658149-131658183	28	10	511	bounded	KIAA1545	KIAA1545 protein (Fragment).
chr12:131691365-131691490	81	7	20	extending	NA	NA
chr12:131707660-131708004	86	19	16	extending	P2RX2	purinergic receptor P2X2 isoform D;purinergic receptor P2X2 isoform C;purinergic rec
chr12:131801482-131801695	2868	5	71	extending	PGAM5	Homo sapiens Bcl-XL-binding protein v68 mRNA, partial cds.;Bcl-XL-binding protein v
chr12:131861887-131861964	265	10	414	bounded	GOLGA3	Golgi autoantigen, golgin subfamily a, 3
chr12:13257680-13258022	1252	64	40	extending	EMP1	epithelial membrane protein 1
chr12:14929932-14930001	5182	2552	6	bounded	MGP	matrix Gla protein
chr12:47504722-47504783	405	2	82	bounded	CACNB3	Homo sapiens cDNA FLJ16588 fis, clone TESTI4001036, highly similar to Dihydropy
chr12:47730936-47732474	3423	55	53	extending	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2
chr12:48474815-48477444	5444	18	31	extending	KIAA1602	Homo sapiens mRNA for KIAA1602 protein, partial cds.;KIAA1602 protein (Fragment)
chr12:48758468-48758627	151	3	23	extending	ACCN2	amiloride-sensitive cation channel 2, neuronal
chr12:48787624-48787850	4150	2	430	bounded	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)
chr12:50734692-50735255	5825	5	199	bounded	NR4A1	nuclear receptor subfamily 4, group A, member 1
chr12:51199793-51199932	22900	4167	45	bounded	KRT5	keratin 5
chr12:51199793-51200000	73240	4167	15	bounded	KRT5	keratin 5
chr12:51579965-51580098	938	20	7	bounded	KRT8	keratin 8
chr12:51780769-51780908	3192	7	664	bounded	IGFBP6	insulin-like growth factor binding protein 6
chr12:54798115-54798369	25	6	54	extending	ZC3H10	zinc finger CCCH-type containing 10
chr12:54999329-54999538	717	4	90	bounded	USP52	ubiquitin specific protease 52
chr12:55863825-55863943	1245	27	3	bounded	LRP1	low density lipoprotein-related protein 1
chr12:55888765-55888867	1856	17	1151	bounded	LRP1	low density lipoprotein-related protein 1
chr12:55890770-55890929	1259	6	70	bounded	LRP1	low density lipoprotein-related protein 1
chr12:55952503-55952604	105	37	24	extending	R3HDM2;KIAA1002	Homo sapiens mRNA for KIAA1002 protein, partial cds.;R3H domain containing 2;R3
chr12:55975432-55975557	146	5	53	extending	R3HDM2	R3H domain containing 2;R3H domain-containing protein 2 (Fragment).
chr12:56207201-56207277	402	6	318	bounded	MBD6	methyl-CpG binding domain protein 6
chr12:56249306-56249485	1121	258	10	extending	KIF5A	kinesin family member 5A
chr12:56296342-56296545	3803	12	562	bounded	BC073932;GEFT	Homo sapiens RAC/CDC42/Rho exchange factor GEFT mRNA, complete cds.;RAC/C
chr12:56300392-56300502	344	65	87	bounded	SLC26A10	solute carrier family 26, member 10;Homo sapiens chromosome 12 putative anion tra
chr12:56398305-56398426	4032	12	28	bounded	OS9	amplified in osteosarcoma isoform 4 precursor;amplified in osteosarcoma isoform 1 p
chr12:56407020-56407279	2616	3	124	bounded	BC019026;CENTG1	Homo sapiens cDNA clone IMAGE:4558254, partial cds.;centaurin, gamma 1;Centau
chr12:56410541-56410664	1774	3	301	extending	CENTG1	centaurin, gamma 1;Centaurin-gamma 1 (ARF-GAP with GTP-binding protein-like, an
chr12:63113467-63113650	773	3	299	bounded	XPOT	tRNA exportin
chr12:6313159-6313292	1280	5	536	extending	TNFRSF1A	tumor necrosis factor receptor 1 precursor
chr12:6334786-6334862	13	2	19	bounded	SCNN1A	sodium channel, nonvoltage-gated 1 alpha;Homo sapiens cDNA: FLJ21883 fis, clone

chr12:6334792-6334862	13	2	19	bounded	SCNN1A	sodium channel, nonvoltage-gated 1 alpha;Homo sapiens cDNA: FLJ21883 fis, clone
chr12:6517176-6517241	13049	40	75	bounded	OK/SW-cl.12;GAPDH	Homo sapiens OK/SW-cl.12 mRNA for glyceraldehyde-3-phosphate dehydrogenase,
chr12:6530122-6530428	351	254	111	extending	HOM-TES-103;DKFZp586I222	hypothetical protein LOC25900 isoform 2;Homo sapiens HOM-TES-103 tumor antige
chr12:6728226-6728409	8924	4	3073	bounded	MLF2	myeloid leukemia factor 2
chr12:6901671-6901826	1504	4	1358	extending	ENO2	enolase 2
chr12:6918048-6918601	17826	4	2084	bounded	ATN1	atrophin-1
chr12:7042675-7042864	2965	2	950	bounded	C1S	complement component 1, s subcomponent
chr12:7133030-7133216	9829	686	2	bounded	C1R	complement component 1, r subcomponent
chr12:7185105-7185315	1748	329	8	extending	CLSTN3	calsyntenin 3
chr12:7200057-7200792	1385	4	13	bounded	KIAA0726;CLSTN3	Homo sapiens mRNA for KIAA0726 protein, partial cds.;calsyntenin 3
chr12:74730578-74730669	768	613	9	bounded	NAP1L1	nucleosome assembly protein 1-like 1
chr12:80185816-80185997	276	12	116	extending	PPFIA2	PTPRF interacting protein alpha 2
chr12:847293-848531	281	3	6	bounded	WNK1;HSN2	hereditary sensory neuropathy, type II;WNK lysine deficient protein kinase 1
chr12:88534722-88534947	826	3	27	bounded	ATP2B1	plasma membrane calcium ATPase 1 isoform 1a;plasma membrane calcium ATPase
chr12:9118423-9118617	8046	155	47	bounded	A2M	alpha-2-macroglobulin precursor
chr12:94129020-94129174	138	5	37	bounded	FGD6	FYVE, RhoGEF and PH domain containing 6
chr12:94953270-94953432	1368	99	5	bounded	LTA4H	leukotriene A4 hydrolase
chr12:97465482-97465689	206	63	9	bounded	TMPO	thymopoietin isoform gamma;thymopoietin isoform beta
chr13:109664130-109664363	874	129	133	extending	COL4A1	alpha 1 type IV collagen preproprotein
chr13:112792383-112792475	36	3	8	bounded	KIAA0362;MCF2L	MCF.2 cell line derived transforming;Ost-II (MCF.2 cell line derived transforming sequ
chr13:22751506-22751617	90	2	26	bounded	SGCG	gamma sarcoglycan
chr13:24153710-24153858	67	2	11	bounded	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha
chr13:28988275-28988450	82	41	4	extending	SLC7A1	solute carrier family 7 (cationic amino acid
chr13:44812847-44813029	15374	29708	10	bounded	TPT1	tumor protein, translationally-controlled 1;TPT1 protein (Tumor protein, translationally-
chr13:44813124-44813212	1017	8	4	bounded	D28408;TPT1	tumor protein, translationally-controlled 1;TPT1 protein (Tumor protein, translationally-
chr13:45440884-45441206	1688	131	6	bounded	KIAA0853;ZC3H13	Homo sapiens mRNA for KIAA0853 protein, partial cds.;zinc finger CCCH-type contai
chr13:45447419-45447607	3017	166	10	bounded	KIAA0853;ZC3H13	Homo sapiens mRNA for KIAA0853 protein, partial cds.;zinc finger CCCH-type contai
chr13:49133169-49133345	146	5	57	bounded	EBRP;EBPL;RP11-432M24.2	Homo sapiens delta8-delta7 sterol isomerase related protein EBRP (EBRP) mRNA, c
chr13:75278195-75278398	29	3	12	isolated	LMO7	LIM domain only 7;LIM domain only 7 (Fragment).
chr14:100381152-100381203	1	2	4	isolated	FP504	Homo sapiens MEG3 mRNA, partial sequence, imprinted gene.;Full-length cDNA clon
chr14:101576326-101576440	968	336	326	bounded	DYNC1H1	dynein, cytoplasmic, heavy polypeptide 1
chr14:101618201-101618484	3379	1388	15	bounded	HSP90AA1	heat shock protein 90kDa alpha (cytosolic),
chr14:101621848-101622040	6986	2001	5	bounded	HSP90AA1;HSPCA	heat shock protein 90kDa alpha (cytosolic),;Full-length cDNA clone CS0CAP007YF18
chr14:101765547-101765741	337	24	3	bounded	MOK;RAGE	RAGE protein.;Homo sapiens mRNA for MOK protein kinase, complete cds.;MAPK/M
chr14:103275569-103276683	4280	2	49	extending	KIAA0771;PPP1R13B	apoptosis-stimulating protein of p53, 1;Homo sapiens mRNA for KIAA0771 protein, p
chr14:104469394-104469737	181	8	35	extending	PLD4	phospholipase D family, member 4
chr14:104754926-104755176	1794	111	7	bounded	BRF;BRF1	transcription initiation factor IIIB isoform 2;transcription initiation factor IIIB isoform 1;tr
chr14:105028838-105028904	35	2	13	bounded	FLJ00116;C14orf80	Full-length cDNA clone CS0DI081YB03 of Placenta of Homo sapiens (human).;Full-le
chr14:105205681-105205947	4447	63	128	bounded	DKFZp686O16217;IGHA2;AK	Ig epsilon chain C region.;Homo sapiens cDNA FLJ43645 fis, clone SYNOV3000302,
chr14:105244829-105244944	1120	3	1193	bounded	IGHA2;abParts;IGHE;DKFZp6	Homo sapiens cDNA FLJ46441 fis, clone THYMU3016518, highly similar to Ig gamm
chr14:105280159-105280363	21123	33494	25	bounded	IGHA2;DKFZp686O16217;abF	Ig epsilon chain C region.;Ig alpha-2 chain C region.;Homo sapiens cDNA FLJ46441 f
chr14:105523704-105524020	6426	4	654	bounded	abParts	Parts of antibodies, mostly variable regions.
chr14:20556203-20556503	1428	681	7562	bounded	NDRG2;KIAA1248	N-myc downstream-regulated gene 2 isoform a;Homo sapiens mRNA for KIAA1248 p
chr14:20569891-20570028	313	61	4	bounded	C14orf8	chromosome 14 open reading frame 8
chr14:22307013-22307220	1197	9	565	bounded	OXA1L	Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like pr
chr14:22317842-22317890	20	26	2	bounded	SLC7A7	solute carrier family 7 (cationic amino acid
chr14:22601978-22602114	1413	213	13	bounded	KIAA0670;ACIN1	apoptotic chromatin condensation inducer 1;Homo sapiens mRNA for KIAA0670 prote
chr14:22863210-22863338	6211	6	528	bounded	PABPN1	Homo sapiens clone FLB2302 mRNA sequence.;poly(A) binding protein, nuclear 1
chr14:23065896-23066022	82	4	15	isolated	THTPA;AX746599	Homo sapiens cDNA FLJ33428 fis, clone BRACE2020742.;Homo sapiens thiamine tri
chr14:23066653-23066853	96	15	5	isolated	THTPA;AX746599	Homo sapiens cDNA FLJ33428 fis, clone BRACE2020742.;Homo sapiens thiamine tri
chr14:23068759-23068817	15	5	17	bounded	ZNF409;THTPA;AX746599	Homo sapiens zinc finger protein 409, mRNA (cDNA clone MGC:141820 IMAGE:400
chr14:23070530-23070770	195	4	7	bounded	ZNF409;THTPA;AX746599	Homo sapiens zinc finger protein 409, mRNA (cDNA clone MGC:141820 IMAGE:400
chr14:23114734-23115059	1554	138	2	bounded	JPH4	junctophilin 4

chr14:23115144-23115505	2798	16	212	bounded	JPH4	junctophilin 4
chr14:23115459-23115505	76	9	212	bounded	JPH4	junctophilin 4
chr14:23597009-23597118	74	8	3	extending	C14orf121	hypothetical protein LOC90668
chr14:23608186-23608305	560	53	2	extending	C14orf121	hypothetical protein LOC90668
chr14:23753356-23753407	50	22	2	bounded	CHMP4A;MDP-1;MDP1	magnesium-dependent phosphatase 1;chromatin modifying protein 4A;Magnesium-de
chr14:23806733-23807004	511	2	157	extending	RABGGTA	Homo sapiens Rab geranylgeranyltransferase, alpha subunit, mRNA (cDNA clone MG
chr14:23835784-23835876	720	176	3	bounded	DHRS1	dehydrogenase/reductase (SDR family) member 1
chr14:23865083-23865211	23	2	8	extending	ADCY4	adenylate cyclase 4
chr14:23870064-23870402	164	2	13	extending	ADCY4	adenylate cyclase 4
chr14:32085318-32085956	307	2	5	bounded	AKAP6	A-kinase anchor protein 6
chr14:32139583-32139749	121	3	48	extending	AKAP6	A-kinase anchor protein 6
chr14:33336414-33336529	42	11	2	bounded	NPAS3	neuronal PAS domain protein 3 isoform 2;neuronal PAS domain protein 3 isoform 1
chr14:35227416-35228960	184	2	10	extending	GARNL1	GTPase activating Rap/RanGAP domain-like 1
chr14:37133857-37133940	942	337	6	bounded	FOXA1	forkhead box A1
chr14:51590047-51590789	631	73	18	extending	C14orf166;NID2	homeobox prox 1;nidogen 2
chr14:54273501-54273755	741	4	68	bounded	SAMD4A	sterile alpha motif domain containing 4
chr14:57897372-57897573	287	55	2	extending	ARID4A	retinoblastoma-binding protein 1 isoform II;retinoblastoma-binding protein 1 isoform I;
chr14:64274514-64274695	400	3	16	bounded	PLEKHG3	pleckstrin homology domain containing, family G,
chr14:66027492-66027575	8	3	5	isolated	MGC88374	Homo sapiens similar to CG32662-PA, mRNA (cDNA clone IMAGE:5163906).;hypoth
chr14:67112209-67112475	1273	4	49	extending	PLEKHH1	pleckstrin homology domain containing, family H
chr14:69063658-69063802	80	12	85	bounded	NA	NA
chr14:69528854-69528943	207	9	95	extending	SMOC1	secreted modular calcium-binding protein 1
chr14:70549470-70549672	141	5	9	bounded	PCNX	pecanex-like 1
chr14:73255761-73255957	248	13	217	bounded	C14orf43;FLJ00335	Homo sapiens cDNA: FLJ21325 fis, clone COL02408, highly similar to AF147723 Ho
chr14:75281586-75281682	201	41	8	extending	TTLL5;KIAA0998	tubulin tyrosine ligase-like family, member 5;Homo sapiens mRNA for KIAA0998 prot
chr14:92187680-92187968	535	11	2	bounded	RIN3	Ras and Rab interactor 3
chr14:93157876-93158940	573	11	7	bounded	KIAA1409	hypothetical protein LOC57578
chr14:93637970-93638074	391	5	88	bounded	FAM14B	hypothetical protein LOC122509
chr14:93664604-93664708	1628	777	17	bounded	FAM14A	TLH29 protein precursor
chr14:93918682-93919180	50701	2673	17	bounded	SERPINA1	serine (or cysteine) proteinase inhibitor, clade;Homo sapiens clone FLB2803 PRO068
chr14:94627293-94627450	261	108	2	bounded	DICER1	dicer1
chr14:98940315-98940394	105	42	3	bounded	SETD3	SET domain containing 3 isoform a
chr14:99038809-99038915	1870	486	3	bounded	CPR4;CCNK	Full-length cDNA clone CS0DA006YC23 of Neuroblastoma of Homo sapiens (human)
chr14:99064308-99064346	2	5	7	isolated	NA	NA
chr15:100129925-100130025	8	2	2	extending	DQ588143	DQ588143
chr15:23171771-23172003	417	3	174	bounded	UBE3A	ubiquitin protein ligase E3A isoform 2;ubiquitin protein ligase E3A isoform 3;ubiquitin
chr15:26157343-26157498	32	6	4	bounded	HERC2	hect domain and RLD 2
chr15:32442831-32442949	476	6	93	extending	AGPAT7	PLSC domain containing protein
chr15:32874173-32874311	3483	117	2	bounded	ACTC1;AK092087	Homo sapiens cDNA FLJ34768 fis, clone NT2NE2002791.;cardiac muscle alpha actin
chr15:37667535-37667735	2611	89	23	extending	THBS1	thrombospondin 1 precursor
chr15:38351717-38352492	1011	115	104	extending	PAK6	p21-activated kinase 6
chr15:38370254-38370676	184	37	10	extending	PLCB2	Homo sapiens mRNA for phospholipase C, beta 2 variant protein.;phospholipase C, b
chr15:38471452-38471516	47	2	21	bounded	C15orf23	Homo sapiens cDNA FLJ14502 fis, clone NT2RM1000244, highly similar to Homo sa
chr15:38824467-38824738	2047	168	4	bounded	FAM82C	family with sequence similarity 82, member C
chr15:39550662-39550843	354	302	3	extending	RTF1	Paf1/RNA polymerase II complex component
chr15:39580953-39581341	269	46	21	extending	ITPKA	1D-myo-inositol-trisphosphate 3-kinase A
chr15:39915078-39915138	99	63	12	extending	PLA2G4B;cPLA2 beta	phospholipase A2, group IVB;CDNA FLJ20807 fis, clone ADSE01784.;Cytosolic phos
chr15:40518523-40519099	2395	67	2	bounded	ZFP106	zinc finger protein 106 homolog
chr15:40815365-40815571	208	49	17	extending	CDAN1	codanin 1
chr15:41873066-41873426	20730	14	6	extending	ELL3;SERF2	Homo sapiens small EDRK-rich factor 2 (SERF2) mRNA, complete cds.;small EDRK-
chr15:41876597-41876731	198	10	5	bounded	ELL3;SERINC4;SERF2	Homo sapiens cDNA FLJ35914 fis, clone TESTI2010354, highly similar to Homo sapi
chr15:60329818-60329903	6	4	3	extending	DQ592483;DQ586930	DQ592483;DQ586930
chr15:60334809-60334916	15	6	2	extending	DQ576734	DQ576734
chr15:61742257-61742456	459	75	12	bounded	HERC1	guanine nucleotide exchange factor p532

chr15:61753594-61754345	604	38	12	bounded	HERC1	guanine nucleotide exchange factor p532
chr15:64582438-64582556	705	39	3175	bounded	RPL4	ribosomal protein L4;Homo sapiens mRNA for ribosomal protein L4 variant protein.
chr15:70280323-70280475	534	5	15	bounded	PKM2	pyruvate kinase 3 isoform 2;pyruvate kinase 3 isoform 1;Homo sapiens Opa-interactin
chr15:70282282-70282354	38	9	4	bounded	PKM2	pyruvate kinase 3 isoform 2;pyruvate kinase 3 isoform 1;Homo sapiens Opa-interactin
chr15:70286474-70286672	23943	14	1874	extending	PKM2	pyruvate kinase 3 isoform 2;pyruvate kinase 3 isoform 1;Homo sapiens Opa-interactin
chr15:71404349-71404838	88	6	9	extending	HCN4	hyperpolarization activated cyclic
chr15:72933415-72933462	616	65	14	bounded	SCAMP2	secretory carrier membrane protein 2
chr15:73017309-73017430	2585	461	2	bounded	COX5A	cytochrome c oxidase subunit Va precursor
chr15:80306846-80306975	95	20	2	extending	EFTUD1	elongation factor Tu GTP binding domain
chr15:87928524-87928762	48	2	14	bounded	C15orf42	leucine-rich repeat kinase 1
chr15:87992490-87993009	217	10	27	extending	KIF7;BC042063	kinesin family member 7;Homo sapiens hypothetical protein LOC254571, mRNA (cDN
chr15:87993976-87994176	85	76	14	bounded	BC042063	Homo sapiens hypothetical protein LOC254571, mRNA (cDNA clone IMAGE:5724194
chr15:89221130-89221297	1261	58	2	extending	FURIN	furin preproprotein
chr15:89262795-89262989	356	2	146	extending	MAN2A2	Homo sapiens PRO2198 mRNA, complete cds.;mannosidase, alpha, class 2A, memb
chr15:89297693-89297946	2487	148	2	bounded	UNC45A;smap-1	smooth muscle cell associated protein-1 isoform;UNC45 homolog A (UNC-45A) (Smo
chr16:1190257-1190809	781	17	9	extending	CACNA1H	calcium channel, voltage-dependent, T type,
chr16:1197002-1197431	110	5	39	extending	CACNA1H	calcium channel, voltage-dependent, T type,
chr16:1246304-1246364	56	2	20	bounded	TPSD1	tryptase delta 1
chr16:1302399-1302605	230	3	41	bounded	UBE2I	ubiquitin-conjugating enzyme E2I
chr16:1357073-1357351	994	6	182	extending	C16orf28;flj23360	hypothetical protein LOC65259;CDNA: FLJ23360 fis, clone HEP15172 (Hypothetical p
chr16:1447256-1447389	873	377	3	extending	CLCN7	chloride channel 7
chr16:15037374-15037606	2630	26	2	bounded	PDXDC1	hypothetical protein LOC23042
chr16:15126848-15127165	18	6	30	extending	PDXDC1;FLJ00285	FLJ00285 protein (Fragment).;hypothetical protein LOC23042
chr16:15626730-15627155	250	6	27	bounded	KIAA0430	limkain b1
chr16:15637404-15637700	503	3	18	bounded	KIAA0430	limkain b1
chr16:15780108-15780201	646	2	655	extending	MYH11;KIAA0866	Homo sapiens mRNA for KIAA0866 protein, partial cds.;smooth muscle myosin heavy
chr16:15839245-15839627	10408	26	2371	extending	MYH11	MYH11 protein.;smooth muscle myosin heavy chain 11 isoform
chr16:1756725-1756803	403	100	2	bounded	MAPK8IP3	mitogen-activated protein kinase 8 interacting
chr16:2061512-2061678	929	68	2	extending	TSC2;SLC9A3R2 variant prote	tuberous sclerosis 2 isoform 4;Homo sapiens mRNA for SLC9A3R2 variant protein, pa
chr16:2074568-2074717	1194	9	636	bounded	TSC2;SLC9A3R2 variant prote	tuberous sclerosis 2 isoform 4;Homo sapiens mRNA for SLC9A3R2 variant protein, pa
chr16:2081425-2081563	607	100	41	bounded	PKD1	polycystin 1 isoform 2 precursor;polycystin 1 isoform 1 precursor
chr16:2089646-2089706	220	10	50	bounded	PKD1	polycystin 1 isoform 2 precursor;polycystin 1 isoform 1 precursor
chr16:2108219-2108464	180	9	6	bounded	PKD1	polycystin 1 isoform 2 precursor;polycystin 1 isoform 1 precursor
chr16:2163790-2164050	437	268	48	extending	TRAF7	ring finger and WD repeat domain 1
chr16:2204140-2204729	3599	89	2	bounded	LOC283871	hypothetical protein LOC283871
chr16:22199069-22199198	749	2	103	bounded	EEF2K	elongation factor-2 kinase
chr16:24849606-24849835	1626	104	4	bounded	ARHGAP17;MST066	nadrin isoform 1;nadrin isoform 2;ARHGAP17 protein.;CDNA FLJ10308 fis, clone NT2
chr16:254637-254716	841	10	416	bounded	ITFG3	integrin alpha FG-GAP repeat containing 3
chr16:274864-275016	1116	5	77	extending	PDIA2	protein disulfide isomerase-associated 2
chr16:2751563-2752809	17327	386	6	bounded	SRRM2	splicing coactivator subunit SRm300
chr16:2830844-2831081	59	3	2	bounded	MGC52282	Hypothetical protein MGC52282.;Homo sapiens cDNA FLJ16659 fis, clone TESTI404
chr16:28754821-28754944	1058	4	182	bounded	ATXN2L;A2LG	ataxin 2 related protein isoform A;ataxin 2 related protein isoform B;ataxin 2 related pr
chr16:28897977-28898129	1209	158	3	extending	SPIN1	spinster
chr16:2919688-2920012	1336	2	18	bounded	FLYWCH1	FLYWCH-type zinc finger 1 isoform b;FLYWCH-type zinc finger 1 isoform a
chr16:29896911-29897006	671	96	4	extending	BOLA2;TAOK2	TAO kinase 2 isoform 2;BolA-like protein 2 isoform b;TAO kinase 2 isoform 1
chr16:29982551-29982599	13	24	17	bounded	ALDOA;BOLA2	BolA-like protein 2 isoform b;aldolase A
chr16:29982551-29982664	44	24	44	bounded	ALDOA;BOLA2	BolA-like protein 2 isoform b;aldolase A
chr16:3013267-3013363	6179	5	2093	bounded	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependant)
chr16:30630393-30630979	2362	180	57	extending	SRCAP	Snf2-related CBP activator protein
chr16:30640947-30641108	637	5	336	bounded	SRCAP	Snf2-related CBP activator protein
chr16:30897967-30898751	3137	130	20	bounded	SETD1A	SET domain containing 1A
chr16:31030129-31030211	327	3	165	bounded	BCKDK	branched chain ketoacid dehydrogenase kinase
chr16:31108862-31108994	8188	758	15	extending	FUS	fusion (involved in t(12;16) in malignant
chr16:31412425-31412603	1213	115	11	bounded	C16orf58	hypothetical protein LOC64755;CDNA FLJ35261 fis, clone PROST2004270.

chr16:3279394-3280554	2445	27	2	bounded	AF251050;ZNF263	zinc finger protein 263;Homo sapiens jerky mRNA, complete cds.
chr16:3680829-3680889	631	149	7	bounded	TRAP1	TNF receptor-associated protein 1
chr16:3760572-3760760	781	77	5	bounded	CREBBP	CREB binding protein isoform b;CREB binding protein isoform a
chr16:4196955-4198106	275	8	4	bounded	DKFZp451C023;SRL	Homo sapiens cDNA FLJ32026 fis, clone NTONG1000214, highly similar to SARCAL
chr16:4331370-4331502	734	69	4	bounded	Magmas	Homo sapiens CGI-136 protein mRNA, complete cds.;mitochondria-associated granul
chr16:45476880-45477025	24	5	2	extending	GPT2	alanine aminotransferase 2
chr16:47872614-47872877	9113	931	9	bounded	CBLN1	cerebellin 1 precursor
chr16:55208801-55209003	297	12	65	extending	MTC;NR_001447;MTF	Homo sapiens MTC (MTC) mRNA, complete cds.;NR_001447;Homo sapiens MTF (M
chr16:55230106-55230179	171	3	58	bounded	MTC;MT1A	metallothionein 1A;Homo sapiens MTC (MTC) mRNA, complete cds.
chr16:553333-554377	6111	2	233	bounded	LOC146325	hypothetical protein LOC146325
chr16:56107748-56107876	141	3	21	bounded	CCDC102A	coiled-coil domain containing 102A
chr16:570752-570973	270	2	30	bounded	PIGQ	phosphatidylinositol glycan anchor biosynthesis,
chr16:57095764-57096054	1191	503	847	extending	NDRG4;smap-8	NDRG family member 4;Homo sapiens mRNA for SMAP-8, complete cds.
chr16:648511-648654	144	2	32	extending	WDR90;KIAA1924	Homo sapiens mRNA for KIAA1924 protein, partial cds.;WD repeat domain 90;CDNA
chr16:65028999-65029105	49	3	5	isolated	BEAN	Homo sapiens cDNA FLJ31580 fis, clone NT2RI2002041.
chr16:65598187-65598221	4	5	43	bounded	FLJ37464;UNQ440	hypothetical protein LOC283848;CDNA FLJ37464 fis, clone BRAWH2011795, weakly
chr16:65758847-65759003	235	3	23	extending	hHSF4;HSF4	heat shock transcription factor 4 isoform b;heat shock transcription factor 4 isoform a;
chr16:66240089-66240378	26	10	9	extending	RLTPR	RGD, leucine-rich repeat, tropomodulin and
chr16:66252859-66253114	1345	158	18	extending	PARD6A	par-6 partitioning defective 6 homolog alpha
chr16:66422620-66422728	609	169	5	bounded	CENPT	Centromere protein T (CENP-T) (Interphase centromere complex protein 22).;centrom
chr16:66468894-66469060	352	2	62	bounded	EDC4	autoantigen RCD8
chr16:66469764-66469851	209	79	3	extending	EDC4	autoantigen RCD8
chr16:66473072-66473513	2864	142	78	extending	EDC4	autoantigen RCD8
chr16:66522085-66522211	37	2	7	extending	CTRL;PSMB10	chymotrypsin-like;proteasome beta 10 subunit proprotein
chr16:68309774-68309934	2073	715	10	bounded	NQO1	NAD(P)H menadione oxidoreductase 1,
chr16:71380058-71380248	408	3	19	bounded	ATBF1	Alpha-fetoprotein enhancer-binding protein (AT motif-binding factor) (AT-binding trans
chr16:84254493-84254721	1828	7	86	bounded	KIAA0182	Homo sapiens mRNA for KIAA0182 protein variant protein.;hypothetical protein LOC2
chr16:85902257-85902403	166	20	558	bounded	FBXO31	CDNA: FLJ22477 fis, clone HRC10815.
chr16:87320130-87320364	1028	5	37	extending	FAM38A	family with sequence similarity 38, member A
chr16:87330057-87330317	660	55	67	bounded	FAM38A	family with sequence similarity 38, member A
chr16:87331468-87331555	273	20	164	bounded	FLJ45121	hypothetical protein LOC400556
chr16:87331637-87331723	322	167	13	bounded	FLJ45121	hypothetical protein LOC400556
chr16:87332477-87332645	524	126	34	bounded	FLJ45121	hypothetical protein LOC400556
chr16:87884534-87884645	324	299	4	bounded	ANKRD11	Homo sapiens mRNA for ankyrin repeat domain 11 variant protein.;ankyrin repeat do
chr16:88514499-88514677	199	3	3	bounded	MC1R;TUBB3	melanocortin 1 receptor;Tubulin, beta, 4.
chr16:8860529-8860656	1706	133	9	bounded	PMM2;CARHSP1	full-length cDNA clone CS0DJ003YA02 of T cells (Jurkat cell line) Cot 10-normalized
chr17:12838806-12839104	627	244	162	bounded	ELAC2	elaC homolog 2;Zinc phosphodiesterase ELAC protein 2 (EC 3.1.26.11) (Ribonucleas
chr17:12849795-12850021	110	33	52	extending	ELAC2	elaC homolog 2
chr17:1509881-1510045	1596	6	326	bounded	PRPF8	U5 snRNP-specific protein
chr17:16981955-16982468	3227	33	146	extending	M-RIP	myosin phosphatase-Rho interacting protein
chr17:17008148-17011954	11331	17	232	extending	M-RIP;KIAA0864	myosin phosphatase-Rho interacting protein;KIAA0864 protein (Fragment).
chr17:17071913-17072200	2322	4	70	extending	FLCN	folliculin isoform 2;Folliculin (Birt-Hogg-Dube syndrome protein) (BHD skin lesion fibro
chr17:17663359-17663481	244	98	4	bounded	SREBF1	Sterol regulatory element binding transcription factor 1 isoform a variant (Fragment).;
chr17:17948599-17948720	165	2	167	extending	DRG2	developmentally regulated GTP binding protein 2;Homo sapiens mRNA for developme
chr17:18086211-18086317	415	16	91	bounded	LLGL1	lethal giant larvae homolog 1
chr17:18129446-18129582	154	12	2	extending	TOP3A	topoisomerase (DNA) III alpha;Homo sapiens full length insert cDNA clone YX60A04.
chr17:19711233-19711322	66	17	2	bounded	ULK2	unc-51-like kinase 2
chr17:20357841-20357966	1	10	7	isolated	NA	NA
chr17:2153677-2153778	133	21	6	bounded	SMG6	Smg-6 homolog, nonsense mediated mRNA decay
chr17:21654820-21655440	545	31	2	bounded	BC070367	Homo sapiens cDNA clone IMAGE:6618390, containing frame-shift errors.
chr17:2217339-2217449	209	2	49	bounded	KIAA0397;RUTBC1	CDNA FLJ43213 fis, clone FEBRA2021339.;RUN and TBC1 domain containing 1
chr17:23708441-23708600	446	242	14	bounded	POLDIP2	DNA polymerase delta interacting protein 2
chr17:23718863-23718966	2637	1460	7	bounded	VTN	vitronectin precursor
chr17:23924866-23925079	7173	11	744	extending	ALDOC	fructose-bisphosphate aldolase C

chr17:23925212-23925365	11725	752	10	bounded	ALDOC	fructose-bisphosphate aldolase C
chr17:23937570-23937617	15	18	6	bounded	SPAG5	sperm associated antigen 5
chr17:23964176-23964291	182	13	16	extending	AK098638;FLJ25006	hypothetical protein LOC124923;Homo sapiens cDNA FLJ25772 fis, clone TST06461
chr17:23982624-23982823	1877	65	9	bounded	KIAA0100	hypothetical protein LOC9703
chr17:24473019-24473101	534	3	226	bounded	MYO18A	myosin 18A isoform a;myosin 18A isoform b
chr17:24475689-24475832	21	3	16	extending	MYO18A	myosin 18A isoform a;myosin 18A isoform b
chr17:24478996-24479688	1179	20	10	extending	MYO18A	myosin 18A isoform a;myosin 18A isoform b
chr17:24927364-24927579	2333	297	4	bounded	GIT1	G protein-coupled receptor kinase interactor 1
chr17:24967846-24968186	772	378	35	extending	CORO6	coronin 6;Coronin-6.
chr17:2545262-2545570	1374	674	59	extending	KIAA0664	hypothetical protein LOC23277
chr17:27398893-27399237	175	4	4	extending	LRRC37B	leucine rich repeat containing 37B
chr17:29977259-29978189	289	2	7	extending	TMEM132E	transmembrane protein 132E
chr17:31173762-31173950	1265	5	460	bounded	TAF15	TBP-associated factor 15 isoform 2;TBP-associated factor 15 isoform 1
chr17:31195594-31195650	999	262	7	bounded	TAF15	TBP-associated factor 15 isoform 2;TBP-associated factor 15 isoform 1
chr17:31196119-31196155	788	15	4381	bounded	TAF15	TBP-associated factor 15 isoform 2;TBP-associated factor 15 isoform 1
chr17:32016623-32016741	1211	3	262	bounded	ZNF403;LZK1	zinc finger protein 403;Homo sapiens C3HC4-type zinc finger protein (LZK1) mRNA, c
chr17:32384602-32384709	677	7	206	bounded	ded;AATF	Homo sapiens Che-1 mRNA, complete cds.;apoptosis antagonizing transcription facto
chr17:33610975-33611067	36	2	22	bounded	NPEPPS	aminopeptidase puromycin sensitive
chr17:33875934-33877098	4069	124	132	extending	ARHGAP23	KIAA1501 protein (Fragment).
chr17:33919706-33920110	1522	30	3	extending	ARHGAP23	KIAA1501 protein (Fragment).
chr17:33954636-33955220	1075	2	4	isolated	SNIP;KIAA1684	Homo sapiens mRNA for KIAA1684 protein, partial cds.;SNAP25-interacting protein
chr17:34118952-34119047	908	67	6	bounded	MLLT6	myeloid/lymphoid or mixed-lineage leukemia
chr17:34121721-34121793	2780	7	630	bounded	MLLT6	myeloid/lymphoid or mixed-lineage leukemia
chr17:34125391-34125529	712	542	13	bounded	MLLT6	myeloid/lymphoid or mixed-lineage leukemia;MLLT6 protein (Fragment).
chr17:34126616-34126760	215	3	132	bounded	MLLT6	myeloid/lymphoid or mixed-lineage leukemia;MLLT6 protein (Fragment).
chr17:3423677-3423890	159	34	2	bounded	TRPV1	transient receptor potential cation channel,
chr17:3423677-3423914	172	34	3	bounded	TRPV1	transient receptor potential cation channel,
chr17:35586706-35586901	68	10	5	isolated	NA	NA
chr17:3674985-3675075	58	24	2	bounded	ELG;C17orf85	Homo sapiens mRNA for ELG protein.;ELG protein
chr17:36925882-36926064	14784	2873	13	extending	KRT15	keratin 15;Homo sapiens cDNA FLJ33285 fis, clone ASTRO2009526, highly similar to
chr17:36928108-36928281	4169	566	6	bounded	KRT15	keratin 15;Homo sapiens cDNA FLJ33285 fis, clone ASTRO2009526, highly similar to
chr17:36928108-36928367	9515	566	5	bounded	KRT15	keratin 15;Homo sapiens cDNA FLJ33285 fis, clone ASTRO2009526, highly similar to
chr17:36993009-36993233	24131	6	20	bounded	KRT14	keratin 14
chr17:36996372-36996612	4599	51	12	bounded	KRT14	keratin 14
chr17:37021936-37022119	157	371	32	bounded	KRT16	keratin 16
chr17:37022232-37022466	486	28	3	bounded	KRT16	keratin 16
chr17:37022354-37022502	948	12	5	bounded	KRT16	keratin 16
chr17:37318760-37318847	340	6	156	extending	ACLY	ATP citrate lyase isoform 2;ATP citrate lyase isoform 1
chr17:37319264-37319479	2448	9	204	extending	ACLY	ATP citrate lyase isoform 2;ATP citrate lyase isoform 1
chr17:37439769-37439879	96	18	15	isolated	NA	NA
chr17:37520433-37520579	1842	36	219	extending	GCN5L2	GCN5 general control of amino-acid synthesis
chr17:37714921-37715032	338	42	2	extending	STAT5A	signal transducer and activator of transcription
chr17:38019393-38019956	1344	1055	278	extending	TUBG1	tubulin, gamma 1
chr17:39294028-39294147	138	18	7	isolated	CD300LG	triggering receptor expressed on myeloid cells
chr17:39519485-39519631	1059	8	722	bounded	HDAC5	histone deacetylase 5 isoform 1;histone deacetylase 5 isoform 3
chr17:39521431-39521492	305	6	285	bounded	HDAC5	histone deacetylase 5 isoform 1;histone deacetylase 5 isoform 3
chr17:39630492-39630645	653	252	8	extending	ATXN7L3	ATXN7L3 protein (Fragment).;ATXN7L3 protein.
chr17:39784623-39784689	778	15	677	bounded	GRN	Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.;granulin precursor
chr17:39830759-39834347	18751	7	92	bounded	GPATCH8	G patch domain containing 8
chr17:4023398-4023431	4	28	3	bounded	ANKFY1	ankyrin repeat and FYVE domain containing 1
chr17:40359308-40359385	22	5	3	bounded	LOC146909	hypothetical protein LOC146909;Hypothetical protein (Fragment).
chr17:41407587-41407679	38	15	3	bounded	MAPT	microtubule-associated protein tau isoform 1;microtubule-associated protein tau isofor
chr17:4215844-4216000	10	7	3	isolated	UBE2G1	ubiquitin-conjugating enzyme E2G 1
chr17:42591595-42591804	30	5	21	isolated	CDC27	cell division cycle protein 27

chr17:43131688-43131860	336	4	164	bounded	TBKBP1	ProSAPiP2 protein
chr17:43413528-43413824	782	281	12	extending	CDK5RAP3;OK/SW-cl.114	CDK5 regulatory subunit associated protein 3;Homo sapiens OK/SW-cl.114 mRNA, c
chr17:43487328-43487511	27	2	3	isolated	NFE2L1;FLJ00380	nuclear factor (erythroid-derived 2)-like 1;Homo sapiens mRNA for FLJ00380 protein.
chr17:4395345-4395389	130	5	155	bounded	MYBBP1A	MYB binding protein 1a
chr17:44280425-44280462	15	144	5	bounded	CALCOCO2	calcium binding and coiled-coil domain 2
chr17:45548366-45548446	88	37	9	bounded	SAMD14	sterile alpha motif domain containing 14
chr17:45581507-45582067	13754	464	6	bounded	PPP1R9B	protein phosphatase 1, regulatory subunit 9B
chr17:4659950-4660288	591	5	45	extending	PLD2	phospholipase D2
chr17:4734316-4734385	181	15	53	bounded	MINK1;MINK	misshapen/NIK-related kinase isoform 4;misshapen/NIK-related kinase isoform 1;Miss
chr17:4792303-4792501	38743	4531	43	bounded	PFN1	profilin 1
chr17:4797092-4797382	1606	380	331	extending	ENO3	enolase 3
chr17:4823703-4823818	1249	75	6	bounded	CAMTA2	calmodulin binding transcription activator 2
chr17:4824038-4824640	3600	8	212	bounded	CAMTA2	calmodulin binding transcription activator 2
chr17:53742872-53743573	725	48	26	extending	BZRAP1	peripheral benzodiazepine receptor-associated
chr17:53953103-53953268	4782	1366	9	bounded	SEPT4;CE5B3 alpha	Homo sapiens CE5B3 alpha mRNA for Bradeion alpha, complete cds.;septin 4 isofor
chr17:55363765-55363878	255	57	2	extending	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide
chr17:56502014-56502440	44	10	8	isolated	BCAS3	Homo sapiens GAOB1 mRNA, complete cds.;breast carcinoma amplified sequence 3
chr17:59261225-59261593	4650	1941	625	bounded	PSMC5	Homo sapiens clone 23598 mRNA, complete cds.;proteasome 26S ATPase subunit 5
chr17:60399812-60400097	706	3	35	bounded	FLJ32065	Homo sapiens cDNA FLJ32065 fis, clone OCBBF1000086.
chr17:63367112-63367234	960	10	49	bounded	BPTF	bromodomain PHD finger transcription factor
chr17:68948546-68948657	39	7	28	isolated	NA	NA
chr17:70276322-70276390	2403	45	2	bounded	SLC9A3R1	solute carrier family 9 (sodium/hydrogen
chr17:70353800-70354011	923	135	7	extending	GRIN2C	N-methyl-D-aspartate receptor subunit 2C
chr17:7037883-7037914	1	3	462	extending	DLG4	postsynaptic density protein 95
chr17:70747051-70747154	62	32	3	bounded	GGA3	Homo sapiens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complet
chr17:7083726-7083923	10	3	9	isolated	NA	NA
chr17:71013497-71013601	384	79	2	bounded	CASKIN2;KIAA1139	cask-interacting protein 2;Homo sapiens mRNA for KIAA1139 protein, partial cds.
chr17:71013981-71014152	120	57	10	extending	CASKIN2;KIAA1139	cask-interacting protein 2;Homo sapiens mRNA for KIAA1139 protein, partial cds.
chr17:71029381-71030197	5858	320	10	extending	TSEN54	tRNA splicing endonuclease 54 homolog;Homo sapiens cDNA FLJ37147 fis, clone B
chr17:71030926-71031011	106	2	30	extending	TSEN54	tRNA splicing endonuclease 54 homolog
chr17:71072051-71072183	649	4	51	bounded	LLGL2	lethal giant larvae homolog 2 isoform c;lethal giant larvae homolog 2 isoform b;lethal
chr17:71324446-71324549	243	87	3	bounded	UNK	zinc finger CCCH-type domain containing 5
chr17:7133573-7133753	3068	230	6	bounded	YBX2	germ cell specific Y-box binding protein
chr17:71522102-71522236	95	16	3	bounded	EVPL	envoplakin
chr17:71661956-71662004	39	2	23	extending	AK093500;RNF157	Homo sapiens cDNA FLJ36181 fis, clone TESTI2026794.;ring finger protein 157
chr17:7170298-7170591	443	148	31	extending	KIAA1787	hypothetical protein LOC84461 isoform 2;hypothetical protein LOC84461 isoform 1;H
chr17:7193988-7194101	109	14	2	bounded	CENTB1	centaurin beta1
chr17:71985339-71985462	116	6	13	bounded	FLJ00080;RHBDF2	FLJ00080 protein (Fragment).;rhomboid, veinlet-like 6 isoform 2;rhomboid, veinlet-like
chr17:72192749-72192817	1526	432	10	bounded	MXRA7	transmembrane anchor protein 1 isoform 1;transmembrane anchor protein 1 isoform
chr17:72243867-72244075	3224	6	11	bounded	MFSD11;ET;SFRS2	splicing factor, arginine/serine-rich 2;Homo sapiens cDNA FLJ35170 fis, clone PLACE
chr17:7273233-7273290	6	4	2	isolated	FGF11	Homo sapiens mRNA for fibroblast growth factor 11 variant protein.
chr17:7309754-7310501	5909	546	8	bounded	ZBTB4	zinc finger and BTB domain containing 4
chr17:7310572-7310853	2605	49	474	bounded	ZBTB4	zinc finger and BTB domain containing 4
chr17:73584837-73585010	180	2	246	extending	KIAA1582;TNRC6C	Homo sapiens mRNA for KIAA1582 protein, partial cds.;trinucleotide repeat containin
chr17:73605361-73605537	143	2	44	extending	TNRC6C	trinucleotide repeat containing 6C
chr17:73712504-73712866	394	24	8	extending	AFMID	arylformamidase;Homo sapiens, clone IMAGE:4804617, mRNA.
chr17:7393515-7393659	177	118	5	extending	TNFSF12;APO3L;TNFSF12-TI	tumor necrosis factor (ligand) superfamily,;Homo sapiens TWEAK mRNA, complete c
chr17:74554275-74554371	170	7	38	bounded	CTRP1;C1QTNF1	C1q and tumor necrosis factor related protein 1;Homo sapiens putative GPCR interac
chr17:7458495-7458720	540	104	4	bounded	FXR2	fragile X mental retardation syndrome related
chr17:75802441-75802722	849	3	204	bounded	SGSH	N-sulfoglucosamine sulfohydrolase (sulfamidase);Homo sapiens mRNA for N-sulfoglu
chr17:75927596-75928751	1499	46	19	extending	RNF213	chromosome 17 open reading frame 27
chr17:76825375-76825476	46	104	3	bounded	C17orf56	hypothetical protein LOC146705
chr17:7695518-7695592	169	3	63	extending	JMJD3	jumonji domain containing 3
chr17:77025430-77025538	131	6	59	extending	KIAA1447	KIAA1447 protein (Fragment).

chr17:77092805-77093247	73593	610	18006	bounded	ACTG1	actin, gamma 1 propeptide
chr17:77093874-77093975	7790	115	6	bounded	ACTG1	actin, gamma 1 propeptide
chr17:77280435-77280767	337	8	3	isolated	NA	NA
chr17:7734983-7735112	1257	649	2	extending	CHD3	chromodomain helicase DNA binding protein 3;Homo sapiens CHD3 mRNA, complete
chr17:77404829-77404871	7	2	3	isolated	P4HB	prolyl 4-hydroxylase, beta subunit precursor;P4HB protein.
chr17:77485820-77486314	2671	102	191	extending	PIG45;PYCR1	Hypothetical protein.;pyrroline-5-carboxylate reductase 1 isoform 1;pyrroline-5-carbox
chr17:77507816-77508240	130	13	3	extending	NOTUM	notum pectinacetylesterase homolog
chr17:7752445-7752872	892	222	261	extending	CHD3	chromodomain helicase DNA binding protein 3;CHD3 protein (Fragment).
chr17:77606063-77606387	2182	681	387	bounded	GPS1	G protein pathway suppressor 1 isoform 2;G protein pathway suppressor 1 isoform 1
chr17:77612035-77612126	403	3	185	bounded	DUS1L	Homo sapiens PP3111 mRNA, complete cds.;PP3111 protein
chr17:77631857-77632040	4141	936	12	bounded	FASN;FASN variant protein	fatty acid synthase;Homo sapiens mRNA for FASN variant protein, partial cds, clone:
chr17:77635678-77635870	13722	489	18	bounded	FASN	fatty acid synthase
chr17:77642047-77642200	3454	105	11	bounded	FASN	fatty acid synthase
chr17:7779065-7779188	161	2	44	bounded	CNTROB	LYST-interacting protein LIP8 isoform beta;LYST-interacting protein LIP8 isoform alph
chr17:7792226-7792370	370	3	50	bounded	CNTROB	LYST-interacting protein LIP8 isoform beta;LYST-interacting protein LIP8 isoform alph
chr17:8098209-8098333	149	36	3	bounded	PFAS	phosphoribosylformylglycinamidine synthase
chr17:8133301-8133517	829	49	4	bounded	MOG1;SLC25A35;RANGNRF;	solute carrier family 25, member 35;Homo sapiens cDNA FLJ40217 fis, clone TESTI2
chr18:10672101-10672289	35	4	4	isolated	FAM38B	hypothetical protein LOC63895
chr18:12449754-12449927	23	2	2	isolated	SPIRE1	KIAA1135 protein (Fragment).;spire homolog 1
chr18:24010925-24010971	13	13	3	bounded	CDH2	cadherin 2, type 1 preproprotein
chr18:27742715-27742974	103	16	5	extending	KIAA1012	hypothetical protein LOC22878;Homo sapiens mRNA for KIAA1012 protein, partial cd
chr18:32483277-32483366	57	22	4	isolated	FHOD3;KIAA1695	Homo sapiens mRNA for KIAA1695 protein, partial cds.;formin homology 2 domain co
chr18:5397436-5397501	5	3	4	isolated	EPB41L3	erythrocyte membrane protein band 4.1-like 3
chr18:678519-678608	71	3	160	extending	ENOSF1	rTS beta protein;Homo sapiens cDNA FLJ36554 fis, clone TRACH2008597, highly sin
chr18:8774665-8774841	415	2	34	bounded	KIAA0802	hypothetical protein LOC23255
chr19:10148968-10149000	9	58	5	bounded	DNMT1	DNA (cytosine-5-)-methyltransferase 1;DNMT1 protein.
chr19:10363235-10363382	9651	2	531	bounded	CDC37	cell division cycle 37 protein;Synthetic construct Homo sapiens mRNA for hypothetical
chr19:1055772-1055928	800	3	106	bounded	GPX4	glutathione peroxidase 4 isoform A precursor;glutathione peroxidase 4 isoform B prec
chr19:1060505-1060592	288	160	7	bounded	SBNO2	KIAA0963
chr19:11223762-11223924	262	3	198	bounded	DOCK6	dedicator of cytokinesis 6
chr19:11419350-11419433	5111	20	2106	bounded	PRKCSH	protein kinase C substrate 80K-H isoform 1;protein kinase C substrate 80K-H isoform
chr19:11420355-11420480	2558	655	60	extending	PRKCSH	protein kinase C substrate 80K-H isoform 1;protein kinase C substrate 80K-H isoform
chr19:1205975-1206060	488	4	475	bounded	MIDN	midnolin
chr19:1206310-1206693	3755	6	81	extending	MIDN	midnolin
chr19:12673160-12673267	408	2	182	bounded	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)
chr19:12673886-12674033	605	128	4	extending	TNPO2	transportin 2 (importin 3, karyopherin beta 2b)
chr19:12703158-12703255	2213	2272	4	bounded	C19orf43	hypothetical protein MGC2803
chr19:12772973-12773077	3991	829	20	bounded	PRDX2	peroxiredoxin 2 isoform a;peroxiredoxin 2 isoform c
chr19:12773886-12774033	12	3	4	isolated	NA	NA
chr19:13062128-13062204	1585	6	359	bounded	NFIX	Nuclear factor 1 X-type (Nuclear factor 1/X) (NF1-X) (NFI-X) (NF-I/X) (CCAAT-box-bin
chr19:13233222-13233424	898	6	103	extending	CACNA1A	calcium channel, alpha 1A subunit isoform 2;calcium channel, alpha 1A subunit isofor
chr19:13270358-13270446	1054	644	2	bounded	CACNA1A	calcium channel, alpha 1A subunit isoform 2;calcium channel, alpha 1A subunit isofor
chr19:13270613-13271167	4669	8	133	bounded	CACNA1A	calcium channel, alpha 1A subunit isoform 2;calcium channel, alpha 1A subunit isofor
chr19:13270975-13271167	2139	4	133	bounded	CACNA1A	calcium channel, alpha 1A subunit isoform 2;calcium channel, alpha 1A subunit isofor
chr19:13786329-13786679	332	16	10	isolated	ZSWIM4	zinc finger, SWIM domain containing 4
chr19:13899706-13900001	1328	354	97	extending	CC2D1A	coiled-coil and C2 domain containing 1A
chr19:1397287-1397340	35	10	41	extending	NA	NA
chr19:14030927-14030975	1	3	11	isolated	NA	NA
chr19:14060692-14060737	72	73	4	bounded	SAMD1	sterile alpha motif domain containing 1
chr19:14061597-14061884	934	90	2	bounded	SAMD1	sterile alpha motif domain containing 1
chr19:14124121-14124244	680	78	6	bounded	LPHN1;BX537706	latrophilin 1 isoform 1 precursor;latrophilin 1 isoform 2 precursor;Homo sapiens mRN
chr19:14124596-14124640	78	113	18	bounded	LPHN1;BX537706	latrophilin 1 isoform 1 precursor;latrophilin 1 isoform 2 precursor;Homo sapiens mRN
chr19:1433401-1433474	110	14	56	bounded	DKFZp434B217;PCSK4	Homo sapiens cDNA FLJ32673 fis, clone TESTI1000138, highly similar to NEUROEN
chr19:1438784-1439091	403	5	14	extending	DKFZp434B217;PCSK4	Homo sapiens cDNA FLJ32673 fis, clone TESTI1000138, highly similar to NEUROEN

chr19:14412955-14413227	3358	211	5	bounded	PKN1	protein kinase N1 isoform 1;protein kinase N1 isoform 2
chr19:14538573-14538743	9672	10	4	extending	NDUFB7	NADH dehydrogenase (ubiquinone) 1 beta
chr19:1484718-1484847	99	4	4	isolated	LOC126520	LOC126520 protein.
chr19:15210554-15210691	461	147	14	bounded	BRD4	bromodomain-containing protein 4 isoform long
chr19:15210707-15210791	1196	6	131	bounded	BRD4	bromodomain-containing protein 4 isoform long
chr19:15214711-15214834	1169	758	19	bounded	BRD4	bromodomain-containing protein 4 isoform long
chr19:15414487-15414559	46	3	59	isolated	DKFZp547M136	CDNA FLJ16504 fis, clone FEBRA2014122, highly similar to WizL.
chr19:16345726-16345773	11	13	7	isolated	eps15R;EPS15L1	Homo sapiens eps15R mRNA, partial cds.;epidermal growth factor receptor pathway
chr19:16396925-16397127	1835	3	295	bounded	eps15R;EPS15L1	Homo sapiens eps15R mRNA, partial cds.;epidermal growth factor receptor pathway
chr19:17376146-17376246	213	2	125	bounded	BST2	bone marrow stromal cell antigen 2
chr19:18031717-18031895	10	6	4	bounded	IL12RB1	interleukin 12 receptor, beta 1 isoform 1
chr19:18408140-18408687	4981	419	137	bounded	DKFZp434A0612;ISYNA1	myo-inositol 1-phosphate synthase A1;Homo sapiens D-myo-inositol-3-phosphate syn
chr19:18422287-18422584	729	64	3	bounded	ELL	elongation factor RNA polymerase II
chr19:18546680-18546712	308	2837	2	bounded	UBA52	ubiquitin and ribosomal protein L40 precursor
chr19:18740553-18740603	127	7	97	bounded	CRTC1;KIAA0616	Homo sapiens mRNA for KIAA0616 protein, partial cds.;mucoepidermoid carcinoma t
chr19:18911747-18911824	29	3	2	isolated	HOMER3	Homer, neuronal immediate early gene, 3
chr19:18976203-18976455	1017	11	96	bounded	SFRS14	splicing factor, arginine/serine-rich 14
chr19:19104126-19104317	663	2	54	extending	TMEM161A;UNQ582	hypothetical protein LOC54929;Homo sapiens cDNA FLJ20422 fis, clone KAT02572.
chr19:19274074-19274185	395	181	2	bounded	SF4	splicing factor 4;Homo sapiens splicing factor 4 (SF4) mRNA, complete cds.
chr19:1931148-1931202	501	641	14	bounded	CSNK1G2	casein kinase 1, gamma 2
chr19:19501173-19501326	242	2	3	extending	FLJ44968	hypothetical protein LOC374887;Homo sapiens cDNA FLJ37657 fis, clone BRHIP201
chr19:1992039-1992107	1212	696	10	bounded	MKNK2;DKFZp586A1021	MAP kinase-interacting serine/threonine kinase 2;MAP kinase-interacting serine/threo
chr19:1997366-1997690	5558	1133	320	extending	MKNK2	MAP kinase-interacting serine/threonine kinase 2
chr19:2389487-2389529	56	2	401	bounded	LMNB2	lamin B2
chr19:2951645-2951705	1170	642	4	bounded	TLE2	transducin-like enhancer protein 2
chr19:3478633-3478812	425	26	43	bounded	FZR1	Fzr1 protein
chr19:34885639-34885724	1787	2	116	bounded	DKFZp762D096;C19orf12	hypothetical protein LOC83636 isoform 2;hypothetical protein LOC83636 isoform 1;H
chr19:3494233-3494450	745	3	4	bounded	C19orf28	hypothetical protein LOC126321 isoform b;hypothetical protein LOC126321 isoform a
chr19:3540829-3540923	57	31	2	extending	GIPC3	PDZ domain protein GIPC3
chr19:3577594-3577686	526	213	3	bounded	C19orf29	chromosome 19 open reading frame 29
chr19:3588534-3588611	57	6	24	isolated	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type
chr19:3915629-3915982	5991	297	3	bounded	DAPK3	death-associated protein kinase 3
chr19:3928213-3928301	42015	10183	44	bounded	EEF2	eukaryotic translation elongation factor 2
chr19:3928817-3929140	128135	7469	121	bounded	EEF2	eukaryotic translation elongation factor 2
chr19:3931655-3931707	2104	33	7819	bounded	EEF2	eukaryotic translation elongation factor 2
chr19:3931839-3931971	36896	7833	32	bounded	EEF2	eukaryotic translation elongation factor 2
chr19:39564211-39564343	1191	1289	4	extending	GPI	glucose phosphate isomerase
chr19:4005755-4006245	3794	5	54	bounded	ZBTB7A	zinc finger and BTB domain containing 7A
chr19:40452546-40452665	1924	797	10	bounded	USF2	Homo sapiens clone TCCCIA00046 mRNA sequence.;Upstream stimulatory factor 2c
chr19:40693338-40693382	30	17	41	isolated	DMKN;UNQ729	Homo sapiens cDNA FLJ38896 fis, clone NOVAR2000352.;dermokine isoform beta
chr19:40939552-40939749	13198	1024	5	bounded	HSPB6	heat shock protein, alpha-crystallin-related,
chr19:40960202-40960281	8	2	3	isolated	SNX26	sorting nexin 26
chr19:41057483-41057575	532	82	2	bounded	APLP1	amyloid precursor-like protein 1 isoform 1;Homo sapiens cDNA FLJ35057 fis, clone O
chr19:41286142-41286723	1857	8	20	bounded	WDR62	WD repeat domain 62
chr19:4173667-4173792	99	21	19	isolated	NA	NA
chr19:43694725-43694854	270	22	29	bounded	RYR1	skeletal muscle ryanodine receptor isoform 2;Homo sapiens mRNA for ryanodine rece
chr19:43699839-43700000	4920	30	7	bounded	RYR1	skeletal muscle ryanodine receptor isoform 2;Homo sapiens mRNA for ryanodine rece
chr19:43700012-43700171	992	7	36	bounded	RYR1	skeletal muscle ryanodine receptor isoform 2;Homo sapiens mRNA for ryanodine rece
chr19:43790470-43790650	120	15	18	extending	MAP4K1	mitogen-activated protein kinase kinase kinase
chr19:43888524-43888585	612	2623	4	bounded	ACTN4	actinin, alpha 4
chr19:44003171-44003260	26	29	15	isolated	ECH1;P/OKcl.14	peroxisomal enoyl-coenzyme A hydratase-like;Homo sapiens P/OKcl.14 mRNA for he
chr19:44013690-44013996	6476	4	7006	extending	ECH1;P/OKcl.14	peroxisomal enoyl-coenzyme A hydratase-like;Homo sapiens P/OKcl.14 mRNA for he
chr19:4445373-4445472	1319	3	233	bounded	HDGF2	hepatoma-derived growth factor-related protein 2
chr19:44590223-44590644	10929	830	2	bounded	ZFP36	zinc finger protein 36, C3H type, homolog

chr19:4468566-4468710	1471	187	698	bounded	KIAA1881	plasma membrane associated protein, S3-12
chr19:4488956-4489933	8357	6	2	bounded	LRG1;HMFT1766	CDNA FLJ45787 fis, clone NETRP2008582, weakly similar to Adipophilin.;leucine-rich
chr19:45022922-45022995	4595	3	1829	bounded	FBL	fibrillarin
chr19:45023211-45023267	471	12	361	bounded	FBL	fibrillarin
chr19:45655902-45656292	4376	355	393	extending	BLVRB	biliverdin reductase B (flavin reductase
chr19:45814846-45815019	316	104	4	extending	LTBP4	Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, comp
chr19:458608-458844	683	2	27	bounded	C19orf20	gene trap ROSA b-geo 22
chr19:45902841-45903020	247	16	6	bounded	ADCK4	Homo sapiens cDNA FLJ12229 fis, clone MAMMA1001181, weakly similar to ABC1 P
chr19:46501717-46501761	534	2363	3	bounded	E1B-AP5;HNRPUL1	E1B-55kDa-associated protein 5 isoform a;Homo sapiens mRNA for E1B-55kDa-asso
chr19:46501918-46502006	4893	25	1564	bounded	E1B-AP5;HNRPUL1	E1B-55kDa-associated protein 5 isoform a;Homo sapiens mRNA for E1B-55kDa-asso
chr19:469889-470414	1331	27	14	bounded	C19orf20	gene trap ROSA b-geo 22
chr19:47218233-47218349	237	48	3	extending	GRIK5	glutamate receptor KA2 precursor
chr19:47438175-47438452	2341	420	4	bounded	GSK3A	glycogen synthase kinase 3 alpha
chr19:47444897-47445730	8192	12	96	bounded	ERF	Ets2 repressor factor;Homo sapiens Ets2 repressor factor, mRNA (cDNA clone MGC:
chr19:486837-487067	1176	1315	5	extending	CDC34	ubiquitin-conjugating enzyme Cdc34
chr19:489678-489790	102	56	5	isolated	CDC34	ubiquitin-conjugating enzyme Cdc34
chr19:492339-492545	3519	626	22	bounded	CDC34	ubiquitin-conjugating enzyme Cdc34
chr19:492339-492552	3848	626	8	bounded	CDC34	ubiquitin-conjugating enzyme Cdc34
chr19:50014202-50014289	3148	4	894	bounded	BCAM	basal cell adhesion molecule isoform 2;basal cell adhesion molecule isoform 1
chr19:50083207-50083353	152	16	5	bounded	PVRL2	poliovirus receptor related 2 isoform delta
chr19:50102901-50103049	10490	15	3572	bounded	APOE	apolipoprotein E precursor
chr19:50150280-50150322	1	3	20	isolated	NA	NA
chr19:50259110-50259329	2342	358	2	extending	SFRS16;SWAP2	splicing factor, arginine/serine-rich 16;Homo sapiens suppressor of white apricot hom
chr19:50355158-50355319	11	4	3	isolated	NA	NA
chr19:51211152-51211321	87	32	19	extending	LOC729440	hypothetical protein LOC729440
chr19:51425205-51425614	113	10	5	extending	IGFL1	insulin growth factor-like family member 1
chr19:5166509-5166573	179	76	5	bounded	PTPRS	protein tyrosine phosphatase, receptor type,
chr19:52467166-52467258	154	41	47	isolated	NA	NA
chr19:52739195-52741049	328	6	5	extending	ZNF541	Zinc finger protein 541.
chr19:52945297-52945355	5505	62	283	bounded	GLTSCR2	glioma tumor suppressor candidate region gene 2;Homo sapiens HSPC271 mRNA, p
chr19:53366923-53367146	214	2	39	bounded	LOC374920	hypothetical protein LOC374920
chr19:53688763-53688929	1073	435	45	bounded	LMTK3	lemur tyrosine kinase 3
chr19:53697978-53698055	122	59	10	bounded	LMTK3	lemur tyrosine kinase 3
chr19:54077068-54077272	71	5	15	extending	TULP2	tubby like protein 2
chr19:54150539-54150588	21	5	6	isolated	BAX	BCL2-associated X protein isoform sigma;Bax zeta.;BCL2-associated X protein isofor
chr19:54173163-54173226	127	10	39	extending	GYS1	glycogen synthase 1 (muscle)
chr19:54298071-54298204	746	5	7	bounded	SNRP70	U1 small nuclear ribonucleoprotein 70 kDa;U1 small nuclear ribonucleoprotein 70 kDa
chr19:54377647-54377936	508	82	19	bounded	TRPM4;TRPM4B	Homo sapiens cation channel TRPM4B (TRPM4B) mRNA, complete cds.;transient re
chr19:54602315-54602365	31	2	60	bounded	FLJ32658	hypothetical protein LOC147872
chr19:54792609-54793082	1476	3	75	bounded	PRR12	Proline-rich protein 12.
chr19:54811142-54811288	666	2	102	bounded	PRR12	Proline-rich protein 12.
chr19:54847875-54848506	11962	12	2	bounded	SR-A1	serine arginine-rich pre-mRNA splicing factor
chr19:54848582-54848774	3681	23	320	bounded	SR-A1	serine arginine-rich pre-mRNA splicing factor
chr19:54990699-54990886	378	296	3	extending	AP2A1	adaptor-related protein complex 2, alpha 1
chr19:55030802-55031014	1514	3	97	bounded	MED25;FP3184	ARC/mediator transcriptional coactivator;Homo sapiens clone TCBAP0758 mRNA se
chr19:55031301-55031475	547	5	96	bounded	MED25;FP3184	ARC/mediator transcriptional coactivator;Homo sapiens clone TCBAP0758 mRNA se
chr19:55068281-55068371	1030	8	168	bounded	AKT1S1	AKT1 substrate 1 (proline-rich)
chr19:55073162-55073310	2082	3	268	extending	TBC1D17	Homo sapiens cDNA FLJ12168 fis, clone MAMMA1000625, weakly similar to GYP7 P
chr19:5543758-5543893	4243	295	5	bounded	SAFB2	scaffold attachment factor B2
chr19:55601251-55601370	201	23	3	bounded	POLD1	polymerase (DNA directed), delta 1, catalytic
chr19:55646349-55646407	3	77	4	extending	MYBPC2	myosin binding protein C, fast type
chr19:56143725-56143841	1803	4	730	bounded	KLK5	kallikrein-related peptidase 5 preproprotein
chr19:56144923-56145069	1170	132	6	bounded	KLK5	kallikrein-related peptidase 5 preproprotein
chr19:56536219-56536534	96	3	5	isolated	NA	NA

chr19:56536219-56537073	178	3	9	extending	BC131493	Homo sapiens cDNA clone IMAGE:40076783, partial cds.
chr19:573582-573743	523	200	10	bounded	POLRMT	mitochondrial DNA-directed RNA polymerase
chr19:5875838-5875911	314	175	5	bounded	RANBP3	RAN binding protein 3 isoform RANBP3-d;RAN binding protein 3 isoform RANBP3-a;
chr19:59309630-59309892	2265	152	336	bounded	TFPT	TCF3 (E2A) fusion partner (in childhood
chr19:59347977-59348179	2255	341	2	extending	CNOT3;FLJ00420;KIAA0691	CCR4-NOT transcription complex, subunit 3;FLJ00420 protein (Fragment).;Homo sap
chr19:5993055-5993101	9	163	3	bounded	RFX2	regulatory factor X2 isoform a;regulatory factor X2 isoform b
chr19:60297841-60297924	295	155	4	bounded	PPP1R12C	protein phosphatase 1, regulatory subunit 12C
chr19:60299047-60299098	170	185	7	bounded	PPP1R12C	protein phosphatase 1, regulatory subunit 12C
chr19:60357210-60357379	4905	1086	5	bounded	TNNI3	troponin I, cardiac
chr19:60362311-60362629	672	5	34	bounded	C19orf51	C19orf51 protein (CDNA FLJ40069 fis, clone TESTI1000094).;hypothetical protein L
chr19:60443006-60443094	453	306	6	bounded	SAPS1	SAPS domain family, member 1
chr19:60444437-60444571	544	6	22	bounded	SAPS1	SAPS domain family, member 1
chr19:60507835-60508100	787	12	163	bounded	BRSK1	BR serine/threonine kinase 1
chr19:60561325-60563159	608	2	6	extending	DKFZp434G1729	Homo sapiens cDNA FLJ46094 fis, clone TESTI2018687.
chr19:60702995-60703591	1211	36	2	extending	NA	NA
chr19:60716190-60716351	117	17	14	extending	NA	NA
chr19:62447103-62447229	11	6	13	isolated	NA	NA
chr19:6312674-6312783	490	7	83	bounded	CLPP	endopeptidase Clp precursor
chr19:6332370-6332475	4254	1175	8	bounded	GTF2F1	general transcription factor IIF, polypeptide 1,
chr19:6365882-6366025	1888	2	3	isolated	KHSRP	KH-type splicing regulatory protein (FUSE
chr19:6366080-6366312	5586	3	1355	extending	KHSRP	KH-type splicing regulatory protein (FUSE
chr19:63755085-63755364	6513	496	459	extending	CHMP2A	chromatin modifying protein 2A
chr19:6637189-6637298	4646	30	1065	bounded	C3	Homo sapiens cDNA FLJ37409 fis, clone BRAMY2028516, highly similar to COMPLE
chr19:6660695-6660739	1502	3470	7	bounded	C3	complement component 3 precursor
chr19:6661650-6661880	5343	1064	2	extending	C3	complement component 3 precursor
chr19:6683967-6684073	351	2	251	extending	GPR108	G protein-coupled receptor 108 isoform 1;Homo sapiens mRNA full length insert cDN
chr19:6705063-6705436	242	7	12	extending	SH2D3A	SH2 domain containing 3A
chr19:7527852-7527968	55	4	5	isolated	PNPLA6;DKFZp564K0223	neuropathy target esterase;Homo sapiens mRNA for neuropathy target esterase.
chr19:755036-755172	994	822	4	bounded	PTBP1	Homo sapiens mRNA for polypyrimidine tract-binding protein 1 isoform c variant protei
chr19:755292-755939	8700	159	867	extending	PTBP1	Homo sapiens mRNA for polypyrimidine tract-binding protein 1 isoform c variant protei
chr19:755532-755690	3126	97	14	bounded	PTBP1	Homo sapiens mRNA for polypyrimidine tract-binding protein 1 isoform c variant protei
chr19:759548-759762	6174	17	216	bounded	PTBP1	Homo sapiens mRNA for polypyrimidine tract-binding protein 1 isoform c variant protei
chr19:7609612-7609986	522	154	84	extending	STXBP2	syntaxin binding protein 2;Homo sapiens mRNA for hunc18b2, complete cds.
chr19:7888586-7888744	261	4	24	isolated	NA	NA
chr19:811617-811777	8698	1125	2	extending	CFD	complement factor D preproprotein
chr19:8287380-8287522	2033	399	19	bounded	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha
chr19:8335090-8335523	1907	3	45	bounded	ANGPTL4	angiopoietin-like 4 protein isoform a precursor;angiopoietin-like 4 protein isoform b pre
chr19:8438421-8438468	261	3	425	bounded	HNRPM	heterogeneous nuclear ribonucleoprotein M
chr19:8461771-8462041	115	26	6	extending	PRAM1	PML-RARA regulated adaptor molecule 1
chr19:8518920-8519201	32	15	20	extending	MYO1F;MYO1F variant protein	Homo sapiens mRNA for MYO1F variant protein, partial cds, clone: hk07299.;myosin
chr19:8566663-8566787	26	2	17	bounded	ADAMTS10	ADAM metallopeptidase with thrombospondin type 1;A disintegrin-like and metalloprot
chr19:883418-883478	125	137	10	bounded	ARID3A	AT rich interactive domain 3A (BRIGHT- like)
chr19:962366-962496	2768	316	6	bounded	C19orf6	membralin isoform 2;membralin isoform 1
chr19:962891-962962	971	955	12	bounded	C19orf6	membralin isoform 2;membralin isoform 1
chr19:971771-971986	2888	314	2	bounded	C19orf6	membralin isoform 2;membralin isoform 1
chr19:983391-983509	408	398	4	extending	CNN2	calponin 2 isoform a;Homo sapiens cDNA: FLJ21182 fis, clone CAS11560, highly sim
chr19:987066-987245	1724	9	153	extending	CNN2	calponin 2 isoform a;Homo sapiens cDNA: FLJ21182 fis, clone CAS11560, highly sim
chr19:995642-995743	59	2	45	bounded	ABCA7	ATP-binding cassette, sub-family A, member 7
chr2:101846721-101846945	429	15	27	bounded	MAP4K4	mitogen-activated protein kinase kinase kinase
chr2:113694140-113694252	42	12	8	extending	PAX8	paired box gene 8 isoform PAX8D;paired box gene 8 isoform PAX8E;paired box gene
chr2:127534633-127534686	378	9	274	extending	BIN1	bridging integrator 1 isoform 10;bridging integrator 1 isoform 8;bridging integrator 1 is
chr2:130833276-130833535	110	29	11	extending	PTPN18	protein tyrosine phosphatase, non-receptor type
chr2:131966250-131966347	2384	898	3	bounded	FAM128B	FAM128B protein (Fragment).
chr2:131991770-131991851	171	99	3	bounded	BC093080	Homo sapiens cDNA FLJ41352 fis, clone BRAWH2014645.

chr2:148957149-148958174	480	12	3	extending	MBD5;KIAA1461	Homo sapiens mRNA for KIAA1461 protein, partial cds.;methyl-CpG binding domain
chr2:149255689-149255819	856	7	63	bounded	EPC2	enhancer of polycomb homolog 2
chr2:152252179-152252493	220	3	5	extending	NEB	nebulin
chr2:161744409-161744518	347	2	103	bounded	TANK	TRAF interacting protein TANK isoform b;TRAF interacting protein TANK isoform a
chr2:1648993-1649242	1145	172	4	bounded	PXDN	Homo sapiens melanoma-associated antigen MG50 mRNA, partial cds.;peroxidasin
chr2:175140943-175141047	374	4	64	bounded	AK002090;WIPF1;BC046497	Homo sapiens cDNA FLJ11228 fis, clone PLACE1008329.;WAS/WASL interacting pr
chr2:179173826-179174143	313	34	54	bounded	AK093733;BC070113;TTN	titin isoform N2-A;Homo sapiens cDNA FLJ36414 fis, clone THYMU2010848.;titin isof
chr2:1791855-1791997	47	17	3	extending	MYT1L	myelin transcription factor 1-like
chr2:179296018-179296668	544	29	70	extending	TTN	Homo sapiens titin (TTN) mRNA, partial cds.;titin isoform N2-B;titin isoform novex-2;tit
chr2:179372459-179372882	545	79	44	extending	TTN	titin isoform N2-A;titin isoform N2-B;titin isoform novex-3;titin isoform novex-2;titin isof
chr2:196890195-196890338	25	4	15	extending	DKFZp686M17164;HECW2	Hypothetical protein DKFZp686M17164.;HECT, C2 and WW domain containing E3 u
chr2:201651903-201651990	641	16	274	bounded	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta
chr2:203763760-203764245	7	66	6	bounded	NBEAL1	Neurobeachin-like 1 (Amyotrophic lateral sclerosis 2 chromosomal region candidate
chr2:203989882-203990049	207	5	24	bounded	ABI2;argBPIB	ArgBPIB protein.;Abl interactor 2 (Abelson interactor 2) (Abi-2) (Abl-binding protein 3)
chr2:210412191-210412399	33	3	2	bounded	KIAA1843	KIAA1843 protein (Fragment).
chr2:216689627-216689792	940	174	4	bounded	XRCC5	ATP-dependent DNA helicase II
chr2:217072238-217072341	55127	23063	60	bounded	RPL37A	RPL37A protein.;ribosomal protein L37a
chr2:218854907-218855108	1787	156	8	bounded	PNKD;TMBIM1	myofibrillogenesis regulator 1 isoform 1;transmembrane BAX inhibitor motif containing
chr2:219224668-219225267	389	16	12	bounded	ZNF142	zinc finger protein 142
chr2:220130309-220131076	2347	88	102	extending	KIAA0657	CDNA FLJ13792 fis, clone THYRO1000072, weakly similar to MYOSIN LIGHT CHAI
chr2:228568469-228568625	236	25	8	bounded	SKIP	sphingosine kinase type 1-interacting protein
chr2:232082087-232082298	40	2	11	bounded	C2orf52	hypothetical protein LOC151477
chr2:232284841-232284945	14384	671	20	extending	PTMA	prothymosin, alpha (gene sequence 28);Homo sapiens prothymosin a14 mRNA, com
chr2:233057755-233058045	59	4	3	extending	ECEL1	endothelin converting enzyme-like 1
chr2:233417000-233417167	1074	107	6	bounded	TNRC15	trinucleotide repeat containing 15
chr2:233417174-233417209	24	5	281	bounded	TNRC15	trinucleotide repeat containing 15
chr2:236981981-236982430	447	4	185	isolated	IQCA	Homo sapiens cDNA: FLJ22527 fis, clone HRC12820.;IQ motif containing with AAA
chr2:238303162-238303224	17	6	6	isolated	LRRFIP1	leucine rich repeat (in FLII) interacting;LRR FLI-I interacting protein 1 (Fragment).
chr2:239689424-239689529	230	5	56	bounded	HDAC4	histone deacetylase 4
chr2:241054148-241054209	198	256	9	bounded	GPC1	glypican 1 precursor
chr2:241359061-241359269	1684	678	48	extending	KIF1A	axonal transport of synaptic vesicles
chr2:242273859-242273965	263	12	168	bounded	DTYMK	deoxythymidylate kinase (thymidylate kinase);Homo sapiens mRNA for deoxythymidyl
chr2:27101963-27102109	2914	3	261	bounded	MAPRE3	microtubule-associated protein, RP/EB family,
chr2:27113450-27113550	781	5	362	bounded	FLJ20254	hypothetical protein LOC54867 isoform 1
chr2:27116723-27116868	190	8	79	bounded	FLJ20254	hypothetical protein LOC54867 isoform 1
chr2:27316069-27316156	1091	619	2	bounded	CAD	carbamoylphosphate synthetase 2/aspartate
chr2:27461187-27461459	5178	2	1519	bounded	PPM1G	Protein phosphatase 1G variant (Fragment).;protein phosphatase 1G
chr2:32626427-32626585	339	2	124	bounded	BIRC6	baculoviral IAP repeat-containing 6
chr2:47256766-47256892	376	13	16	isolated	CALM2	calmodulin 2
chr2:47919502-47919643	91	13	3	bounded	FBXO11	F-box only protein 11 isoform 3;F-box only protein 11 isoform 2;F-box only protein 11
chr2:54724964-54725257	2178	153	5	extending	SPTBN1	spectrin, beta, non-erythrocytic 1 isoform 2;spectrin, beta, non-erythrocytic 1 isoform 1
chr2:66648089-66648228	551	50	4	extending	MEIS1	Meis homeobox 1;Homo sapiens cDNA FLJ40855 fis, clone TRACH2016317, highly s
chr2:71670764-71670926	118	2	54	extending	DYSF	dysferlin
chr2:74506065-74506126	106	3	47	bounded	WDR54	WD repeat domain 54
chr2:85426480-85426575	68	2	3	isolated	RETSAT	all-trans-13,14-dihydroretinol saturase
chr2:85633866-85634129	481	39	3	bounded	GGCX	gamma-glutamyl carboxylase
chr2:85659646-85659801	3874	2	327	bounded	VAMP8	vesicle-associated membrane protein 8
chr2:85673582-85673707	1476	427	2	bounded	VAMP5	vesicle-associated membrane protein 5
chr2:86300604-86300755	43	4	4	isolated	REEP1	receptor expression enhancing protein 1
chr2:86307997-86308032	1	5	3	isolated	REEP1	receptor expression enhancing protein 1
chr2:96216195-96216379	437	3	97	bounded	STARD7	START domain containing 7
chr2:96389629-96389714	22	3	10	bounded	NCAPH	non-SMC condensin I complex, subunit H;Homo sapiens non-SMC condensin I compl
chr2:96830536-96830598	5	2	3	isolated	CNNM4	cyclin M4
chr2:96895130-96895393	993	25	72	extending	SEMA4C	semaphorin 4C

chr2:99154234-99154324	39	2	10	extending	MITD1;MRPL30	Homo sapiens HSPC249 mRNA, complete cds.;39S ribosomal protein L30, mitochonc
chr2:99414635-99414834	162	3	23	isolated	REV1	REV1-like isoform 2;REV1-like isoform 1
chr20:1063857-1063949	1443	2	140	bounded	PSMF1	OTTHUMP00000029954.;proteasome inhibitor subunit 1 isoform 2;proteasome inhibit
chr20:1195298-1195456	49	8	7	extending	SNPH	syntaphilin
chr20:1225690-1225896	78	3	23	extending	SNPH	syntaphilin
chr20:13656977-13657112	72	2	41	extending	ESF1	ABT1-associated protein
chr20:17588985-17589173	1422	6	152	bounded	KIAA1398;RRBP1	ribosome binding protein 1;Hypothetical protein (Fragment).
chr20:20527323-20527463	12	3	14	isolated	C20orf74	hypothetical protein LOC57186
chr20:2788885-2789043	335	83	4	extending	VPS16	vacuolar protein sorting 16 isoform 3;vacuolar protein sorting 16 isoform 1;Homo sapie
chr20:2790422-2790545	618	3	8	extending	VPS16	vacuolar protein sorting 16 isoform 3;vacuolar protein sorting 16 isoform 1;Homo sapie
chr20:29527872-29528249	165	9	3	bounded	REM1	RAS-like GTP-binding protein REM
chr20:29565945-29566198	4275	2	234	bounded	HM13	minor histocompatibility antigen 13 isoform 2;minor histocompatibility antigen 13 isofor
chr20:2975260-2975546	2927	450	19	extending	MRPS26	mitochondrial ribosomal protein S26
chr20:29914035-29914185	382	57	17	bounded	DUSP15	Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16) (Vaccinia virus VH
chr20:32806186-32806296	294	55	19	bounded	NCOA6	nuclear receptor coactivator 6
chr20:32911433-32911541	407	279	7	bounded	GGTL3	gamma-glutamyltransferase-like 3;Gamma-glutamyltransferase 4 precursor (EC 2.3.2.
chr20:33305917-33305973	47	2	36	bounded	MMP24	matrix metalloproteinase 24 preproprotein
chr20:33518511-33518794	258	2	33	extending	C-NAP1;CEP250	centrosomal protein 2 isoform 1;centrosomal protein 2 isoform 2;Homo sapiens cep25
chr20:36690984-36691059	4	2	3	isolated	NA	NA
chr20:36691559-36691707	48	4	5	isolated	NA	NA
chr20:39235474-39235867	3225	104	211	extending	PLCG1	phospholipase C gamma 1 isoform a;phospholipase C gamma 1 isoform b
chr20:43969723-43969801	557	6	369	extending	PLTP	phospholipid transfer protein isoform b;phospholipid transfer protein isoform a;Homo s
chr20:44008075-44008430	7134	138	52	extending	C20orf67;PCIF1	Homo sapiens mRNA for posphorylated CTD interacting factor PCIF1, complete cds.;p
chr20:44099301-44099452	266	121	14	extending	SLC12A5	Solute carrier family 12, (Potassium-chloride transporter) member 5.;solute carrier fam
chr20:44105679-44105979	533	57	156	extending	SLC12A5	solute carrier family 12 member 5
chr20:45564532-45564645	18	17	3	isolated	NCOA3	nuclear receptor coactivator 3 isoform b;nuclear receptor coactivator 3 isoform a
chr20:45713316-45713427	226	8	47	bounded	NCOA3	nuclear receptor coactivator 3 isoform b;nuclear receptor coactivator 3 isoform a
chr20:47864955-47865133	565	3	18	bounded	SLC9A8	Na+/H+ exchanger isoform 8
chr20:48241317-48241394	698	5	9	bounded	CEBPB	CCAAT/enhancer binding protein beta
chr20:49762822-49763020	732	35	35	extending	ATP9A	ATPase, Class II, type 9A
chr20:50215810-50215965	254	20	3	bounded	ZFP64	zinc finger protein 64 isoform c;zinc finger protein 64 isoform b;zinc finger protein 64 is
chr20:54639668-54640319	2228	459	81	extending	TFAP2C	transcription factor AP-2 gamma
chr20:56911949-56912035	25916	743	12972	bounded	GNASL;GNAS	GNAS complex locus isoform d;GNAS complex locus isoform f;GNAS complex locus i
chr20:5852333-5852746	19471	3	493	bounded	CHGB	chromogranin B precursor
chr20:60011621-60011725	65	17	82	bounded	TAF4	TBP-associated factor 4
chr20:60209134-60209521	1224	92	24	bounded	GTPBP5;DKFZp434C0935	GTP binding protein 5;Homo sapiens cDNA FLJ10741 fis, clone NT2RP3001529, wea
chr20:60305485-60305924	81	3	20	isolated	NA	NA
chr20:60319353-60319467	174	60	7	bounded	LAMA5	laminin alpha 5
chr20:60342015-60342151	293	388	8	bounded	LAMA5	laminin alpha 5
chr20:61515205-61515378	426	6	84	bounded	KCNQ2	potassium voltage-gated channel KQT-like protein
chr20:61530145-61530232	112	5	63	extending	KCNQ2	potassium voltage-gated channel KQT-like protein
chr20:61590715-61591018	29564	2515	7	extending	EEF1A2	eukaryotic translation elongation factor 1 alpha
chr20:61743905-61744090	2431	213	9	bounded	STMN3	SCG10-like-protein
chr20:61745475-61745728	3189	6	425	bounded	STMN3	SCG10-like-protein
chr20:61797394-61797447	94	8	196	bounded	RTEL1;TNFRSF6B	Regulator of telomere elongation helicase 1 (EC 3.6.1.-) (Helicase- like protein NHL).;t
chr20:62139724-62139999	340	10	12	bounded	PRR17	proline rich 17;Homo sapiens cDNA FLJ27267 fis, clone TMS00367.
chr21:16141853-16141966	17	12	18	isolated	USP25	ubiquitin specific protease 25
chr21:26269254-26269403	8183	1761	9	bounded	APP	amyloid beta A4 protein precursor, isoform c;amyloid beta A4 protein precursor, isofor
chr21:31414557-31415026	10227	3	130	bounded	TIAM1	T-cell lymphoma invasion and metastasis 1
chr21:43937499-43937692	383	58	2	bounded	RRP1B	ribosomal RNA processing 1 homolog B
chr21:44126813-44126924	13	3	3	extending	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3
chr21:44569464-44569554	2048	966	2	bounded	PFKL	Homo sapiens mRNA for liver phosphofructokinase isoform a variant protein.;liver pho
chr21:46230868-46231123	13265	352	22	extending	COL6A1	collagen, type VI, alpha 1 precursor
chr21:46235331-46235383	440	82	515	bounded	COL6A1	collagen, type VI, alpha 1 precursor

chr21:46242050-46242104	253	21	381	bounded	COL6A1	collagen, type VI, alpha 1 precursor
chr21:46246989-46247052	1673	11	2844	bounded	COL6A1	collagen, type VI, alpha 1 precursor;Homo sapiens collagen, type VI, alpha 1, mRNA (
chr21:46369608-46369959	3313	538	616	extending	COL6A2	alpha 2 type VI collagen isoform 2C2a precursor;alpha 2 type VI collagen isoform 2C2
chr21:46610927-46611404	805	87	4	bounded	PCNT	pericentrin (kendrin)
chr22:16400101-16400405	597	18	8	bounded	CECR2	Cat eye syndrome critical region protein 2.
chr22:16442643-16442730	69	2	5	bounded	SLC25A18	solute carrier
chr22:17550903-17551156	1062	144	2	bounded	CLTCL1	Homo sapiens cDNA FLJ43941 fis, clone TESTI4014265, moderately similar to Clathr
chr22:17643162-17643353	197	3	78	bounded	CLTCL1	Homo sapiens cDNA FLJ43941 fis, clone TESTI4014265, moderately similar to Clathr
chr22:18245613-18245787	467	104	7	extending	TXNRD2;TRXR2A	Homo sapiens mRNA for thioredoxin reductase II alpha, partial cds.;thioredoxin reduc
chr22:19115305-19116133	582	12	78	extending	SCARF2	scavenger receptor class F, member 2 isoform 1;scavenger receptor class F, member
chr22:19710094-19710197	70	9	2	extending	HP2XM;P2RXL1	purinergic receptor P2X-like 1, orphan receptor;Homo sapiens mRNA for HUMAN P2
chr22:20491955-20492135	1184	2	239	bounded	MAPK1	mitogen-activated protein kinase 1
chr22:21079523-21079768	182	145	3	bounded	abParts	Parts of antibodies, mostly variable regions.
chr22:21385384-21385658	6428	5986	18	bounded	abParts;DKFZp667J0810	Parts of antibodies, mostly variable regions.;Homo sapiens cDNA FLJ43597 fis, clone
chr22:21560296-21560439	52	8	70	bounded	DKFZp667J0810;abParts;IGL	Parts of antibodies, mostly variable regions.;Homo sapiens mRNA for immunoglobulin
chr22:21587794-21587870	1	84	304	extending	abParts	Parts of antibodies, mostly variable regions.
chr22:21587908-21588045	2	9	11	isolated	abParts	Parts of antibodies, mostly variable regions.
chr22:21831085-21831440	69	5	14	extending	RAB36	RAB36, member RAS oncogene family
chr22:22452769-22452856	23	17	8	bounded	MMP11	Homo sapiens PP13850 mRNA, complete cds.;matrix metalloproteinase 11 prepropro
chr22:22455598-22455680	12	15	69	bounded	MMP11	Homo sapiens PP13850 mRNA, complete cds.;matrix metalloproteinase 11 prepropro
chr22:22566560-22566769	43684	6	3410	extending	BC036909;MIF	Homo sapiens macrophage migration inhibitory factor (MIF) mRNA, complete cds.;ma
chr22:22892607-22892943	11185	35	4	bounded	KIAA0330;CABIN1	calcineurin binding protein 1;Homo sapiens mRNA for KIAA0330 gene, partial cds.
chr22:22903559-22903785	3185	39	737	bounded	CABIN1	calcineurin binding protein 1
chr22:28018489-28018595	961	3	414	bounded	EWSR1	Ewing sarcoma breakpoint region 1 isoform EWS-b;Ewing sarcoma breakpoint region
chr22:29068189-29068246	1229	2819	18	bounded	SF3A1	splicing factor 3a, subunit 1, 120kDa isoform 1
chr22:29859095-29859221	445	2	99	bounded	PIB5PA	phosphatidylinositol (4,5) bisphosphate;Homo sapiens cDNA FLJ35540 fis, clone SPL
chr22:33991555-33991596	21	4	78	bounded	HMG2L1	high-mobility group protein 2-like 1 isoform b;high-mobility group protein 2-like 1 isofor
chr22:35011113-35011343	6014	547	13	extending	MYH9	myosin, heavy polypeptide 9, non-muscle
chr22:35034800-35034862	14	6	6	isolated	MYH9	myosin, heavy polypeptide 9, non-muscle
chr22:35047738-35047812	202	3	176	extending	MYH9	myosin, heavy polypeptide 9, non-muscle
chr22:36356922-36357052	1313	10	233	bounded	GGA1	golgi associated, gamma adaptin ear containing,
chr22:36939784-36939842	270	2	229	bounded	MAFF	transcription factor MAFF
chr22:36940373-36940696	1046	230	2	bounded	MAFF	transcription factor MAFF
chr22:36957192-36957286	155	2	30	extending	C22orf5	Homo sapiens mRNA for putative MAPK activating protein, complete cds, clone: FM0
chr22:37442579-37442951	2036	3	23	extending	GTPBP1	GTP binding protein 1
chr22:37867298-37867387	676	11	506	extending	CBX7	chromobox homolog 7;Chromobox-like 7.
chr22:38153978-38154134	988	5	143	bounded	MAP3K7IP1;SYBGRIB	mitogen-activated protein kinase kinase kinase 7;Mitogen-activated protein kinase kin
chr22:38389622-38389792	122	3	15	extending	CACNA1I	calcium channel, voltage-dependent, T type,
chr22:38410250-38410449	157	3	5	extending	CACNA1I	calcium channel, voltage-dependent, T type,
chr22:39143291-39143398	155	18	7	bounded	MKL1	megakaryoblastic leukemia 1 protein
chr22:39144687-39145334	2831	3	45	bounded	MKL1	megakaryoblastic leukemia 1 protein
chr22:40414744-40414931	389	628	2	extending	NHP2L1	NHP2 non-histone chromosome protein 2-like 1
chr22:41359258-41359350	5	10	9	extending	CYB5R3	cytochrome b5 reductase isoform 1;cytochrome b5 reductase isoform 2
chr22:42257770-42258177	86	5	3	extending	FLJ23588	CAP-binding protein complex interacting protein
chr22:48577457-48577648	616	157	8	bounded	BRD1	bromodomain containing protein 1
chr22:48741094-48741135	144	329	9	bounded	PIM3	pim-3 oncogene
chr22:49047081-49047167	261	3	143	extending	MAPK11	mitogen-activated protein kinase 11
chr22:49047490-49047730	713	146	126	extending	MAPK11	mitogen-activated protein kinase 11
chr22:49062410-49063106	2457	296	4	extending	Nbla00445;PLXNB2;KIAA0315	Plexin-B2 precursor (MM1).;Hypothetical protein Nbla00445 (Fragment).;Homo sapien
chr22:49063606-49064001	4313	173	331	extending	PLXNB2;KIAA0315	Plexin-B2 precursor (MM1).;Homo sapiens mRNA for KIAA0315 gene, partial cds.
chr22:49063608-49063742	1649	41	436	bounded	PLXNB2;KIAA0315	Plexin-B2 precursor (MM1).;Homo sapiens mRNA for KIAA0315 gene, partial cds.
chr22:49066315-49066457	403	10	220	extending	PLXNB2;KIAA0315	Plexin-B2 precursor (MM1).;Homo sapiens mRNA for KIAA0315 gene, partial cds.
chr22:49095389-49095495	159	2	47	extending	FAM116B	hypothetical protein LOC414918
chr22:49095606-49095691	243	48	3	bounded	FAM116B	hypothetical protein LOC414918

chr22:49226096-49226250	483	5	2	bounded	SAPS2	SAPS domain family member 2.;SAPS domain family, member 2
chr22:49239807-49240049	1419	232	5	extending	SBF1	SBF1 protein (Fragment).;SET binding factor 1 isoform a
chr22:49251445-49251620	482	29	2	extending	SBF1	SET binding factor 1 isoform a
chr22:49388518-49388655	787	186	49	bounded	MAPK8IP2	mitogen-activated protein kinase 8 interacting
chr22:49388740-49388793	173	9	86	bounded	MAPK8IP2	mitogen-activated protein kinase 8 interacting
chr22:49388975-49389014	20	2	151	bounded	MAPK8IP2	mitogen-activated protein kinase 8 interacting
chr22:49390835-49391028	1989	3	238	extending	MAPK8IP2	mitogen-activated protein kinase 8 interacting
chr22:49505478-49505545	1945	257	3	bounded	SHANK3	proline-rich synapse-associated protein 2
chr3:101979818-101979882	45	60	2	bounded	ABI3BP	Target of Nesh-SH3 precursor (Tarsh) (Nesh-binding protein) (NeshBP) (ABI gene fan
chr3:10352813-10352984	265	16	114	bounded	ATP2B2;ATP2B2 variant prote	Homo sapiens mRNA for ATP2B2 variant protein, partial cds, clone: fg06458.;plasma
chr3:116877916-116878147	3447	3	268	bounded	GAP43	growth associated protein 43
chr3:124501657-124501778	178	22	3	bounded	ADCY5	adenylate cyclase 5
chr3:12588622-12588872	918	3	273	bounded	MKRN2	makorin, ring finger protein, 2
chr3:128862151-128862692	5580	7	84	bounded	PODXL2	endoglycan
chr3:130481329-130481448	834	7	133	bounded	C3orf37	hypothetical protein LOC56941
chr3:13374695-13374895	567	3	56	extending	NUP210	nucleoporin 210
chr3:13626014-13626173	268	41	2	extending	FBLN2	fibulin 2 precursor, isoform a;fibulin 2 precursor, isoform b
chr3:139600001-139600104	812	189	85	extending	MRAS	muscle RAS oncogene homolog
chr3:14175041-14175396	1069	2	17	bounded	XPC	xeroderma pigmentosum, complementation group C
chr3:14940513-14940649	479	2	8	extending	FGD5	FYVE, RhoGEF and PH domain containing 5
chr3:151962910-151963279	1482	231	3	bounded	SIAH2	seven in absentia homolog 2
chr3:153017895-153018066	48	4	31	bounded	AADAC	arylacetamide deacetylase
chr3:159911221-159911404	889	34	23	bounded	RARRES1	retinoic acid receptor responder (tazarotene
chr3:169225005-169225076	302	2	221	extending	GOLPH4	golgi phosphoprotein 4
chr3:169229702-169229780	278	152	4	extending	GOLPH4	golgi phosphoprotein 4
chr3:169229702-169229784	286	152	180	extending	GOLPH4	golgi phosphoprotein 4
chr3:169233002-169233307	3016	163	3	bounded	GOLPH4	golgi phosphoprotein 4
chr3:180228124-180228294	96	16	20	bounded	ZMAT3	p53 target zinc finger protein isoform 2;p53 target zinc finger protein isoform 1
chr3:184954605-184954847	292	19	11	extending	YEATS2	YEATS domain containing 2
chr3:185356109-185356278	617	2	184	bounded	DVL3	dishevelled 3
chr3:185431229-185431299	32	8	2	isolated	NA	NA
chr3:185439042-185439355	329	50	13	extending	DKFZp761K032	Hypothetical protein DKFZp761K032 (Fragment).
chr3:185780884-185781360	951	34	55	extending	EPHB3	ephrin receptor EphB3 precursor
chr3:186873023-186873093	47	47	2	bounded	IGF2BP2	insulin-like growth factor 2 mRNA binding
chr3:196937222-196939114	320	15	14	extending	MUC20	mucin 20
chr3:197096080-197096250	819	308	15	bounded	TNK2	tyrosine kinase, non-receptor, 2 isoform 1;tyrosine kinase, non-receptor, 2 isoform 2;H
chr3:197099690-197099874	2509	3	266	extending	TNK2	tyrosine kinase, non-receptor, 2 isoform 1;tyrosine kinase, non-receptor, 2 isoform 2
chr3:197195862-197196005	2	38	95	bounded	BC071730	Homo sapiens full length insert cDNA clone ZC24D06.
chr3:198215169-198215448	900	120	7	extending	MFI2;BC032042	melanoma-associated antigen p97 isoform 1,;Homo sapiens cDNA clone IMAGE:481
chr3:32753909-32753986	241	15	66	bounded	CNOT10	CCR4-NOT transcription complex, subunit 10
chr3:33533477-33533658	373	21	2	bounded	CLASP2;KIAA0627	Homo sapiens mRNA for KIAA0627 protein, partial cds.;CLIP-associating protein 2
chr3:33881788-33881926	840	4	74	bounded	PDCD6IP	programmed cell death 6 interacting protein
chr3:36875213-36875389	89	12	19	extending	KIAA0342	KIAA0342 protein (Fragment).
chr3:36877401-36877655	146	19	2	isolated	NA	NA
chr3:37335591-37335689	200	2	66	bounded	GOLGA4	golgi autoantigen, golgin subfamily a, 4
chr3:39146574-39146853	105	29	15	extending	STI2;TTC21A	tetratricopeptide repeat domain 21A;Homo sapiens mRNA for TRP domain containing
chr3:39153675-39153882	259	5	17	extending	STI2;TTC21A	tetratricopeptide repeat domain 21A;Homo sapiens mRNA for TRP domain containing
chr3:42676133-42676324	714	3	30	bounded	ZBTB47	zinc finger protein 651
chr3:45052020-45052243	3665	206	12	bounded	CLEC3B	C-type lectin domain family 3, member B
chr3:47020571-47020704	512	175	6	bounded	FLJ00341	FLJ00341 protein (Fragment).
chr3:47136676-47141042	3233	16	19	extending	SETD2	Histone-lysine N-methyltransferase SETD2 (EC 2.1.1.43) (SET domain- containing pr
chr3:47514780-47514960	682	48	3	extending	TMEM103	hypothetical protein LOC54859;CDNA FLJ20211 fis, clone COLF1807.
chr3:48577847-48577999	310	26	8	extending	COL7A1	alpha 1 type VII collagen precursor
chr3:48602896-48602994	286	154	4	bounded	COL7A1	alpha 1 type VII collagen precursor

chr3:48607512-48607596	489	69	264	bounded	COL7A1	alpha 1 type VII collagen precursor
chr3:48691290-48691406	236	4	51	extending	NCKIPSD	NCK interacting protein with SH3 domain isoform
chr3:49111943-49112084	1536	4	410	bounded	QARS	glutaminyl-tRNA synthetase;QARS protein (Fragment).
chr3:49374927-49375063	4411	6	1357	extending	RHOA	ras homolog gene family, member A
chr3:49719258-49719335	176	2	47	bounded	RNF123;DKFZp434A0610	Homo sapiens FP1477 mRNA, complete cds.;ring finger protein 123
chr3:50070171-50070440	1425	5	944	bounded	RBM6	RBM6 protein.;RNA binding motif protein 6
chr3:51391920-51392042	46	9	35	isolated	DOCK3	dedicator of cytokinesis 3
chr3:52256030-52256282	258	71	4	bounded	PPM1M	protein phosphatase 1M (PP2C domain containing);Protein phosphatase 2C isoform
chr3:52397474-52397665	160	6	9	bounded	DNAH1;KIAA1410	Homo sapiens mRNA for KIAA1410 protein, partial cds.;dynein, axonemal, heavy poly
chr3:52418610-52418799	717	220	649	extending	BAP1	BRCA1 associated protein-1
chr3:52498602-52498734	1104	3	64	bounded	NISCH;KIAA0975	Homo sapiens mRNA for KIAA0975 protein, partial cds.;nischarin
chr3:52536885-52537129	874	173	466	extending	NT5DC2	5'-nucleotidase domain containing 2
chr3:52702464-52702863	2662	504	493	extending	GNL3	guanine nucleotide binding protein-like 3
chr3:52790963-52791121	457	2	60	extending	ITIH1	inter-alpha (globulin) inhibitor H1
chr3:56580235-56580370	44	2	11	extending	CCDC66	Homo sapiens cDNA FLJ38369 fis, clone FEBRA2001828.;coiled-coil domain containi
chr3:62739887-62740159	4	6	2	isolated	CADPS	Ca2+-dependent secretion activator isoform 1;Ca2+-dependent secretion activator iso
chr3:63983991-63984155	2759	358	4	bounded	PFAAP4;PSMD6	proteasome (prosome, macropain) 26S subunit,;KIAA0107 isoform.
chr3:70083619-70083727	15	8	23	extending	MITF	microphthalmia-associated transcription factor
chr3:9414108-9414411	87	32	2	extending	AK093640;AL110136;SETD5;	Homo sapiens mRNA for KIAA1757 protein, partial cds.;SET domain containing 5;Hor
chr3:9518203-9518322	11	4	2	bounded	LHFPL4	lipoma HMGIC fusion partner-like 4
chr4:110963041-110963093	22	5	94	bounded	NOLA1	nucleolar protein family A, member 1
chr4:1232704-1232849	1020	270	2	bounded	CTBP1	C-terminal binding protein 1 isoform 1;C-terminal binding protein 1 isoform 2
chr4:144600976-144601090	147	13	16	bounded	GAB1	GRB2-associated binding protein 1 isoform b;GRB2-associated binding protein 1 isof
chr4:154463250-154463430	248	26	6	extending	TRIM2	tripartite motif-containing 2
chr4:155707091-155707373	6848	172	5	extending	FGB	fibrinogen, beta chain preproprotein;Homo sapiens cDNA clone IMAGE:4071515, part
chr4:155726140-155726217	34387	75	25	bounded	FGA	fibrinogen, alpha polypeptide isoform alpha;Homo sapiens fibrinogen alpha chain, mR
chr4:155726588-155726739	25781	3	10	bounded	FGA	fibrinogen, alpha polypeptide isoform alpha;Homo sapiens fibrinogen alpha chain, mR
chr4:159311068-159311371	413	58	2	bounded	C4orf18;AK126266	Homo sapiens cDNA FLJ39473 fis, clone PROST2012890.;hypothetical protein LOC5
chr4:160496688-160496760	124	6	43	bounded	RAPGEF2	Rap guanine nucleotide exchange factor 2 (Neural RAP guanine nucleotide exchange
chr4:1706804-1706850	108	3	301	bounded	TACC3	transforming, acidic coiled-coil containing
chr4:1771272-1771325	159	72	4	bounded	FGFR3	fibroblast growth factor receptor 3 isoform 1;Fibroblast growth factor receptor 3 isofor
chr4:186764733-186765497	140	4	8	extending	ArgBP2b;ArgBP2a;SORBS2	Arg/Abl-interacting protein ArgBP2b (Fragment).;Arg/Abl-interacting protein ArgBP2a.;
chr4:38986651-38986805	416	60	2	bounded	RFC1	replication factor C large subunit
chr4:39376253-39376405	4119	8	480	bounded	LIG;HIP2	huntingtin interacting protein 2;Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19)
chr4:68211452-68211504	7	18	2	bounded	UBE1L2	ubiquitin-activating enzyme E1-like 2
chr4:68885340-68885514	2453	74	22	bounded	YTHDC1	splicing factor YT521-B isoform 1;splicing factor YT521-B isoform 2
chr4:68885551-68885763	1606	10	106	bounded	YTHDC1	splicing factor YT521-B isoform 1;splicing factor YT521-B isoform 2
chr4:717124-717255	6	2	4	isolated	PCGF3;RNF3A	Homo sapiens mRNA for RNF3A (DONG1) ring finger protein.;ring finger protein 3
chr4:77055085-77055162	89	3	13	bounded	ASAHL	N-acylsphingosine amidohydrolase-like protein
chr4:7789693-7789841	117	10	12	extending	SORCS2	VPS10 domain receptor protein SORCS 2
chr4:83591185-83591422	594	18	79	extending	ENOPH1;MASA	Homo sapiens masA mRNA, complete cds.;Enolase-phosphatase E1 (EC 3.1.3.77) (2
chr4:87862392-87862611	181	5	9	bounded	PTPN13	protein tyrosine phosphatase, non-receptor type
chr4:89411271-89411434	16	2	3	extending	PPM1K	protein phosphatase 1K (PP2C domain containing)
chr5:102324796-102324832	31	2	68	bounded	PAM	peptidylglycine alpha-amidating monooxygenase;Homo sapiens mRNA for peptidylgly
chr5:1130948-1131103	496	11	7	bounded	SLC12A7	solute carrier family 12 (potassium/chloride
chr5:1133549-1133716	4	3	4	isolated	SLC12A7	solute carrier family 12 (potassium/chloride
chr5:131561913-131562032	68	49	2	extending	P4HA2	prolyl 4-hydroxylase, alpha II subunit isoform 2;prolyl 4-hydroxylase, alpha II subunit is
chr5:132140699-132140850	305	43	7	bounded	SEPT8	Septin-8.
chr5:133889473-133889600	18	2	60	bounded	PHF15;FLJ00195	Protein Jade-2 (PHD finger protein 15).;PHD finger protein 15;Homo sapiens mRNA f
chr5:134288828-134289299	226	24	7	isolated	PCBD2	pterin-4 alpha-carbinolamine dehydratase 2
chr5:137809059-137809186	391	3	192	bounded	REEP2	receptor expression enhancing protein 2
chr5:138766216-138766336	58	29	9	extending	LOC202051	Homo sapiens cDNA FLJ25874 fis, clone CBR02446.;Hypothetical protein LOC20205
chr5:140004754-140004852	78	2	23	bounded	TMCO6	transmembrane and coiled-coil domains 6
chr5:140004754-140004867	108	2	2	bounded	TMCO6	transmembrane and coiled-coil domains 6

chr5:140888204-140888326	255	66	5	bounded	DIAPH1	diaphanous 1 isoform 1;diaphanous 1 isoform 2
chr5:145590410-145590673	862	26	64	extending	RBM27	RNA-binding protein 27 (RNA-binding motif protein 27).
chr5:149493342-149493764	1712	52	122	extending	PDGFRB	platelet-derived growth factor receptor beta
chr5:149611738-149611788	124	254	5	bounded	CAMK2A	calcium/calmodulin-dependent protein kinase IIA
chr5:149753141-149753308	885	7	142	bounded	TCOF1	Treacher Collins-Franceschetti syndrome 1
chr5:149911508-149911649	274	98	3	extending	NDST1	N-deacetylase/N-sulfotransferase (heparan
chr5:150387663-150387880	12268	1775	10	bounded	GPX3	Homo sapiens extracellular glutathione peroxidase mRNA, complete cds.;plasma glut
chr5:150387663-150387884	17028	1775	12	bounded	GPX3	Homo sapiens extracellular glutathione peroxidase mRNA, complete cds.;plasma glut
chr5:150490859-150491043	633	8	699	extending	ANXA6	annexin VI isoform 2;annexin VI isoform 1;Homo sapiens cDNA FLJ44888 fis, clone B
chr5:150871919-150871968	126	837	3	bounded	FAT2;KIAA0811	FAT tumor suppressor 2 precursor;KIAA0811 protein (Fragment).
chr5:166734781-166735056	9	2	6	bounded	NA	NA
chr5:171716300-171716383	5	9	11	isolated	SH3PXD2B	SH3 and PX domains 2B
chr5:172215700-172215920	35	2	42	isolated	ERGIC1	endoplasmic reticulum-golgi intermediate
chr5:172968847-172969038	3445	65	3	bounded	FAM44B	hypothetical protein LOC91272
chr5:175986038-175986123	2040	6	1567	bounded	SNCB	beta-synuclein
chr5:176730957-176731196	215	110	28	extending	RGS14	regulator of G-protein signalling 14;Homo sapiens regulator of G protein signaling RG
chr5:176763462-176763697	171	6	20	bounded	F12	Homo sapiens mRNA for coagulation factor XII-Mie, complete cds.;coagulation factor
chr5:176850104-176850200	410	3	223	bounded	PDLIM7	PDZ and LIM domain 7 isoform 4;Homo sapiens ENIGMA protein mRNA, complete c
chr5:177589547-177589673	285	29	2	bounded	pp9286;AGXT2L2	Alanine-glyoxylate aminotransferase 2-like 2.;alanine-glyoxylate aminotransferase 2-li
chr5:178945403-178945476	100	38	3	extending	RUFY1	RUN and FYVE domain-containing 1 isoform b;RUN and FYVE domain-containing 1 i
chr5:178977591-178977667	1811	4	775	bounded	HNRPH1	Homo sapiens cDNA FLJ34954 fis, clone NTONG2002582, highly similar to HETERO
chr5:178982699-178982771	1437	19	836	bounded	HNRPH1	Homo sapiens cDNA FLJ34954 fis, clone NTONG2002582, highly similar to HETERO
chr5:180584043-180584418	6014	21	308	bounded	AX748230;TRIM41a;TRIM41	Homo sapiens mRNA for hypothetical protein, partial cds, similar to ret finger protein.;
chr5:32268824-32268871	3	6	4	bounded	MTMR12	myotubularin related protein 12
chr5:39324678-39324810	262	5	23	bounded	C9	complement component 9
chr5:40870080-40870124	10420	6	1818	bounded	RPL37	ribosomal protein L37
chr5:43197108-43197790	556	15	3	extending	ZNF131	zinc finger protein 131;Homo sapiens cDNA FLJ32781 fis, clone TESTI2002149, high
chr5:56567550-56567607	75	182	3	bounded	GPBP1;DKFZp434G1730	vasculin;Homo sapiens cDNA: FLJ21154 fis, clone CAS09752.
chr5:68447509-68447772	202	29	3	bounded	SLC30A5;ZTL1	Zinc transporter ZTL1.;zinc transporter ZTL1 isoform 1;Homo sapiens putative diseas
chr5:80845203-80845318	151	47	3	extending	SSBP2;DKFZp564C0362	single-stranded DNA binding protein 2;HSPC116.
chr5:86744251-86744395	618	55	2	bounded	CCNH	cyclin H
chr5:944858-944969	363	3	42	bounded	DKFZp434D0711;BRD9	bromodomain containing 9 isoform 2;bromodomain containing 9 isoform 1;Homo sapi
chr6:109870439-109870780	336	89	34	extending	SMPD2	sphingomyelin phosphodiesterase 2, neutral
chr6:109881534-109882135	2149	27	54	extending	MICAL1	microtubule associated monoxygenase, calponin
chr6:139736184-139736782	16213	3	547	bounded	CITED2	Cbp/p300-interacting transactivator, with
chr6:152631983-152632117	610	59	27	extending	SYNE1	nesprin 1 isoform longer;nesprin 1 longest;nesprin 1 isoform beta
chr6:168109286-168109805	1385	273	3	bounded	MLLT4	myeloid/lymphoid or mixed-lineage leukemia
chr6:17736865-17737290	438	34	2	bounded	NUP153	nucleoporin 153kDa
chr6:29972807-29972908	2	114	9	isolated	HLA-A*0226;HLA-G	major histocompatibility complex, class I, G;Homo sapiens MHC class I antigen HLA-
chr6:30003971-30004084	151	16	28	bounded	BC035647;AK097625;HLA-A*	major histocompatibility complex, class I, G;Homo sapiens MHC class I antigen HLA-
chr6:30336971-30337235	1716	2	96	bounded	FLJ45422	hypothetical protein LOC441140
chr6:30659364-30659450	191	61	42	bounded	ABCF1	ATP-binding cassette, sub-family F, member 1
chr6:30661635-30661731	251	80	6	bounded	ABCF1	ATP-binding cassette, sub-family F, member 1
chr6:30722225-30722331	92	32	7	bounded	C6orf134	hypothetical protein LOC79969 isoform 2;hypothetical protein LOC79969 isoform 1
chr6:30800025-30800153	8714	36	31	bounded	TUBB;TUBB2C	tubulin, beta polypeptide;tubulin, beta, 2
chr6:30968986-30969179	818	19	304	extending	DDR1 variant protein;DDR1	discoidin domain receptor family, member 1;Homo sapiens mRNA for DDR1 variant p
chr6:30972384-30972621	1045	12	147	bounded	DDR1 variant protein;DDR1	discoidin domain receptor family, member 1;Homo sapiens mRNA for DDR1 variant p
chr6:30989567-30989739	440	32	4	bounded	KIAA1885;VARS2;GTF2H4	general transcription factor IIH, polypeptide 4,;Homo sapiens mRNA for KIAA1885 pro
chr6:31220443-31220829	1217	82	129	extending	HCR;CCHCR1	StAR-binding protein;Homo sapiens HCR (a-helix coiled-coil rod homologue) mRNA,
chr6:31432542-31432713	1846	38	921	bounded	HLA-B	major histocompatibility complex, class I, B;MHC class I antigen (Fragment).
chr6:31608536-31608664	1776	204	2	bounded	BAT1	Homo sapiens mRNA for HLA-B associated transcript 1 variant protein.;HLA-B associ
chr6:31622234-31622315	1369	1015	2	bounded	ATP6V1G2;BAT1	ATPase, H+ transporting, lysosomal, V1 subunit;HLA-B associated transcript 1
chr6:31699488-31699669	2567	494	5	extending	BAT2	HLA-B associated transcript-2 isoform b;HLA-B associated transcript-2 isoform a
chr6:31705397-31705601	2843	19	118	bounded	BAT2	HLA-B associated transcript-2 isoform b;HLA-B associated transcript-2 isoform a

chr6:31706895-31707003	643	1589	4	bounded	BAT2	HLA-B associated transcript-2 isoform b;HLA-B associated transcript-2 isoform a
chr6:31739609-31740248	3572	286	2	bounded	BAT4	HLA-B associated transcript 4
chr6:31842001-31842520	312	7	3	extending	C6orf27;G7c	NG37 protein;Homo sapiens mRNA for G7c protein (G7c gene located in the class III
chr6:32039188-32039315	235	3	71	bounded	SKIV2L	superkiller viralicidic activity 2-like homolog
chr6:32125753-32126061	359	369	4	bounded	TNXB	tenascin XB isoform 1
chr6:32129143-32129413	586	665	25	bounded	TNXB	tenascin XB isoform 1
chr6:32129143-32129466	1558	665	459	extending	TNXB	tenascin XB isoform 1
chr6:32154788-32155081	943	140	3	bounded	TNXB	Homo sapiens tenascin XB (TNXB), transcript variant XB, mRNA.;tenascin XB isofor
chr6:32225292-32225414	177	18	7	bounded	C6orf31;PRRT1	NG5 protein;Homo sapiens full length insert cDNA clone YI44H12.;Chromosome 6 op
chr6:32226123-32226263	383	85	9	bounded	C6orf31;PRRT1	NG5 protein;Homo sapiens full length insert cDNA clone YI44H12.;Chromosome 6 op
chr6:33052013-33052219	5510	7	484	bounded	DKFZp313H139;BRD2	bromodomain containing protein 2;Hypothetical protein DKFZp313H139.;Homo sapie
chr6:33144774-33144877	407	174	2	bounded	HLA-DPA1	major histocompatibility complex, class II, DP
chr6:33356429-33356738	2353	130	8	bounded	WDR46	WD repeat domain 46
chr6:33394752-33394860	1255	348	8	bounded	DAXX	death-associated protein 6
chr6:34468019-34468178	773	243	5	bounded	NUDT3	nudix-type motif 3
chr6:35048336-35048398	7	6	2	isolated	ANKS1A	Homo sapiens cDNA clone IMAGE:4618556, partial cds.;ankyrin repeat and sterile al
chr6:37713941-37714067	840	4	30	bounded	GPIM;MDGA1	Homo sapiens glycosyl-phosphatidyl-inositol-MAM (GPIM) mRNA, complete cds.;MA
chr6:37721948-37722129	2125	13	29	extending	GPIM;MDGA1	Homo sapiens glycosyl-phosphatidyl-inositol-MAM (GPIM) mRNA, complete cds.;MA
chr6:40507445-40508848	314	2	4	bounded	LRFN2	leucine rich repeat and fibronectin type III
chr6:41766717-41766803	184	121	6	bounded	TFEB	transcription factor EB;Homo sapiens mRNA for transcription factor EB (TFEB gene),
chr6:41766843-41766951	455	14	110	bounded	TFEB	transcription factor EB;Homo sapiens mRNA for transcription factor EB (TFEB gene),
chr6:43065327-43065401	761	310	3	bounded	PPP2R5D	delta isoform of regulatory subunit B56, protein;Delta isoform of regulatory subunit B5
chr6:43065327-43065440	818	310	7	extending	PPP2R5D	delta isoform of regulatory subunit B56, protein;Delta isoform of regulatory subunit B5
chr6:43082227-43082395	676	4	183	bounded	PPP2R5D	delta isoform of regulatory subunit B56, protein;Delta isoform of regulatory subunit B5
chr6:43148939-43149016	751	332	12	bounded	DKFZp761H229;KLC4	Homo sapiens cDNA FLJ30731 fis, clone FEBRA2000105, moderately similar to KIN
chr6:43304977-43305121	2350	186	4	bounded	C6orf108	putative c-Myc-responsive isoform 1;putative c-Myc-responsive isoform 2
chr6:43322323-43322481	139	4	10	bounded	TTBK1	tau tubulin kinase 1
chr6:43358797-43360028	1003	10	24	bounded	TTBK1	tau tubulin kinase 1
chr6:43614927-43615205	31	4	48	isolated	XPO5	exportin 5
chr6:46322444-46322609	614	42	4	bounded	DSCR1L1	Down syndrome critical region gene 1-like 1;Down syndrome critical region gene 1-like
chr6:74286323-74286470	5	441	27	bounded	EEF1A1	eukaryotic translation elongation factor 1 alpha;EEF1A1 protein (Fragment).;Homo sa
chr6:90422204-90422270	155	116	3	bounded	MDN1	MDN1, midasin homolog
chr6:94025793-94025906	22	6	3	bounded	EPHA7	ephrin receptor EphA7
chr6:99903704-99903994	179	9	2	bounded	C6orf168	hypothetical protein LOC84553
chr6:99955141-99956227	9128	90	121	bounded	BC033061;C6orf111;DKFZp56	Homo sapiens, clone IMAGE:4934129, mRNA.;Homo sapiens HSPC261 mRNA, parti
chr7:100008665-100008754	133	53	2	bounded	FLJ00248	Homo sapiens mRNA for FLJ00248 protein.
chr7:100013223-100013279	284	753	15	bounded	LRCH4;PP14183	Homo sapiens PP14183 mRNA, complete cds.;leucine-rich repeats and calponin hom
chr7:100640332-100640674	2911	520	188	extending	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase
chr7:100641847-100641969	2684	1333	3	bounded	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase
chr7:101713033-101713085	306	667	10	bounded	CUTL1;Nbla10317	Homo sapiens neuroblastoma cDNA, clone:Nbla10317, full insert sequence.;CCAAT
chr7:12381161-12381378	6	2	4	isolated	NA	NA
chr7:128268460-128268569	6645	639	35	bounded	FLNC	gamma filamin
chr7:128285626-128285804	3471	864	5	bounded	FLNC	gamma filamin
chr7:136849136-136849411	25	168	8	isolated	DGKI;DGKi	diacylglycerol kinase, iota;Diacylglycerol kinase, iota variant (Fragment).
chr7:139303919-139304032	14	4	10	bounded	TBXAS1	thromboxane A synthase 1 (platelet, cytochrome
chr7:139383984-139384230	105	23	2	extending	PARP12	zinc finger CCCH-type domain containing 1
chr7:141507394-141507482	3	3	4	extending	NA	NA
chr7:141512367-141512522	8	2	2	isolated	NA	NA
chr7:142206636-142206733	12	15	18	bounded	TCRBV13S1-TCRBJ2S1;TCR	Homo sapiens mRNA for T-cell receptor beta chain, partial cds, clone:TCRVB.3.;Hom
chr7:142790016-142790147	4950	2913	4	bounded	ZYX	zyxin
chr7:142790202-142790537	5261	9	409	bounded	ZYX	zyxin
chr7:1445002-1445129	121	88	3	bounded	FLJ00139;MICALL2	Homo sapiens cDNA: FLJ23471 fis, clone HSI11969.;MICAL-like 2 isoform 2;MICAL-li
chr7:149048077-149048151	40	13	24	bounded	KIAA1862;KRBA1	KIAA1862 protein;Homo sapiens mRNA for KIAA1862 protein, partial cds.
chr7:149104957-149105039	4	3	9	isolated	AK127639	CDNA FLJ45737 fis, clone JCMLC2002751, weakly similar to Von Willebrand factor.

chr7:149110868-149111043	27	2	5	isolated	AK127639	CDNA FLJ45737 fis, clone JCMLC2002751, weakly similar to Von Willebrand factor.
chr7:149119323-149119414	7	3	3	bounded	KIAA2036	Homo sapiens mRNA for KIAA2036 protein.
chr7:149129806-149129976	59	9	16	isolated	NA	NA
chr7:149131496-149131625	18	7	3	isolated	NA	NA
chr7:149132017-149132108	21	4	14	isolated	NA	NA
chr7:149140582-149140661	39	20	6	isolated	NA	NA
chr7:149143911-149144110	104	4	4	isolated	NA	NA
chr7:149148898-149149144	179	5	2	isolated	NA	NA
chr7:149149884-149150219	146	12	13	extending	AK123170;AY927596;AY9275	Homo sapiens cDNA FLJ36112 fis, clone TESTI2022023, weakly similar to Bos taurus
chr7:150399421-150399625	5811	6	78	bounded	SLC4A2	solute carrier family 4, anion exchanger, member
chr7:150684150-150684241	1446	17	180	bounded	NUB1	NEDD8 ultimate buster-1
chr7:151485779-151485940	173	114	12	bounded	MLL3;KIAA1506;DKFZp434D2	myeloid/lymphoid or mixed-lineage leukemia 3;Homo sapiens ALR-like protein mRNA,
chr7:154721192-154721340	3641	3	207	bounded	INSIG1	insulin induced gene 1 isoform 1;insulin induced gene 1 isoform 3;insulin induced gen
chr7:155196694-155196910	526	2	110	bounded	PRR8	proline rich 8
chr7:156495115-156495441	111	15	9	bounded	HLXB9	homeo box HB9
chr7:156702322-156702395	67	22	5	bounded	UBE3C	ubiquitin protein ligase E3C
chr7:23276219-23276319	2430	2	640	bounded	GPNMB	glycoprotein (transmembrane) nmb isoform b;glycoprotein (transmembrane) nmb isofo
chr7:23706933-23707012	115	3	21	bounded	C7orf46	hypothetical protein LOC340277;Homo sapiens cDNA FLJ45875 fis, clone OCBBF30
chr7:2380691-2380767	640	21	1376	bounded	EIF3S9	eukaryotic translation initiation factor 3,
chr7:2381551-2381688	3498	12	138	bounded	EIF3S9	eukaryotic translation initiation factor 3,
chr7:2551097-2551216	395	2	24	bounded	C7orf27	HEAT repeat domain-containing protein C7orf27 precursor.;hypothetical protein LOC2
chr7:2584402-2584686	176	26	76	extending	IQCE	IQ motif containing E;IQCE protein.
chr7:26199720-26199812	20117	7410	30	bounded	HNRPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
chr7:27822493-27822634	152	95	3	bounded	TAX1BP1	Tax1 (human T-cell leukemia virus type I)
chr7:29961325-29961501	2685	3	1137	bounded	SCRN1	secernin 1
chr7:32576157-32576303	87	14	3	extending	KIAA0241	hypothetical protein LOC23080
chr7:34085122-34085323	56	3	3	bounded	BMPER	BMP-binding endothelial regulator precursor
chr7:44231887-44232015	89	3	4	isolated	CAMKB;CAMK2B	calcium/calmodulin-dependent protein kinase IIB;Homo sapiens calcium/calmodulin-d
chr7:44496533-44496670	2172	178	6	bounded	NUDCD3	NudC domain containing 3
chr7:44576139-44576232	4373	1641	3	bounded	DDX21;DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56;Homo sapiens DEAD-box RNA helicase
chr7:44588171-44588297	2339	247	3	bounded	TMED4	transmembrane emp24 protein transport domain;Homo sapiens mRNA for putative N
chr7:45088232-45092236	5720	97	85	extending	KIAA0363	KIAA0363 protein (Fragment).
chr7:4791572-4791841	649	81	36	extending	KIAA0415	hypothetical protein LOC9907
chr7:51078574-51078858	805	36	6	bounded	COBL	cordon-bleu homolog
chr7:51223105-51223149	2	3	7	isolated	COBL	cordon-bleu homolog;Protein cordon-bleu.
chr7:5318660-5319008	530	106	4	extending	KIAA1856	KIAA1856 protein
chr7:66097712-66097844	717	187	5	bounded	SBDS	Shwachman-Bodian-Diamond syndrome protein
chr7:69869036-69869277	988	39	23	extending	AUTS2	autism susceptibility candidate 2
chr7:72659402-72659686	723	8	118	bounded	MLXIPL;WBSCR14	Williams Beuren syndrome chromosome region 14;Williams-Beuren syndrome chrom
chr7:73240585-73240671	30	2	3	isolated	EIF4H	Homo sapiens eukaryotic translation initiation factor 4H, mRNA (cDNA clone MGC:19
chr7:75448771-75448854	1323	598	4	bounded	POR	cytochrome P450 reductase
chr7:75715442-75715532	618	203	4	bounded	BC029292	Homo sapiens hypothetical protein FLJ37078, mRNA (cDNA clone IMAGE:5182276).
chr7:75727160-75727282	678	139	4	bounded	BC029292	Homo sapiens hypothetical protein FLJ37078, mRNA (cDNA clone IMAGE:5182276).
chr7:75749985-75750126	571	5	108	bounded	FLJ37078;BC096755	Homo sapiens cDNA FLJ35271 fis, clone PROST2005886.;hypothetical protein LOC2
chr7:82433023-82433739	375	9	4	extending	NA	NA
chr7:867547-867627	608	2	567	bounded	UNC84A;KIAA0810	unc-84 homolog A;Homo sapiens mRNA for KIAA0810 protein, partial cds.
chr7:910289-910429	1356	109	8	bounded	CENTA1	centaurin, alpha 1
chr7:91530712-91530750	3	8	3	isolated	AKAP9	A-kinase anchor protein 9 isoform 2;A-kinase anchor protein 9 isoform 3;A-kinase anc
chr7:91601423-91601596	2514	30	11	bounded	CYP51A1	cytochrome P450, family 51
chr7:98346072-98346166	54	4	20	bounded	TRRAP	transformation/transcription domain-associated
chr8:101802795-101803056	9539	978	6	bounded	PABPC1	Homo sapiens cDNA FLJ37875 fis, clone BRSSN2018771, highly similar to POLYADE
chr8:103736970-103737044	251	18	11	bounded	KLF10	Kruppel-like factor 10 isoform a
chr8:125401508-125401605	248	40	2	bounded	TMEM65	hypothetical protein LOC157378
chr8:125637164-125637827	1288	81	24	bounded	MTSS1	metastasis suppressor 1
chr8:12914564-12914737	256	3	22	bounded	KIAA1456	Homo sapiens mRNA for KIAA1456 protein, partial cds.;hypothetical protein LOC5760

chr8:134361653-134361692	274	12	728	bounded	NDRG1	N-myc downstream regulated gene 1
chr8:141747550-141747699	2166	332	14	bounded	PTK2;DKFZp666O0110	Homo sapiens mRNA for PTK2 protein tyrosine kinase 2 isoform b variant protein.;PTK
chr8:143359128-143359592	376	13	44	isolated	TSNARE1	t-SNARE domain containing 1;Hypothetical protein (Fragment).
chr8:143606908-143607006	5	14	3	isolated	BAI1	brain-specific angiogenesis inhibitor 1
chr8:143621937-143622071	222	5	85	extending	BAI1	brain-specific angiogenesis inhibitor 1
chr8:144691316-144691555	348	52	3	bounded	ZC3H3	zinc finger CCCH-type domain containing 3
chr8:144734244-144734467	5862	3	1329	extending	EEF1D	eukaryotic translation elongation factor 1 delta
chr8:145186753-145186967	337	34	4	extending	OPLAH	5-oxoprolinase (ATP-hydrolysing)
chr8:145238940-145239035	12	5	5	bounded	KIAA1875	KIAA1875 protein
chr8:145550039-145550146	406	2	149	bounded	C8orfK29;FBL6;FBXL6	F-box and leucine-rich repeat protein 6 isoform;C8orfK29 protein.;Homo sapiens F-box
chr8:145570050-145570134	9	5	6	bounded	ADCK5	Homo sapiens cDNA FLJ35454 fis, clone SMINT2004473.;aarF domain containing kin
chr8:145595474-145595701	965	305	57	extending	CPSF1	cleavage and polyadenylation specific factor 1,
chr8:145663750-145663821	336	7	227	bounded	KIFC2	kinesin family member C2
chr8:145663905-145664021	309	199	4	bounded	KIFC2	kinesin family member C2
chr8:145664706-145664841	2903	5	394	extending	KIFC2	kinesin family member C2
chr8:146248776-146249126	1520	88	2	extending	C8orf33	hypothetical protein LOC65265;Homo sapiens full length insert cDNA clone ZB85G04.
chr8:1987683-1987842	240	32	3	extending	MYOM2	myomesin 2
chr8:21994075-21994202	78	40	5	extending	EPB49	erythrocyte membrane protein band 4.9 (dematin)
chr8:22040495-22040793	1504	335	4	bounded	HR	hairless protein isoform a;hairless protein isoform b
chr8:22470173-22470387	848	224	4	extending	SORBS3	vinexin beta (SH3-containing adaptor molecule-1)
chr8:26540648-26540770	838	194	61	extending	DPYSL2	dihydropyrimidinase-like 2
chr8:27344310-27344708	1542	181	8	extending	PTK2B	PTK2B protein tyrosine kinase 2 beta isoform b;PTK2B protein tyrosine kinase 2 beta i
chr8:27517725-27517797	5801	4843	25	bounded	CLU	clusterin isoform 1;clusterin isoform 2
chr8:28273138-28273260	338	3	10	bounded	ZNF395	zinc finger protein 395
chr8:42299022-42299173	714	169	5	extending	IKBKB;IKK-beta	Homo sapiens mRNA for inhibitor of kappa light polypeptide gene enhancer in B-cells,
chr8:48882251-48882286	64	187	21	bounded	PRKDC	protein kinase, DNA-activated, catalytic
chr8:62726163-62726229	536	215	5	bounded	ASPH	aspartate beta-hydroxylase isoform a;aspartate beta-hydroxylase isoform c;aspartate b
chr8:71201395-71201836	302	2	28	extending	NCOA2	nuclear receptor coactivator 2
chr8:93092379-93092495	109	2	33	bounded	RUNX1T1	Homo sapiens runt-related transcription factor 1; translocated to, 1 (cyclin D-related),
chr9:100633843-100634060	210	6	64	extending	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide
chr9:114988350-114988454	88	19	2	bounded	KIAA0674	KIAA0674 protein (Fragment).
chr9:116091273-116091396	149	4	211	extending	KIAA1870;COL27A1	collagen, type XXVII, alpha 1;Homo sapiens mRNA for KIAA1870 protein, partial cds.
chr9:123134533-123134656	6255	4348	7	bounded	GSN	gelsolin isoform b;gelsolin isoform a precursor
chr9:123583564-123583618	1312	396	35	bounded	DAB2IP	DAB2 interacting protein isoform 1;DAB2 interacting protein isoform 2
chr9:125213876-125213929	6	6	19	isolated	DENND1A;KIAA1608	DENN/MADD domain containing 1A isoform 1;DENN/MADD domain containing 1A isc
chr9:128495221-128495423	290	2	10	extending	LMX1B	LIM homeobox transcription factor 1, beta
chr9:129205787-129205903	252	3	86	bounded	SLC2A8	solute carrier family 2, (facilitated glucose
chr9:129925064-129925234	3444	3	891	bounded	PTGES2	prostaglandin E synthase 2 isoform 1;Homo sapiens cDNA FLJ14038 fis, clone HEMB
chr9:129980809-129981076	2273	137	11	bounded	CIZ1;Ciz1	Cip1-interacting zinc finger protein;Homo sapiens Ciz1 mRNA, complete cds.
chr9:129981299-129981515	2204	17	354	bounded	CIZ1;Ciz1	Cip1-interacting zinc finger protein;Homo sapiens Ciz1 mRNA, complete cds.
chr9:130059890-130060298	3015	178	475	extending	GOLGA2	Golgi autoantigen, golgin subfamily a, 2
chr9:130226245-130226372	1389	11	204	bounded	CEECAM1	cerebral endothelial cell adhesion molecule 1
chr9:130390909-130390992	818	693	8	bounded	SPTAN1	spectrin, alpha, non-erythrocytic 1
chr9:130458641-130458673	13	536	7	bounded	WDR34	WD repeat domain 34
chr9:132247392-132247505	26	5	19	isolated	NA	NA
chr9:132247887-132248074	64	18	2	isolated	NA	NA
chr9:132258420-132258517	10	2	3	extending	DKFZp434P0216	Homo sapiens cDNA FLJ36264 fis, clone THYMU2002815, weakly similar to AXONIN-
chr9:132283980-132284249	94	28	4	bounded	DKFZp434P0216	Homo sapiens cDNA FLJ36264 fis, clone THYMU2002815, weakly similar to AXONIN-
chr9:132295492-132295812	169	25	7	bounded	AK074396	CDNA FLJ23816 fis, clone HSI02685.
chr9:132719275-132719445	260	2	82	bounded	ABL1	v-abl Abelson murine leukemia viral oncogene
chr9:133301828-133301874	55	295	6	bounded	KIAA0515	KIAA0515 protein.
chr9:135220194-135220456	3198	10	137	bounded	SURF4	surfeit 4
chr9:135269606-135269898	1337	324	8	bounded	XPMC2H;vWF-CP;REXO4	Homo sapiens vWF-CP(ADAMTS13) mRNA for von Willebrand factor-cleaving protea
chr9:135395541-135395681	162	68	2	bounded	ADAMTSL2	ADAMTS-like 2
chr9:137119720-137119806	1018	2	141	bounded	OLFM1	olfactomedin related ER localized protein;Noelin precursor (Neuronal olfactomedin-rela

chr9:137725637-137725702	11	3	2	bounded	SOHLH1	spermatogenesis and oogenesis specific basic
chr9:138396097-138396303	158	24	4	bounded	SNAPC4	small nuclear RNA activating complex,
chr9:138691696-138691895	1381	142	3	extending	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2
chr9:138736353-138736574	1670	3	198	bounded	AK054908;FAM69B	Homo sapiens cDNA FLJ30346 fis, clone BRACE2007527.;hypothetical protein LOC1
chr9:138806220-138806307	235	184	4	bounded	TMEM141	transmembrane protein 141
chr9:138821845-138821963	275	44	4	bounded	KIAA1984;AK055547	hypothetical protein LOC84960;Homo sapiens cDNA FLJ30985 fis, clone HHDPC200
chr9:138851619-138851793	2242	807	4	bounded	C9orf86;pp8875	Homo sapiens pp8875 mRNA, complete cds.;hypothetical protein LOC55684
chr9:138851858-138851935	637	13	247	bounded	C9orf86;pp8875	Homo sapiens pp8875 mRNA, complete cds.;hypothetical protein LOC55684
chr9:138863416-138863562	392	2	3	bounded	PHPT1;DKFZp564M173	Homo sapiens clone 24870 mRNA sequence.;phosphohistidine phosphatase 1
chr9:139030564-139031011	2590	352	60	extending	KIAA1062;ABCA2	ATP-binding cassette, sub-family A, member 2;Homo sapiens mRNA for KIAA1062 pr
chr9:139170942-139171310	1642	311	175	extending	GRIN1;hNMDAR1-3b	NMDA receptor 1 isoform NR1-2 precursor;NMDA receptor 1 isoform NR1-3 precurso
chr9:139194725-139194857	159	82	5	extending	ANAPC2	anaphase-promoting complex subunit 2
chr9:139200511-139200629	292	6	37	bounded	ANAPC2	anaphase-promoting complex subunit 2
chr9:139443576-139443656	37	5	25	bounded	NOXA1	NADPH oxidase activator 1
chr9:139768444-139768579	489	318	3	extending	EHMT1	euchromatic histone methyltransferase 1
chr9:27170238-27170376	112	15	2	extending	TEK	TEK tyrosine kinase, endothelial precursor
chr9:33452675-33452811	974	3	66	bounded	NOL6	nucleolar protein family 6 alpha isoform;nucleolar protein family 6 gamma isoform;Ho
chr9:33453245-33453435	652	19	7	bounded	NOL6	nucleolar protein family 6 alpha isoform;nucleolar protein family 6 gamma isoform;Ho
chr9:33454877-33454964	248	51	5	bounded	NOL6	nucleolar protein family 6 alpha isoform;nucleolar protein family 6 gamma isoform;Ho
chr9:33961649-33961735	238	57	9	bounded	UBAP2;KIAA1491	Homo sapiens mRNA for KIAA1491 protein, partial cds.;ubiquitin associated protein 2
chr9:34967540-34967638	58	2	44	extending	KIAA1045	Protein KIAA1045.
chr9:35388886-35389031	344	2	147	bounded	UNC13B	UNC13 (C. elegans)-like
chr9:35550607-35550848	1106	5	255	bounded	RUSC2	RUN and SH3 domain containing 2
chr9:461212-461326	16	2	4	isolated	ANKRD15	ankyrin repeat domain protein 15 isoform a
chr9:5822690-5822845	139	45	2	bounded	KIAA1815	hypothetical protein LOC79956
chr9:79175626-79175885	560	42	52	extending	VPS13A	vacuolar protein sorting 13A isoform A;vacuolar protein sorting 13A isoform B;vacuola
chr9:91116016-91116086	2958	2	297	bounded	CKS2	CDC28 protein kinase 2
chr9:94024605-94024775	970	2	217	extending	IARS	IARS protein.;isoleucyl-tRNA synthetase
chr9:94049476-94049654	973	4	100	bounded	IARS	IARS protein.;isoleucyl-tRNA synthetase
chr9:94073646-94073758	613	7	82	bounded	IARS	IARS protein.;isoleucyl-tRNA synthetase
chr9:94912624-94912737	840	2	2	bounded	C9orf89	chromosome 9 open reading frame 89;Homo sapiens cDNA FLJ33154 fis, clone UTE
chr9:95092081-95092184	90	43	6	extending	WNK2	WNK lysine deficient protein kinase 2
chr9:95099956-95100000	107	262	3	bounded	WNK2	WNK lysine deficient protein kinase 2
chr9:95100032-95100170	392	49	88	bounded	WNK2	WNK lysine deficient protein kinase 2
chr9:96408918-96408990	1229	33	2	bounded	FBP1	fructose-1,6-bisphosphatase 1
chrX:100759137-100759230	406	5	246	extending	ARMCX6	armadillo repeat containing, X-linked 6
chrX:106846576-106846697	853	516	2	bounded	TSC22D3	TSC22 domain family, member 3 isoform 1;TSC22 domain family, member 3 isoform
chrX:109447483-109447854	365	34	2	bounded	AMMECR1	AMMECR1 protein isoform 1;AMMECR1 protein isoform 2
chrX:118111658-118111766	15	4	3	isolated	NA	NA
chrX:12750744-12750824	177	132	2	bounded	PRPS2	phosphoribosyl pyrophosphate synthetase 2
chrX:128886754-128886852	154	5	41	bounded	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein,
chrX:152689407-152689730	193	12	18	extending	PLXNB3	plexin B3
chrX:152692508-152692993	551	73	21	extending	PLXNB3	plexin B3
chrX:152789439-152789828	1889	109	27	extending	L1CAM	L1 cell adhesion molecule isoform 1 precursor;Homo sapiens L1CAM mRNA for L1 ce
chrX:153243976-153244140	15481	8	634	extending	FLNA	filamin A, alpha
chrX:153284242-153284376	723	12	140	bounded	DNASE1L1;QM	deoxyribonuclease I-like 1 precursor;Homo sapiens mRNA expressed only in placenta
chrX:153416274-153416539	43	3	2	isolated	G6PD	glucose-6-phosphate dehydrogenase isoform a;glucose-6-phosphate dehydrogenase
chrX:16780460-16780672	354	8	172	extending	RBBP7	Retinoblastoma binding protein 7.;retinoblastoma binding protein 7
chrX:18834534-18834853	150	16	63	extending	PHKA2	phosphorylase kinase, alpha 2 (liver)
chrX:23711696-23711921	1134	629	175	bounded	SAT1;SSAT-1	Homo sapiens SSAT-1 mRNA for diamine acetyltransferase 1, complete cds.;spermid
chrX:37964893-37965001	540	109	3	bounded	SRPX	sushi-repeat-containing protein, X-linked
chrX:40479394-40479546	39	25	4	bounded	CRSP2	cofactor required for Sp1 transcriptional
chrX:46968728-46968918	10903	670	4	extending	PCTK1	PCTAIRE protein kinase 1
chrX:47310995-47311123	1176	3	185	bounded	ARAF	v-raf murine sarcoma 3611 viral oncogene
chrX:48267315-48267404	767	3	267	bounded	EBP	emopamil binding protein (sterol isomerase)

chrX:48432669-48432767	202	2	95	bounded	WAS	Wiskott-Aldrich syndrome protein
chrX:48559306-48559403	554	4	63	bounded	KIAA0901;HDAC6	histone deacetylase 6;Homo sapiens mRNA for KIAA0901 protein, partial cds.
chrX:48719661-48719783	931	148	8	bounded	GRIPAP1	GRIP1 associated protein 1 isoform 1;GRIP1 associated protein 1 isoform 2
chrX:48722571-48722655	1152	298	12	bounded	GRIPAP1	GRIP1 associated protein 1 isoform 1;GRIP1 associated protein 1 isoform 2
chrX:48811656-48812570	1478	28	22	bounded	CCDC120	coiled-coil domain containing 120
chrX:53130668-53130773	1479	3	431	bounded	HRIHFB2216;TSPYL2	TSPY-like 2 variant (Fragment).;TSPY-like 2;Homo sapiens HRIHFB2216 mRNA, part
chrX:53132006-53132217	9939	12	1442	bounded	HRIHFB2216;TSPYL2	TSPY-like 2 variant (Fragment).;TSPY-like 2;Homo sapiens HRIHFB2216 mRNA, part
chrX:53456903-53457110	1047	6	98	bounded	SMC1A;SMC1L1	Homo sapiens MSTP142 mRNA, complete cds.;structural maintenance of chromosom
chrX:53591746-53591959	1188	6	779	bounded	HUWE1	HECT, UBA and WWE domain containing 1
chrX:69285336-69285419	121	71	2	extending	IGBP1	immunoglobulin binding protein 1
chrX:70277210-70277354	651	228	3	bounded	MED12	mediator of RNA polymerase II transcription,
chrX:70277364-70277432	56	24	37	bounded	MED12	mediator of RNA polymerase II transcription,
chrX:71275016-71277346	734	4	2	bounded	LOC340527	hypothetical protein LOC340527
chrX:76794260-76794423	884	135	2	bounded	ATRX	transcriptional regulator ATRX isoform 2;transcriptional regulator ATRX isoform 3;trans

[1] List of predicted exons (n=1413) with mRNA-SEQ reads supporting both junctions and the exon body. The exon prediction source, reads counts summed over all tissues, and gene names are presented. The novel exons are classified by their location with respect to other exons as "isolated" (do not overlap any know exons), "Extending" (exon overlaps but is longer than previous exon),"Bounded" (the exons is shorter than a previous known exon).

Table S4. Fraction of differentially regulated alternative transcript events among subsets of tissues and cell lines.

Cell lines (n=5)

Event type	No. events observed	No. significant events	Observed fraction significant	Estimated fraction significant[1]
Skipped exon	5163	849	0.16	0.24
RI	97	10	0.10	0.14
A5SS	1308	213	0.16	0.26
A3SS	2484	653	0.26	0.32
MXE	59	14	0.24	0.27
AFE	8386	997	0.12	0.25
ALE	4129	434	0.11	0.17
3' Tandem	4717	412	0.09	0.18

Cerebellum (n=6)

Event type	No. events observed	No. significant events	Observed fraction significant	Estimated fraction significant[1]
Skipped exon	5479	1018	0.19	0.30
RI	119	24	0.20	N/A[2]
A5SS	1298	295	0.23	0.36
A3SS	2550	686	0.27	0.41
MXE	75	7	0.09	0.26
AFE	8657	818	0.09	0.25
ALE	4508	254	0.06	0.10
3' Tandem	4863	820	0.17	0.27

Tissues excluding cerebellum (n=9)

Event type	No. events observed	No. significant events	Observed fraction significant	Estimated fraction significant[1]
Skipped exon	7698	3755	0.49	0.59
RI	140	64	0.46	0.59
A5SS	1616	770	0.48	0.60
A3SS	3290	1476	0.45	0.59
MXE	97	48	0.49	0.71
AFE	9806	3389	0.35	0.50
ALE	5021	1762	0.35	0.39
3' Tandem	5119	3139	0.61	0.72

[1] The estimated fraction of significant events was determined using a curve fitting approach, as described in Supplementary Information.

[2] Too few data available to estimate value.

Table S5. Skipped Exon Switch Scores.[1]

Gene	Event[2]	Switch score[4]	Tissue 1	Tissue 1 inclusion level[3]	Tissue 2	Tissue 2 inclusion level[3]	Gene description
L1CAM	chrX:152782017-152782028:-	1.00	cerebellum	1.00	MB435	0.00	L1 cell adhesion molecule isoform 1 precursor,L1 ce
ATP5C1	chr10:7888943-7888979:+	1.00	MCF7	1.00	skel. muscle	0.00	ATP synthase, H+ transporting, mitochondrial F1,AT
AP1B1,DKFZp686A	chr22:28065743-28065763:-	1.00	HME	0.00	brain	1.00	adaptor-related protein complex 1 beta 1 subunit,ada
PHKB	chr16:46055294-46055405:+	1.00	HME	1.00	skel. muscle	0.00	phosphorylase kinase, beta isoform b,phosphorylase
MAP7D2	chrX:19983773-19983871:-	1.00	brain	1.00	testes	0.00	Homo sapiens cDNA FLJ14503 fis, clone NT2RM10
MLF1	chr3:159793865-159793909:+	1.00	heart	1.00	testes	0.00	myeloid leukemia factor 1,CDNA FLJ39570 fis, clone
MYOM1	chr18:3119230-3119517:-	1.00	skel. muscle	0.00	testes	1.00	myomesin 1
CTRP1,C1QTNF1	chr17:74541994-74542210:+	1.00	MB435	1.00	adipose	0.00	C1q and tumor necrosis factor related protein 1,C1q
PHLDB1,KIAA0638	chr11:118018182-118018322:+	1.00	cerebellum	1.00	MB435	0.00	Homo sapiens mRNA for KIAA0638 protein, partial c
TPM3	chr1:152411129-152411204:-	1.00	MCF7	1.00	skel. muscle	0.01	tropomyosin 3 isoform 2,tropomyosin 3 isoform 3,
BIN1	chr2:127534642-127534686:-	1.00	adipose	0.00	skel. muscle	1.00	bridging integrator 1 isoform 4,bridging integrator 1 i
PHKB	chr16:46055311-46055405:+	1.00	HME	1.00	skel. muscle	0.01	phosphorylase kinase, beta isoform b,phosphorylase
PDLIM3	chr4:186672851-186673038:-	0.99	BT474	1.00	skel. muscle	0.01	PDZ and LIM domain protein 3 (Actinin-associated L
DKFZp566P0524,A	chr10:61498401-61506212:-	0.99	BT474	0.01	brain	1.00	ankyrin 3 isoform 1,ankyrin 3 isoform 1,Ankyrin 3 iso
AK055197,TPM1	chr15:61140450-61140525:+	0.99	MCF7	1.00	heart	0.01	tropomyosin 1 alpha chain isoform 6,Homo sapiens
PLEKHA1	chr10:124177782-124177926:+	0.99	HME	0.01	colon	1.00	Homo sapiens mRNA for pleckstrin homology doma
DKFZp434H012	chr6:39185068-39189474:-	0.99	MCF7	1.00	testes	0.01	hypothetical protein LOC55776,hypothetical protein
SMG7	chr1:181782861-181783010:+	0.99	cerebellum	1.00	MB435	0.01	SMG-7 homolog isoform 1,SMG-7 homolog isoform
SPTAN1	chr9:130411751-130411765:+	0.98	cerebellum	0.98	HME	0.00	Homo sapiens SPTAN1 mRNA for non-erythrocytic
AJ008131,AX72130	chr17:40679655-40679754:+	0.98	cerebellum	1.00	lymph node	0.02	formin-like 1,Homo sapiens CLL-associated antigen
MEF2D	chr1:154712910-154712930:-	0.98	adipose	0.02	skel. muscle	1.00	MADS box transcription enhancer factor 2,,MADS b
FHL1	chrX:135119068-135119267:+	0.98	cerebellum	1.00	skel. muscle	0.02	four and a half LIM domains 1,four and a half LIM do
SHF	chr15:43253066-43253206:-	0.98	HME	0.02	brain	1.00	Homo sapiens cDNA FLJ37072 fis, clone BRACE20
PLEKHA1	chr10:124177782-124177822:+	0.98	HME	0.02	colon	1.00	Homo sapiens mRNA for pleckstrin homology doma
PLEKHA1	chr10:124177782-124177852:+	0.98	HME	0.02	colon	1.00	Homo sapiens mRNA for pleckstrin homology doma
TPM2	chr9:35674729-35674804:-	0.98	colon	0.01	skel. muscle	0.99	tropomyosin 2 (beta) isoform 2
ADAM15	chr1:153301004-153301217:+	0.98	cerebellum	1.00	adipose	0.02	a disintegrin and metalloproteinase domain 15,a disi
MARK4,MARKL1	chr19:50493241-50493320:+	0.97	cerebellum	1.00	testes	0.03	MAP/microtubule affinity-regulating kinase 4 (EC 2.7
AK055197,TPM1	chr15:61140965-61141040:+	0.97	cerebellum	1.00	T47D	0.03	tropomyosin 1 alpha chain isoform 6,Homo sapiens
TPM2	chr9:35675061-35675136:-	0.97	colon	0.99	skel. muscle	0.02	tropomyosin 2 (beta) isoform 2
SFRS14	chr19:18963149-18963362:-	0.97	MCF7	1.00	testes	0.03	splicing factor, arginine/serine-rich 14,splicing factor,
CSDE1,KIAA0885	chr1:115085671-115085817:-	0.97	MCF7	0.00	skel. muscle	0.97	upstream of NRAS isoform 2,upstream of NRAS iso
ARHGEF11,ARHGE	chr1:155174834-155174929:-	0.97	cerebellum	1.00	MCF7	0.03	Rho guanine nucleotide exchange factor (GEF) 11,R
PDLIM5,LIM	chr4:95725160-95725177:+	0.96	HME	0.00	heart	0.96	PDZ and LIM domain 5 isoform b,PDZ and LIM dom
BDTN,DTNB	chr2:25495888-25495908:-	0.96	cerebellum	1.00	testes	0.04	dystrobrevin, beta isoform 1,dystrobrevin, beta isofo
LOC113179	chr19:1862889-1864446:+	0.95	HME	1.00	brain	0.05	CDNA FLJ34737 fis, clone MESAN2008415, moder
PALLD,KIAA0992	chr4:170082959-170083004:+	0.95	HME	0.00	heart	0.95	palladin,palladin,KIAA0992 protein (Fragment).,SIH0
SCRIB	chr8:144961710-144961772:-	0.95	cerebellum	1.00	BT474	0.05	scribble isoform a
ABLIM1,AK057834	chr10:116197629-116197769:-	0.95	cerebellum	0.05	HME	1.00	actin-binding LIM protein 1 isoform a,actin-binding L
FMNL3,KIAA2014	chr12:48326689-48326803:-	0.95	colon	1.00	lymph node	0.05	formin-like 3 isoform 1,Homo sapiens mRNA for KIA
SYNE2,KIAA1011,	chr14:63751757-63751825:+	0.95	skel. muscle	1.00	testes	0.05	Nesprin-2 (Nuclear envelope spectrin repeat protein
ITGA7 variant prote	chr12:54380313-54380444:-	0.95	colon	1.00	skel. muscle	0.05	Homo sapiens mRNA for ITGA7 variant protein, part
n/a	chr22:28409009-28409053:+	0.95	skel. muscle	1.00	testes	0.05	neurofibromin 2 isoform 5,neurofibromin 2 isoform 2,
AK055197,TPM1	chr15:61123309-61123404:+	0.94	MCF7	1.00	colon	0.06	tropomyosin 1 alpha chain isoform 6,Homo sapiens
ABLIM1,AK057834	chr10:116197629-116197775:-	0.94	cerebellum	0.06	HME	1.00	actin-binding LIM protein 1 isoform a,actin-binding L
NCDN	chr1:35796344-35796672:+	0.94	cerebellum	0.06	HME	1.00	neurochondrin isoform 1,neurochondrin isoform 2,
AK055197,TPM1	chr15:61123279-61123404:+	0.94	MCF7	1.00	colon	0.06	tropomyosin 1 alpha chain isoform 6,Homo sapiens
PDLIM7	chr5:176851414-176851532:-	0.94	MCF7	1.00	skel. muscle	0.06	PDZ and LIM domain 7 isoform 1,Homo sapiens EN
n/a	chr19:1224493-1224714:+	0.94	BT474	1.00	colon	0.06	n/a
n/a	chr21:26291546-26291602:-	0.94	cerebellum	0.06	HME	1.00	amyloid beta A4 protein precursor, isoform a,amyloi
CDC42SE1	chr1:149295751-149295886:-	0.94	cerebellum	1.00	MB435	0.07	CDC42 small effector 1,CDC42 small effector 1,
MAP4K4	chr2:101843719-101843880:+	0.93	HME	1.00	brain	0.07	mitogen-activated protein kinase kinase kinase,mito
FLNC	chr7:128277266-128277364:+	0.93	adipose	1.00	skel. muscle	0.07	gamma filamin,gamma filamin,
SFRS14	chr19:18965457-18965549:-	0.93	cerebellum	0.07	MCF7	1.00	splicing factor, arginine/serine-rich 14,splicing factor
DBN1	chr5:176819210-176819347:-	0.93	MCF7	0.00	brain	0.93	drebrin 1 isoform b,drebrin 1 isoform a,
ANK2	chr4:114515369-114515551:+	0.93	cerebellum	0.07	testes	1.00	ankyrin 2 isoform 1,ankyrin 2 isoform 2,ankyrin 2 is
SYNGAP1,ZBTB9	chr6:33518208-33518249:+	0.93	brain	0.93	lymph node	0.00	synaptic Ras GTPase activating protein 1,zinc finge
AK055197,TPM1	chr15:61122958-61123083:+	0.93	colon	0.95	heart	0.02	tropomyosin 1 alpha chain isoform 6,Homo sapiens
ANK2	chr4:114513138-114513230:+	0.93	brain	0.07	heart	1.00	ankyrin 2 isoform 1,ankyrin 2 isoform 2,ankyrin 2 iso
BX537745,ATP2B4	chr1:201968974-201969151:+	0.92	cerebellum	1.00	adipose	0.08	plasma membrane calcium ATPase 4 isoform 4a,Ho
ODF2	chr9:130262650-130262766:+	0.92	MCF7	1.00	testes	0.08	outer dense fiber of sperm tails 2 isoform 1,outer de
C1orf103	chr1:111295433-111296960:-	0.92	HME	0.08	testes	1.00	receptor-interacting factor 1 isoform 1,receptor-inter
CAPZB	chr1:19541833-19541945:-	0.92	heart	1.00	testes	0.08	F-actin capping protein beta subunit
RPN2	chr20:35300219-35300266:+	0.92	liver	0.08	skel. muscle	1.00	ribophorin II precursor,ribophorin II precursor,riboph
PICALM variant pro	chr11:85378941-85379090:-	0.92	cerebellum	1.00	breast	0.08	phosphatidylinositol-binding clathrin assembly,phosp
FLJ10916	chr2:88265962-88266358:+	0.92	breast	1.00	testes	0.08	hypothetical protein LOC55258,Homo sapiens cDNA
FLJ10916	chr2:88265962-88266113:+	0.92	breast	1.00	skel. muscle	0.08	hypothetical protein LOC55258,Homo sapiens cDNA
DKFZp666D023,GU	chr1:226395448-226395831:+	0.92	MCF7	0.08	heart	1.00	guanylate kinase 1,guanylate kinase 1,Homo sapien
HYAL2	chr3:50333801-50334208:-	0.92	HME	1.00	heart	0.08	hyaluronoglucosaminidase 2,hyaluronoglucosaminid
EPB41L3,KIAA0987	chr18:5388020-5388142:-	0.91	cerebellum	0.93	adipose	0.02	erythrocyte membrane protein band 4.1-like 3,erythr
CR620931,MORF4	chrX:102820083-102820204:-	0.91	MCF7	1.00	brain	0.09	MORF-related gene X,MORF-related gene X,MORF

EEN-B2-L1,SH3GL	chr15:82069026-82069222:+	0.91	brain	0.09	testes	1.00	SH3-domain GRB2-like 3,Homo sapiens EEN-B2-L1
CR620931,MORF4L	chrX:102820083-102820235:-	0.91	MCF7	1.00	brain	0.10	MORF-related gene X,MORF-related gene X,MORF
CCDC95,FLJ00210	chr16:29920034-29923479:+	0.91	breast	1.00	skel. muscle	0.10	coiled-coil domain containing 95,coiled-coil domain
n/a	chr14:100371829-100371969:+	0.90	cerebellum	0.10	testes	1.00	n/a
n/a	chr14:23104865-23104941:-	0.90	cerebellum	0.10	MCF7	1.00	n/a
CLTB	chr5:175756086-175756139:-	0.90	cerebellum	0.90	breast	0.00	clathrin, light polypeptide isoform b,clathrin, light poly
RP11-155N3.2,DO	chr13:98258895-98258930:-	0.90	adipose	0.00	brain	0.90	dedicator of cytokinesis 9,Homo sapiens mRNA for
n/a	chr17:5270015-5272255:+	0.90	cerebellum	1.00	skel. muscle	0.10	n/a
KIAA0864	chr17:17024646-17024708:+	0.90	HME	1.00	brain	0.11	myosin phosphatase-Rho interacting protein,myosin
APBB1	chr11:6379783-6379788:-	0.89	cerebellum	0.89	adipose	0.00	amyloid beta A4 precursor protein-binding,,amyloid
n/a	chr14:100371826-100371969:+	0.89	cerebellum	0.11	testes	1.00	n/a
RPS24	chr10:79469968-79469989:+	0.89	cerebellum	0.99	MB435	0.10	ribosomal protein S24 isoform a,ribosomal protein S
AK124433,MAGI1	chr3:65319779-65319867:-	0.89	breast	0.00	brain	0.89	membrane associated guanylate kinase, WW and P
CARM1	chr19:10893051-10893119:+	0.88	cerebellum	1.00	MB435	0.12	coactivator-associated arginine,coactivator-associate
C21orf2	chr21:44578372-44580115:-	0.88	cerebellum	1.00	adipose	0.12	hypothetical protein LOC755,Uncharacterized protei
PIP5K1C	chr19:3584435-3584518:-	0.88	cerebellum	0.97	lymph node	0.09	phosphatidylinositol-4-phosphate 5-kinase, type
MAP4K4	chr2:101846715-101846945:+	0.88	MB435	0.05	brain	0.93	mitogen-activated protein kinase kinase kinase,mito
CADM2	chr3:86111004-86111123:+	0.88	adipose	1.00	brain	0.12	immunoglobulin superfamily, member 4D,immunoglo
SUPT5H	chr19:44640774-44640785:+	0.88	cerebellum	0.12	T47D	1.00	suppressor of Ty 5 homolog,suppressor of Ty 5 hom
PACSIN2	chr22:41602838-41602960:-	0.88	cerebellum	0.12	breast	1.00	protein kinase C and casein kinase substrate in,prote
DKFZp434H202,AT	chr17:37914116-37914133:+	0.87	cerebellum	0.87	MCF7	0.00	ATPase, H+ transporting, lysosomal V0 subunit a,AT
RPS24	chr10:79467729-79467746:+	0.87	BT474	0.00	skel. muscle	0.87	ribosomal protein S24 isoform a,ribosomal protein S
n/a	chr2:149683863-149683923:+	0.87	MCF7	0.05	testes	0.92	n/a
QRSL1	chr6:107206777-107206952:+	0.87	lymph node	0.13	testes	1.00	Glutaminyl-tRNA synthase (Glutamine-hydrolyzing)-
SMARCC2	chr12:54844354-54844419:-	0.87	BT474	1.00	colon	0.13	SWI/SNF-related matrix-associated,SWI/SNF-relate
SERPINA1	chr14:93924650-93924750:-	0.87	HME	1.00	testes	0.13	serine (or cysteine) proteinase inhibitor, clade,serine
SERPINA1	chr14:93924650-93924753:-	0.87	HME	1.00	testes	0.13	serine (or cysteine) proteinase inhibitor, clade,serine
MCAT	chr22:41863031-41863248:-	0.87	BT474	1.00	brain	0.13	mitochondrial malonyltransferase isoform a,mitochor
n/a	chr16:69270719-69270727:-	0.87	MCF7	0.04	skel. muscle	0.91	n/a
HMGN3	chr6:79968492-79968591:-	0.87	MB435	0.13	skel. muscle	1.00	high mobility group nucleosomal binding domain 3,hi
ODF2	chr9:130262613-130262766:+	0.86	MCF7	1.00	testes	0.14	outer dense fiber of sperm tails 2 isoform 1,outer der
MAPT	chr17:41405061-41405147:+	0.86	skel. muscle	0.90	testes	0.04	microtubule-associated protein tau isoform 1,microtu
TRIP10	chr19:6697040-6697207:+	0.86	MB435	0.06	skel. muscle	0.92	thyroid hormone receptor interactor 10,Cdc42-intera
TNS1,DKFZp434G1	chr2:218403335-218403358:-	0.86	breast	0.07	heart	0.93	tensin,tensin,tensin,CDNA: FLJ21295 fis, clone COL
ITGA7 variant prote	chr12:54379921-54380040:-	0.86	colon	0.04	skel. muscle	0.90	Homo sapiens mRNA for ITGA7 variant protein, part
CD44	chr11:35184235-35184366:+	0.86	MCF7	0.12	HME	0.97	CD44 antigen isoform 1 precursor,CD44 antigen isof
DKFZp666D023,GU	chr1:226395448-226395612:+	0.85	MCF7	0.15	heart	1.00	guanylate kinase 1,guanylate kinase 1,Homo sapien
CLEC4M	chr19:7736071-7736154:+	0.85	liver	1.00	lymph node	0.15	C-type lectin domain family 4, member M isoform,C-
RP11-275G3.2	chr1:211253058-211253383:-	0.85	cerebellum	0.15	HME	1.00	Hypothetical protein (Novel protein).
TNK2	chr3:197080765-197080809:-	0.85	T47D	0.06	skel. muscle	0.91	tyrosine kinase, non-receptor, 2 isoform 1,tyrosine ki
KIAA0465,MACF1	chr1:39707806-39707874:+	0.85	MB435	0.01	heart	0.86	microfilament and actin filament cross-linker,microfil
n/a	chr17:24436748-24436792:-	0.84	cerebellum	0.16	skel. muscle	1.00	n/a
n/a	chr9:116848510-116848782:-	0.84	BT474	1.00	colon	0.16	tenascin C (hexabrachion)
n/a	chr22:28409009-28409068:+	0.84	HME	0.88	testes	0.04	neurofibromin 2 isoform 5,neurofibromin 2 isoform 2,
AX747817	chr22:29826871-29827035:+	0.84	cerebellum	1.00	colon	0.16	smoothelin isoform b,smoothelin isoform c,smootheli
VEGF,VEGF41,VE	chr6:43857671-43857802:+	0.84	cerebellum	1.00	MB435	0.16	vascular endothelial growth factor A isoform e,vascu
ASPH	chr8:62757552-62757596:-	0.84	cerebellum	0.85	breast	0.02	aspartate beta-hydroxylase isoform a,aspartate beta
F11R	chr1:159274965-159275108:-	0.83	breast	1.00	MCF7	0.17	F11 receptor isoform a precursor,F11 receptor isofor
PCYT2	chr17:77458372-77458425:-	0.83	BT474	0.89	testes	0.06	phosphate cytidylyltransferase 2, ethanolamine,Hom
WNK1	chr12:860148-860426:+	0.83	cerebellum	1.00	adipose	0.17	WNK lysine deficient protein kinase 1,Serine/threoni
SORBS1,KIAA1296	chr10:97121073-97121174:-	0.83	heart	0.17	skel. muscle	1.00	sorbin and SH3 domain containing 1 isoform 4,sorbi
KIAA0819	chr22:16690410-16690547:-	0.82	cerebellum	1.00	MB435	0.18	Uncharacterized protein KIAA0819.
C14orf173	chr14:104252666-104252722:+	0.82	MB435	0.18	liver	1.00	hypothetical protein LOC64423 isoform 2,hypothetic
GUSB	chr7:65082149-65082333:-	0.82	cerebellum	0.18	breast	1.00	glucuronidase, beta
SOCS7	chr17:33774161-33774265:+	0.82	BT474	0.18	brain	1.00	suppressor of cytokine signaling 7,suppressor of cyt
CR620931,MORF4L	chrX:102820083-102820184:-	0.82	MCF7	1.00	brain	0.18	MORF-related gene X,MORF-related gene X,MORF
SPTAN1	chr9:130395083-130395142:+	0.82	MCF7	1.00	testes	0.18	Homo sapiens SPTAN1 mRNA for non-erythrocytic
PPP3CB	chr10:74869636-74869665:-	0.82	cerebellum	1.00	colon	0.18	protein phosphatase 3 (formerly 2B), catalytic,protei
RAB11FIP1	chr8:37847954-37849855:-	0.82	MCF7	1.00	MB435	0.18	RAB11 family interacting protein 1 isoform 3,RAB11
EPB41L1	chr20:34246665-34246700:+	0.82	brain	0.98	testes	0.16	erythrocyte membrane protein band 4.1-like 1,erythr
TCF3	chr19:1566284-1566519:-	0.82	breast	1.00	colon	0.18	TCF3 protein.,TCF3 protein.,Homo sapiens cDNA: F
FLJ20186	chr16:88543326-88543422:+	0.81	cerebellum	0.87	lymph node	0.06	differentially expressed in FDCP 8 isoform 1,differen
ZNF638,NP220	chr2:71429391-71430909:+	0.81	cerebellum	1.00	liver	0.19	zinc finger protein 638,zinc finger protein 638,zinc fin
n/a	chr3:39519030-39519409:+	0.81	brain	0.19	testes	1.00	n/a
FLJ20186	chr16:88543329-88543422:+	0.81	cerebellum	0.86	lymph node	0.05	differentially expressed in FDCP 8 isoform 1,differen
n/a	chr2:159241497-159241625:+	0.81	cerebellum	1.00	testes	0.19	n/a
U2AF1	chr21:43394545-43394611:-	0.81	brain	0.19	lymph node	1.00	U2 small nuclear RNA auxillary factor 1 isoform,U2
ACTN1	chr14:68415459-68415539:-	0.81	MCF7	1.00	colon	0.20	actinin, alpha 1,actinin, alpha 1,actinin, alpha 1,actini
KIAA1818,KIAA149	chr12:131031987-131032094:+	0.81	adipose	0.20	testes	1.00	Homo sapiens mRNA for KIAA1498 protein, partial c
AP1S2	chrX:15768541-15768635:-	0.80	adipose	0.00	heart	0.80	adaptor-related protein complex 1 sigma 2,Homo sa
ARHGAP5	chr14:31629459-31633343:+	0.80	cerebellum	1.00	lymph node	0.20	Rho GTPase activating protein 5 isoform b,Rho GTP
SAMD4B	chr19:44536486-44536546:+	0.80	lymph node	0.04	testes	0.85	sterile alpha motif domain containing 4B,sterile alph
KIAA0843,ABLIM3	chr5:148600432-148600530:+	0.80	cerebellum	0.84	adipose	0.04	actin binding LIM protein family, member 3,actin bin
CALD1	chr7:134298111-134298225:+	0.80	cerebellum	0.80	HME	0.00	caldesmon 1 isoform 3,caldesmon 1 isoform 2,calde
SAT1,SSAT-1	chrX:23712332-23712441:+	0.80	cerebellum	0.90	adipose	0.10	spermidine/spermine N1-acetyltransferase,Homo sa
TJP1	chr15:27799273-27799512:-	0.80	brain	1.00	testes	0.20	tight junction protein 1 isoform a,tight junction protein
ERGIC3	chr20:33605557-33605571:+	0.80	cerebellum	0.80	breast	0.00	serologically defined breast cancer antigen 84,serolo

BAIAP2	chr17:76699309-76699354:+	0.79	BT474	0.90	MB435	0.10	BAI1-associated protein 2 isoform 1,Homo sapiens
C5orf16	chr5:140998706-140998772:+	0.79	brain	1.00	lymph node	0.21	chromosome 5 open reading frame 16,chromosom
COASY	chr17:37967900-37968031:+	0.79	T47D	0.08	lymph node	0.87	coenzyme A synthase isoform a,coenzyme A syntha
SHOC2	chr10:112713873-112714809:+	0.79	HME	1.00	T47D	0.21	soc-2 suppressor of clear homolog,soc-2 suppresso
ASNS	chr7:97338967-97339244:-	0.79	MCF7	0.21	skel. muscle	1.00	asparagine synthetase,asparagine synthetase,aspar
SREBP-1	chr17:17667557-17667646:-	0.79	brain	1.00	lymph node	0.21	sterol regulatory element binding transcription,Sterol
DST,BPAG1,KIAA0	chr6:56435803-56435913:-	0.79	cerebellum	0.21	MCF7	1.00	dystonin isoform 1eB precursor,DST protein (Fragm
SRRM1	chr1:24862261-24862302:+	0.79	cerebellum	1.00	lymph node	0.22	serine/arginine repetitive matrix 1
ODZ2	chr5:167571317-167571337:+	0.79	HME	0.04	heart	0.83	odz, odd Oz/ten-m homolog 2,odz, odd Oz/ten-m ho
KIAA0968	chr5:149599460-149599492:-	0.78	brain	0.13	skel. muscle	0.91	calcium/calmodulin-dependent protein kinase IIA,cal
KIAA1217,DKFZp6	chr10:24823435-24823539:+	0.78	adipose	0.80	skel. muscle	0.02	hypothetical protein LOC56243,hypothetical protein
AKT2	chr19:45462969-45463098:-	0.78	cerebellum	1.00	colon	0.22	v-akt murine thymoma viral oncogene homolog 2
KIAA1873,CAPRIN	chr12:30763280-30765116:-	0.78	cerebellum	1.00	lymph node	0.22	C1q domain containing 1 isoform 2,C1q domain con
FXR1	chr3:182175795-182175886:+	0.78	T47D	0.15	skel. muscle	0.93	fragile X mental retardation-related protein 1,fragile
aml1,RUNX1,AML1	chr21:35128577-35128768:-	0.78	breast	1.00	MB435	0.22	runt-related transcription factor 1 isoform a,runt-rela
MRPL55	chr1:226362761-226363345:-	0.78	breast	1.00	BT474	0.22	mitochondrial ribosomal protein L55 isoform a,mitoc
CSPG2,VCAN	chr5:82850924-82853884:+	0.78	MB435	1.00	colon	0.22	chondroitin sulfate proteoglycan 2 (versican),chondr
APLP2,CR602481	chr11:129512361-129512396:+	0.78	cerebellum	0.99	BT474	0.21	amyloid beta (A4) precursor-like protein 2,amyloid be
NCDN	chr1:35796344-35796411:+	0.78	cerebellum	0.22	HME	1.00	neurochondrin isoform 1,neurochondrin isoform 2,
ARHGAP17,RICH1,	chr16:24858186-24858419:-	0.78	cerebellum	1.00	skel. muscle	0.22	nadrin isoform 1,nadrin isoform 2,nadrin isoform 1,R
SIX5	chr19:50961448-50962253:-	0.78	BT474	1.00	skel. muscle	0.22	sine oculis homeobox homolog 5,Homo sapiens cD
p70 S6Kb,RPS6KB	chr11:66957173-66957241:+	0.78	cerebellum	0.23	MCF7	1.00	ribosomal protein S6 kinase, 70kDa, polypeptide,rib
KIF1B	chr1:10261742-10261783:+	0.77	cerebellum	1.00	skel. muscle	0.23	kinesin family member 1B isoform b,kinesin family m
NRAP	chr10:115392683-115392787:-	0.77	heart	0.07	skel. muscle	0.84	nebulin-related anchoring protein isoform S
ANKRD9	chr14:102044731-102044936:-	0.77	cerebellum	1.00	breast	0.23	ankyrin repeat domain 9,ankyrin repeat domain 9,an
NAGLU	chr17:37942942-37943089:+	0.77	HME	1.00	colon	0.23	alpha-N-acetylglucosaminidase precursor
NR4A1	chr12:50732547-50732696:+	0.77	adipose	0.80	skel. muscle	0.03	nuclear receptor subfamily 4, group A, member 1,nu
PB1	chr3:52563780-52563935:-	0.77	T47D	1.00	lymph node	0.23	polybromo 1 isoform 2,polybromo 1 isoform 4,polybr
SENP5	chr3:198096419-198097962:+	0.77	cerebellum	1.00	brain	0.23	SUMO1/sentrin specific protease 5
CLTA	chr9:36200622-36200657:+	0.77	cerebellum	0.77	breast	0.00	clathrin, light polypeptide A isoform a,Homo sapiens
DTX3	chr12:56285394-56285781:+	0.77	T47D	1.00	brain	0.24	deltex 3 homolog,deltex 3 homolog,deltex 3 homolo
CTTN	chr11:69945224-69945334:+	0.76	BT474	0.94	heart	0.18	cortactin isoform a,cortactin isoform b,
CEACAM1	chr19:47707568-47707620:-	0.76	liver	0.18	lymph node	0.94	carcinoembryonic antigen-related cell adhesion,carc
KIAA0182	chr16:84225021-84225239:+	0.76	MCF7	0.24	colon	1.00	hypothetical protein LOC23199,hypothetical protein
FMNL2,KIAA1902	chr2:153210194-153210240:+	0.76	MB435	0.81	brain	0.05	formin-like 2,CDNA FLJ16308 fis, clone PUAEN200
ANXA6	chr5:150470381-150470398:-	0.76	breast	0.93	BT474	0.17	annexin VI isoform 1,annexin VI isoform 2,annexin V
SUV39H2	chr10:14963505-14963650:+	0.76	MB435	0.24	testes	1.00	Histone-lysine N-methyltransferase, H3 lysine-9 spe
KIAA1217,DKFZp6	chr10:24871818-24873416:+	0.76	breast	1.00	MB435	0.24	hypothetical protein LOC56243,hypothetical protein
C19orf28	chr19:3493774-3493975:-	0.76	cerebellum	1.00	MB435	0.24	hypothetical protein LOC126321 isoform a,hypotheti
KIAA0428,MBNL1	chr3:153499884-153500846:+	0.76	cerebellum	1.00	breast	0.24	muscleblind-like 1 isoform e,muscleblind-like 1 isofo
RPS24	chr10:79467729-79467757:+	0.76	BT474	0.00	skel. muscle	0.76	ribosomal protein S24 isoform a,ribosomal protein S
MAP2K7,MKK7	chr19:7876693-7876740:+	0.76	skel. muscle	0.95	testes	0.19	mitogen-activated protein kinase kinase 7,mitogen-a
DKFZp451I083,MY	chr12:100584653-100584706:+	0.76	skel. muscle	0.01	testes	0.76	myosin binding protein C, slow type isoform 3,myosi
SORBS1,KIAA1296	chr10:97125720-97125803:-	0.75	skel. muscle	1.00	testes	0.25	sorbin and SH3 domain containing 1 isoform 4,sorbi
DKFZp451I083,MY	chr12:100600513-100600571:+	0.75	skel. muscle	0.05	testes	0.80	myosin binding protein C, slow type isoform 3,myosi
SH3GLB2	chr9:130811553-130811567:-	0.75	cerebellum	0.75	MCF7	0.00	SH3-containing protein SH3GLB2,SH3-containing p
RGL1,ARHGAP9	chr12:56153653-56153758:-	0.75	lymph node	0.25	testes	1.00	Rho GTPase activating protein 9 isoform 1,Rho GTP
FLJ20186	chr16:88543326-88543547:+	0.75	cerebellum	0.78	lymph node	0.03	differentially expressed in FDCP 8 isoform 1,differen
MCFD2	chr2:46989666-46989820:-	0.75	cerebellum	0.25	breast	1.00	multiple coagulation factor deficiency 2,multiple coa
MFN2	chr1:11964454-11964758:+	0.75	cerebellum	0.25	colon	1.00	mitofusin 2
BCAS2	chr1:114920832-114920902:-	0.75	colon	0.25	heart	1.00	breast carcinoma amplified sequence 2
LRP8	chr1:53487640-53487816:-	0.75	cerebellum	1.00	MB435	0.25	low density lipoprotein receptor-related protein,low d
ARRB1	chr11:74660393-74660416:-	0.75	MB435	0.25	brain	1.00	arrestin beta 1 isoform A,arrestin beta 1 isoform B,
SNRP70	chr19:54297183-54298656:+	0.74	cerebellum	0.77	MB435	0.03	U1 small nuclear ribonucleoprotein 70 kDa,U1 small
BCAR1	chr16:73828582-73828743:-	0.74	BT474	1.00	adipose	0.26	breast cancer anti-estrogen resistance 1,breast can
SNIP,P140,KIAA16	chr17:33957521-33957643:-	0.74	cerebellum	0.26	BT474	1.00	SNAP25-interacting protein,SNAP25-interacting pro
PTPRF	chr1:43851026-43851058:+	0.74	MCF7	0.00	colon	0.74	protein tyrosine phosphatase, receptor type, F,prote
HM13	chr20:29619542-29619688:+	0.74	lymph node	0.03	skel. muscle	0.77	minor histocompatibility antigen 13 isoform 3,minor h
TMED2	chr12:122638111-122638131:+	0.74	cerebellum	0.00	skel. muscle	0.74	coated vesicle membrane protein
TTF1	chr9:134266663-134268036:-	0.74	MCF7	1.00	adipose	0.26	transcription termination factor, RNA polymerase,tra
C9orf3,APO	chr9:96884678-96884822:+	0.74	MCF7	1.00	skel. muscle	0.26	aminopeptidase O,aminopeptidase O,aminopeptidas
AB231751	chr11:63288916-63289302:-	0.74	cerebellum	1.00	colon	0.26	Homo sapiens mRNA for hypothetical protein, partial
DOK2,DOK-2	chr8:21825686-21825967:-	0.74	breast	1.00	lymph node	0.26	docking protein 2,docking protein 2,Homo sapiens d
KIAA0134	chr19:52571970-52572044:+	0.74	HME	0.84	testes	0.10	Homo sapiens cDNA FLJ41051 fis, clone SMINT100
ABLIM1,AK057834	chr10:116203128-116203232:-	0.74	HME	0.01	heart	0.75	actin-binding LIM protein 1 isoform a,actin-binding L
BIN1	chr2:127542209-127542301:-	0.74	cerebellum	0.74	breast	0.00	bridging integrator 1 isoform 4,bridging integrator 1 i
C9orf7	chr9:135320265-135320390:+	0.74	liver	1.00	testes	0.26	Uncharacterized protein C9orf7.
CLIP2,KIAA0291	chr7:73425198-73425302:+	0.74	cerebellum	0.78	colon	0.05	CAP-GLY domain containing linker protein 2,CAP-G
MBD1	chr18:46054554-46054718:-	0.73	HME	1.00	MB435	0.27	methyl-CpG binding domain protein 1 isoform 3,met
SMRTE,NCOR2	chr12:123424912-123424962:-	0.73	cerebellum	0.83	HME	0.10	nuclear receptor co-repressor 2 isoform 1,nuclear re
FLJ10241	chr19:46631017-46631179:-	0.73	HME	1.00	lymph node	0.27	hypothetical protein LOC55101,hypothetical protein
Rabex5,RABGEF1	chr7:65874305-65874500:+	0.73	T47D	1.00	colon	0.27	RAB guanine nucleotide exchange factor (GEF) 1,H
MADD	chr11:47304865-47304934:+	0.73	brain	0.27	testes	1.00	MAP-kinase activating death domain-containing,MA
FLJ20186	chr16:88543329-88543547:+	0.73	cerebellum	0.75	lymph node	0.02	differentially expressed in FDCP 8 isoform 1,differen
SUPT5H	chr19:44640771-44640785:+	0.73	cerebellum	0.02	testes	0.75	suppressor of Ty 5 homolog,suppressor of Ty 5 hom
ABI1	chr10:27084590-27084676:-	0.73	cerebellum	1.00	lymph node	0.27	abl-interactor 1 isoform a,abl-interactor 1 isoform b,a
TMEM168	chr7:112210989-112212244:-	0.73	HME	1.00	testes	0.27	hypothetical protein LOC64418

EPSIN,EPN1	chr19:60892475-60892549:+	0.73	cerebellum	0.27	HME	1.00	epsin 1,Homo sapiens EH domain-binding mitotic ph
CALD1	chr7:134270979-134271056:+	0.73	HME	0.03	colon	0.76	caldesmon 1 isoform 3,caldesmon 1 isoform 2,calde
ZNF397	chr18:31076353-31076846:+	0.73	cerebellum	1.00	testes	0.28	Zinc finger protein 397 (Zinc finger and SCAN doma
PDLIM5,LIM	chr4:95715790-95716208:+	0.73	breast	1.00	skel. muscle	0.28	PDZ and LIM domain 5 isoform b,PDZ and LIM dom
LGALS8	chr1:234772838-234772963:+	0.73	BT474	0.28	testes	1.00	galectin 8 isoform a,galectin 8 isoform b,
THTPA	chr14:23095792-23096353:+	0.72	T47D	1.00	colon	0.28	thiamine triphosphatase,thiamine triphosphatase,Ho
KIF1A,KIF1A varian	chr2:241360660-241360686:-	0.72	cerebellum	0.72	BT474	0.00	axonal transport of synaptic vesicles,Homo sapiens
KIAA0406	chr20:36073331-36075673:-	0.72	breast	1.00	liver	0.28	hypothetical protein LOC9675,hypothetical protein L
JKTBP,HNRPDL	chr4:83565740-83565844:-	0.72	MCF7	0.75	brain	0.03	heterogeneous nuclear ribonucleoprotein D-like,hete
p70 S6Kb,RPS6KB	chr11:66957173-66957263:+	0.72	cerebellum	0.28	MCF7	1.00	ribosomal protein S6 kinase, 70kDa, polypeptide,rib
MAP7D2	chrX:19983773-19983838:-	0.72	cerebellum	0.72	testes	0.00	Homo sapiens cDNA FLJ14503 fis, clone NT2RM10
NEXN	chr1:78163461-78163502:+	0.72	heart	0.97	skel. muscle	0.25	nexilin (F actin binding protein),Nexilin.,Homo sapier
FMNL2,KIAA1902	chr2:153210194-153210287:+	0.72	MB435	0.79	brain	0.07	formin-like 2,CDNA FLJ16308 fis, clone PUAEN200
BCHE	chr3:167029999-167031523:-	0.72	brain	1.00	testes	0.28	butyrylcholinesterase precursor,Homo sapiens butyr
ABI1	chr10:27100010-27100024:-	0.72	cerebellum	1.00	lymph node	0.28	abl-interactor 1 isoform a,abl-interactor 1 isoform b,a
F11R	chr1:159274965-159275087:-	0.72	breast	1.00	MCF7	0.28	F11 receptor isoform a precursor,F11 receptor isofor
MPST	chr22:35749739-35749914:+	0.72	liver	1.00	testes	0.28	3-mercaptopyruvate sulfurtransferase,3-mercaptopy
MYL6,MLC-3	chr12:54840677-54840721:+	0.72	HME	0.86	lymph node	0.15	myosin, light chain 6, alkali, smooth muscle and,Hom
THTPA	chr14:23095792-23096088:+	0.72	T47D	1.00	colon	0.28	thiamine triphosphatase,thiamine triphosphatase,Ho
SORBS1,KIAA1296	chr10:97164241-97164609:-	0.71	cerebellum	0.29	breast	1.00	sorbin and SH3 domain containing 1 isoform 4,sorbi
LTBP4	chr19:45808898-45809140:+	0.71	breast	1.00	MB435	0.29	latent transforming growth factor beta binding,latent
KIAA0621,ARHGAF	chr5:142566956-142567231:+	0.71	cerebellum	0.29	breast	1.00	GTPase regulator associated with the focal,GTPase
FAM63A	chr1:149245412-149245897:-	0.71	cerebellum	1.00	testes	0.29	hypothetical protein LOC55793 isoform 1,hypothetic
NDUFV3	chr21:43196361-43197455:+	0.71	cerebellum	0.29	BT474	1.00	NADH-ubiquinone oxidoreductase flavoprotein 3
MDC1	chr6:30783322-30784113:-	0.71	HME	1.00	testes	0.29	mediator of DNA damage checkpoint 1,mediator of
KIAA0858,AK12345	chr13:75277616-75277897:+	0.71	brain	1.00	heart	0.29	LIM domain only 7,Homo sapiens mRNA for KIAA08
SMARCC2	chr12:54852988-54853080:-	0.71	brain	1.00	colon	0.29	SWI/SNF-related matrix-associated,SWI/SNF-relate
THTPA	chr14:23095792-23096083:+	0.71	T47D	1.00	colon	0.29	thiamine triphosphatase,thiamine triphosphatase,Ho
NR1H3	chr11:47237307-47237386:+	0.71	T47D	0.04	adipose	0.74	nuclear receptor subfamily 1, group H, member 3,n
PKIG	chr20:42644640-42644786:+	0.71	BT474	0.12	skel. muscle	0.82	cAMP-dependent protein kinase inhibitor gamma,cA
PHLDB1,KIAA0638	chr11:118031780-118031812:+	0.71	MB435	0.00	brain	0.71	Homo sapiens mRNA for KIAA0638 protein, partial c
PPCDC	chr15:73107641-73107847:+	0.70	BT474	0.30	T47D	1.00	phosphopantothenoylcysteine decarboxylase
RTN4	chr2:55105726-55108125:-	0.70	cerebellum	1.00	breast	0.30	reticulon 4 isoform A,reticulon 4 isoform D,reticulon
DKFZp566P0524,A	chr10:61489462-61489770:-	0.70	MCF7	1.00	brain	0.30	ankyrin 3 isoform 1,ankyrin 3 isoform 1,Ankyrin 3 iso
BAI2,BAI 2	chr1:31982381-31982545:-	0.70	cerebellum	0.30	T47D	1.00	brain-specific angiogenesis inhibitor 2,brain-specific
SFRS3	chr6:36675576-36676031:+	0.70	colon	0.75	liver	0.05	splicing factor, arginine/serine-rich 3,Homo sapiens
LTBP1	chr2:33421409-33421534:+	0.70	HME	1.00	colon	0.30	latent transforming growth factor beta binding,latent
PEX19	chr1:158519944-158520053:-	0.70	T47D	0.97	lymph node	0.27	peroxisomal biogenesis factor 19,Peroxisomal bioge
AP2M1	chr3:185381127-185381132:+	0.70	cerebellum	1.00	MB435	0.30	adaptor-related protein complex 2, mu 1 subunit,ada
BAT2D1,KIAA1096	chr1:169825131-169825367:+	0.70	T47D	1.00	testes	0.30	HBxAg transactivated protein 2,Homo sapiens mRN
HM13	chr20:29619542-29619744:+	0.70	lymph node	0.02	skel. muscle	0.72	minor histocompatibility antigen 13 isoform 3,minor
ERC1	chr12:1242461-1242592:+	0.70	cerebellum	0.30	BT474	1.00	RAB6-interacting protein 2 isoform epsilon,RAB6-int
SCHIP1	chr3:161086690-161089426:+	0.70	breast	1.00	colon	0.30	schwannomin interacting protein 1,Schwannomin int
WSB1	chr17:22658897-22659060:+	0.70	cerebellum	1.00	adipose	0.31	WD repeat and SOCS box-containing 1 isoform 1,W
DKFZp451I083,MY	chr12:100600513-100600580:+	0.70	skel. muscle	0.03	testes	0.73	myosin binding protein C, slow type isoform 3,myosi
WSB1	chr17:22658897-22659072:+	0.69	cerebellum	1.00	adipose	0.31	WD repeat and SOCS box-containing 1 isoform 1,W
EPB41L3,KIAA098	chr18:5384676-5384792:-	0.69	adipose	0.31	colon	1.00	erythrocyte membrane protein band 4.1-like 3,erythr
NFIX	chr19:13050427-13050549:+	0.69	brain	0.95	skel. muscle	0.26	Nuclear factor 1 X-type (Nuclear factor 1/X) (NF1-X)
LRRFIP2	chr3:37082719-37082820:-	0.69	skel. muscle	1.00	testes	0.31	leucine rich repeat (in FLII) interacting,leucine rich re
TCF20	chr22:40894559-40894686:-	0.69	cerebellum	1.00	lymph node	0.31	transcription factor 20 isoform 2
ZFAND5	chr9:74168206-74168342:-	0.69	cerebellum	1.00	adipose	0.31	zinc finger protein 216,zinc finger protein 216,zinc fi
FNBP1,AL049935	chr9:131725944-131726126:-	0.69	cerebellum	1.00	lymph node	0.31	formin binding protein 1,Homo sapiens mRNA; cDN
TCF3	chr19:1563206-1563432:-	0.69	breast	1.00	adipose	0.31	TCF3 protein.,TCF3 protein.,Homo sapiens cDNA: F
SH3GLB2	chr9:130815108-130815119:-	0.69	cerebellum	0.69	MCF7	0.00	SH3-containing protein SH3GLB2,SH3-containing p
ADAM15	chr1:153301004-153301075:+	0.69	T47D	0.77	testes	0.08	a disintegrin and metalloproteinase domain 15,a disi
BIN1	chr2:127526301-127526408:-	0.69	cerebellum	0.69	skel. muscle	0.00	bridging integrator 1 isoform 4,bridging integrator 1 i
ITGB4	chr17:71262731-71262889:+	0.69	MCF7	0.00	adipose	0.69	integrin beta 4 isoform 1 precursor,integrin beta 4 is
SLC2A8	chr9:129204657-129204853:+	0.69	cerebellum	1.00	skel. muscle	0.31	solute carrier family 2, (facilitated glucose,solute ca
WNK1	chr12:859000-859458:+	0.69	skel. muscle	1.00	testes	0.31	WNK lysine deficient protein kinase 1,Serine/threoni
KIAA1033	chr12:104029033-104029172:+	0.69	HME	1.00	lymph node	0.31	hypothetical protein LOC23325,hypothetical protein
PRKCDBP	chr11:6297463-6297558:-	0.69	MB435	0.12	colon	0.81	protein kinase C, delta binding protein
SLC6A6	chr3:14484600-14484724:+	0.68	breast	1.00	lymph node	0.32	solute carrier family 6 (neurotransmitter,Homo sapie
AXIN1	chr16:336149-337107:-	0.68	cerebellum	1.00	T47D	0.32	axin 1 isoform a,axin 1 isoform b,
TMEM126B	chr11:85019837-85020008:+	0.68	BT474	0.09	adipose	0.77	hypothetical protein LOC55863,hypothetical protein
CTTN	chr11:69944154-69944264:+	0.68	breast	1.00	brain	0.32	cortactin isoform a,cortactin isoform b,
RPS24	chr10:79467203-79469989:+	0.68	cerebellum	0.68	MB435	0.00	ribosomal protein S24 isoform a,ribosomal protein S
BPTF	chr17:63302134-63302322:+	0.68	cerebellum	1.00	BT474	0.32	Homo sapiens BPTF mRNA for bromodomain PHD
IMPDH2	chr3:49038432-49038503:-	0.68	BT474	0.01	skel. muscle	0.69	inosine monophosphate dehydrogenase 2
n/a	chr5:42840515-42842967:-	0.68	cerebellum	1.00	adipose	0.32	n/a
FLJ00246,MASK-B	chr5:139856289-139857047:+	0.68	cerebellum	1.00	T47D	0.32	MASK-4E-BP3 protein,ankyrin repeat and KH doma
PRMT7	chr16:66903442-66903580:+	0.68	MCF7	1.00	BT474	0.32	protein arginine N-methyltransferase 7,protein argini
n/a	chr14:101761185-101762498:-	0.68	cerebellum	1.00	testes	0.32	n/a
RNASE1	chr14:20340248-20340318:-	0.67	adipose	0.14	brain	0.81	pancreatic ribonuclease precursor,pancreatic ribonu
YIPF1,DKFZp761P	chr1:54127505-54127724:-	0.67	HME	0.33	MB435	1.00	Yip1 domain family, member 1,Yip1 domain family,
CDK2	chr12:54649526-54649627:+	0.67	adipose	1.00	lymph node	0.33	cyclin-dependent kinase 2 isoform 1,cyclin-depende
C1orf144,RP11-430	chr1:16590457-16590506:+	0.67	cerebellum	0.87	lymph node	0.20	putative MAPK activating protein PM20,PM21,Putati
ACADM	chr1:75966662-75966761:+	0.67	HME	1.00	colon	0.33	acyl-Coenzyme A dehydrogenase, C-4 to C-12,Hom

KIAA0999	chr11:116243872-116244015:-	0.67	breast	1.00	brain	0.33	KIAA0999 protein,KIAA0999 protein.,KIAA0999 pro
UBXD5,RP11-569G	chr1:26500004-26500102:-	0.67	cerebellum	0.11	testes	0.78	socius isoform 1,socius isoform 3,socius isoform 1,S
DKFZp434K249,RN	chr11:494824-494996:-	0.67	T47D	0.77	lymph node	0.10	ribonuclease/angiogenin inhibitor,ribonuclease/angio
C9orf18	chr9:123971745-123971856:+	0.67	colon	0.06	testes	0.73	hypothetical protein LOC254956
DKFZp434I0612	chr1:20979425-20979620:-	0.67	adipose	0.10	lymph node	0.77	Homo sapiens HP1-BP74 protein mRNA, complete
BRD8	chr5:137532058-137532276:-	0.67	MCF7	1.00	testes	0.33	bromodomain containing 8 isoform 1,bromodomain
NFATC3	chr16:66713391-66714525:+	0.67	cerebellum	0.33	breast	1.00	cytoplasmic nuclear factor of activated T-cells,cytop
CD47	chr3:109253476-109253507:-	0.67	MCF7	0.33	brain	1.00	CD47 antigen isoform 1 precursor,CD47 antigen iso
VEGF,VEGF41,VE	chr6:43857671-43857767:+	0.67	MB435	0.14	heart	0.80	vascular endothelial growth factor A isoform e,vascu
RNASE1	chr14:20340248-20340330:-	0.67	adipose	0.13	brain	0.79	pancreatic ribonuclease precursor,pancreatic ribonu
C20orf199	chr20:47330847-47330908:+	0.67	MCF7	0.87	lymph node	0.21	Homo sapiens NS5ATP6-regulated protein 1, compl
n/a	chr20:47330847-47330908:-	0.67	MCF7	0.87	lymph node	0.21	n/a
AKAP8L,HRIHFB20	chr19:15370441-15370577:-	0.67	cerebellum	0.67	skel. muscle	0.01	A kinase (PRKA) anchor protein 8-like,Homo sapien
ZBTB44,CR615509	chr11:129635961-129637034:-	0.67	breast	1.00	MCF7	0.34	BTB (POZ) domain containing 15,BTB (POZ) domai
STK39	chr2:168630075-168630137:-	0.66	MCF7	1.00	MB435	0.34	serine threonine kinase 39 (STE20/SPS1 homolog,
LTBP3	chr11:65064060-65064200:-	0.66	MB435	0.18	adipose	0.84	latent transforming growth factor beta binding,latent
EPB41	chr1:29295254-29295703:+	0.66	cerebellum	0.34	BT474	1.00	erythrocyte membrane protein band 4.1,erythrocyte
DKFZp564J1082,E	chr6:131230292-131230414:-	0.66	breast	1.00	brain	0.34	erythrocyte membrane protein band 4.1-like 2,Hypot
ANKS6	chr9:100592207-100592709:-	0.66	cerebellum	1.00	testes	0.34	sterile alpha motif domain containing 6,sterile alpha
DKFZp547H1810,M	chr3:48003877-48003927:-	0.66	HME	0.00	skel. muscle	0.66	microtubule-associated protein 4 isoform 1,microtub
AKR1A1	chr1:45806744-45806943:+	0.66	MCF7	0.34	adipose	1.00	aldo-keto reductase family 1, member A1,aldo-keto
DKFZp564D0478,C	chr1:27530063-27530215:+	0.66	lymph node	0.85	testes	0.19	Homo sapiens hypothetical protein SB71 mRNA, co
C10orf84	chr10:120091229-120091429:-	0.66	cerebellum	0.21	skel. muscle	0.87	hypothetical protein LOC63877
n/a	chr10:75541673-75541876:+	0.66	HME	0.23	colon	0.89	vinculin isoform meta-VCL
CSDA	chr12:10753774-10753980:-	0.66	MB435	0.75	skel. muscle	0.10	cold shock domain protein A,cold shock domain pro
TCF20	chr22:40894559-40894653:-	0.66	cerebellum	1.00	lymph node	0.34	transcription factor 20 isoform 2
PTK2B	chr8:27359228-27359353:+	0.66	cerebellum	1.00	lymph node	0.34	PTK2B protein tyrosine kinase 2 beta isoform b,PTK
MLX	chr17:37974014-37974103:+	0.65	adipose	0.25	testes	0.90	transcription factor-like protein 4 isoform,transcriptio
TRPM2	chr21:44671321-44671422:+	0.65	cerebellum	0.84	MB435	0.19	transient receptor potential cation channel,,transient
ASPSCR1	chr17:77566240-77566521:+	0.65	lymph node	0.69	testes	0.04	alveolar soft part sarcoma chromosome region,,alve
KBTBD2	chr7:32885572-32886079:-	0.65	MB435	0.35	brain	1.00	kelch repeat and BTB (POZ) domain containing 2
KIAA0983,THOC5	chr22:28276717-28276832:-	0.65	MCF7	0.79	adipose	0.14	THO complex 5,THO complex 5,THO complex 5,TH
TPST1	chr7:65342747-65343692:+	0.65	MB435	1.00	T47D	0.35	tyrosylprotein sulfotransferase 1
RP11-66D17.7-007	chr1:154970425-154970909:+	0.65	cerebellum	1.00	skel. muscle	0.35	hypothetical protein LOC51093
RMND1	chr6:151808136-151808653:-	0.65	cerebellum	1.00	testes	0.35	required for meiotic nuclear division 1 homolog,requi
FBLN2	chr3:13638276-13638416:+	0.65	skel. muscle	1.00	testes	0.36	fibulin 2 precursor, isoform b
n/a	chr7:101823429-101823989:+	0.65	T47D	1.00	lymph node	0.36	n/a
ARRB2	chr17:4565031-4565087:+	0.64	cerebellum	0.80	colon	0.15	arrestin, beta 2 isoform 1,arrestin, beta 2 isoform 2,a
KIAA0428,MBNL1	chr3:153656746-153656840:+	0.64	breast	1.00	colon	0.36	muscleblind-like 1 isoform e,muscleblind-like 1 isofo
U2AF1	chr21:43393632-43393698:-	0.64	heart	1.00	lymph node	0.36	U2 small nuclear RNA auxillary factor 1 isoform,U2
PELI3	chr11:65992880-65992951:+	0.64	cerebellum	0.36	MB435	1.00	pellino 3 alpha,pellino 3 alpha,Protein pellino homol
SFRS6	chr20:41521207-41521474:+	0.64	cerebellum	1.00	breast	0.36	arginine/serine-rich splicing factor 6,arginine/serine-
NUMA1 variant prot	chr11:71401095-71401136:-	0.64	brain	0.33	skel. muscle	0.97	nuclear mitotic apparatus protein 1,Homo sapiens m
ZNF271	chr18:31124972-31125194:+	0.64	breast	0.19	brain	0.83	zinc finger protein 271,zinc finger protein 271,zinc fi
POLR2D	chr2:128326969-128327149:-	0.64	BT474	1.00	HME	0.36	DNA directed RNA polymerase II polypeptide D,Hom
PTK2,DKFZp666O0	chr8:142004942-142005030:-	0.64	BT474	0.18	testes	0.82	PTK2 protein tyrosine kinase 2 isoform b,PTK2 prote
EIF4G2,CR611226	chr11:10779784-10779897:-	0.64	cerebellum	1.00	liver	0.36	eukaryotic translation initiation factor 4,eukaryotic tra
HYPA,PRPF40A	chr2:153243816-153243869:-	0.64	BT474	0.16	skel. muscle	0.80	Homo sapiens HSPC225 mRNA, complete cds.,Hom
TPM3	chr1:152408405-152408483:-	0.64	cerebellum	0.36	breast	1.00	tropomyosin 3 isoform 2,tropomyosin 3 isoform 3,
ST3GAL1	chr8:134557144-134558025:-	0.64	breast	1.00	MCF7	0.36	sialyltransferase 4A,sialyltransferase 4A,
KIAA1845,CAPN10	chr2:241184024-241184611:+	0.64	cerebellum	1.00	testes	0.36	calpain 10 isoform a,calpain 10 isoform c,calpain 10
ZMYND11	chr10:257135-257296:+	0.64	HME	1.00	skel. muscle	0.37	zinc finger, MYND domain containing 11 isoform,zin
RABEP1	chr17:5332240-5332633:+	0.63	cerebellum	1.00	HME	0.37	rabaptin, RAB GTPase binding effector protein 1,rab
AK025749,NAT12	chr14:56927428-56928199:+	0.63	cerebellum	1.00	brain	0.37	N-acetyltransferase 12,Homo sapiens cDNA: FLJ21
SLC2A8	chr9:129199476-129199638:+	0.63	adipose	1.00	colon	0.37	solute carrier family 2, (facilitated glucose,solute ca
C7orf44	chr7:43638349-43639532:-	0.63	cerebellum	1.00	MB435	0.37	hypothetical protein LOC55744,hypothetical protein
ACTR1B	chr2:97643466-97643541:-	0.63	cerebellum	1.00	skel. muscle	0.37	ARP1 actin-related protein 1 homolog B,
SOLH	chr16:526030-526143:+	0.63	adipose	0.19	lymph node	0.82	small optic lobes,Homo sapiens, Similar to small opt
TRPT1	chr11:63748148-63748258:-	0.63	cerebellum	1.00	BT474	0.37	tRNA phosphotransferase 1 isoform 2,tRNA phosph
SGCE	chr7:94066945-94066971:-	0.63	cerebellum	0.37	HME	1.00	sarcoglycan, epsilon,sarcoglycan, epsilon,sarcoglyc
PFKFB3	chr10:6310165-6310187:+	0.63	adipose	0.02	skel. muscle	0.66	6-phosphofructo-2-kinase/fructose-2,,Homo sapiens
SAMD4A,KIAA1053	chr14:54273492-54273755:+	0.63	cerebellum	0.20	skel. muscle	0.84	sterile alpha motif domain containing 4,sterile alpha
DKFZp762G166,EX	chr14:68745894-68746273:+	0.63	cerebellum	1.00	breast	0.37	exonuclease 3'-5' domain-like 2,exonuclease 3'-5' d
PRMT7	chr16:66903446-66903580:+	0.63	MCF7	1.00	BT474	0.37	protein arginine N-methyltransferase 7,protein argini
IMPDH1	chr7:127836579-127836774:-	0.63	MB435	0.37	lymph node	1.00	inosine monophosphate dehydrogenase 1 isoform a,
SNRP70	chr19:54297183-54297254:+	0.63	cerebellum	0.64	MB435	0.01	U1 small nuclear ribonucleoprotein 70 kDa,U1 small
SEPT4,CE5B3 alph	chr17:53959042-53959338:-	0.63	brain	1.00	lymph node	0.37	septin 4 isoform 3,septin 4 isoform 2,septin 4 isofor
CUGBP1,AK05465	chr11:47477581-47477732:-	0.63	MCF7	0.13	skel. muscle	0.76	CUG triplet repeat, RNA-binding protein 1,CUG tripl
DST,BPAG1,KIAA0	chr6:56437442-56437513:-	0.63	MB435	0.00	skel. muscle	0.63	dystonin isoform 1eB precursor,DST protein (Fragm
SRRM2	chr16:2759864-2760229:+	0.63	cerebellum	0.75	testes	0.12	splicing coactivator subunit SRm300,splicing coactiv
ZC3H11A	chr1:202032044-202032352:+	0.63	MCF7	0.37	adipose	1.00	zinc finger CCCH-type containing 11A,zinc finger C
GIPC1	chr19:14464669-14464724:-	0.63	cerebellum	0.30	heart	0.92	regulator of G-protein signalling 19 interacting,regula
KIAA0670,ACIN1	chr14:22606363-22607720:-	0.63	MCF7	0.67	heart	0.04	apoptotic chromatin condensation inducer 1,apoptot
DKFZp564O1863,F	chr12:27004715-27004828:+	0.62	breast	1.00	skel. muscle	0.38	FGFR1 oncogene partner 2,HSPC123-like protein.,
KIAA1818,KIAA149	chr12:131071577-131071819:+	0.62	BT474	1.00	testes	0.38	Homo sapiens mRNA for KIAA1498 protein, partial
BRD8	chr5:137530106-137530315:-	0.62	cerebellum	1.00	MB435	0.38	bromodomain containing 8 isoform 1,bromodomain
ArgBP2b,ArgBP2a,	chr4:186781062-186782642:-	0.62	brain	0.62	heart	0.00	sorbin and SH3 domain containing 2 isoform 1,sorbi

BC051442,PPP2R5	chr14:101453921-101454037:+	0.62	MB435	0.38	heart	1.00	CDNA FLJ16473 fis, clone BRHIP3026052, highly si
GGA1	chr22:36350834-36351029:+	0.62	BT474	1.00	lymph node	0.38	golgi associated, gamma adaptin ear containing,,gol
MTA1	chr14:105005720-105005731:+	0.62	cerebellum	0.62	MB435	0.00	metastasis associated protein,Homo sapiens mRNA
SNRP70	chr19:54297183-54297242:+	0.62	cerebellum	0.63	MB435	0.02	U1 small nuclear ribonucleoprotein 70 kDa,U1 small
SLC44A2,DKFZp66	chr19:10614573-10614697:+	0.62	BT474	0.01	skel. muscle	0.63	CTL2 protein,CTL2 protein,Homo sapiens clone 246
DKFZp761E2216,C	chr7:150467999-150468136:+	0.62	cerebellum	0.38	BT474	1.00	centaurin, gamma 3 isoform a,centaurin, gamma 3 is
DTX3	chr12:56285621-56285781:+	0.62	T47D	1.00	brain	0.38	deltex 3 homolog,deltex 3 homolog,deltex 3 homolo
KIF23	chr15:67520161-67520472:+	0.62	T47D	0.38	testes	1.00	kinesin family member 23 isoform 2
CTPS	chr1:41245708-41245804:+	0.62	MCF7	1.00	lymph node	0.38	CTP synthase,CTP synthase,
RNPS1	chr16:2254575-2254762:-	0.62	HME	0.29	brain	0.90	RNA-binding protein S1, serine-rich domain,RNA-bi
PLSCR3	chr17:7237187-7237407:-	0.61	MCF7	0.39	colon	1.00	phospholipid scramblase 3,phospholipid scramblase
NDRG2,KIAA1248	chr14:20560863-20560904:-	0.61	cerebellum	0.32	skel. muscle	0.94	N-myc downstream-regulated gene 2 isoform a,N-m
CR592254,NR_003	chr6:86444232-86444469:-	0.61	cerebellum	0.23	T47D	0.85	full-length cDNA clone CS0DI004YM02 of Placenta
NR1H3	chr11:47237918-47238106:+	0.61	cerebellum	0.39	breast	1.00	nuclear receptor subfamily 1, group H, member 3,n
TBRG4,NR_002990	chr7:45110223-45110380:-	0.61	HME	1.00	testes	0.39	cell cycle progression 2 protein isoform 2,cell cycle p
ATXN2L,A2LG	chr16:28755271-28755307:+	0.61	MCF7	0.15	testes	0.76	ataxin 2 related protein isoform C,ataxin 2 related pr
STRA13	chr17:77570806-77570859:-	0.61	HME	0.70	lymph node	0.09	stimulated by retinoic acid 13,Homo sapiens stimulat
CR622423,ADD1	chr4:2898167-2898200:+	0.61	cerebellum	0.62	lymph node	0.01	adducin 1 (alpha) isoform d,adducin 1 (alpha) isofor
HCFC1R1	chr16:3013476-3013532:-	0.61	heart	0.29	liver	0.89	host cell factor C1 regulator 1 (XPO1 dependant),ho
GAA	chr17:75690205-75690284:+	0.61	T47D	1.00	lymph node	0.39	acid alpha-glucosidase preproprotein,acid alpha-glu
BCAS1	chr20:52016852-52017019:-	0.61	BT474	1.00	brain	0.39	breast carcinoma amplified sequence 1,breast carci
PGPEP1	chr19:18329193-18329425:+	0.61	breast	1.00	lymph node	0.39	Homo sapiens mRNA for putative pyroglutamyl-pepti
DKFZp451I083,MY	chr12:100602291-100602333:+	0.61	skel. muscle	0.99	testes	0.38	myosin binding protein C, slow type isoform 3,myosi
PCQAP	chr22:19259400-19259519:+	0.61	BT474	0.62	colon	0.01	positive cofactor 2, glutamine/Q-rich-associated,posi
NPEPL1	chr20:56677753-56677915:+	0.61	breast	1.00	lymph node	0.40	syntaxin 16 isoform a,syntaxin 16 isoform b,syntaxin
MPI	chr15:72969832-72970048:+	0.60	BT474	1.00	MB435	0.40	Mannose phosphate isomerase isoform.
UNQ154,TMEM77	chr1:111483646-111483856:-	0.60	cerebellum	0.40	breast	1.00	hypothetical protein LOC128338,Homo sapiens cDN
ZNF313	chr20:47991527-47991655:+	0.60	HME	1.00	brain	0.40	zinc finger protein 313,Homo sapiens clone 25071 a
PALM	chr19:691352-691483:+	0.60	adipose	1.00	brain	0.40	paralemmin isoform 2
FUBP3	chr9:132499875-132499946:+	0.60	T47D	0.40	adipose	1.00	far upstream element (FUSE) binding protein 3,Far
UBXD5,RP11-569G	chr1:26500004-26500131:-	0.60	cerebellum	0.08	testes	0.68	socius isoform 1,socius isoform 3,socius isoform 1,S
MFN2	chr1:11964618-11964758:+	0.60	cerebellum	0.40	colon	1.00	mitofusin 2
MLXIP	chr12:121182792-121182883:+	0.60	cerebellum	0.40	breast	1.00	MLX interacting protein,MLX interacting protein,ML
LIG1	chr19:53357331-53357420:-	0.60	cerebellum	0.40	HME	1.00	DNA ligase I,Homo sapiens mRNA for DNA ligase I
MMACHC	chr1:45845580-45846596:+	0.60	MB435	0.12	T47D	0.72	methylmalonic aciduria (cobalamin deficiency),meth
TMEM142B	chr7:101863636-101863785:+	0.60	MCF7	1.00	lymph node	0.40	transmembrane protein 142B,transmembrane protei
GAK	chr4:880248-880337:-	0.60	cerebellum	1.00	colon	0.40	cyclin G associated kinase,cyclin G associated kinas
n/a	chr14:105206493-105206543:-	0.60	lymph node	1.00	testes	0.40	n/a
hNedd5,SEPT2	chr2:241904518-241904628:+	0.60	BT474	0.23	HME	0.82	septin 2,septin 2,septin 2,septin 2,septin 2,Homo sa
peptidylglycine alph	chr5:102388737-102388937:+	0.60	breast	0.40	MB435	1.00	peptidylglycine alpha-amidating monooxygenase,pe
CAMLG	chr5:134107576-134107641:+	0.60	adipose	0.33	brain	0.93	calcium modulating ligand,Homo sapiens calcium m
BAIAP2	chr17:76699309-76699350:+	0.60	MB435	0.03	liver	0.63	BAI1-associated protein 2 isoform 1,Homo sapiens
GOLGA2	chr9:130069294-130069374:-	0.60	BT474	0.13	adipose	0.72	Golgi autoantigen, golgin subfamily a, 2,Golgi autoa
SNED1,FLJ00133,A	chr2:241661354-241661452:+	0.59	adipose	1.00	lymph node	0.41	6720455I24Rik homolog,6720455I24Rik homolog,In
JAG2	chr14:104688373-104688486:-	0.59	HME	0.41	T47D	1.00	jagged 2 isoform a precursor,jagged 2 isoform b pre
MOCS1	chr6:39984809-39984856:-	0.59	breast	1.00	lymph node	0.41	molybdenum cofactor synthesis-step 1 protein,moly
PUM2	chr2:20341825-20342061:-	0.59	HME	1.00	MB435	0.41	pumilio homolog 2,pumilio homolog 2,pumilio homol
ARRB2	chr17:4565057-4565087:+	0.59	cerebellum	0.90	colon	0.31	arrestin, beta 2 isoform 1,arrestin, beta 2 isoform 2,a
n/a	chr3:185538869-185539011:+	0.59	cerebellum	1.00	adipose	0.41	n/a
BMPR2	chr2:203128220-203129499:+	0.59	cerebellum	0.41	breast	1.00	bone morphogenetic protein receptor type II,Homo s
MMS19L,MMS19	chr10:99226582-99226710:-	0.59	HME	1.00	testes	0.41	MMS19-like (MET18 homolog, S. cerevisiae),MMS1
FLJ00056,FLJ1035	chr14:20625319-20625462:+	0.59	breast	1.00	lymph node	0.41	hypothetical protein LOC55701,CDNA FLJ10357 fis,
graf-2,ARHGAP10	chr4:149203749-149203901:+	0.59	lymph node	0.41	skel. muscle	1.00	Rho GTPase activating protein 10,Rho GTPase acti
RBM6	chr3:49979635-49981185:+	0.59	MCF7	1.00	colon	0.41	RNA binding motif protein 6,RBM6 protein.,RBM6 p
peptidylglycine alph	chr5:102388734-102388937:+	0.59	cerebellum	0.41	MB435	1.00	peptidylglycine alpha-amidating monooxygenase,pe
LTBP4	chr19:45814635-45814788:+	0.59	HME	1.00	colon	0.41	latent transforming growth factor beta binding,latent
TMEM16A	chr11:69634880-69634945:+	0.59	BT474	0.41	liver	1.00	transmembrane protein 16A,transmembrane protein
BAT3	chr6:31715256-31715402:-	0.59	MB435	0.36	colon	0.95	HLA-B associated transcript-3 isoform a,HLA-B ass
ZNF313	chr20:47991505-47991655:+	0.59	HME	1.00	brain	0.42	zinc finger protein 313,Homo sapiens clone 25071 a
GALE	chr1:23997964-23998089:-	0.58	BT474	0.42	T47D	1.00	UDP-galactose-4-epimerase,Homo sapiens cDNA F
MARK2	chr11:63428034-63428195:+	0.58	T47D	0.65	lymph node	0.07	MAP/microtubule affinity-regulating kinase 2,MAP/mi
PRKCZ	chr1:2066688-2066810:+	0.58	cerebellum	0.05	testes	0.64	protein kinase C, zeta isoform 1,protein kinase C, ze
NQO2	chr6:2960763-2960876:+	0.58	adipose	0.42	skel. muscle	1.00	NAD(P)H dehydrogenase, quinone 2,NAD(P)H dehy
DUSP10	chr1:219978899-219979752:-	0.58	cerebellum	1.00	lymph node	0.42	dual specificity phosphatase 10 isoform a,dual speci
MINK1,MINK	chr17:4734299-4734385:+	0.58	cerebellum	0.58	MB435	0.00	misshapen/NIK-related kinase isoform 2,misshapen/
FBXL3	chr13:76493649-76493997:-	0.58	breast	1.00	colon	0.42	F-box and leucine-rich repeat protein 3
CBY1	chr22:37393968-37394083:+	0.58	cerebellum	1.00	BT474	0.42	PKD2 interactor, golgi and endoplasmic reticulum,P
TCEB1	chr8:75039276-75039414:-	0.58	cerebellum	1.00	heart	0.42	elongin C,elongin C,elongin C,elongin C,
ZC3H11A	chr1:202032044-202032247:+	0.58	MCF7	0.42	adipose	1.00	zinc finger CCCH-type containing 11A,zinc finger C
WAC	chr10:28924668-28924976:+	0.58	cerebellum	1.00	breast	0.42	WW domain-containing adapter with a coiled-coil,W
ATXN2L,A2LG	chr16:28755148-28755312:+	0.58	brain	0.42	heart	1.00	ataxin 2 related protein isoform C,ataxin 2 related pr
n/a	chr10:28924668-28924976:-	0.58	cerebellum	1.00	breast	0.42	n/a
FXC1,TIM9b	chr11:6459563-6459658:+	0.58	HME	1.00	lymph node	0.42	fracture callus 1 homolog,Homo sapiens small zinc f
R3HDM2,KIAA1002	chr12:55968907-55968960:-	0.58	MCF7	0.00	skel. muscle	0.58	R3H domain containing 2,R3H domain-containing pr
C14orf153	chr14:103107713-103107910:+	0.58	BT474	1.00	brain	0.42	hypothetical protein LOC84334,Homo sapiens mRN
TOM1L2	chr17:17694932-17694991:-	0.58	brain	0.42	colon	1.00	target of myb1-like 2 isoform 1,target of myb1-like 2
PXN	chr12:119138116-119138276:-	0.58	HME	1.00	colon	0.42	paxillin,Homo sapiens mRNA for Paxillin variant prot

SPG21	chr15:63062898-63062984:-	0.58	BT474	0.38	testes	0.96	spastic paraplegia 21,spastic paraplegia 21,
LYRM1	chr16:20834379-20834537:+	0.58	breast	1.00	heart	0.43	LYR motif containing 1,LYR motif containing 1,
DKFZp666K145,HP	chr10:100179538-100179636:-	0.57	cerebellum	0.34	adipose	0.92	Homo sapiens mRNA; cDNA DKFZp666K145 (from
SNAPC5	chr15:64574722-64574811:-	0.57	MB435	1.00	lymph node	0.43	small nuclear RNA activating complex,
n/a	chr22:37021339-37021399:-	0.57	MB435	0.06	T47D	0.63	n/a
SCARB1	chr12:123833182-123833310:-	0.57	liver	1.00	testes	0.43	scavenger receptor class B, member 1 isoform 1,sca
TMEM142B	chr7:101863654-101863785:+	0.57	MCF7	1.00	lymph node	0.43	transmembrane protein 142B,transmembrane protei
C14orf108	chr14:56810715-56811360:+	0.57	BT474	1.00	lymph node	0.43	hypothetical protein LOC55745,Uncharacterized pro
HIRIP3	chr16:29912728-29913665:-	0.57	cerebellum	1.00	BT474	0.43	HIRA interacting protein 3,Homo sapiens mRNA for
GEMIN7	chr19:50275005-50275127:+	0.57	cerebellum	0.21	HME	0.78	gemin 7,gemin 7,gemin 7,
PEX5	chr12:7246104-7246214:+	0.57	brain	0.43	testes	1.00	peroxisomal biogenesis factor 5,peroxisomal biogen
C1orf43	chr1:152458936-152459037:-	0.57	adipose	0.43	lymph node	1.00	hypothetical protein LOC25912 isoform 1,hypothetica
POLB	chr8:42315687-42315744:+	0.57	heart	0.37	testes	0.94	polymerase (DNA directed), beta,polymerase (DNA
SRRM2	chr16:2758507-2758601:+	0.57	HME	0.60	skel. muscle	0.03	splicing coactivator subunit SRm300,splicing coactiv
ART3	chr4:77222001-77222712:+	0.57	MB435	0.43	heart	1.00	ADP-ribosyltransferase 3,Homo sapiens mRNA for
PLCD1	chr3:38142657-38142836:-	0.57	MCF7	0.43	HME	1.00	phospholipase C, delta 1
PCBP2	chr12:52147856-52147894:+	0.57	liver	0.67	lymph node	0.10	poly(rC)-binding protein 2 isoform b,poly(rC)-binding
TNNT1	chr19:60349614-60349646:-	0.57	lymph node	0.25	skel. muscle	0.81	troponin T1, skeletal, slow,troponin T1, skeletal, slow
DMWD	chr19:50979739-50979813:-	0.57	adipose	0.35	testes	0.92	dystrophia myotonica-containing WD repeat motif,dy
TJP2	chr9:71055771-71056100:+	0.57	breast	1.00	colon	0.43	tight junction protein 2 (zona occludens 2),tight juncti
BDTN,DTNB	chr2:25463662-25463751:-	0.57	breast	1.00	brain	0.43	dystrobrevin, beta isoform 1,dystrobrevin, beta isofor
NRP1	chr10:33511632-33511682:-	0.57	heart	1.00	lymph node	0.43	neuropilin 1 isoform b,neuropilin 1 isoform c,neuropil
SH3KBP1	chrX:19473961-19474089:-	0.57	HME	1.00	heart	0.43	SH3-domain kinase binding protein 1 isoform a,SH3-
KIAA0196	chr8:126165137-126165446:-	0.57	BT474	1.00	HME	0.43	hypothetical protein LOC9897,Homo sapiens mRNA
CREB3L2	chr7:137263436-137263652:-	0.57	breast	1.00	MB435	0.43	cAMP responsive element binding protein 3-like,cAM
BIN1	chr2:127525200-127525289:-	0.57	cerebellum	1.00	MB435	0.43	bridging integrator 1 isoform 4,bridging integrator 1 i
NR_002588,DKFZp	chr3:187988793-187988903:+	0.57	BT474	0.57	skel. muscle	0.01	eukaryotic translation initiation factor 4A2,Homo sapi
NR_002588,DKFZp	chr3:187988793-187988899:+	0.57	BT474	0.57	skel. muscle	0.00	eukaryotic translation initiation factor 4A2,Homo sapi
BCAS3	chr17:56820761-56820851:+	0.57	BT474	0.62	colon	0.05	breast carcinoma amplified sequence 3,Homo sapie
COBL	chr7:51118249-51118419:-	0.57	cerebellum	0.44	BT474	1.00	cordon-bleu homolog,cordon-bleu homolog,cordon-b
MBD1	chr18:46055738-46055812:-	0.56	adipose	0.00	testes	0.56	methyl-CpG binding domain protein 1 isoform 3,meth
NR4A1	chr12:50723853-50723962:+	0.56	adipose	0.18	skel. muscle	0.74	nuclear receptor subfamily 4, group A, member 1,nu
KIAA1398,RRBP1	chr20:17608644-17608720:-	0.56	HME	0.19	adipose	0.75	ribosome binding protein 1,ribosome binding protein
TCEA2	chr20:62165689-62165746:+	0.56	lymph node	0.63	testes	0.07	transcription elongation factor A protein 2,Homo sapi
TBRG1,FLJ00213	chr11:124001579-124001715:+	0.56	colon	1.00	lymph node	0.44	transforming growth factor beta regulator 1,NIAM.,tra
DKFZp547K246,TM	chr4:931497-931942:+	0.56	T47D	1.00	brain	0.44	hypothetical protein LOC84286,Homo sapiens cDNA
RWDD1	chr6:117001914-117002027:+	0.56	cerebellum	0.59	skel. muscle	0.03	RWD domain containing 1 isoform b,RWD domain c
HNRPAB	chr5:177569739-177569879:+	0.56	BT474	0.31	skel. muscle	0.87	heterogeneous nuclear ribonucleoprotein AB,hetero
NDRG2,KIAA1248	chr14:20561985-20562095:-	0.56	HME	1.00	brain	0.44	N-myc downstream-regulated gene 2 isoform a,N-m
HRNBP2,RBM9	chr22:34482098-34482137:-	0.56	HME	0.44	MB435	1.00	RNA binding motif protein 9 isoform 1,RNA binding
NCOA6	chr20:32791828-32794806:-	0.56	cerebellum	1.00	liver	0.44	nuclear receptor coactivator 6
C12orf32	chr12:2864690-2864961:+	0.56	cerebellum	1.00	brain	0.44	chromosome 12 open reading frame 32,chromosom
KIAA0621,ARHGAF	chr5:142566956-142567066:+	0.56	cerebellum	0.44	breast	1.00	GTPase regulator associated with the focal,GTPase
ArgBP2b,ArgBP2a,	chr4:186809932-186809976:-	0.56	brain	1.00	colon	0.44	sorbin and SH3 domain containing 2 isoform 1,sorbi
DKFZp566D244,PA	chr15:70328640-70328709:-	0.56	cerebellum	0.56	MCF7	0.00	poly (ADP-ribose) polymerase family, member 6,Ho
ITGA6	chr2:173074746-173074875:+	0.56	HME	1.00	MB435	0.44	integrin alpha chain, alpha 6 isoform a
RGN	chrX:46834119-46834334:+	0.56	cerebellum	1.00	liver	0.44	regucalcin,regucalcin,
MTERFD2	chr2:241687484-241687982:-	0.56	BT474	1.00	MB435	0.44	MTERF domain containing 2,MTERF domain contai
ZNF655,VIK	chr7:98997447-98998053:+	0.56	cerebellum	1.00	adipose	0.44	zinc finger protein 655 isoform b,zinc finger protein 6
AMN1	chr12:31753494-31753626:-	0.56	brain	0.44	skel. muscle	1.00	antagonist of mitotic exit network 1 homolog,Homo s
KIAA1217,DKFZp6	chr10:24871628-24871705:+	0.56	adipose	0.15	skel. muscle	0.70	hypothetical protein LOC56243,hypothetical protein
ZFYVE19	chr15:38892189-38892392:+	0.56	cerebellum	0.45	breast	1.00	zinc finger, FYVE domain containing 19,Zinc finger
MFN2	chr1:11964614-11964762:+	0.55	cerebellum	0.45	colon	1.00	mitofusin 2
ECHDC2	chr1:53143294-53144871:-	0.55	cerebellum	1.00	BT474	0.45	enoyl Coenzyme A hydratase domain containing 2
DKFZp547O175	chr12:121991307-121991495:-	0.55	MCF7	1.00	testes	0.45	ATP-binding cassette, sub-family B (MDR/TAP),,AT
RTN2	chr19:50688258-50688476:-	0.55	MB435	0.45	T47D	1.00	reticulon 2 isoform B,reticulon 2 isoform D,
DMKN,UNQ729	chr19:40680389-40680423:-	0.55	HME	0.76	adipose	0.20	dermokine isoform beta,dermokine isoform beta,der
EMP3	chr19:53522590-53522733:+	0.55	adipose	1.00	lymph node	0.45	epithelial membrane protein 3
SC4MOL	chr4:166473942-166474227:+	0.55	BT474	0.45	MB435	1.00	sterol-C4-methyl oxidase-like isoform 1,sterol-C4-m
C12orf32	chr12:2864710-2864919:+	0.55	cerebellum	1.00	brain	0.45	chromosome 12 open reading frame 32,chromosom
GL004,C2orf33	chr2:227915705-227915779:+	0.55	MB435	0.07	skel. muscle	0.62	hypothetical protein LOC56947,hypothetical protein
ATXN2L,A2LG	chr16:28755148-28755307:+	0.55	brain	0.45	heart	1.00	ataxin 2 related protein isoform C,ataxin 2 related pr
AB073649,MAP7	chr6:136746502-136746612:-	0.55	MCF7	0.45	testes	1.00	microtubule-associated protein 7,microtubule-associ
PLSCR3	chr17:7237644-7237879:-	0.55	MB435	0.45	T47D	1.00	phospholipid scramblase 3,phospholipid scramblase
BPTF	chr17:63312706-63312894:+	0.55	cerebellum	1.00	MCF7	0.45	Homo sapiens BPTF mRNA for bromodomain PHD
ANKRD17	chr4:74224112-74224864:-	0.55	cerebellum	1.00	MB435	0.45	ankyrin repeat domain protein 17 isoform a,ankyrin r
MR1B	chr1:179287994-179288269:+	0.55	T47D	0.45	lymph node	1.00	MHC class I related protein 1 isoform B (Major histo
ECHDC1	chr6:127679288-127679340:-	0.55	breast	1.00	MB435	0.45	enoyl Coenzyme A hydratase domain containing 1,E
NS5ATP2,HDDC2	chr6:125661559-125661661:-	0.55	MCF7	0.62	lymph node	0.07	HD domain containing 2,Homo sapiens CGI-130 pro
ACADM	chr1:75966674-75966761:+	0.55	HME	1.00	colon	0.45	acyl-Coenzyme A dehydrogenase, C-4 to C-12,Hom
RBM6	chr3:49979907-49981185:+	0.55	MCF7	1.00	colon	0.45	RNA binding motif protein 6,RBM6 protein.,RBM6 p
BC008049,ZMIZ2,H	chr7:44766275-44766352:+	0.55	cerebellum	0.81	lymph node	0.26	zinc finger, MIZ-type containing 2 isoform 2,zinc fing
TJP2	chr9:71054111-71054221:+	0.55	cerebellum	0.45	breast	1.00	tight junction protein 2 (zona occludens 2),tight juncti
CR592254,NR_003	chr6:86444391-86444469:-	0.55	cerebellum	0.37	T47D	0.92	full-length cDNA clone CS0DI004YM02 of Placenta
RAG1AP1,RP11-54	chr1:153376661-153376822:+	0.55	HME	0.46	colon	1.00	stromal cell protein,Novel protein.,
C1orf38	chr1:28081069-28082141:+	0.55	breast	1.00	testes	0.46	Induced by contact to basement membrane 1 protei
n/a	chr7:101825072-101825150:+	0.54	cerebellum	0.46	MCF7	1.00	n/a

DDEF2	chr2:9448642-9448776:+	0.54	cerebellum	0.85	BT474	0.30	development- and differentiation-enhancing,develop
PDLIM5,LIM	chr4:95716117-95716208:+	0.54	HME	1.00	skel. muscle	0.46	PDZ and LIM domain 5 isoform b,PDZ and LIM doma
CAST	chr5:96088254-96088319:+	0.54	heart	0.86	skel. muscle	0.31	calpastatin isoform a,calpastatin isoform h,calpastati
DKFZp761E2216,Cl	chr7:150448540-150448765:+	0.54	MB435	0.12	lymph node	0.66	centaurin, gamma 3 isoform a,centaurin, gamma 3 is
n/a	chr14:22899604-22899882:-	0.54	T47D	1.00	colon	0.46	embryonal Fyn-associated substrate isoform 1,embry
MOCS1	chr6:39984794-39984856:-	0.54	breast	1.00	lymph node	0.46	molybdenum cofactor synthesis-step 1 protein,molyl
C12orf32	chr12:2864710-2864961:+	0.54	cerebellum	1.00	brain	0.46	chromosome 12 open reading frame 32,chromosom
PPP2R4	chr9:130930064-130930168:+	0.54	adipose	0.61	brain	0.07	protein phosphatase 2A, regulatory subunit B',Homo
SAR1A	chr10:71591381-71591500:-	0.54	breast	1.00	colon	0.46	SAR1a gene homolog 1
n/a	chr11:64289999-64290203:-	0.54	HME	0.87	liver	0.34	splicing factor 1 isoform 2,splicing factor 1 isoform 3,
mm-1,PFDN5	chr12:51976481-51977975:+	0.54	cerebellum	1.00	lymph node	0.46	prefoldin subunit 5 isoform gamma,Homo sapiens m
NTAN1	chr16:15049355-15049457:-	0.54	MB435	0.81	lymph node	0.27	N-terminal Asn amidase
ENTPD6,CD39L2	chr20:25135158-25135226:+	0.54	cerebellum	0.21	MB435	0.75	ectonucleoside triphosphate diphosphohydrolase,ect
FN1	chr2:215945077-215945343:-	0.54	cerebellum	1.00	brain	0.46	fibronectin 1 isoform 1 preproprotein,fibronectin 1 isc
SEMA6A	chr5:115831178-115831342:-	0.54	cerebellum	0.46	T47D	1.00	sema domain, transmembrane domain (TM), and,ser
ADAR2g	chr21:45420073-45421007:+	0.54	cerebellum	1.00	brain	0.47	RNA-specific adenosine deaminase B1 isoform 4,RN
KIAA1114,TRO	chrX:54965736-54966926:+	0.54	cerebellum	1.00	brain	0.47	trophinin isoform 5,trophinin isoform 2,Homo sapiens
C6orf134	chr6:30718524-30718767:+	0.53	cerebellum	1.00	MCF7	0.47	hypothetical protein LOC79969 isoform 2,hypothetica
HEXIM2	chr17:40595638-40595785:+	0.53	MB435	1.00	skel. muscle	0.47	hexamthylene bis-acetamide inducible 2,hexamthyle
CROCC,KIAA0445	chr1:17170547-17170729:+	0.53	cerebellum	0.75	adipose	0.21	ciliary rootlet coiled-coil, rootletin,ciliary rootlet coiled
KIAA0723,DKFZp68	chr5:138671747-138671915:+	0.53	brain	1.00	lymph node	0.47	matrin 3,matrin 3,matrin 3,matrin 3,matrin 3,matrin 3,
FBXO18	chr10:5984989-5985144:+	0.53	adipose	0.47	testes	1.00	F-box only protein, helicase, 18 isoform 2,F-box only
APLP2,CR602481	chr11:129498717-129498884:+	0.53	cerebellum	0.83	testes	0.30	amyloid beta (A4) precursor-like protein 2,amyloid be
C1orf85,AF086351,	chr1:154531174-154531431:-	0.53	BT474	1.00	testes	0.47	kidney predominant protein NCU-G1,kidney predomi
SEMA3F	chr3:50187533-50187625:+	0.53	HME	0.95	adipose	0.41	semaphorin 3F,semaphorin 3F,
MTA1	chr14:105004089-105004124:+	0.53	cerebellum	1.00	testes	0.47	metastasis associated protein,Homo sapiens mRNA
AK128131	chr17:74610839-74610931:-	0.53	brain	1.00	colon	0.47	Homo sapiens cDNA FLJ42653 fis, clone BRACE30
ASPM	chr1:195336184-195340938:-	0.53	MCF7	1.00	T47D	0.47	asp (abbreastal spindle)-like, microcephaly,asp (abb
CDKN3,AY257479	chr14:53936362-53936444:+	0.53	MB435	0.43	testes	0.96	cyclin-dependent kinase inhibitor 3,cyclin-dependent
DKFZp586K0821	chr11:47547828-47548019:+	0.53	MCF7	0.89	MB435	0.36	Protein-tyrosine phosphatase mitochondrial 1, mitoch
n/a	chr11:47547828-47548019:-	0.53	MCF7	0.89	MB435	0.36	n/a
SFRS6	chr20:41521207-41521371:+	0.53	cerebellum	1.00	MB435	0.47	arginine/serine-rich splicing factor 6,arginine/serine-r
KCNC4	chr1:110576366-110576742:+	0.53	cerebellum	0.47	testes	1.00	Shaw-related voltage-gated potassium channel,Sha
DPH3,AK023203	chr3:16280666-16280740:-	0.53	lymph node	0.88	testes	0.35	zinc finger, CSL domain containing 2 isoform 2,Hom
KIAA0964,DLGAP4	chr20:34561059-34561138:+	0.53	brain	0.55	testes	0.02	disks large-associated protein 4 isoform a,CDNA FL
ZNF326	chr1:90245492-90245897:+	0.53	cerebellum	1.00	brain	0.47	zinc finger protein 326 isoform 2
MGRN1,KIAA0544	chr16:4670034-4670099:+	0.53	cerebellum	0.47	skel. muscle	1.00	mahogunin, ring finger 1,mahogunin, ring finger 1,ma
HMGCR	chr5:74686637-74686795:+	0.53	MCF7	1.00	brain	0.47	3-hydroxy-3-methylglutaryl-Coenzyme A reductase,3
DKFZp313I142,FLJ	chr5:176891560-176891807:-	0.53	MCF7	1.00	HME	0.47	Homo sapiens mRNA for KIAA1931 protein, partial c
RCE1	chr11:66369547-66369609:+	0.53	HME	1.00	lymph node	0.47	prenyl protein peptidase RCE1 isoform 1,prenyl prot
BC033061,C6orf11	chr6:99970946-99971025:-	0.53	lymph node	0.47	skel. muscle	1.00	splicing factor, arginine/serine-rich 130,splicing facto
MFN2	chr1:11964614-11964758:+	0.53	cerebellum	0.47	colon	1.00	mitofusin 2
TMEM159	chr16:21079800-21079830:+	0.53	T47D	0.09	colon	0.62	promethin,Homo sapiens clone 24796 mRNA seque
RAB11FIP3	chr16:481135-481269:+	0.53	cerebellum	1.00	colon	0.47	rab11-family interacting protein 3
LRRFIP2	chr3:37107962-37108033:-	0.53	MB435	1.00	testes	0.47	leucine rich repeat (in FLII) interacting,leucine rich re
BAX	chr19:54150617-54150668:+	0.53	BT474	1.00	lymph node	0.47	BCL2-associated X protein isoform sigma,BCL2-ass
HTRG,SAP30BP	chr17:71179491-71179538:+	0.53	heart	1.00	lymph node	0.47	transcriptional regulator protein,transcriptional regula
STAU1	chr20:47215941-47216229:-	0.53	BT474	0.47	brain	1.00	staufen isoform a,staufen isoform c,staufen isoform
NSMCE2	chr8:126183475-126183570:+	0.53	BT474	0.47	HME	1.00	non-SMC element 2 homolog (MMS21, S.,non-SMC
PCDHGB3,PCDHG	chr5:140838145-140838297:+	0.53	MB435	0.48	colon	1.00	protocadherin gamma subfamily A, 11 isoform 1,prot
NSMCE2	chr8:126183438-126183570:+	0.52	HME	1.00	lymph node	0.48	non-SMC element 2 homolog (MMS21, S.,non-SMC
SETMAR	chr3:4329582-4330445:+	0.52	MCF7	1.00	testes	0.48	SET domain and mariner transposase fusion,SETM
GL004,C2orf33	chr2:227925474-227925533:+	0.52	lymph node	0.48	skel. muscle	1.00	hypothetical protein LOC56947,hypothetical protein
SPOCD1,BC069257	chr1:32052139-32053560:-	0.52	T47D	0.75	testes	0.23	SPOC domain containing 1,SPOC domain containin
CD151	chr11:824530-824745:+	0.52	cerebellum	1.00	lymph node	0.48	CD151 antigen,CD151 antigen,CD151 antigen,CD1
ZMIZ1	chr10:80740687-80740947:+	0.52	MCF7	0.89	lymph node	0.36	retinoic acid induced 17,retinoic acid induced 17,retir
FLJ00043	chr11:65107639-65107812:+	0.52	MCF7	1.00	lymph node	0.48	signal-induced proliferation-associated protein,signa
n/a	chr17:5272115-5272255:+	0.52	cerebellum	1.00	skel. muscle	0.48	n/a
CP110,KIAA0419	chr16:19444542-19444684:+	0.52	cerebellum	0.22	MB435	0.75	CP110 protein,Homo sapiens KIAA0419 mRNA, part
PPM1K	chr4:89418316-89418818:-	0.52	cerebellum	1.00	MCF7	0.48	protein phosphatase 1K (PP2C domain containing),
NIN,KIAA1565	chr14:50292960-50295098:-	0.52	cerebellum	1.00	lymph node	0.48	ninein isoform 2,Homo sapiens mRNA for KIAA1565
ECHDC2	chr1:53144779-53144871:-	0.52	HME	0.31	liver	0.84	enoyl Coenzyme A hydratase domain containing 2
AK055197,TPM1	chr15:61143316-61143442:+	0.52	breast	1.00	colon	0.48	tropomyosin 1 alpha chain isoform 6,Homo sapiens
AK2,AK2A	chr1:33269732-33269849:-	0.52	cerebellum	0.54	testes	0.02	adenylate kinase 2 isoform b,Homo sapiens AK2A m
SLC29A2	chr11:65890478-65890611:-	0.52	cerebellum	1.00	MCF7	0.48	solute carrier family 29 (nucleoside,solute carrier fam
CD300A	chr17:69981270-69981608:+	0.52	adipose	0.48	lymph node	1.00	CMRF35-H antigen precursor (CMRF35-H9) (CMRF
CROCC,KIAA0445	chr1:17170547-17170708:+	0.52	cerebellum	0.73	adipose	0.21	ciliary rootlet coiled-coil, rootletin,ciliary rootlet coiled
MECP2	chrX:153010836-153010959:-	0.52	MB435	1.00	colon	0.48	methyl CpG binding protein 2,methyl CpG binding pr
APIP	chr11:34873133-34873233:-	0.52	MCF7	1.00	lymph node	0.48	APAF1 interacting protein
FLJ00147	chr11:11858300-11858503:+	0.52	HME	1.00	skel. muscle	0.48	ubiquitin specific protease 47,ubiquitin specific prote
MMAB	chr12:108483431-108483517:-	0.52	T47D	0.17	testes	0.69	cob(I)alamin adenosyltransferase precursor,cob(I)ala
POMT1	chr9:133369397-133369548:+	0.52	T47D	0.74	testes	0.22	protein-O-mannosyltransferase 1 isoform b,protein-C
USP21	chr1:159396780-159396920:+	0.52	T47D	0.69	colon	0.17	ubiquitin-specific protease 21,ubiquitin-specific prote
OPN3	chr1:239834185-239834504:-	0.52	HME	1.00	brain	0.48	opsin 3 isoform 1,opsin 3 isoform 3,
FER1L3	chr10:95142664-95142702:-	0.52	MCF7	0.48	MB435	1.00	Fer-1-like 3, myoferlin (C. elegans).
PPM1K	chr4:89418320-89418818:-	0.52	cerebellum	1.00	MCF7	0.49	protein phosphatase 1K (PP2C domain containing),
LYSMD4	chr15:98089446-98089735:-	0.52	cerebellum	1.00	testes	0.49	LysM, putative peptidoglycan-binding, domain,Homo

NEDD9	chr6:11321500-11321946:-	0.52	breast	1.00	liver	0.49	Homo sapiens mRNA full length insert cDNA clone
IKBKB,IKK-beta,AX	chr8:42265316-42265403:+	0.52	MB435	0.49	adipose	1.00	inhibitor of kappa light polypeptide gene,Homo sapie
TGFBR2	chr3:30639695-30639769:+	0.51	heart	0.75	testes	0.24	transforming growth factor, beta receptor II
HCDI,C14orf124	chr14:23981155-23981306:-	0.51	cerebellum	1.00	lymph node	0.49	hypothetical protein LOC56948,hypothetical protein
PCBP4	chr3:51970997-51971144:-	0.51	cerebellum	0.77	MB435	0.25	poly(rC) binding protein 4 isoform c,poly(rC) binding
FAM14B	chr14:93633594-93633777:+	0.51	cerebellum	0.56	testes	0.05	hypothetical protein LOC122509,hypothetical protei
n/a	chr10:104930978-104931075:-	0.51	MCF7	0.85	testes	0.34	n/a
NFIC	chr19:3404761-3404914:+	0.51	T47D	0.80	testes	0.29	nuclear factor I/C isoform 1
STARD10,NY-CO-2	chr11:72092845-72093027:-	0.51	HME	0.92	lymph node	0.41	START domain containing 10,START domain contai
CD59	chr11:33709546-33709590:-	0.51	MCF7	0.08	skel. muscle	0.59	CD59 antigen p18-20,CD59 antigen p18-20,CD59 a
SOCS7	chr17:33774717-33775442:+	0.51	cerebellum	0.24	testes	0.75	suppressor of cytokine signaling 7,suppressor of cyt
SEC12,PREB	chr2:27208602-27208775:-	0.51	cerebellum	0.49	breast	1.00	prolactin regulatory element binding protein,PREB p
FAM63A	chr1:149241265-149242068:-	0.51	cerebellum	1.00	HME	0.49	hypothetical protein LOC55793 isoform 1,hypothetic
FAM3A	chrX:153389336-153389407:-	0.51	MCF7	0.49	lymph node	1.00	family 3, member A protein,Homo sapiens cDNA: FL
XHRIP110,RXRIP1	chr5:176328162-176328898:-	0.51	cerebellum	1.00	HME	0.49	Retinoid X receptor-interacting protein 110 (Recepto
ACCN3,ABCB8,ASI	chr7:150361625-150361937:+	0.51	cerebellum	1.00	MCF7	0.49	amiloride-sensitive cation channel 3 isoform a,amilo
SYT7	chr11:61071225-61071356:-	0.51	BT474	0.40	brain	0.91	synaptotagmin VII,Homo sapiens synaptotagmin VII
YIPF1,DKFZp761P	chr1:54121374-54121537:-	0.51	liver	1.00	testes	0.49	Yip1 domain family, member 1,Yip1 domain family,
CR609046,PDE4DI	chr1:143571116-143571355:-	0.51	breast	1.00	lymph node	0.49	phosphodiesterase 4D interacting protein isoform,ph
C10orf116	chr10:88719937-88719999:+	0.51	cerebellum	1.00	BT474	0.49	adipose specific 2
MBD1	chr18:46053702-46053839:-	0.51	cerebellum	1.00	BT474	0.49	methyl-CpG binding domain protein 1 isoform 3,met
ABI1	chr10:27087997-27088170:-	0.51	breast	1.00	brain	0.49	abl-interactor 1 isoform a,abl-interactor 1 isoform b,a
ZNF76	chr6:35369506-35369670:+	0.51	cerebellum	1.00	MB435	0.49	zinc finger protein 76 (expressed in testis),zinc finge
ABI2,argBPIB	chr2:203967668-203967814:+	0.51	MB435	1.00	brain	0.49	abl interactor 2,abl interactor 2,Abl interactor 2 (Abel
RANBP3	chr19:5908929-5908984:-	0.51	cerebellum	1.00	BT474	0.49	RAN binding protein 3 isoform RANBP3-b,RAN bindi
LOC553158,ARHG	chr22:43509571-43509706:+	0.51	breast	1.00	MB435	0.49	proline rich 5 (renal) isoform 2,proline rich 5 (renal) i
DKFZp434B172	chr3:43048763-43050049:+	0.51	cerebellum	1.00	liver	0.49	Homo sapiens cDNA FLJ33682 fis, clone BRAWH2
PRKAG1	chr12:47685793-47685902:-	0.51	breast	1.00	heart	0.49	AMP-activated protein kinase, noncatalytic,AMP-acti
FKRP	chr19:51943612-51943814:+	0.51	breast	1.00	MB435	0.50	fukutin-related protein,fukutin-related protein,fukutin-
HTF9C	chr22:18480641-18480757:-	0.51	breast	1.00	skel. muscle	0.50	HpaII tiny fragments locus 9C,HpaII tiny fragments l
RFXANK	chr19:19168995-19169060:+	0.51	MB435	0.50	adipose	1.00	regulatory factor X-associated,regulatory factor X-as
HNRPH1	chr5:178975153-178975202:-	0.50	BT474	0.45	adipose	0.95	heterogeneous nuclear ribonucleoprotein H1,hetero
GATS	chr7:99646953-99647553:-	0.50	cerebellum	1.00	MB435	0.50	opposite strand transcription unit to STAG3,opposit
TRIP12	chr2:230433366-230433491:-	0.50	adipose	0.13	brain	0.64	thyroid hormone receptor interactor 12,thyroid horm
ARMCX4	chrX:100630087-100630958:+	0.50	cerebellum	1.00	MB435	0.50	Homo sapiens cDNA FLJ39636 fis, clone SMINT200
PLEKHM2	chr1:15920411-15920470:+	0.50	brain	0.48	skel. muscle	0.99	Pleckstrin homology domain containing, family M (W
ABHD14B	chr3:51980516-51980948:-	0.50	cerebellum	1.00	MB435	0.50	abhydrolase domain containing 14B,abhydrolase do
PAK4	chr19:44350710-44350782:+	0.50	breast	1.00	adipose	0.50	p21-activated kinase 4 isoform 1,Serine/threonine-p
ABI1	chr10:27087997-27088173:-	0.50	breast	1.00	brain	0.50	abl-interactor 1 isoform a,abl-interactor 1 isoform b,a
DKFZp686B20267,	chr3:184292891-184293027:-	0.50	MCF7	1.00	lymph node	0.50	methylcrotonoyl-Coenzyme A carboxylase 1,Homo s
CECR5	chr22:16010432-16010635:-	0.50	adipose	0.50	testes	1.00	cat eye syndrome chromosome region, candidate 5,
C20orf100,TOX2	chr20:42127766-42128161:+	0.50	adipose	0.50	lymph node	1.00	chromosome 20 open reading frame 100,Homo sap
GGA1	chr22:36350922-36351029:+	0.50	BT474	1.00	lymph node	0.50	golgi associated, gamma adaptin ear containing,,gol
KIAA1343	chr1:209552685-209552926:+	0.50	MCF7	1.00	adipose	0.50	Homo sapiens mRNA for KIAA1343 protein, partial c
FN1	chr2:215953779-215954048:-	0.50	breast	0.14	MB435	0.64	fibronectin 1 isoform 1 preproprotein,fibronectin 1 is
BCAT2	chr19:54002825-54003305:-	0.50	cerebellum	0.55	BT474	0.05	branched chain aminotransferase 2,,BCAT2 protein
NAB2	chr12:55773457-55773648:+	0.50	HME	1.00	lymph node	0.50	NGFI-A binding protein 2
MLPH	chr2:238093292-238093411:+	0.50	BT474	1.00	MB435	0.50	melanophilin isoform 1,melanophilin isoform 2,mela
TMEM11	chr17:21054841-21055132:-	0.50	HME	0.10	heart	0.60	transmembrane protein 11,Homo sapiens transmem
POLR1D	chr13:27093474-27094146:+	0.50	breast	1.00	brain	0.50	polymerase (RNA) I polypeptide D isoform 2,Homo s
SP100	chr2:230990550-230990624:+	0.50	colon	0.38	liver	0.88	nuclear antigen Sp100 isoform 2,nuclear antigen Sp
RP11-235O14.2	chr9:76883062-76883318:-	0.50	cerebellum	0.28	lymph node	0.77	nicotinamide riboside kinase 1,Nicotinamide riboside
MRPL33	chr2:27850795-27850901:+	0.50	liver	0.61	lymph node	0.11	mitochondrial ribosomal protein L33 isoform a,mitoc
NTRK2	chr9:86474415-86474623:+	0.50	breast	0.84	lymph node	0.34	neurotrophic tyrosine kinase, receptor, type 2,neurot
STMN4	chr8:27155111-27155191:-	0.50	cerebellum	0.34	brain	0.84	stathmin-like-protein RB3,Stathmin-4 (Stathmin-like
AK095785,TCF25	chr16:88502875-88503016:+	0.50	cerebellum	0.14	BT474	0.64	NULP1,Homo sapiens cDNA FLJ38466 fis, clone FE
AX747817	chr22:29819770-29819862:+	0.50	HME	0.01	heart	0.51	smoothelin isoform b,smoothelin isoform c,smootheli
eps15R,EPS15L1	chr19:16333590-16333795:-	0.50	cerebellum	1.00	T47D	0.50	epidermal growth factor receptor pathway,epidermal
MAPKAP1,DKFZp6	chr9:127474416-127474743:-	0.50	breast	0.50	MCF7	1.00	mitogen-activated protein kinase associated,mitogen
ZNF142	chr2:219224668-219225267:-	0.50	cerebellum	0.50	BT474	1.00	zinc finger protein 142,zinc finger protein 142,zinc fi
MPI	chr15:72969947-72970048:+	0.50	MB435	0.50	T47D	1.00	Mannose phosphate isomerase isoform.
RHBDD2	chr7:75348619-75348744:+	0.50	brain	0.34	lymph node	0.84	rhomboid, veinlet-like 7 isoform a
MPI	chr15:72969950-72970048:+	0.50	MB435	0.50	T47D	1.00	Mannose phosphate isomerase isoform.
ARL1	chr12:100323753-100323890:-	0.50	cerebellum	1.00	adipose	0.50	ADP-ribosylation factor-like 1,Homo sapiens ADP-ri
ATG4D	chr19:10518515-10518791:+	0.50	cerebellum	0.50	breast	1.00	APG4 autophagy 4 homolog D
SAPS2	chr22:49222283-49222363:+	0.50	MB435	0.23	T47D	0.73	SAPS domain family, member 2,SAPS domain fami
CDC42	chr1:22273174-22273299:+	0.50	breast	0.52	skel. muscle	0.03	cell division cycle 42 isoform 1,cell division cycle 42
SIRT6	chr19:4131779-4131906:-	0.50	T47D	1.00	skel. muscle	0.51	sirtuin 6,Mono-ADP-ribosyltransferase sirtuin-6 (EC
CCDC82	chr11:95756774-95757573:-	0.50	cerebellum	1.00	adipose	0.51	coiled-coil domain containing 82
MIZF	chr11:118499488-118499604:+	0.50	BT474	0.20	lymph node	0.69	MBD2 (methyl-CpG-binding protein)-interacting,MB
AK026621,TSPAN1	chr10:82218283-82218423:+	0.49	BT474	0.78	MB435	0.28	tetraspanin 14,tetraspanin 14,Homo sapiens cDNA:
SULF2	chr20:45721550-45721603:-	0.49	MCF7	0.51	adipose	1.00	sulfatase 2 isoform a precursor,sulfatase 2 isoform b
LOC88523,PFAAP5	chr13:32007906-32009164:-	0.49	cerebellum	1.00	colon	0.51	Homo sapiens phosphonoformate immuno-associat
PUS3	chr11:125271012-125271435:-	0.49	HME	0.25	T47D	0.75	pseudouridylate synthase 3
KIAA1491	chr9:33963181-33963235:-	0.49	BT474	1.00	skel. muscle	0.51	ubiquitin associated protein 2,ubiquitin associated pr
AK055197,TPM1	chr15:61143316-61143394:+	0.49	breast	1.00	colon	0.51	tropomyosin 1 alpha chain isoform 6,Homo sapiens
SAR1A	chr10:71591381-71591693:-	0.49	cerebellum	1.00	colon	0.51	SAR1a gene homolog 1

PTPRF	chr1:43841869-43842447:+	0.49	cerebellum	0.51	MCF7	1.00	protein tyrosine phosphatase, receptor type, F,prote
TMEM142B	chr7:101863677-101863785:+	0.49	MCF7	1.00	lymph node	0.51	transmembrane protein 142B,transmembrane protei
SCAMP3	chr1:153498072-153498149:-	0.49	cerebellum	1.00	colon	0.51	secretory carrier membrane protein 3 isoform 1,secr
SMEK2	chr2:55679056-55679679:-	0.49	MCF7	1.00	BT474	0.51	SMEK homolog 2, suppressor of mek1,SMEK homol
RXRB	chr6:33274924-33275171:-	0.49	cerebellum	1.00	MCF7	0.51	retinoid X receptor, beta,retinoid X receptor, beta,Ho
HCDI,C14orf124	chr14:23981144-23981306:-	0.49	cerebellum	1.00	lymph node	0.51	hypothetical protein LOC56948,hypothetical protein
ZNF7	chr8:146025232-146025793:+	0.49	cerebellum	0.51	MCF7	1.00	CDNA FLJ38706 fis, clone KIDNE2002795, moderat
TMTC4	chr13:100120615-100120824:-	0.49	BT474	0.51	testes	1.00	transmembrane and tetratricopeptide repeat,transme
PAK4	chr19:44350710-44350792:+	0.49	BT474	0.93	adipose	0.45	p21-activated kinase 4 isoform 1,Serine/threonine-pr
DAZAP1	chr19:1376877-1376959:+	0.49	cerebellum	0.51	brain	1.00	DAZ associated protein 1 isoform b,DAZ associated
CAMK1	chr3:9782443-9782574:-	0.49	MB435	1.00	colon	0.51	calcium/calmodulin-dependent protein kinase I,Hom
RP11-307C12.7	chr1:153228660-153228807:+	0.49	breast	1.00	lymph node	0.51	flavin adenine dinucleotide synthetase isoform,flavin
CCDC76	chr1:100386038-100386470:+	0.49	cerebellum	1.00	testes	0.51	coiled-coil domain containing 76
LIG,HIP2	chr4:39423767-39423825:+	0.49	BT474	0.51	MB435	1.00	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.1
TROVE2,CR60799	chr1:191304787-191305387:+	0.49	breast	0.51	MCF7	1.00	60kD Ro/SSA autoantigen isoform 2,TROVE domai
ARL6IP2	chr2:38423914-38424158:-	0.49	HME	0.51	colon	1.00	ADP-ribosylation factor-like 6 interacting,ARL6IP2 pr
OPA1	chr3:194817661-194817768:+	0.49	BT474	0.51	T47D	1.00	optic atrophy 1 isoform 8,optic atrophy 1 isoform 6,o
n/a	chr8:67997113-67997181:-	0.49	HME	0.94	brain	0.46	n/a
HOM-TES-103,DKF	chr12:6530825-6530930:-	0.48	cerebellum	0.13	lymph node	0.61	hypothetical protein LOC25900 isoform 4,hypothetic
AK095785,TCF25	chr16:88502875-88502992:+	0.48	cerebellum	0.14	BT474	0.63	NULP1,Homo sapiens cDNA FLJ38466 fis, clone FE
USP21	chr1:159396743-159396920:+	0.48	T47D	0.63	colon	0.15	ubiquitin-specific protease 21,ubiquitin-specific prote
PLCD1	chr3:38148091-38148133:-	0.48	breast	1.00	lymph node	0.52	phospholipase C, delta 1
ADAMTS13,vWF-Cl	chr9:135312853-135313037:+	0.48	cerebellum	1.00	T47D	0.52	ADAM metallopeptidase with thrombospondin type 1
DKFZp686O1389,D	chrX:151841920-151842009:+	0.48	HME	0.52	testes	1.00	Hypothetical protein DKFZp686B22130 (Fragment).,
KRIT1	chr7:91712677-91712845:-	0.48	cerebellum	1.00	T47D	0.52	krev interaction trapped 1 isoform 1,krev interaction
UNQ6118,IL17RC	chr3:9935019-9935093:+	0.48	T47D	0.94	adipose	0.46	interleukin 17 receptor C isoform 2 precursor,interleu
KIAA1067,EXOC7	chr17:71598005-71598073:-	0.48	T47D	0.58	testes	0.10	exocyst complex component 7 isoform b,exocyst co
STK40	chr1:36606036-36606272:-	0.48	MB435	0.26	skel. muscle	0.74	Serine/threonine-protein kinase 40 (EC 2.7.11.1) (SI
ZNF384	chr12:6651777-6651959:-	0.48	MCF7	0.08	testes	0.56	nuclear matrix transcription factor 4 isoform a,nuclea
KBTBD3	chr11:105452444-105452644:-	0.48	T47D	1.00	brain	0.52	BTB and kelch domain containing 3,BTB and kelch
BAT3	chr6:31720063-31720170:-	0.48	liver	0.64	testes	0.16	HLA-B associated transcript-3 isoform a,HLA-B ass
PTPRS	chr19:5169798-5169809:-	0.48	cerebellum	1.00	MB435	0.52	protein tyrosine phosphatase, receptor type,,protein
SLC39A13,DKFZp4	chr11:47391527-47391634:+	0.48	adipose	1.00	lymph node	0.52	solute carrier family 39 (zinc transporter),,Homo sapi
DKFZp566D244,PA	chr15:70330240-70330349:-	0.48	cerebellum	1.00	MCF7	0.52	poly (ADP-ribose) polymerase family, member 6,Ho
CRYL1	chr13:19911732-19911893:-	0.48	cerebellum	0.25	brain	0.72	Lambda-crystallin (CRYL1 protein) (Crystallin, lamb
LIG,HIP2	chr4:39455697-39455825:+	0.48	cerebellum	1.00	skel. muscle	0.52	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.1
ABI2,argBPIB	chr2:203969753-203969935:+	0.48	cerebellum	0.82	heart	0.35	abl interactor 2,abl interactor 2,Abl interactor 2 (Abel
ADCYAP1R1	chr7:31106266-31106349:+	0.48	cerebellum	1.00	brain	0.52	adenylate cyclase activating polypeptide 1,adenylate
TMEM173	chr5:138841247-138841473:-	0.48	breast	1.00	colon	0.52	hypothetical protein LOC340061
WDR54	chr2:74502755-74503010:+	0.48	cerebellum	1.00	lymph node	0.52	WD repeat domain 54
SCPEP1	chr17:52430745-52430858:+	0.48	breast	1.00	MCF7	0.53	serine carboxypeptidase 1 precursor protein
RBED1,DKFZp667	chr2:85435710-85435804:+	0.48	HME	1.00	lymph node	0.53	RNA binding motif and ELMO domain 1,CDNA: FLJ
IFT88	chr13:20162844-20162954:+	0.48	MB435	1.00	T47D	0.53	intraflagellar transport 88 homolog isoform 1,intrafla
MGLL,monoglycerid	chr3:128912109-128912198:-	0.47	brain	0.44	colon	0.92	monoglyceride lipase isoform 2,monoglyceride lipas
KIAA0955,CARD8	chr19:53433452-53433601:-	0.47	breast	1.00	lymph node	0.53	caspase recruitment domain family, member 8,casp
NUDT22	chr11:63751616-63751714:+	0.47	BT474	0.16	T47D	0.63	nudix (nucleoside diphosphate linked moiety,nudix (
SETD3	chr14:98997282-98997430:-	0.47	adipose	0.53	lymph node	1.00	SET domain containing 3 isoform a,SET domain co
RNF185	chr22:29913033-29913256:+	0.47	cerebellum	1.00	testes	0.53	ring finger protein 185,Homo sapiens cDNA: FLJ233
PDPR,KIAA1990	chr16:68744795-68744977:+	0.47	MB435	0.53	adipose	1.00	pyruvate dehydrogenase phosphatase regulatory,py
BC070247,SVIL	chr10:29855896-29855991:-	0.47	colon	0.53	heart	1.00	supervillin isoform 2,Homo sapiens cDNA clone IMA
TRPM4,TRPM4B	chr19:54406084-54406156:+	0.47	MCF7	1.00	MB435	0.53	transient receptor potential cation channel,,Transient
GUSB	chr7:65072704-65072788:-	0.47	cerebellum	0.53	breast	1.00	glucuronidase, beta
RNF38	chr9:36380464-36380613:-	0.47	adipose	0.57	colon	0.09	ring finger protein 38 isoform 2,ring finger protein 38
NDRG2,KIAA1248	chr14:20562029-20562095:-	0.47	HME	1.00	brain	0.53	N-myc downstream-regulated gene 2 isoform a,N-m
SULT1A1,OK/SW-c	chr16:28528753-28529013:-	0.47	cerebellum	0.53	breast	1.00	sulfotransferase family, cytosolic, 1A,,Homo sapiens
hRFI,BC029038	chr12:120339690-120340097:+	0.47	cerebellum	1.00	MCF7	0.53	Homo sapiens hRFI mRNA for hypothetical protein,
DKFZp451P074,SM	chr2:88174151-88174189:+	0.47	heart	0.95	skel. muscle	0.48	SET and MYND domain containing 1,SET and MYN
ADRM1	chr20:60312912-60312936:+	0.47	MB435	0.53	colon	1.00	adhesion regulating molecule 1 precursor,adhesion
AL138795.4,C1orf5	chr1:148518675-148518776:+	0.47	cerebellum	0.53	lymph node	1.00	hypothetical protein LOC79630,hypothetical protein
CD47	chr3:109257057-109257103:-	0.47	brain	0.00	testes	0.47	CD47 antigen isoform 1 precursor,CD47 antigen iso
BCAT2	chr19:54001586-54001786:-	0.47	breast	1.00	HME	0.53	branched chain aminotransferase 2,,BCAT2 protein
SNHG3-RCC1	chr1:28729622-28729672:+	0.47	MCF7	0.22	HME	0.69	regulator of chromosome condensation 1 isoform,re
RHBDD2	chr7:75348619-75348740:+	0.47	brain	0.39	lymph node	0.85	rhomboid, veinlet-like 7 isoform a
SBF1	chr22:49242329-49242406:-	0.47	skel. muscle	0.84	testes	0.37	SET binding factor 1 isoform a,SET binding factor 1
FKRP	chr19:51943612-51943762:+	0.47	breast	1.00	MB435	0.53	fukutin-related protein,fukutin-related protein,fukutin-
PTPRF	chr1:43840329-43840355:+	0.47	BT474	0.91	HME	0.44	protein tyrosine phosphatase, receptor type, F,prote
IFT20	chr17:23683299-23683535:-	0.47	cerebellum	0.67	colon	0.20	intraflagellar transport protein IFT20,Intraflagellar tr
UPP1	chr7:48107946-48108104:+	0.47	cerebellum	0.62	MB435	0.15	uridine phosphorylase 1,uridine phosphorylase 1,uri
SUPT4H1	chr17:53847686-53848322:-	0.47	cerebellum	0.54	MCF7	1.00	suppressor of Ty 4 homolog 1,Homo sapiens cDNA
CR609046,PDE4DI	chr1:143583053-143583238:-	0.46	cerebellum	0.54	skel. muscle	1.00	phosphodiesterase 4D interacting protein isoform,ph
MFGE8	chr15:87243891-87244046:-	0.46	MCF7	0.54	brain	1.00	milk fat globule-EGF factor 8 protein,milk fat globule
CDK5RAP2	chr9:122209111-122209347:-	0.46	MCF7	1.00	testes	0.54	CDK5 regulatory subunit associated protein 2,CDK5
CSNK1D,BC04700	chr17:77797141-77797204:-	0.46	MCF7	1.00	lymph node	0.54	casein kinase 1, delta isoform 2,casein kinase 1, del
C1orf128	chr1:23978515-23978558:+	0.46	cerebellum	1.00	lymph node	0.54	thioredoxin family Trp26
LDLRAD3	chr11:36014229-36014375:+	0.46	cerebellum	1.00	T47D	0.54	low density lipoprotein receptor class A domain
AX747833	chr14:72815742-72815885:-	0.46	BT474	0.47	T47D	0.93	numb homolog isoform 1,numb homolog isoform 3,n
BCL2L12	chr19:54865285-54865557:+	0.46	HME	1.00	skel. muscle	0.54	BCL2-like 12 isoform 1,BCL2-like 12 isoform 3,

SRCAP	chr16:30641385-30641570:+	0.46	cerebellum	0.47	colon	0.01	Snf2-related CBP activator protein,Snf2-related CB
C12orf52	chr12:112108373-112108504:+	0.46	MCF7	1.00	MB435	0.54	hypothetical protein LOC84934,hypothetical protein
DKFZp547M136	chr19:15399921-15400319:-	0.46	cerebellum	1.00	lymph node	0.54	CDNA FLJ16504 fis, clone FEBRA2014122, highly s
ARHGEF10	chr8:1778926-1779009:+	0.46	MB435	0.54	adipose	1.00	Rho guanine nucleotide exchange factor 10,Rho gu
MEGF8	chr19:47567342-47567474:+	0.46	BT474	0.54	T47D	1.00	Homo sapiens mRNA for MEGF8, partial cds.,MEG
DKFZp666A163,BT	chr11:13423147-13423276:-	0.46	HME	0.23	testes	0.69	K+ channel tetramerization protein,Homo sapiens G
ALG11,UTP14C	chr13:51496143-51497074:+	0.46	BT474	0.03	lymph node	0.49	asparagine-linked glycosylation 11 homolog (S.,UTP
SMRTE,NCOR2	chr12:123377908-123378132:-	0.46	cerebellum	1.00	breast	0.54	nuclear receptor co-repressor 2 isoform 1,nuclear re
GAA	chr17:75690205-75690319:+	0.46	T47D	1.00	skel. muscle	0.54	acid alpha-glucosidase preproprotein,acid alpha-glu
PIGV	chr1:26993191-26994312:+	0.46	cerebellum	1.00	MCF7	0.54	phosphatidylinositol glycan class V,Homo sapiens c
EFHD2	chr1:15626233-15626367:+	0.46	T47D	1.00	lymph node	0.54	EF hand domain family, member D2
C1orf50	chr1:43005767-43005882:+	0.46	breast	1.00	testes	0.54	hypothetical protein LOC79078
LAT,SPIN1	chr16:28900723-28900878:+	0.46	cerebellum	1.00	lymph node	0.54	linker for activation of T cells isoform b,linker for acti
n/a	chr11:57262712-57263087:+	0.46	cerebellum	0.54	BT474	1.00	n/a
FLJ00313	chr1:16842110-16842227:-	0.46	T47D	0.76	lymph node	0.30	Homo sapiens mRNA for FLJ00313 protein.,Homo s
ENTPD6,CD39L2	chr20:25135715-25136033:+	0.46	MCF7	0.54	liver	1.00	ectonucleoside triphosphate diphosphohydrolase,ect
BCL7B	chr7:72595814-72595910:-	0.46	cerebellum	1.00	lymph node	0.54	B-cell CLL/lymphoma 7B isoform 1,Homo sapiens m
AOS1,SAE1	chr19:52392330-52392474:+	0.46	BT474	0.54	brain	1.00	SUMO-1 activating enzyme subunit 1,Homo sapiens
EPSIN,EPN1	chr19:60880224-60880396:+	0.46	cerebellum	0.01	T47D	0.47	epsin 1,Homo sapiens EH domain-binding mitotic ph
WNK2	chr9:95102154-95102252:+	0.46	colon	0.54	heart	1.00	WNK lysine deficient protein kinase 2
n/a	chr7:23191214-23191442:+	0.46	cerebellum	0.54	breast	1.00	n/a
AXIN1	chr16:281191-281298:-	0.46	cerebellum	0.54	MCF7	0.09	axin 1 isoform a,axin 1 isoform b,
NELF	chr9:139469512-139469580:-	0.46	cerebellum	1.00	testes	0.55	nasal embryonic LHRH factor,nasal embryonic LHR
SAMD4A,KIAA1053	chr14:54320808-54320915:+	0.45	heart	0.51	testes	0.06	sterile alpha motif domain containing 4,sterile alpha
ELMO2	chr20:44460743-44460817:-	0.45	HME	0.47	brain	0.92	engulfment and cell motility 2,OTTHUMP000000317
FBXO38	chr5:147786969-147787703:+	0.45	cerebellum	1.00	MCF7	0.55	F-box protein 38 isoform b,F-box protein 38 isoform
RIT1	chr1:154147071-154147219:-	0.45	MCF7	0.55	BT474	1.00	Ras-like without CAAX 1
MRPS18B	chr6:30698588-30698654:+	0.45	breast	1.00	lymph node	0.55	mitochondrial ribosomal protein S18B
SFRS8	chr12:130814954-130815184:+	0.45	cerebellum	1.00	lymph node	0.55	splicing factor, arginine/serine-rich 8,SFRS8 protein
TRPT1	chr11:63748849-63749018:-	0.45	cerebellum	0.55	breast	1.00	tRNA phosphotransferase 1 isoform 2,tRNA phosph
SSAT2	chr17:7470986-7471087:-	0.45	cerebellum	1.00	adipose	0.55	Homo sapiens polyamine N-acetyltransferase (SSAT
MAPKAP1,DKFZp6	chr9:127308410-127308517:-	0.45	MCF7	1.00	MB435	0.55	mitogen-activated protein kinase associated,mitogen
n/a	chr19:40445289-40445435:+	0.45	HME	0.10	testes	0.55	LISCH protein isoform 1,LISCH protein isoform 3,LIS
U2AF2	chr19:60864949-60865008:+	0.45	cerebellum	0.45	BT474	0.00	U2 (RNU2) small nuclear RNA auxiliary factor 2,U2
SUOX	chr12:54682594-54682771:+	0.45	cerebellum	0.55	breast	1.00	sulfite oxidase,sulfite oxidase,sulfite oxidase,sulfite
RAF1	chr3:12622700-12622798:-	0.45	cerebellum	1.00	BT474	0.55	v-raf-1 murine leukemia viral oncogene homolog
RABL5	chr7:100748125-100749033:-	0.45	cerebellum	1.00	BT474	0.55	RAB, member RAS oncogene family-like 5
PRMT7	chr16:66907301-66907478:+	0.45	cerebellum	1.00	heart	0.55	protein arginine N-methyltransferase 7,protein argini
ZBTB43	chr9:128610893-128611015:+	0.45	skel. muscle	0.41	testes	0.86	zinc finger protein 297B
C7orf46	chr7:23690643-23690816:+	0.45	adipose	0.12	testes	0.57	hypothetical protein LOC340277,Homo sapiens cDN
CR592254,NR_003	chr6:86444232-86444312:-	0.45	HME	1.00	skel. muscle	0.55	full-length cDNA clone CS0DI004YM02 of Placenta
C6orf31,AL050203	chr6:32226123-32226661:-	0.45	MB435	1.00	testes	0.55	Chromosome 6 open reading frame 31.,Homo sapie
GLYCTK1,GLYCTK	chr3:52299360-52299775:+	0.45	adipose	0.55	liver	1.00	CG9886-like,Homo sapiens glycerate kinase 1 (GLY
PHF8	chrX:54036759-54037061:-	0.45	lymph node	0.30	testes	0.75	PHD finger protein 8,PHD finger protein 8,PHD finge
TEAD2	chr19:54551028-54551039:-	0.45	breast	0.54	MB435	0.09	TEA domain family member 2,TEA domain family m
HGFL,MGC17330	chr22:30015301-30015379:-	0.45	cerebellum	0.55	HME	1.00	HGFL protein,Homo sapiens HGFL(S) protein (HGF
WDR54	chr2:74502788-74503010:+	0.45	cerebellum	1.00	lymph node	0.55	WD repeat domain 54
FDPS	chr1:153556272-153556343:+	0.45	cerebellum	1.00	MB435	0.55	farnesyl diphosphate synthase,Farnesyl pyrophosph
ACADVL	chr17:7064507-7064576:+	0.45	cerebellum	1.00	HME	0.55	acyl-Coenzyme A dehydrogenase, very long chain,a
ENTPD6,CD39L2	chr20:25135712-25136033:+	0.45	MCF7	0.55	liver	1.00	ectonucleoside triphosphate diphosphohydrolase,ect
MANBAL	chr20:35360580-35360696:+	0.45	BT474	0.55	testes	0.10	mannosidase, beta A, lysosomal-like,Homo sapiens
FBXO38	chr5:147786969-147787478:+	0.45	cerebellum	1.00	MCF7	0.55	F-box protein 38 isoform b,F-box protein 38 isoform
KIAA0430	chr16:15626730-15627158:-	0.45	cerebellum	1.00	colon	0.55	limkain b1,limkain b1,
KRIT1	chr7:91712715-91712845:-	0.45	MCF7	1.00	T47D	0.55	krev interaction trapped 1 isoform 1,krev interaction
ZNF394	chr7:98934275-98934401:-	0.45	cerebellum	1.00	adipose	0.55	zinc finger protein 99,Homo sapiens cDNA FLJ1229
UNQ2531,TMEM25	chr11:117909345-117909476:+	0.45	adipose	0.55	colon	1.00	transmembrane protein 25,Homo sapiens cDNA FLJ
LOC55565	chr16:70453180-70453346:-	0.45	cerebellum	1.00	MCF7	0.55	hypothetical protein LOC55565,Homo sapiens clone
KIAA0833,CAMTA1	chr1:6802828-6802897:+	0.45	T47D	1.00	brain	0.55	calmodulin-binding transcription activator 1,CAMTA1
SHARPIN	chr8:145225972-145226096:-	0.45	BT474	1.00	liver	0.55	Homo sapiens hSIPL1A mRNA for shank-interacting
CAMLG	chr5:134104652-134105112:+	0.45	breast	0.55	heart	1.00	calcium modulating ligand,Homo sapiens calcium m
DNAJA3	chr16:4444813-4444929:+	0.45	BT474	0.66	testes	0.21	DnaJ (Hsp40) homolog, subfamily A, member 3
PTPRS	chr19:5167731-5167778:-	0.45	cerebellum	0.05	adipose	0.50	protein tyrosine phosphatase, receptor type,,protein
ARHGEF10	chr8:1815621-1815737:+	0.45	HME	0.55	testes	1.00	Rho guanine nucleotide exchange factor 10,Rho gu
GL004,C2orf33	chr2:227920186-227920344:+	0.45	cerebellum	1.00	testes	0.55	hypothetical protein LOC56947,hypothetical protein
PUM1	chr1:31210108-31210344:-	0.45	breast	1.00	colon	0.55	pumilio 1 isoform 1,pumilio 1 isoform 2,pumilio 1 isof
MAP4K4	chr2:101854388-101854579:+	0.45	adipose	0.31	testes	0.75	mitogen-activated protein kinase kinase kinase,mito
n/a	chr22:16947878-16948024:+	0.44	MB435	0.86	colon	0.41	n/a
MGC13114	chr16:624890-625064:-	0.44	MCF7	1.00	HME	0.56	hypothetical protein LOC84326 isoform h,hypothetic
UBN1	chr16:4867387-4867476:+	0.44	MB435	0.56	adipose	1.00	ubinuclein 1,ubinuclein 1,
NAF1,TNIP1	chr5:150393362-150393553:-	0.44	cerebellum	1.00	brain	0.56	TNFAIP3 interacting protein 1,TNFAIP3 interacting p
OS9	chr12:56400149-56400313:+	0.44	MB435	0.46	T47D	0.90	amplified in osteosarcoma isoform 2 precursor,ampli
U2AF1L4	chr19:40927367-40927479:-	0.44	cerebellum	0.75	testes	0.30	U2 small nuclear RNA auxiliary factor 1-like 4,Homo
RP5-890O3.8-016,	chr1:1248424-1248530:-	0.44	cerebellum	0.46	HME	0.02	Novel protein (Fragment).,Homo sapiens cDNA FLJ
DKFZp547P055	chr12:102871322-102871442:-	0.44	BT474	0.56	liver	1.00	Homo sapiens cDNA FLJ13975 fis, clone Y79AA100
UNC84A,KIAA0810	chr7:856086-856196:+	0.44	MCF7	1.00	MB435	0.56	unc-84 homolog A,unc-84 homolog A,Homo sapiens
KIAA0716,DOCK4	chr7:111162346-111162459:-	0.44	MB435	1.00	brain	0.56	dedicator of cytokinesis 4,Homo sapiens mRNA for
ZNF628	chr19:60545395-60545560:+	0.44	cerebellum	0.56	HME	1.00	zinc finger protein 628

KIAA0859,AK09481	chr1:170017751-170017883:+	0.44	cerebellum	1.00	HME	0.56	CGI-01 protein isoform 1,CGI-01 protein isoform 2,C
THSD1	chr13:51858164-51858322:-	0.44	adipose	0.56	colon	1.00	thrombospondin type I domain-containing 1,thrombo
ARNT	chr1:149081524-149081568:-	0.44	MCF7	0.56	MB435	1.00	aryl hydrocarbon receptor nuclear translocator
C10orf104	chr10:73653652-73653820:+	0.44	BT474	0.87	lymph node	0.43	hypothetical protein LOC119504,hypothetical protei
FLJ12949	chr19:10536605-10537466:-	0.44	cerebellum	1.00	colon	0.56	hypothetical protein LOC65095 isoform 1,hypothetic
NFX1	chr9:33284418-33285425:+	0.44	cerebellum	1.00	skel. muscle	0.56	nuclear transcription factor, X-box binding 1,nuclear
HNRPR	chr1:23539932-23540097:-	0.44	cerebellum	0.77	MB435	0.33	heterogeneous nuclear ribonucleoprotein R,heteroge
YAP1	chr11:101561959-101562078:+	0.44	adipose	0.30	colon	0.74	Yes-associated protein 1, 65 kD,Yes-associated prot
CLK2	chr1:153505123-153505207:-	0.44	BT474	0.57	colon	1.00	CDC-like kinase 2,CDC-like kinase 2 isoform 2,CDC
AK124197,PRDM2	chr1:13977500-13981913:+	0.44	cerebellum	1.00	colon	0.57	retinoblastoma protein-binding zinc finger,Homo sapi
PRUNE	chr1:149267886-149268044:+	0.44	adipose	0.25	skel. muscle	0.69	prune homolog,Prune homolog (Drosophila).,prune
CASC4	chr15:42482377-42482544:+	0.44	cerebellum	1.00	T47D	0.57	cancer susceptibility candidate 4 isoform a,cancer s
SDSL	chr12:112351348-112351487:+	0.44	breast	1.00	MB435	0.57	serine dehydratase-like
ELK1,Elk1	chrX:47394264-47394369:-	0.44	HME	0.18	testes	0.62	ELK1 protein,ELK1 protein,Homo sapiens Elk1 mR
TORC2,CRTC2	chr1:152190360-152190766:-	0.43	cerebellum	0.57	breast	1.00	transducer of regulated cAMP response,Homo sapie
GALE	chr1:23995586-23995663:-	0.43	BT474	0.57	MB435	1.00	UDP-galactose-4-epimerase,Homo sapiens cDNA F
UBE2A	chrX:118599498-118599587:+	0.43	MB435	1.00	brain	0.57	ubiquitin-conjugating enzyme E2A isoform 1,ubiquiti
AP1B1,DKFZp686A	chr22:28055701-28055709:-	0.43	MB435	0.12	adipose	0.56	adaptor-related protein complex 1 beta 1 subunit,ada
PPM2C	chr8:94999315-94999349:+	0.43	brain	0.54	testes	0.11	pyruvate dehydrogenase phosphatase precursor,pyr
C7orf26	chr7:6613693-6614007:+	0.43	cerebellum	0.47	colon	0.04	hypothetical protein LOC79034,hypothetical protein
n/a	chr14:20231546-20231649:+	0.43	liver	0.89	lymph node	0.46	n/a
HNMT	chr2:138441137-138441426:+	0.43	breast	0.10	colon	0.53	histamine N-methyltransferase isoform 1,histamine
APEH	chr3:49687620-49687746:+	0.43	cerebellum	0.57	breast	1.00	N-acylaminoacyl-peptide hydrolase
TCOF1	chr5:149751300-149751413:+	0.43	HME	0.74	lymph node	0.30	Treacher Collins-Franceschetti syndrome 1,Treache
MGC7036	chr12:122481008-122481159:-	0.43	breast	0.57	MCF7	1.00	hypothetical protein LOC196383
KIAA0946,ZDHHC1	chr12:75715345-75715448:+	0.43	adipose	0.57	brain	1.00	huntingtin interacting protein 14,Homo sapiens mRN
TXNDC14,KIAA038	chr11:57315433-57315721:+	0.43	cerebellum	1.00	colon	0.57	catenin (cadherin-associated protein), delta 1,cateni
GCAT	chr22:36535902-36536110:+	0.43	BT474	0.57	T47D	1.00	glycine C-acetyltransferase precursor
CNOT4	chr7:134699146-134699358:-	0.43	colon	1.00	testes	0.57	CCR4-NOT transcription complex, subunit 4,CCR4-
WIPI2	chr7:5199275-5199328:+	0.43	BT474	0.64	testes	0.21	WD repeat domain, phosphoinositide interacting 2,W
PLD3	chr19:45563300-45563332:+	0.43	HME	0.83	colon	0.40	phospholipase D3 isoform 2,phospholipase D3 isofo
VSIG4,Z39Ig	chrX:65169035-65169316:-	0.43	colon	1.00	heart	0.57	V-set and immunoglobulin domain containing 4,V-se
ELN	chr7:73118210-73118263:+	0.43	adipose	0.20	colon	0.63	elastin isoform a,elastin isoform e,elastin isoform d,e
FASTK,DKFZp667F	chr7:150407520-150407942:-	0.43	cerebellum	1.00	colon	0.57	Fas-activated serine/threonine kinase isoform 1,Fas-
DOK1	chr2:74636529-74636713:+	0.43	MB435	1.00	adipose	0.57	docking protein 1,DOK1 protein.,docking protein 1,
NNAT	chr20:35584174-35584254:+	0.43	cerebellum	0.25	colon	0.68	neuronatin isoform alpha,neuronatin isoform beta,
SH3BP2	chr4:2801018-2801672:+	0.43	cerebellum	1.00	heart	0.57	SH3-domain binding protein 2,SH3-domain binding
GOSR2	chr17:42367394-42367534:+	0.43	MCF7	1.00	skel. muscle	0.57	golgi SNAP receptor complex member 2 isoform B,g
PLA2G5	chr1:20288869-20288975:+	0.43	heart	0.54	testes	0.97	phospholipase A2, group V precursor,Homo sapiens
DKFZp686M10160,	chr1:226002016-226002557:+	0.43	cerebellum	1.00	heart	0.57	chromosome 1 open reading frame 142,chromosom
GPI7,PIGG	chr4:514225-514534:+	0.43	MB435	0.57	T47D	1.00	GPI ethanolamine phosphate transferase 2 (EC 2.-.-
FAM63A	chr1:149241265-149241423:-	0.43	HME	0.57	T47D	1.00	hypothetical protein LOC55793 isoform 1,hypothetic
CCBL1,BC022468	chr9:130647453-130647617:-	0.43	cerebellum	0.57	MB435	1.00	cytoplasmic cysteine conjugate-beta lyase,cytoplasm
NRM29,NRM	chr6:30765032-30765208:-	0.43	BT474	1.00	testes	0.57	nurim,Homo sapiens multispanning nuclear envelop
DYRK2	chr12:66329844-66329992:+	0.43	breast	0.57	colon	1.00	dual-specificity tyrosine-(Y)-phosphorylation,dual-sp
CRIM1	chr2:36477261-36477434:+	0.43	breast	1.00	colon	0.57	cysteine-rich motor neuron 1
C14orf112	chr14:69879128-69879199:-	0.43	BT474	1.00	lymph node	0.57	hypothetical protein LOC51241
RSAD1	chr17:45912240-45912444:+	0.43	cerebellum	1.00	MB435	0.58	radical S-adenosyl methionine domain containing
MAD1L1,MAD1	chr7:2236710-2236925:-	0.43	cerebellum	1.00	MB435	0.58	MAD1-like 1 protein,MAD1-like 1 protein,MAD1-like
TRPT1	chr11:63749834-63749917:-	0.43	MCF7	0.42	skel. muscle	0.84	tRNA phosphotransferase 1 isoform 2,tRNA phosph
CD46,Y07713	chr1:206007747-206007791:+	0.43	HME	0.82	adipose	0.39	CD46 antigen, complement regulatory protein,CD46
AF283776	chr2:175694418-175694514:-	0.42	cerebellum	1.00	testes	0.58	activating transcription factor 2,Homo sapiens cDNA
PTBP1	chr19:756513-756569:+	0.42	T47D	1.00	lymph node	0.58	polypyrimidine tract-binding protein 1 isoform,polypy
C16orf48	chr16:66256400-66256572:-	0.42	cerebellum	1.00	MB435	0.58	hypothetical protein LOC84080,Uncharacterized pro
ZNF639	chr3:180525524-180525804:+	0.42	MB435	1.00	lymph node	0.58	zinc finger protein 639,zinc finger protein 639,
ARID5A	chr2:96578785-96578923:+	0.42	breast	0.47	adipose	0.90	Homo sapiens AT rich interactive domain 5A (MRF1
SYNCRIP,CR58996	chr6:86407729-86407888:-	0.42	T47D	0.58	testes	1.00	synaptotagmin binding, cytoplasmic RNA,synaptotag
EXOSC8	chr13:36474410-36474446:+	0.42	cerebellum	1.00	lymph node	0.58	exosome component 8,exosome component 8,Hom
TEX261	chr2:71072468-71072621:-	0.42	breast	1.00	lymph node	0.58	testis expressed sequence 261
FOLR2	chr11:71607265-71607426:+	0.42	breast	1.00	testes	0.58	folate receptor 2 precursor
TMEM126B	chr11:85020379-85020500:+	0.42	MCF7	1.00	lymph node	0.58	hypothetical protein LOC55863,hypothetical protein
ANAPC11	chr17:77444724-77444786:+	0.42	BT474	0.45	skel. muscle	0.88	APC11 anaphase promoting complex subunit 11,AP
CLIM1b	chr4:16116561-16116703:-	0.42	colon	1.00	lymph node	0.58	LIM domain binding 2,LIM domain binding 2,LIM do
n/a	chr17:5270015-5270343:+	0.42	cerebellum	1.00	adipose	0.58	n/a
FAM3A	chrX:153389336-153389386:-	0.42	MCF7	0.58	lymph node	1.00	family 3, member A protein,Homo sapiens cDNA: FL
D2HGDH,pp13479	chr2:242323221-242323604:+	0.42	cerebellum	0.58	MCF7	1.00	D-2-hydroxyglutarate dehydrogenase precursor,Hom
ATXN2	chr12:110375864-110376032:-	0.42	adipose	0.58	testes	1.00	ataxin 2,ataxin 2,ataxin 2,Homo sapiens cDNA FLJ4
MAZ,MAZi,CR5927	chr16:29728362-29728586:+	0.42	breast	0.23	T47D	0.65	MYC-associated zinc finger protein isoform 1,Homo
MRO	chr18:46581717-46581872:-	0.42	brain	0.58	testes	1.00	maestro,maestro,
CCNDBP1,DIP1	chr15:41265310-41265723:+	0.42	cerebellum	1.00	BT474	0.58	cyclin D-type binding-protein 1 isoform 1,cyclin D-typ
MTDH	chr8:98781158-98781256:+	0.42	HME	1.00	lymph node	0.58	LYRIC/3D3
IRF7	chr11:604174-604399:-	0.42	colon	1.00	testes	0.58	interferon regulatory factor 7 isoform d,Homo sapien
KIAA1949	chr6:30760164-30761802:-	0.42	cerebellum	1.00	MCF7	0.58	Protein KIAA1949.,Protein KIAA1949.,
MATN2	chr8:99108820-99109233:+	0.42	cerebellum	0.58	breast	1.00	matrilin 2 isoform a precursor,matrilin 2 isoform b pre
ARFGAP3	chr22:41536763-41536894:-	0.42	MB435	1.00	adipose	0.58	ADP-ribosylation factor GTPase activating
CR594125,SNX12	chrX:70198418-70198542:-	0.42	cerebellum	0.58	MCF7	1.00	sorting nexin 12,sorting nexin 12,Homo sapiens cDN
ARHGAP23	chr17:33908182-33908278:+	0.42	cerebellum	1.00	testes	0.58	KIAA1501 protein (Fragment).

MLPH	chr2:238107946-238108029:+	0.42	MCF7	0.11	MB435	0.53	melanophilin isoform 1,melanophilin isoform 2,melan
RAD23A	chr19:12920311-12920370:+	0.42	cerebellum	0.58	HME	1.00	UV excision repair protein RAD23 homolog A,UV ex
AFF4	chr5:132261821-132261983:-	0.42	BT474	1.00	adipose	0.58	ALL1 fused gene from 5q31,ALL1 fused gene from
FN1	chr2:215945077-215945268:-	0.42	HME	0.84	brain	0.42	fibronectin 1 isoform 1 preproprotein,fibronectin 1 iso
SAE2	chr19:39613321-39613404:+	0.42	MCF7	1.00	skel. muscle	0.58	SUMO-1 activating enzyme subunit 2,SUMO-1 activ
MAD1L1,MAD1	chr7:2236710-2236885:-	0.42	cerebellum	1.00	MB435	0.58	MAD1-like 1 protein,MAD1-like 1 protein,MAD1-like
n/a	chr12:6179849-6179992:+	0.42	cerebellum	1.00	breast	0.58	CD9 antigen,CD9 antigen,
TULP3	chr12:2900190-2900349:+	0.42	MB435	1.00	testes	0.58	tubby like protein 3,Homo sapiens tubby like protein
MUTYH,hMYH	chr1:45571177-45571583:-	0.42	cerebellum	0.58	MCF7	1.00	mutY homolog isoform 2,mutY homolog isoform 1,m
RNF4	chr4:2461862-2462027:+	0.42	MCF7	1.00	brain	0.58	ring finger protein 4,ring finger protein 4,
ECHDC1	chr6:127693647-127693868:-	0.42	breast	1.00	lymph node	0.58	enoyl Coenzyme A hydratase domain containing 1,E
DKFZp586I1223,P	chr7:102735279-102735391:+	0.42	cerebellum	0.59	breast	1.00	mitochondrial processing peptidase beta subunit,Ho
SPRED2	chr2:65415243-65415411:-	0.42	MB435	1.00	adipose	0.59	sprouty-related protein with EVH-1 domain 2
AMOTL1	chr11:94167825-94167974:+	0.42	BT474	0.47	adipose	0.89	angiomotin like 1,angiomotin like 1,
LSM14A	chr19:39409153-39409209:+	0.42	brain	0.58	lymph node	0.16	LSM14 homolog A,LSM14 homolog A,LSM14 homol
POP5	chr12:119501960-119502109:-	0.41	MCF7	0.59	T47D	1.00	processing of precursor 5, ribonuclease P/MRP
C15orf17	chr15:72985672-72985759:-	0.41	BT474	1.00	lymph node	0.59	hypothetical protein LOC57184,hypothetical protein
CDK10	chr16:88283161-88283233:+	0.41	MCF7	1.00	lymph node	0.59	cyclin-dependent kinase 10 isoform 2,cyclin-depend
UBXD7,KIAA0794	chr3:197618514-197618661:-	0.41	cerebellum	0.59	MB435	1.00	UBX domain-containing protein 7.,Homo sapiens m
ACO1	chr9:32376369-32376436:+	0.41	HME	0.00	skel. muscle	0.41	aconitase 1,aconitase 1,
CIB2	chr15:76203102-76203136:-	0.41	adipose	0.56	testes	0.98	DNA-dependent protein kinase catalytic,CIB2 protei
CALU	chr7:128181552-128181745:+	0.41	breast	1.00	skel. muscle	0.59	calumenin precursor,calumenin precursor,Calumeni
IL4R	chr16:27265289-27265440:+	0.41	breast	1.00	MCF7	0.59	interleukin 4 receptor alpha chain isoform a,interleuk
IKBKB,IKK-beta,AX	chr8:42265309-42265403:+	0.41	BT474	1.00	lymph node	0.59	inhibitor of kappa light polypeptide gene,Homo sapie
DPH5	chr1:101263453-101263610:-	0.41	MCF7	1.00	lymph node	0.59	diphthine synthase isoform b,diphthine synthase isof
n/a	chr8:52935958-52936359:-	0.41	cerebellum	1.00	adipose	0.59	n/a
LOC113386	chr19:63515375-63515640:+	0.41	cerebellum	1.00	testes	0.59	hypothetical protein LOC113386,Homo sapiens cDN
n/a	chr6:32267903-32268005:-	0.41	MB435	1.00	testes	0.59	n/a
ACADVL	chr17:7064507-7064572:+	0.41	cerebellum	1.00	HME	0.59	acyl-Coenzyme A dehydrogenase, very long chain,a
CBLB,Nbla00127	chr3:106883013-106883144:-	0.41	adipose	1.00	lymph node	0.59	Cas-Br-M (murine) ecotropic retroviral,Cas-Br-M (mu
NDUFS2	chr1:159439851-159439957:+	0.41	breast	1.00	lymph node	0.59	NADH dehydrogenase (ubiquinone) Fe-S protein 2,,
METTL1	chr12:56449822-56450006:-	0.41	MCF7	0.59	T47D	1.00	methyltransferase-like protein 1 isoform c
ZFP41	chr8:144422905-144423065:+	0.41	cerebellum	1.00	testes	0.59	zinc finger protein 41 homolog,zinc finger protein 41
AX747833	chr14:72820542-72820826:-	0.41	cerebellum	1.00	adipose	0.59	numb homolog isoform 1,numb homolog isoform 3,n
GNB1	chr1:1760489-1760537:-	0.41	adipose	1.00	colon	0.59	guanine nucleotide-binding protein, beta-1
MKRN1	chr7:139818152-139818280:-	0.41	T47D	1.00	liver	0.59	makorin, ring finger protein, 1,makorin, ring finger pr
SUMF2,DKFZp566I	chr7:56109361-56109405:+	0.41	MB435	0.89	T47D	0.49	sulfatase modifying factor 2 isoform a,sulfatase modi
MAGED2	chrX:54852880-54853371:+	0.41	cerebellum	1.00	skel. muscle	0.59	melanoma antigen family D, 2,melanoma antigen fa
RANBP3	chr19:5902404-5902607:-	0.41	adipose	0.43	testes	0.84	RAN binding protein 3 isoform RANBP3-b,RAN bindi
ZDHHC7	chr16:83579870-83579980:-	0.41	adipose	0.42	lymph node	0.82	zinc finger, DHHC domain containing 7
CSAD	chr12:51851324-51851492:-	0.41	T47D	0.59	adipose	1.00	cysteine sulfinic acid decarboxylase-related,cysteine
DHX57	chr2:38948828-38949057:-	0.41	MB435	0.59	T47D	1.00	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57,Pu
CXXC5	chr5:139039616-139039709:+	0.41	T47D	0.15	testes	0.56	CXXC finger 5,Hypothetical protein (CXXC5 protein)
MPI	chr15:72969921-72970048:+	0.41	breast	1.00	MB435	0.59	Mannose phosphate isomerase isoform.
hTTY1s,TTYH1	chr19:59638820-59638865:+	0.41	cerebellum	0.89	testes	0.49	tweety 1 isoform 1,tweety 1 isoform 2,Homo sapiens
HMGCS1	chr5:43343625-43343683:-	0.41	BT474	0.39	HME	0.80	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1,
PXMP4	chr20:31762022-31762220:-	0.41	T47D	0.59	liver	1.00	peroxisomal membrane protein 4 isoform a,peroxiso
UBP1	chr3:33425186-33425293:-	0.41	brain	0.42	lymph node	0.01	upstream binding protein 1 (LBP-1a)
EIF4G1 variant prot	chr3:185515971-185516027:+	0.41	brain	0.60	liver	1.00	eukaryotic translation initiation factor 4,eukaryotic tra
RGN	chrX:46824660-46825279:+	0.41	cerebellum	0.64	liver	0.23	regucalcin,regucalcin,
PQLC2	chr1:19511810-19511970:+	0.41	MCF7	0.60	T47D	1.00	PQ loop repeat containing 2 isoform 1,PQ loop repea
PLA2G6,iPLA2	chr22:36854222-36854383:-	0.41	brain	0.60	testes	1.00	phospholipase A2, group VI isoform a,phospholipase
UBTF	chr17:39645238-39645348:-	0.41	T47D	0.65	skel. muscle	0.24	upstream binding transcription factor, RNA,upstrea
TXNDC14,KIAA038	chr11:57339963-57340049:+	0.41	BT474	0.41	MB435	0.00	catenin (cadherin-associated protein), delta 1,cateni
PIK4CB	chr1:149563845-149564017:-	0.41	skel. muscle	0.75	testes	0.35	phosphatidylinositol 4-kinase, catalytic, beta,phosph
DKFZp313M0720,T	chr12:43982064-43982143:+	0.41	MB435	1.00	lymph node	0.60	transmembrane protein 16F,Homo sapiens cDNA FL
NUBP2	chr16:1776740-1776957:+	0.41	MCF7	0.46	lymph node	0.87	nucleotide binding protein 2 (MinD homolog, E.,Hom
TINF2	chr14:23780066-23780822:-	0.40	cerebellum	1.00	brain	0.60	TERF1 (TRF1)-interacting nuclear factor 2,TERF1-i
VWA1	chr1:1362170-1362727:+	0.40	cerebellum	1.00	skel. muscle	0.60	von Willebrand factor A domain-related protein,von
SYNE1,KIAA0796,K	chr6:152493548-152493606:-	0.40	cerebellum	0.60	heart	1.00	nesprin 1 isoform longer,Homo sapiens mRNA for K
SLC29A2	chr11:65893107-65893246:-	0.40	cerebellum	1.00	BT474	0.60	solute carrier family 29 (nucleoside,solute carrier fa
ASXL1,ASXH1	chr20:30481365-30481517:+	0.40	adipose	0.56	lymph node	0.16	additional sex combs like 1,Homo sapiens ASXH1 m
SPIN1	chr9:90231117-90231326:+	0.40	BT474	1.00	T47D	0.60	spindlin,spindlin,
UFD1,UFD1L	chr22:17842993-17843125:-	0.40	cerebellum	1.00	lymph node	0.60	ubiquitin fusion degradation 1-like isoform A,ubiquiti
TRAPPC6A	chr19:50360225-50360292:-	0.40	MCF7	0.60	HME	1.00	trafficking protein particle complex 6A,Trafficking pr
C5orf28	chr5:43489517-43489902:-	0.40	MCF7	1.00	MB435	0.60	hypothetical protein LOC64417,hypothetical protein
TXNDC14,KIAA038	chr11:57315540-57315721:+	0.40	cerebellum	1.00	colon	0.60	catenin (cadherin-associated protein), delta 1,cateni
EAPP	chr14:34068315-34068432:-	0.40	breast	1.00	lymph node	0.60	E2F-associated phosphoprotein
BC044624,PBX1	chr1:163055933-163056045:+	0.40	brain	1.00	testes	0.60	pre-B-cell leukemia transcription factor 1,Pre-B-cell l
KIAA1845,CAPN10	chr2:241184409-241184611:+	0.40	cerebellum	1.00	testes	0.60	calpain 10 isoform a,calpain 10 isoform c,calpain 10
ADCK1	chr14:77461860-77462057:+	0.40	breast	1.00	testes	0.60	aarF domain containing kinase 1,aarF domain contai
METTL9	chr16:21531467-21531657:+	0.40	BT474	1.00	testes	0.60	methyltransferase like 9 isoform 1,methyltransferase
PHLDB1,KIAA0638	chr11:118010850-118010979:+	0.40	cerebellum	0.45	breast	0.05	Homo sapiens mRNA for KIAA0638 protein, partial c
PDCD10	chr3:168925883-168925955:-	0.40	BT474	0.03	brain	0.43	programmed cell death 10,programmed cell death 1
APOBEC3D,bK150	chr22:37751021-37751300:+	0.40	MB435	1.00	lymph node	0.60	Probable DNA dC->dU-editing enzyme APOBEC-3D
QDPR	chr4:17119992-17120084:-	0.40	BT474	1.00	colon	0.60	quinoid dihydropteridine reductase,Homo sapiens c
ELN	chr7:73093482-73093517:+	0.40	adipose	1.00	testes	0.60	elastin isoform a,elastin isoform e,elastin isoform d,e

GPR146	chr7:1062266-1062410:+	0.40	breast	0.83	adipose	0.43	G protein-coupled receptor 146,G protein-coupled r
EMP3	chr19:53522590-53522692:+	0.40	adipose	1.00	lymph node	0.60	epithelial membrane protein 3
GATS	chr7:99648606-99648692:-	0.40	brain	0.60	skel. muscle	1.00	opposite strand transcription unit to STAG3,opposit
NR_002588,DKFZp	chr3:187985445-187985584:+	0.40	MCF7	0.60	T47D	1.00	eukaryotic translation initiation factor 4A2,Homo sapi
NME1-NME2,NME2	chr17:46594088-46594163:+	0.40	cerebellum	1.00	HME	0.60	NME1-NME2 protein,non-metastatic cells 2, protein
MMP28	chr17:31124298-31124521:-	0.40	breast	0.60	testes	1.00	matrix metalloproteinase 28 isoform 1,matrix metallo
DUSP22	chr6:280114-280163:+	0.40	adipose	0.60	skel. muscle	1.00	dual specificity phosphatase 22,dual specificity phos
MGC14376	chr17:1564415-1564497:-	0.40	adipose	1.00	testes	0.60	hypothetical protein LOC84981,hypothetical protein
n/a	chr8:144974824-144974874:+	0.40	cerebellum	0.75	MCF7	0.35	n/a
SIAHBP1	chr8:144974824-144974874:-	0.40	cerebellum	0.75	MCF7	0.35	fuse-binding protein-interacting repressor,fuse-bindi
HCDI,C14orf124	chr14:23981224-23981306:-	0.40	cerebellum	1.00	lymph node	0.60	hypothetical protein LOC56948,hypothetical protein
MS4A7	chr11:59909137-59909271:+	0.40	adipose	0.60	liver	1.00	membrane-spanning 4-domains, subfamily A, mem
YAP1	chr11:101561959-101562072:+	0.40	adipose	0.36	colon	0.76	Yes-associated protein 1, 65 kD,Yes-associated prot
BID	chr22:16606569-16606779:-	0.40	MCF7	1.00	adipose	0.60	BH3 interacting domain death agonist isoform 2,BH3
FOLR2	chr11:71607253-71607426:+	0.40	breast	1.00	testes	0.61	folate receptor 2 precursor
SIGIRR	chr11:396843-396993:-	0.40	breast	1.00	liver	0.61	Single Ig IL-1-related receptor (Single Ig IL-1R-relate
CHES1	chr14:88726481-88726546:-	0.40	adipose	0.52	skel. muscle	0.91	checkpoint suppressor 1,checkpoint suppressor 1,c
FLJ00246,MASK-B	chr5:139895131-139895307:+	0.39	cerebellum	1.00	breast	0.61	MASK-4E-BP3 protein,ankyrin repeat and KH doma
PPP1CA	chr11:66925115-66925279:-	0.39	cerebellum	0.61	heart	1.00	protein phosphatase 1, catalytic subunit, alpha,prote
TMEM164,AK09412	chrX:109133385-109134048:+	0.39	breast	1.00	lymph node	0.61	hypothetical protein LOC84187,Homo sapiens cDNA
DYNLL2	chr17:53519442-53519582:+	0.39	HME	1.00	lymph node	0.61	dynein light chain 2
TRERF1	chr6:42338976-42339284:-	0.39	MCF7	0.61	HME	1.00	Transcriptional-regulating factor 1 (Transcriptional-re
SFRS10	chr3:187132059-187132334:-	0.39	adipose	0.04	skel. muscle	0.44	splicing factor, arginine/serine-rich 10,Homo sapiens
GUSB	chr7:65077341-65077493:-	0.39	colon	0.81	testes	0.42	glucuronidase, beta
ECSIT	chr19:11490890-11491008:-	0.39	cerebellum	0.61	MCF7	1.00	evolutionarily conserved signaling intermediate,Hom
SFRS10	chr3:187127083-187127216:-	0.39	cerebellum	0.61	brain	1.00	splicing factor, arginine/serine-rich 10,Homo sapiens
AX746484,RP11-82	chr9:116183161-116183547:-	0.39	breast	1.00	T47D	0.61	AT-hook transcription factor,AT-hook transcription fa
NUBP2	chr16:1776759-1776957:+	0.39	MCF7	0.50	lymph node	0.89	nucleotide binding protein 2 (MinD homolog, E.,Hom
KIAA0515	chr9:133359613-133359694:+	0.39	cerebellum	0.70	MB435	0.31	Homo sapiens mRNA for KIAA0515 protein, partial c
OSBPL1A	chr18:20011975-20012157:-	0.39	breast	1.00	MB435	0.61	oxysterol-binding protein-like 1A isoform B,oxysterol-
GIPC1	chr19:14454501-14454818:-	0.39	cerebellum	1.00	testes	0.61	regulator of G-protein signalling 19 interacting,regula
AK124197,PRDM2	chr1:13972160-13972270:+	0.39	breast	1.00	lymph node	0.61	retinoblastoma protein-binding zinc finger,Homo sapi
PHSECRG2,C16orf	chr16:15885366-15885563:-	0.39	breast	1.00	liver	0.61	hypothetical protein LOC123811,Homo sapiens cDN
CR621085	chr6:36550544-36550817:+	0.39	MCF7	0.61	testes	1.00	full-length cDNA clone CS0DF015YM03 of Fetal brai
VEGF,VEGF41,VE	chr6:43856447-43856518:+	0.39	HME	0.57	skel. muscle	0.18	vascular endothelial growth factor A isoform e,vascu
TSPO	chr22:41885160-41885370:+	0.39	breast	1.00	lymph node	0.61	translocator protein (18kDa) isoform PBR,translocat
BANP	chr16:86656374-86656439:+	0.39	lymph node	0.34	testes	0.73	BTG3 associated nuclear protein isoform b,BTG3 as
UGP2	chr2:63923177-63923237:+	0.39	cerebellum	0.08	breast	0.47	UDP-glucose pyrophosphorylase 2 isoform a,UDP-g
ZCCHC9	chr5:80636316-80636716:+	0.39	cerebellum	0.61	breast	1.00	zinc finger, CCHC domain containing 9,zinc finger,
IQWD1	chr1:166258850-166258909:+	0.39	skel. muscle	0.90	testes	0.52	IQ motif and WD repeats 1 isoform a,IQ motif and W
n/a	chr16:66258631-66258929:+	0.39	cerebellum	1.00	adipose	0.61	n/a
MGC4172	chr17:32030213-32030305:+	0.39	cerebellum	0.61	colon	1.00	short-chain dehydrogenase/reductase
ZNF434	chr16:3387193-3387745:-	0.39	cerebellum	1.00	BT474	0.61	zinc finger protein 434,zinc finger protein 434,
LOC124512	chr17:72234647-72234890:+	0.39	MB435	1.00	lymph node	0.61	hypothetical protein LOC124512,Homo sapiens hyp
ING4	chr12:6632657-6632823:-	0.39	cerebellum	0.61	breast	1.00	inhibitor of growth family, member 4,inhibitor of gro
FAM44B	chr5:172972740-172972864:-	0.39	cerebellum	1.00	lymph node	0.61	hypothetical protein LOC91272
MKKS	chr20:10341178-10342579:-	0.39	cerebellum	1.00	BT474	0.61	McKusick-Kaufman syndrome protein,McKusick-Kau
EEFSEC	chr3:129466150-129466314:+	0.39	MB435	1.00	skel. muscle	0.61	eukaryotic elongation factor,,Homo sapiens MJ0495-
PDHA1	chrX:19282530-19282622:+	0.39	cerebellum	1.00	colon	0.61	pyruvate dehydrogenase (lipoamide) alpha 1
PILRA	chr7:99825447-99825665:+	0.39	cerebellum	0.68	adipose	0.29	paired immunoglobulin-like type 2 receptor alpha,pai
ZDHHC16	chr10:99201837-99202031:+	0.39	cerebellum	0.61	MCF7	1.00	Abl-philin 2 isoform 2,Abl-philin 2 isoform 2,
C10orf119	chr10:121585042-121585206:-	0.39	cerebellum	1.00	skel. muscle	0.61	chromosome 10 open reading frame 119,Homo sapi
C6orf48,G8	chr6:31912180-31912273:+	0.39	MCF7	0.39	adipose	0.01	G8 protein,G8 protein,Homo sapiens mRNA for G8
LYRM1	chr16:20821309-20821540:+	0.39	colon	0.08	lymph node	0.46	LYR motif containing 1,LYR motif containing 1,
ASPH	chr8:62721863-62721991:-	0.39	MCF7	1.00	lymph node	0.62	aspartate beta-hydroxylase isoform a,aspartate beta-
SPECC1	chr17:20048238-20049817:+	0.39	cerebellum	1.00	T47D	0.62	spectrin domain with coiled-coils 1 NSP5b3b,spectri
GGCX	chr2:85641449-85641619:-	0.39	BT474	1.00	liver	0.62	gamma-glutamyl carboxylase
GSTT1	chr22:22706822-22706998:-	0.38	MCF7	1.00	testes	0.62	glutathione S-transferase theta 1,Homo sapiens glut
PITPNB	chr22:26580842-26580927:-	0.38	breast	1.00	brain	0.62	phosphatidylinositol transfer protein, beta
H2AFY,AX747819	chr5:134716535-134716634:-	0.38	BT474	0.96	colon	0.58	H2A histone family, member Y isoform 3,H2A histon
n/a	chr20:33683499-33683570:-	0.38	MCF7	1.00	adipose	0.62	n/a
EGFL7,ve-statin	chr9:138684442-138684603:+	0.38	MB435	0.62	T47D	1.00	EGF-like-domain, multiple 7,EGF-like-domain, multi
CLK2	chr1:153505123-153505210:-	0.38	BT474	0.62	adipose	1.00	CDC-like kinase 2,CDC-like kinase 2 isoform 2,CDC
BCL2L12	chr19:54862091-54862230:+	0.38	MB435	0.62	T47D	1.00	BCL2-like 12 isoform 1,BCL2-like 12 isoform 3,
DKFZp666A163,BT	chr11:13423147-13423304:-	0.38	HME	0.31	testes	0.69	K+ channel tetramerization protein,Homo sapiens G
BCS1L	chr2:219233004-219233133:+	0.38	cerebellum	1.00	MB435	0.62	BCS1-like,BCS1-like,BCS1-like,BCS1-like,BCS1-lik
KLHL24	chr3:184843962-184844024:+	0.38	heart	1.00	skel. muscle	0.62	DRE1 protein,DRE1 protein,DRE1 protein,
ABHD14B	chr3:51980516-51980754:-	0.38	cerebellum	1.00	MB435	0.62	abhydrolase domain containing 14B,abhydrolase do
ETFA	chr15:74374987-74375133:-	0.38	MCF7	0.62	brain	1.00	electron transfer flavoprotein, alpha,electron transfer
NDE1,AX747846	chr16:15701087-15701212:+	0.38	MB435	1.00	testes	0.62	nuclear distribution gene E homolog 1,nuclear distrib
ALKBH2	chr12:108012197-108012395:-	0.38	BT474	1.00	HME	0.62	alkB, alkylation repair homolog 2,alkB, alkylation rep
MPPE1	chr18:11874878-11875042:-	0.38	cerebellum	0.58	skel. muscle	0.20	metallophosphoesterase 1 precursor,metallophosph
TSC2,SLC9A3R2 v	chr16:2038589-2038755:+	0.38	MCF7	1.00	heart	0.62	tuberous sclerosis 2 isoform 1,tuberous sclerosis 2 i
HAGH	chr16:1809117-1809225:-	0.38	cerebellum	1.00	lymph node	0.62	hydroxyacyl glutathione hydrolase isoform 2,hydroxy
ZNF385	chr12:53055895-53056005:-	0.38	breast	1.00	BT474	0.62	zinc finger protein 385,zinc finger protein 385,zinc fi
KIAA1815	chr9:5795027-5795217:-	0.38	MCF7	0.62	HME	1.00	hypothetical protein LOC79956,hypothetical protein
RSU1	chr10:16898978-16899089:-	0.38	MCF7	0.93	heart	0.55	ras suppressor protein 1 isoform 1,ras suppressor p

CR609046,PDE4DII	chr1:143585234-143585386:-	0.38	cerebellum	0.62	brain	1.00	phosphodiesterase 4D interacting protein isoform,ph
CACNA1H	chr16:1202512-1202529:+	0.38	adipose	0.63	testes	0.25	calcium channel, voltage-dependent, T type,,calcium
n/a	chr6:3209407-3209558:+	0.38	cerebellum	0.62	lymph node	1.00	n/a
KIAA0891	chr3:49129496-49129798:-	0.38	adipose	1.00	testes	0.62	ubiquitin specific protease 19,ubiquitin specific prote
PKNOX2	chr11:124726390-124726498:+	0.38	cerebellum	0.62	brain	1.00	PBX/knotted 1 homeobox 2,Homo sapiens mRNA fo
TRAD,RFFL	chr17:30372503-30372913:-	0.38	breast	1.00	liver	0.62	Homo sapiens mRNA for Trad, complete cds.,rififylin
PRPF3	chr1:148567403-148567549:+	0.38	cerebellum	0.62	BT474	1.00	PRP3 pre-mRNA processing factor 3 homolog
KIAA0999	chr11:116251792-116251935:-	0.38	brain	0.51	testes	0.89	KIAA0999 protein,KIAA0999 protein.,KIAA0999 prot
RPS6KL1	chr14:74443891-74443986:-	0.38	cerebellum	0.62	testes	1.00	ribosomal protein S6 kinase-like 1,Homo sapiens cD
PHF15,FLJ00195	chr5:133940357-133940485:+	0.38	breast	0.62	BT474	1.00	Homo sapiens mRNA for hypothetical protein (ORF1
HOIL-1	chr20:349515-349675:+	0.38	MB435	0.62	T47D	1.00	Homo sapiens HOIL-1 mRNA for ubiquitin ligase, co
n/a	chr4:15295571-15295680:+	0.38	cerebellum	0.00	testes	0.38	n/a
BCLAF1	chr6:136629860-136630006:-	0.38	cerebellum	1.00	BT474	0.62	BCL2-associated transcription factor 1 isoform,BCL2
n/a	chr14:72946398-72946529:-	0.38	cerebellum	0.62	adipose	1.00	n/a
RPUSD3	chr3:9855716-9855855:-	0.38	MCF7	1.00	BT474	0.62	RNA pseudouridylate synthase domain containing,R
HT036-ISO,RP11-5	chr1:43691161-43691262:-	0.38	cerebellum	0.84	MB435	0.47	Novel protein (HT036).,Homo sapiens HT036-ISO (H
IQWD1	chr1:166251643-166251813:+	0.38	heart	0.62	skel. muscle	1.00	IQ motif and WD repeats 1 isoform a,IQ motif and W
GTF3C5	chr9:134907295-134907514:+	0.38	cerebellum	1.00	colon	0.62	general transcription factor IIIC, polypeptide,general
B7,LRRC23	chr12:6892155-6892452:+	0.38	MB435	0.62	skel. muscle	1.00	leucine-rich repeat-containing protein 23,leucine-rich
LENG8,KIAA1932	chr19:59654283-59654371:+	0.38	breast	1.00	lymph node	0.63	leukocyte receptor cluster (LRC) member 8,Homo sa
APOL1	chr22:34983075-34983128:+	0.38	lymph node	1.00	testes	0.63	apolipoprotein L1 isoform b precursor,apolipoprotein
CAMKK2,KIAA0787	chr12:120170792-120170920:-	0.38	cerebellum	1.00	adipose	0.63	calcium/calmodulin-dependent protein kinase,calciu
RHPN1	chr8:144529838-144529966:+	0.38	MCF7	1.00	lymph node	0.63	rhophilin 1
ZNHIT3	chr17:31916892-31916923:+	0.38	cerebellum	0.63	MCF7	1.00	thyroid hormone receptor interactor 3 isoform 2,thyro
IL4R	chr16:27279588-27279637:+	0.37	HME	1.00	lymph node	0.63	interleukin 4 receptor alpha chain isoform a,interleuk
C6orf162	chr6:88097129-88097149:+	0.37	brain	0.37	heart	0.00	hypothetical protein LOC57150,hypothetical protein L
UNQ6408,TOR2A	chr9:129536399-129536664:-	0.37	BT474	1.00	MB435	0.63	Torsin-2A precursor (Torsin family 2 member A) (To
EPN3	chr17:45971244-45971324:+	0.37	MCF7	0.63	HME	1.00	epsin 3,Homo sapiens epsin 3 mRNA, complete cds.
KIAA1093,TNRC6B	chr22:38990638-38992986:+	0.37	cerebellum	1.00	lymph node	0.63	trinucleotide repeat containing 6B isoform 1,Homo sa
CHCHD7	chr8:57287875-57288022:+	0.37	MCF7	0.42	lymph node	0.04	coiled-coil-helix-coiled-coil-helix domain,coiled-coil-h
ASCC2,DKFZp586	chr22:28558234-28558331:-	0.37	breast	1.00	lymph node	0.63	activating signal cointegrator 1 complex subunit,Hom
PALM2-AKAP2,KIA	chr9:111958420-111958598:+	0.37	adipose	0.51	colon	0.88	PALM2-AKAP2 protein isoform 1,PALM2-AKAP2 pro
MICALL1	chr22:36647925-36648379:+	0.37	breast	1.00	lymph node	0.63	molecule interacting with Rab13
FLOT2	chr17:24235369-24235459:-	0.37	cerebellum	0.63	BT474	1.00	flotillin 2
CCND3	chr6:42016086-42016301:-	0.37	BT474	1.00	colon	0.63	cyclin D3,Homo sapiens mRNA for cyclin D3 variant
CNTFR	chr9:34571093-34571203:-	0.37	brain	1.00	testes	0.63	ciliary neurotrophic factor receptor,ciliary neurotrophi
IFRG15,TOR1AIP2	chr1:178112997-178113131:-	0.37	T47D	1.00	adipose	0.63	interferon responsive gene 15,torsin A interacting pro
METTL3	chr14:21038477-21038664:-	0.37	cerebellum	1.00	testes	0.63	methyltransferase like 3,Homo sapiens cDNA FLJ20
PITPNC1	chr17:63113644-63113762:+	0.37	breast	1.00	brain	0.63	phosphatidylinositol transfer protein,,phosphatidylino
MAD1L1,MAD1	chr7:2236710-2236888:-	0.37	cerebellum	1.00	MB435	0.63	MAD1-like 1 protein,MAD1-like 1 protein,MAD1-like
CHCHD7	chr8:57287875-57288002:+	0.37	MCF7	0.42	lymph node	0.05	coiled-coil-helix-coiled-coil-helix domain,coiled-coil-h
n/a	chr19:16625846-16625936:-	0.37	colon	0.55	liver	0.92	n/a
KIAA0819	chr22:16685713-16685826:-	0.37	cerebellum	1.00	lymph node	0.63	Uncharacterized protein KIAA0819.
MYBBP1A	chr17:4390392-4390528:-	0.37	cerebellum	1.00	lymph node	0.63	MYB binding protein 1a,MYB binding protein 1a,Hom
FLJ10241	chr19:46634123-46634217:-	0.37	MCF7	0.63	MB435	1.00	hypothetical protein LOC55101,hypothetical protein L
MAP7D1	chr1:36413086-36413196:+	0.37	cerebellum	1.00	MB435	0.63	arginine/proline rich coiled-coil 1,arginine/proline rich
NDUFA3	chr19:59301472-59301565:+	0.37	MB435	0.00	T47D	0.37	NADH dehydrogenase (ubiquinone) 1 alpha,Homo s
VEGF,VEGF41,VE	chr6:43856447-43856500:+	0.37	heart	0.55	skel. muscle	0.18	vascular endothelial growth factor A isoform e,vascu
DKFZp761D1923	chr7:30152318-30152440:+	0.37	HME	1.00	adipose	0.63	Homo sapiens cDNA FLJ30904 fis, clone FEBRA20
FOXJ3	chr1:42516606-42516930:-	0.37	skel. muscle	1.00	testes	0.63	forkhead box J3,forkhead box J3,
MRPL47	chr3:180803134-180803279:-	0.37	BT474	1.00	testes	0.63	mitochondrial ribosomal protein L47 isoform a,mitoch
NPM3	chr10:103532586-103532671:-	0.37	MCF7	0.63	BT474	1.00	nucleophosmin/nucleoplasmin 3
TMEM50A	chr1:25551960-25552052:+	0.37	adipose	1.00	brain	0.63	small membrane protein 1
DDR1 variant protei	chr6:30971160-30971270:+	0.37	MCF7	1.00	adipose	0.63	Homo sapiens mRNA for DDR1 variant protein, parti
PPP4C,PPX	chr16:30000022-30000132:+	0.37	cerebellum	0.63	breast	1.00	protein phosphatase 4 (formerly X), catalytic,Homo s
HM13	chr20:29606210-29606293:+	0.37	cerebellum	0.63	skel. muscle	1.00	minor histocompatibility antigen 13 isoform 3,minor h
NDUFS1	chr2:206725388-206725479:-	0.37	cerebellum	1.00	BT474	0.64	NADH dehydrogenase (ubiquinone) Fe-S protein 1,
GSTT1	chr22:22711700-22711787:-	0.37	cerebellum	0.52	heart	0.89	glutathione S-transferase theta 1,Homo sapiens glut
IFI27,P27	chr14:93647758-93647872:+	0.37	cerebellum	1.00	heart	0.64	interferon, alpha-inducible protein 27,Homo sapiens
CSDE1,KIAA0885	chr1:115081615-115081707:-	0.37	heart	0.10	testes	0.46	upstream of NRAS isoform 2,upstream of NRAS isof
SMRTE,NCOR2	chr12:123378046-123378132:-	0.37	cerebellum	1.00	breast	0.64	nuclear receptor co-repressor 2 isoform 1,nuclear re
ENTPD6,CD39L2	chr20:25149868-25149969:+	0.37	cerebellum	1.00	HME	0.64	ectonucleoside triphosphate diphosphohydrolase,ect
AHDC1	chr1:27757403-27757628:-	0.37	breast	1.00	testes	0.64	Homo sapiens cDNA clone IMAGE:5588836, **** W
MAGOH	chr1:53471802-53471912:-	0.36	MCF7	0.94	lymph node	0.57	mago-nashi homolog
SEMA6A	chr5:115836480-115836530:-	0.36	adipose	0.04	brain	0.40	sema domain, transmembrane domain (TM), and,se
KHDRBS3	chr8:136726484-136726542:+	0.36	MB435	1.00	testes	0.64	KH domain containing, RNA binding, signal,KH dom
G30888,POLM,Pol	chr7:44080255-44080654:-	0.36	cerebellum	1.00	skel. muscle	0.64	polymerase (DNA directed), mu,POLM protein.,Hom
CAMK2G	chr10:75249296-75249409:-	0.36	T47D	0.27	brain	0.63	calcium/calmodulin-dependent protein kinase II,calci
UFD1,UFD1L	chr22:17843019-17843125:-	0.36	cerebellum	1.00	lymph node	0.64	ubiquitin fusion degradation 1-like isoform A,ubiquiti
YIPF2	chr19:10899306-10899392:-	0.36	BT474	0.64	HME	1.00	Yip1 domain family, member 2,Yip1 domain family,
ADAM15	chr1:153300515-153300589:+	0.36	HME	0.51	adipose	0.87	a disintegrin and metalloproteinase domain 15,a disi
MYO1B,myh-1	chr2:191975603-191975689:+	0.36	HME	0.04	MB435	0.40	myosin IB,myosin IB,Hypothetical protein (Fragment)
DAB2	chr5:39418477-39419130:-	0.36	cerebellum	1.00	heart	0.64	disabled homolog 2,disabled homolog 2,
CD302	chr2:160348116-160348226:-	0.36	liver	1.00	lymph node	0.64	CD302 antigen
P53TG1	chr7:86812295-86812485:-	0.36	liver	0.75	testes	0.39	Homo sapiens mRNA for P53TG1-A, complete cds.,
FLCN	chr17:17075833-17075921:-	0.36	cerebellum	1.00	MCF7	0.64	folliculin isoform 1,Folliculin (Birt-Hogg-Dube syndro
TSC2,SLC9A3R2 v	chr16:2067600-2067728:+	0.36	BT474	0.39	MB435	0.02	tuberous sclerosis 2 isoform 1,tuberous sclerosis 2 i

SYNGR2	chr17:73679186-73679325:+	0.36	MB435	1.00	lymph node	0.64	synaptogyrin 2,Homo sapiens mRNA for synaptogyri
IFI27,P27	chr14:93647724-93647872:+	0.36	cerebellum	1.00	heart	0.64	interferon, alpha-inducible protein 27,Homo sapiens
UBN1	chr16:4861157-4861303:+	0.36	cerebellum	1.00	adipose	0.64	ubinuclein 1,ubinuclein 1,
TOR3A	chr1:177321386-177321651:+	0.36	MB435	1.00	testes	0.64	torsin family 3, member A,Torsin-3A precursor (Torsi
DKFZp434P167,DK	chr8:145287861-145287980:+	0.36	cerebellum	0.71	HME	0.35	Hypothetical protein DKFZp434I0113 (Fragment).,K
NAALADL1	chr11:64570237-64570574:-	0.36	adipose	1.00	testes	0.64	N-acetylated alpha-linked acidic
BRWD2,AX747838,	chr10:122640218-122640389:+	0.36	HME	1.00	T47D	0.64	bromodomain and WD repeat domain containing 2,H
FMNL2,KIAA1902	chr2:153208179-153208304:+	0.36	cerebellum	0.39	brain	0.03	formin-like 2,CDNA FLJ16308 fis, clone PUAEN200
MIRO-2,RHOT2	chr16:660676-660774:+	0.36	BT474	1.00	testes	0.64	ras homolog gene family, member T2,Homo sapiens
SUSD3	chr9:94877887-94878075:+	0.36	BT474	1.00	lymph node	0.64	sushi domain containing 3,sushi domain containing
DKFZp586B0320,T	chr3:9760908-9761192:+	0.36	MCF7	1.00	MB435	0.64	tubulin tyrosine ligase-like family, member 3,tubulin t
KIAA0693,SS18L1	chr20:60162732-60162916:+	0.36	cerebellum	0.04	HME	0.40	SS18-like protein 1,Homo sapiens mRNA for KIAA06
AX747133,BRUNOL	chr18:33093142-33093225:-	0.36	cerebellum	0.51	brain	0.87	bruno-like 4, RNA binding protein,bruno-like 4, RNA
CSAD	chr12:51841178-51841242:-	0.36	cerebellum	0.55	adipose	0.91	cysteine sulfinic acid decarboxylase-related,cysteine
n/a	chr6:3209442-3209558:+	0.36	cerebellum	0.64	lymph node	1.00	n/a
FLJ22222	chr17:77945496-77945708:-	0.36	HME	0.11	lymph node	0.47	hypothetical protein LOC79701 isoform 2
PBX3	chr9:127717786-127718027:+	0.36	MCF7	0.64	BT474	1.00	pre-B-cell leukemia transcription factor 3,Pre-B-cell l
dJ402G11.5,SELO	chr22:48993024-48993240:+	0.36	cerebellum	0.40	MB435	0.04	selenoprotein O,Homo sapiens PNAS-21 mRNA, co
Icap-1a,ITGB1BP1	chr2:9476206-9476312:-	0.36	breast	1.00	lymph node	0.64	integrin cytoplasmic domain-associated protein 1,inte
DNM1	chr9:130055201-130055237:+	0.36	cerebellum	0.96	brain	0.60	dynamin 1 isoform 2,dynamin 1 isoform 1,Homo sapi
ZFYVE9	chr1:52504915-52505091:+	0.36	cerebellum	0.64	HME	1.00	zinc finger, FYVE domain containing 9 isoform 3,zinc
UNC84A,KIAA0810	chr7:855683-855766:+	0.36	cerebellum	0.64	MCF7	1.00	unc-84 homolog A,unc-84 homolog A,Homo sapiens
PHF14	chr7:10988524-10989311:+	0.36	MCF7	1.00	brain	0.64	PHD finger protein 14 isoform 1,PHD finger protein 1
SLC7A6	chr16:66857997-66858125:+	0.36	MCF7	1.00	BT474	0.64	solute carrier family 7 (cationic amino acid,solute car
AK095179	chr17:8307363-8307397:+	0.36	colon	0.39	lymph node	0.03	Homo sapiens cDNA FLJ37860 fis, clone BRSSN20
PLD3	chr19:45563604-45563677:+	0.36	cerebellum	0.64	MB435	1.00	phospholipase D3 isoform 2,phospholipase D3 isofo
DKFZp781C0423,D	chr20:33780798-33780863:-	0.36	breast	1.00	lymph node	0.64	Homo sapiens cDNA FLJ44170 fis, clone THYMU20
CA12	chr15:61407350-61407382:-	0.36	HME	0.65	T47D	1.00	carbonic anhydrase XII isoform 1 precursor,carbonic
AX747833	chr14:72820542-72820835:-	0.36	cerebellum	1.00	MB435	0.65	numb homolog isoform 1,numb homolog isoform 3,n
CCDC95,FLJ00210	chr16:29920034-29920352:+	0.36	breast	1.00	MB435	0.65	coiled-coil domain containing 95,coiled-coil domain c
FBXO44	chr1:11641177-11641272:+	0.36	cerebellum	0.52	brain	0.16	F-box protein 44 isoform 1,F-box protein 44 isoform
PHLDB1,KIAA0638	chr11:118020575-118020619:+	0.36	cerebellum	0.36	T47D	0.00	Homo sapiens mRNA for KIAA0638 protein, partial c
MYO1B,myh-1	chr2:191973720-191973806:+	0.36	BT474	0.84	MB435	0.48	myosin IB,myosin IB,Hypothetical protein (Fragment)
ATP13A2,DKFZp76	chr1:17192711-17192917:-	0.36	cerebellum	1.00	BT474	0.65	ATPase type 13A2,ATPase type 13A2,Cation-transp
LOC113386	chr19:63515344-63515640:+	0.36	cerebellum	1.00	testes	0.65	hypothetical protein LOC113386,Homo sapiens cDN
TMEM177	chr2:120154878-120155169:+	0.36	cerebellum	1.00	testes	0.65	hypothetical protein LOC80775,Homo sapiens cDNA
DPYSL4	chr10:133866140-133866319:+	0.36	cerebellum	1.00	testes	0.65	dihydropyrimidinase-like 4
n/a	chr11:64297478-64297553:-	0.35	breast	1.00	lymph node	0.65	splicing factor 1 isoform 2,splicing factor 1 isoform 3,
ST6GALNAC6,RP1	chr9:129700056-129700110:-	0.35	breast	1.00	lymph node	0.65	ST6,OTTHUMP00000022210.,ST6,
UNQ169,TMEM59	chr1:54283953-54284047:-	0.35	MCF7	1.00	skel. muscle	0.65	thymic dendritic cell-derived factor 1,thymic dendritic
SEC31B,AF279139	chr10:102239755-102240069:-	0.35	cerebellum	1.00	lymph node	0.65	Homo sapiens secretory pathway component Sec31
KIAA1509	chr14:90821492-90821933:-	0.35	BT474	0.46	lymph node	0.81	KIAA1509 protein.
KIAA0265	chr7:129523997-129524083:+	0.35	MB435	0.43	testes	0.78	hypothetical protein LOC23008,hypothetical protein
NDUFA3	chr19:59301475-59301565:+	0.35	MB435	0.00	T47D	0.35	NADH dehydrogenase (ubiquinone) 1 alpha,Homo s
ENO1,DKFZp666C	chr1:8853471-8853529:-	0.35	cerebellum	0.00	skel. muscle	0.35	enolase 1,Alpha-enolase (EC 4.2.1.11) (2-phospho-
C3orf18	chr3:50577901-50578296:-	0.35	cerebellum	1.00	testes	0.65	hypothetical protein LOC51161,hypothetical protein
C9orf9	chr9:134752577-134752779:+	0.35	colon	0.61	testes	0.97	Rsb-66 protein,Uncharacterized protein C9orf9.,
SLTM	chr15:56978960-56979374:-	0.35	breast	1.00	testes	0.65	modulator of estrogen induced transcription,modulat
NHP2L1	chr22:40408306-40408537:-	0.35	T47D	0.02	testes	0.37	NHP2 non-histone chromosome protein 2-like 1,NHP
RTKN	chr2:74520186-74520612:-	0.35	MB435	0.17	brain	0.52	rhotekin isoform c
RNF14	chr5:141334553-141334704:+	0.35	brain	0.65	testes	1.00	ring finger protein 14 isoform 1,ring finger protein 14
KIAA0955,CARD8	chr19:53413940-53414081:-	0.35	MB435	1.00	testes	0.65	caspase recruitment domain family, member 8,caspa
PLXNB3,KIAA1206	chrX:152685522-152686562:+	0.35	cerebellum	1.00	MB435	0.65	plexin B3,Homo sapiens mRNA for KIAA1206 protei
TIE1	chr1:43546054-43546182:+	0.35	breast	0.52	testes	0.87	tyrosine kinase with immunoglobulin-like and
THYN1	chr11:133623913-133624063:-	0.35	breast	1.00	MB435	0.65	thymocyte nuclear protein 1 isoform 1,thymocyte nuc
pp9286,AGXT2L2	chr5:177572580-177572710:-	0.35	breast	1.00	lymph node	0.65	alanine-glyoxylate aminotransferase 2-like 2,Homo s
DECR1	chr8:91098528-91098730:+	0.35	cerebellum	1.00	brain	0.65	2,4-dienoyl CoA reductase 1 precursor
ANXA11	chr10:81925843-81925891:-	0.35	MCF7	0.83	colon	0.48	annexin A11,annexin A11,
ZFP64	chr20:50215810-50215971:-	0.35	MCF7	1.00	MB435	0.65	zinc finger protein 64 isoform a,zinc finger protein 64
SCMH1	chr1:41424380-41424509:-	0.35	breast	1.00	MB435	0.65	sex comb on midleg homolog 1 isoform 2,sex comb
C7orf26	chr7:6613693-6613753:+	0.35	adipose	0.10	testes	0.45	hypothetical protein LOC79034,hypothetical protein
PCK2	chr14:23639044-23639262:+	0.35	cerebellum	1.00	MCF7	0.65	mitochondrial phosphoenolpyruvate carboxykinase,
n/a	chr7:100674008-100674140:-	0.35	BT474	1.00	lymph node	0.65	n/a
CDC42SE2	chr5:130679572-130679736:+	0.35	MCF7	1.00	T47D	0.65	CDC42 small effector 2,CDC42 small effector 2,CD
GSTO2	chr10:106024974-106025082:+	0.35	HME	0.65	testes	1.00	glutathione S-transferase omega 2
PILRB,FDFACT2	chr7:99788932-99789571:+	0.35	breast	0.65	BT474	1.00	paired immunoglobulin-like type 2 receptor beta,Hom
UNC84B	chr22:37480593-37480657:-	0.35	breast	0.54	colon	0.19	unc-84 homolog B,unc-84 homolog B,
PAPD4	chr5:78980641-78980769:+	0.35	cerebellum	1.00	BT474	0.65	PAP associated domain containing 4,PAP associate
MGC13114	chr16:625613-625775:-	0.35	breast	1.00	MB435	0.65	hypothetical protein LOC84326 isoform h,hypothetic
CDKN3,AY257479	chr14:53936367-53936444:+	0.35	T47D	0.60	testes	0.94	cyclin-dependent kinase inhibitor 3,cyclin-dependent
LOC124512	chr17:72234647-72234855:+	0.35	lymph node	0.65	testes	1.00	hypothetical protein LOC124512,Homo sapiens hyp
BOK	chr2:242147543-242147791:+	0.35	cerebellum	1.00	BT474	0.65	BCL2-related ovarian killer,Homo sapiens cDNA FLJ
SPHK-2	chr19:53820960-53821431:+	0.35	breast	1.00	adipose	0.65	sphingosine kinase 2,sphingosine kinase 2,sphingos
TRIM37	chr17:54536436-54536537:-	0.35	cerebellum	1.00	testes	0.65	tripartite motif-containing 37 protein,tripartite motif-c
LSM14B	chr20:60134677-60134890:+	0.35	cerebellum	0.65	MCF7	1.00	LSM14 protein homolog B (Protein FAM61B).,LSM1
KIAA0657,OBSL1	chr2:220131150-220131425:-	0.35	cerebellum	1.00	breast	0.65	CDNA FLJ13792 fis, clone THYRO1000072, weakly
RILP	chr17:1496950-1497033:-	0.35	breast	1.00	testes	0.65	Rab interacting lysosomal protein

COPZ2	chr17:43464521-43464598:-	0.35	MB435	1.00	skel. muscle	0.65	coatomer protein complex, subunit zeta 2
NUB1	chr7:150702116-150702262:+	0.35	cerebellum	1.00	lymph node	0.65	NEDD8 ultimate buster-1,NEDD8 ultimate buster-1,
TUBD1	chr17:55322974-55323184:-	0.35	MCF7	0.76	BT474	0.42	delta-tubulin,delta-tubulin,
MINK1,MINK	chr17:4736473-4736583:+	0.35	breast	1.00	testes	0.65	misshapen/NIK-related kinase isoform 2,misshapen/
ANGPTL4	chr19:8340103-8340216:+	0.35	HME	0.65	brain	1.00	angiopoietin-like 4 protein isoform a precursor,angio
IRAK1	chrX:152932687-152932923:-	0.35	cerebellum	1.00	skel. muscle	0.65	interleukin-1 receptor-associated kinase 1,interleukin
TRERF1	chr6:42339036-42339284:-	0.35	MCF7	0.66	HME	1.00	Transcriptional-regulating factor 1 (Transcriptional-re
NOVA1	chr14:26011366-26011437:-	0.35	cerebellum	0.96	brain	0.61	neuro-oncological ventral antigen 1 isoform 1,neuro-
GOLGA4	chr3:37377738-37377800:+	0.35	BT474	1.00	HME	0.66	golgi autoantigen, golgin subfamily a, 4,golgi autoant
n/a	chr8:48802315-48802408:-	0.35	cerebellum	1.00	MB435	0.66	n/a
APOC1	chr19:50111287-50111567:+	0.34	breast	0.55	lymph node	0.89	apolipoprotein C-I precursor,apolipoprotein C-I precu
JOSD2	chr19:55702643-55702768:-	0.34	breast	1.00	T47D	0.66	Josephin domain containing 2,Josephin domain cont
LRRC20	chr10:71806214-71806358:-	0.34	heart	0.66	skel. muscle	1.00	leucine rich repeat containing 20 isoform 1
NENF	chr1:210682511-210682590:+	0.34	cerebellum	0.66	HME	1.00	SCIRP10-related protein
REEP4	chr8:22052384-22052519:-	0.34	MCF7	0.66	BT474	1.00	receptor expression enhancing protein 4
NFE2L1,FLJ00380	chr17:43489393-43489482:+	0.34	cerebellum	0.03	colon	0.38	nuclear factor (erythroid-derived 2)-like 1,nuclear fac
SH3BP5	chr3:15273364-15273624:-	0.34	cerebellum	0.66	MCF7	1.00	SH3-domain binding protein 5 (BTK-associated),SH
ADSL	chr22:39090830-39091006:+	0.34	cerebellum	1.00	testes	0.66	adenylosuccinate lyase,adenylosuccinate lyase,Hom
pt-wd,STRAP	chr12:15927742-15927877:+	0.34	cerebellum	1.00	adipose	0.66	serine/threonine kinase receptor associated,Homo s
CCDC95,FLJ00210	chr16:29920236-29920352:+	0.34	cerebellum	0.66	BT474	1.00	coiled-coil domain containing 95,coiled-coil domain
SLTM	chr15:56978960-56979428:-	0.34	breast	1.00	testes	0.66	modulator of estrogen induced transcription,modulat
ECGF1	chr22:49314791-49315014:-	0.34	breast	1.00	HME	0.66	endothelial cell growth factor 1,endothelial cell grow
COPS3	chr17:17120074-17120203:-	0.34	BT474	0.66	HME	1.00	COP9 constitutive photomorphogenic homolog
KTN1	chr14:55200426-55200512:+	0.34	HME	1.00	heart	0.66	kinectin 1 isoform a,kinectin 1 isoform a,kinectin 1 is
n/a	chr12:6179811-6179992:+	0.34	cerebellum	1.00	breast	0.66	CD9 antigen,CD9 antigen,
n/a	chr4:15295607-15295680:+	0.34	cerebellum	0.00	testes	0.34	n/a
TINAGL1	chr1:31815288-31815646:+	0.34	breast	1.00	T47D	0.66	P3ECSL,P3ECSL,
HEATR5B,KIAA141	chr2:37082953-37083219:-	0.34	cerebellum	1.00	brain	0.66	HEAT repeat containing 5B,Homo sapiens mRNA fo
GFRA2	chr8:21696043-21696357:-	0.34	brain	0.66	testes	1.00	GDNF family receptor alpha 2 preproprotein,GDNF f
AGPAT7	chr15:32440893-32441025:-	0.34	MCF7	0.66	HME	1.00	PLSC domain containing protein
ITM2A	chrX:78505576-78505707:-	0.34	breast	1.00	heart	0.66	integral membrane protein 2A
KLHL25	chr15:84112252-84114055:-	0.34	cerebellum	1.00	adipose	0.66	BTB/POZ KELCH domain protein
C10orf104	chr10:73649824-73650143:+	0.34	T47D	0.50	testes	0.16	hypothetical protein LOC119504,hypothetical protei
DECR1	chr8:91098607-91098730:+	0.34	cerebellum	1.00	brain	0.66	2,4-dienoyl CoA reductase 1 precursor
CAMTA2	chr17:4830211-4830305:-	0.34	cerebellum	1.00	skel. muscle	0.66	calmodulin binding transcription activator 2,calmodul
SNX5	chr20:17897018-17897100:-	0.34	breast	1.00	MCF7	0.66	sorting nexin 5,Homo sapiens sorting nexin 5 (SNX5
RP11-432M24.2	chr13:49135194-49135332:-	0.34	liver	0.90	lymph node	0.56	Homo sapiens delta8-delta7 sterol isomerase relate
C11orf67	chr11:77229713-77229754:+	0.34	breast	0.52	heart	0.18	hypothetical protein LOC28971,UPF0366 protein C1
KIAA1845,CAPN10	chr2:241184024-241184242:+	0.34	cerebellum	0.38	testes	0.04	calpain 10 isoform a,calpain 10 isoform c,calpain 10
PDLIM2,FLJ00072	chr8:22505009-22505126:+	0.34	cerebellum	0.66	HME	1.00	PDZ and LIM domain 2 isoform 2,PDZ and LIM dom
NUP98	chr11:3663779-3664000:-	0.34	cerebellum	1.00	breast	0.66	nucleoporin 98kD isoform 1,nucleoporin 98kD isofor
PPP6C	chr9:126960341-126960482:-	0.34	MCF7	1.00	adipose	0.66	protein phosphatase 6, catalytic subunit
CROP/Luc7A,CRO	chr17:46169647-46169839:+	0.34	cerebellum	0.48	BT474	0.82	cisplatin resistance-associated overexpressed,cispla
BTN2A1	chr6:26566814-26566925:+	0.34	MB435	1.00	brain	0.66	butyrophilin, subfamily 2, member A1 isoform 1,buty
TNFSF12-TNFSF1	chr17:7397628-7397866:+	0.34	lymph node	0.53	testes	0.19	tumor necrosis factor ligand superfamily, member,tu
TRIM26	chr6:30280412-30280521:-	0.34	MCF7	1.00	skel. muscle	0.66	tripartite motif-containing 26,tripartite motif-containin
RHOC	chr1:113049245-113049313:-	0.34	breast	0.49	MB435	0.16	ras homolog gene family, member C precursor,ras h
DLG4	chr17:7035936-7036045:-	0.34	MB435	0.66	skel. muscle	1.00	postsynaptic density protein 95
KIAA0424,ARHGE	chrX:62890909-62891281:-	0.34	cerebellum	1.00	MB435	0.66	Cdc42 guanine exchange factor 9,Homo sapiens KI
LOC161931	chr16:82786922-82787151:+	0.34	adipose	0.59	testes	0.93	hypothetical protein LOC161931,hypothetical protei
APOBEC3D,bK150	chr22:37741546-37741702:+	0.34	HME	1.00	lymph node	0.66	Probable DNA dC->dU-editing enzyme APOBEC-3D
SCARB1	chr12:123860673-123860788:-	0.34	cerebellum	0.66	breast	1.00	scavenger receptor class B, member 1 isoform 1,sc
KIAA1064	chr19:52264189-52264440:-	0.34	cerebellum	1.00	MCF7	0.66	Homo sapiens mRNA for KIAA1064 protein, partial
DOM3Z	chr6:32047076-32047481:-	0.34	breast	1.00	colon	0.66	DOM-3 homolog Z,Protein Dom3Z (Dom-3 homolog
VPS11	chr11:118447516-118447763:+	0.34	cerebellum	1.00	testes	0.66	vacuolar protein sorting 11
MFN2	chr1:11965167-11965234:+	0.34	heart	0.38	skel. muscle	0.71	mitofusin 2
KIAA1534,OSBPL5	chr11:3098227-3098430:-	0.34	breast	1.00	MB435	0.66	oxysterol-binding protein-like protein 5 isoform,oxyst
DAXX	chr6:33397474-33397729:-	0.34	cerebellum	0.66	breast	1.00	death-associated protein 6,death-associated protein
MLL5	chr7:104538160-104538285:+	0.34	cerebellum	0.66	MCF7	1.00	myeloid/lymphoid or mixed-lineage leukemia 5,myel
DKFZp434K1421,C	chr17:25469224-25469317:+	0.34	breast	1.00	T47D	0.66	coiled-coil domain containing 55 isoform 1,Homo sa
PSMA2,DKFZp686	chr7:42932660-42932792:-	0.34	MB435	0.66	brain	1.00	proteasome alpha 2 subunit,Hypothetical protein DK
LOC113386	chr19:63515344-63515581:+	0.34	cerebellum	1.00	testes	0.66	hypothetical protein LOC113386,Homo sapiens cD
KIAA0424,ARHGE	chrX:62890920-62891281:-	0.34	cerebellum	1.00	BT474	0.66	Cdc42 guanine exchange factor 9,Homo sapiens K
SENP6	chr6:76469081-76469508:+	0.34	MCF7	1.00	skel. muscle	0.66	SUMO1/sentrin specific protease 6,SUMO1/sentrin
C15orf24,ORF3	chr15:32175388-32175502:-	0.34	cerebellum	1.00	liver	0.66	chromosome 15 open reading frame 24,Homo sapi
POGZ	chr1:149680028-149680186:-	0.34	HME	1.00	testes	0.66	pogo transposable element with ZNF domain,pogo
FCER1G	chr1:159454400-159454491:+	0.34	breast	1.00	lymph node	0.67	Fc fragment of IgE, high affinity I, receptor,Fc fragm
VRK3	chr19:55192573-55192639:-	0.34	MCF7	0.67	adipose	1.00	vaccinia related kinase 3 isoform 1,vaccinia related
RGL2	chr6:33374210-33374406:-	0.34	cerebellum	0.67	breast	1.00	ral guanine nucleotide dissociation,ral guanine nucl
DKFZp547H1810,M	chr3:47869657-47869846:-	0.34	cerebellum	0.67	breast	1.00	microtubule-associated protein 4 isoform 1,microtub
NARG2,BRCC1	chr15:58557428-58557560:-	0.34	HME	1.00	MB435	0.67	NMDA receptor regulated 2 isoform b,NMDA recept
TOP3b,TOP3B	chr22:20654582-20654778:-	0.34	cerebellum	1.00	lymph node	0.67	topoisomerase (DNA) III beta,topoisomerase (DNA)
TIA1	chr2:70309695-70309727:-	0.34	MB435	0.71	lymph node	0.38	TIA1 protein isoform 2,TIA1 protein isoform 1,Homo
UBE2J2	chr1:1192976-1193235:-	0.34	cerebellum	0.67	breast	1.00	ubiquitin conjugating enzyme E2, J2 isoform 1,ubiqu
SMARCA2	chr9:2018987-2019247:+	0.33	cerebellum	1.00	skel. muscle	0.67	SWI/SNF related, matrix associated, actin depende
SMPDL3A	chr6:123158521-123158734:+	0.33	MB435	1.00	skel. muscle	0.67	acid sphingomyelinase-like phosphodiesterase 3A,
AACS,DKFZp666F2	chr12:124187161-124187363:+	0.33	breast	1.00	BT474	0.67	acetoacetyl-CoA synthetase,Homo sapiens mRNA

MRPL22	chr5:154310574-154310691:+	0.33	HME	1.00	heart	0.67	mitochondrial ribosomal protein L22 isoform a,mitoc
C11orf79	chr11:60962052-60962161:+	0.33	T47D	0.33	skel. muscle	0.67	hypothetical protein LOC54949
LRP16	chr11:63539300-63539329:-	0.33	MCF7	0.63	skel. muscle	0.96	LRP16 protein
C20orf199	chr20:47330429-47330514:+	0.33	adipose	0.95	skel. muscle	0.62	Homo sapiens NS5ATP6-regulated protein 1, comp
n/a	chr20:47330429-47330514:-	0.33	adipose	0.95	skel. muscle	0.62	n/a
AF251050,ZNF263	chr16:3276024-3276150:+	0.33	MCF7	0.85	T47D	0.51	zinc finger protein 263,Homo sapiens zinc finger pro
ARFIP2	chr11:6458129-6458269:-	0.33	cerebellum	1.00	adipose	0.67	ADP-ribosylation factor interacting protein 2,ADP-rib
OK/SW-cl.69	chr20:61977598-61977672:+	0.33	lymph node	0.67	skel. muscle	1.00	tumor protein D52-like 2 isoform a,tumor protein D5
RNMTL1	chr17:633073-633317:+	0.33	cerebellum	1.00	liver	0.67	RNA methyltransferase like 1
LIMS2	chr2:128116094-128116244:-	0.33	breast	1.00	lymph node	0.67	LIM and senescent cell antigen-like domains 2,LIM
HSPC142	chr19:17245713-17245833:+	0.33	cerebellum	1.00	BT474	0.67	hypothetical protein LOC29086,hypothetical protein
SIL1	chr5:138390389-138390580:-	0.33	cerebellum	1.00	heart	0.67	SIL1 protein precursor,SIL1 protein precursor,SIL1
AK124433,MAGI1	chr3:65336460-65336663:-	0.33	cerebellum	0.73	breast	0.39	membrane associated guanylate kinase, WW and
SMRTE,NCOR2	chr12:123507605-123507661:-	0.33	BT474	1.00	adipose	0.67	nuclear receptor co-repressor 2 isoform 1,nuclear re
FBXO18	chr10:5988006-5988601:+	0.33	cerebellum	1.00	adipose	0.67	F-box only protein, helicase, 18 isoform 2,F-box onl
HM13	chr20:29600141-29600257:+	0.33	BT474	0.35	liver	0.02	minor histocompatibility antigen 13 isoform 3,minor
C1orf2	chr1:153490499-153490609:-	0.33	T47D	1.00	adipose	0.67	hypothetical protein LOC10712 isoform a,Homo sap
NAP1L4	chr11:2927033-2927070:-	0.33	MB435	0.04	brain	0.37	nucleosome assembly protein 1-like 4,Homo sapien
KIAA0911,CLSTN1	chr1:9720143-9720199:-	0.33	cerebellum	1.00	testes	0.67	calsyntenin 1 isoform 1,calsyntenin 1 isoform 2,cals
ZNF75A	chr16:3298314-3298837:+	0.33	BT474	0.21	T47D	0.54	zinc finger protein 75a,Homo sapiens cDNA FLJ315
SRRM2	chr16:2746336-2746608:+	0.33	cerebellum	0.92	heart	0.59	splicing coactivator subunit SRm300,splicing coacti
KIAA0859,AK09481	chr1:170026215-170026379:+	0.33	breast	1.00	adipose	0.67	CGI-01 protein isoform 1,CGI-01 protein isoform 2,
ELOVL1	chr1:43604526-43604674:-	0.33	T47D	0.43	adipose	0.10	elongation of very long chain fatty acids,elongation
PPM1F	chr22:20630215-20630480:-	0.33	cerebellum	1.00	T47D	0.67	protein phosphatase 1F,protein phosphatase 1F,
SRCAP	chr16:30640011-30640298:+	0.33	breast	1.00	MB435	0.67	Snf2-related CBP activator protein,Snf2-related CB
HEXDC	chr17:77991638-77991778:+	0.33	cerebellum	0.67	lymph node	1.00	hexosaminidase (glycosyl hydrolase family 20,,CDN
KIAA0653,ICOSLG	chr21:44481178-44481528:-	0.33	BT474	0.67	MB435	1.00	inducible T-cell co-stimulator ligand,Homo sapiens
TRA16	chr19:19174279-19174384:-	0.33	adipose	0.67	colon	1.00	TR4 orphan receptor associated protein TRA16,Hor
RNF38	chr9:36346300-36346470:-	0.33	cerebellum	1.00	skel. muscle	0.67	ring finger protein 38 isoform 2,ring finger protein 38
KIAA0397,RUTBC1	chr17:2217315-2217449:+	0.33	HME	0.50	MB435	0.17	RUN and TBC1 domain containing 1,RUN and TBC
SLC39A4	chr8:145609429-145609581:-	0.33	HME	1.00	MB435	0.67	solute carrier family 39 (zinc transporter),,Homo sap
AK025296,FLJ2027	chr4:40133215-40133421:-	0.33	breast	1.00	colon	0.67	hypothetical protein LOC54502,hypothetical protein
ERCC1	chr19:50609061-50609132:-	0.33	BT474	1.00	testes	0.67	excision repair cross-complementing 1 isofrom 2,Ho
PDCD6,ALG-2,KIA	chr5:357292-359869:+	0.33	cerebellum	1.00	testes	0.67	arylhydrocarbon receptor repressor,arylhydrocarbon
CAV2	chr7:115927550-115927737:+	0.33	breast	1.00	lymph node	0.67	caveolin 2 isoform a and b,caveolin 2 isoform c,Hon
PCQAP	chr22:19269142-19269302:+	0.33	breast	1.00	brain	0.67	positive cofactor 2, glutamine/Q-rich-associated,pos
TNK2	chr3:197078437-197078526:-	0.33	cerebellum	0.67	HME	1.00	tyrosine kinase, non-receptor, 2 isoform 1,tyrosine k
SH3BP2	chr4:2803448-2803503:+	0.33	BT474	0.62	lymph node	0.95	SH3-domain binding protein 2,SH3-domain binding
C18orf1	chr18:13633358-13633411:+	0.33	brain	0.87	testes	0.55	hypothetical protein LOC753 isoform gamma 1,hyp
ARHGEF7,Nbla103	chr13:110655637-110655721:+	0.33	cerebellum	1.00	adipose	0.68	Rho guanine nucleotide exchange factor 7 isoform,
ZNF207	chr17:27721132-27721214:+	0.33	HME	1.00	T47D	0.68	zinc finger protein 207 isoform a,zinc finger protein
ABCD4,PMP69	chr14:73826483-73826574:-	0.33	cerebellum	0.68	BT474	1.00	ATP-binding cassette, sub-family D, member 4,Hom
S100A4	chr1:151784570-151784618:-	0.32	colon	0.40	heart	0.07	S100 calcium-binding protein A4
AK025296,FLJ2027	chr4:40133215-40133418:-	0.32	breast	1.00	colon	0.68	hypothetical protein LOC54502,hypothetical protein
UNC84A,KIAA0810	chr7:838668-838764:+	0.32	brain	1.00	colon	0.68	unc-84 homolog A,unc-84 homolog A,Homo sapien
UBXD5,RP11-569G	chr1:26501891-26501996:-	0.32	MB435	0.68	T47D	1.00	socius isoform 1,socius isoform 3,socius isoform 1,
LOC219854	chr11:124477238-124477423:-	0.32	cerebellum	1.00	T47D	0.68	hypothetical protein LOC219854,Homo sapiens cD
DPF2	chr11:64868627-64868668:+	0.32	cerebellum	0.68	skel. muscle	1.00	D4, zinc and double PHD fingers family 2,D4, zinc a
LOC554235	chr19:55707996-55708080:-	0.32	cerebellum	0.60	brain	0.93	hypothetical protein LOC554235
GLRB	chr4:158293320-158293612:+	0.32	cerebellum	0.68	brain	1.00	glycine receptor, beta
GCAT	chr22:36535980-36536110:+	0.32	MB435	0.68	T47D	1.00	glycine C-acetyltransferase precursor
RNF121	chr11:71345921-71345958:+	0.32	MCF7	0.68	skel. muscle	1.00	ring finger protein 121 isoform 1,ring finger protein 1
IFNAR2	chr21:33554772-33554902:+	0.32	MB435	1.00	lymph node	0.68	interferon alpha/beta receptor 2 isoform a,interferon
AX746969,G6PC3	chr17:39507863-39507981:+	0.32	cerebellum	1.00	skel. muscle	0.68	glucose-6-phosphatase catalytic subunit 3,Homo sa
KIAA0905,SEC31A	chr4:83982317-83982658:-	0.32	cerebellum	1.00	colon	0.68	SEC31 homolog A isoform 4,SEC31 homolog A iso
ATP2B2,ATP2B2 v	chr3:10395927-10395968:-	0.32	cerebellum	0.46	brain	0.14	plasma membrane calcium ATPase 2 isoform 1,pla
PAP2-a1,PPAP2A	chr5:54822545-54822699:-	0.32	adipose	0.02	skel. muscle	0.34	phosphatidic acid phosphatase type 2A isoform 2,H
SORBS1,KIAA1296	chr10:97144748-97144822:-	0.32	heart	0.68	skel. muscle	1.00	sorbin and SH3 domain containing 1 isoform 4,sorbi
R3HDM2,KIAA1002	chr12:55972622-55972717:-	0.32	breast	1.00	lymph node	0.68	R3H domain containing 2,R3H domain-containing p
CLDND1	chr3:99722667-99722971:-	0.32	cerebellum	1.00	heart	0.68	claudin domain containing 1 protein isoform a,claudi
DNAL4	chr22:37508614-37508821:-	0.32	MCF7	0.68	adipose	1.00	dynein light chain 4, axonemal
GBA2	chr9:35731669-35731887:-	0.32	breast	1.00	T47D	0.68	CDNA FLJ33048 fis, clone TRACH1000030, weakly
C14orf129,CR5970	chr14:95915778-95915878:+	0.32	MCF7	1.00	lymph node	0.68	hypothetical protein LOC51527,hypothetical protein
YY1AP1	chr1:153924486-153924616:-	0.32	cerebellum	1.00	BT474	0.68	YY1-associated protein isoform 3,YY1-associated p
DDEF1	chr8:131173401-131173571:-	0.32	breast	1.00	brain	0.68	development and differentiation enhancing factor,de
DKFZp666D023,GU	chr1:226402695-226402863:+	0.32	cerebellum	1.00	MB435	0.68	guanylate kinase 1,guanylate kinase 1,Homo sapie
TINAGL1	chr1:31815322-31815646:+	0.32	breast	1.00	T47D	0.68	P3ECSL,P3ECSL,
FMNL3,KIAA2014	chr12:48338492-48338644:-	0.32	MB435	0.62	adipose	0.94	formin-like 3 isoform 1,Homo sapiens mRNA for KI
HNRPD	chr4:83511705-83511761:-	0.32	liver	0.93	lymph node	0.61	heterogeneous nuclear ribonucleoprotein D,heterog
n/a	chr14:74482669-74482731:-	0.32	HME	0.68	testes	0.36	placental growth factor, vascular endothelial,placent
DKFZp666D023,GU	chr1:226402695-226402780:+	0.32	cerebellum	1.00	skel. muscle	0.68	guanylate kinase 1,guanylate kinase 1,Homo sapie
MXRA8,UNQ662	chr1:1280693-1280995:-	0.32	breast	1.00	skel. muscle	0.68	matrix-remodelling associated 8,matrix-remodelling
MPI	chr15:72976405-72976613:+	0.32	breast	1.00	lymph node	0.68	Mannose phosphate isomerase isoform.
UNP,USP4	chr3:49291251-49291339:-	0.32	breast	1.00	colon	0.68	ubiquitin specific protease, proto-oncogene,ubiquiti
IL32	chr16:3057556-3057615:+	0.32	liver	0.67	lymph node	0.35	interleukin 32 isoform A,interleukin 32 isoform B,inte
MON1A	chr3:49923963-49924448:-	0.32	cerebellum	1.00	adipose	0.68	CDNA FLJ34699 fis, clone MESAN2002186.
STOML1	chr15:72064053-72064265:-	0.32	adipose	1.00	testes	0.68	stomatin (EPB72)-like 1,stomatin (EPB72)-like 1,sto

TNK2	chr3:197093319-197093596:-	0.32	cerebellum	1.00	breast	0.68	tyrosine kinase, non-receptor, 2 isoform 1,tyrosine k
HSPH1	chr13:30615929-30616060:-	0.32	cerebellum	1.00	lymph node	0.68	heat shock 105kD,heat shock 105kD,heat shock 10
MAPT	chr17:41423081-41423278:+	0.32	T47D	0.32	brain	0.00	microtubule-associated protein tau isoform 1,microt
ILK	chr11:6585852-6586017:+	0.32	MB435	1.00	brain	0.68	integrin-linked kinase,integrin-linked kinase,integrin-
DGKA,DAGK1	chr12:54618562-54618611:+	0.32	HME	1.00	lymph node	0.68	diacylglycerol kinase, alpha 80kDa,diacylglycerol ki
ZNF207	chr17:27712600-27712647:+	0.32	BT474	1.00	testes	0.68	zinc finger protein 207 isoform a,zinc finger protein
KIAA0319L	chr1:35680434-35680524:-	0.32	cerebellum	1.00	brain	0.68	polycystic kidney disease 1-like isoform a,polycystic
ERG	chr21:38694366-38694437:-	0.32	adipose	0.68	lymph node	1.00	v-ets erythroblastosis virus E26 oncogene like,v-ets
FLJ10241	chr19:46634137-46634217:-	0.32	breast	1.00	MCF7	0.68	hypothetical protein LOC55101,hypothetical protein
R3HDM2,KIAA1002	chr12:55969059-55969090:-	0.32	MCF7	0.68	lymph node	1.00	R3H domain containing 2,R3H domain-containing p
UNP,USP4	chr3:49323951-49324091:-	0.32	cerebellum	0.77	HME	0.45	ubiquitin specific protease, proto-oncogene,ubiquiti
RBM5	chr3:50122816-50122900:+	0.32	cerebellum	0.68	MB435	1.00	RNA binding motif protein 5,RNA binding motif prote
LARP5	chr10:861005-861256:-	0.32	cerebellum	1.00	adipose	0.68	La ribonucleoprotein domain family, member 5
PPP2R4	chr9:130922613-130922710:+	0.32	cerebellum	1.00	adipose	0.68	protein phosphatase 2A, regulatory subunit B',Hom
ZNF202	chr11:123116035-123116454:-	0.32	MB435	0.68	testes	0.36	zinc finger protein 202,zinc finger protein 202,zinc fi
STOML1	chr15:72064053-72064262:-	0.32	brain	1.00	testes	0.68	stomatin (EPB72)-like 1,stomatin (EPB72)-like 1,sto
OATL1,TBC1D25	chrX:48288201-48288355:+	0.32	cerebellum	1.00	MB435	0.68	TBC1 domain family, member 25,OATL1 protein.,O
n/a	chr5:179155191-179155463:+	0.32	breast	0.68	colon	1.00	n/a
DKFZp762M186,PG	chr17:73922555-73922703:+	0.32	MCF7	1.00	adipose	0.68	phosphatidylglycerophosphate synthase 1,Hypothet
MASP1	chr3:188486307-188486538:-	0.32	colon	0.83	heart	0.52	mannan-binding lectin serine protease 1 isoform,ma
CHURC1	chr14:64462478-64462551:+	0.32	liver	0.69	testes	1.00	churchill domain containing 1,churchill domain conta
MKRN2	chr3:12585374-12585502:+	0.32	MB435	1.00	T47D	0.69	makorin, ring finger protein, 2,makorin, ring finger p
C21orf11,FAM3B	chr21:41616720-41616863:+	0.32	BT474	0.69	testes	1.00	family with sequence similarity 3, member B,family
FAM14B	chr14:93637913-93638158:+	0.32	MCF7	1.00	BT474	0.69	hypothetical protein LOC122509,hypothetical protei
SMRTE,NCOR2	chr12:123391101-123391250:-	0.32	breast	1.00	heart	0.69	nuclear receptor co-repressor 2 isoform 1,nuclear re
WARS	chr14:99905177-99905348:-	0.32	breast	1.00	MB435	0.69	tryptophanyl-tRNA synthetase isoform b,tryptophany
DAXX	chr6:33397474-33397732:-	0.32	breast	1.00	heart	0.69	death-associated protein 6,death-associated protein
KIAA0515	chr9:133311609-133311850:+	0.31	cerebellum	1.00	skel. muscle	0.69	Homo sapiens mRNA for KIAA0515 protein, partial
LRCH4,PP14183	chr7:100012645-100012948:-	0.31	cerebellum	1.00	heart	0.69	leucine-rich repeats and calponin homology (CH),le
DAP3	chr1:153953421-153953543:+	0.31	breast	0.69	BT474	1.00	death-associated protein 3,death-associated protein
SERPINA1	chr14:93924891-93925100:-	0.31	T47D	0.62	lymph node	0.93	serine (or cysteine) proteinase inhibitor, clade,serine
HSF1	chr8:145507122-145507205:+	0.31	BT474	0.39	colon	0.07	heat shock transcription factor 1,Homo sapiens hea
RP4-659I19.2	chr1:231172278-231172487:+	0.31	cerebellum	1.00	lymph node	0.69	hypothetical protein LOC84284
MGC3207	chr19:13737768-13737943:+	0.31	breast	1.00	MCF7	0.69	hypothetical protein LOC84245 isoform 2
SERF2,AK022435,	chr15:41871466-41871845:+	0.31	cerebellum	1.00	breast	0.69	Huntingtin interacting protein K,CDNA FLJ20431 fis,
C19orf46	chr19:41196086-41196164:-	0.31	colon	0.69	lymph node	1.00	hypothetical protein LOC163183,Homo sapiens cD
LTBP4	chr19:45814635-45814766:+	0.31	MCF7	1.00	adipose	0.69	latent transforming growth factor beta binding,latent
ZADH1	chr14:73415552-73415761:+	0.31	cerebellum	1.00	MCF7	0.69	zinc binding alcohol dehydrogenase, domain,zinc bi
SPTAN1	chr9:130430025-130430042:+	0.31	cerebellum	1.00	lymph node	0.69	Homo sapiens SPTAN1 mRNA for non-erythrocytic
USP52	chr12:54998288-54998485:-	0.31	MCF7	1.00	liver	0.69	ubiquitin specific protease 52,ubiquitin specific prote
ZNF384	chr12:6658090-6658137:-	0.31	colon	0.50	lymph node	0.19	nuclear matrix transcription factor 4 isoform a,nucle
TTC8	chr14:88411123-88411206:+	0.31	MCF7	0.69	BT474	1.00	tetratricopeptide repeat domain 8 isoform B,tetratric
KIAA1439,NFIA,AF	chr1:61664725-61664816:+	0.31	BT474	1.00	T47D	0.69	nuclear factor I/A,Nuclear factor 1 A-type (Nuclear f
CSAD	chr12:51851933-51852039:-	0.31	cerebellum	0.69	BT474	1.00	cysteine sulfinic acid decarboxylase-related,cysteine
RAB3IL1	chr11:61430514-61430732:-	0.31	breast	1.00	brain	0.69	RAB3A interacting protein (rabin3)-like 1
UBQLN1	chr9:85471085-85471168:-	0.31	cerebellum	1.00	testes	0.69	ubiquilin 1 isoform 1,ubiquilin 1 isoform 2,
CLTC	chr17:55119144-55119164:+	0.31	brain	0.31	liver	0.00	clathrin heavy chain 1,clathrin heavy chain 1,clathri
AZI1,KIAA1118	chr17:76781131-76781238:-	0.31	cerebellum	1.00	MB435	0.69	5-azacytidine induced 1 isoform a,5-azacytidine ind
UNQ572,GLT8D1	chr3:52713780-52714008:-	0.31	cerebellum	1.00	T47D	0.69	glycosyltransferase 8 domain containing 1,glycosylt
SNRPC	chr6:34833667-34833709:+	0.31	T47D	1.00	lymph node	0.69	small nuclear ribonucleoprotein polypeptide C
PPP1CA	chr11:66925115-66925246:-	0.31	cerebellum	0.69	heart	1.00	protein phosphatase 1, catalytic subunit, alpha,prote
APH1A,PSF	chr1:148506981-148507015:-	0.31	HME	0.69	MB435	1.00	anterior pharynx defective 1 homolog A isoform,ante
SHMT2	chr12:55911531-55911610:+	0.31	cerebellum	0.69	HME	1.00	serine hydroxymethyltransferase 2,Homo sapiens c
ZNF511	chr10:134973270-134973471:+	0.31	cerebellum	1.00	lymph node	0.69	Zinc finger protein 511.,Homo sapiens cDNA FLJ34
FKSG37,CHRDL2	chr11:74090285-74090339:-	0.31	colon	0.59	testes	0.90	chordin-like 2,Chordin-like protein 2 precursor (Chor
CNOT8	chr5:154222960-154223148:+	0.31	cerebellum	1.00	HME	0.69	CCR4-NOT transcription complex, subunit 8,CCR4-
WDR33	chr2:128187627-128188065:-	0.31	cerebellum	1.00	T47D	0.69	WD repeat domain 33 isoform 1,WD repeat domain
NFATC2IP	chr16:28873387-28873504:+	0.31	cerebellum	1.00	colon	0.69	nuclear factor of activated T-cells,,nuclear factor of
DCUN1D2	chr13:113186156-113186372:-	0.31	cerebellum	1.00	testes	0.69	DCN1, defective in cullin neddylation 1, domain,Hon
KIAA0864	chr17:16987595-16987708:+	0.31	breast	1.00	heart	0.69	myosin phosphatase-Rho interacting protein,myosin
LTBR	chr12:6367825-6367932:+	0.31	breast	1.00	lymph node	0.69	lymphotoxin beta receptor,lymphotoxin beta recepto
DKFZp434O158,VE	chr12:94142087-94142143:+	0.31	BT474	0.04	skel. muscle	0.35	transmembrane protein vezatin,transmembrane pro
ZRANB2	chr1:71303949-71304023:-	0.31	breast	0.54	colon	0.85	zinc finger protein 265 isoform 2,zinc finger protein
TSPAN15	chr10:70913453-70913638:+	0.31	cerebellum	1.00	skel. muscle	0.69	transmembrane 4 superfamily member 15
RAG1AP1,RP11-54	chr1:153375928-153376051:+	0.31	MB435	0.69	colon	1.00	stromal cell protein,Novel protein.,
CR626060	chr11:1726821-1726932:-	0.31	cerebellum	1.00	T47D	0.69	Homo sapiens similar to RIKEN cDNA 6330512M04
ZDHHC11,UNQ598	chr5:876504-877208:-	0.31	BT474	1.00	T47D	0.69	zinc finger, DHHC domain containing 11,Homo sapi
KIN27,PRKACA	chr19:14065440-14065604:-	0.31	cerebellum	1.00	MB435	0.69	cAMP-dependent protein kinase catalytic subunit,Pr
K-sam,FGFR2	chr10:123314942-123315208:-	0.31	cerebellum	0.69	T47D	1.00	fibroblast growth factor receptor 2 isoform 1,fibrobla
DDX42,DKFZp586A	chr17:59218126-59218362:+	0.31	cerebellum	1.00	breast	0.69	DEAD box polypeptide 42 protein,DEAD box polype
KIAA1186,MTP18	chr22:29153109-29153390:+	0.31	BT474	1.00	MB435	0.69	mitochondrial protein 18 kDa isoform a,mitochondri
STX3	chr11:59311086-59311185:+	0.31	BT474	1.00	MB435	0.69	syntaxin 3A
TRMT1	chr19:13081729-13081815:-	0.31	breast	1.00	testes	0.69	TRM1 tRNA methyltransferase 1,TRM1 tRNA methy
CNOT10	chr3:32753906-32753986:+	0.31	cerebellum	0.69	skel. muscle	1.00	CCR4-NOT transcription complex, subunit 10,CCR4
BCS1L	chr2:219233906-219234274:+	0.31	cerebellum	1.00	breast	0.69	BCS1-like,BCS1-like,BCS1-like,BCS1-like,BCS1-lik
GNPDA2	chr4:44418858-44419016:-	0.31	cerebellum	0.69	HME	1.00	glucosamine-6-phosphate deaminase 2,glucosamin
KIAA0319L	chr1:35744800-35745323:-	0.31	cerebellum	1.00	BT474	0.69	polycystic kidney disease 1-like isoform a,polycystic

LAT,SPIN1	chr16:28902608-28902779:+	0.31	cerebellum	1.00	HME	0.69	linker for activation of T cells isoform b,linker for acti
ANXA7	chr10:74830567-74830621:-	0.31	breast	1.00	BT474	0.69	annexin VII isoform 2,annexin VII isoform 1,annexin
SYT15	chr10:46389255-46389459:-	0.31	cerebellum	1.00	lymph node	0.69	synaptotagmin XV isoform a,synaptotagmin XV isof
C10orf104	chr10:73649818-73650143:+	0.31	T47D	0.52	testes	0.22	hypothetical protein LOC119504,hypothetical protei
HSKM-B	chr1:212545153-212545216:+	0.31	breast	0.69	BT474	1.00	Homo sapiens HSKM-B (HSKM-B) mRNA, complet
TEX264	chr3:51683327-51683618:+	0.31	cerebellum	1.00	liver	0.69	testis expressed sequence 264,testis expressed se
PKD1	chr16:2081425-2081599:-	0.31	cerebellum	1.00	colon	0.69	polycystin 1 isoform 1 precursor,polycystin 1 isoform
FAM63A	chr1:149241265-149241411:-	0.31	MCF7	0.69	T47D	1.00	hypothetical protein LOC55793 isoform 1,hypothetic
PIGS	chr17:23912567-23912774:-	0.31	MCF7	1.00	BT474	0.69	phosphatidylinositol glycan anchor biosynthesis,,GP
TMEM63B	chr6:44211043-44211081:+	0.31	MCF7	1.00	testes	0.69	transmembrane protein 63B,transmembrane protei
PRODH	chr22:17298503-17298711:-	0.31	cerebellum	0.69	BT474	1.00	proline dehydrogenase (oxidase) 1,proline dehydrog
RWDD1	chr6:117000714-117000841:+	0.31	cerebellum	0.32	adipose	0.01	RWD domain containing 1 isoform b,RWD domain
POU6F1	chr12:49876849-49876977:-	0.31	cerebellum	0.70	colon	1.00	POU domain, class 6, transcription factor 1,POU do
LRRC45	chr17:77580708-77580800:+	0.31	cerebellum	1.00	MB435	0.70	leucine rich repeat containing 45
SGCA	chr17:45599728-45599847:+	0.31	adipose	1.00	lymph node	0.70	sarcoglycan, alpha (50kDa dystrophin-associated,A
RNB6,EVL,AX7471	chr14:99673830-99673892:+	0.31	breast	1.00	brain	0.70	Enah/Vasp-like,Enah/Vasp-like,Homo sapiens RNB
SEZ6L2	chr16:29814081-29814282:-	0.31	MB435	0.57	T47D	0.88	seizure related 6 homolog (mouse)-like 2 isoform,se
C1orf50	chr1:43011821-43011907:+	0.31	cerebellum	0.70	HME	1.00	hypothetical protein LOC79078
AOF2	chr1:23243507-23243566:+	0.31	cerebellum	0.56	HME	0.87	amine oxidase (flavin containing) domain 2
NENF	chr1:210682530-210682590:+	0.30	cerebellum	0.70	HME	1.00	SCIRP10-related protein
DKFZp434D0516,W	chr14:23656021-23656093:+	0.30	BT474	0.70	liver	1.00	WD repeat domain 23 isoform 1,WD repeat domain
HCA58,AX746620,F	chr20:33950706-33950984:+	0.30	breast	1.00	testes	0.70	PHD finger protein 20,PHD finger protein 20,Homo
YIF1A	chr11:65809428-65809583:-	0.30	cerebellum	1.00	MCF7	0.70	Yip1 interacting factor homolog,Yip1 interacting fact
MGC71993,C17orf4	chr17:6860953-6861057:+	0.30	MCF7	1.00	heart	0.70	hypothetical protein LOC124944,hypothetical protei
DKFZp779G0129,S	chr2:182501133-182501250:+	0.30	MCF7	0.70	HME	1.00	sperm specific antigen 2,SSFA2 protein (Hypothetic
KIAA0955,CARD8	chr19:53444592-53444702:-	0.30	adipose	0.79	lymph node	0.48	caspase recruitment domain family, member 8,casp
ISOC2	chr19:60658815-60659024:-	0.30	MCF7	1.00	BT474	0.70	isochorismatase domain containing 2,Isochorismata
SF3B14	chr2:24150450-24150568:-	0.30	adipose	1.00	skel. muscle	0.70	splicing factor 3B, 14 kDa subunit
CD46,Y07713	chr1:206030221-206030313:+	0.30	BT474	0.01	HME	0.31	CD46 antigen, complement regulatory protein,CD46
CLP-36,PDLIM1	chr10:97021380-97021531:-	0.30	breast	0.70	MCF7	1.00	PDZ and LIM domain 1 (elfin),Homo sapiens mRNA
RBM35A	chr8:95774081-95774231:+	0.30	MCF7	0.60	BT474	0.91	RNA binding motif protein 35A isoform 1,RNA bindi
AF131776,CAMKB,	chr7:44245713-44245787:-	0.30	cerebellum	1.00	skel. muscle	0.70	calcium/calmodulin-dependent protein kinase IIB,ca
RAB7L1	chr1:204010584-204010837:-	0.30	cerebellum	1.00	breast	0.70	RAB7, member RAS oncogene family-like 1,RAB7,
USP48	chr1:21922978-21923175:-	0.30	cerebellum	1.00	HME	0.70	ubiquitin specific protease 48 isoform a,ubiquitin sp
CHD3	chr17:7751644-7751745:+	0.30	breast	1.00	MCF7	0.70	chromodomain helicase DNA binding protein 3,CHD
KIAA1582,TNRC6C	chr17:73605421-73605537:+	0.30	cerebellum	0.70	testes	1.00	trinucleotide repeat containing 6C,trinucleotide repe
CLUAP1,KIAA0643	chr16:3494721-3494832:+	0.30	cerebellum	1.00	lymph node	0.70	clusterin associated protein 1 isoform 1,clusterin as
DKFZp686E22155,	chr1:24618368-24618717:+	0.30	breast	1.00	MCF7	0.70	NIPA-like domain containing 3,Hypothetical protein
TNRC5,FLJ00338	chr6:43010094-43010314:+	0.30	cerebellum	1.00	HME	0.70	trinucleotide repeat containing 5 isoform 1,trinucleot
ATG16L1,FLJ1003	chr2:233838277-233838528:+	0.30	cerebellum	1.00	testes	0.70	APG16 autophagy 16-like isoform 1,APG16 autopha
EPB41L1	chr20:34225100-34225290:+	0.30	cerebellum	1.00	testes	0.70	erythrocyte membrane protein band 4.1-like 1,erythr
CD276	chr15:71778980-71779112:+	0.30	BT474	1.00	colon	0.70	CD276 antigen isoform b,CD276 antigen isoform b,
ATOX1	chr5:151111458-151111533:-	0.30	colon	1.00	lymph node	0.70	antioxidant protein 1
DKFZp564E0123,C	chr16:56032185-56032396:-	0.30	breast	1.00	T47D	0.70	cytokine induced apoptosis inhibitor 1,cytokine indu
GPR108	chr19:6686633-6686715:-	0.30	breast	0.70	HME	1.00	G protein-coupled receptor 108 isoform 1,G protein-
DKFZp313I142,FLJ	chr5:176890889-176891128:-	0.30	MCF7	1.00	HME	0.70	Homo sapiens mRNA for KIAA1931 protein, partial
PTK7,DKFZp434L0	chr6:43220916-43221148:+	0.30	cerebellum	1.00	MCF7	0.70	PTK7 protein tyrosine kinase 7 isoform a,PTK7 prot
NCOA7	chr6:126217859-126218079:+	0.30	cerebellum	1.00	HME	0.70	nuclear receptor coactivator 7,nuclear receptor coa
SFRS7,HSSG1	chr2:38829544-38829992:-	0.30	colon	0.02	lymph node	0.33	splicing factor, arginine/serine-rich 7,Homo sapiens
MFAP2	chr1:17176191-17176280:-	0.30	MB435	1.00	adipose	0.70	microfibrillar-associated protein 2 precursor,microfib
FKBP5,AIG6	chr6:35666885-35666975:-	0.30	HME	1.00	lymph node	0.70	FK506 binding protein 5,FK506 binding protein 5,Ho
KIAA0858,AK12345	chr13:75279617-75280336:+	0.30	brain	1.00	heart	0.70	LIM domain only 7,Homo sapiens mRNA for KIAA0
MRPL14	chr6:44192256-44192344:-	0.30	cerebellum	1.00	lymph node	0.70	mitochondrial ribosomal protein L14
PRNPIP	chr1:44486198-44486297:-	0.30	cerebellum	1.00	brain	0.70	prion protein interacting protein,Homo sapiens clon
TNK2	chr3:197078437-197078532:-	0.30	cerebellum	0.70	HME	1.00	tyrosine kinase, non-receptor, 2 isoform 1,tyrosine k
METTL1	chr12:56451144-56451307:-	0.30	MCF7	1.00	testes	0.70	methyltransferase-like protein 1 isoform c
SEH1L	chr18:12945462-12945608:+	0.30	BT474	1.00	testes	0.70	sec13-like protein isoform 1,sec13-like protein isofo
UBE2B	chr5:133751915-133752003:+	0.30	cerebellum	1.00	colon	0.70	ubiquitin-conjugating enzyme E2B
DKFZp586P1420,M	chr6:74239809-74240098:+	0.30	cerebellum	1.00	BT474	0.70	mitochondrial translation optimization 1 homolog,Ho
C7orf27	chr7:2551069-2551216:-	0.30	breast	1.00	BT474	0.70	HEAT repeat domain-containing protein C7orf27 pr
EEF1D	chr8:144739532-144739603:-	0.30	BT474	1.00	colon	0.70	eukaryotic translation elongation factor 1 delta,euka
RTEL1,TNFRSF6B	chr20:61791299-61791445:+	0.30	cerebellum	0.70	MCF7	1.00	regulator of telomere elongation helicase 1,regulato
USF2	chr19:40452546-40452746:+	0.30	heart	0.70	skel. muscle	1.00	upstream stimulatory factor 2 isoform 1,upstream st
EP300	chr22:39872689-39872766:+	0.30	HME	0.70	adipose	1.00	E1A binding protein p300
CHURC1	chr14:64462481-64462551:+	0.30	liver	0.70	skel. muscle	1.00	churchill domain containing 1,churchill domain conta
TUT1,FLJ00132	chr11:62105434-62105749:-	0.30	cerebellum	1.00	MCF7	0.70	RNA binding motif protein 21,Homo sapiens cDNA:
KIAA0905,SEC31A	chr4:83982362-83982658:-	0.30	cerebellum	1.00	colon	0.70	SEC31 homolog A isoform 4,SEC31 homolog A iso
PTOV1,ACID2,UN	chr19:55054158-55054245:+	0.30	brain	0.00	lymph node	0.30	prostate tumor overexpressed gene 1,prostate tum
n/a	chr19:55054158-55054245:-	0.30	brain	0.00	lymph node	0.30	n/a
AKR1A1	chr1:45790695-45790822:+	0.30	lymph node	0.13	testes	0.43	aldo-keto reductase family 1, member A1,aldo-keto
DCTN3	chr9:34606027-34606110:-	0.30	breast	1.00	brain	0.70	dynactin 3 isoform 2
C15orf24,ORF3	chr15:32175388-32175507:-	0.30	cerebellum	1.00	liver	0.70	chromosome 15 open reading frame 24,Homo sapi
WBP5	chrX:102498667-102498745:+	0.30	MB435	0.62	brain	0.92	WW domain binding protein 5,WW domain binding
ABHD12	chr20:25248835-25248954:-	0.30	cerebellum	0.70	MCF7	1.00	abhydrolase domain containing 12 isoform a,abhydr
FRAG1	chr11:3801689-3801941:+	0.30	cerebellum	1.00	skel. muscle	0.70	FGF receptor activating protein 1 isoform.,FGF rece
ASL	chr7:65184225-65184419:+	0.30	cerebellum	0.70	breast	1.00	argininosuccinate lyase isoform 1,argininosuccinate
ACLY	chr17:37306399-37306428:-	0.30	T47D	0.93	testes	0.64	ATP citrate lyase isoform 1,ATP citrate lyase isofor

TCF7L2	chr10:114910368-114910440:+	0.30	adipose	0.36	colon	0.06	transcription factor 7-like 2 (T-cell specific,,Transcrip
C17orf62,PP3439	chr17:78000596-78000645:-	0.30	colon	0.14	lymph node	0.43	hypothetical protein LOC79415,hypothetical protein
ZCCHC11	chr1:52719683-52719895:-	0.30	lymph node	1.00	testes	0.70	zinc finger, CCHC domain containing 11 isoform,zin
C2orf30	chr2:53888940-53889101:+	0.30	MB435	1.00	testes	0.70	chromosome 2 open reading frame 30,chromosome
n/a	chr9:138805899-138806050:+	0.30	BT474	0.70	heart	1.00	n/a
PICALM variant prot	chr11:85365314-85365373:-	0.30	cerebellum	1.00	lymph node	0.70	phosphatidylinositol-binding clathrin assembly,phos
P15RS	chr18:31867669-31867798:-	0.30	cerebellum	1.00	skel. muscle	0.70	hypothetical protein FLJ10656,P15RS protein.,hypo
C16orf57	chr16:56601334-56601517:+	0.30	breast	1.00	T47D	0.70	hypothetical protein LOC79650,Homo sapiens cDN
NCSTN	chr1:158593455-158593667:+	0.30	cerebellum	1.00	heart	0.70	Nicastrin precursor.,nicastrin precursor,
KIAA0494	chr1:46926612-46926803:-	0.30	MCF7	1.00	MB435	0.70	hypothetical protein LOC9813,hypothetical protein L
OPN3	chr1:239834345-239834504:-	0.30	BT474	0.84	brain	0.54	opsin 3 isoform 1,opsin 3 isoform 3,
KIAA0319L	chr1:35686361-35686520:-	0.30	cerebellum	1.00	lymph node	0.71	polycystic kidney disease 1-like isoform a,polycystic
DKFZp761E2216,Cl	chr7:150466163-150466333:+	0.30	breast	1.00	adipose	0.71	centaurin, gamma 3 isoform a,centaurin, gamma 3 i
n/a	chr2:66649686-66649781:+	0.30	cerebellum	1.00	testes	0.71	n/a
MCFD2	chr2:46988453-46988612:-	0.30	breast	1.00	lymph node	0.71	multiple coagulation factor deficiency 2,multiple coa
PSMD4	chr1:149501309-149501401:+	0.30	BT474	0.68	adipose	0.98	proteasome 26S non-ATPase subunit 4 isoform 2,p
MRPL52	chr14:22372467-22372538:+	0.29	cerebellum	1.00	lymph node	0.71	mitochondrial ribosomal protein L52 isoform a,mitoc
SERGEF	chr11:17937593-17937759:-	0.29	cerebellum	1.00	skel. muscle	0.71	deafness locus associated putative guanine,Secreti
KIAA0843,ABLIM3	chr5:148602247-148602294:+	0.29	cerebellum	1.00	colon	0.71	actin binding LIM protein family, member 3,actin bin
ERBB2IP	chr5:65406608-65406814:+	0.29	MCF7	1.00	brain	0.71	ERBB2 interacting protein isoform 2,ERBB2 interact
NMNAT3,FKSG76	chr3:140775130-140775212:-	0.29	breast	1.00	testes	0.71	nicotinamide nucleotide adenylyltransferase 3,Homo
EPS8L2	chr11:696674-696801:+	0.29	BT474	0.02	liver	0.32	epidermal growth factor receptor pathway,epiderma
FAM3A	chrX:153393832-153393929:-	0.29	MB435	0.08	testes	0.37	family 3, member A protein,Homo sapiens cDNA: F
FLJ00160	chrX:128986646-128987035:+	0.29	cerebellum	1.00	adipose	0.71	Homo sapiens cDNA FLJ11362 fis, clone HEMBA1
SHC1	chr1:153207304-153207357:-	0.29	cerebellum	0.71	BT474	1.00	SHC (Src homology 2 domain containing),SHC (Src
PILRB,FDFACT2	chr7:99789454-99789571:+	0.29	BT474	1.00	MB435	0.71	paired immunoglobulin-like type 2 receptor beta,Ho
DKFZp313I142,FLJ	chr5:176891560-176891738:-	0.29	cerebellum	0.71	MCF7	1.00	Homo sapiens mRNA for KIAA1931 protein, partial
PXMP3	chr8:78060978-78061087:-	0.29	BT474	0.71	heart	1.00	peroxin 2,peroxin 2,peroxin 2,
ARHGAP1	chr11:46660177-46660308:-	0.29	cerebellum	1.00	heart	0.71	Rho GTPase activating protein 1
TSPAN9	chr12:3063080-3063146:+	0.29	adipose	0.95	colon	0.66	tetraspanin 9
YTHDF2	chr1:28941502-28943085:+	0.29	cerebellum	1.00	liver	0.71	high glucose-regulated protein 8,high glucose-regul
POLR3H,dJ347H13	chr22:40266649-40266745:-	0.29	cerebellum	1.00	brain	0.71	polymerase (RNA) III (DNA directed) polypeptide,po
GLTSCR1,BC0320	chr19:52877045-52877221:+	0.29	adipose	1.00	skel. muscle	0.71	glioma tumor suppressor candidate region gene 1,H
RBM34	chr1:233390449-233390585:-	0.29	BT474	0.71	MB435	1.00	RNA binding motif protein 34,Homo sapiens mRNA;
ANKS3,KIAA1977	chr16:4716981-4717179:-	0.29	colon	0.71	lymph node	1.00	ankyrin repeat and sterile alpha motif domain,ANKS
PAPOLA	chr14:96098909-96098983:+	0.29	MB435	1.00	lymph node	0.71	poly(A) polymerase alpha,poly(A) polymerase alpha
TMEM98	chr17:28282458-28282533:+	0.29	breast	1.00	MB435	0.71	hypothetical protein LOC26022,hypothetical protein
AKAP1	chr17:52540306-52540408:+	0.29	colon	0.00	testes	0.29	Homo sapiens unknown protein mRNA, partial cds.
MGC3207	chr19:13737768-13737879:+	0.29	MCF7	0.71	lymph node	1.00	hypothetical protein LOC84245 isoform 2
DKFZp434L0130	chr10:32183000-32183140:-	0.29	cerebellum	0.78	MB435	0.49	Rho GTPase activating protein 12,Rho GTPase acti
ARHGAP4	chrX:152828819-152829052:-	0.29	cerebellum	0.71	breast	1.00	Rho GTPase activating protein 4,Rho GTPase activ
AP3D1	chr19:2063859-2064412:-	0.29	cerebellum	1.00	heart	0.71	adaptor-related protein complex 3, delta 1,adaptor-
STXBP1	chr9:129486468-129486593:+	0.29	cerebellum	0.29	MB435	0.00	syntaxin binding protein 1 isoform a,syntaxin binding
UBE1C	chr3:69211953-69211994:-	0.29	BT474	0.71	brain	1.00	ubiquitin-activating enzyme E1C isoform 1,ubiquitin-
AAAS	chr12:51994802-51994900:-	0.29	breast	0.71	MCF7	1.00	achalasia, adrenocortical insufficiency,,achalasia, a
ADNP	chr20:48978595-48978769:-	0.29	BT474	1.00	HME	0.71	activity-dependent neuroprotector,activity-dependen
QDPR	chr4:17102953-17103061:-	0.29	cerebellum	1.00	liver	0.71	quinoid dihydropteridine reductase,Homo sapiens c
mm-1,PFDN5	chr12:51975890-51976326:+	0.29	MB435	0.71	heart	1.00	prefoldin subunit 5 isoform gamma,Homo sapiens m
KIAA0428,MBNL1	chr3:153633196-153633399:+	0.29	MCF7	1.00	BT474	0.71	muscleblind-like 1 isoform e,muscleblind-like 1 isofo
FMO3	chr1:169349771-169350126:+	0.29	adipose	0.71	liver	1.00	flavin containing monooxygenase 3 isoform 1,flavin
CLDND1	chr3:99722667-99722976:-	0.29	cerebellum	1.00	heart	0.71	claudin domain containing 1 protein isoform a,claudi
AK097119,KNS2	chr14:103223171-103223301:+	0.29	adipose	0.63	testes	0.92	Homo sapiens kinesin light chain 1S (KNS2) mRNA
HTATIP	chr11:65237395-65237550:+	0.29	colon	0.73	testes	0.44	HIV-1 Tat interactive protein, 60kDa isoform 2,HIV-1
ASRGL1	chr11:61915843-61915982:+	0.29	cerebellum	0.31	testes	0.03	asparaginase-like 1 protein,asparaginase-like 1 prot
CHID1	chr11:898542-898645:-	0.29	breast	0.20	HME	0.49	chitinase domain containing 1,chitinase domain con
PCYT2	chr17:77460044-77460489:-	0.29	cerebellum	1.00	colon	0.71	phosphate cytidylyltransferase 2, ethanolamine,Hom
NDUFA8	chr9:123954345-123954508:-	0.29	breast	0.71	brain	1.00	NADH dehydrogenase (ubiquinone) 1 alpha
HERPUD2	chr7:35641270-35641593:-	0.29	cerebellum	0.71	breast	1.00	HERPUD family member 2,HERPUD family membe
DEDD2	chr19:47412672-47413037:-	0.29	cerebellum	1.00	adipose	0.71	death effector domain-containing DNA binding,Hom
hSSH-3,SSH3	chr11:66831596-66831784:+	0.29	cerebellum	1.00	MCF7	0.71	slingshot homolog 3,Homo sapiens mRNA for hSSH
FLJ00100,FLJ0000	chr7:100294608-100294719:+	0.29	cerebellum	1.00	lymph node	0.71	solute carrier family 12 (potassium/chloride,FLJ0001
derp10,COPS7A	chr12:6707353-6707428:+	0.29	HME	1.00	lymph node	0.71	COP9 complex subunit 7a,COP9 complex subunit 7
TMPIT	chr7:75454792-75454856:-	0.29	breast	1.00	testes	0.71	transmembrane protein induced by tumor necrosis,
SNAP91	chr6:84358893-84358976:-	0.29	cerebellum	0.71	brain	1.00	Clathrin coat assembly protein AP180 (Clathrin coat
ASRGL1	chr11:61880373-61880515:+	0.29	cerebellum	0.71	brain	1.00	asparaginase-like 1 protein,asparaginase-like 1 prot
POLR3H,dJ347H13	chr22:40258609-40258695:-	0.29	cerebellum	0.71	breast	1.00	polymerase (RNA) III (DNA directed) polypeptide,po
GUSB	chr7:65081821-65081963:-	0.29	cerebellum	0.71	MCF7	1.00	glucuronidase, beta
LOC197322	chr16:87692500-87692672:+	0.29	MCF7	0.71	testes	1.00	hypothetical protein LOC197322,Homo sapiens cD
DKFZp434C191,CH	chr8:23162668-23162839:+	0.29	cerebellum	1.00	MCF7	0.71	CHMP family, member 7,Homo sapiens cDNA FLJ1
KIAA1341,MYEF2	chr15:46230589-46230660:-	0.29	cerebellum	0.13	testes	0.42	myelin gene expression factor 2,Homo sapiens mR
SYNJ2	chr6:158369776-158370046:+	0.29	MCF7	1.00	BT474	0.72	synaptojanin 2,synaptojanin 2,synaptojanin 2,synap
n/a	chr12:120231887-120232049:+	0.29	cerebellum	1.00	lymph node	0.72	n/a
TARS	chr5:33484404-33484594:+	0.29	cerebellum	0.72	breast	1.00	threonyl-tRNA synthetase,Homo sapiens cDNA FLJ
AK026621,TSPAN1	chr10:82259037-82259207:+	0.29	breast	1.00	MCF7	0.72	tetraspanin 14,tetraspanin 14,Homo sapiens cDNA:
MAOB	chrX:43583058-43583195:-	0.28	cerebellum	1.00	skel. muscle	0.72	amine oxidase (flavin-containing)
LBR	chr1:223664616-223664741:-	0.28	BT474	1.00	colon	0.72	lamin B receptor,lamin B receptor,
TETRAN	chr4:2903080-2903188:-	0.28	T47D	1.00	adipose	0.72	tetracycline transporter-like protein,Homo sapiens te

APH1A,PSF	chr1:148506981-148507151:-	0.28	cerebellum	1.00	HME	0.72	anterior pharynx defective 1 homolog A isoform,ante
L26953,CSNK1A1	chr5:148877550-148877633:-	0.28	cerebellum	1.00	skel. muscle	0.72	casein kinase 1, alpha 1 isoform 1,casein kinase 1,
TMLHE	chrX:154427951-154428132:-	0.28	MCF7	1.00	HME	0.72	Trimethyllysine dioxygenase, mitochondrial precurso
PTK2,DKFZp666O0	chr8:141958752-141958918:-	0.28	T47D	0.72	adipose	1.00	PTK2 protein tyrosine kinase 2 isoform b,PTK2 prot
DCTN3	chr9:34604039-34604195:-	0.28	cerebellum	1.00	adipose	0.72	dynactin 3 isoform 2
Kid,CR592785,KIF2	chr16:29722221-29722430:+	0.28	MCF7	1.00	BT474	0.72	kinesin family member 22,Homo sapiens mRNA for
n/a	chr4:174688526-174688804:+	0.28	colon	1.00	heart	0.72	n/a
FHL3	chr1:38236222-38236391:-	0.28	breast	1.00	MCF7	0.72	four and a half LIM domains 3,four and a half LIM do
MAPT	chr17:41443513-41443605:+	0.28	brain	0.54	skel. muscle	0.83	microtubule-associated protein tau isoform 1,microtu
LGTN	chr1:204839440-204839589:-	0.28	breast	1.00	heart	0.72	ligatin
RCP9	chr7:65230126-65230162:+	0.28	HME	1.00	adipose	0.72	calcitonin gene-related peptide-receptor,calcitonin g
EHMT1,KIAA1876	chr9:139725240-139725303:+	0.28	MCF7	1.00	lymph node	0.72	euchromatic histone methyltransferase 1,Homo sap
MTMR14	chr3:9706648-9706827:+	0.28	BT474	1.00	lymph node	0.72	jumpy isoform 2,jumpy isoform 1,jumpy isoform 3,ju
ZNF462,RP11-508	chr9:108741018-108741209:+	0.28	MB435	0.72	testes	1.00	zinc finger protein 462,zinc finger protein 462,OTTH
MGC10334	chr1:1252079-1252275:+	0.28	cerebellum	1.00	BT474	0.72	hypothetical protein LOC80772
TCIRG1,TIRC7	chr11:67574530-67574707:+	0.28	breast	1.00	HME	0.72	T-cell, immune regulator 1 isoform a,T-cell, immune
SLC41A3	chr3:127252476-127252583:-	0.28	breast	1.00	lymph node	0.72	solute carrier family 41, member 3 isoform 1,solute
MRVI1,AK002039	chr11:10604089-10604706:-	0.28	adipose	1.00	brain	0.72	JAW1-related protein isoform b,JAW1-related protei
TBL1X	chrX:9581585-9581729:+	0.28	MCF7	0.72	testes	1.00	transducin beta-like 1X,transducin beta-like 1X,trans
PIGF	chr2:46695580-46695828:-	0.28	HME	0.72	MB435	1.00	phosphatidylinositol glycan, class F isoform 1
HNRPR	chr1:23532598-23532711:-	0.28	cerebellum	1.00	heart	0.72	heterogeneous nuclear ribonucleoprotein R,heterog
GRHPR	chr9:37414842-37414983:+	0.28	cerebellum	1.00	brain	0.72	Homo sapiens MSTP035 mRNA, complete cds.,CD
FLJ20186	chr16:88548198-88548285:+	0.28	cerebellum	0.72	adipose	1.00	differentially expressed in FDCP 8 isoform 1,differen
n/a	chr18:75780172-75780388:-	0.28	cerebellum	1.00	T47D	0.72	n/a
PFDN1,AX748200	chr5:139660185-139660351:-	0.28	BT474	1.00	liver	0.72	prefoldin subunit 1,Homo sapiens mRNA for prefold
DKFZp686E14208	chr1:46799737-46799901:-	0.28	MCF7	1.00	testes	0.72	Hypothetical protein DKFZp686E14208 (MAP kinas
NUB1	chr7:150702116-150702220:+	0.28	cerebellum	1.00	lymph node	0.72	NEDD8 ultimate buster-1,NEDD8 ultimate buster-1,
RHOC	chr1:113049245-113049268:-	0.28	breast	0.35	lymph node	0.07	ras homolog gene family, member C precursor,ras
BCAP29,AK000878	chr7:107008327-107008545:+	0.28	cerebellum	1.00	BT474	0.72	B-cell receptor-associated protein BAP29 isoform,H
TMEM57	chr1:25655731-25655909:+	0.28	liver	0.72	skel. muscle	1.00	transmembrane protein 57
PPP4C,PPX	chr16:30001568-30001669:+	0.28	breast	0.72	colon	1.00	protein phosphatase 4 (formerly X), catalytic,Homo
DNALI1	chr1:37797515-37799923:+	0.28	cerebellum	1.00	T47D	0.72	dynein, axonemal, light intermediate chain 1
FPGS	chr9:129610658-129610805:+	0.28	cerebellum	0.72	breast	1.00	folylpolyglutamate synthase isoform a precursor,foly
SLC26A10	chr12:56294566-56294655:+	0.28	brain	0.72	colon	1.00	RAC/CDC42 exchange factor isoform 2,RAC/CDC4
UCC1,EPDR1	chr7:37954967-37955175:+	0.28	cerebellum	0.72	breast	1.00	ependymin related protein 1 precursor,Homo sapien
MYH11,KIAA0866	chr16:15710161-15710199:-	0.28	colon	0.91	testes	0.63	smooth muscle myosin heavy chain 11 isoform,smo
HIF3A,HIF-3A4	chr19:51500342-51500487:+	0.28	adipose	0.72	colon	1.00	hypoxia-inducible factor-3 alpha isoform c,hypoxia-i
OATP-E,SLCO4A1	chr20:60769809-60769981:+	0.28	MB435	0.72	adipose	1.00	solute carrier organic anion transporter family,Homo
ECHDC2	chr1:53135697-53135744:-	0.28	breast	1.00	testes	0.72	enoyl Coenzyme A hydratase domain containing 2
ZDHHC16	chr10:99203546-99203593:+	0.28	HME	1.00	lymph node	0.72	Abl-philin 2 isoform 2,Abl-philin 2 isoform 2,
HDAC11	chr3:13517213-13517289:+	0.28	MCF7	0.72	colon	1.00	histone deacetylase 11,histone deacetylase 11,
KIAA0556	chr16:27658863-27659742:+	0.28	cerebellum	1.00	BT474	0.72	CDNA FLJ40166 fis, clone TESTI2016197.
GSK3B	chr3:121044792-121044890:-	0.28	cerebellum	0.72	MCF7	1.00	glycogen synthase kinase 3 beta,Homo sapiens gly
ORMDL2	chr12:54499142-54499224:+	0.28	MCF7	0.72	T47D	1.00	ORMDL2
NCK2	chr2:105864216-105864937:+	0.28	heart	0.72	liver	1.00	NCK adaptor protein 2 isoform A,NCK adaptor prote
AK026365,C1orf71	chr1:244821437-244821866:+	0.28	cerebellum	1.00	BT474	0.72	hypothetical protein LOC163882,Homo sapiens cD
COPZ1	chr12:53020514-53020666:+	0.28	cerebellum	0.97	lymph node	0.69	coatomer protein complex, subunit zeta 1,Homo sa
GRIN1,hNMDAR1-3	chr9:139162425-139162487:+	0.28	cerebellum	0.83	brain	0.55	NMDA receptor 1 isoform NR1-3 precursor,NMDA r
RBM38	chr20:55401741-55401795:+	0.28	adipose	0.94	colon	0.66	RNA-binding region containing protein 1 isoform,RN
EML2,DKFZp564P0	chr19:50821803-50821937:-	0.28	cerebellum	1.00	MCF7	0.72	echinoderm microtubule associated protein like,Ho
DKFZp686E14208	chr1:46818789-46818886:-	0.28	cerebellum	1.00	MB435	0.72	Hypothetical protein DKFZp686E14208 (MAP kinas
C14orf172	chr14:103066040-103066399:+	0.28	cerebellum	1.00	lymph node	0.72	hypothetical protein LOC115708
MTERFD2	chr2:241685331-241685515:-	0.28	cerebellum	1.00	testes	0.72	MTERF domain containing 2,MTERF domain contai
AKT2	chr19:45434004-45434132:-	0.28	breast	1.00	HME	0.72	v-akt murine thymoma viral oncogene homolog 2
TCEAL8	chrX:102396189-102396261:-	0.28	cerebellum	1.00	colon	0.72	transcription elongation factor A (SII)-like 8,transcrip
TUFT1	chr1:149801191-149801265:+	0.28	BT474	0.52	MB435	0.24	tuftelin 1,tuftelin 1,
n/a	chr22:20987469-20987662:+	0.28	cerebellum	1.00	HME	0.72	n/a
NQO1	chr16:68306368-68306481:-	0.28	breast	1.00	T47D	0.72	NAD(P)H menadione oxidoreductase 1,,NAD(P)H m
HCDI,C14orf124	chr14:23980720-23980841:-	0.28	cerebellum	1.00	lymph node	0.72	hypothetical protein LOC56948,hypothetical protein
PSMA4	chr15:76621880-76622042:+	0.28	MCF7	1.00	colon	0.72	proteasome alpha 4 subunit,PSMA4 protein.,PSMA
MFSD3	chr8:145706551-145706698:+	0.28	breast	1.00	MCF7	0.72	major facilitator superfamily domain containing
NEXN	chr1:78155839-78156030:+	0.28	breast	0.72	heart	1.00	nexilin (F actin binding protein),Nexilin.,Homo sapie
KIAA1186,MTP18	chr22:29153227-29153390:+	0.28	MB435	0.72	colon	1.00	mitochondrial protein 18 kDa isoform a,mitochondri
LIG3	chr17:30334134-30334684:+	0.28	cerebellum	1.00	MB435	0.72	ligase III, DNA, ATP-dependent isoform beta,ligase
KIAA1186,MTP18	chr22:29153158-29153390:+	0.28	BT474	1.00	MB435	0.72	mitochondrial protein 18 kDa isoform a,mitochondri
C2,DKFZp779M031	chr6:32003711-32003920:+	0.28	breast	1.00	lymph node	0.73	complement component 2 precursor,complement c
LIG,HIP2	chr4:39433672-39433754:+	0.28	HME	1.00	lymph node	0.73	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.
NT5C3L	chr17:37237204-37237404:-	0.28	breast	1.00	skel. muscle	0.73	5'-nucleotidase, cytosolic III-like,Homo sapiens 5'-nu
CLDND1	chr3:99723187-99723230:-	0.28	MCF7	0.00	brain	0.28	claudin domain containing 1 protein isoform a,claudi
ILKAP	chr2:238758561-238758667:-	0.28	cerebellum	1.00	lymph node	0.73	integrin-linked kinase-associated protein,integrin-lin
MFNG	chr22:36198427-36198512:-	0.28	adipose	0.73	lymph node	1.00	O-fucosylpeptide,Homo sapiens cDNA clone IMAG
GPS1	chr17:77603421-77603607:+	0.28	HME	0.03	testes	0.30	G protein pathway suppressor 1 isoform 2,G protein
SURF2	chr9:135216647-135216826:+	0.27	breast	1.00	heart	0.73	surfeit 2
BMF	chr15:38183673-38183833:-	0.27	BT474	0.73	lymph node	1.00	Bcl2 modifying factor isoform bmf-1,Bcl2 modifying
CAMKK2,KIAA0787	chr12:120196242-120196771:-	0.27	MCF7	1.00	MB435	0.73	calcium/calmodulin-dependent protein kinase,calciu
GPATCH4	chr1:154834451-154834537:-	0.27	MCF7	1.00	skel. muscle	0.73	G patch domain containing 4 isoform 2,G patch dom
GMFG	chr19:44517741-44517790:-	0.27	colon	1.00	lymph node	0.73	glia maturation factor, gamma,glia maturation factor

KCTD17	chr22:35786809-35786908:+	0.27	HME	1.00	brain	0.73	potassium channel tetramerisation domain,potassiu
NOL3	chr16:65765566-65765858:+	0.27	cerebellum	1.00	adipose	0.73	nucleolar protein 3,Nucleolar protein 3 (Apoptosis re
FLJ10081,KIAA131	chr2:96631580-96631802:-	0.27	cerebellum	1.00	colon	0.73	hypothetical protein LOC55683,hypothetical protein
NOL3	chr16:65765566-65765868:+	0.27	cerebellum	1.00	adipose	0.73	nucleolar protein 3,Nucleolar protein 3 (Apoptosis re
BCL2L12	chr19:54862088-54862230:+	0.27	MCF7	1.00	testes	0.73	BCL2-like 12 isoform 1,BCL2-like 12 isoform 3,
PHGDHL1	chr13:98651684-98651822:+	0.27	adipose	0.03	testes	0.30	CDNA PSEC0110 fis, clone PLACE1010021, highly
SH3TC1,FLJ00164	chr4:8269584-8269794:+	0.27	adipose	0.46	lymph node	0.73	SH3 domain and tetratricopeptide repeats 1,SH3 do
EMP3	chr19:53522590-53522630:+	0.27	MB435	0.56	lymph node	0.29	epithelial membrane protein 3
RP5-890O3.8-016,	chr1:1237683-1237744:-	0.27	HME	1.00	lymph node	0.73	Novel protein (Fragment).,Homo sapiens cDNA FLJ
SLC19A1	chr21:45782109-45782350:-	0.27	MCF7	1.00	T47D	0.73	solute carrier family 19 member 1,SLC19A1 protein.
AX747565,PEF1	chr1:31873410-31873710:-	0.27	cerebellum	1.00	testes	0.73	penta-EF hand domain containing 1,penta-EF hand
KIAA0101	chr15:62455995-62456157:-	0.27	BT474	0.73	MB435	1.00	hypothetical protein LOC9768 isoform 1,hypothetica
RNPEP	chr1:200233070-200233305:+	0.27	cerebellum	0.73	breast	1.00	arginyl aminopeptidase (aminopeptidase B),Homo s
FRAG1	chr11:3789056-3789230:+	0.27	HME	1.00	MB435	0.73	FGF receptor activating protein 1 isoform.,FGF rece
YBX1	chr1:42934457-42934546:+	0.27	BT474	1.00	skel. muscle	0.73	nuclease sensitive element binding protein 1
EFNA1	chr1:153372603-153372668:+	0.27	BT474	0.73	adipose	1.00	ephrin A1 isoform a precursor,ephrin A1 isoform b p
LOC150223	chr22:20313299-20313476:-	0.27	MCF7	1.00	adipose	0.73	hypothetical protein LOC150223,Homo sapiens hyp
DAP3	chr1:153965457-153965537:+	0.27	HME	1.00	T47D	0.73	death-associated protein 3,death-associated protein
AGPAT2	chr9:138690858-138690953:-	0.27	heart	1.00	skel. muscle	0.73	1-acylglycerol-3-phosphate O-acyltransferase 2,1-a
FN5,C11orf75	chr11:92872090-92872162:-	0.27	liver	1.00	lymph node	0.73	hypothetical protein LOC56935,Homo sapiens FN5
MGC16824,DKFZp	chr16:19569205-19569282:+	0.27	cerebellum	1.00	brain	0.73	hypothetical protein LOC57020,hypothetical protein
LRRFIP1	chr2:238332111-238332203:+	0.27	heart	1.00	skel. muscle	0.73	leucine rich repeat (in FLII) interacting,leucine rich r
RABGAP1,DKFZp5	chr9:124759111-124759309:+	0.27	cerebellum	0.73	adipose	1.00	CDNA FLJ12346 fis, clone MAMMA1002297, highly
EIF5	chr14:102870479-102870687:+	0.27	cerebellum	1.00	lymph node	0.73	eukaryotic translation initiation factor 5,eukaryotic tr
AIP	chr11:67011053-67011232:+	0.27	cerebellum	1.00	liver	0.73	aryl hydrocarbon receptor interacting protein
ZC3HC1	chr7:129451339-129451582:-	0.27	cerebellum	1.00	lymph node	0.73	zinc finger, C3HC type 1,zinc finger, C3HC type 1,
PHKA2	chrX:18879143-18879311:-	0.27	cerebellum	1.00	MB435	0.73	phosphorylase kinase, alpha 2 (liver),phosphorylase
PCBP3	chr21:46158293-46158436:+	0.27	cerebellum	0.69	testes	0.42	poly(rC) binding protein 3,poly(rC) binding protein 3,
AK124433,MAGI1	chr3:65336460-65336627:-	0.27	cerebellum	0.72	breast	0.45	membrane associated guanylate kinase, WW and
UCK2	chr1:164139043-164139140:+	0.27	cerebellum	0.73	MCF7	1.00	uridine-cytidine kinase 2
SLC29A2	chr11:65892584-65892718:-	0.27	MCF7	0.73	BT474	1.00	solute carrier family 29 (nucleoside,solute carrier fa
LRRFIP1	chr2:238324582-238324653:+	0.27	heart	0.73	skel. muscle	1.00	leucine rich repeat (in FLII) interacting,leucine rich r
RENBP	chrX:152860597-152860678:-	0.27	cerebellum	1.00	lymph node	0.73	renin binding protein
CLDND1	chr3:99723187-99723237:-	0.27	brain	0.27	colon	0.00	claudin domain containing 1 protein isoform a,claud
METAP2	chr12:94403786-94403888:+	0.27	cerebellum	1.00	lymph node	0.73	methionyl aminopeptidase 2,methionyl aminopeptid
IMPDH2	chr3:49040685-49040759:-	0.27	MCF7	0.73	BT474	1.00	inosine monophosphate dehydrogenase 2
HCR,CCHCR1	chr6:31230252-31230555:-	0.27	cerebellum	1.00	testes	0.73	StAR-binding protein,Homo sapiens HCR (a-helix c
GTF3A	chr13:26898391-26898478:+	0.27	lymph node	0.01	skel. muscle	0.28	Homo sapiens cDNA FLJ25264 fis, clone STM0505
CHD5,KIAA0444	chr1:6089042-6089156:-	0.27	cerebellum	0.74	testes	0.47	chromodomain helicase DNA binding protein 5,Hom
NECAP2	chr1:16654900-16654975:+	0.27	breast	1.00	MCF7	0.73	adaptin-ear-binding coat-associated protein 2,adapt
KIAA1597,SYTL2	chr11:85106174-85106221:-	0.27	MCF7	0.48	MB435	0.75	synaptotagmin-like 2 isoform c,synaptotagmin-like 2
hasc-1,SLC7A10	chr19:38398515-38398719:-	0.27	adipose	0.73	testes	1.00	solute carrier family 7, member 10,CDNA FLJ20839
AK094678,BC0489	chr11:763522-763629:-	0.27	breast	1.00	MCF7	0.73	Parkinson disease 7 domain containing 1,PDDC1 p
NAGK,N-Acetylgluc	chr2:71151140-71151224:+	0.27	cerebellum	0.73	HME	1.00	N-Acetylglucosamine kinase,Homo sapiens mRNA
MGAT1	chr5:180168254-180168682:-	0.27	cerebellum	1.00	adipose	0.73	mannosyl (alpha-1,3-)-glycoprotein,mannosyl (alpha
KIF1A,KIF1A varian	chr2:241345409-241345684:-	0.27	cerebellum	0.10	BT474	0.37	axonal transport of synaptic vesicles,Homo sapiens
IL13RA1	chrX:117764945-117765083:+	0.27	MCF7	1.00	adipose	0.73	interleukin 13 receptor, alpha 1 precursor,interleuki
RPUSD3	chr3:9860149-9860285:-	0.27	cerebellum	1.00	MCF7	0.73	RNA pseudouridylate synthase domain containing,
RABEP2	chr16:28843225-28843437:-	0.27	cerebellum	1.00	heart	0.73	rabaptin, RAB GTPase binding effector protein 2,ra
CCAR1	chr10:70152218-70152340:+	0.27	cerebellum	1.00	HME	0.73	cell-cycle and apoptosis regulatory protein 1,Homo
KIAA1813,LZTS2	chr10:102753254-102753913:+	0.27	cerebellum	1.00	lymph node	0.73	leucine zipper, putative tumor suppressor 2,Homo s
DKFZp564N1363	chr20:34288218-34288302:+	0.27	T47D	0.28	adipose	0.01	hypothetical protein LOC25980,hypothetical protein
SH2B,SH2B1	chr16:28784834-28785855:+	0.27	cerebellum	1.00	MCF7	0.73	SH2-B gamma signaling protein.,SH2 domain-conta
DOM3Z	chr6:32047076-32047437:-	0.27	breast	1.00	colon	0.73	DOM-3 homolog Z,Protein Dom3Z (Dom-3 homolog
CASK	chrX:41299797-41299832:-	0.27	adipose	1.00	lymph node	0.73	calcium/calmodulin-dependent serine protein,calciu
PICALM variant prot	chr11:85366761-85366784:-	0.27	MCF7	1.00	MB435	0.73	phosphatidylinositol-binding clathrin assembly,phos
MTMR14	chr3:9694668-9694742:+	0.27	MCF7	1.00	MB435	0.73	jumpy isoform 2,jumpy isoform 1,jumpy isoform 3,ju
LPHN1	chr19:14132405-14132508:-	0.27	cerebellum	1.00	MB435	0.73	latrophilin 1 isoform 1 precursor,latrophilin 1 isoform
RASSF3	chr12:63368263-63368500:+	0.27	breast	1.00	MB435	0.73	Ras association (RalGDS/AF-6) domain family 3,Ra
hNedd5,SEPT2	chr2:241914087-241914201:+	0.27	cerebellum	1.00	BT474	0.73	septin 2,septin 2,septin 2,septin 2,septin 2,Homo sa
CDCA3	chr12:6830258-6830434:-	0.27	MCF7	0.73	HME	1.00	trigger of mitotic entry 1,Homo sapiens cDNA FLJ34
CAMTA2	chr17:4826108-4826179:-	0.27	breast	1.00	MB435	0.73	calmodulin binding transcription activator 2,calmodu
MTMR14	chr3:9714395-9714550:+	0.27	lymph node	0.73	skel. muscle	1.00	jumpy isoform 2,jumpy isoform 1,jumpy isoform 3,ju
TARBP2	chr12:52182071-52182235:+	0.27	HME	1.00	adipose	0.73	TAR RNA binding protein 2 isoform b,TAR RNA bin
ATP2C1	chr3:132096124-132096309:+	0.27	cerebellum	1.00	T47D	0.73	calcium-transporting ATPase 2C1 isoform 1c,calciu
CDC42SE2	chr5:130679568-130679736:+	0.27	MCF7	1.00	T47D	0.73	CDC42 small effector 2,CDC42 small effector 2,CD
STAT1	chr2:191586496-191586649:-	0.27	MCF7	1.00	MB435	0.73	signal transducer and activator of transcription,sign
MXI1	chr10:111994576-111994621:+	0.27	brain	1.00	skel. muscle	0.73	MAX interactor 1 isoform b,MAX interactor 1 isoform
PDCD2	chr6:170731015-170731118:-	0.27	MCF7	1.00	MB435	0.73	programmed cell death 2 isoform 1,programmed ce
NAALADL1	chr11:64570237-64570410:-	0.27	adipose	1.00	testes	0.73	N-acetylated alpha-linked acidic
RALY	chr20:32125286-32125333:+	0.27	HME	0.65	lymph node	0.91	RNA binding protein (autoantigenic,,RNA binding pr
FAM114A1	chr4:38556087-38556442:+	0.27	breast	1.00	adipose	0.73	hypothetical protein LOC92689
WIPI2	chr7:5220692-5220861:+	0.27	cerebellum	1.00	liver	0.73	WD repeat domain, phosphoinositide interacting 2,
NPAP60L,NUP50	chr22:43950439-43950625:+	0.27	HME	1.00	adipose	0.73	nucleoporin 50kDa isoform a,nucleoporin 50kDa iso
FES	chr15:89235216-89235425:+	0.27	breast	0.73	adipose	1.00	V-FES feline sarcoma viral/V-FPS fujinami avian,V-
HSPG2	chr1:22087748-22087798:-	0.27	colon	0.86	testes	0.60	Homo sapiens mRNA for Basement membrane-spe
VWA1	chr1:1362565-1362727:+	0.27	cerebellum	1.00	skel. muscle	0.73	von Willebrand factor A domain-related protein,von

JFP10,CCDC78	chr16:715414-715581:-	0.27	cerebellum	1.00	MB435	0.73	coiled-coil domain containing 78 isoform 2,Hypothet
UMPS	chr3:125936630-125936783:+	0.27	BT474	0.73	MB435	1.00	uridine monophosphate synthase,uridine monophos
ATXN2	chr12:110438341-110438550:-	0.27	cerebellum	1.00	brain	0.73	ataxin 2,ataxin 2,ataxin 2,Homo sapiens cDNA FLJ4
PZR,MPZL1	chr1:166011925-166012027:+	0.27	adipose	0.74	colon	1.00	myelin protein zero-like 1 isoform a,myelin protein z
ZNF512	chr2:27660029-27660087:+	0.27	cerebellum	0.81	HME	0.54	zinc finger protein 512,ZNF512 protein.,ZNF512 pro
LAMA5	chr20:60318870-60319023:-	0.27	cerebellum	1.00	MCF7	0.74	laminin alpha 5
GAL3ST4	chr7:99602061-99602364:-	0.27	MB435	1.00	testes	0.74	galactose-3-O-sulfotransferase 4,galactose-3-O-sulf
WBSCR22	chr7:72736033-72736266:+	0.27	cerebellum	1.00	liver	0.74	Williams Beuren syndrome chromosome region 22,
MMACHC	chr1:45929233-45929369:+	0.27	BT474	1.00	MB435	0.74	methylmalonic aciduria (cobalamin deficiency),meth
FAM118B	chr11:125604330-125604398:+	0.27	MB435	1.00	T47D	0.74	hypothetical protein LOC79607,hypothetical protein
PITPNM2	chr12:122040287-122040448:-	0.27	adipose	0.74	colon	1.00	phosphatidylinositol transfer protein,
PALLD,KIAA0992	chr4:170035449-170036120:+	0.27	MCF7	1.00	skel. muscle	0.74	palladin,palladin,KIAA0992 protein (Fragment).,SIH
CCDC95,FLJ00210	chr16:29923390-29923479:+	0.27	cerebellum	0.45	testes	0.71	coiled-coil domain containing 95,coiled-coil domain
KIAA1267	chr17:41472240-41472428:-	0.26	breast	1.00	HME	0.74	hypothetical protein LOC284058,hypothetical protei
BCL6	chr3:188927213-188927380:-	0.26	cerebellum	1.00	T47D	0.74	B-cell lymphoma 6 protein,B-cell lymphoma 6 protei
BIRC6	chr2:32686026-32686214:+	0.26	cerebellum	1.00	skel. muscle	0.74	baculoviral IAP repeat-containing 6
ROD1	chr9:114077945-114078114:-	0.26	HME	1.00	T47D	0.74	ROD1 regulator of differentiation 1,ROD1 regulator
RAB3A	chr19:18174323-18174550:-	0.26	cerebellum	1.00	heart	0.74	RAB3A, member RAS oncogene family
U79272,YIPF6	chrX:67648416-67648544:+	0.26	adipose	0.74	heart	1.00	Yip1 domain family, member 6,Homo sapiens cDNA
HIBDL,N-PAC	chr16:4821981-4822223:-	0.26	cerebellum	1.00	heart	0.74	cytokine-like nuclear factor n-pac,Homo sapiens un
ZNF187	chr6:28347779-28348095:+	0.26	cerebellum	0.74	MCF7	1.00	zinc finger protein 187,zinc finger protein 187,zinc fi
COL16A1	chr1:31917992-31918039:-	0.26	adipose	0.16	colon	0.43	alpha 1 type XVI collagen precursor,alpha 1 type X
DKFZp762D096,C1	chr19:34891001-34891170:-	0.26	breast	1.00	lymph node	0.74	hypothetical protein LOC83636 isoform 1,hypothetic
C22orf5,DKFZp686	chr22:36972737-36972837:-	0.26	cerebellum	0.00	adipose	0.26	chromosome 22 open reading frame 5,Homo sapie
DNM1L	chr12:32782066-32782143:+	0.26	cerebellum	1.00	HME	0.74	dynamin 1-like protein isoform 1,dynamin 1-like prot
DKFZp762I052	chr9:139092323-139092493:+	0.26	MB435	0.74	T47D	1.00	Hypothetical protein DKFZp762I052 (OTTHUMP000
hMmTRA1b,PLSCR	chr3:147737017-147737042:-	0.26	MB435	0.74	brain	1.00	phospholipid scramblase 1,phospholipid scramblase
ZNF767,UNQ5808	chr7:148949070-148949196:-	0.26	cerebellum	1.00	lymph node	0.74	zinc finger family member 767,Homo sapiens cDNA
C6orf48,G8	chr6:31912183-31912273:+	0.26	MCF7	0.27	adipose	0.01	G8 protein,G8 protein,Homo sapiens mRNA for G8
RETSAT	chr2:85424633-85424799:-	0.26	breast	1.00	T47D	0.74	all-trans-13,14-dihydroretinol saturase
PLD3	chr19:45563409-45563677:+	0.26	BT474	1.00	lymph node	0.74	phospholipase D3 isoform 2,phospholipase D3 isof
LOC653319,FLJ001	chr16:65772962-65773101:-	0.26	cerebellum	0.57	testes	0.30	hypothetical protein LOC653319,Homo sapiens mR
RAB4B	chr19:45981523-45981585:+	0.26	BT474	1.00	skel. muscle	0.74	ras-related GTP-binding protein 4b,Homo sapiens r
TNIP2	chr4:2716222-2716470:-	0.26	breast	1.00	T47D	0.74	A20-binding inhibitor of NF-kappaB activation 2,A20
SIAHBP1	chr8:144978471-144978557:-	0.26	brain	1.00	lymph node	0.74	fuse-binding protein-interacting repressor,fuse-bindi
CAP2	chr6:17622059-17622164:+	0.26	cerebellum	1.00	BT474	0.74	adenylyl cyclase-associated protein 2
DAB2	chr5:39424164-39424226:-	0.26	breast	1.00	colon	0.74	disabled homolog 2,disabled homolog 2,
KIAA0465,MACF1	chr1:39719179-39719289:+	0.26	cerebellum	0.01	HME	0.27	microfilament and actin filament cross-linker,microfil
COQ6	chr14:73498193-73498359:+	0.26	cerebellum	1.00	breast	0.74	coenzyme Q6 homolog isoform a,Homo sapiens C
ASB1	chr2:239009091-239009393:+	0.26	cerebellum	1.00	MB435	0.74	ankyrin repeat and SOCS box-containing protein
FAM32A	chr19:16162331-16162388:+	0.26	cerebellum	1.00	lymph node	0.74	hypothetical protein LOC26017
ELAVL1	chr19:8401542-8401751:-	0.26	cerebellum	1.00	MCF7	0.74	ELAV-like 1
APCDD1	chr18:10458466-10458649:+	0.26	breast	1.00	testes	0.74	adenomatosis polyposis coli down-regulated 1
ILF3	chr19:10656092-10656152:+	0.26	adipose	0.35	lymph node	0.09	interleukin enhancer binding factor 3 isoform a,inter
ATP2B3	chrX:152488255-152488408:+	0.26	cerebellum	0.74	brain	1.00	Homo sapiens cDNA FLJ37181 fis, clone BRALZ20
VCP	chr9:35068138-35068340:-	0.26	MCF7	1.00	MB435	0.74	valosin-containing protein,Homo sapiens transitiona
mccb,MCCC2	chr5:70958223-70958336:+	0.26	MCF7	1.00	liver	0.74	methylcrotonoyl-Coenzyme A carboxylase 2 (beta),
03/02/08	chr19:8401542-8401751:+	0.26	cerebellum	1.00	MCF7	0.74	membrane-associated ring finger (C3HC4) 2,memb
ARHGAP4	chrX:152829570-152829647:-	0.26	MB435	0.74	lymph node	1.00	Rho GTPase activating protein 4,Rho GTPase activ
HECTD1,KIAA1131	chr14:30667569-30668264:-	0.26	cerebellum	0.74	breast	1.00	HECT domain containing 1,HECT domain containin
VISA,KIAA1271	chr20:3786282-3786456:+	0.26	cerebellum	1.00	BT474	0.74	Mitochondrial antiviral-signaling protein (Interferon-b
PCYT2	chr17:77456550-77456615:-	0.26	cerebellum	0.74	breast	1.00	phosphate cytidylyltransferase 2, ethanolamine,Hom
n/a	chr17:18086782-18086861:-	0.26	cerebellum	1.00	lymph node	0.74	n/a
AK130824,WDR20	chr14:101731028-101731210:+	0.26	cerebellum	1.00	MB435	0.74	WD repeat domain 20 isoform 2,WD repeat domain
THRAP5	chr19:827974-828180:-	0.26	cerebellum	1.00	lymph node	0.74	Thyroid hormone receptor-associated protein compl
ITGA7 variant protei	chr12:54366253-54366365:-	0.26	lymph node	0.00	skel. muscle	0.26	Homo sapiens mRNA for ITGA7 variant protein, par
ANKRD15	chr9:722378-722617:+	0.26	breast	1.00	brain	0.74	ankyrin repeat domain protein 15 isoform a,ankyrin
PPT1	chr1:40315101-40315172:-	0.26	cerebellum	1.00	breast	0.74	palmitoyl-protein thioesterase 1
POLR3GL	chr1:144169292-144169360:-	0.26	breast	1.00	lymph node	0.74	polymerase (RNA) III (DNA directed) polypeptide
LRP11	chr6:150215832-150215989:-	0.26	cerebellum	1.00	colon	0.74	low density lipoprotein receptor-related protein,low
C11orf51	chr11:71500106-71500190:-	0.26	MCF7	1.00	adipose	0.74	hypothetical protein LOC25906,hypothetical protein
ITPA,OK/SW-cl.9	chr20:3141904-3142029:+	0.26	breast	1.00	HME	0.74	inosine triphosphatase isoform a,inosine triphospha
STOML1	chr15:72068502-72068651:-	0.26	MB435	1.00	adipose	0.74	stomatin (EPB72)-like 1,stomatin (EPB72)-like 1,sto
EPB49	chr8:21994262-21994327:+	0.26	colon	0.97	skel. muscle	0.71	erythrocyte membrane protein band 4.9 (dematin),e
n/a	chr17:63814679-63815447:+	0.26	cerebellum	1.00	T47D	0.74	n/a
DKFZp547H1810,M	chr3:47935213-47935335:-	0.26	breast	1.00	skel. muscle	0.74	microtubule-associated protein 4 isoform 1,microtub
TMEM127	chr2:96294603-96294977:-	0.26	cerebellum	1.00	heart	0.74	hypothetical protein LOC55654,hypothetical protein
TJAP1	chr6:43553803-43553948:+	0.26	cerebellum	1.00	skel. muscle	0.74	tight junction protein 4 (peripheral),tight junction pro
DEGS2	chr14:99685058-99685800:-	0.26	cerebellum	1.00	BT474	0.74	sphingolipid C4-hydroxylase/delta 4-desaturase
AF251050,ZNF263	chr16:3275060-3275240:+	0.26	cerebellum	0.74	MCF7	1.00	zinc finger protein 263,Homo sapiens zinc finger pro
TXNDC14,KIAA038	chr11:57318058-57318129:+	0.26	MCF7	1.00	colon	0.74	catenin (cadherin-associated protein), delta 1,cateni
AK094014,AK0948	chrX:44901904-44902077:-	0.26	breast	1.00	colon	0.74	CDNA FLJ37558 fis, clone BRCOC1000087.,Homo
SFRS2	chr17:72243449-72243552:-	0.26	cerebellum	0.31	MCF7	0.06	splicing factor, arginine/serine-rich 2,splicing factor,
RP11-529I10.4	chr10:103358582-103358684:+	0.26	MB435	0.74	T47D	1.00	DPCD protein
ZDHHC16	chr10:99205386-99205530:+	0.26	MCF7	0.74	BT474	1.00	Abl-philin 2 isoform 2,Abl-philin 2 isoform 2,
TBRG4,NR_00299	chr7:45110662-45110833:-	0.26	MCF7	1.00	lymph node	0.74	cell cycle progression 2 protein isoform 2,cell cycle
ARVCF	chr22:18338739-18338858:-	0.26	cerebellum	0.42	testes	0.68	armadillo repeat protein,armadillo repeat protein,Ho

AKR1A1	chr1:45800048-45800132:+	0.26	breast	1.00	MCF7	0.74	aldo-keto reductase family 1, member A1,aldo-keto
PRMT5	chr14:22467546-22467664:-	0.26	cerebellum	0.74	MCF7	1.00	protein arginine methyltransferase 5 isoform b,prote
DKFZp434D0516,W	chr14:23655966-23656093:+	0.26	cerebellum	1.00	HME	0.74	WD repeat domain 23 isoform 1,WD repeat domain
EPHB4	chr7:100240724-100240879:-	0.26	breast	1.00	T47D	0.74	ephrin receptor EphB4 precursor,ephrin receptor Ep
DHODH	chr16:70612524-70612711:+	0.26	breast	0.74	MCF7	1.00	dihydroorotate dehydrogenase isoform 2
PDLIM7	chr5:176849378-176850200:-	0.26	breast	1.00	colon	0.75	PDZ and LIM domain 7 isoform 1,Homo sapiens EN
OSBPL2,KIAA0772	chr20:60264508-60264672:+	0.26	cerebellum	1.00	MB435	0.75	oxysterol-binding protein-like protein 2 isoform,oxyst
OSBPL2,KIAA0772	chr20:60268468-60268576:+	0.25	cerebellum	1.00	MCF7	0.75	oxysterol-binding protein-like protein 2 isoform,oxyst
AMDHD2	chr16:2510771-2510907:+	0.25	MCF7	1.00	colon	0.75	amidohydrolase domain containing 2,amidohydrolas
SGTA	chr19:2718578-2718684:-	0.25	cerebellum	1.00	breast	0.75	small glutamine-rich tetratricopeptide
TOR3A	chr1:177318698-177318811:+	0.25	MCF7	0.75	HME	1.00	torsin family 3, member A,Torsin-3A precursor (Tors
C2,DKFZp779M031	chr6:32004488-32004673:+	0.25	breast	0.75	adipose	1.00	complement component 2 precursor,complement c
PCCMT,ICMT	chr1:6216121-6216290:-	0.25	HME	0.75	MB435	1.00	isoprenylcysteine carboxyl methyltransferase,Homo
MTMR12	chr5:32269636-32269797:-	0.25	MCF7	0.75	BT474	1.00	myotubularin related protein 12
KIAA1637,NCOA5	chr20:44141433-44141499:-	0.25	cerebellum	0.75	BT474	1.00	nuclear receptor coactivator 5,nuclear receptor coac
TCEA3	chr1:23618157-23618219:-	0.25	T47D	0.75	liver	1.00	transcription elongation factor A (SII), 3
C17orf62,PP3439	chr17:77997788-77997861:-	0.25	T47D	1.00	lymph node	0.75	hypothetical protein LOC79415,hypothetical protein
PRAME	chr22:21229232-21229350:-	0.25	MB435	0.75	T47D	1.00	preferentially expressed antigen in melanoma,prefe
THRAP3	chr1:36497570-36497672:+	0.25	cerebellum	1.00	T47D	0.75	thyroid hormone receptor associated protein 3,thyro
PHF21A,KIAA1696	chr11:45916284-45916439:-	0.25	cerebellum	1.00	heart	0.75	BRAF35/HDAC2 complex,BRAF35/HDAC2 complex
SLC39A6	chr18:31960180-31960977:-	0.25	cerebellum	0.75	breast	1.00	solute carrier family 39 (zinc transporter),,solute carr
NR_003042	chr1:76027432-76027629:+	0.25	cerebellum	1.00	heart	0.75	Rab geranylgeranyltransferase, beta subunit,Rab ge
UFD1,UFD1L	chr22:17839210-17839331:-	0.25	MCF7	1.00	lymph node	0.75	ubiquitin fusion degradation 1-like isoform A,ubiquiti
RABL5	chr7:100748957-100749033:-	0.25	cerebellum	1.00	adipose	0.75	RAB, member RAS oncogene family-like 5
NDUFA12	chr12:93912077-93912164:-	0.25	cerebellum	1.00	MB435	0.75	13kDa differentiation-associated protein
GPBP1L1	chr1:45923835-45923879:-	0.25	BT474	0.49	testes	0.74	GC-rich promoter binding protein 1-like 1,GC-rich pr
KRTCAP3	chr2:27518950-27519134:+	0.25	MCF7	0.75	colon	1.00	keratinocyte associated protein 3,keratinocyte asso
GAK	chr4:888425-888567:-	0.25	cerebellum	1.00	breast	0.75	cyclin G associated kinase,cyclin G associated kina
PRKAR2A	chr3:48764613-48764754:-	0.25	breast	1.00	testes	0.75	cAMP-dependent protein kinase, regulatory,cAMP-d
HDAC3	chr5:140994562-140994704:-	0.25	cerebellum	1.00	MB435	0.75	histone deacetylase 3,histone deacetylase 3,
WNK1	chr12:850692-850775:+	0.25	HME	0.33	T47D	0.58	WNK lysine deficient protein kinase 1,Serine/threoni
DKFZp547H1810,M	chr3:47892179-47892394:-	0.25	cerebellum	0.75	breast	1.00	microtubule-associated protein 4 isoform 1,microtub
n/a	chr14:103248965-103249021:-	0.25	BT474	0.65	MB435	0.90	n/a
TAPBP	chr6:33388972-33389232:-	0.25	cerebellum	1.00	heart	0.75	tapasin isoform 3 precursor,tapasin isoform 2 precur
PIGQ,GPI1	chr16:572249-572310:+	0.25	skel. muscle	0.75	testes	1.00	phosphatidylinositol glycan anchor biosynthesis,,Pho
RHOC	chr1:113049198-113049313:-	0.25	breast	0.34	BT474	0.09	ras homolog gene family, member C precursor,ras h
PPOX	chr1:159403753-159403900:+	0.25	cerebellum	1.00	adipose	0.75	protoporphyrinogen oxidase,Homo sapiens cDNA FL
CGI149,VPS24	chr2:86622886-86622946:-	0.25	MCF7	1.00	lymph node	0.75	vacuolar protein sorting 24 isoform 1,vacuolar protei
KLF6	chr10:3812298-3812421:-	0.25	cerebellum	1.00	breast	0.75	Krueppel-like factor 6 (Core promoter element-bindi
NUP98	chr11:3722315-3722455:-	0.25	HME	1.00	lymph node	0.75	nucleoporin 98kD isoform 1,nucleoporin 98kD isofor
FDPS	chr1:153556209-153556343:+	0.25	cerebellum	1.00	MB435	0.75	farnesyl diphosphate synthase,Farnesyl pyrophosph
OCIM,MYEOV	chr11:68819276-68819538:+	0.25	MB435	0.75	T47D	1.00	myeloma overexpressed,myeloma overexpressed,H
TMEM127	chr2:96294603-96294954:-	0.25	cerebellum	1.00	heart	0.75	hypothetical protein LOC55654,hypothetical protein
C1QC	chr1:22843091-22843284:+	0.25	breast	1.00	lymph node	0.75	complement component 1, q subcomponent, gamm
ETHE1	chr19:48722507-48722651:-	0.25	cerebellum	1.00	breast	0.75	ETHE1 protein
SURF5	chr9:135203216-135203376:-	0.25	cerebellum	1.00	BT474	0.75	surfeit 5 isoform b
MGC29891	chr1:149356492-149356616:+	0.25	MCF7	0.75	T47D	1.00	GA repeat binding protein, beta 2,GA repeat binding
AK127087,IARS	chr9:94088639-94088721:-	0.25	MCF7	1.00	skel. muscle	0.75	isoleucyl-tRNA synthetase,isoleucyl-tRNA synthetas
RPS6KL1	chr14:74458434-74458941:-	0.25	MCF7	1.00	BT474	0.75	ribosomal protein S6 kinase-like 1,Homo sapiens cD
FLJ32065	chr17:60399822-60400097:-	0.25	MCF7	1.00	BT474	0.75	Homo sapiens cDNA FLJ32065 fis, clone OCBBF10
CLN3	chr16:28410304-28410382:-	0.25	breast	1.00	lymph node	0.75	CLN3 protein.,ceroid-lipofuscinosis, neuronal 3,Hom
PLCD3	chr17:40545757-40545906:-	0.25	cerebellum	0.75	breast	1.00	phospholipase C delta 3
PILRB,FDFACT2	chr7:99788932-99789042:+	0.25	cerebellum	0.75	breast	1.00	paired immunoglobulin-like type 2 receptor beta,Hom
APEH	chr3:49686926-49687058:+	0.25	cerebellum	0.75	breast	1.00	N-acylaminoacyl-peptide hydrolase
CINP	chr14:101886009-101886138:-	0.25	cerebellum	1.00	skel. muscle	0.75	Homo sapiens from HeLa cyclin-dependent kinase 2
ZADH1,ZNF410	chr14:73458522-73458662:+	0.25	colon	1.00	testes	0.75	clones 23667 and 23775 zinc finger protein,Homo sa
ZNF341	chr20:31796570-31796766:+	0.25	lymph node	1.00	testes	0.75	zinc finger protein 341,Homo sapiens cDNA FLJ146
TDRD7	chr9:99230563-99230775:+	0.25	MCF7	1.00	MB435	0.75	tudor domain containing 7
SESN2	chr1:28472456-28472606:+	0.25	breast	1.00	skel. muscle	0.75	sestrin 2
MYD88	chr3:38156359-38156493:+	0.25	MCF7	1.00	MB435	0.75	myeloid differentiation primary response gene,myelo
ANK1	chr8:41638105-41638239:-	0.25	brain	1.00	testes	0.75	ankyrin 1 isoform 5,ankyrin 1 isoform 6,ankyrin 1 iso
ZBTB3	chr11:62131714-62131869:-	0.25	cerebellum	0.75	breast	1.00	zinc finger and BTB domain containing 3
TEAD4	chr12:2974165-2974419:+	0.25	breast	0.75	MCF7	1.00	TEA domain family member 4 isoform 1,TEA domai
RAN	chr12:129923082-129923127:+	0.25	breast	1.00	lymph node	0.75	ras-related nuclear protein,ras-related nuclear protei
MEOX1	chr17:39076382-39076554:-	0.25	adipose	1.00	skel. muscle	0.75	mesenchyme homeobox 1 isoform 3,mesenchyme h
ARMCX6	chrX:100759149-100759230:-	0.25	cerebellum	1.00	lymph node	0.75	armadillo repeat containing, X-linked 6,armadillo rep
KLHL20	chr1:172010067-172010200:+	0.25	breast	1.00	BT474	0.75	kelch-like 20,KLHL20 protein.,
BTN2A2	chr6:26493222-26493569:+	0.25	MCF7	1.00	MB435	0.75	butyrophilin, subfamily 2, member A2 isoform a,buty
FLJ20920	chr17:45904788-45904939:+	0.25	cerebellum	0.75	breast	1.00	hypothetical protein LOC80221
SRR	chr17:2165601-2165772:+	0.25	cerebellum	1.00	T47D	0.75	serine racemase,serine racemase,Homo sapiens se
SEZ6L2	chr16:29791527-29791565:-	0.25	cerebellum	0.26	brain	0.51	seizure related 6 homolog (mouse)-like 2 isoform,sei
RP5-890O3.8-016,	chr1:1245699-1246336:-	0.25	cerebellum	1.00	lymph node	0.75	Novel protein (Fragment).,Homo sapiens cDNA FLJ
C17orf68	chr17:8087028-8087191:-	0.25	cerebellum	0.75	MCF7	1.00	hypothetical protein LOC80169
KIAA1835,RANGA	chr22:39987396-39987530:-	0.25	cerebellum	1.00	testes	0.75	Ran GTPase activating protein 1,Ran GTPase activ
DKFZp686O1389,D	chrX:151878899-151879096:+	0.25	MCF7	1.00	adipose	0.75	Hypothetical protein DKFZp686B22130 (Fragment).,
RPLP2	chr11:800233-800357:+	0.25	cerebellum	1.00	HME	0.75	ribosomal protein P2,ribosomal protein P2,
PUM1	chr1:31187432-31187557:-	0.25	cerebellum	0.75	breast	1.00	pumilio 1 isoform 1,pumilio 1 isoform 2,pumilio 1 iso

CLCN7	chr16:1455269-1455340:-	0.25	cerebellum	1.00	BT474	0.75	chloride channel 7,chloride channel 7,Homo sapiens
AP2M1	chr3:185381127-185381223:+	0.25	HME	0.31	MB435	0.06	adaptor-related protein complex 2, mu 1 subunit,ada
HSD17B6	chr12:55453890-55454216:+	0.25	cerebellum	1.00	testes	0.75	hydroxysteroid (17-beta) dehydrogenase 6
MIZF	chr11:118502855-118503045:+	0.25	BT474	1.00	colon	0.75	MBD2 (methyl-CpG-binding protein)-interacting,MBD
BCAS3	chr17:56800470-56800637:+	0.25	cerebellum	0.75	breast	1.00	breast carcinoma amplified sequence 3,Homo sapie
FLJ00369,ARHGEF	chr19:47102449-47102612:+	0.25	cerebellum	1.00	testes	0.75	Rho guanine nucleotide exchange factor 1 isoform,H
NDRG3	chr20:34716618-34716656:-	0.25	MB435	0.02	colon	0.27	N-myc downstream-regulated gene 3 isoform a,N-my
DUS2L	chr16:66616819-66616898:+	0.25	BT474	0.75	testes	1.00	dihydrouridine synthase 2-like, SMM1 homolog,dihy
KIAA0319L	chr1:35682349-35682491:-	0.25	cerebellum	1.00	BT474	0.75	polycystic kidney disease 1-like isoform a,polycystic
DPM1	chr20:48990809-48990877:-	0.25	MB435	1.00	T47D	0.75	dolichyl-phosphate mannosyltransferase,Homo sapi
FLT3LG	chr19:54673978-54674116:+	0.25	breast	0.83	lymph node	0.59	fms-related tyrosine kinase 3 ligand,FLT3LG protein.
HMG2L1	chr22:33988316-33988414:+	0.25	BT474	0.63	HME	0.38	high-mobility group protein 2-like 1 isoform a,high-m
WNK2	chr9:95058402-95058557:+	0.25	cerebellum	0.75	testes	1.00	WNK lysine deficient protein kinase 2
SNX7	chr1:98976381-98976533:+	0.25	MCF7	1.00	lymph node	0.75	sorting nexin 7 isoform a,sorting nexin 7 isoform b,
TEAD4	chr12:2996825-2996953:+	0.25	MB435	0.75	adipose	1.00	TEA domain family member 4 isoform 1,TEA domai
DKFZp781C0423,D	chr20:33791861-33791933:-	0.25	MB435	0.21	T47D	0.46	Homo sapiens cDNA FLJ44170 fis, clone THYMU20
AX765705,PARD3	chr10:34779251-34779382:-	0.25	MCF7	0.76	skel. muscle	1.00	partitioning-defective protein 3 homolog,partitioning-
CCAR1	chr10:70186036-70186246:+	0.25	MCF7	1.00	T47D	0.76	cell-cycle and apoptosis regulatory protein 1,Homo s
IL6R	chr1:152675069-152675210:+	0.25	HME	1.00	colon	0.76	interleukin 6 receptor isoform 2 precursor
RPLP2	chr11:800235-800357:+	0.25	cerebellum	1.00	HME	0.76	ribosomal protein P2,ribosomal protein P2,
PLCD1	chr3:38150447-38150504:-	0.25	breast	1.00	lymph node	0.76	phospholipase C, delta 1
XYLT2	chr17:45789478-45789612:+	0.25	MCF7	0.76	BT474	1.00	xylosyltransferase II
CALU	chr7:128181819-128182012:+	0.25	BT474	0.37	colon	0.13	calumenin precursor,calumenin precursor,Calumeni

[1] Switch scores are provided for tissue-biased skipped exons for which there exist at least 20 reads in 2 tissues and switch score >= .25.
[2] The "Event" column contains coordinates which denote the skipped exon, and strand of the annotated transcript.
[3] Inclusion levels for the skipped exon are provided in the two tissues exhibiting the highest and lowest inclusion levels.
[4] The switch score is derived from the absolute difference between inclusion levels in the two displayed tissues.

Table S6. Mutually exclusive exon switch scores.[1]

Gene	Event[2]	Switch score[4]	Tissue 1	Tissue 1 inclusion level[3]	Tissue 2	Tissue 2 inclusion level[3]	Gene description
FMNL2,KIAA1902	chr2:153208179-153208304,chr2:153210194-153210240:+	0.96	cerebellum	1.00	MB435	0.04	formin-like 2,CDNA FLJ16308 fis, clone PUAEN2006335.,
DLG3	chrX:69629951-69630050,chrX:69631983-69632028:+	0.95	MCF7	1.00	brain	0.05	synapse-associated protein 102 isoform a
SLC25A3,OK/SW-c	chr12:97513342-97513466,chr12:97513636-97513757:+	0.93	BT474	0.00	skel. muscle	0.93	solute carrier family 25 member 3 isoform a,Homo sapiens mRNA for OK/SW-CL
PKM2	chr15:70282583-70282417,chr15:70282015-70281849:-	0.88	T47D	0.03	skel. muscle	0.91	pyruvate kinase 3 isoform 1,Homo sapiens Opa-interacting protein OIP3 mRNA,
n/a	chr15:70281849-70282015,chr15:70282417-70282583:+	0.88	T47D	0.97	skel. muscle	0.09	n/a
A2BP1	chr16:7654932-7654971,chr16:7661560-7661602:+	0.86	brain	0.86	skel. muscle	0.00	ataxin 2-binding protein 1 isoform 2,ataxin 2-binding protein 1 isoform 1,ataxin 2-
UBE1	chrX:46941290-46941367,chrX:46942510-46942698:+	0.84	lymph node	0.07	skel. muscle	0.91	Ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity comple
QTRT1	chr19:10767737-10767875,chr19:10769056-10769194:+	0.83	BT474	0.99	brain	0.16	dynamin 2 isoform 2,dynamin 2 isoform 4,dynamin 2 isoform 4,dynamin 2 isoform
WASF3	chr13:26148686-26148861,chr13:26152172-26152338:+	0.81	cerebellum	0.81	colon	0.00	WAS protein family, member 3
PHKB	chr16:46256297-46256387,chr16:46257354-46257444:+	0.76	MB435	0.00	skel. muscle	0.76	phosphorylase kinase, beta isoform b,phosphorylase kinase, beta isoform a,Hom
MAPK14	chr6:36171742-36171821,chr6:36175943-36176022:+	0.76	cerebellum	0.14	colon	0.90	mitogen-activated protein kinase 14 isoform 2,mitogen-activated protein kinase 1
n/a	chr8:125640254-125640135,chr8:125639297-125639103:-	0.71	cerebellum	0.71	skel. muscle	0.00	n/a
MEF2C	chr5:88092901-88092758,chr5:88092698-88092561:-	0.70	colon	1.00	skel. muscle	0.30	MADS box transcription enhancer factor 2,,MADS box transcription enhancer fact
SLC39A14	chr8:22323404-22323573,chr8:22325495-22325664:+	0.67	MB435	0.00	liver	0.67	solute carrier family 39 (zinc transporter),
SLC7A2	chr8:17456361-17456500,chr8:17456747-17456883:+	0.66	MCF7	0.77	skel. muscle	0.11	solute carrier family 7, member 2 isoform 2,solute carrier family 7, member 2 isof
n/a	chr19:43892737-43892822,chr19:43893756-43893841:+	0.65	cerebellum	0.35	liver	1.00	n/a
COL13A1	chr10:71382644-71382730,chr10:71383710-71383787:+	0.58	cerebellum	0.38	MB435	0.96	alpha 1 type XIII collagen isoform 1,alpha 1 type XIII collagen isoform 6,alpha 1 ty
n/a	chr1:153300676-153300746,chr1:153301004-153301075:+	0.55	cerebellum	0.56	T47D	0.01	n/a
BCS1L	chr2:219233004-219233133,chr2:219233274-219233388:+	0.53	BT474	0.85	HME	0.32	BCS1-like,BCS1-like,BCS1-like,BCS1-like,BCS1-like,
SFRS14	chr19:18965549-18965457,chr19:18963362-18963149:-	0.53	cerebellum	0.36	skel. muscle	0.89	splicing factor, arginine/serine-rich 14,splicing factor, arginine/serine-rich 14,splic
PLD3	chr19:45563300-45563332,chr19:45563409-45563677:+	0.52	cerebellum	0.31	heart	0.83	phospholipase D3 isoform 2,phospholipase D3 isoform 1,phospholipase D3 isofo
ATE1	chr10:123649499-123649371,chr10:123648474-123648346:-	0.52	skel. muscle	0.29	testes	0.80	arginyltransferase 1 isoform 1,Homo sapiens arginine-tRNA-protein transferase 1
n/a	chr22:27990207-27989824,chr22:27987414-27987189:-	0.48	cerebellum	1.00	T47D	0.52	n/a
C20orf199	chr20:47331696-47331762,chr20:47332683-47332947:+	0.48	MCF7	0.76	T47D	0.28	Homo sapiens NS5ATP6-regulated protein 1, complete sequence.,Homo sapiens
n/a	chr19:1566519-1566284,chr19:1563429-1563206:-	0.47	T47D	0.70	colon	0.23	n/a
BAT2D1,KIAA1096	chr1:169825131-169825367,chr1:169826914-169826962:+	0.47	cerebellum	1.00	BT474	0.54	HBxAg transactivated protein 2,Homo sapiens mRNA for KIAA1096 protein, parti
PLEKHB2	chr2:131600727-131600829,chr2:131606945-131607034:+	0.45	BT474	0.21	brain	0.66	pleckstrin homology domain containing, family B,pleckstrin homology domain con
n/a	chrX:152714312-152714453,chrX:152714577-152714775:+	0.44	MB435	0.47	lymph node	0.02	n/a
DLG1	chr3:198287953-198287854,chr3:198287138-198287105:-	0.42	HME	0.58	skel. muscle	1.00	discs, large homolog 1,discs, large homolog 1,
DNM1	chr9:130026351-130026489,chr9:130028135-130028273:+	0.41	cerebellum	0.63	brain	0.21	dynamin 1 isoform 2,dynamin 1 isoform 1,Homo sapiens mRNA for dynamin 1 iso
DGKA,DAGK1	chr12:54618562-54618611,chr12:54618689-54618749:+	0.39	HME	0.98	lymph node	0.60	diacylglycerol kinase, alpha 80kDa,diacylglycerol kinase, alpha 80kDa,diacylglyc
MAPK9	chr5:179607532-179607461,chr5:179607116-179607045:-	0.38	cerebellum	0.38	MCF7	0.00	mitogen-activated protein kinase 9 isoform JNK2,mitogen-activated protein kinas
DTX3	chr12:56285394-56285781,chr12:56286039-56286079:+	0.38	MCF7	1.00	brain	0.62	deltex 3 homolog,deltex 3 homolog,deltex 3 homolog,deltex 3 homolog,
n/a	chr1:210682511-210682590,chr1:210684306-210684407:+	0.37	cerebellum	0.15	adipose	0.52	n/a
OGDH	chr7:44653568-44653658,chr7:44653781-44653883:+	0.36	cerebellum	0.36	breast	0.00	oxoglutarate (alpha-ketoglutarate) dehydrogenase,oxoglutarate (alpha-ketoglutar
PFKP	chr10:3152084-3152236,chr10:3157289-3157441:+	0.35	skel. muscle	1.00	testes	0.65	Phosphofructokinase, platelet.
n/a	chr11:35176244-35176369,chr11:35182635-35182763:+	0.35	MB435	0.06	T47D	0.41	n/a
n/a	chr19:45022995-45022894,chr19:45022784-45022713:-	0.34	HME	0.83	brain	0.50	n/a
ZBTB7B	chr1:153249358-153249497,chr1:153253115-153253193:+	0.33	T47D	0.55	lymph node	0.88	kruppel-related zinc finger protein hcKrox,kruppel-related zinc finger protein hcKr
C19orf6	chr19:962194-962095,chr19:962094-961990:-	0.33	breast	0.98	colon	0.66	membralin isoform 2
FLJ20186	chr16:88543326-88543422,chr16:88543474-88543547:+	0.32	HME	0.95	adipose	0.63	differentially expressed in FDCP 8 isoform 1,differentially expressed in FDCP 8 is
CKLFSF1,CMTM1,	chr16:65149594-65149752,chr16:65154476-65154621:+	0.32	HME	0.36	adipose	0.68	chemokine-like factor superfamily 1 isoform 14,chemokine-like factor superfamily
ACTN4	chr19:43910426-43910506,chr19:43910796-43910861:+	0.31	cerebellum	0.69	BT474	1.00	actinin, alpha 4,Homo sapiens actinin, alpha 4, mRNA (cDNA clone MGC:12692
n/a	chr3:187987610-187987747,chr3:187988006-187988067:+	0.29	cerebellum	0.72	breast	0.43	n/a
DIABLO	chr12:121275248-121275145,chr12:121275144-121275012:-	0.29	liver	0.06	lymph node	0.35	diablo isoform 1 precursor,diablo isoform 3 precursor,
ITPA,OK/SW-cl.9	chr20:3141815-3141872,chr20:3141904-3142029:+	0.28	MCF7	0.75	lymph node	0.46	inosine triphosphatase isoform a,inosine triphosphatase isoform b,Homo sapiens
n/a	chr6:34312959-34312997,chr6:34316492-34316637:+	0.28	T47D	0.67	lymph node	0.39	n/a
n/a	chr18:72829471-72829439,chr18:72825845-72825719:-	0.27	cerebellum	0.27	lymph node	0.00	n/a
n/a	chr19:18409570-18409409,chr19:18408687-18408494:-	0.27	cerebellum	0.47	adipose	0.20	n/a

PHF1	chr6:33490710-33490899,chr6:33491016-33491084:+	0.26	colon	0.54	heart	0.28	PHD finger protein 1 isoform a
ACP1	chr2:262037-262150,chr2:262192-262305:+	0.23	BT474	0.72	skel. muscle	0.95	acid phosphatase 1 isoform d,Homo sapiens mRNA for acid phosphatase 1 isof
COL5A1	chr9:136861643-136861711,chr9:136861775-136861843:+	0.23	breast	0.50	testes	0.73	alpha 1 type V collagen preproprotein
n/a	chr4:114689334-114689262,chr4:114688321-114688249:-	0.23	cerebellum	0.75	heart	0.97	n/a
MTHFSD	chr16:85143399-85143286,chr16:85143253-85143140:-	0.22	T47D	0.92	testes	0.70	methenyltetrahydrofolate synthetase domain,methenyltetrahydrofolate synthetase
n/a	chr2:73316186-73316281,chr2:73318188-73318323:+	0.22	skel. muscle	0.99	testes	0.76	n/a
DYNLRB1	chr20:32581317-32581699,chr20:32584989-32585070:+	0.22	BT474	0.45	MB435	0.23	Homo sapiens bithoraxoid-like protein mRNA, complete cds.,Homo sapiens bitho
n/a	chr9:138805899-138806050,chr9:138806051-138806303:+	0.22	HME	0.90	colon	0.68	n/a
C1orf151	chr1:19799868-19800052,chr1:19816339-19816417:+	0.21	colon	0.24	testes	0.03	chromosome 1 open reading frame 151 protein,Homo sapiens cDNA FLJ36999 fi
n/a	chr12:7039317-7039356,chr12:7039404-7039482:+	0.21	colon	0.80	heart	0.60	n/a
n/a	chr15:22754978-22755108,chr15:22755565-22755705:+	0.21	cerebellum	0.21	colon	0.00	n/a
n/a	chr22:19235723-19235774,chr22:19239223-19239435:+	0.20	BT474	0.59	T47D	0.39	n/a
n/a	chr4:186797183-186797025,chr4:186796310-186796227:-	0.17	colon	0.92	heart	0.75	n/a
n/a	chr14:100368602-100368731,chr14:100371826-100371969:+	0.15	cerebellum	0.42	testes	0.27	n/a
TEGT,CR623040	chr12:48422002-48422165,chr12:48423467-48423615:+	0.13	MCF7	1.00	T47D	0.87	testis enhanced gene transcript (BAX inhibitor,testis enhanced gene transcript (B
NCDN	chr1:35796344-35796411,chr1:35796412-35796672:+	0.12	brain	0.99	testes	0.87	neurochondrin isoform 1,neurochondrin isoform 2,
n/a	chr1:21375438-21375255,chr1:21310463-21310403:-	0.11	MB435	1.00	colon	0.89	n/a
MEF2A	chr15:98029051-98029182,chr15:98029248-98029385:+	0.10	HME	0.86	heart	0.76	MADS box transcription enhancer factor 2,,MADS box transcription enhancer fac
EIF3S2	chr1:32464359-32464471,chr1:32464591-32464718:+	0.10	BT474	0.33	brain	0.43	eukaryotic translation initiation factor 3,,eukaryotic translation initiation factor 3,,
SCDR10,HSD11B1	chr19:5635792-5635916,chr19:5635976-5636130:+	0.10	MB435	0.28	brain	0.38	short-chain dehydrogenase/reductase 10 isoform,short-chain dehydrogenase/red
APEX1	chr14:19993577-19993702,chr14:19993737-19993772:+	0.09	cerebellum	1.00	liver	0.91	APEX nuclease,APEX nuclease,APEX nuclease,APEX nuclease,
TNNT3	chr11:1914020-1914060,chr11:1914769-1914809:+	0.09	breast	0.09	adipose	0.00	Homo sapiens cDNA FLJ32406 fis, clone SKMUS2000416, highly similar to TRO
n/a	chr20:43877436-43877586,chr20:43877587-43877791:+	0.09	HME	0.00	testes	0.09	n/a
APEX1	chr14:19993577-19993702,chr14:19993734-19993772:+	0.09	cerebellum	1.00	liver	0.91	APEX nuclease,APEX nuclease,APEX nuclease,APEX nuclease,
P4HA2	chr5:131561972-131561913,chr5:131561863-131561798:-	0.07	HME	0.83	testes	0.90	prolyl 4-hydroxylase, alpha II subunit isoform 2,prolyl 4-hydroxylase, alpha II subu
GRIA2	chr4:158501612-158501726,chr4:158502140-158502254:+	0.07	cerebellum	0.57	brain	0.50	glutamate receptor, ionotropic, AMPA 2 isoform 1,glutamate receptor, ionotropic,
EPS8L2	chr11:696596-696801,chr11:698575-698643:+	0.05	HME	0.89	T47D	0.84	epidermal growth factor receptor pathway,epidermal growth factor receptor pathw
n/a	chr12:122709930-122709975,chr12:122710016-122710084:+	0.05	cerebellum	0.00	MB435	0.05	n/a
n/a	chr20:10147742-10147861,chr20:10188005-10188049:+	0.05	cerebellum	0.95	brain	1.00	n/a
TCF7L2	chr10:114908416-114908466,chr10:114910368-114910440:+	0.04	adipose	0.77	testes	0.72	transcription factor 7-like 2 (T-cell specific,,Transcription factor 7-like 2 (HMG box
DKFZp451I083,MY	chr12:100532405-100532440,chr12:100544781-100544819:+	0.04	breast	0.96	testes	1.00	myosin binding protein C, slow type isoform 3,myosin binding protein C, slow type
n/a	chr11:43870167-43870255,chr11:43875321-43875480:+	0.03	MB435	0.97	skel. muscle	1.00	n/a
mm-1,PFDN5	chr12:51975890-51975992,chr12:51976505-51976602:+	0.03	breast	1.00	testes	0.97	prefoldin subunit 5 isoform gamma,Homo sapiens mRNA for MM-1 alpha, comple
MYL6,MLC-3	chr12:54839549-54839673,chr12:54839674-54839781:+	0.03	cerebellum	0.03	brain	0.00	myosin, light chain 6, alkali, smooth muscle and,Homo sapiens MLC-3 mRNA for
n/a	chr10:33236077-33235997,chr10:33235514-33235399:-	0.03	heart	1.00	skel. muscle	0.97	n/a
n/a	chr20:10147742-10147861,chr20:10166621-10166674:+	0.02	cerebellum	0.89	brain	0.90	n/a
n/a	chr19:11408110-11408326,chr19:11408355-11408544:+	0.02	cerebellum	0.99	breast	1.00	n/a
n/a	chr20:10147742-10147861,chr20:10162859-10162985:+	0.00	cerebellum	0.97	brain	0.97	n/a

[1] Switch scores are provided for tissue-biased MXEs for which there exist at least 20 reads in 2 tissues.

[2] The "Event" column contains coordinates which denote the MXEs, and strand of the annotated transcript.

[3] Inclusion levels for the first MXE are provided in the two tissues exhibiting the highest and lowest inclusion levels.

[4] The switch score is derived from the absolute difference between inclusion levels in the two displayed tissues.

Table S7. Enrichment of categories in genes with high switch score skipped exons versus low switch score skipped exons.[1]

Fisher-test (pvalue)	DAVID functional category	High switch score, in cat.	Low switch score, in cat.	High switch score, not in cat.	Low switch score, not in cat.	log2(Obs / Exp)	Category type
1.3E-134	12477932	747	674	30	718	0.99	hsa_PUBMED_ID
3.1E-79	CELLULAR_PROCESS	619	537	158	855	1.05	hsa_GOTERM_BP_1
1.7E-72	PHYSIOLOGICAL_PROCESS	600	525	177	867	1.03	hsa_GOTERM_BP_1
1.3E-65	CELLULAR_PHYSIOLOGICAL_PROCESS	569	493	208	899	1.05	hsa_GOTERM_BP_2
2.3E-52	similarity	552	519	225	873	0.93	hsa_SP_COMMENT_TYPE
2.2E-49	CELL	522	478	255	914	0.97	hsa_GOTERM_CC_1
6.9E-48	METABOLISM	459	379	318	1013	1.12	hsa_GOTERM_BP_2
1.7E-44	PRIMARY_METABOLISM	431	350	346	1042	1.14	hsa_GOTERM_BP_3
2.6E-43	BINDING	488	448	289	944	0.96	hsa_GOTERM_MF_1
2.6E-43	BINDING	488	448	289	944	0.96	hsa_GOTERM_MF_ALL
1.8E-42	CELLULAR_METABOLISM	427	353	350	1039	1.12	hsa_GOTERM_BP_3
7.5E-38	subcellular_location	442	399	335	993	0.99	hsa_SP_COMMENT_TYPE
5.1E-32	14702039	373	322	404	1070	1.05	hsa_PUBMED_ID
5.4E-29	INTRACELLULAR	403	384	374	1008	0.91	hsa_GOTERM_CC_2
4.0E-28	CATALYTIC_ACTIVITY	309	249	468	1143	1.15	hsa_GOTERM_MF_1
4.0E-28	CATALYTIC_ACTIVITY	309	249	468	1143	1.15	hsa_GOTERM_MF_ALL
1.8E-24	function	432	459	345	933	0.75	hsa_SP_COMMENT_TYPE
1.4E-23	MACROMOLECULE_METABOLISM	297	256	480	1136	1.06	hsa_GOTERM_BP_3
1.6E-19	tissue_specificity	286	263	491	1129	0.96	hsa_SP_COMMENT_TYPE
3.9E-19	sequence_conflict	337	342	440	1050	0.82	hsa_UP_SEQ_FEATURE
1.7E-18	BIOLOGICAL_PROCESS_UNKNOWN	337	346	440	1046	0.8	hsa_GOTERM_BP_1
3.9E-18	ORGANELLE	320	323	457	1069	0.83	hsa_GOTERM_CC_1
3.9E-18	INTRACELLULAR_ORGANELLE	320	323	457	1069	0.83	hsa_GOTERM_CC_2
3.9E-18	INTRACELLULAR_ORGANELLE	320	323	457	1069	0.83	hsa_GOTERM_CC_3
2.9E-17	MEMBRANE	222	187	555	1205	1.09	hsa_GOTERM_CC_2
4.6E-16	MOLECULAR_FUNCTION_UNKNOWN	321	339	456	1053	0.76	hsa_GOTERM_MF_1
4.6E-16	MOLECULAR_FUNCTION_UNKNOWN	321	339	456	1053	0.76	hsa_GOTERM_MF_ALL
5.6E-16	BP00216:_BIOLOGICAL_PROCESS_UNCLASSIFIED	317	334	460	1058	0.77	hsa_PANTHER_TERM_BP
9.8E-16	TRANSPORT	164	120	613	1272	1.29	hsa_GOTERM_BP_3
9.8E-16	TRANSPORT	164	120	613	1272	1.29	hsa_GOTERM_BP_4
1.4E-15	INTRINSIC_TO_MEMBRANE	162	119	615	1273	1.29	hsa_GOTERM_CC_3
1.4E-15	INTEGRAL_TO_MEMBRANE	162	119	615	1273	1.29	hsa_GOTERM_CC_4
2.1E-15	MEMBRANE-BOUND_ORGANELLE	283	286	494	1106	0.83	hsa_GOTERM_CC_2
2.1E-15	INTRACELLULAR_MEMBRANE-BOUND_ORGANELLE	283	286	494	1106	0.83	hsa_GOTERM_CC_3
2.1E-15	INTRACELLULAR_MEMBRANE-BOUND_ORGANELLE	283	286	494	1106	0.83	hsa_GOTERM_CC_4

2.5E-15	CYTOPLASM	224	201	553	1191	1	hsa_GOTERM_CC_3
6.6E-15	MF00208:_MOLECULAR_FUNCTION_UNCLASSIFIED	304	322	473	1070	0.76	hsa_PANTHER_TERM_MF
1.4E-14	CELLULAR_MACROMOLECULE_METABOLISM	190	160	587	1232	1.09	hsa_GOTERM_BP_4
3.0E-14	LOCALIZATION	185	155	592	1237	1.1	hsa_GOTERM_BP_2
3.6E-14	BIOPOLYMER_METABOLISM	197	172	580	1220	1.04	hsa_GOTERM_BP_4
4.6E-14	CELLULAR_PROTEIN_METABOLISM	184	155	593	1237	1.09	hsa_GOTERM_BP_5
7.2E-14	ESTABLISHMENT_OF_LOCALIZATION	183	155	594	1237	1.08	hsa_GOTERM_BP_3
1.1E-13	PROTEIN_METABOLISM	197	175	580	1217	1.01	hsa_GOTERM_BP_4
1.6E-13	NUCLEIC_ACID_BINDING	170	140	607	1252	1.12	hsa_GOTERM_MF_2
1.6E-13	NUCLEIC_ACID_BINDING	170	140	607	1252	1.12	hsa_GOTERM_MF_ALL
2.5E-13	subunit	296	322	481	1070	0.72	hsa_SP_COMMENT_TYPE
2.7E-13	BP00060:_PROTEIN_METABOLISM_AND_MODIFICATIC	144	108	633	1284	1.26	hsa_PANTHER_TERM_BP
5.7E-12	hypothetical_protein	221	220	556	1172	0.85	hsa_SP_PIR_KEYWORDS
5.8E-12	catalytic_activity	153	127	624	1265	1.11	hsa_SP_COMMENT_TYPE
6.5E-12	NUCLEOBASE,_NUCLEOSIDE,_NUCLEOTIDE_AND_NU	187	172	590	1220	0.96	hsa_GOTERM_BP_4
1.4E-11	BP00031:_NUCLEOSIDE,_NUCLEOTIDE_AND_NUCLEIC	138	110	639	1282	1.17	hsa_PANTHER_TERM_BP
2.2E-11	transmembrane	128	98	649	1294	1.23	hsa_SP_PIR_KEYWORDS
7.7E-11	membrane	152	132	625	1260	1.04	hsa_SP_PIR_KEYWORDS
2.3E-10	transmembrane_region	119	93	658	1299	1.2	hsa_UP_SEQ_FEATURE
4.8E-10	HYDROLASE_ACTIVITY	112	86	665	1306	1.22	hsa_GOTERM_MF_2
4.8E-10	HYDROLASE_ACTIVITY	112	86	665	1306	1.22	hsa_GOTERM_MF_ALL
6.4E-10	sequence_variant	171	164	606	1228	0.9	hsa_UP_SEQ_FEATURE
6.4E-10	PROTEIN_BINDING	255	287	522	1105	0.67	hsa_GOTERM_MF_2
6.4E-10	PROTEIN_BINDING	255	287	522	1105	0.67	hsa_GOTERM_MF_ALL
7.7E-10	TRANSFERASE_ACTIVITY	111	86	666	1306	1.21	hsa_GOTERM_MF_2
7.7E-10	TRANSFERASE_ACTIVITY	111	86	666	1306	1.21	hsa_GOTERM_MF_ALL
2.0E-09	TRANSITION_METAL_ION_BINDING	110	87	667	1305	1.18	hsa_GOTERM_MF_4
2.0E-09	TRANSITION_METAL_ION_BINDING	110	87	667	1305	1.18	hsa_GOTERM_MF_ALL
2.4E-09	BIOPOLYMER_MODIFICATION	119	98	658	1294	1.12	hsa_GOTERM_BP_5
3.8E-09	repeat	163	159	614	1233	0.88	hsa_SP_PIR_KEYWORDS
5.0E-09	SIGNAL_TRANSDUCER_ACTIVITY	125	108	652	1284	1.05	hsa_GOTERM_MF_1
5.0E-09	SIGNAL_TRANSDUCER_ACTIVITY	125	108	652	1284	1.05	hsa_GOTERM_MF_ALL
9.0E-09	TRANSPORTER_ACTIVITY	85	60	692	1332	1.34	hsa_GOTERM_MF_1
9.0E-09	TRANSPORTER_ACTIVITY	85	60	692	1332	1.34	hsa_GOTERM_MF_ALL
1.1E-08	CATION_BINDING	141	132	636	1260	0.94	hsa_GOTERM_MF_3
1.1E-08	CATION_BINDING	141	132	636	1260	0.94	hsa_GOTERM_MF_ALL
1.1E-08	CELL_COMMUNICATION	165	165	612	1227	0.84	hsa_GOTERM_BP_2
1.2E-08	SIGNAL_TRANSDUCTION	155	151	622	1241	0.88	hsa_GOTERM_BP_3
1.5E-08	MF00042:_NUCLEIC_ACID_BINDING	111	93	666	1299	1.1	hsa_PANTHER_TERM_MF
1.8E-08	nuclear_protein	151	147	626	1245	0.88	hsa_SP_PIR_KEYWORDS
3.7E-08	zinc	85	63	692	1329	1.27	hsa_SP_PIR_KEYWORDS

4.6E-08	ION_BINDING	148	146	629	1246	0.86	hsa_GOTERM_MF_2
4.6E-08	METAL_ION_BINDING	148	146	629	1246	0.86	hsa_GOTERM_MF_3
4.6E-08	ION_BINDING	148	146	629	1246	0.86	hsa_GOTERM_MF_ALL
4.6E-08	METAL_ION_BINDING	148	146	629	1246	0.86	hsa_GOTERM_MF_ALL
9.2E-08	BP00102:_SIGNAL_TRANSDUCTION	103	88	674	1304	1.07	hsa_PANTHER_TERM_BP
9.3E-08	polymorphism	127	119	650	1273	0.94	hsa_SP_PIR_KEYWORDS
1.1E-07	ZINC_ION_BINDING	91	73	686	1319	1.16	hsa_GOTERM_MF_5
1.1E-07	ZINC_ION_BINDING	91	73	686	1319	1.16	hsa_GOTERM_MF_ALL
1.5E-07	metal-binding	103	89	674	1303	1.05	hsa_SP_PIR_KEYWORDS
2.7E-07	splice_variant	226	268	551	1124	0.6	hsa_UP_SEQ_FEATURE
2.7E-07	PROTEIN_LOCALIZATION	75	56	702	1336	1.26	hsa_GOTERM_BP_3
2.9E-07	NUCLEOTIDE_BINDING	109	99	668	1293	0.98	hsa_GOTERM_MF_2
2.9E-07	NUCLEOTIDE_BINDING	109	99	668	1293	0.98	hsa_GOTERM_MF_ALL
3.2E-07	NUCLEUS	170	184	607	1208	0.73	hsa_GOTERM_CC_3
3.2E-07	NUCLEUS	170	184	607	1208	0.73	hsa_GOTERM_CC_4
3.2E-07	NUCLEUS	170	184	607	1208	0.73	hsa_GOTERM_CC_5
3.6E-07	cofactor	59	38	718	1354	1.48	hsa_SP_COMMENT_TYPE
4.0E-07	BP00141:_TRANSPORT	55	34	722	1358	1.54	hsa_PANTHER_TERM_BP
4.9E-07	transferase	80	63	697	1329	1.19	hsa_SP_PIR_KEYWORDS
6.1E-07	alternative_products	229	277	548	1115	0.57	hsa_SP_COMMENT_TYPE
7.5E-07	alternative_splicing	227	275	550	1117	0.56	hsa_SP_PIR_KEYWORDS
8.2E-07	CELL_ORGANIZATION_AND_BIOGENESIS	122	120	655	1272	0.87	hsa_GOTERM_BP_3
9.6E-07	ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	73	56	704	1336	1.22	hsa_GOTERM_BP_4
9.6E-07	PROTEIN_TRANSPORT	73	56	704	1336	1.22	hsa_GOTERM_BP_4
9.6E-07	PROTEIN_TRANSPORT	73	56	704	1336	1.22	hsa_GOTERM_BP_5
9.8E-07	INTRACELLULAR_PROTEIN_TRANSPORT	70	53	707	1339	1.24	hsa_GOTERM_BP_5
1.3E-06	CELLULAR_LIPID_METABOLISM	43	23	734	1369	1.74	hsa_GOTERM_BP_4
1.3E-06	CELLULAR_LIPID_METABOLISM	43	23	734	1369	1.74	hsa_GOTERM_BP_5
1.3E-06	PURINE_NUCLEOTIDE_BINDING	87	74	690	1318	1.07	hsa_GOTERM_MF_3
1.3E-06	PURINE_NUCLEOTIDE_BINDING	87	74	690	1318	1.07	hsa_GOTERM_MF_ALL
1.3E-06	INTRACELLULAR_TRANSPORT	76	61	701	1331	1.16	hsa_GOTERM_BP_4
1.3E-06	INTRACELLULAR_TRANSPORT	76	61	701	1331	1.16	hsa_GOTERM_BP_5
1.4E-06	BIOSYNTHESIS	84	71	693	1321	1.08	hsa_GOTERM_BP_3
1.5E-06	CELLULAR_LOCALIZATION	77	62	700	1330	1.15	hsa_GOTERM_BP_3
1.5E-06	ESTABLISHMENT_OF_CELLULAR_LOCALIZATION	77	62	700	1330	1.15	hsa_GOTERM_BP_4
1.5E-06	CELLULAR_LOCALIZATION	77	62	700	1330	1.15	hsa_GOTERM_BP_4
1.5E-06	ESTABLISHMENT_OF_CELLULAR_LOCALIZATION	77	62	700	1330	1.15	hsa_GOTERM_BP_5
2.2E-06	RECEPTOR_ACTIVITY	62	45	715	1347	1.3	hsa_GOTERM_MF_2
2.2E-06	RECEPTOR_ACTIVITY	62	45	715	1347	1.3	hsa_GOTERM_MF_ALL
2.3E-06	pathway	58	40	719	1352	1.38	hsa_SP_COMMENT_TYPE
2.4E-06	LIPID_METABOLISM	51	33	726	1359	1.47	hsa_GOTERM_BP_4

2.8E-06	zinc-finger	65	49	712	1343	1.25	hsa_SP_PIR_KEYWORDS
3.7E-06	REGULATION_OF_PHYSIOLOGICAL_PROCESS	156	174	621	1218	0.68	hsa_GOTERM_BP_2
5.2E-06	PROTEIN_COMPLEX	100	96	677	1296	0.9	hsa_GOTERM_CC_1
6.3E-06	BP00125:_INTRACELLULAR_PROTEIN_TRAFFIC	61	46	716	1346	1.25	hsa_PANTHER_TERM_BP
6.9E-06	BP00193:_DEVELOPMENTAL_PROCESSES	76	65	701	1327	1.07	hsa_PANTHER_TERM_BP
1.0E-05	REGULATION_OF_CELLULAR_PHYSIOLOGICAL_PROC	147	165	630	1227	0.67	hsa_GOTERM_BP_3
1.1E-05	transport	58	44	719	1348	1.24	hsa_SP_PIR_KEYWORDS
1.1E-05	BP00019:_LIPID,_FATTY_ACID_AND_STEROID_METAB	43	27	734	1365	1.51	hsa_PANTHER_TERM_BP
1.2E-05	BP00103:_CELL_SURFACE_RECEPTOR_MEDIATED_SI	39	23	738	1369	1.6	hsa_PANTHER_TERM_BP
1.2E-05	REGULATION_OF_BIOLOGICAL_PROCESS	164	191	613	1201	0.62	hsa_GOTERM_BP_1
1.3E-05	hydrolase	66	54	711	1338	1.13	hsa_SP_PIR_KEYWORDS
1.5E-05	LIGASE_ACTIVITY	48	33	729	1359	1.38	hsa_GOTERM_MF_2
1.5E-05	LIGASE_ACTIVITY	48	33	729	1359	1.38	hsa_GOTERM_MF_ALL
1.5E-05	RESPONSE_TO_STIMULUS	98	97	679	1295	0.86	hsa_GOTERM_BP_1
2.0E-05	receptor	47	32	730	1360	1.4	hsa_SP_PIR_KEYWORDS
2.2E-05	DEVELOPMENT	115	122	662	1270	0.76	hsa_GOTERM_BP_1
2.2E-05	PLASMA_MEMBRANE	71	62	706	1330	1.04	hsa_GOTERM_CC_3
2.8E-05	CELLULAR_BIOSYNTHESIS	72	64	705	1328	1.01	hsa_GOTERM_BP_4
2.9E-05	TRANSFERASE_ACTIVITY,_TRANSFERRING_PHOSPH	64	54	713	1338	1.09	hsa_GOTERM_MF_3
2.9E-05	TRANSFERASE_ACTIVITY,_TRANSFERRING_PHOSPH	64	54	713	1338	1.09	hsa_GOTERM_MF_ALL
3.0E-05	MF00170:_LIGASE	34	19	743	1373	1.68	hsa_PANTHER_TERM_MF
3.1E-05	nucleotide-binding	73	65	704	1327	1.01	hsa_SP_PIR_KEYWORDS
3.3E-05	ADENYL_NUCLEOTIDE_BINDING	70	62	707	1330	1.02	hsa_GOTERM_MF_4
3.3E-05	ADENYL_NUCLEOTIDE_BINDING	70	62	707	1330	1.02	hsa_GOTERM_MF_ALL
3.3E-05	REGULATION_OF_CELLULAR_PROCESS	150	175	627	1217	0.62	hsa_GOTERM_BP_2
3.7E-05	REGULATION_OF_CELLULAR_METABOLISM	95	96	682	1296	0.83	hsa_GOTERM_BP_4
3.8E-05	BP00071:_PROTEOLYSIS	40	26	737	1366	1.46	hsa_PANTHER_TERM_BP
4.8E-05	REGULATION_OF_METABOLISM	101	105	676	1287	0.79	hsa_GOTERM_BP_3
5.0E-05	C00001:H2O	39	25	738	1367	1.48	hsa_KEGG_COMPOUND
6.4E-05	BP00108:_RECEPTOR_PROTEIN_TYROSINE_KINASE_	16	4	761	1388	2.84	hsa_PANTHER_TERM_BP
7.1E-05	MF00271:_OTHER_MEMBRANE_TRAFFIC_PROTEIN	13	2	764	1390	3.54	hsa_PANTHER_TERM_MF
7.2E-05	glycosylation_site:N-linked_(GlcNAc...)	84	83	693	1309	0.86	hsa_UP_SEQ_FEATURE
7.4E-05	CARBOHYDRATE_METABOLISM	51	40	726	1352	1.19	hsa_GOTERM_BP_4
7.7E-05	TRANSCRIPTION	95	98	682	1294	0.8	hsa_GOTERM_BP_5
7.9E-05	helix	106	114	671	1278	0.74	hsa_UP_SEQ_FEATURE
8.1E-05	domain	70	64	707	1328	0.97	hsa_SP_COMMENT_TYPE
8.3E-05	PTM	107	115	670	1277	0.74	hsa_SP_COMMENT_TYPE
9.6E-05	domain:Ig-like_C2-type_2	11	1	766	1391	4.3	hsa_UP_SEQ_FEATURE
9.6E-05	repeat:WD_4	11	1	766	1391	4.3	hsa_UP_SEQ_FEATURE
9.6E-05	domain:Ig-like_C2-type_1	11	1	766	1391	4.3	hsa_UP_SEQ_FEATURE
9.7E-05	signal_peptide	74	70	703	1322	0.92	hsa_UP_SEQ_FEATURE

1.0E-04	INTRINSIC_TO_PLASMA_MEMBRANE	43	31	734	1361	1.31	hsa_GOTERM_CC_4
1.0E-04	INTEGRAL_TO_PLASMA_MEMBRANE	43	31	734	1361	1.31	hsa_GOTERM_CC_5
1.1E-04	PS50294:PS50294	14	3	763	1389	3.06	hsa_PROSITE_NAME
1.1E-04	strand	109	120	668	1272	0.7	hsa_UP_SEQ_FEATURE
1.1E-04	BP00063:_PROTEIN_MODIFICATION	66	60	711	1332	0.98	hsa_PANTHER_TERM_BP
1.3E-04	signal	72	69	705	1323	0.9	hsa_SP_PIR_KEYWORDS
1.3E-04	NON-MEMBRANE-BOUND_ORGANELLE	69	65	708	1327	0.93	hsa_GOTERM_CC_2
1.3E-04	INTRACELLULAR_NON-MEMBRANE-BOUND_ORGANEI	69	65	708	1327	0.93	hsa_GOTERM_CC_3
1.3E-04	INTRACELLULAR_NON-MEMBRANE-BOUND_ORGANEI	69	65	708	1327	0.93	hsa_GOTERM_CC_4
1.4E-04	TISSUE_DEVELOPMENT	44	33	733	1359	1.26	hsa_GOTERM_BP_2
1.7E-04	turn	107	118	670	1274	0.7	hsa_UP_SEQ_FEATURE
1.7E-04	MITOCHONDRION	49	40	728	1352	1.13	hsa_GOTERM_CC_4
1.7E-04	MITOCHONDRION	49	40	728	1352	1.13	hsa_GOTERM_CC_5
1.7E-04	SM00320:WD40	12	2	765	1390	3.43	hsa_SMART_NAME
1.8E-04	glycoprotein	88	92	689	1300	0.78	hsa_SP_PIR_KEYWORDS
1.9E-04	REGULATION_OF_NUCLEOBASE,_NUCLEOSIDE,_NUC	85	88	692	1304	0.79	hsa_GOTERM_BP_5
2.0E-04	IONOTROPIC_GLUTAMATE_RECEPTOR_PATHWAY	0	20	777	1372	#NUM!	hsa_PANTHER_PATHWAY
2.3E-04	HYDROLASE_ACTIVITY,_ACTING_ON_ESTER_BONDS	39	28	738	1364	1.32	hsa_GOTERM_MF_3
2.3E-04	HYDROLASE_ACTIVITY,_ACTING_ON_ESTER_BONDS	39	28	738	1364	1.32	hsa_GOTERM_MF_ALL
2.4E-04	BP00064:_PROTEIN_PHOSPHORYLATION	41	31	736	1361	1.24	hsa_PANTHER_TERM_BP
2.4E-04	PDGF_SIGNALING_PATHWAY	17	6	760	1386	2.34	hsa_PANTHER_PATHWAY
2.5E-04	BP00061:_PROTEIN_BIOSYNTHESIS	18	7	759	1385	2.2	hsa_PANTHER_TERM_BP
2.5E-04	MANGANESE_ION_BINDING	10	1	767	1391	4.16	hsa_GOTERM_MF_5
2.5E-04	MANGANESE_ION_BINDING	10	1	767	1391	4.16	hsa_GOTERM_MF_ALL
2.5E-04	manganese	10	1	767	1391	4.16	hsa_SP_PIR_KEYWORDS
2.5E-04	wd_repeat	13	3	764	1389	2.96	hsa_SP_PIR_KEYWORDS
2.6E-04	DNA_BINDING	78	79	699	1313	0.82	hsa_GOTERM_MF_3
2.6E-04	DNA_BINDING	78	79	699	1313	0.82	hsa_GOTERM_MF_ALL
2.6E-04	PS00061:ADH_SHORT	8	0	769	1392	#DIV/0!	hsa_PROSITE_NAME
2.8E-04	BP00289:_OTHER_METABOLISM	33	22	744	1370	1.43	hsa_PANTHER_TERM_BP
3.2E-04	ECTODERM_DEVELOPMENT	27	16	750	1376	1.6	hsa_GOTERM_BP_3
3.2E-04	BP00246:_ECTODERM_DEVELOPMENT	25	14	752	1378	1.68	hsa_PANTHER_TERM_BP
3.5E-04	MF00141:_HYDROLASE	38	28	739	1364	1.28	hsa_PANTHER_TERM_MF
3.8E-04	mitochondrion	45	37	732	1355	1.12	hsa_SP_PIR_KEYWORDS
3.8E-04	PROTEIN_BIOSYNTHESIS	43	34	734	1358	1.18	hsa_GOTERM_BP_5
3.8E-04	MF00123:_OXIDOREDUCTASE	36	26	741	1366	1.31	hsa_PANTHER_TERM_MF
4.2E-04	oxidoreductase	34	24	743	1368	1.34	hsa_SP_PIR_KEYWORDS
4.2E-04	MF00001:_RECEPTOR	38	29	739	1363	1.23	hsa_PANTHER_TERM_MF
4.2E-04	2.7.1.112	11	2	766	1390	3.3	hsa_EC_NUMBER
4.2E-04	INTERLEUKIN_SIGNALING_PATHWAY	11	2	766	1390	3.3	hsa_PANTHER_PATHWAY
4.2E-04	fad	11	2	766	1390	3.3	hsa_SP_PIR_KEYWORDS

4.8E-04	OXIDOREDUCTASE_ACTIVITY	46	39	731	1353	1.08	hsa_GOTERM_MF_2
4.8E-04	OXIDOREDUCTASE_ACTIVITY	46	39	731	1353	1.08	hsa_GOTERM_MF_ALL
4.8E-04	kinase	46	39	731	1353	1.08	hsa_SP_PIR_KEYWORDS
5.0E-04	MF00283:_UBIQUITIN-PROTEIN_LIGASE	16	6	761	1386	2.26	hsa_PANTHER_TERM_MF
5.4E-04	MACROMOLECULE_BIOSYNTHESIS	47	40	730	1352	1.07	hsa_GOTERM_BP_4
5.4E-04	MACROMOLECULE_BIOSYNTHESIS	47	40	730	1352	1.07	hsa_GOTERM_BP_5
5.9E-04	STEROID_METABOLISM	19	9	758	1383	1.92	hsa_GOTERM_BP_5
5.9E-04	MF00086:_OTHER_TRANSPORTER	19	9	758	1383	1.92	hsa_PANTHER_TERM_MF
5.9E-04	BP00290:_LIPID_METABOLISM	12	3	765	1389	2.84	hsa_PANTHER_TERM_BP
5.9E-04	repeat:WD_1	12	3	765	1389	2.84	hsa_UP_SEQ_FEATURE
5.9E-04	repeat:WD_2	12	3	765	1389	2.84	hsa_UP_SEQ_FEATURE
5.9E-04	repeat:WD_3	12	3	765	1389	2.84	hsa_UP_SEQ_FEATURE
6.4E-04	PD000093:SH2	9	1	768	1391	4.01	hsa_PRODOM_NAME
6.4E-04	carbohydrate_metabolism	9	1	768	1391	4.01	hsa_SP_PIR_KEYWORDS
6.4E-04	repeat:WD_5	9	1	768	1391	4.01	hsa_UP_SEQ_FEATURE
6.4E-04	domain:Ig-like_C2-type_3	9	1	768	1391	4.01	hsa_UP_SEQ_FEATURE
6.7E-04	CYTOSOL	25	15	752	1377	1.58	hsa_GOTERM_CC_4
7.0E-04	VESICLE-MEDIATED_TRANSPORT	51	46	726	1346	0.99	hsa_GOTERM_BP_4
7.0E-04	VESICLE-MEDIATED_TRANSPORT	51	46	726	1346	0.99	hsa_GOTERM_BP_5
7.0E-04	KINASE_ACTIVITY	51	46	726	1346	0.99	hsa_GOTERM_MF_4
7.0E-04	KINASE_ACTIVITY	51	46	726	1346	0.99	hsa_GOTERM_MF_ALL
7.1E-04	CELL_CYCLE	63	62	714	1330	0.86	hsa_GOTERM_BP_3
7.1E-04	ATP_BINDING	63	62	714	1330	0.86	hsa_GOTERM_MF_5
7.1E-04	ATP_BINDING	63	62	714	1330	0.86	hsa_GOTERM_MF_ALL
7.6E-04	INTRACELLULAR_SIGNALING_CASCADE	66	67	711	1325	0.82	hsa_GOTERM_BP_4
8.1E-04	AROMATIC_COMPOUND_METABOLISM	17	7	760	1385	2.12	hsa_GOTERM_BP_4
8.2E-04	CARBOXYLIC_ACID_METABOLISM	36	28	741	1364	1.2	hsa_GOTERM_BP_5
8.5E-04	PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	22	12	755	1380	1.72	hsa_GOTERM_MF_4
8.5E-04	PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY	22	12	755	1380	1.72	hsa_GOTERM_MF_ALL
8.6E-04	atp-binding	55	52	722	1340	0.92	hsa_SP_PIR_KEYWORDS
9.6E-04	BP00111:_INTRACELLULAR_SIGNALING_CASCADE	37	29	740	1363	1.19	hsa_PANTHER_TERM_BP
9.8E-04	CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANS	62	62	715	1330	0.84	hsa_GOTERM_BP_4
1.0E-03	EMBRYONIC_DEVELOPMENT	10	2	767	1390	3.16	hsa_GOTERM_BP_2
1.1E-03	CELLULAR_COMPONENT_UNKNOWN	37	30	740	1362	1.14	hsa_GOTERM_CC_1
1.1E-03	MF00131:_TRANSFERASE	45	40	732	1352	1.01	hsa_PANTHER_TERM_MF
1.2E-03	MF00126:_DEHYDROGENASE	22	13	755	1379	1.6	hsa_PANTHER_TERM_MF
1.2E-03	BP00034:_DNA_METABOLISM	17	8	760	1384	1.93	hsa_PANTHER_TERM_BP
1.2E-03	flavoprotein	13	4	764	1388	2.54	hsa_SP_PIR_KEYWORDS
1.3E-03	COFACTOR_BINDING	11	3	766	1389	2.72	hsa_GOTERM_MF_2
1.3E-03	COENZYME_BINDING	11	3	766	1389	2.72	hsa_GOTERM_MF_3
1.3E-03	ELECTROCHEMICAL_POTENTIAL-DRIVEN_TRANSPOR	11	3	766	1389	2.72	hsa_GOTERM_MF_3

1.3E-03	PORTER_ACTIVITY	11	3	766	1389	2.72	hsa_GOTERM_MF_4
1.3E-03	ELECTROCHEMICAL_POTENTIAL-DRIVEN_TRANSPOR	11	3	766	1389	2.72	hsa_GOTERM_MF_ALL
1.3E-03	COFACTOR_BINDING	11	3	766	1389	2.72	hsa_GOTERM_MF_ALL
1.3E-03	COENZYME_BINDING	11	3	766	1389	2.72	hsa_GOTERM_MF_ALL
1.3E-03	PORTER_ACTIVITY	11	3	766	1389	2.72	hsa_GOTERM_MF_ALL
1.4E-03	LYASE_ACTIVITY	19	10	758	1382	1.77	hsa_GOTERM_MF_2
1.4E-03	LYASE_ACTIVITY	19	10	758	1382	1.77	hsa_GOTERM_MF_ALL
1.4E-03	MF00036:_TRANSCRIPTION_FACTOR	58	58	719	1334	0.84	hsa_PANTHER_TERM_MF
1.4E-03	ORGANIC_ACID_METABOLISM	36	29	741	1363	1.15	hsa_GOTERM_BP_4
1.4E-03	protease	21	12	756	1380	1.65	hsa_SP_PIR_KEYWORDS
1.5E-03	BP00199:_NEUROGENESIS	23	14	754	1378	1.56	hsa_PANTHER_TERM_BP
1.5E-03	HYDROLASE_ACTIVITY,_ACTING_ON_ACID_ANHYDRI	33	26	744	1366	1.19	hsa_GOTERM_MF_4
1.5E-03	PYROPHOSPHATASE_ACTIVITY	33	26	744	1366	1.19	hsa_GOTERM_MF_5
1.5E-03	HYDROLASE_ACTIVITY,_ACTING_ON_ACID_ANHYDRI	33	26	744	1366	1.19	hsa_GOTERM_MF_ALL
1.5E-03	PYROPHOSPHATASE_ACTIVITY	33	26	744	1366	1.19	hsa_GOTERM_MF_ALL
1.5E-03	3d-structure	98	115	679	1277	0.61	hsa_SP_PIR_KEYWORDS
1.5E-03	disease	85	96	692	1296	0.67	hsa_SP_COMMENT_TYPE
1.6E-03	sh2_domain	8	1	769	1391	3.84	hsa_SP_PIR_KEYWORDS
1.6E-03	RECEPTOR_BINDING	44	40	733	1352	0.98	hsa_GOTERM_MF_2
1.6E-03	RECEPTOR_BINDING	44	40	733	1352	0.98	hsa_GOTERM_MF_3
1.6E-03	RECEPTOR_BINDING	44	40	733	1352	0.98	hsa_GOTERM_MF_ALL
1.7E-03	PHOSPHORUS_METABOLISM	53	52	724	1340	0.87	hsa_GOTERM_BP_4
1.7E-03	PHOSPHATE_METABOLISM	53	52	724	1340	0.87	hsa_GOTERM_BP_5
1.8E-03	General_function_prediction_only	18	9	759	1383	1.84	hsa_COG_KOG_ONTOLOGY
1.9E-03	ELECTRON_TRANSPORT	23	15	754	1377	1.46	hsa_GOTERM_BP_4
1.9E-03	ELECTRON_TRANSPORT	23	15	754	1377	1.46	hsa_GOTERM_BP_5
1.9E-03	MF00153:_PROTEASE	23	15	754	1377	1.46	hsa_PANTHER_TERM_MF
1.9E-03	disease_mutation	57	58	720	1334	0.82	hsa_SP_PIR_KEYWORDS
2.0E-03	MF00039:_OTHER_TRANSCRIPTION_FACTOR	14	6	763	1386	2.06	hsa_PANTHER_TERM_MF
2.1E-03	DOUBLE-STRANDED_RNA_BINDING	6	0	771	1392	#DIV/0!	hsa_GOTERM_MF_4
2.1E-03	DOUBLE-STRANDED_RNA_BINDING	6	0	771	1392	#DIV/0!	hsa_GOTERM_MF_ALL
2.1E-03	METHYLMALONYL_PATHWAY	6	0	771	1392	#DIV/0!	hsa_PANTHER_PATHWAY
2.1E-03	BP00147:_OTHER_TRANSPORT	6	0	771	1392	#DIV/0!	hsa_PANTHER_TERM_BP
2.1E-03	MEMBRANE_LIPID_METABOLISM	13	5	764	1387	2.22	hsa_GOTERM_BP_5
2.1E-03	ORGANELLE_ORGANIZATION_AND_BIOGENESIS	52	51	725	1341	0.87	hsa_GOTERM_BP_4
2.1E-03	PEPTIDASE_ACTIVITY	26	18	751	1374	1.37	hsa_GOTERM_MF_3
2.1E-03	PEPTIDASE_ACTIVITY	26	18	751	1374	1.37	hsa_GOTERM_MF_ALL
2.1E-03	TRANSCRIPTION_REGULATOR_ACTIVITY	77	86	700	1306	0.68	hsa_GOTERM_MF_1
2.1E-03	TRANSCRIPTION_REGULATOR_ACTIVITY	77	86	700	1306	0.68	hsa_GOTERM_MF_ALL
2.4E-03	CARBOHYDRATE_TRANSPORT	9	2	768	1390	3.01	hsa_GOTERM_BP_4
2.4E-03	CARBOHYDRATE_TRANSPORT	9	2	768	1390	3.01	hsa_GOTERM_BP_5

2.4E-03	Ubl_conjugation_pathway	9	2	768	1390	3.01	hsa_SP_PIR_KEYWORDS
2.4E-03	LIPID_BIOSYNTHESIS	18	10	759	1382	1.69	hsa_GOTERM_BP_4
2.4E-03	LIPID_BIOSYNTHESIS	18	10	759	1382	1.69	hsa_GOTERM_BP_5
2.4E-03	LIPID_BINDING	18	10	759	1382	1.69	hsa_GOTERM_MF_2
2.4E-03	LIPID_BINDING	18	10	759	1382	1.69	hsa_GOTERM_MF_ALL
2.4E-03	MF00087:_TRANSFER/CARRIER_PROTEIN	18	10	759	1382	1.69	hsa_PANTHER_TERM_MF
2.4E-03	HYDROLASE_ACTIVITY,_ACTING_ON_ACID_ANHYDRI	33	27	744	1365	1.13	hsa_GOTERM_MF_3
2.4E-03	HYDROLASE_ACTIVITY,_ACTING_ON_ACID_ANHYDRI	33	27	744	1365	1.13	hsa_GOTERM_MF_ALL
2.7E-03	CHANNEL_OR_PORE_CLASS_TRANSPORTER_ACTIVI	15	7	762	1385	1.94	hsa_GOTERM_MF_2
2.7E-03	CHANNEL_OR_PORE_CLASS_TRANSPORTER_ACTIVI	15	7	762	1385	1.94	hsa_GOTERM_MF_ALL
2.7E-03	BP00137:_PROTEIN_TARGETING_AND_LOCALIZATION	15	7	762	1385	1.94	hsa_PANTHER_TERM_BP
2.7E-03	MF00107:_KINASE	36	31	741	1361	1.06	hsa_PANTHER_TERM_MF
2.8E-03	LIGASE_ACTIVITY,_FORMING_CARBON-NITROGEN_B	31	25	746	1367	1.15	hsa_GOTERM_MF_3
2.8E-03	LIGASE_ACTIVITY,_FORMING_CARBON-NITROGEN_B	31	25	746	1367	1.15	hsa_GOTERM_MF_ALL
3.1E-03	BP00040:_MRNA_TRANSCRIPTION	58	61	719	1331	0.77	hsa_PANTHER_TERM_BP
3.2E-03	transit_peptide	29	23	748	1369	1.18	hsa_SP_PIR_KEYWORDS
3.5E-03	ORGANISMAL_PHYSIOLOGICAL_PROCESS	75	85	702	1307	0.66	hsa_GOTERM_BP_2
3.6E-03	GENERATION_OF_PRECURSOR_METABOLITES_AND_	43	41	734	1351	0.91	hsa_GOTERM_BP_4
3.6E-03	NUCLEOSIDE-TRIPHOSPHATASE_ACTIVITY	30	24	747	1368	1.16	hsa_GOTERM_MF_ALL
3.6E-03	BP00047:_PRE-MRNA_PROCESSING	23	16	754	1376	1.36	hsa_PANTHER_TERM_BP
3.6E-03	MF00267:_MEMBRANE_TRAFFIC_PROTEIN	23	16	754	1376	1.36	hsa_PANTHER_TERM_MF
3.7E-03	UBIQUITIN-PROTEIN_LIGASE_ACTIVITY	27	21	750	1371	1.2	hsa_GOTERM_MF_ALL
3.7E-03	BP00001:_CARBOHYDRATE_METABOLISM	38	34	739	1358	1	hsa_PANTHER_TERM_BP
3.9E-03	RNA_METABOLISM	44	42	733	1350	0.91	hsa_GOTERM_BP_5
4.1E-03	CARBON-CARBON_LYASE_ACTIVITY	7	1	770	1391	3.65	hsa_GOTERM_MF_3
4.1E-03	CARBON-CARBON_LYASE_ACTIVITY	7	1	770	1391	3.65	hsa_GOTERM_MF_ALL
4.2E-03	GTP_BINDING	19	12	758	1380	1.5	hsa_GOTERM_MF_ALL
4.2E-03	PHOSPHORIC_MONOESTER_HYDROLASE_ACTIVITY	19	12	758	1380	1.5	hsa_GOTERM_MF_ALL
4.2E-03	GUANYL_NUCLEOTIDE_BINDING	19	12	758	1380	1.5	hsa_GOTERM_MF_ALL
4.2E-03	EXTRACELLULAR_SPACE	12	5	765	1387	2.1	hsa_GOTERM_CC_2
4.2E-03	PHOSPHOLIPID_BINDING	12	5	765	1387	2.1	hsa_GOTERM_MF_3
4.2E-03	PHOSPHOLIPID_BINDING	12	5	765	1387	2.1	hsa_GOTERM_MF_ALL
4.2E-03	MF00119:_SYNTHASE	12	5	765	1387	2.1	hsa_PANTHER_TERM_MF
4.4E-03	RNA_BINDING	48	48	729	1344	0.84	hsa_GOTERM_MF_3
4.4E-03	RNA_BINDING	48	48	729	1344	0.84	hsa_GOTERM_MF_ALL
4.7E-03	ION_CHANNEL_ACTIVITY	11	4	766	1388	2.3	hsa_GOTERM_MF_3
4.7E-03	ION_CHANNEL_ACTIVITY	11	4	766	1388	2.3	hsa_GOTERM_MF_ALL
5.1E-03	MF00197:_MISCELLANEOUS_FUNCTION	34	30	743	1362	1.02	hsa_PANTHER_TERM_MF
5.6E-03	CIRCULATION	8	2	769	1390	2.84	hsa_GOTERM_BP_3
5.8E-03	COATED_MEMBRANE	0	12	777	1380	-infinity	hsa_GOTERM_CC_3
5.9E-03	CARBOHYDRATE_TRANSPORTER_ACTIVITY	5	0	772	1392	NA	hsa_GOTERM_MF_2

6.2E-03	TRANSCRIPTION_FACTOR_ACTIVITY	35	32	742	1360	0.97	hsa_GOTERM_MF_2
6.2E-03	BP00036:_DNA_REPAIR	13	6	764	1386	1.96	hsa_PANTHER_TERM_BP
6.4E-03	BP00142:_ION_TRANSPORT	20	14	757	1378	1.36	hsa_PANTHER_TERM_BP
6.4E-03	BP00281:_ONCOGENESIS	20	14	757	1378	1.36	hsa_PANTHER_TERM_BP
6.9E-03	RESPONSE_TO_STRESS	55	60	722	1332	0.72	hsa_GOTERM_BP_2
1.1E-02	RESPONSE_TO_BIOTIC_STIMULUS	53	59	724	1333	0.69	hsa_GOTERM_BP_2
1.3E-02	SYNAPSE	7	2	770	1390	2.65	hsa_GOTERM_CC_1
1.5E-02	caution	61	72	716	1320	0.6	hsa_SP_COMMENT_TYPE
1.7E-02	interaction	78	98	699	1294	0.51	hsa_SP_COMMENT_TYPE
1.8E-02	MEMBRANE-ENCLOSED_LUMEN	33	33	744	1359	0.84	hsa_GOTERM_CC_1
2.4E-02	STRUCTURAL_MOLECULE_ACTIVITY	35	37	742	1355	0.76	hsa_GOTERM_MF_1

[1] All skipped exons were ranked according to switch scores. Genes with the top 1000 skipped exons (high switch scores) were compared with the genes encoding the bottom 1500 skipped exons (low switch scores). Gene sets were downloaded from DAVID (NIH; see complete list of 68 types of categories at http://david.abcc.ncifcrf.gov/) including Gene Ontology categories, PANTHER classifications, Protein domain categories from PFAM, SMART and BLOCKS, sets of genes that co-occur in publications, and others. Genes names were mapped to DAVID's internal IDs and a fisher's exact test was used to evaluate significance of enriched or depleted categories from all gene sets. P-values shown are not multiple test corrected.

Table S8. Motifs enriched in introns flanking SEs differentially regulated in tissues and cell lines.

Motif	Intron region[1]	SE expression[2]	Tissue	P-value[3]
UCUCUC	upstream	increased	cerebellum	1.1E-16
CUCUCU	upstream	increased	cerebellum	4.6E-14
UGCAUG	downstream	increased	skel. muscle	8.7E-12
ACUAAC	downstream	increased	skel. muscle	1.6E-07
GCAUGU	downstream	increased	skel. muscle	2.0E-07
AUGGCA	downstream	increased	heart	3.3E-07
UGCAUG	downstream	decreased	MCF7	3.8E-07
GACCCC	upstream	increased	HME	5.2E-07
GCAGCA	downstream	decreased	cerebellum	5.4E-07
CAGCAG	downstream	decreased	cerebellum	7.4E-07
UCUAAC	downstream	increased	skel. muscle	9.3E-07
CUCUUG	downstream	increased	heart	1.1E-06
CUCUCU	upstream	decreased	colon	1.2E-06
ACCUUU	downstream	increased	T47D	1.6E-06
ACUAAC	downstream	decreased	cerebellum	1.7E-06
GUCUUG	upstream	decreased	MCF7	2.0E-06
CCUUCC	downstream	increased	breast	2.2E-06
AGCAAG	downstream	increased	HME	2.6E-06
AAUGGC	downstream	increased	heart	2.9E-06
CUAACC	downstream	increased	skel. muscle	3.1E-06
UUGGAC	upstream	decreased	HME	3.6E-06
AGCAAG	downstream	increased	T47D	3.8E-06
GCUAAC	upstream	increased	cerebellum	3.8E-06
CUCCUC	upstream	increased	cerebellum	4.4E-06
UCUCUC	upstream	decreased	brain	4.8E-06
UAACAC	upstream	decreased	breast	5.1E-06
GUAUGU	upstream	increased	BT474	5.8E-06
ACCACC	upstream	decreased	cerebellum	6.4E-06
UCUCUC	upstream	decreased	colon	6.7E-06
GGUGGU	upstream	decreased	T47D	7.0E-06
GGGAAC	upstream	decreased	BT474	7.8E-06
CUCUCU	upstream	decreased	brain	8.0E-06
CAAAGU	upstream	increased	breast	8.3E-06
CUGUGC	downstream	increased	cerebellum	8.9E-06
GUGUGU	downstream	decreased	heart	8.9E-06
ACACAC	upstream	decreased	HME	9.3E-06
GGGCUC	upstream	increased	adipose	9.7E-06
GCAUGU	upstream	increased	cerebellum	9.8E-06
CUACCC	upstream	decreased	T47D	1.0E-05
UCUCUC	upstream	decreased	MB435	1.2E-05
AUGUAU	upstream	increased	BT474	1.2E-05
UAACCU	upstream	increased	brain	1.2E-05
GUAAAC	upstream	decreased	HME	1.3E-05
GUGGAC	upstream	decreased	HME	1.3E-05
AUUAUU	downstream	increased	MCF7	1.3E-05
ACACAC	downstream	decreased	colon	1.3E-05
UAGUAC	downstream	increased	testes	1.4E-05
CUCUCU	upstream	decreased	MB435	1.4E-05
UGUGGA	upstream	decreased	heart	1.4E-05
UUUUGG	downstream	increased	BT474	1.4E-05
CUACUA	downstream	decreased	BT474	1.5E-05
CUCUCU	upstream	increased	brain	1.5E-05
UGUGUG	downstream	decreased	heart	1.6E-05
ACACAC	upstream	increased	lymph node	1.6E-05
AAAUCC	upstream	increased	T47D	1.6E-05
UCCCAU	downstream	decreased	BT474	1.6E-05
CUAACC	upstream	increased	cerebellum	1.7E-05
UCUAAC	downstream	decreased	lymph node	1.7E-05
UGCAGG	downstream	decreased	liver	1.8E-05
GCUGGC	downstream	increased	cerebellum	1.8E-05

CAGUCC	downstream	decreased	BT474	1.8E-05
AUCAUA	downstream	increased	colon	1.8E-05
GAUUAU	downstream	decreased	lymph node	2.0E-05
UCUCUC	upstream	decreased	adipose	2.0E-05
AUCUCU	upstream	increased	adipose	2.0E-05
AGCAGC	downstream	decreased	cerebellum	2.2E-05
GUGCAU	downstream	increased	skel. muscle	2.3E-05
AUAUAU	downstream	increased	MCF7	2.4E-05
UGGUUU	downstream	increased	BT474	2.6E-05
CAGCAG	downstream	increased	testes	2.6E-05
GCUUCC	upstream	increased	MCF7	2.6E-05
UAUAUA	downstream	increased	HME	2.7E-05
GUGUGU	downstream	increased	brain	2.7E-05
CCCCAG	downstream	decreased	BT474	2.7E-05
GGUAAA	upstream	increased	liver	2.8E-05
UAGCUG	downstream	increased	MCF7	2.8E-05
CAAACC	upstream	decreased	BT474	2.8E-05
GGCACC	downstream	decreased	breast	2.8E-05
CCAGAA	upstream	increased	testes	3.0E-05
CUGAGU	upstream	increased	testes	3.2E-05
CACUAA	upstream	increased	cerebellum	3.4E-05
GGCUAC	downstream	increased	liver	3.4E-05
GUCCAC	downstream	decreased	heart	3.5E-05
AAGAUU	downstream	decreased	breast	3.5E-05
GUGACU	downstream	decreased	adipose	3.7E-05
UGCAGG	downstream	increased	HME	3.7E-05
UCCAGC	downstream	decreased	cerebellum	3.7E-05
CCCUUG	upstream	decreased	heart	3.8E-05
GUACAC	upstream	decreased	skel. muscle	4.0E-05
GGUAGG	downstream	decreased	testes	4.3E-05
CCCUCA	upstream	increased	lymph node	4.3E-05
CACACA	upstream	increased	lymph node	4.4E-05
UAUGUA	upstream	increased	BT474	4.4E-05
CAUGUG	upstream	increased	cerebellum	4.4E-05
GUGUAG	downstream	decreased	liver	4.5E-05
AUGUUU	downstream	decreased	testes	4.8E-05
ACACAC	upstream	decreased	MCF7	4.8E-05
GUAGCC	downstream	increased	heart	4.8E-05
CCCCAG	downstream	decreased	T47D	4.9E-05
UAAUAA	upstream	decreased	skel. muscle	5.0E-05
UGAGUG	upstream	increased	testes	5.0E-05
AGGGUU	upstream	increased	breast	5.1E-05
UUUGGA	upstream	increased	breast	5.2E-05
UGUGCA	downstream	increased	cerebellum	5.3E-05
AUGGGU	downstream	increased	testes	5.4E-05
UACUGA	downstream	decreased	BT474	5.6E-05
GGACUC	upstream	increased	BT474	5.7E-05
GACUCC	upstream	increased	HME	5.7E-05
AUAUCC	upstream	decreased	T47D	5.8E-05
ACUAUU	downstream	increased	MCF7	5.8E-05
CUUGUG	downstream	decreased	MB435	5.8E-05
CUAAAC	downstream	decreased	heart	5.9E-05
CCAAGC	upstream	increased	breast	6.0E-05
GACAUG	upstream	decreased	lymph node	6.1E-05
UAUCAU	upstream	decreased	brain	6.3E-05
AACUAC	downstream	increased	skel. muscle	6.5E-05
UGGAUG	downstream	decreased	lymph node	6.6E-05
GUAUCU	upstream	decreased	breast	6.7E-05
UACAAC	downstream	decreased	liver	6.8E-05
AUUAUU	downstream	decreased	brain	6.8E-05
AGCCAC	upstream	increased	liver	6.9E-05
UCUGAG	upstream	increased	lymph node	6.9E-05
UGUAUG	upstream	increased	BT474	7.0E-05
GACUGU	upstream	increased	adipose	7.1E-05

AGGGUA	downstream	increased	HME	7.3E-05
CAAUGA	upstream	increased	heart	7.4E-05
AUAAUC	upstream	decreased	T47D	7.5E-05
UGGACC	upstream	decreased	HME	7.6E-05
UCUUCU	downstream	increased	BT474	7.7E-05
AGUGCC	upstream	decreased	HME	7.8E-05
CUGAAU	downstream	decreased	breast	7.8E-05
GCAGCA	downstream	increased	colon	8.1E-05
AACUAC	downstream	decreased	HME	8.2E-05
UCUCUC	upstream	increased	brain	8.4E-05
UUGUUA	downstream	decreased	BT474	8.4E-05
UGUGCU	downstream	increased	heart	8.4E-05
AACUAC	downstream	decreased	MB435	8.5E-05
GCACCU	downstream	decreased	cerebellum	8.5E-05
GCAUCC	downstream	decreased	HME	8.7E-05
GUUUAC	downstream	increased	MCF7	8.7E-05
CCUCAA	upstream	decreased	MB435	8.7E-05
AUAACU	downstream	increased	adipose	8.8E-05
GCAUGG	downstream	increased	skel. muscle	8.8E-05
AUGUUC	upstream	increased	cerebellum	9.0E-05
UGUAUC	upstream	decreased	breast	9.0E-05
GCAGCA	downstream	increased	testes	9.1E-05
UCUUGC	downstream	increased	heart	9.1E-05
AUGGGU	upstream	increased	T47D	9.2E-05
UAACCU	downstream	decreased	lymph node	9.3E-05
GUAAGC	downstream	increased	MCF7	9.4E-05
CCCUAG	upstream	decreased	cerebellum	9.6E-05
GGUAAA	upstream	increased	brain	9.7E-05
GUGCCA	upstream	increased	brain	9.9E-05
ACAUGC	downstream	increased	liver	1.0E-04
UCUGUC	upstream	decreased	lymph node	1.0E-04
CAUAAC	downstream	increased	adipose	1.0E-04
GACAUC	downstream	decreased	breast	1.0E-04
UGCAUG	downstream	increased	cerebellum	1.0E-04
UUAAAA	upstream	increased	HME	1.0E-04
UAAAAG	upstream	decreased	skel. muscle	1.1E-04
GGAUAC	upstream	increased	MCF7	1.1E-04
AGCAUA	downstream	decreased	BT474	1.1E-04
ACAUGG	upstream	decreased	skel. muscle	1.1E-04
CUGGAG	upstream	decreased	breast	1.1E-04
AUGUUC	downstream	decreased	colon	1.1E-04
GACCCC	upstream	increased	BT474	1.1E-04
GGGGUA	upstream	increased	skel. muscle	1.1E-04
GGACUC	upstream	increased	HME	1.2E-04
AUCCUA	upstream	decreased	BT474	1.2E-04
GUUCCC	downstream	increased	MB435	1.2E-04
GCUGAC	upstream	increased	BT474	1.2E-04
UAACCU	upstream	increased	cerebellum	1.2E-04
UUUUGA	downstream	increased	lymph node	1.2E-04
AGGUAG	downstream	increased	MB435	1.2E-04
GACUAA	upstream	increased	cerebellum	1.2E-04
GAGACU	upstream	decreased	breast	1.3E-04
AAUCCU	upstream	decreased	BT474	1.3E-04
AUGUCU	upstream	decreased	heart	1.3E-04
CACCUA	downstream	increased	adipose	1.3E-04
ACUACU	downstream	decreased	HME	1.3E-04
CAGACA	downstream	decreased	colon	1.3E-04
ACUGCC	upstream	increased	heart	1.3E-04
UUAUUA	downstream	decreased	T47D	1.3E-04
GUCAUG	downstream	increased	breast	1.3E-04
AGGUAG	downstream	decreased	cerebellum	1.4E-04
GGAGGA	upstream	increased	breast	1.4E-04
CCACCA	upstream	increased	T47D	1.4E-04
AUCACU	downstream	increased	lymph node	1.4E-04

UUGCAC	downstream	decreased	cerebellum	1.4E-04
UCUCUC	upstream	decreased	breast	1.4E-04
UGGUUU	downstream	increased	HME	1.4E-04
UAUACA	downstream	increased	MB435	1.5E-04
UAAUAA	downstream	increased	skel. muscle	1.5E-04
CUUCUU	downstream	increased	T47D	1.5E-04
UCCAAG	upstream	increased	BT474	1.5E-04
GGGCUC	upstream	increased	breast	1.5E-04
GUGUGU	downstream	decreased	colon	1.5E-04
UGAAAA	downstream	increased	skel. muscle	1.5E-04
GGUAUC	upstream	decreased	breast	1.5E-04
AUCUGA	downstream	decreased	adipose	1.5E-04
CUGGUA	upstream	increased	MB435	1.5E-04
UACUAA	downstream	increased	skel. muscle	1.5E-04
ACUAGA	downstream	decreased	liver	1.5E-04
UCAGCU	downstream	increased	breast	1.5E-04
GUACUU	downstream	increased	brain	1.6E-04
ACAACA	upstream	increased	lymph node	1.6E-04
AAGCUC	upstream	increased	HME	1.6E-04
UAGGCC	downstream	decreased	liver	1.6E-04
UGCUCU	downstream	decreased	cerebellum	1.6E-04
CUCACC	downstream	decreased	cerebellum	1.6E-04
GAACUA	downstream	increased	MB435	1.6E-04
UAAUAA	upstream	increased	liver	1.6E-04
CUCAUU	upstream	decreased	breast	1.6E-04
AGCUGG	downstream	decreased	adipose	1.6E-04
AAUGGC	downstream	increased	skel. muscle	1.6E-04
CAUGCA	downstream	increased	MB435	1.6E-04
GUACUC	downstream	decreased	colon	1.6E-04
CAAGCC	upstream	increased	breast	1.7E-04
CAGCAA	upstream	decreased	skel. muscle	1.7E-04
AUAUAU	downstream	increased	HME	1.7E-04
UACACC	upstream	decreased	testes	1.7E-04
GGCAAG	upstream	increased	MCF7	1.7E-04
UCUAUC	upstream	increased	brain	1.7E-04
UGCAGG	downstream	decreased	cerebellum	1.7E-04
ACUGCC	downstream	increased	skel. muscle	1.7E-04
GAAAGG	upstream	increased	MB435	1.7E-04
ACACAC	upstream	increased	colon	1.7E-04
AAGGUU	upstream	increased	breast	1.7E-04
AUGAGU	upstream	increased	heart	1.7E-04
ACCUUU	downstream	decreased	colon	1.7E-04
UACAAG	upstream	decreased	breast	1.8E-04
GGCUUA	upstream	increased	BT474	1.8E-04
GGUAAA	upstream	decreased	BT474	1.8E-04
CUAGAG	upstream	increased	adipose	1.8E-04
CUAAGA	downstream	increased	brain	1.8E-04
UUUAGA	downstream	increased	MB435	1.8E-04
GGCUAA	upstream	decreased	MCF7	1.8E-04
ACACAC	downstream	increased	testes	1.8E-04
CUGGAC	upstream	increased	heart	1.8E-04
GCAGGC	downstream	decreased	HME	1.9E-04
CUCAGU	upstream	decreased	MCF7	1.9E-04
ACUGGG	downstream	decreased	MCF7	1.9E-04
GACUCA	upstream	decreased	T47D	1.9E-04
GGUACU	downstream	increased	BT474	1.9E-04
GUUGAC	upstream	increased	MCF7	2.0E-04
UACCUU	downstream	increased	T47D	2.0E-04
AAUGGA	upstream	increased	T47D	2.0E-04
AGUGUU	downstream	increased	cerebellum	2.1E-04
GCAUCA	upstream	decreased	breast	2.1E-04
UGCAUG	downstream	increased	heart	2.1E-04
CCAGAA	downstream	decreased	MCF7	2.1E-04
CUAACC	downstream	decreased	cerebellum	2.1E-04

CCUCUA	upstream	decreased	breast	2.1E-04
CUCUAG	upstream	decreased	MB435	2.1E-04
CACACA	upstream	decreased	T47D	2.1E-04
AACUAC	downstream	increased	brain	2.1E-04
CACCUG	downstream	increased	MCF7	2.1E-04
AGGGCA	downstream	decreased	adipose	2.1E-04
UCUAGG	downstream	increased	lymph node	2.2E-04
CACACA	upstream	decreased	HME	2.2E-04
GGACUC	upstream	increased	T47D	2.2E-04
CAUCUC	upstream	increased	adipose	2.2E-04
GACCCC	downstream	increased	MB435	2.2E-04
GGGUAG	downstream	increased	heart	2.2E-04
GUUAAC	downstream	decreased	HME	2.2E-04
AGCAGC	downstream	increased	testes	2.3E-04
GUUUUA	downstream	increased	heart	2.3E-04
GAAAGG	upstream	increased	testes	2.3E-04
UGUAGG	upstream	increased	testes	2.3E-04
AACUUC	upstream	increased	breast	2.3E-04
GGUUAC	upstream	increased	breast	2.3E-04
GUUUUA	downstream	increased	skel. muscle	2.3E-04
ACUAUC	upstream	increased	adipose	2.3E-04
UAAGAU	upstream	decreased	adipose	2.4E-04
ACAUUU	downstream	increased	colon	2.4E-04
UCUCUC	downstream	increased	brain	2.4E-04
AGCUAC	upstream	increased	breast	2.4E-04
AUAUGU	downstream	decreased	HME	2.4E-04
CUCUAC	upstream	decreased	T47D	2.4E-04
AGCCCA	downstream	decreased	testes	2.4E-04
UGUCAU	downstream	decreased	brain	2.5E-04
UGACCC	upstream	decreased	breast	2.5E-04
CCCUAA	upstream	decreased	brain	2.5E-04
AAAAGU	upstream	decreased	MCF7	2.5E-04
CAUGUC	upstream	decreased	HME	2.5E-04
UGGAGG	upstream	decreased	adipose	2.5E-04
GGUGCU	downstream	decreased	BT474	2.5E-04
GCCUGA	upstream	decreased	liver	2.5E-04
GCCAUC	upstream	decreased	brain	2.5E-04
ACCUCU	downstream	decreased	cerebellum	2.6E-04
AACUUG	downstream	decreased	cerebellum	2.6E-04
AGCUGG	downstream	increased	MCF7	2.6E-04
GAUACC	upstream	increased	MCF7	2.6E-04
GAUUAA	upstream	increased	breast	2.6E-04
UACUCU	upstream	decreased	adipose	2.6E-04
ACAUCA	downstream	increased	MCF7	2.7E-04
GUGUAU	upstream	decreased	MCF7	2.7E-04
CCAAAA	upstream	increased	BT474	2.7E-04
AAACCU	upstream	increased	heart	2.7E-04
GGGCAC	downstream	increased	BT474	2.8E-04
CACACA	downstream	decreased	colon	2.8E-04
AUUAUG	downstream	increased	T47D	2.8E-04
AACUAA	downstream	decreased	colon	2.8E-04
UCCAAA	upstream	increased	lymph node	2.8E-04
CAAGCU	upstream	increased	adipose	2.8E-04
ACUGCC	downstream	decreased	MB435	2.8E-04
UUACUA	downstream	decreased	HME	2.8E-04
GGUUGG	upstream	increased	breast	2.9E-04
CUAGUC	downstream	increased	testes	2.9E-04
UAAGGU	upstream	decreased	BT474	2.9E-04
AAGGGA	downstream	decreased	cerebellum	2.9E-04
UUAUAC	upstream	increased	adipose	2.9E-04
GACUAG	downstream	decreased	T47D	2.9E-04
GUGUGC	downstream	increased	skel. muscle	2.9E-04
CUGCCC	downstream	decreased	lymph node	2.9E-04
CUGUCU	upstream	decreased	brain	3.0E-04

GUGUGG	upstream	increased	cerebellum	3.0E-04
UGCUGC	upstream	increased	MB435	3.0E-04
CCCAAA	downstream	increased	breast	3.0E-04
AGCAUA	downstream	increased	testes	3.0E-04
CUGCAU	upstream	increased	MCF7	3.0E-04
ACACAC	upstream	decreased	T47D	3.0E-04
AAAACU	downstream	increased	breast	3.0E-04
GUAUUU	upstream	increased	colon	3.0E-04
GCACAA	upstream	increased	adipose	3.0E-04
GACCCU	upstream	decreased	breast	3.0E-04
UUGAAA	downstream	increased	skel. muscle	3.0E-04
AUCAUA	downstream	decreased	MCF7	3.0E-04
ACUGAC	upstream	decreased	MB435	3.0E-04
UCCCCA	downstream	decreased	BT474	3.1E-04
AAGUGU	downstream	increased	heart	3.1E-04
GAGUAA	downstream	increased	brain	3.1E-04
UUAUCU	downstream	decreased	heart	3.1E-04
UAGCAA	downstream	increased	breast	3.2E-04
AUGAAA	downstream	decreased	skel. muscle	3.2E-04
CUCUCU	downstream	increased	brain	3.2E-04
GCCUGC	downstream	increased	skel. muscle	3.2E-04
UGUGUG	downstream	decreased	colon	3.2E-04
GAUAUC	upstream	increased	breast	3.2E-04
AGUUCC	downstream	decreased	BT474	3.3E-04
GGUUUA	upstream	increased	MB435	3.3E-04
AGCCCA	downstream	increased	MCF7	3.3E-04
UGUCUG	downstream	decreased	colon	3.3E-04
ACUACU	downstream	decreased	MCF7	3.3E-04
GGGUCC	upstream	increased	MB435	3.3E-04
ACAACU	upstream	decreased	liver	3.3E-04
CUGAUC	downstream	decreased	adipose	3.4E-04
UUGGUG	upstream	increased	BT474	3.4E-04
UUCUAA	downstream	increased	skel. muscle	3.4E-04
ACUGGC	upstream	increased	heart	3.4E-04
AUCUAA	upstream	increased	heart	3.4E-04
CUAAUU	upstream	decreased	HME	3.4E-04
ACUUGU	downstream	decreased	MB435	3.4E-04
UCUUGC	upstream	increased	heart	3.4E-04
CCCUUC	upstream	decreased	T47D	3.4E-04
GACCUA	downstream	increased	adipose	3.4E-04
AGACAA	downstream	increased	testes	3.4E-04
UACUAA	downstream	decreased	HME	3.4E-04
CAGUAA	downstream	decreased	brain	3.5E-04
GAGAGA	downstream	increased	breast	3.5E-04
UUGGAC	upstream	decreased	MB435	3.5E-04
AAGUGG	upstream	increased	cerebellum	3.5E-04

[1] Motifs were counted in the region -150 to -30 upstream of the 5'ss for “upstream”, and in the region +10 to +150 downstream of the 3'ss for “downstream”.

[2] Motifs were counted in the regions flanking skipped exons whos expression was determined to be significantly increased or decreased in each tissue.

[3] Significance relative to control hexamers was assessed using a binomial test (see Supplementary Information). Only motifs passing Bonferroni cutoff (1/no. motifs tested, ~4000) are shown. Given ~4000 motifs, 15 tissues, 2 regions, and 2 directions of regulation, the expected false discovery rate of the entire analysis is ~60/362 (17%)

Table S9. Hexamer S:B values in skipped exons and tandem UTRs.[1]

6-mer	Introns flanking skipped exons		Tandem UTRs	
	S:B	p value	S:B	p value
ACTAAC	8.26	**5.8E-52**	1.56	**6.1E-04**
GCATGC	5.37	**2.8E-33**	3.18	**1.7E-27**
TGCATG	4.94	**4.0E-82**	3.78	**3.6E-114**
CTAACC	4.43	**6.0E-21**	1.04	4.3E-01
TACTAA	3.91	**1.8E-14**	1.26	**6.1E-03**
CACTAA	3.90	**9.9E-19**	2.10	**1.9E-13**
GGTAAG	3.63	**4.3E-07**	1.35	1.8E-02
GCTAAC	3.59	**5.8E-09**	1.14	2.5E-01
ACTAAT	3.24	**1.6E-14**	1.57	**2.2E-07**
GCATGA	3.06	**6.6E-12**	2.40	**2.1E-23**
GCATGT	2.86	**4.5E-16**	2.87	**2.3E-49**
ATAACC	2.78	**1.1E-05**	1.05	3.8E-01
CTAACA	2.72	**1.2E-07**	1.28	2.3E-02
GCATGG	2.69	**2.4E-11**	1.73	**1.1E-07**
ATTAAC	2.56	**3.5E-07**	1.49	**1.8E-05**
GCTTGC	2.52	**1.3E-07**	1.64	**5.7E-05**
TTAACC	2.51	**8.2E-08**	1.26	2.3E-02
CTGCAT	2.47	**1.8E-12**	1.65	**6.1E-11**
CAATGC	2.46	**2.1E-04**	1.12	2.4E-01
CTAACT	2.43	**5.8E-07**	1.05	3.7E-01
TCTAAC	2.39	**8.9E-06**	1.43	**1.7E-03**
TTGCAT	2.38	**8.4E-12**	1.66	**7.8E-15**
AGCATG	2.37	**1.8E-07**	2.20	**8.3E-24**
CTAATT	2.31	**6.7E-09**	1.05	2.6E-01
GATTAA	2.22	**6.3E-05**	1.20	2.7E-02
GCCAAC	2.21	**2.1E-03**	1.43	1.1E-02
CATAAC	2.19	**2.2E-03**	0.98	5.6E-01
GACTAA	2.17	**1.9E-03**	1.12	2.3E-01
CAACTA	2.16	**7.9E-03**	0.92	7.3E-01
CATGAC	2.15	**5.7E-04**	0.95	6.6E-01
GTACCA	2.15	**3.7E-03**	2.01	**3.3E-09**
TGGCAT	2.14	**3.6E-07**	0.96	6.7E-01
CTGATC	2.10	**1.7E-04**	0.95	6.5E-01
AACTAA	2.09	**2.6E-05**	1.09	2.0E-01
TAACCA	2.08	**5.5E-05**	1.50	**1.5E-05**
GACAAC	2.07	4.1E-02	0.77	9.2E-01
TGACAA	2.07	**1.7E-04**	1.05	3.3E-01
CAGCAA	2.05	**2.0E-04**	1.12	1.2E-01
TAACCC	2.05	**5.1E-04**	0.97	5.9E-01
TCTAGC	2.04	**3.6E-03**	0.82	9.1E-01
TTTAAC	2.04	**9.2E-07**	1.34	**5.0E-06**
GCTAAT	2.02	**2.0E-03**	1.13	1.6E-01
GGTTAG	2.01	**5.4E-03**	0.77	9.5E-01
ACTGGC	2.00	**1.5E-03**	0.93	7.0E-01
TGCAAT	1.98	**2.0E-03**	2.11	**4.1E-24**

CAGGTA	1.97	**2.8E-03**	1.56	**3.5E-05**
TTGCTA	1.97	**1.4E-04**	1.27	**4.6E-03**
GACAAT	1.96	2.1E-02	1.87	**1.0E-08**
CATTAA	1.96	**1.4E-04**	1.33	**1.8E-05**
GCATAA	1.96	**8.5E-03**	1.11	2.1E-01
TTAACA	1.94	**9.7E-06**	1.13	5.1E-02
CTTAAC	1.94	**1.3E-03**	1.08	2.8E-01
CATGCC	1.94	**5.6E-05**	0.87	8.9E-01
GCAAAC	1.92	1.3E-02	1.17	1.3E-01
GCAATT	1.90	**6.2E-03**	1.18	7.4E-02
GCTTTA	1.90	**1.5E-04**	1.83	**6.6E-17**
AATTGC	1.90	**3.4E-03**	1.13	1.1E-01
CATGGC	1.87	**4.5E-04**	1.05	3.5E-01
GATCAA	1.86	2.9E-02	1.05	3.8E-01
TAACCT	1.86	**2.2E-04**	0.99	5.7E-01
GGCTTC	1.86	**2.0E-04**	1.25	1.9E-02
TGGTAA	1.85	**8.5E-04**	0.96	6.8E-01
GTGCAT	1.85	**6.5E-04**	1.99	**1.5E-13**
GTTTGC	1.84	**2.3E-04**	1.87	**1.1E-13**
TTGACC	1.83	**5.1E-03**	1.19	7.7E-02
GCCTGC	1.83	**4.0E-05**	1.85	**5.6E-08**
ACAACT	1.82	1.6E-02	0.91	8.0E-01
GGTTTG	1.82	**1.8E-04**	1.07	2.3E-01
ATGTAC	1.81	**7.2E-03**	1.95	**2.2E-15**
GGATTG	1.80	**8.7E-03**	0.55	1.0E+00
GACCAC	1.80	2.2E-02	1.70	**2.9E-04**
GAACCC	1.80	1.5E-02	0.83	8.8E-01
AGCTAA	1.79	**7.7E-03**	0.76	9.9E-01
TTGGCT	1.79	**2.3E-05**	1.27	**1.7E-03**
GCTTGG	1.78	**4.6E-04**	1.39	**2.6E-03**
CTAGCC	1.78	2.3E-02	1.03	4.6E-01
GTTAGA	1.78	1.0E-02	0.99	5.4E-01
TGGCTT	1.78	**2.2E-07**	1.45	**8.3E-08**
ATTGGC	1.77	1.2E-02	1.37	**9.3E-03**
GTTGGC	1.77	**6.6E-03**	1.43	**2.7E-03**
TAGCTG	1.77	**4.8E-03**	1.01	4.9E-01
TAGCTT	1.77	**8.2E-04**	1.25	**8.2E-03**
TTGCTT	1.76	**2.3E-08**	1.30	**8.9E-07**
GTCCAA	1.76	3.0E-02	0.96	6.2E-01
TGTTAA	1.76	**7.4E-05**	1.11	3.5E-02
GGTAAA	1.75	**7.2E-03**	0.93	7.5E-01
ACCAGC	1.75	**3.4E-03**	2.01	**1.6E-13**
ATGGCA	1.75	**1.9E-03**	1.14	9.9E-02
CATGAA	1.75	**1.4E-03**	1.24	**5.1E-03**
CAGGTC	1.75	**7.7E-03**	1.08	3.2E-01
CATGGT	1.74	**2.0E-03**	0.84	9.5E-01
CCATGA	1.74	**4.3E-03**	0.92	7.8E-01
TAGCCA	1.74	1.1E-02	1.43	**4.0E-04**
GTAGCT	1.73	**7.0E-03**	1.18	7.9E-02
GTCTGC	1.73	**1.7E-03**	1.21	7.9E-02

GCTTAA	1.73	1.3E-02	1.14	1.1E-01
GTTAAT	1.73	**3.0E-03**	1.34	**2.0E-04**
TTGACA	1.73	**1.6E-03**	1.25	**5.9E-03**
GCTAGC	1.73	5.6E-02	1.22	2.0E-01
TTAATC	1.73	**2.6E-03**	1.22	1.8E-02
CCTAAC	1.72	1.6E-02	0.42	1.0E+00
GGCATG	1.72	**8.6E-04**	1.07	3.1E-01
TTCTAA	1.72	**1.4E-04**	1.08	9.7E-02
CTAGCT	1.71	1.7E-02	0.92	7.4E-01
GATACA	1.71	3.7E-02	0.66	1.0E+00
CTGCCT	1.71	**1.6E-06**	1.53	**3.1E-10**
GGTGGG	1.71	**1.5E-06**	1.22	3.0E-02
GGAGGG	1.71	**2.6E-06**	0.92	7.8E-01
TGCTAC	1.70	2.4E-02	1.62	**5.6E-05**
CTCTAA	1.70	**2.9E-03**	0.78	9.9E-01
GCTGCT	1.69	**6.5E-05**	2.88	**1.3E-59**
GATAAC	1.69	7.4E-02	0.86	8.3E-01
TAAAGC	1.69	**5.3E-03**	1.52	**8.9E-08**
TACAAA	1.69	**4.8E-03**	0.76	1.0E+00
CTCAAT	1.68	4.2E-02	0.92	7.5E-01
TGCTAA	1.68	**3.0E-03**	1.47	**3.3E-06**
ATCTAA	1.68	1.8E-02	0.85	9.4E-01
AATGCA	1.68	**1.8E-03**	1.22	**3.0E-03**
TTGATT	1.67	**1.1E-04**	1.04	2.8E-01
ATCCAC	1.67	3.3E-02	0.76	9.6E-01
CTTGGC	1.67	**6.9E-04**	1.11	1.8E-01
TTAGCT	1.67	**5.5E-03**	1.05	3.2E-01
GTAGAC	1.67	4.4E-02	1.22	1.1E-01
TGTAGC	1.66	1.3E-02	1.78	**3.0E-09**
TTCAGC	1.66	**3.5E-03**	0.91	8.4E-01
CACCAC	1.66	**8.1E-03**	0.43	1.0E+00
TAGCTC	1.65	2.7E-02	0.90	7.7E-01
AAATTG	1.65	**5.7E-04**	0.91	9.4E-01
AGAAGC	1.65	**6.5E-03**	0.97	6.4E-01
CTGCTT	1.65	**7.7E-06**	1.46	**2.8E-08**
GAATGT	1.64	**2.8E-03**	1.91	**1.9E-26**
AGGTCT	1.64	**8.0E-03**	1.17	1.0E-01
GCATAC	1.64	1.6E-01	0.95	6.3E-01
AGGTAA	1.63	2.3E-02	1.08	2.6E-01
CTAATC	1.63	5.1E-02	1.14	2.1E-01
CTGGCA	1.63	**1.6E-03**	1.17	6.1E-02
GATTGC	1.63	3.4E-02	1.01	5.0E-01
TAACAA	1.63	1.3E-02	1.22	1.3E-02
GCTGCC	1.62	**7.5E-04**	1.76	**1.8E-07**
TTTGTC	1.62	**4.8E-05**	1.14	3.3E-02
CTGCTG	1.62	**4.7E-05**	2.09	**1.0E-29**
GCAGGC	1.62	**5.6E-03**	1.41	**5.1E-03**
ACAGGT	1.61	1.8E-02	0.83	9.5E-01
TACAAG	1.61	6.4E-02	1.22	5.4E-02
TTTGAT	1.61	**3.7E-04**	1.17	**3.5E-03**

TTAGTG	1.61	**9.0E-03**	1.07	2.5E-01
GGATAA	1.61	5.7E-02	0.92	7.5E-01
GAAATC	1.61	1.4E-02	0.92	8.0E-01
TAACAC	1.61	2.7E-02	1.03	4.3E-01
TCTAAT	1.60	**4.2E-03**	1.44	**5.0E-06**
TAATCA	1.60	1.5E-02	1.31	**1.4E-03**
TGCAGC	1.60	**5.6E-03**	1.29	**7.7E-03**
CTGCCA	1.60	**7.9E-04**	1.68	**4.1E-10**
TGCATC	1.60	2.2E-02	1.29	1.3E-02
AATGCT	1.60	**2.3E-03**	0.98	6.4E-01
TGAAGG	1.59	**7.3E-03**	1.16	5.0E-02
AGTAAC	1.59	2.9E-02	1.05	3.8E-01
GACCAT	1.59	6.1E-02	1.15	1.7E-01
GCACTA	1.58	7.0E-02	2.03	**1.8E-08**
TCTGCT	1.58	**6.8E-05**	1.27	**9.4E-04**
CTGGCT	1.58	**3.1E-04**	1.14	7.0E-02
TGGTGG	1.58	**5.2E-04**	0.83	9.7E-01
TGCTTA	1.57	**8.0E-03**	1.26	**2.9E-03**
GGCTAC	1.57	1.1E-01	1.08	3.6E-01
GGGTGG	1.57	**9.1E-05**	1.25	2.8E-02
TAACTG	1.57	**9.1E-03**	1.07	2.4E-01
TGCTTG	1.56	**4.2E-04**	1.52	**6.8E-08**
TGGAAT	1.56	**4.5E-03**	1.07	1.9E-01
ATGCAT	1.56	**5.4E-03**	1.69	**1.0E-12**
CATTGC	1.56	1.8E-02	1.29	**9.1E-03**
TTATGA	1.56	**9.8E-03**	1.02	3.9E-01
GGTAGG	1.56	3.2E-02	0.98	5.8E-01
GTGGAC	1.56	5.6E-02	1.41	1.3E-02
GCTGGC	1.56	**3.7E-03**	1.82	**2.0E-07**
TTTGCA	1.56	**1.5E-04**	1.90	**9.1E-38**
ACCACC	1.55	2.1E-02	0.81	9.2E-01
AAGCTT	1.55	**7.4E-03**	1.40	**8.4E-06**
GACATC	1.55	8.0E-02	1.26	5.3E-02
TGCCAA	1.55	3.0E-02	2.88	**6.9E-55**
GGTGGC	1.55	**4.5E-03**	0.96	6.4E-01
GCAGCC	1.55	**5.6E-03**	1.42	**2.4E-03**
TAATCT	1.55	**7.9E-03**	1.08	2.1E-01
TCTTGA	1.54	**6.8E-03**	0.94	8.0E-01
GCTTCA	1.54	1.7E-02	1.11	1.8E-01
GAGCAG	1.54	**4.9E-03**	1.03	4.1E-01
GCTGCA	1.54	1.1E-02	1.69	**5.0E-09**
ACTAAG	1.54	8.3E-02	0.65	1.0E+00
CAATTA	1.54	6.7E-02	1.17	7.5E-02
GCAGGT	1.54	1.8E-02	0.95	6.8E-01
GTCTAA	1.54	8.4E-02	1.27	3.9E-02
TAGAGC	1.54	6.1E-02	0.82	9.0E-01
GGCTGC	1.54	**4.3E-03**	1.55	**1.2E-04**
CTCAAG	1.53	3.3E-02	0.68	1.0E+00
AACTTC	1.53	2.8E-02	0.77	9.9E-01
ATCAAG	1.53	7.1E-02	0.92	7.5E-01

AGCCAA	1.52	3.6E-02	1.41	**1.0E-04**
ATGGCT	1.52	1.4E-02	1.17	5.8E-02
GCAACT	1.52	1.0E-01	1.18	1.4E-01
TCCATT	1.52	**2.6E-03**	0.79	1.0E+00
CCATTG	1.52	3.3E-02	0.83	9.6E-01
GCTTGT	1.52	1.3E-02	1.53	**2.1E-06**
GCTACA	1.52	1.0E-01	1.14	2.0E-01
CATGAT	1.51	2.7E-02	0.90	8.5E-01
GCCTCC	1.51	**3.7E-03**	0.87	8.8E-01
GCAATC	1.51	2.4E-01	1.13	2.6E-01
GTGCAC	1.51	7.7E-02	1.78	**1.5E-06**
ACACCA	1.50	5.8E-02	0.85	9.2E-01
GGGAGG	1.50	**9.0E-05**	1.02	4.4E-01
GTTTGA	1.50	1.9E-02	1.02	4.3E-01
GCTCAA	1.50	7.9E-02	0.59	1.0E+00
ATTGAC	1.50	7.2E-02	1.03	4.4E-01
TAATTA	1.50	**4.4E-03**	1.05	2.2E-01
GCTGTC	1.50	1.7E-02	1.19	6.3E-02
ATGACA	1.50	3.7E-02	0.79	9.9E-01
TAGCCT	1.50	6.6E-02	1.09	2.6E-01
CATAAT	1.50	2.9E-02	0.97	6.2E-01
GAATGG	1.49	2.6E-02	1.01	4.8E-01
TCCAGA	1.49	2.3E-02	1.19	2.6E-02
GGTTAA	1.49	9.1E-02	1.42	**7.4E-04**
GCTTCT	1.49	**8.9E-04**	1.27	**2.2E-03**
TGCTGC	1.49	**2.7E-03**	2.72	**3.8E-51**
ATGTGC	1.49	2.8E-02	1.50	**2.9E-06**
GTTTAC	1.49	4.7E-02	3.20	**2.3E-59**
TCCAAT	1.49	1.1E-01	1.06	3.6E-01
AGTTAG	1.48	5.3E-02	0.90	7.9E-01
CCTGCC	1.48	**4.2E-04**	1.39	**2.5E-04**
CCATAT	1.48	8.5E-02	0.97	6.0E-01
AACCAG	1.48	4.6E-02	1.17	7.0E-02
AATGGT	1.48	3.5E-02	0.99	5.5E-01
GTCTTG	1.48	1.4E-02	1.17	6.2E-02
GGAACC	1.48	8.0E-02	1.19	1.7E-01
ATGGTA	1.48	6.0E-02	1.18	5.5E-02
TAACAT	1.48	1.4E-02	1.15	3.8E-02
ACCATA	1.47	1.3E-01	0.94	6.9E-01
GTGCTT	1.47	**8.2E-03**	1.70	**1.0E-12**
GATGTC	1.47	8.2E-02	0.86	8.9E-01
CTGCAC	1.47	2.3E-02	1.25	2.0E-02
AAAGGT	1.47	4.5E-02	1.12	9.2E-02
GCTGAT	1.47	4.9E-02	0.94	7.1E-01
AAGATC	1.47	1.0E-01	0.95	6.7E-01
CAAAGC	1.46	6.0E-02	1.48	**3.3E-05**
TGTCTG	1.46	**1.1E-03**	1.24	**1.9E-03**
AAGGTC	1.46	1.0E-01	1.27	4.4E-02
TTTAAT	1.46	**7.5E-04**	1.01	3.6E-01
CATGTA	1.46	4.3E-02	1.47	**6.1E-07**

AAGCAC	1.46	8.6E-02	2.24	**8.8E-22**
TCATTA	1.46	2.7E-02	0.88	9.3E-01
CACTGC	1.46	1.3E-02	1.27	**5.3E-03**
CATGCA	1.46	3.7E-02	1.08	2.4E-01
CTGAAT	1.46	1.7E-02	1.01	4.7E-01
TTAGAT	1.46	3.4E-02	0.98	6.1E-01
ACTAAA	1.46	3.7E-02	0.89	9.3E-01
ACACTA	1.46	1.4E-01	2.54	**2.3E-20**
TGATCT	1.46	2.8E-02	0.83	9.8E-01
TTGAAA	1.45	**2.7E-03**	1.05	1.5E-01
TGCTTC	1.45	**1.8E-03**	1.25	**3.9E-03**
GGTGAG	1.45	2.4E-02	0.64	1.0E+00
AATGGC	1.45	6.4E-02	1.26	2.1E-02
TTGTCT	1.45	**1.1E-03**	1.25	**6.7E-04**
TTCTGC	1.45	**1.7E-03**	1.14	5.4E-02
AGGTCC	1.45	9.9E-02	1.17	1.9E-01
GTGGTA	1.45	9.1E-02	1.00	5.2E-01
GACAGC	1.45	8.4E-02	0.96	6.3E-01
GGCCAC	1.45	4.8E-02	0.92	7.3E-01
TAACTC	1.45	7.1E-02	1.11	2.1E-01
CTGTAC	1.44	7.9E-02	1.69	**6.5E-08**
ATCTGC	1.44	4.2E-02	1.10	2.0E-01
CTAATG	1.44	5.3E-02	1.21	4.3E-02
TGCAGG	1.44	1.6E-02	0.79	9.9E-01
CAGCTG	1.44	**7.0E-03**	1.28	**2.0E-03**
TTGGTC	1.44	5.1E-02	1.35	**3.1E-03**
CCTGAC	1.43	2.5E-02	0.78	9.7E-01
GGTGCC	1.43	7.1E-02	2.62	**2.0E-17**
ATCAAC	1.43	1.8E-01	0.73	9.7E-01
TGGTAG	1.43	7.0E-02	1.33	1.1E-02
TCACTA	1.43	8.9E-02	0.91	7.7E-01
TTTCTG	1.43	**9.0E-05**	1.17	**6.9E-04**
AGCTGC	1.43	2.6E-02	1.78	**9.4E-11**
AATTAA	1.43	1.0E-02	0.95	8.2E-01
ATTTCA	1.43	**4.2E-03**	0.99	5.5E-01
ACAATA	1.43	1.1E-01	1.26	**7.1E-03**
CTGCAA	1.43	7.3E-02	0.77	9.9E-01
CTTAGC	1.43	1.1E-01	1.01	5.0E-01
ATTAGC	1.43	1.4E-01	0.84	9.2E-01
GTGGGC	1.43	1.9E-02	1.20	1.1E-01
GGTAGC	1.43	1.7E-01	1.42	2.1E-02
CACAAC	1.43	2.0E-01	0.90	7.7E-01
CAATCA	1.42	1.7E-01	1.75	**1.9E-07**
TGGCTG	1.42	**5.4E-03**	1.25	**4.6E-03**
ATTAAA	1.42	**6.7E-03**	1.30	**1.0E-11**
AAAGCC	1.42	7.1E-02	1.30	**1.6E-03**
TGCTTT	1.42	**2.0E-04**	1.50	**5.6E-18**
TTCCAA	1.42	2.6E-02	1.20	**6.0E-03**
CACTAC	1.41	2.5E-01	1.82	**1.1E-05**
TGTGGG	1.41	**6.5E-03**	0.99	5.5E-01

AGCTTG	1.41	3.8E-02	1.23	2.3E-02
GTCACT	1.41	5.9E-02	0.96	6.6E-01
TGACCA	1.41	5.1E-02	1.80	**7.0E-11**
TTGTCC	1.41	3.1E-02	0.95	6.9E-01
ATTAGT	1.41	8.5E-02	1.09	2.0E-01
CTTCAT	1.41	1.0E-02	0.83	9.9E-01
ATTGCA	1.41	6.9E-02	1.36	**1.7E-04**
GCTGAC	1.41	7.5E-02	1.20	1.1E-01
ATAATC	1.41	1.0E-01	0.91	8.1E-01
ATTTAA	1.41	**5.9E-03**	1.03	2.7E-01
CAAAGG	1.41	5.3E-02	1.14	9.2E-02
AAATGC	1.41	3.1E-02	1.04	3.0E-01
TTGGTG	1.40	1.8E-02	1.35	**2.0E-04**
GGCTGT	1.40	2.0E-02	1.08	2.5E-01
AGCAAC	1.40	1.5E-01	1.15	1.4E-01
CTCCAT	1.40	2.0E-02	0.76	9.9E-01
AGGATC	1.40	1.3E-01	0.83	9.0E-01
ATTACC	1.40	1.8E-01	0.92	7.4E-01
TTAATT	1.40	**4.0E-03**	0.97	7.6E-01
TTCAAA	1.40	2.0E-02	0.83	1.0E+00
TAAATG	1.40	1.3E-02	1.22	**7.3E-05**
ATTGCT	1.40	3.4E-02	1.25	**2.8E-03**
TGGGGA	1.39	**6.8E-03**	0.75	1.0E+00
CTGCAG	1.39	**6.8E-03**	0.94	7.8E-01
CAGTAA	1.39	7.1E-02	0.97	6.3E-01
TTAGCC	1.39	1.3E-01	1.13	1.7E-01
TTAGTT	1.39	2.4E-02	1.01	4.7E-01
GTGACC	1.39	7.3E-02	1.46	**2.0E-03**
GTGTTG	1.39	3.5E-02	1.17	4.1E-02
CAGCCC	1.39	1.9E-02	0.98	6.0E-01
ATTGGT	1.39	9.5E-02	1.01	4.5E-01
CTAGGA	1.39	1.1E-01	0.69	9.9E-01
GTTGCT	1.39	5.6E-02	1.25	1.1E-02
TCAACC	1.39	1.7E-01	0.67	9.9E-01
AAATGT	1.39	**5.8E-03**	1.21	**1.2E-05**
AACCCT	1.39	6.5E-02	0.74	9.9E-01
TAAAGG	1.39	7.4E-02	1.25	**3.6E-03**
GCACAC	1.39	1.3E-01	1.34	1.5E-02
GCAGCA	1.38	5.5E-02	1.24	1.7E-02
CTGGAT	1.38	6.2E-02	1.03	4.2E-01
TGAAAG	1.38	3.1E-02	0.88	9.6E-01
ATTTGC	1.38	4.0E-02	1.47	**7.5E-08**
CCTGGC	1.38	1.5E-02	1.08	2.6E-01
AGCTCT	1.38	2.3E-02	0.88	9.2E-01
GACTAG	1.38	1.8E-01	0.54	1.0E+00
AATTAG	1.38	7.1E-02	0.89	9.1E-01
CCAAGA	1.38	9.4E-02	0.87	9.2E-01
ATGCAG	1.38	6.5E-02	0.94	7.5E-01
CTTGAA	1.38	4.2E-02	1.59	**4.1E-14**
CATGTG	1.38	2.5E-02	1.01	4.7E-01

TCTGCA	1.38	**9.7E-03**	1.22	**6.5E-03**
GCAGCT	1.38	4.6E-02	1.75	**3.5E-10**
GACCTT	1.38	7.4E-02	0.98	6.0E-01
GATTGG	1.38	1.4E-01	0.96	6.4E-01
GAAGTG	1.38	6.6E-02	0.85	9.5E-01
ATGATC	1.37	1.5E-01	0.68	1.0E+00
CATGCT	1.37	3.2E-02	1.18	6.0E-02
TCTGGC	1.37	4.5E-02	1.20	4.5E-02
GGCATT	1.37	7.3E-02	1.17	6.5E-02
GGCAGC	1.37	4.1E-02	2.19	**2.4E-13**
ATGACT	1.37	8.3E-02	0.96	6.9E-01
GCAGTG	1.37	2.8E-02	0.78	9.9E-01
TTGTTT	1.37	**7.7E-05**	1.00	5.0E-01
CTACAC	1.37	2.1E-01	0.73	9.6E-01
CTTGGT	1.37	3.4E-02	1.03	4.0E-01
GGAATT	1.37	6.9E-02	0.97	6.3E-01
CAGAGC	1.37	3.5E-02	1.05	3.2E-01
TTGTTA	1.37	2.8E-02	1.10	7.4E-02
CTAATA	1.36	1.1E-01	1.47	**1.2E-05**
CTACAT	1.36	1.3E-01	0.68	1.0E+00
CATTGT	1.36	4.5E-02	1.07	1.9E-01
ATGTTG	1.36	4.5E-02	0.83	9.9E-01
TTAAGG	1.36	9.1E-02	0.86	9.4E-01
TACCAG	1.36	1.4E-01	1.32	**7.2E-03**
GGCTTA	1.36	1.4E-01	1.04	4.0E-01
TATAGG	1.36	1.9E-01	1.02	4.6E-01
TAGGAA	1.36	4.8E-02	1.00	5.0E-01
TTTGAC	1.36	5.4E-02	1.31	**6.7E-04**
GTGATC	1.36	1.4E-01	0.81	9.4E-01
TCTAAA	1.36	4.7E-02	0.79	1.0E+00
GCAGAA	1.36	7.4E-02	0.87	9.4E-01
TTGTCA	1.36	4.7E-02	1.09	1.3E-01
CTGGAA	1.36	4.0E-02	1.30	**2.3E-04**
TGAATG	1.36	2.3E-02	1.67	**3.1E-17**
TGATAC	1.36	1.8E-01	1.04	4.1E-01
CATTGG	1.36	1.1E-01	0.84	9.3E-01
TTGCAA	1.35	1.0E-01	1.45	**1.6E-06**
AGGAGC	1.35	6.4E-02	0.87	8.7E-01
GATGCA	1.35	1.5E-01	1.08	2.8E-01
CATCTA	1.35	1.9E-01	1.11	2.3E-01
ATTGTT	1.35	2.6E-02	0.98	6.3E-01
CTCTGC	1.35	1.1E-02	0.90	8.7E-01
TTTTAA	1.35	**4.6E-04**	0.99	6.9E-01
GTTGGT	1.35	7.8E-02	1.17	8.7E-02
AAGCAA	1.35	7.3E-02	0.99	5.4E-01
CCTGAA	1.35	6.2E-02	0.72	1.0E+00
TAATGA	1.35	5.0E-02	0.99	5.9E-01
TAGTCC	1.35	2.1E-01	0.66	9.9E-01
AGCAAA	1.35	5.3E-02	0.84	9.9E-01
CCTGCT	1.35	1.5E-02	1.05	3.1E-01

AACCTT	1.35	7.5E-02	0.68	1.0E+00
TGTCAG	1.35	4.4E-02	1.04	3.6E-01
CCAATA	1.35	2.5E-01	1.45	**7.9E-04**
TGCTAG	1.34	1.5E-01	1.74	**2.0E-06**
TTCCAT	1.34	2.5E-02	0.88	9.5E-01
GGTCTG	1.34	7.0E-02	1.17	1.0E-01
ATTAAT	1.34	3.5E-02	0.93	8.8E-01
TGCCTG	1.34	1.6E-02	1.42	**3.0E-06**
TGGCAG	1.34	2.7E-02	1.44	**4.2E-05**
GAATAG	1.34	1.4E-01	0.84	9.2E-01
AGTTCA	1.34	1.1E-01	0.80	9.9E-01
ACCTGC	1.34	7.0E-02	1.18	8.0E-02
TACAAC	1.34	2.7E-01	0.81	9.2E-01
CCTGCA	1.34	2.8E-02	1.09	2.1E-01
TCCAAA	1.34	6.3E-02	1.12	6.8E-02
CCATCC	1.34	5.5E-02	0.65	1.0E+00
TAACTT	1.34	3.8E-02	1.19	**7.5E-03**
GGGGGG	1.34	1.1E-01	0.65	9.4E-01
TGCCAT	1.34	4.5E-02	1.44	**3.4E-06**
ATTCTA	1.34	7.9E-02	0.94	7.7E-01
TGTGCT	1.34	**9.4E-03**	1.42	**7.5E-07**
TTGCCA	1.34	6.5E-02	1.67	**2.8E-12**
CCAACC	1.34	1.3E-01	0.51	1.0E+00
CTGCTA	1.34	1.3E-01	2.05	**1.8E-13**
ACCATG	1.33	1.3E-01	0.60	1.0E+00
ATAAGT	1.33	1.5E-01	0.78	9.9E-01
GGTCAC	1.33	1.8E-01	1.03	4.4E-01
CTTGTT	1.33	1.9E-02	1.22	**2.2E-03**
GCAGAC	1.33	1.7E-01	0.87	8.2E-01
ACCTCA	1.33	8.2E-02	1.72	**4.9E-12**
CCACTA	1.33	1.8E-01	1.11	2.7E-01
CCAGCT	1.33	4.1E-02	1.07	2.3E-01
TTTGCT	1.33	**6.5E-03**	1.37	**1.7E-09**
GAGCTG	1.33	4.7E-02	0.96	6.7E-01
TTGTGG	1.33	4.5E-02	1.28	**1.4E-03**
CATTCA	1.33	6.3E-02	0.75	1.0E+00
CTTTAA	1.33	3.3E-02	1.03	3.4E-01
GATCTA	1.32	2.6E-01	1.09	3.1E-01
GCCAGA	1.32	1.2E-01	1.19	5.6E-02
TAATTT	1.32	1.0E-02	1.04	1.4E-01
TGCAGT	1.32	5.1E-02	0.91	8.9E-01
GTCAAC	1.32	3.3E-01	0.76	9.3E-01
TGAAAT	1.32	2.6E-02	0.97	7.1E-01
GATTAG	1.32	2.2E-01	0.84	8.8E-01
TTTACT	1.32	3.3E-02	1.06	1.7E-01
AATGTT	1.32	3.6E-02	1.06	1.2E-01
CATACT	1.32	1.8E-01	0.77	9.8E-01
CAAAGA	1.32	1.2E-01	1.69	**4.5E-14**
GCCATT	1.32	1.1E-01	1.55	**2.2E-07**
CAGCAT	1.32	8.4E-02	1.12	1.1E-01

TCAAGT	1.32	1.3E-01	0.98	5.9E-01
CCTGAT	1.32	1.1E-01	0.83	9.3E-01
TATGAT	1.31	1.6E-01	0.89	8.9E-01
TTTTAT	1.31	**3.0E-03**	1.22	**9.7E-11**
GAGTTA	1.31	1.5E-01	0.76	9.7E-01
GAATGC	1.31	1.4E-01	1.69	**1.6E-06**
TGGATG	1.31	9.0E-02	0.78	9.9E-01
AGCAAT	1.31	1.7E-01	1.74	**4.0E-12**
TGACCT	1.31	5.2E-02	1.17	4.6E-02
GCTTCC	1.31	6.4E-02	1.20	4.0E-02
TGCCTA	1.31	1.5E-01	1.27	2.0E-02
AGTTGG	1.31	8.8E-02	0.85	9.3E-01
ACTGCA	1.31	8.1E-02	0.79	9.9E-01
GGTGCT	1.31	9.4E-02	4.45	**2.2E-96**
TTTGTT	1.31	**1.1E-03**	1.03	2.2E-01
GATCTG	1.31	1.5E-01	0.88	8.5E-01
GTCTGG	1.30	8.8E-02	1.25	2.9E-02
GATGGT	1.30	1.6E-01	0.91	8.0E-01
TTATAA	1.30	5.4E-02	0.95	8.3E-01
TGCTGA	1.30	4.8E-02	1.25	**3.9E-03**
TCTGAC	1.30	8.1E-02	1.03	4.2E-01
TTTGAA	1.30	2.1E-02	1.10	2.3E-02
CCTTGA	1.30	1.0E-01	1.01	4.8E-01
TTAACT	1.30	7.7E-02	1.17	1.3E-02
TTAAAT	1.30	2.1E-02	0.97	8.1E-01
ATGCTT	1.30	4.8E-02	1.27	**4.2E-04**
GGGCTC	1.30	8.2E-02	1.31	3.3E-02
CCACCA	1.30	9.4E-02	0.79	9.8E-01
TAGTGC	1.30	2.3E-01	1.50	**1.5E-03**
GTTGTC	1.30	1.7E-01	1.17	1.1E-01
AGCAGC	1.30	8.7E-02	1.35	**7.7E-04**
ACTTCT	1.30	6.3E-02	0.66	1.0E+00
TCAACA	1.30	1.6E-01	0.75	9.9E-01
CATCAT	1.30	1.4E-01	0.70	1.0E+00
AGCTGG	1.30	6.0E-02	0.91	8.4E-01
TTTAGT	1.30	6.2E-02	0.85	9.9E-01
CTGGTT	1.30	6.7E-02	1.14	6.4E-02
TTGGTT	1.29	3.5E-02	1.01	4.4E-01
TGTGAC	1.29	1.0E-01	1.41	**9.4E-05**
GTGGGT	1.29	5.9E-02	0.87	8.9E-01
GTCAGA	1.29	1.7E-01	1.13	1.5E-01
CTGGTG	1.29	7.4E-02	1.45	**3.6E-05**
GGCATA	1.29	2.3E-01	0.95	6.4E-01
TGTGTG	1.29	**4.7E-03**	1.08	7.2E-02
AAAGCT	1.29	9.0E-02	1.29	**1.2E-04**
CATAGT	1.29	1.8E-01	0.69	1.0E+00
TGGTTG	1.29	8.7E-02	0.96	6.9E-01
TGTAAC	1.29	1.4E-01	2.04	**1.3E-20**
AGATCC	1.29	2.1E-01	0.92	7.2E-01
TTTATT	1.29	**4.1E-03**	1.41	**1.7E-30**

GAGAAG	1.29	7.5E-02	0.71	1.0E+00
GAGGGC	1.29	7.9E-02	1.05	4.0E-01
GGTAAC	1.29	2.5E-01	0.89	7.7E-01
TTTACA	1.29	6.9E-02	1.61	**4.5E-21**
GTGGAA	1.29	1.1E-01	0.85	9.5E-01
CTAAAC	1.29	2.0E-01	1.02	4.5E-01
CCAATT	1.29	2.1E-01	0.75	9.8E-01
GCTTTC	1.29	6.8E-02	1.12	1.0E-01
CATCCA	1.29	1.3E-01	0.61	1.0E+00
TGGCAC	1.29	1.5E-01	1.33	**7.3E-03**
TAACAG	1.29	1.5E-01	0.97	6.3E-01
GTTCAT	1.28	1.5E-01	0.92	8.1E-01
GCTCTG	1.28	3.8E-02	1.11	1.5E-01
TTTGGA	1.28	5.1E-02	1.08	1.2E-01
TTGAAG	1.28	9.7E-02	1.00	5.1E-01
GCTTTG	1.28	3.8E-02	1.35	**2.7E-05**
GGGTAA	1.28	2.2E-01	0.81	9.1E-01
TCAATA	1.28	2.2E-01	1.88	**2.7E-15**
AAGGAA	1.28	4.3E-02	0.75	1.0E+00
TATCAA	1.28	2.0E-01	0.85	9.4E-01
ACCAGA	1.28	1.6E-01	0.84	9.3E-01
GGGCCA	1.28	1.0E-01	1.25	5.3E-02
TCCTGC	1.28	4.7E-02	1.05	3.0E-01
AATTCA	1.28	9.7E-02	0.90	9.2E-01
TAAATT	1.28	4.7E-02	1.01	4.3E-01
CAGCTC	1.28	8.7E-02	0.91	8.2E-01
AGCTTT	1.28	5.5E-02	1.47	**2.1E-10**
TAGCAC	1.27	2.6E-01	1.78	**2.7E-06**
GCCAGG	1.27	7.2E-02	1.21	4.5E-02
GTTGCA	1.27	1.8E-01	1.35	**2.3E-03**
TCTTGC	1.27	7.9E-02	1.22	2.7E-02
AGAACC	1.27	2.1E-01	0.85	9.0E-01
TAGAAC	1.27	2.4E-01	0.74	9.9E-01
TGGTGC	1.27	1.2E-01	3.15	**4.1E-49**
CCCAAT	1.27	2.6E-01	0.49	1.0E+00
AGGCTC	1.27	1.6E-01	1.08	3.1E-01
TTGGGC	1.27	1.5E-01	1.07	3.2E-01
AAGTGG	1.27	1.2E-01	0.85	9.5E-01
GTTGTG	1.27	1.3E-01	1.08	2.3E-01
CTGTTG	1.27	7.3E-02	0.93	8.1E-01
GCCACA	1.27	1.3E-01	0.85	9.2E-01
CTACCA	1.27	2.7E-01	1.05	3.8E-01
TCAGCA	1.27	1.1E-01	1.11	1.2E-01
AAAGCA	1.27	7.9E-02	1.23	**2.8E-04**
GTGGCT	1.27	6.5E-02	1.28	**4.5E-03**
GAGCCT	1.27	1.3E-01	0.99	5.5E-01
CATCCT	1.27	9.0E-02	0.51	1.0E+00
CTAAGT	1.27	2.5E-01	1.00	5.1E-01
GCTGTG	1.27	5.4E-02	1.62	**1.4E-10**
TGTGGA	1.27	8.7E-02	1.17	3.3E-02

TTGGTA	1.27	1.6E-01	1.14	7.8E-02
GCTCCA	1.27	1.7E-01	0.84	8.9E-01
TCAGAC	1.27	1.9E-01	0.97	6.0E-01
GGGTCA	1.27	1.7E-01	0.94	6.9E-01
GGATGC	1.26	2.1E-01	1.12	2.4E-01
CTTCAC	1.26	1.4E-01	0.79	9.8E-01
GACATA	1.26	2.8E-01	0.58	1.0E+00
TTACTA	1.26	1.6E-01	1.02	4.5E-01
GTAGCA	1.26	2.3E-01	1.72	**5.5E-07**
TCTAGA	1.26	1.8E-01	0.90	8.4E-01
ATGCAC	1.26	2.4E-01	1.62	**5.4E-06**
TACATC	1.26	2.6E-01	0.95	6.7E-01
GTACTT	1.26	1.7E-01	1.48	**2.2E-06**
AGGTGC	1.26	1.7E-01	2.30	**3.3E-15**
GGAAGT	1.26	1.6E-01	0.84	9.4E-01
TTGAGT	1.26	1.3E-01	0.75	1.0E+00
TAGATA	1.26	2.2E-01	0.97	6.2E-01
GGAAGG	1.26	7.2E-02	0.95	7.3E-01
TGGTTA	1.26	1.8E-01	1.24	1.3E-02
GAAGCT	1.26	1.5E-01	0.94	7.5E-01
TGACAT	1.26	1.3E-01	1.08	1.9E-01
TGCAAC	1.26	2.6E-01	0.58	1.0E+00
AATCAC	1.25	2.1E-01	0.96	6.7E-01
AGTTTC	1.25	1.2E-01	0.94	7.6E-01
TGTTGC	1.25	1.2E-01	1.19	2.1E-02
GTGGGA	1.25	8.6E-02	0.73	1.0E+00
CTGTGG	1.25	5.6E-02	1.29	**1.4E-03**
AAGGCT	1.25	1.6E-01	1.04	3.7E-01
GTAGTT	1.25	2.1E-01	1.49	**1.0E-05**
AACTGT	1.25	1.4E-01	1.05	2.6E-01
CAAACC	1.25	2.3E-01	0.68	1.0E+00
TTTCAA	1.25	7.8E-02	1.00	4.8E-01
GGGGGC	1.25	1.4E-01	1.26	1.8E-01
ATCCAT	1.25	1.8E-01	0.73	1.0E+00
ACCAAC	1.25	2.8E-01	0.87	8.3E-01
AACTTG	1.25	1.5E-01	1.26	**2.1E-03**
CAAAAT	1.24	1.1E-01	0.80	1.0E+00
GTGTTA	1.24	2.0E-01	1.35	**7.0E-04**
AGGCTT	1.24	1.5E-01	1.13	9.7E-02
AACTGC	1.24	2.0E-01	1.19	5.0E-02
GCTCTT	1.24	1.1E-01	0.96	6.8E-01
GGCTCT	1.24	1.2E-01	1.01	4.9E-01
CTTGAT	1.24	1.6E-01	1.14	8.7E-02
GTTTAA	1.24	1.3E-01	1.11	5.1E-02
TCACCT	1.24	1.0E-01	0.83	9.7E-01
GTGAAC	1.24	2.4E-01	1.20	7.9E-02
CAGGCA	1.24	1.2E-01	0.91	8.2E-01
CTTCTG	1.24	5.1E-02	0.97	6.4E-01
TTTCTA	1.24	5.9E-02	1.42	**8.1E-14**
TGGAGC	1.24	1.5E-01	0.88	8.6E-01

TGAACT	1.24	1.6E-01	1.02	4.2E-01
CACAGC	1.24	1.5E-01	0.78	9.9E-01
CACCAT	1.24	2.2E-01	0.43	1.0E+00
AGTTTG	1.24	1.2E-01	1.12	6.4E-02
CTGATT	1.24	1.2E-01	0.82	9.9E-01
CTGAAG	1.24	1.2E-01	0.89	9.0E-01
CTGCCC	1.24	4.9E-02	1.07	2.7E-01
ACATCC	1.24	2.4E-01	0.54	1.0E+00
GGGCCC	1.24	1.5E-01	2.04	**2.2E-04**
ACAGAC	1.23	2.3E-01	0.92	7.8E-01
TGATTG	1.23	1.7E-01	0.96	6.9E-01
ATTCAA	1.23	1.8E-01	0.89	9.0E-01
GCATCC	1.23	2.5E-01	0.86	8.3E-01
CAGTTC	1.23	1.9E-01	0.79	9.8E-01
TTAAGT	1.23	1.5E-01	0.86	9.7E-01
GGGGAC	1.23	1.8E-01	1.11	2.7E-01
AGAGCC	1.23	1.6E-01	0.95	6.8E-01
CTGCTC	1.23	9.4E-02	1.17	6.5E-02
TAGGTC	1.23	3.4E-01	0.87	7.9E-01
GTTTGG	1.23	1.3E-01	1.25	**5.7E-03**
CCATAA	1.23	2.6E-01	1.25	3.7E-02
GGGCTG	1.23	6.7E-02	1.31	**9.0E-03**
TCTCTC	1.23	2.4E-02	0.44	1.0E+00
CTAGAT	1.23	3.1E-01	0.88	8.4E-01
TGTTGT	1.23	7.1E-02	0.83	1.0E+00
AATGTG	1.23	1.2E-01	1.35	**1.1E-06**
AACCAC	1.23	2.8E-01	1.13	1.7E-01
TGATCA	1.23	2.0E-01	0.80	9.7E-01
GCCAAG	1.23	2.1E-01	1.49	**6.8E-05**
TGTCTT	1.23	4.0E-02	1.19	**1.3E-03**
AAGTAC	1.23	2.8E-01	1.09	2.6E-01
TAATAA	1.22	1.3E-01	1.35	**2.6E-11**
TGAAGT	1.22	1.6E-01	0.90	9.2E-01
GGTCTT	1.22	1.9E-01	0.96	6.6E-01
AGGTAG	1.22	2.3E-01	1.13	1.7E-01
TGGGTT	1.22	1.2E-01	0.85	9.5E-01
CAAGTT	1.22	2.1E-01	0.96	6.8E-01
CAGACT	1.22	2.0E-01	0.90	8.4E-01
GGCTGA	1.22	1.6E-01	0.80	9.8E-01
CTCAAC	1.22	2.8E-01	0.43	1.0E+00
CAGAAG	1.22	1.5E-01	0.81	9.9E-01
CATCAA	1.22	2.9E-01	1.02	4.6E-01
TGGTGA	1.22	1.6E-01	0.90	8.7E-01
GCCAAT	1.22	3.4E-01	1.76	**7.0E-06**
AAGGTA	1.22	2.5E-01	1.36	**8.5E-04**
GGCAGG	1.22	9.0E-02	1.06	3.3E-01
GACTCA	1.22	2.3E-01	0.59	1.0E+00
TGTACA	1.22	2.2E-01	2.43	**9.5E-56**
AAATCA	1.22	1.5E-01	0.76	1.0E+00
TAGTTT	1.22	1.3E-01	1.19	**2.1E-03**

TGTTTA	1.22	8.7E-02	1.49	**3.6E-16**
TGTAAG	1.22	2.2E-01	1.05	3.1E-01
GAAATT	1.21	1.4E-01	0.77	1.0E+00
TGCTAT	1.21	2.3E-01	1.31	**1.2E-03**
ACCAAT	1.21	3.4E-01	1.12	2.1E-01
TGCTGG	1.21	8.8E-02	1.20	2.0E-02
ATCATG	1.21	2.2E-01	1.19	3.2E-02
AAATTA	1.21	1.0E-01	0.75	1.0E+00
TCAAAG	1.21	2.2E-01	0.87	9.3E-01
AACATT	1.21	1.4E-01	0.82	1.0E+00
TGGAAA	1.21	1.1E-01	0.92	9.3E-01
CCATGT	1.21	1.7E-01	0.85	9.6E-01
CTTAAA	1.21	1.4E-01	0.78	1.0E+00
CAGTGC	1.21	1.7E-01	1.47	**1.3E-04**
TTGCAC	1.21	2.4E-01	3.08	**5.2E-52**
TTGGCA	1.21	1.5E-01	1.39	**1.0E-04**
CAATAT	1.21	2.7E-01	1.32	**1.1E-03**
TTATTT	1.21	2.4E-02	1.33	**3.0E-22**
GTTGAA	1.21	2.1E-01	1.04	3.3E-01
GTAAAG	1.21	2.3E-01	1.26	**7.8E-03**
GGAATG	1.21	1.9E-01	1.49	**1.0E-05**
CTTTGA	1.21	1.2E-01	1.06	2.3E-01
TATAAA	1.21	1.3E-01	1.06	9.4E-02
ATTGAT	1.21	2.2E-01	0.92	8.4E-01
CATGGA	1.21	2.3E-01	0.87	9.0E-01
AATCTA	1.21	2.7E-01	0.92	7.8E-01
GCTTAT	1.21	2.3E-01	1.10	1.9E-01
GTGTCA	1.21	2.6E-01	1.24	2.6E-02
GGAGCC	1.21	2.0E-01	0.93	7.0E-01
TCATTG	1.20	1.7E-01	0.86	9.5E-01
AACCCA	1.20	2.5E-01	0.77	9.8E-01
GTGGCA	1.20	2.0E-01	1.00	5.3E-01
TGGACT	1.20	2.2E-01	1.26	1.5E-02
GTGTGC	1.20	1.6E-01	1.34	**2.8E-03**
GCAGTT	1.20	2.3E-01	0.90	8.7E-01
TCCATG	1.20	2.0E-01	0.85	9.4E-01
GTTAGT	1.20	2.6E-01	1.09	2.8E-01
TGATAA	1.20	2.3E-01	1.01	4.6E-01
ATGCCA	1.20	2.3E-01	1.38	**2.2E-04**
CACCTC	1.20	1.9E-01	0.76	9.9E-01
TGCAAG	1.20	2.7E-01	1.28	1.5E-02
ATGCCC	1.20	2.4E-01	0.77	9.6E-01
GGCTTT	1.20	1.1E-01	1.31	**2.4E-04**
GGAGAA	1.19	1.7E-01	0.76	1.0E+00
TAGCAT	1.19	2.4E-01	1.35	**9.2E-04**
GTTGAG	1.19	2.6E-01	0.54	1.0E+00
TGGGCT	1.19	1.3E-01	1.08	2.4E-01
TTAGAA	1.19	1.9E-01	0.84	1.0E+00
CACTTA	1.19	2.4E-01	0.73	1.0E+00
AATTTC	1.19	1.6E-01	0.83	1.0E+00

TTTTGC	1.19	1.0E-01	1.35	**3.1E-08**
ATCATA	1.19	2.9E-01	0.91	8.1E-01
CCTTTC	1.19	9.4E-02	0.89	9.2E-01
ACTGCT	1.19	1.9E-01	1.16	5.3E-02
GCTTGA	1.19	2.7E-01	1.08	2.8E-01
TGGACC	1.19	3.1E-01	1.58	**1.3E-03**
GTTAAC	1.19	3.2E-01	1.44	**1.3E-03**
GTTTGT	1.19	1.0E-01	1.18	**3.5E-03**
AACCTG	1.19	2.4E-01	0.73	1.0E+00
TCAAGC	1.19	3.1E-01	0.97	6.2E-01
ATTTTA	1.18	7.1E-02	0.93	9.7E-01
CTGTGA	1.18	1.6E-01	1.91	**8.7E-24**
GTTGCC	1.18	3.0E-01	1.37	**7.8E-03**
GCTGAA	1.18	2.5E-01	0.97	6.4E-01
GATTGA	1.18	3.2E-01	0.73	9.9E-01
TTGATA	1.18	2.5E-01	1.42	**2.2E-06**
TATTCA	1.18	2.0E-01	0.99	5.7E-01
GAACCA	1.18	3.1E-01	1.25	3.5E-02
AGCCTG	1.18	1.6E-01	0.91	8.4E-01
GGGGTC	1.18	2.4E-01	1.01	5.1E-01
TCTTAG	1.18	2.2E-01	0.71	1.0E+00
TGTAGT	1.18	2.6E-01	1.26	**2.3E-03**
CTGTCC	1.18	1.4E-01	0.91	8.2E-01
AGAGCT	1.18	1.9E-01	0.73	1.0E+00
GAAGCA	1.18	2.4E-01	1.08	2.1E-01
GTAGTC	1.18	4.0E-01	0.86	8.4E-01
GGATCT	1.18	2.9E-01	0.66	1.0E+00
CCATAG	1.18	3.2E-01	0.80	9.3E-01
CTGACT	1.18	1.8E-01	0.91	8.1E-01
AGTAAA	1.18	2.0E-01	0.92	8.8E-01
TGCCAG	1.18	1.9E-01	1.66	**3.2E-09**
ATGAAT	1.18	1.9E-01	0.88	9.6E-01
GGATTT	1.18	2.1E-01	0.77	1.0E+00
GGCCAG	1.18	1.8E-01	1.57	**1.5E-05**
GGGCAG	1.17	1.4E-01	1.14	1.4E-01
GACACC	1.17	3.4E-01	0.65	9.9E-01
GCTAAA	1.17	3.3E-01	1.05	3.6E-01
CCAGGG	1.17	1.7E-01	1.66	**4.3E-07**
AATGTA	1.17	2.1E-01	1.54	**1.1E-17**
AGCTGA	1.17	2.2E-01	0.84	9.7E-01
TATTAA	1.17	1.7E-01	1.26	**2.5E-06**
GCAGGG	1.17	1.8E-01	1.09	2.6E-01
GAAAGC	1.17	2.7E-01	0.96	6.7E-01
CAATTG	1.17	3.7E-01	0.68	9.9E-01
CTTTAG	1.17	2.3E-01	1.01	4.7E-01
TGAAAC	1.17	2.5E-01	0.81	9.9E-01
AATTGA	1.17	2.2E-01	0.61	1.0E+00
TTAGGC	1.17	3.4E-01	1.13	2.3E-01
GGTTGC	1.17	3.4E-01	0.91	7.6E-01
CCAAAG	1.17	2.4E-01	2.52	**2.4E-51**

TGACAG	1.17	2.2E-01	0.89	8.8E-01
ATAGCT	1.17	3.0E-01	0.87	8.9E-01
CAACTT	1.17	2.7E-01	0.83	9.6E-01
ATCCAA	1.17	3.5E-01	0.90	8.1E-01
AAGAAA	1.17	1.3E-01	0.73	1.0E+00
ATAACA	1.17	2.9E-01	0.73	1.0E+00
AATCCA	1.17	3.0E-01	0.99	5.5E-01
TTCCTG	1.17	1.2E-01	0.95	7.7E-01
TTTATC	1.17	2.1E-01	0.95	7.7E-01
TTGTTC	1.17	1.9E-01	0.87	9.6E-01
ATGTAA	1.17	2.1E-01	1.33	**1.3E-07**
GGATGA	1.17	2.9E-01	0.93	7.2E-01
GCTGGA	1.17	2.1E-01	0.92	8.1E-01
CTGTAG	1.17	2.5E-01	1.14	8.8E-02
GGAGCT	1.17	2.4E-01	0.92	7.7E-01
CTTTAC	1.17	2.8E-01	1.14	1.1E-01
TCAGCT	1.17	2.0E-01	0.78	1.0E+00
CAATAA	1.17	3.3E-01	2.68	**1.9E-76**
AATCAT	1.17	2.6E-01	1.13	6.3E-02
CTTATG	1.17	2.7E-01	0.87	8.8E-01
TTGAAT	1.17	1.9E-01	1.06	1.7E-01
GCAGTA	1.17	3.4E-01	1.34	**6.2E-03**
AGCAGA	1.17	2.2E-01	0.95	7.3E-01
TACTGC	1.17	3.3E-01	1.32	**9.6E-03**
ATGGAT	1.17	2.8E-01	0.86	9.4E-01
TTCATG	1.17	2.2E-01	0.93	8.5E-01
GAATTC	1.17	2.8E-01	0.86	9.4E-01
AACTAG	1.17	3.6E-01	0.94	6.9E-01
TAGATC	1.16	3.8E-01	0.88	8.0E-01
CACAAA	1.16	2.8E-01	0.95	7.1E-01
TCTTGT	1.16	1.5E-01	1.25	**7.5E-04**
ATGGTG	1.16	2.4E-01	0.74	1.0E+00
TCAGGC	1.16	2.8E-01	1.13	1.6E-01
ACACAA	1.16	3.6E-01	0.73	1.0E+00
TATTTG	1.16	1.6E-01	1.22	**3.8E-05**
ATAAGC	1.16	3.6E-01	1.23	5.3E-02
TGGAAG	1.16	2.1E-01	0.91	8.8E-01
TATTAC	1.16	3.2E-01	1.09	2.1E-01
CCTGTG	1.16	1.6E-01	1.21	1.4E-02
TGCAGA	1.16	2.2E-01	0.94	7.9E-01
GGAGCA	1.16	2.5E-01	1.03	4.2E-01
CATAAG	1.16	3.6E-01	0.87	8.6E-01
CCAAAC	1.16	3.3E-01	0.95	6.8E-01
GCCTAA	1.16	3.5E-01	1.02	4.7E-01
TCAAAA	1.16	2.1E-01	0.64	1.0E+00
TTTCTT	1.16	3.5E-02	1.03	2.4E-01
GGTAGA	1.16	3.2E-01	0.87	8.3E-01
GGCCAT	1.16	3.0E-01	1.35	1.1E-02
TGGCTC	1.16	2.0E-01	1.04	3.7E-01
ACTGAA	1.16	2.4E-01	1.03	3.4E-01

TGTTTG	1.16	1.2E-01	1.14	1.1E-02
TCTCAA	1.16	2.4E-01	0.60	1.0E+00
CTACTA	1.16	4.0E-01	0.70	9.9E-01
AACCCC	1.16	3.0E-01	0.34	1.0E+00
AGTCTA	1.16	3.8E-01	0.94	7.0E-01
ATCAGA	1.15	2.9E-01	0.68	1.0E+00
TTAGAG	1.15	3.0E-01	0.67	1.0E+00
CACATG	1.15	2.7E-01	0.65	1.0E+00
CAGATC	1.15	3.5E-01	0.64	1.0E+00
ATAGTA	1.15	3.2E-01	0.58	1.0E+00
TTCTGT	1.15	9.5E-02	1.21	**9.2E-05**
TAGTGG	1.15	3.4E-01	0.89	8.0E-01
AAAGGC	1.15	3.1E-01	1.12	1.3E-01
TTTGTG	1.15	1.3E-01	1.31	**1.6E-07**
CCAGAG	1.15	2.3E-01	1.19	3.7E-02
TATCCA	1.15	3.3E-01	0.85	9.1E-01
CTTCTC	1.15	1.4E-01	0.75	1.0E+00
ACAATG	1.15	3.6E-01	0.97	6.4E-01
AGGTAT	1.15	3.4E-01	1.04	4.0E-01
ACAAAT	1.15	2.6E-01	0.88	9.7E-01
TTTTGT	1.15	6.8E-02	1.31	**6.1E-15**
AGGGCT	1.15	2.2E-01	1.65	**6.1E-08**
CTTGCC	1.15	2.5E-01	1.10	1.9E-01
ATTTTG	1.15	1.4E-01	1.38	**2.4E-14**
CACACT	1.15	2.8E-01	1.08	2.5E-01
CTGACA	1.15	2.7E-01	1.25	1.4E-02
TCAGGG	1.15	2.4E-01	1.95	**1.0E-13**
GAATAC	1.15	4.0E-01	0.98	5.7E-01
TGTCAC	1.15	2.7E-01	1.02	4.5E-01
CTGATA	1.15	3.1E-01	0.83	9.3E-01
TTACAT	1.14	2.5E-01	1.12	5.7E-02
CCTTCA	1.14	2.3E-01	0.90	8.6E-01
TGGTAC	1.14	3.8E-01	2.12	**6.4E-11**
TTATAC	1.14	3.4E-01	1.49	**2.4E-06**
ATTTGT	1.14	1.8E-01	1.27	**6.9E-07**
GTTTCT	1.14	1.4E-01	1.03	3.0E-01
TGATTA	1.14	2.7E-01	0.90	8.7E-01
CCCTGA	1.14	2.3E-01	0.65	1.0E+00
AGGTGG	1.14	2.2E-01	0.64	1.0E+00
CTAAAA	1.14	2.6E-01	0.62	1.0E+00
AGCTCA	1.14	2.9E-01	0.89	8.6E-01
TTTGGT	1.14	1.8E-01	1.16	**9.8E-03**
TTTAAG	1.14	2.3E-01	0.96	7.9E-01
GGCTCC	1.14	2.8E-01	1.41	**5.1E-03**
TAGTAC	1.14	4.2E-01	1.06	3.9E-01
ACTCAA	1.14	3.7E-01	0.60	1.0E+00
AAGTCT	1.14	2.9E-01	0.85	9.6E-01
ACAGCC	1.14	3.0E-01	0.85	9.1E-01
AATCTT	1.14	2.6E-01	0.93	8.3E-01
ATTGCC	1.14	3.5E-01	1.23	3.8E-02

AACAAG	1.14	3.2E-01	0.76	9.9E-01
GATTCA	1.14	3.5E-01	0.80	9.7E-01
GAATTA	1.14	3.1E-01	0.93	8.3E-01
TTGTGA	1.14	2.5E-01	1.31	**5.0E-05**
GGGTTA	1.14	3.8E-01	0.91	7.4E-01
GTGTGT	1.14	1.4E-01	1.03	3.1E-01
GATTTG	1.14	2.8E-01	1.21	1.2E-02
TGGAGG	1.13	2.4E-01	0.68	1.0E+00
TCATCC	1.13	3.0E-01	0.46	1.0E+00
CTCTGG	1.13	2.1E-01	1.34	**5.3E-04**
CAAGGG	1.13	3.2E-01	0.99	5.6E-01
TTTTTA	1.13	9.0E-02	1.08	**5.2E-03**
TGTGCA	1.13	2.5E-01	1.77	**2.0E-16**
ACCATC	1.13	3.8E-01	0.67	1.0E+00
CCAGGC	1.13	2.3E-01	1.01	4.8E-01
CAACAC	1.13	3.9E-01	0.67	9.9E-01
AGGCAG	1.13	2.2E-01	1.06	2.5E-01
AGTGGG	1.13	2.5E-01	0.72	1.0E+00
AAGCCT	1.13	3.1E-01	1.30	**2.8E-03**
CTAGCA	1.13	3.8E-01	1.31	2.9E-02
AAAATG	1.13	1.9E-01	0.90	9.8E-01
GAGGAC	1.13	3.3E-01	0.79	9.4E-01
CTCATT	1.13	2.3E-01	0.87	9.4E-01
GCCAGT	1.13	3.4E-01	1.18	7.0E-02
GCCTGA	1.13	3.0E-01	0.92	7.7E-01
GGGTAC	1.13	4.1E-01	1.16	2.5E-01
CCCTTT	1.13	1.9E-01	0.72	1.0E+00
TTCAGG	1.13	2.9E-01	1.24	**5.3E-03**
TCCAGG	1.13	2.6E-01	0.86	9.2E-01
TAAACC	1.13	3.6E-01	1.33	**2.2E-03**
GGTGGT	1.13	2.9E-01	0.65	1.0E+00
ACCTGA	1.13	3.2E-01	0.59	1.0E+00
GCTGTT	1.13	2.7E-01	1.19	1.6E-02
GGAGGC	1.13	2.6E-01	0.83	9.4E-01
TGGGAG	1.13	2.1E-01	0.71	1.0E+00
AGAATG	1.13	2.9E-01	0.96	7.1E-01
TGTTGG	1.13	2.7E-01	1.08	1.8E-01
GTCTAC	1.13	4.8E-01	0.67	9.8E-01
TGTGCC	1.13	2.5E-01	2.34	**1.1E-28**
GGCAGA	1.13	2.7E-01	0.74	1.0E+00
TACTGA	1.13	3.2E-01	0.98	6.1E-01
TGATCC	1.13	3.5E-01	0.64	1.0E+00
CAGAAC	1.13	3.4E-01	1.00	5.1E-01
TGCTGT	1.13	2.0E-01	1.62	**1.4E-15**
CTTTAT	1.13	2.3E-01	1.00	4.9E-01
AGCTTA	1.13	3.6E-01	1.28	1.0E-02
TGACCC	1.13	3.1E-01	0.75	9.7E-01
CTGACC	1.12	2.8E-01	0.95	6.7E-01
GGAGTA	1.12	4.1E-01	0.70	9.9E-01
GGGCAC	1.12	3.3E-01	1.14	2.2E-01

GGAAAT	1.12	3.0E-01	0.97	6.8E-01
CTGGGC	1.12	2.2E-01	1.25	1.5E-02
TTCATT	1.12	1.8E-01	0.84	1.0E+00
TGGTTT	1.12	1.9E-01	1.04	2.5E-01
GAAGCC	1.12	3.4E-01	1.58	**1.9E-05**
TTCTTT	1.12	9.1E-02	0.88	1.0E+00
TCTGGT	1.12	2.8E-01	1.04	3.4E-01
AAGTGA	1.12	3.0E-01	0.85	9.8E-01
TTTTCT	1.12	7.9E-02	1.11	**1.6E-03**
AATCAA	1.12	3.4E-01	0.96	6.8E-01
TTCTTG	1.12	2.0E-01	0.96	7.2E-01
GAGAGC	1.12	3.5E-01	0.84	8.9E-01
AAGGCA	1.12	3.3E-01	0.83	9.8E-01
TCTTTA	1.12	2.4E-01	0.83	1.0E+00
TCCATA	1.12	3.7E-01	0.93	7.4E-01
GGTACT	1.12	4.2E-01	2.22	**1.4E-11**
TGGCAA	1.12	3.6E-01	1.24	1.5E-02
ATTGGG	1.12	3.6E-01	0.85	8.9E-01
GAAACA	1.12	3.2E-01	0.75	1.0E+00
CCAATC	1.12	4.4E-01	1.27	8.6E-02
TTGTGC	1.11	3.2E-01	1.68	**1.8E-10**
TGTCCT	1.11	2.2E-01	1.11	9.2E-02
TGGTGT	1.11	2.8E-01	1.14	7.7E-02
TCTGCC	1.11	2.4E-01	1.02	4.2E-01
AGGTGA	1.11	3.3E-01	0.63	1.0E+00
AGTGCA	1.11	3.3E-01	1.29	**4.7E-03**
GGTAAT	1.11	3.8E-01	0.88	8.3E-01
TGTTTT	1.11	9.9E-02	0.97	8.0E-01
AGGAGG	1.11	2.5E-01	0.48	1.0E+00
CCCTGG	1.11	2.4E-01	0.87	8.9E-01
CATAGG	1.11	4.2E-01	0.75	9.6E-01
AGAGCA	1.11	3.1E-01	0.91	8.6E-01
TTATTA	1.11	2.6E-01	1.05	1.6E-01
TGCTCA	1.11	3.1E-01	1.00	5.3E-01
GGGCTA	1.11	4.1E-01	1.54	**6.5E-03**
TGGCCT	1.11	2.6E-01	1.29	**2.5E-03**
TTGGAA	1.11	2.8E-01	1.05	2.5E-01
TGTTCA	1.11	3.0E-01	0.95	7.6E-01
CTACAA	1.11	4.5E-01	0.70	9.9E-01
TCAATT	1.11	3.7E-01	0.78	9.9E-01
TGACTA	1.11	3.8E-01	1.15	1.5E-01
TTGGCC	1.11	3.3E-01	0.99	5.7E-01
AGCATC	1.11	3.8E-01	0.78	9.8E-01
GTAAAT	1.11	3.1E-01	2.13	**3.0E-49**
GGAATA	1.11	3.8E-01	0.87	9.2E-01
AGCCCA	1.11	3.4E-01	0.71	1.0E+00
TGCTCC	1.11	3.1E-01	0.88	8.4E-01
TTCACA	1.10	3.2E-01	0.80	1.0E+00
GTGGTT	1.10	3.2E-01	1.07	2.5E-01
TCACTC	1.10	3.4E-01	0.71	1.0E+00

GAAGGC	1.10	3.7E-01	1.35	**9.0E-03**
TTGTAA	1.10	3.0E-01	2.09	**8.1E-59**
TTCTAG	1.10	3.1E-01	0.98	5.9E-01
ATGGTT	1.10	3.3E-01	0.90	8.9E-01
TTTACC	1.10	3.5E-01	1.22	1.5E-02
TGGGCC	1.10	3.1E-01	1.11	2.4E-01
AAATGA	1.10	2.9E-01	0.78	1.0E+00
GCTCAG	1.10	3.2E-01	1.34	**1.2E-03**
ACCACA	1.10	3.8E-01	0.72	1.0E+00
GCTACC	1.10	4.5E-01	1.88	**4.3E-05**
TGTGTT	1.10	2.1E-01	1.18	**9.5E-04**
ATGAAC	1.10	3.9E-01	0.91	8.1E-01
GTTATC	1.10	4.3E-01	1.05	3.8E-01
TTAATA	1.10	3.0E-01	1.20	**1.7E-04**
GAGGGA	1.10	3.0E-01	0.64	1.0E+00
AGGGCA	1.10	3.2E-01	0.93	7.5E-01
TATTTT	1.10	1.6E-01	1.50	**5.0E-54**
GTGATA	1.10	3.9E-01	0.74	9.9E-01
AATAGC	1.10	4.1E-01	1.10	2.4E-01
ATATGA	1.10	4.0E-01	0.85	9.6E-01
AAACCC	1.10	3.9E-01	0.64	1.0E+00
TACACC	1.10	4.5E-01	1.01	5.1E-01
ATAAAG	1.10	3.7E-01	1.59	**2.3E-18**
AGGAAC	1.10	3.9E-01	1.00	5.1E-01
TGCCTC	1.10	2.9E-01	1.34	**2.4E-04**
GATCCT	1.10	3.9E-01	0.84	8.9E-01
TATGGT	1.10	4.0E-01	1.02	4.4E-01
CAACAA	1.10	4.2E-01	0.77	9.9E-01
GGTGTC	1.10	3.8E-01	1.29	3.8E-02
ATCAAA	1.10	3.6E-01	0.99	5.8E-01
GGTGAT	1.10	3.7E-01	0.67	1.0E+00
TAGGCC	1.10	4.4E-01	1.04	4.4E-01
CTCTCT	1.10	1.9E-01	0.41	1.0E+00
AACTTT	1.10	2.9E-01	0.94	8.6E-01
AGTTAA	1.10	3.5E-01	0.73	1.0E+00
TCTCTG	1.10	2.3E-01	0.88	9.5E-01
CAGTGT	1.10	3.2E-01	1.32	**7.7E-05**
GTGCCT	1.10	3.5E-01	4.23	**1.2E-114**
ATTCAG	1.09	3.4E-01	0.85	9.8E-01
CCCAGA	1.09	3.3E-01	0.79	9.8E-01
GGTCCT	1.09	3.6E-01	0.97	6.0E-01
GCTAAG	1.09	4.2E-01	1.01	4.9E-01
ACTTAA	1.09	3.5E-01	0.76	1.0E+00
CCTTAA	1.09	3.8E-01	1.87	**4.6E-16**
CAATCC	1.09	4.6E-01	0.85	8.3E-01
CACAGA	1.09	3.6E-01	0.82	9.8E-01
TTTTGA	1.09	2.5E-01	1.15	**1.8E-03**
TCAGTC	1.09	3.9E-01	0.54	1.0E+00
GCCATG	1.09	3.8E-01	1.22	4.1E-02
ATGTCC	1.09	4.0E-01	0.82	9.4E-01

GTTAAA	1.09	3.5E-01	0.96	7.1E-01
CTTTGC	1.09	2.8E-01	1.30	**4.0E-04**
CTCAGG	1.09	3.2E-01	2.83	**6.2E-46**
CTTTGT	1.09	2.5E-01	1.24	**9.9E-05**
GAATTG	1.09	3.8E-01	0.78	1.0E+00
TAAGGA	1.09	3.7E-01	0.78	9.9E-01
TGGTCC	1.09	3.9E-01	1.25	6.3E-02
CAGTTG	1.09	3.8E-01	0.91	8.5E-01
AGCAGG	1.09	3.4E-01	1.02	4.5E-01
CTGGCC	1.09	3.2E-01	1.16	1.1E-01
TAGACA	1.09	4.1E-01	1.34	**8.7E-03**
CAAGTC	1.09	4.2E-01	0.71	9.9E-01
ACATTG	1.09	3.9E-01	1.08	2.1E-01
CATTAC	1.09	4.4E-01	0.87	8.5E-01
CAGCAG	1.09	3.2E-01	1.14	6.1E-02
CCACAT	1.09	3.8E-01	0.57	1.0E+00
TAGGAT	1.09	4.1E-01	0.74	9.9E-01
GTCAAA	1.09	4.5E-01	0.92	7.7E-01
TACCAA	1.09	4.3E-01	1.44	**1.2E-04**
TTTAGA	1.09	3.4E-01	0.91	9.2E-01
ATACAA	1.09	4.2E-01	0.64	1.0E+00
ACATTA	1.09	4.0E-01	0.99	5.5E-01
TGACTC	1.09	3.7E-01	0.79	9.7E-01
AGACTA	1.09	4.4E-01	0.96	6.5E-01
AGACCA	1.09	4.0E-01	1.06	3.0E-01
TCTGGG	1.09	3.1E-01	1.09	1.8E-01
CCCATA	1.09	4.4E-01	0.66	9.9E-01
AGCTGT	1.09	3.5E-01	1.28	**6.1E-04**
TCCAAG	1.09	3.9E-01	1.06	3.1E-01
ATGTTC	1.09	3.6E-01	0.89	9.0E-01
CTATAC	1.09	4.8E-01	0.70	9.8E-01
CACTGG	1.09	3.7E-01	1.23	2.4E-02
TGTGGT	1.09	3.1E-01	1.19	1.2E-02
ATATTG	1.08	3.7E-01	1.09	1.2E-01
TGAATA	1.08	3.6E-01	1.22	**1.4E-03**
GGTCCC	1.08	3.9E-01	0.86	8.1E-01
ACTAGG	1.08	4.5E-01	0.55	1.0E+00
GGCTTG	1.08	3.8E-01	1.40	**3.2E-03**
GCCACC	1.08	3.9E-01	0.93	7.2E-01
TCAGCC	1.08	3.8E-01	0.76	9.9E-01
GAGGTC	1.08	4.1E-01	0.81	9.2E-01
TCTAGG	1.08	4.1E-01	0.99	5.5E-01
ATTCAC	1.08	4.0E-01	0.80	9.8E-01
TAGTTA	1.08	4.1E-01	0.94	7.4E-01
ACCCAC	1.08	4.0E-01	0.48	1.0E+00
TCAGAG	1.08	3.6E-01	0.91	8.4E-01
CACCTA	1.08	4.4E-01	0.72	9.8E-01
TAGAAA	1.08	3.5E-01	0.91	9.4E-01
TTATGC	1.08	4.2E-01	2.02	**8.3E-14**
CCTCCA	1.08	3.4E-01	0.80	9.8E-01

CAGCCT	1.08	3.2E-01	0.78	1.0E+00
CATGTT	1.08	3.4E-01	1.07	1.6E-01
ACATAA	1.08	4.1E-01	0.87	9.3E-01
TCATGA	1.08	4.1E-01	0.77	9.9E-01
GGTCCA	1.08	4.5E-01	1.44	1.3E-02
AGAAAT	1.08	3.4E-01	0.88	9.9E-01
CAAGAG	1.08	4.0E-01	0.71	1.0E+00
CTCCTG	1.08	3.1E-01	0.69	1.0E+00
GTGCTG	1.08	3.3E-01	1.63	**2.9E-09**
TGACTT	1.08	3.3E-01	1.04	2.9E-01
CCAAGT	1.08	4.1E-01	0.87	9.2E-01
TAGTTG	1.08	4.1E-01	1.05	3.5E-01
GAGAGA	1.08	3.6E-01	0.64	1.0E+00
GCAAGG	1.08	4.1E-01	0.68	9.9E-01
TCATGC	1.08	4.0E-01	0.98	5.8E-01
ACAGTT	1.08	3.9E-01	0.83	9.9E-01
TAGATT	1.08	4.0E-01	1.15	5.6E-02
GCAGAG	1.08	3.6E-01	0.96	6.8E-01
ACCTGG	1.08	3.8E-01	0.71	1.0E+00
TTGATG	1.08	3.8E-01	1.00	5.3E-01
CAAGGA	1.08	4.2E-01	0.82	9.6E-01
ACAGCA	1.08	4.0E-01	0.80	9.9E-01
CATGTC	1.08	4.1E-01	1.08	2.8E-01
TGAGCT	1.08	3.6E-01	0.96	6.8E-01
TGGATC	1.08	4.4E-01	1.07	3.4E-01
CATTCT	1.07	3.4E-01	0.77	1.0E+00
ATTATT	1.07	3.3E-01	0.78	1.0E+00
CTTATC	1.07	4.4E-01	0.75	9.8E-01
GACACT	1.07	4.4E-01	1.30	1.3E-02
GCAATG	1.07	4.5E-01	1.21	5.5E-02
CAAGTG	1.07	4.2E-01	1.10	1.8E-01
GATAGC	1.07	4.9E-01	0.92	6.9E-01
GAGACC	1.07	4.2E-01	0.84	9.0E-01
GGGTCC	1.07	4.1E-01	1.29	7.5E-02
AGTCTG	1.07	4.0E-01	0.73	1.0E+00
ATTTAC	1.07	4.1E-01	1.32	**3.5E-04**
TCAGAT	1.07	4.1E-01	0.96	6.8E-01
GTGCTA	1.07	4.5E-01	2.25	**2.0E-17**
GTGGCC	1.07	3.9E-01	1.43	**2.7E-03**
GGTTTC	1.07	4.0E-01	0.86	9.4E-01
TTTGGC	1.07	3.9E-01	1.15	5.4E-02
TAAGCC	1.07	4.4E-01	1.32	2.1E-02
TAATTC	1.07	3.9E-01	0.94	7.5E-01
CAAGAA	1.07	4.2E-01	0.86	9.6E-01
ACCTAA	1.07	4.7E-01	0.65	1.0E+00
TTTAAA	1.07	2.7E-01	0.94	9.8E-01
AATAAG	1.07	4.3E-01	0.78	1.0E+00
TTTAGC	1.07	4.2E-01	1.10	1.6E-01
GGGGCT	1.07	3.7E-01	0.94	6.8E-01
GGCAAA	1.07	4.3E-01	1.04	3.6E-01

TTAATG	1.07	3.8E-01	1.06	1.7E-01
TGACAC	1.07	4.5E-01	1.00	5.1E-01
TCCTGA	1.07	3.6E-01	0.75	1.0E+00
CAGCTA	1.07	4.5E-01	0.82	9.6E-01
ACAAAG	1.07	4.3E-01	0.88	9.2E-01
TCTGTG	1.07	3.2E-01	1.16	1.6E-02
ACCTTC	1.07	4.0E-01	0.64	1.0E+00
AGTTGA	1.07	4.2E-01	0.86	9.4E-01
GGCACT	1.07	4.3E-01	1.20	8.9E-02
GGCATC	1.07	4.5E-01	0.72	9.7E-01
AGCCTT	1.07	3.9E-01	1.57	**1.1E-09**
AGCCAG	1.07	3.8E-01	1.12	1.0E-01
TGTGAT	1.07	3.7E-01	1.22	**2.8E-03**
ACATTC	1.07	4.3E-01	1.43	**1.7E-05**
TCTGAT	1.07	4.0E-01	0.96	6.9E-01
AGGGTA	1.07	4.5E-01	1.12	2.3E-01
TACAGG	1.07	4.4E-01	0.65	1.0E+00
TAAACT	1.07	4.1E-01	1.24	**7.6E-04**
GTCCTT	1.06	3.9E-01	0.95	7.1E-01
GCAGGA	1.06	4.0E-01	0.88	8.9E-01
GTAACT	1.06	4.3E-01	1.26	1.0E-02
TGTTAC	1.06	4.3E-01	1.26	**6.2E-03**
ATCAAT	1.06	4.7E-01	0.94	7.3E-01
CCAGAT	1.06	4.4E-01	0.72	1.0E+00
GTACAA	1.06	4.8E-01	1.82	**2.4E-08**
TTAGGA	1.06	4.2E-01	0.85	9.6E-01
GCACAA	1.06	4.7E-01	2.30	**3.1E-19**
CTATAA	1.06	4.5E-01	0.78	9.9E-01
GGGTTT	1.06	3.9E-01	0.77	1.0E+00
ATGAAG	1.06	4.2E-01	1.20	1.3E-02
AAGAGC	1.06	4.4E-01	0.95	6.9E-01
TCATCA	1.06	4.3E-01	0.77	9.9E-01
CATATT	1.06	4.0E-01	1.03	3.5E-01
CCTGGA	1.06	3.9E-01	1.03	3.9E-01
GTTGGG	1.06	4.2E-01	0.82	9.4E-01
ATCTGA	1.06	4.2E-01	0.60	1.0E+00
AATAAC	1.06	4.3E-01	0.98	5.8E-01
GAAGGA	1.06	4.0E-01	0.82	9.8E-01
CCCATC	1.06	4.1E-01	0.51	1.0E+00
TATAAC	1.06	4.7E-01	0.82	9.4E-01
AATTTG	1.06	3.8E-01	1.01	4.6E-01
CTTGCT	1.06	3.6E-01	1.21	1.1E-02
TCCCAT	1.06	4.0E-01	0.70	1.0E+00
GGACTC	1.06	4.6E-01	1.11	2.9E-01
ACTGTT	1.06	4.1E-01	1.12	6.2E-02
AGAACT	1.06	4.3E-01	0.86	9.6E-01
ACTGCC	1.06	4.2E-01	2.26	**1.4E-17**
TGCACA	1.06	4.3E-01	2.04	**5.2E-22**
TGCCAC	1.06	4.2E-01	0.95	6.7E-01
ATTTGA	1.06	3.9E-01	1.03	3.3E-01

GAATTT	1.06	3.9E-01	1.00	5.0E-01
TACCAT	1.06	4.7E-01	0.92	7.6E-01
TAATGG	1.06	4.4E-01	1.00	5.0E-01
GGGTGA	1.05	4.3E-01	0.68	1.0E+00
TTATTC	1.05	4.0E-01	1.09	1.1E-01
TTGCTC	1.05	4.2E-01	1.14	1.1E-01
AAACCA	1.05	4.3E-01	1.16	2.2E-02
GAACTA	1.05	4.8E-01	1.11	2.2E-01
CTGTAT	1.05	4.2E-01	1.70	**5.6E-17**
GACCCT	1.05	4.3E-01	0.97	5.9E-01
ACATGG	1.05	4.4E-01	0.67	1.0E+00
TGAAAA	1.05	3.9E-01	0.88	9.9E-01
CATAGC	1.05	4.9E-01	1.13	2.2E-01
GCTGTA	1.05	4.6E-01	1.65	**1.4E-08**
CAGAAT	1.05	4.3E-01	0.79	1.0E+00
TGGGCA	1.05	4.0E-01	1.11	1.6E-01
GTTAAG	1.05	4.8E-01	0.85	9.1E-01
CCAGAA	1.05	4.3E-01	1.00	5.3E-01
TGCATA	1.05	4.5E-01	1.42	**2.4E-05**
CAAGCA	1.05	4.7E-01	0.91	8.1E-01
CATCTG	1.05	4.1E-01	1.01	4.8E-01
TGTAAA	1.05	4.1E-01	2.15	**8.3E-86**
ATGTCT	1.05	4.2E-01	1.14	5.8E-02
TTTCCA	1.05	3.7E-01	1.03	3.0E-01
CAGGCC	1.05	4.2E-01	1.01	4.7E-01
GCAACA	1.05	4.7E-01	0.94	7.0E-01
GGTTCA	1.05	4.7E-01	0.82	9.4E-01
ATGTGG	1.05	4.3E-01	0.81	9.8E-01
CAGGTT	1.05	4.5E-01	1.03	4.1E-01
CCATTC	1.05	4.4E-01	0.82	9.6E-01
ATCCTG	1.05	4.3E-01	0.68	1.0E+00
AAGGAG	1.05	4.3E-01	0.73	1.0E+00
TCAACT	1.05	4.7E-01	0.99	5.4E-01
GAGATG	1.04	4.4E-01	0.56	1.0E+00
ACCTTG	1.04	4.5E-01	0.90	8.4E-01
CTGTCT	1.04	3.8E-01	0.92	8.6E-01
ACTCTA	1.04	4.8E-01	0.62	1.0E+00
TGTTGA	1.04	4.3E-01	1.06	2.2E-01
GAATCC	1.04	4.9E-01	0.96	6.4E-01
CTATCC	1.04	5.0E-01	0.69	9.7E-01
AATGAC	1.04	4.6E-01	0.88	9.0E-01
AAGGAT	1.04	4.7E-01	0.79	9.9E-01
TAATTG	1.04	4.4E-01	1.02	3.9E-01
GCTCCT	1.04	4.4E-01	1.01	4.8E-01
GACAGG	1.04	4.6E-01	0.75	9.8E-01
GTCCTG	1.04	4.4E-01	1.21	4.8E-02
TCATTT	1.04	3.9E-01	0.93	9.4E-01
CCATTA	1.04	4.8E-01	1.16	1.1E-01
GGTGTG	1.04	4.4E-01	0.87	9.2E-01
GACCTC	1.04	4.7E-01	1.09	2.7E-01

CAATTC	1.04	5.0E-01	1.02	4.5E-01
GTGTGA	1.04	4.4E-01	0.90	8.9E-01
GAGCAC	1.04	4.8E-01	1.47	**1.7E-03**
ATTCAT	1.04	4.4E-01	0.69	1.0E+00
ACTGAC	1.04	4.8E-01	1.32	1.2E-02
AACCAA	1.04	4.7E-01	1.53	**9.0E-08**
TCTGTC	1.04	4.0E-01	0.87	9.4E-01
GTTCCA	1.04	4.8E-01	0.93	7.4E-01
TAGCAA	1.04	4.9E-01	1.34	**1.3E-03**
GCATTC	1.04	4.8E-01	1.31	1.3E-02
TCAAAC	1.04	4.8E-01	0.82	9.6E-01
GCCTTC	1.04	4.5E-01	1.50	**2.6E-05**
TATGAC	1.04	5.1E-01	1.08	3.2E-01
GCCATC	1.04	4.8E-01	1.21	8.9E-02
CTGTGC	1.04	4.3E-01	1.68	**5.7E-10**
TCACAT	1.03	4.7E-01	0.61	1.0E+00
GCCCAT	1.03	4.9E-01	0.68	9.9E-01
AGTGAC	1.03	4.8E-01	1.06	3.3E-01
CAGCTT	1.03	4.5E-01	1.12	8.5E-02
TATGCC	1.03	5.0E-01	1.37	**9.3E-03**
GGCAAT	1.03	5.1E-01	1.35	1.5E-02
AGAGAA	1.03	4.4E-01	0.73	1.0E+00
GCTATT	1.03	4.9E-01	1.35	**1.1E-03**
TACATT	1.03	4.6E-01	1.14	1.9E-02
ATGCTG	1.03	4.5E-01	1.25	**3.7E-03**
TGATTT	1.03	4.2E-01	1.06	1.4E-01
GTGGTG	1.03	4.6E-01	0.80	9.8E-01
ATGGAG	1.03	4.7E-01	0.51	1.0E+00
TTTTAC	1.03	4.4E-01	1.21	**3.1E-04**
TAATGC	1.03	4.8E-01	1.33	**2.9E-03**
TCAGGT	1.03	4.9E-01	1.62	**1.6E-07**
TCTCCA	1.03	4.4E-01	0.81	9.9E-01
AGACTG	1.03	4.8E-01	1.07	2.6E-01
TGTGGC	1.03	4.7E-01	1.45	**2.7E-05**
ATTGAA	1.03	4.7E-01	0.75	1.0E+00
TCTGAA	1.03	4.6E-01	0.97	6.8E-01
CAGGTG	1.03	4.7E-01	0.90	8.5E-01
CAAGCT	1.03	5.0E-01	1.12	1.7E-01
TAGCTA	1.03	5.2E-01	0.88	8.3E-01
AACCTC	1.03	5.0E-01	0.83	9.4E-01
GAATAT	1.02	4.9E-01	0.79	1.0E+00
GGGGCC	1.02	4.8E-01	1.55	1.4E-02
AATTCC	1.02	4.9E-01	0.78	9.9E-01
CTTCCT	1.02	4.4E-01	0.76	1.0E+00
GGGTAG	1.02	5.0E-01	1.02	4.8E-01
AGGGAG	1.02	4.6E-01	0.72	1.0E+00
TGGCCA	1.02	4.8E-01	1.03	3.9E-01
TTCATC	1.02	4.8E-01	0.89	8.9E-01
ATAAAT	1.02	4.7E-01	1.13	**9.8E-04**
CCTTTT	1.02	4.4E-01	0.80	1.0E+00

TATTGG	1.02	5.1E-01	0.99	5.6E-01
CATTCC	1.02	4.9E-01	2.23	**4.4E-23**
CAGGAA	1.02	4.8E-01	1.28	**5.7E-04**
GTTTAG	1.02	5.0E-01	0.93	7.5E-01
ATGTAT	1.02	4.8E-01	1.30	**8.6E-07**
TTTAGG	1.02	5.0E-01	0.99	5.6E-01
ATTCCC	1.02	5.0E-01	0.67	1.0E+00
CCTCAC	1.02	4.9E-01	0.82	9.5E-01
CCACCT	1.02	4.8E-01	0.72	1.0E+00
AACACT	1.02	5.1E-01	1.27	**2.0E-03**
TGTAGA	1.02	5.0E-01	1.64	**4.4E-11**
GCACCA	1.02	5.2E-01	1.21	1.0E-01
GTTCAG	1.02	5.1E-01	0.89	8.6E-01
CTTTCT	1.02	4.6E-01	0.88	9.9E-01
CAGAGA	1.01	4.9E-01	0.95	7.3E-01
CAATAC	1.01	5.4E-01	1.06	3.8E-01
GGTAGT	1.01	5.3E-01	0.90	7.7E-01
ATCTCA	1.01	5.0E-01	0.75	1.0E+00
GGGCAT	1.01	5.1E-01	0.89	8.0E-01
AGACCC	1.01	5.1E-01	0.62	1.0E+00
GAGAAA	1.01	4.9E-01	0.71	1.0E+00
TTATCA	1.01	5.1E-01	0.91	8.4E-01
AACATG	1.01	5.1E-01	0.78	1.0E+00
CAGGGG	1.01	5.0E-01	0.81	9.3E-01
GCAAAG	1.01	5.2E-01	1.03	4.2E-01
AAATCC	1.01	5.2E-01	0.69	1.0E+00
ACAAGA	1.01	5.2E-01	0.91	8.1E-01
AAACTT	1.01	5.0E-01	0.90	9.7E-01
TCCTGT	1.01	4.9E-01	1.02	4.1E-01
AGACAG	1.01	5.1E-01	0.54	1.0E+00
TAGTTC	1.01	5.3E-01	1.06	3.4E-01
ATTTCC	1.01	5.0E-01	0.83	9.9E-01
TCACCA	1.01	5.2E-01	1.02	4.3E-01
AGGGTG	1.01	5.0E-01	0.80	9.6E-01
GAGCCC	1.01	5.1E-01	0.95	6.6E-01
TTTCAT	1.01	4.9E-01	1.02	3.8E-01
TACAGC	1.01	5.4E-01	0.90	8.1E-01
CTGAGC	1.01	5.1E-01	1.12	1.5E-01
TTAAAC	1.01	5.1E-01	1.09	1.2E-01
CTGTGT	1.01	4.9E-01	1.04	3.0E-01
GCAAAA	1.01	5.2E-01	0.92	8.4E-01
TCCTGG	1.01	5.0E-01	1.02	4.3E-01
AGGAAT	1.01	5.1E-01	0.95	7.4E-01
AATTAT	1.01	5.1E-01	0.83	1.0E+00
TTAAGC	1.01	5.3E-01	1.14	1.1E-01
AGGCCT	1.01	5.1E-01	1.01	4.9E-01
ATAATT	1.01	5.1E-01	0.72	1.0E+00
GAATAA	1.01	5.2E-01	1.39	**3.2E-07**
ATGGGG	1.01	5.2E-01	0.51	1.0E+00
TGTACC	1.01	5.3E-01	1.87	**2.7E-10**

CAACTC	1.00	5.4E-01	0.87	8.3E-01
TAAGCA	1.00	5.3E-01	1.24	**8.2E-03**
GATGGC	1.00	5.4E-01	1.30	3.0E-02
GATCAT	1.00	5.3E-01	0.79	9.5E-01
ACTTCA	1.00	5.2E-01	0.82	9.9E-01
AGGGCC	1.00	5.2E-01	0.99	5.5E-01
CCTACA	1.00	5.4E-01	0.68	9.9E-01
GAGAAC	1.00	5.4E-01	0.77	9.8E-01
CAGGGA	1.00	5.1E-01	1.49	**4.2E-06**
AGAATT	1.00	5.2E-01	0.73	1.0E+00
ACTTGA	1.00	5.3E-01	1.83	**9.7E-20**
TCCAGT	1.00	5.2E-01	0.66	1.0E+00
AGAGAG	1.00	5.2E-01	0.53	1.0E+00
CCAAGC	1.00	5.4E-01	1.18	1.1E-01
AAACTA	1.00	5.3E-01	0.78	1.0E+00
CCTGGT	1.00	5.2E-01	1.13	1.4E-01
CCTTCT	1.00	5.1E-01	0.71	1.0E+00
ATGTCA	1.00	5.3E-01	0.96	6.7E-01
AAGACA	1.00	5.3E-01	0.87	9.3E-01
GCTCCC	1.00	5.2E-01	0.94	6.7E-01
GTAAAC	1.00	5.4E-01	1.71	**8.8E-08**
GTTCTT	1.00	5.2E-01	0.89	9.4E-01
AGCACC	1.00	5.3E-01	0.85	8.8E-01
GCATAT	1.00	5.4E-01	1.24	2.1E-02
TATAGT	1.00	5.3E-01	1.01	4.8E-01
TGAATT	1.00	5.2E-01	1.00	5.2E-01
ATGATG	1.00	5.3E-01	0.75	1.0E+00
TGTGAA	1.00	5.2E-01	1.71	**7.0E-24**
GAAGAA	1.00	5.3E-01	0.80	1.0E+00
AGACAA	1.00	5.4E-01	1.25	**9.5E-03**
ATGCAA	1.00	5.4E-01	1.68	**9.1E-11**
GGGATT	1.00	5.3E-01	0.49	1.0E+00
AAGAAC	1.00	5.4E-01	0.82	9.7E-01
ACATTT	1.00	5.2E-01	0.99	5.7E-01
GGAATC	1.00	5.5E-01	0.84	8.9E-01
GTAACC	1.00	5.5E-01	1.54	**1.0E-03**
TCTATA	1.00	5.4E-01	1.10	1.5E-01
CAAATA	1.00	5.4E-01	1.03	3.4E-01
ACTAGT	1.00	5.6E-01	1.24	6.4E-02
GGGATA	1.00	5.5E-01	0.79	9.4E-01
TAGCAG	1.00	5.4E-01	1.28	1.5E-02
GTAGCC	1.00	5.5E-01	1.16	2.2E-01
ACTGTA	1.00	5.4E-01	1.89	**2.6E-24**
ACAAGT	1.00	5.4E-01	0.87	8.9E-01
CAAATT	1.00	5.4E-01	0.91	9.2E-01
ATTGTC	1.00	5.4E-01	1.08	2.3E-01
TAGTAA	1.00	5.4E-01	0.99	5.6E-01
GGTGCA	1.00	5.4E-01	1.57	**1.4E-04**
GTTGGA	1.00	5.4E-01	0.89	8.3E-01
CAAATG	0.99	5.4E-01	0.88	9.6E-01

ATTGGA	0.99	5.5E-01	0.92	8.0E-01
GCTTTT	0.99	5.4E-01	1.27	**9.2E-06**
TAAATA	0.99	5.4E-01	1.36	**7.8E-16**
GGGGTG	0.99	5.4E-01	0.69	1.0E+00
AATGAA	0.99	5.4E-01	0.88	9.9E-01
CAGGCT	0.99	5.4E-01	0.76	1.0E+00
ACAAGC	0.99	5.6E-01	1.55	**3.1E-04**
GGTATG	0.99	5.6E-01	0.77	9.4E-01
ATAAAC	0.99	5.5E-01	1.65	**4.8E-15**
TCAAGA	0.99	5.5E-01	0.64	1.0E+00
TCACTG	0.99	5.5E-01	1.12	8.1E-02
ATCATT	0.99	5.5E-01	0.70	1.0E+00
AAGCAT	0.99	5.5E-01	1.22	**7.9E-03**
CACAAG	0.99	5.6E-01	1.03	4.1E-01
CCAGAC	0.99	5.5E-01	1.15	1.6E-01
TCTGTT	0.99	5.5E-01	0.91	9.4E-01
CAGCCA	0.99	5.5E-01	0.99	5.4E-01
CCTACC	0.99	5.6E-01	0.91	7.4E-01
CAAGGC	0.99	5.5E-01	0.87	8.4E-01
GAGCTC	0.99	5.5E-01	1.12	2.3E-01
CAGTAG	0.99	5.6E-01	0.85	9.1E-01
AGGTTT	0.99	5.5E-01	1.00	5.2E-01
AAGGTT	0.99	5.6E-01	0.91	8.6E-01
GAAGGT	0.99	5.6E-01	0.94	7.1E-01
ATGAAA	0.99	5.6E-01	0.83	1.0E+00
TAAAAT	0.99	5.6E-01	0.81	1.0E+00
GATAAA	0.99	5.6E-01	0.97	6.5E-01
ACACTT	0.99	5.6E-01	0.86	9.5E-01
CCACAA	0.98	5.6E-01	0.74	9.9E-01
TTAAAA	0.98	5.7E-01	0.77	1.0E+00
GGAAGC	0.98	5.6E-01	1.14	1.2E-01
ATAATG	0.98	5.6E-01	0.92	8.7E-01
GACTAC	0.98	5.9E-01	1.36	4.4E-02
AGAAGA	0.98	5.6E-01	0.77	1.0E+00
AAGTTT	0.98	5.6E-01	0.95	8.0E-01
CCATTT	0.98	5.7E-01	1.06	2.0E-01
AATTGT	0.98	5.6E-01	1.03	3.2E-01
CTGAAA	0.98	5.6E-01	0.89	9.6E-01
TAGGAC	0.98	5.7E-01	1.11	2.6E-01
TCCATC	0.98	5.6E-01	0.69	1.0E+00
TCAAGG	0.98	5.7E-01	0.96	6.5E-01
AAATTC	0.98	5.7E-01	0.78	1.0E+00
GTGCAG	0.98	5.7E-01	0.98	5.9E-01
TTCTCT	0.98	5.9E-01	0.74	1.0E+00
CACCAA	0.98	5.7E-01	1.53	**6.7E-05**
TGGGTA	0.98	5.7E-01	0.79	9.7E-01
TGAAGA	0.98	5.7E-01	1.10	9.4E-02
TCTTTT	0.98	6.0E-01	0.78	1.0E+00
CTCCTC	0.98	5.8E-01	0.55	1.0E+00
GCCCTG	0.98	5.8E-01	0.99	5.5E-01

TTGCCT	0.98	5.8E-01	1.62	**1.5E-12**
CAGGGC	0.98	5.7E-01	1.32	**1.0E-02**
CTAAGC	0.98	5.7E-01	1.23	8.7E-02
CTCACC	0.98	5.7E-01	0.72	9.9E-01
TAAGAC	0.98	5.7E-01	1.10	2.6E-01
AATCCC	0.98	5.7E-01	0.51	1.0E+00
CCAACT	0.98	5.7E-01	0.76	9.8E-01
AATACT	0.98	5.7E-01	0.97	6.8E-01
AAAGGA	0.98	5.8E-01	0.80	1.0E+00
GGGAGC	0.98	5.7E-01	1.04	4.1E-01
GTGTTT	0.98	5.9E-01	1.30	**4.1E-07**
AGTTCC	0.98	5.7E-01	0.64	1.0E+00
ACCTAC	0.98	5.8E-01	0.82	8.9E-01
TAGGTA	0.98	5.7E-01	0.74	9.8E-01
CTAAGG	0.98	5.7E-01	0.79	9.3E-01
TATTTC	0.98	5.9E-01	1.02	3.5E-01
AGTTTA	0.98	5.8E-01	1.10	9.0E-02
TATTGA	0.98	5.8E-01	1.18	1.9E-02
GTAGGC	0.98	5.8E-01	1.18	2.1E-01
AATAAA	0.98	5.9E-01	2.22	**2.5E-218**
GATAGA	0.98	5.8E-01	0.58	1.0E+00
AGGACT	0.97	5.8E-01	1.08	2.7E-01
CATTTT	0.97	6.1E-01	1.11	**7.1E-03**
GACCCA	0.97	5.8E-01	0.78	9.5E-01
GGTTCT	0.97	5.8E-01	1.12	1.5E-01
TTATCC	0.97	5.8E-01	1.05	3.5E-01
CCTCCT	0.97	6.0E-01	0.77	1.0E+00
AAACTC	0.97	5.8E-01	0.73	1.0E+00
GATCCC	0.97	5.8E-01	0.77	9.2E-01
AGTAGC	0.97	5.8E-01	0.63	1.0E+00
CACCTT	0.97	5.9E-01	1.00	4.9E-01
CCTGTC	0.97	5.9E-01	0.86	9.3E-01
GCTGGG	0.97	6.1E-01	0.98	6.1E-01
CATTTC	0.97	6.1E-01	1.04	2.6E-01
CTTAAG	0.97	5.9E-01	0.88	9.1E-01
CCATGG	0.97	5.9E-01	0.67	1.0E+00
CTGAAC	0.97	5.8E-01	0.89	8.4E-01
TATACA	0.97	5.9E-01	1.07	2.1E-01
CCAGCA	0.97	5.9E-01	1.34	**3.6E-04**
GGACTG	0.97	5.9E-01	0.99	5.4E-01
TATATG	0.97	5.9E-01	1.03	3.5E-01
CTAAAG	0.97	5.9E-01	0.90	8.5E-01
TAGGCT	0.97	5.9E-01	1.12	2.0E-01
GCCTTG	0.97	5.9E-01	2.06	**2.6E-16**
AATATA	0.97	6.0E-01	0.85	1.0E+00
GTCACA	0.97	5.9E-01	1.09	2.3E-01
TGAATC	0.97	5.9E-01	1.04	3.8E-01
GATCCA	0.97	5.9E-01	0.80	9.2E-01
CATTAT	0.97	5.9E-01	1.02	4.4E-01
CCAAAA	0.97	5.9E-01	1.21	**3.9E-03**

TGATAG	0.97	5.9E-01	0.65	1.0E+00
CTCCAA	0.97	5.9E-01	0.73	9.9E-01
TGCCTT	0.97	6.2E-01	3.18	**2.2E-118**
AACAAA	0.96	6.1E-01	0.76	1.0E+00
CTTGAC	0.96	5.9E-01	1.22	4.9E-02
GCTTAC	0.96	5.9E-01	0.68	9.8E-01
TGGATT	0.96	6.0E-01	1.03	3.9E-01
GGGTGT	0.96	6.0E-01	0.97	6.0E-01
AATGCC	0.96	5.9E-01	1.74	**1.4E-08**
CTAGAA	0.96	6.0E-01	0.91	8.6E-01
AAAAGC	0.96	6.0E-01	1.08	1.3E-01
TGTACT	0.96	6.0E-01	1.67	**3.5E-12**
GGGCTT	0.96	6.0E-01	1.38	**1.7E-03**
TTGTAG	0.96	6.0E-01	1.41	**7.5E-06**
AGTGTT	0.96	6.1E-01	1.41	**8.6E-08**
GGGAAG	0.96	6.2E-01	0.81	9.8E-01
AACTCC	0.96	5.9E-01	0.52	1.0E+00
ATGAGC	0.96	6.0E-01	0.80	9.6E-01
TGAAGC	0.96	6.0E-01	1.19	4.4E-02
TTCAGA	0.96	6.1E-01	1.04	2.7E-01
GTTTCC	0.96	6.1E-01	0.81	9.8E-01
AGTGGA	0.96	6.0E-01	0.80	9.8E-01
GCATTA	0.96	5.9E-01	1.79	**1.6E-09**
TTCACC	0.96	6.0E-01	0.80	9.8E-01
GCCACT	0.96	6.0E-01	0.83	9.5E-01
GAGGGT	0.96	6.0E-01	0.82	9.2E-01
AGGGGT	0.96	6.0E-01	0.52	1.0E+00
AGGCAA	0.96	6.0E-01	1.00	5.0E-01
TTTCAC	0.96	6.2E-01	0.81	1.0E+00
CTCACT	0.96	6.2E-01	0.49	1.0E+00
GGAGGT	0.96	6.1E-01	0.56	1.0E+00
CTCTTA	0.96	6.1E-01	0.62	1.0E+00
TGAGTT	0.96	6.2E-01	0.75	1.0E+00
GGCCTC	0.96	6.2E-01	1.25	4.5E-02
CTCAGC	0.96	6.1E-01	0.79	9.9E-01
TAGGGT	0.96	6.0E-01	0.73	9.7E-01
TAAAAC	0.96	6.1E-01	0.86	9.9E-01
TGAACC	0.96	6.0E-01	0.95	6.8E-01
GGAACA	0.96	6.0E-01	1.04	3.8E-01
GCTATA	0.96	6.0E-01	1.00	5.3E-01
CACCTG	0.96	6.2E-01	0.78	9.9E-01
GGTGAA	0.96	6.0E-01	0.70	1.0E+00
GCCTAG	0.96	6.0E-01	0.88	7.9E-01
CTAGGT	0.96	6.0E-01	0.67	9.9E-01
CTTCTA	0.96	6.2E-01	0.69	1.0E+00
TTGTAC	0.96	6.1E-01	2.27	**2.1E-33**
CACAGG	0.96	6.1E-01	0.85	9.3E-01
CAATTT	0.95	6.2E-01	0.70	1.0E+00
CCCATT	0.95	6.2E-01	0.68	1.0E+00
AAGCAG	0.95	6.3E-01	0.97	6.3E-01

CCAATG	0.95	6.0E-01	1.04	4.1E-01
GTCTGT	0.95	6.5E-01	1.02	4.1E-01
AGATGT	0.95	6.2E-01	1.09	1.5E-01
CCTCAA	0.95	6.1E-01	0.77	9.9E-01
AACTTA	0.95	6.2E-01	0.78	9.9E-01
GGCCTT	0.95	6.2E-01	1.67	**1.6E-07**
AGTGAA	0.95	6.3E-01	0.67	1.0E+00
CATTAG	0.95	6.1E-01	0.80	9.6E-01
GATGAA	0.95	6.2E-01	0.63	1.0E+00
CCTTGC	0.95	6.3E-01	1.34	**4.8E-03**
AGCCCC	0.95	6.3E-01	0.55	1.0E+00
CAGGAC	0.95	6.2E-01	1.11	2.3E-01
ATAGGT	0.95	6.1E-01	0.74	9.8E-01
TGCCCT	0.95	6.6E-01	1.00	5.1E-01
CTTTCC	0.95	6.7E-01	0.81	9.9E-01
CAGATG	0.95	6.3E-01	1.00	5.2E-01
GAGTAG	0.95	6.2E-01	0.47	1.0E+00
TCTTCA	0.95	6.5E-01	0.92	8.8E-01
AACTCA	0.95	6.2E-01	0.96	6.9E-01
GCCTGG	0.95	6.6E-01	1.12	1.4E-01
AAGAAT	0.95	6.4E-01	0.84	9.9E-01
GGTCAG	0.95	6.3E-01	0.88	8.5E-01
TCACAG	0.95	6.4E-01	0.71	1.0E+00
CATATG	0.95	6.2E-01	0.78	9.8E-01
GACAAA	0.94	6.2E-01	1.10	1.6E-01
ATTAGA	0.94	6.2E-01	0.86	9.4E-01
AGAATA	0.94	6.4E-01	0.90	9.2E-01
GCCCCC	0.94	6.4E-01	0.65	9.6E-01
GCATTG	0.94	6.2E-01	1.37	**1.6E-03**
ACATGA	0.94	6.3E-01	0.80	9.9E-01
GGTTAC	0.94	6.1E-01	1.32	5.9E-02
CATTTG	0.94	6.7E-01	1.03	3.0E-01
ACTCAC	0.94	6.3E-01	0.69	9.9E-01
TCATCT	0.94	6.6E-01	0.89	9.3E-01
GCTCTA	0.94	6.2E-01	1.03	4.5E-01
GATAGG	0.94	6.2E-01	0.33	1.0E+00
TATAAT	0.94	6.5E-01	0.84	1.0E+00
TTAGCA	0.94	6.3E-01	1.37	**2.2E-04**
GAAGTC	0.94	6.2E-01	0.80	9.5E-01
GTGCAA	0.94	6.2E-01	2.24	**2.4E-18**
AGAGAC	0.94	6.3E-01	0.75	9.9E-01
GTTCAC	0.94	6.2E-01	1.16	1.6E-01
GAACTC	0.94	6.2E-01	0.71	9.9E-01
CTCACA	0.94	6.4E-01	0.75	9.9E-01
CTTACA	0.94	6.3E-01	0.69	1.0E+00
AAGCCC	0.94	6.3E-01	1.17	1.3E-01
AAATCT	0.94	6.5E-01	0.73	1.0E+00
TTTGTA	0.94	6.8E-01	2.08	**7.9E-88**
GCTATG	0.94	6.2E-01	1.19	1.3E-01
TGTATG	0.94	6.5E-01	1.26	**4.9E-04**

GCCTAT	0.94	6.2E-01	0.94	6.7E-01
TGGATA	0.94	6.3E-01	0.93	7.6E-01
TAGACC	0.94	6.2E-01	0.93	6.8E-01
GCCATA	0.94	6.2E-01	2.35	**1.1E-13**
TGCAAA	0.94	6.4E-01	1.25	**7.9E-04**
TGAGTC	0.94	6.4E-01	0.87	8.8E-01
GGGAGA	0.94	6.7E-01	0.67	1.0E+00
TTCAAC	0.94	6.3E-01	0.89	8.6E-01
ATGATT	0.94	6.5E-01	0.74	1.0E+00
TCTGGA	0.94	6.6E-01	1.12	9.7E-02
TTCACT	0.94	6.7E-01	0.79	1.0E+00
AACCAT	0.94	6.3E-01	0.76	1.0E+00
ACAGTA	0.94	6.3E-01	1.08	2.0E-01
TTCAAT	0.94	6.4E-01	1.20	1.6E-02
ATTGTG	0.94	6.5E-01	1.25	**1.1E-03**
GAAGGG	0.94	6.6E-01	1.00	5.3E-01
CTGGAC	0.94	6.4E-01	1.45	**1.5E-03**
TTGTGT	0.94	7.1E-01	1.19	**8.4E-04**
TTCCTC	0.94	7.1E-01	0.68	1.0E+00
TTAGAC	0.93	6.3E-01	1.44	**2.6E-03**
TTTCCT	0.93	7.6E-01	0.91	9.7E-01
AGTAGA	0.93	6.5E-01	0.68	1.0E+00
ACATCA	0.93	6.4E-01	0.63	1.0E+00
TACAGT	0.93	6.4E-01	1.28	**1.3E-03**
TATAGA	0.93	6.4E-01	1.18	3.6E-02
GGGGAG	0.93	6.9E-01	0.89	8.3E-01
TCAGAA	0.93	6.7E-01	0.92	8.9E-01
TCCTTT	0.93	7.4E-01	0.77	1.0E+00
GTCCTA	0.93	6.3E-01	0.62	1.0E+00
GACTTA	0.93	6.4E-01	0.92	7.4E-01
GAGCCA	0.93	6.6E-01	1.18	5.4E-02
TTACAA	0.93	6.5E-01	1.08	1.8E-01
TTGGAC	0.93	6.3E-01	1.61	**3.7E-05**
TTGGAT	0.93	6.6E-01	0.99	5.7E-01
AAAGAT	0.93	6.7E-01	0.88	9.7E-01
TAGAGA	0.93	6.5E-01	0.78	1.0E+00
TATGTT	0.93	6.9E-01	0.90	9.5E-01
CAATGG	0.93	6.3E-01	0.73	9.8E-01
TAAGAT	0.93	6.6E-01	0.81	9.8E-01
CTTAGT	0.93	6.5E-01	0.75	9.9E-01
CTATAT	0.93	6.4E-01	1.13	1.1E-01
TCTTAA	0.93	6.8E-01	0.74	1.0E+00
TATGGC	0.93	6.3E-01	1.26	5.1E-02
AGATAG	0.93	6.4E-01	0.58	1.0E+00
TAGAGG	0.93	6.5E-01	0.67	1.0E+00
GATATC	0.93	6.3E-01	0.36	1.0E+00
TGTATC	0.93	6.5E-01	1.21	1.9E-02
CCATCA	0.93	6.5E-01	0.89	8.3E-01
GAGGGG	0.93	6.9E-01	0.54	1.0E+00
GTGAAA	0.93	6.8E-01	0.90	9.2E-01

AGGTAC	0.93	6.3E-01	1.36	1.9E-02
ATGTGA	0.93	6.8E-01	1.34	**1.7E-05**
CTCATC	0.93	6.7E-01	0.78	9.7E-01
TTTTCA	0.93	7.6E-01	1.16	**5.9E-04**
AGTCAA	0.92	6.4E-01	0.74	9.9E-01
ATGATA	0.92	6.5E-01	0.69	1.0E+00
TTCTTA	0.92	7.1E-01	0.96	7.5E-01
GTCTGA	0.92	6.6E-01	0.99	5.7E-01
GATGAT	0.92	6.6E-01	0.67	1.0E+00
TGTTCT	0.92	7.5E-01	0.89	9.7E-01
TTGAAC	0.92	6.6E-01	0.87	9.4E-01
TGTCAT	0.92	6.8E-01	0.82	9.9E-01
AGGGGC	0.92	6.9E-01	0.65	1.0E+00
AATTGG	0.92	6.6E-01	0.95	7.0E-01
CAAGCC	0.92	6.4E-01	1.43	**2.9E-03**
AGAAAA	0.92	7.3E-01	0.73	1.0E+00
TCATAG	0.92	6.5E-01	0.91	8.1E-01
CCAGTG	0.92	6.8E-01	1.14	9.7E-02
AATGTC	0.92	6.7E-01	1.18	2.4E-02
CTTCAA	0.92	6.6E-01	0.78	1.0E+00
TTGTTG	0.92	7.1E-01	0.86	9.8E-01
CAAACA	0.92	6.6E-01	0.72	1.0E+00
GACTTC	0.92	6.6E-01	0.95	6.8E-01
TGGCCC	0.92	6.9E-01	0.78	9.5E-01
CAACAG	0.92	6.6E-01	0.83	9.4E-01
ATCTTT	0.92	7.2E-01	0.98	6.4E-01
CTTTTC	0.92	7.8E-01	0.80	1.0E+00
AGCCTC	0.92	6.9E-01	0.80	9.8E-01
GCAAAT	0.92	6.7E-01	0.98	5.9E-01
TCACTT	0.92	7.1E-01	0.81	1.0E+00
TACCTG	0.92	6.7E-01	1.16	8.2E-02
AGCATA	0.92	6.5E-01	0.91	8.0E-01
TCCTAC	0.92	6.5E-01	0.82	9.0E-01
TATATT	0.92	7.3E-01	1.25	**7.0E-08**
ACTGAT	0.92	6.8E-01	0.85	9.6E-01
ATTAGG	0.92	6.5E-01	0.69	1.0E+00
AAGGGT	0.92	6.8E-01	0.95	6.8E-01
ACAACA	0.92	6.5E-01	0.66	1.0E+00
AGGGTC	0.92	6.7E-01	1.02	4.5E-01
AATATT	0.92	7.4E-01	0.93	9.6E-01
TCCTCC	0.92	7.4E-01	0.61	1.0E+00
GATTTC	0.92	7.0E-01	1.05	3.1E-01
GTACTA	0.92	6.4E-01	1.30	4.3E-02
GCCCAA	0.92	6.5E-01	0.83	8.8E-01
TGCACC	0.92	6.7E-01	1.25	5.5E-02
TGTTTC	0.92	7.8E-01	0.93	8.7E-01
GACCTG	0.91	6.8E-01	0.82	9.2E-01
GGACTT	0.91	6.7E-01	1.24	2.8E-02
CCCAGC	0.91	7.4E-01	0.93	7.7E-01
TCCAAC	0.91	6.5E-01	0.74	9.7E-01

GGCTGG	0.91	7.5E-01	1.14	1.1E-01
GAACAT	0.91	6.7E-01	0.83	9.5E-01
GACATT	0.91	6.8E-01	1.14	5.7E-02
CATTTA	0.91	7.2E-01	0.89	9.7E-01
AGATCA	0.91	6.7E-01	0.73	1.0E+00
CATGGG	0.91	6.9E-01	0.72	9.9E-01
GACTGT	0.91	6.8E-01	1.47	**4.1E-05**
TTAGTC	0.91	6.5E-01	0.94	6.9E-01
AACACC	0.91	6.6E-01	0.84	8.8E-01
AGCTCC	0.91	6.8E-01	0.79	9.6E-01
ATGACC	0.91	6.6E-01	1.11	2.6E-01
GTGCCA	0.91	6.8E-01	2.45	**1.6E-25**
CTCTCA	0.91	7.2E-01	0.51	1.0E+00
TTACTG	0.91	7.0E-01	1.20	**9.3E-03**
GATGAC	0.91	6.5E-01	0.95	6.6E-01
TCATAC	0.91	6.5E-01	0.91	7.6E-01
AGGCCA	0.91	7.0E-01	0.97	6.2E-01
TTCTAT	0.91	7.1E-01	1.20	**4.3E-03**
TCATAA	0.91	6.9E-01	0.96	7.0E-01
CAGACA	0.91	6.9E-01	0.72	1.0E+00
TATCTC	0.91	6.8E-01	0.67	1.0E+00
TATCAT	0.91	6.7E-01	0.80	9.9E-01
AATCCT	0.91	6.9E-01	0.81	9.8E-01
CAAGGT	0.91	6.7E-01	1.17	9.6E-02
GAGTTC	0.91	6.7E-01	0.53	1.0E+00
GAGGTG	0.91	7.0E-01	0.65	1.0E+00
ACTGGT	0.91	6.8E-01	1.41	**6.8E-04**
GCTCTC	0.91	7.0E-01	0.74	9.8E-01
TTTTGG	0.91	7.7E-01	0.87	9.9E-01
ATTCTG	0.91	7.4E-01	0.92	8.9E-01
TCTCAT	0.91	7.4E-01	0.58	1.0E+00
GCAAGA	0.91	6.7E-01	0.92	7.6E-01
TAATCC	0.91	6.9E-01	0.56	1.0E+00
AGAAAG	0.91	7.6E-01	0.64	1.0E+00
ACAAAA	0.91	7.2E-01	0.63	1.0E+00
TATGAA	0.91	7.1E-01	1.11	7.6E-02
AGGAAG	0.91	7.6E-01	0.88	9.6E-01
TGATGA	0.91	7.1E-01	0.74	1.0E+00
GCTGAG	0.91	7.2E-01	0.71	1.0E+00
ATGTTT	0.91	7.9E-01	1.06	1.1E-01
TGCACT	0.91	7.0E-01	2.32	**1.3E-35**
AAGTCC	0.90	6.7E-01	0.93	7.4E-01
AGCCTA	0.90	6.7E-01	0.85	8.7E-01
GTCTTC	0.90	7.2E-01	1.34	**1.5E-03**
AGCTTC	0.90	7.1E-01	0.92	7.8E-01
GGATCA	0.90	6.7E-01	0.79	9.5E-01
TTCTGA	0.90	7.8E-01	1.00	5.4E-01
ACAGAA	0.90	7.2E-01	0.91	8.9E-01
AACTCT	0.90	7.2E-01	0.64	1.0E+00
GGTTGT	0.90	6.9E-01	1.16	1.2E-01

TTTATA	0.90	7.7E-01	1.38	**9.8E-20**
ATGTTA	0.90	7.2E-01	1.18	**9.0E-03**
TATAAG	0.90	6.8E-01	0.96	6.7E-01
AATGAG	0.90	7.0E-01	0.70	1.0E+00
AGAAAC	0.90	7.1E-01	0.90	9.2E-01
GTCACC	0.90	6.8E-01	1.04	4.2E-01
TCTTGG	0.90	7.6E-01	0.88	9.2E-01
TAGGCA	0.90	6.9E-01	0.91	7.8E-01
TGAACA	0.90	7.0E-01	1.09	1.7E-01
TTATGT	0.90	7.4E-01	1.13	1.9E-02
AATTTA	0.90	7.7E-01	0.97	7.5E-01
AACAGT	0.90	7.0E-01	1.02	4.4E-01
AGAGGG	0.90	7.5E-01	0.59	1.0E+00
TATGGA	0.90	6.9E-01	0.82	9.7E-01
ATATCC	0.90	6.7E-01	0.55	1.0E+00
GTTCTG	0.90	7.5E-01	0.91	8.6E-01
GCACAT	0.89	6.9E-01	1.66	**2.6E-07**
CTCTTG	0.89	7.8E-01	0.95	7.5E-01
AAGTGC	0.89	7.0E-01	1.90	**1.5E-15**
AAGTCA	0.89	7.2E-01	0.73	1.0E+00
GTTGTA	0.89	6.9E-01	1.58	**1.4E-08**
CCTCTG	0.89	7.9E-01	1.08	1.8E-01
TTACTC	0.89	7.1E-01	0.82	9.4E-01
AAATAA	0.89	8.0E-01	1.17	**8.0E-07**
AGTACT	0.89	6.9E-01	1.30	**8.7E-03**
ATATTT	0.89	8.2E-01	1.21	**1.7E-08**
CTTGAG	0.89	7.3E-01	0.64	1.0E+00
AAGCCA	0.89	7.3E-01	1.75	**1.1E-14**
ATTATA	0.89	7.4E-01	0.72	1.0E+00
ATTTGG	0.89	7.6E-01	1.09	1.3E-01
CTTGTC	0.89	7.4E-01	1.29	**7.3E-03**
TAGAAT	0.89	7.3E-01	0.99	5.5E-01
GTTCTA	0.89	7.0E-01	0.97	6.3E-01
TCTCTT	0.89	8.6E-01	0.67	1.0E+00
AGTTGC	0.89	6.9E-01	1.20	6.1E-02
CCCTAA	0.89	7.0E-01	0.77	9.5E-01
CAACTG	0.89	6.9E-01	0.84	9.2E-01
AATTCT	0.89	7.6E-01	0.77	1.0E+00
CACATT	0.89	7.4E-01	0.84	9.8E-01
GAACAC	0.89	6.7E-01	0.90	8.1E-01
CTTCAG	0.89	7.6E-01	0.92	8.5E-01
ATGGAC	0.89	6.9E-01	1.45	**2.9E-03**
CATCTC	0.89	7.7E-01	0.73	1.0E+00
CACTTT	0.89	7.9E-01	1.29	**8.1E-06**
AAAGAA	0.89	8.0E-01	0.70	1.0E+00
AGGTTC	0.89	6.9E-01	0.83	9.2E-01
TTGCTG	0.89	8.1E-01	1.64	**1.0E-13**
CTAGTC	0.89	6.7E-01	0.61	1.0E+00
CAACAT	0.89	7.1E-01	0.55	1.0E+00
TAAATC	0.89	7.2E-01	1.21	1.2E-02

AATTTT	0.89	8.4E-01	0.71	1.0E+00
ATTTCT	0.89	8.5E-01	1.09	3.3E-02
GTGTCC	0.89	7.4E-01	0.84	9.2E-01
CACCAG	0.88	7.4E-01	1.19	5.2E-02
ATACTA	0.88	6.9E-01	1.07	3.1E-01
AGGATG	0.88	7.5E-01	0.68	1.0E+00
GCCCAG	0.88	7.8E-01	1.04	3.6E-01
CTTTTG	0.88	8.3E-01	0.98	6.2E-01
AGTTAT	0.88	7.3E-01	0.86	9.6E-01
CTGGGA	0.88	8.0E-01	0.74	1.0E+00
ACCACT	0.88	7.1E-01	1.53	**2.0E-05**
TGGGAT	0.88	7.7E-01	0.57	1.0E+00
AGAGAT	0.88	7.5E-01	0.54	1.0E+00
ATGCCT	0.88	7.5E-01	1.30	**9.7E-04**
GTGCCC	0.88	7.4E-01	1.44	**3.7E-03**
CTGTTT	0.88	8.6E-01	0.91	9.5E-01
AAAAGG	0.88	7.6E-01	0.77	1.0E+00
AGAATC	0.88	7.2E-01	0.63	1.0E+00
TTCCTT	0.88	8.8E-01	0.75	1.0E+00
GTAGAA	0.88	7.2E-01	1.01	4.7E-01
GTAGTG	0.88	7.0E-01	1.21	9.1E-02
GGACAT	0.88	7.1E-01	1.11	2.3E-01
CCAAGG	0.88	7.4E-01	0.98	6.0E-01
GGTTGA	0.88	7.1E-01	0.77	9.6E-01
GCCAGC	0.88	7.4E-01	1.65	**1.5E-05**
CTCTGT	0.88	8.5E-01	0.77	1.0E+00
GGGAAT	0.88	7.3E-01	0.88	8.7E-01
TCTTTG	0.88	8.5E-01	1.06	1.6E-01
TATTCT	0.88	7.9E-01	1.01	4.5E-01
GTTACA	0.88	7.1E-01	1.19	5.7E-02
TGCATT	0.88	8.0E-01	1.36	**3.1E-07**
AGATTC	0.88	7.3E-01	0.61	1.0E+00
CTGGTA	0.88	7.2E-01	0.99	5.5E-01
GTTCCT	0.88	7.7E-01	0.82	9.7E-01
GCATCA	0.88	7.0E-01	0.86	8.7E-01
TCATGG	0.88	7.4E-01	0.89	8.6E-01
AAGCTA	0.88	7.1E-01	1.09	2.1E-01
GCATTT	0.88	8.0E-01	1.17	**5.0E-03**
AGTGTC	0.88	7.4E-01	1.11	2.0E-01
AATAGT	0.88	7.4E-01	0.92	8.0E-01
CCTAAA	0.88	7.3E-01	0.79	9.9E-01
GAGGAG	0.88	8.0E-01	0.58	1.0E+00
TAAGTC	0.88	7.1E-01	0.87	8.4E-01
CATCCC	0.88	7.6E-01	0.69	1.0E+00
CAAACT	0.88	7.4E-01	0.90	8.7E-01
CTTTTT	0.87	9.3E-01	0.81	1.0E+00
TGATGC	0.87	7.2E-01	1.13	1.5E-01
CCCTGC	0.87	8.3E-01	1.18	8.2E-02
CAGTGA	0.87	7.9E-01	0.78	1.0E+00
ATACAG	0.87	7.2E-01	0.80	9.8E-01

GTGTGG	0.87	8.0E-01	1.10	1.8E-01
GACTTG	0.87	7.3E-01	1.25	1.5E-02
CTTGTA	0.87	7.5E-01	1.80	**1.8E-16**
GCTTAG	0.87	7.1E-01	1.28	3.9E-02
AAGCTC	0.87	7.2E-01	0.91	7.8E-01
TGATGT	0.87	7.8E-01	0.90	9.2E-01
AGGTTA	0.87	7.2E-01	1.07	2.9E-01
AAAACT	0.87	8.0E-01	0.77	1.0E+00
TCATTC	0.87	7.9E-01	0.91	8.5E-01
CACAGT	0.87	7.6E-01	0.77	1.0E+00
CTTGCA	0.87	7.8E-01	1.51	**1.1E-05**
ACAAAC	0.87	7.2E-01	0.66	1.0E+00
CTAGGC	0.87	7.0E-01	0.96	6.2E-01
TCACAA	0.87	7.3E-01	1.07	2.5E-01
GAGTTT	0.87	7.9E-01	0.75	1.0E+00
ACCTCC	0.87	7.6E-01	0.64	1.0E+00
TGTCTC	0.87	8.5E-01	0.83	9.8E-01
AAGGGA	0.87	7.9E-01	0.92	8.3E-01
TTAAGA	0.87	7.8E-01	0.90	9.4E-01
CCTTAT	0.87	7.4E-01	1.21	3.4E-02
TTAGTA	0.87	7.5E-01	0.96	6.8E-01
CTGGGG	0.87	8.6E-01	0.76	9.9E-01
TTGACT	0.87	7.8E-01	0.96	7.0E-01
TTCAAG	0.87	7.6E-01	0.68	1.0E+00
GTTTCA	0.87	8.0E-01	0.98	6.2E-01
GGGCAA	0.87	7.4E-01	0.82	9.2E-01
TGGCTA	0.86	7.4E-01	0.84	9.1E-01
TATTGC	0.86	7.3E-01	1.66	**1.6E-07**
GACCAG	0.86	7.5E-01	1.00	5.1E-01
TAAACA	0.86	7.9E-01	1.00	4.9E-01
AAGTTC	0.86	7.5E-01	0.81	9.8E-01
ATAGCA	0.86	7.3E-01	1.02	4.4E-01
ATGAGT	0.86	7.4E-01	0.74	1.0E+00
ATTCCT	0.86	8.1E-01	0.91	8.9E-01
GAAAAG	0.86	8.0E-01	0.75	1.0E+00
AACAGA	0.86	7.7E-01	0.80	9.9E-01
TTCATA	0.86	7.9E-01	1.03	3.6E-01
CCTAGC	0.86	7.1E-01	0.83	8.6E-01
ATGCTC	0.86	7.4E-01	0.94	7.1E-01
GATTTA	0.86	7.6E-01	1.00	5.0E-01
TGTCAA	0.86	7.4E-01	1.22	1.5E-02
TATTGT	0.86	8.0E-01	1.41	**9.0E-09**
GTGCTC	0.86	7.6E-01	1.53	**2.7E-04**
GCTAGG	0.86	7.1E-01	0.69	9.7E-01
AGATGA	0.86	7.8E-01	0.58	1.0E+00
AGCATT	0.86	7.9E-01	1.13	5.0E-02
AGTGTG	0.86	8.1E-01	0.96	6.8E-01
TGTCTA	0.86	7.5E-01	0.97	6.3E-01
CTCTAG	0.86	7.7E-01	0.73	9.9E-01
GAATCA	0.86	7.4E-01	0.79	9.8E-01

GTTATA	0.86	7.4E-01	0.90	8.3E-01
CATCAC	0.86	7.4E-01	0.74	9.9E-01
GCATCT	0.86	7.7E-01	0.96	6.4E-01
ATCCCA	0.86	7.7E-01	0.55	1.0E+00
GGTTTA	0.86	7.6E-01	1.02	4.4E-01
ATCAGC	0.86	7.2E-01	0.86	8.8E-01
CTTTTA	0.86	8.8E-01	0.83	1.0E+00
AATGAT	0.86	8.0E-01	0.75	1.0E+00
TGGGTG	0.86	8.5E-01	1.13	1.2E-01
TTCTGG	0.86	8.6E-01	1.03	3.7E-01
TACATG	0.86	7.6E-01	0.89	9.0E-01
TGCCCA	0.86	8.3E-01	1.09	1.9E-01
AAGCTG	0.86	8.0E-01	1.30	**7.0E-04**
AGCAGT	0.86	7.9E-01	0.99	5.5E-01
CCTCAT	0.85	8.1E-01	0.88	8.8E-01
CTTTCA	0.85	8.6E-01	0.94	8.1E-01
CCATAC	0.85	7.0E-01	0.86	8.1E-01
ATATGG	0.85	7.4E-01	0.86	9.0E-01
GGACCC	0.85	7.6E-01	1.02	4.7E-01
ATAGTC	0.85	7.1E-01	0.83	8.8E-01
GGTATT	0.85	7.7E-01	1.15	9.8E-02
ATACTC	0.85	7.1E-01	0.84	8.8E-01
ATGGCC	0.85	7.5E-01	1.13	2.0E-01
GGTTGG	0.85	7.9E-01	0.98	5.9E-01
TAGTGT	0.85	7.7E-01	1.57	**4.2E-07**
TTTCAG	0.85	9.1E-01	1.06	1.5E-01
AATTAC	0.85	7.6E-01	0.99	5.7E-01
TCTAGT	0.85	7.5E-01	0.99	5.6E-01
GGTGGA	0.85	7.9E-01	0.66	1.0E+00
CTATTT	0.85	8.4E-01	1.35	**1.5E-08**
ACTACA	0.85	7.1E-01	0.99	5.6E-01
TAGTAG	0.85	7.4E-01	0.67	1.0E+00
CTAAAT	0.85	7.8E-01	0.93	8.2E-01
ATAAGG	0.85	7.2E-01	0.96	6.5E-01
GAAAGG	0.85	8.2E-01	0.69	1.0E+00
AATAAT	0.85	8.4E-01	0.64	1.0E+00
CAGAGG	0.85	8.4E-01	0.77	9.9E-01
TTGTAT	0.85	8.3E-01	1.65	**1.8E-28**
TAGTCA	0.85	7.4E-01	0.93	7.2E-01
ATAGTT	0.85	7.8E-01	0.99	5.7E-01
AAGGGG	0.85	8.1E-01	0.67	1.0E+00
TTAGGT	0.85	7.5E-01	0.79	9.8E-01
TTCTCA	0.85	9.0E-01	0.92	8.8E-01
GGACTA	0.85	7.1E-01	0.54	1.0E+00
TTATGG	0.84	7.7E-01	1.01	4.9E-01
CACACC	0.84	7.7E-01	0.71	9.9E-01
CAACCA	0.84	7.3E-01	0.80	9.6E-01
ACTTTG	0.84	8.7E-01	1.05	2.6E-01
AGGATA	0.84	7.3E-01	0.71	1.0E+00
GGATGG	0.84	8.1E-01	0.70	1.0E+00

CTTCTT	0.84	9.1E-01	0.51	1.0E+00
GTGATG	0.84	8.0E-01	0.93	7.7E-01
TACACT	0.84	7.6E-01	1.31	1.4E-02
TTCCCT	0.84	9.1E-01	0.52	1.0E+00
GTAGAG	0.84	7.7E-01	0.54	1.0E+00
TATCCT	0.84	7.8E-01	0.78	9.8E-01
CCACAG	0.84	8.6E-01	0.89	8.7E-01
CTCTTT	0.84	9.4E-01	0.65	1.0E+00
TACTTT	0.84	8.8E-01	0.86	9.9E-01
GACTGA	0.84	7.8E-01	0.99	5.4E-01
AGCACA	0.84	7.9E-01	1.89	**3.0E-17**
ACTAGC	0.84	7.1E-01	0.95	6.3E-01
GAGCTT	0.84	8.0E-01	1.07	2.6E-01
TGTATA	0.84	8.2E-01	1.90	**4.4E-38**
GTCTCC	0.84	8.3E-01	0.69	1.0E+00
TCCACT	0.84	8.0E-01	0.67	1.0E+00
TCAGTT	0.84	8.5E-01	0.80	1.0E+00
AATGGA	0.84	8.1E-01	0.91	8.6E-01
TCCCTT	0.84	9.0E-01	0.65	1.0E+00
GGGATC	0.84	7.4E-01	0.92	7.0E-01
GGGACC	0.84	7.9E-01	1.68	**1.6E-04**
AATAGA	0.83	8.0E-01	0.98	5.9E-01
GGCTAG	0.83	7.5E-01	1.10	3.3E-01
CCACTT	0.83	8.1E-01	0.86	9.4E-01
TAAGAA	0.83	8.5E-01	0.83	1.0E+00
GGCCCC	0.83	8.2E-01	1.16	2.6E-01
AACAGG	0.83	7.8E-01	0.80	9.7E-01
AAGACC	0.83	7.5E-01	0.80	9.6E-01
GAAAGA	0.83	8.3E-01	0.63	1.0E+00
GTATCA	0.83	7.4E-01	0.83	9.2E-01
GGCCTG	0.83	8.6E-01	1.24	3.5E-02
CTAGTT	0.83	7.7E-01	1.14	1.2E-01
TTCCTA	0.83	8.5E-01	1.00	5.2E-01
AACAGC	0.83	7.8E-01	0.82	9.5E-01
ATTAAG	0.83	8.0E-01	1.18	3.4E-02
ATAACT	0.83	8.0E-01	0.94	7.6E-01
ACTGGA	0.83	7.9E-01	1.79	**4.1E-12**
TTACCA	0.83	8.0E-01	1.10	1.6E-01
CCTCCC	0.83	9.4E-01	0.74	1.0E+00
CAGTCT	0.83	8.2E-01	0.83	9.7E-01
ACAGGA	0.83	8.0E-01	0.77	9.9E-01
GTAATG	0.83	8.0E-01	1.16	8.2E-02
CAGGAG	0.83	8.7E-01	0.63	1.0E+00
TATGTG	0.83	8.5E-01	0.99	5.4E-01
GGCTAA	0.83	7.4E-01	0.80	9.3E-01
GTGTAA	0.83	8.0E-01	1.72	**8.2E-12**
TTTTAG	0.83	9.1E-01	0.93	9.0E-01
GGCACA	0.83	8.0E-01	1.11	2.2E-01
AATCAG	0.83	8.0E-01	0.95	7.2E-01
TTTTTT	0.83	1.0E+00	0.51	1.0E+00

CCCCAA	0.83	8.3E-01	0.41	1.0E+00
GTTTTT	0.83	9.6E-01	0.74	1.0E+00
GTGACA	0.83	8.0E-01	0.93	7.6E-01
GGCAAC	0.83	7.4E-01	0.92	7.0E-01
ACACTG	0.83	8.2E-01	1.31	**3.7E-04**
CAGGGT	0.83	8.5E-01	1.40	**5.1E-04**
AATCTC	0.83	7.9E-01	0.81	9.7E-01
GCACTG	0.83	8.2E-01	2.11	**4.2E-17**
TATGTA	0.83	8.4E-01	1.40	**5.9E-09**
CTCCCT	0.83	9.2E-01	0.71	1.0E+00
ACTACT	0.83	7.5E-01	1.63	**8.1E-06**
ACAGGC	0.83	8.0E-01	0.70	1.0E+00
TCTCCT	0.83	9.3E-01	0.56	1.0E+00
AGGGAC	0.83	8.3E-01	1.24	4.6E-02
AGGCAT	0.83	8.2E-01	0.88	8.9E-01
ACTATC	0.83	7.3E-01	0.53	1.0E+00
CCCAGG	0.82	9.0E-01	1.19	3.4E-02
ACATGT	0.82	8.4E-01	0.98	6.1E-01
TTTGAG	0.82	9.0E-01	0.78	1.0E+00
AGACAC	0.82	7.7E-01	0.78	9.8E-01
ATCTAG	0.82	7.5E-01	1.19	1.0E-01
CACTGA	0.82	8.5E-01	1.23	**8.5E-03**
ATCTGG	0.82	8.1E-01	0.89	8.5E-01
GTCAGG	0.82	8.3E-01	0.84	9.1E-01
TATGCT	0.82	8.0E-01	1.21	3.0E-02
TTACCT	0.82	8.4E-01	1.11	1.1E-01
GATATA	0.82	7.6E-01	0.85	9.1E-01
AGTGAT	0.82	8.3E-01	0.77	1.0E+00
ACTCTT	0.82	8.7E-01	0.54	1.0E+00
CTCCAG	0.82	8.9E-01	0.74	1.0E+00
CACTTC	0.82	8.3E-01	0.67	1.0E+00
TCTTTC	0.82	9.6E-01	0.69	1.0E+00
CTTTGG	0.82	9.2E-01	1.03	3.4E-01
AGATTT	0.82	8.8E-01	0.98	6.2E-01
CCAGGT	0.82	8.3E-01	0.88	8.7E-01
ATTATG	0.82	8.2E-01	1.46	**9.3E-07**
CCTTGG	0.82	8.8E-01	0.89	8.8E-01
TCCTTC	0.82	9.2E-01	0.60	1.0E+00
ATGTGT	0.82	9.1E-01	0.95	7.9E-01
ATCTAC	0.82	7.3E-01	0.72	9.8E-01
TAAAGT	0.82	8.5E-01	1.10	6.7E-02
CCTTTG	0.82	9.2E-01	1.07	2.2E-01
TAACTA	0.82	7.8E-01	0.94	7.2E-01
TGGTTC	0.82	8.2E-01	1.26	1.3E-02
CACTCA	0.82	8.2E-01	0.61	1.0E+00
GAAGTT	0.82	8.3E-01	0.82	9.8E-01
TGGGGG	0.82	9.1E-01	0.73	9.9E-01
ACTTGT	0.82	8.5E-01	1.25	**3.6E-03**
TTAAAG	0.82	8.8E-01	1.11	3.2E-02
ATTACA	0.82	8.4E-01	0.62	1.0E+00

AGAGGC	0.82	8.4E-01	1.05	3.6E-01
GCACTT	0.82	8.2E-01	1.98	**7.5E-23**
GTTAGC	0.82	7.6E-01	1.11	2.7E-01
GAAATG	0.82	8.9E-01	0.81	1.0E+00
AAATAG	0.81	8.6E-01	0.78	1.0E+00
CCACAC	0.81	8.2E-01	0.68	1.0E+00
TTATAT	0.81	9.0E-01	1.04	2.2E-01
AGGGTT	0.81	8.3E-01	0.99	5.6E-01
CCAGTA	0.81	7.9E-01	0.98	5.7E-01
ACTGTG	0.81	8.8E-01	1.76	**7.6E-17**
TCCTCA	0.81	9.1E-01	0.77	1.0E+00
ACCTCT	0.81	8.7E-01	1.24	1.1E-02
ATAGAC	0.81	7.4E-01	1.11	2.5E-01
GAGGAT	0.81	8.1E-01	0.41	1.0E+00
TGGACA	0.81	8.3E-01	1.28	**7.5E-03**
GGCAAG	0.81	8.1E-01	0.78	9.5E-01
GGACAC	0.81	7.8E-01	0.82	8.9E-01
CTCTTC	0.81	9.3E-01	0.64	1.0E+00
CAGGAT	0.81	8.2E-01	0.89	8.4E-01
AGCCAC	0.81	8.5E-01	0.90	8.5E-01
TGGTCA	0.81	8.3E-01	1.20	4.0E-02
TATGTC	0.81	8.0E-01	0.95	6.8E-01
TAGGTG	0.81	8.0E-01	0.80	9.6E-01
CATGAG	0.81	8.3E-01	0.61	1.0E+00
TGAGAA	0.81	8.9E-01	0.70	1.0E+00
GACTGG	0.81	8.2E-01	1.15	1.5E-01
TCCCAA	0.81	8.5E-01	0.48	1.0E+00
TATCAG	0.81	8.0E-01	0.78	9.8E-01
ATTTTC	0.81	9.5E-01	0.95	8.4E-01
TTTTTG	0.81	9.8E-01	0.85	1.0E+00
AGGAAA	0.81	9.2E-01	0.81	1.0E+00
ACCCTT	0.81	8.4E-01	0.83	9.4E-01
ACACAT	0.81	8.4E-01	0.60	1.0E+00
AACAAT	0.81	8.0E-01	1.04	3.3E-01
TGTGTC	0.81	9.3E-01	0.99	5.5E-01
CACTGT	0.81	8.8E-01	1.61	**7.5E-12**
GTATTG	0.81	8.0E-01	1.58	**1.6E-06**
CCCTCC	0.81	9.5E-01	0.74	9.9E-01
GGTGTA	0.81	7.7E-01	1.45	**3.8E-03**
GCAGAT	0.81	8.1E-01	0.67	1.0E+00
TTATTG	0.81	8.8E-01	1.09	1.0E-01
CTCCTT	0.81	9.3E-01	0.58	1.0E+00
AAAGTG	0.81	8.7E-01	0.86	9.9E-01
AGTGCT	0.81	8.8E-01	1.05	3.1E-01
GCACAG	0.81	8.5E-01	1.23	3.1E-02
GAGGCT	0.81	8.7E-01	0.85	9.5E-01
GTGGGG	0.81	9.3E-01	0.92	7.6E-01
ACAGCT	0.81	8.5E-01	1.01	4.7E-01
CTCTCC	0.80	9.4E-01	0.55	1.0E+00
TAGTAT	0.80	8.1E-01	0.88	8.9E-01

CAGTTT	0.80	9.2E-01	0.86	9.9E-01
TTCAGT	0.80	9.1E-01	0.79	1.0E+00
TGCCCC	0.80	8.9E-01	0.68	9.9E-01
TAAGCT	0.80	8.2E-01	1.46	**9.4E-05**
GTGGAG	0.80	8.6E-01	0.80	9.7E-01
CCATGC	0.80	8.3E-01	0.58	1.0E+00
CCTAGA	0.80	7.9E-01	0.85	8.9E-01
CTGTTC	0.80	9.0E-01	0.88	9.2E-01
GTTAGG	0.80	7.9E-01	0.67	9.9E-01
CACAAT	0.80	7.7E-01	1.28	1.4E-02
TGTGAG	0.80	8.7E-01	0.89	9.0E-01
GTTTTG	0.80	9.6E-01	0.95	8.3E-01
CCAGCC	0.80	9.2E-01	0.98	5.8E-01
ATAGAA	0.80	8.4E-01	0.70	1.0E+00
ACCAAA	0.80	8.3E-01	2.80	**1.9E-63**
AGTCCC	0.80	8.3E-01	0.63	1.0E+00
AAACCT	0.80	8.4E-01	0.72	1.0E+00
GAGAAT	0.80	8.6E-01	0.73	1.0E+00
GTGATT	0.80	8.7E-01	1.16	3.7E-02
GATTGT	0.80	8.3E-01	1.14	9.4E-02
AAAGGG	0.80	8.8E-01	1.02	4.2E-01
TTTCTC	0.80	9.8E-01	0.80	1.0E+00
TAGACT	0.80	8.1E-01	1.26	2.9E-02
CATAAA	0.80	8.4E-01	0.81	1.0E+00
ATGGTC	0.80	7.8E-01	0.90	7.6E-01
TGTATT	0.80	9.2E-01	1.56	**1.8E-25**
TCAGTA	0.80	8.5E-01	0.93	8.0E-01
AGTTTT	0.80	9.5E-01	0.93	9.3E-01
CCCACT	0.80	8.8E-01	0.55	1.0E+00
GTCCCA	0.80	8.3E-01	0.78	9.7E-01
GAAGTA	0.80	8.1E-01	0.82	9.6E-01
GAACTT	0.80	8.4E-01	1.02	4.4E-01
CCCTCT	0.80	9.3E-01	0.53	1.0E+00
ACCCCA	0.80	8.9E-01	0.38	1.0E+00
AAATGG	0.80	8.9E-01	1.01	4.5E-01
CCCAAG	0.80	8.5E-01	0.69	1.0E+00
GACTTT	0.80	8.8E-01	0.91	8.8E-01
GTCCAT	0.80	8.2E-01	0.99	5.5E-01
CTATGG	0.80	7.8E-01	0.99	5.4E-01
GTCATA	0.80	7.8E-01	0.78	9.6E-01
CTATCA	0.80	7.7E-01	0.83	9.0E-01
GCAAGT	0.80	8.0E-01	0.77	9.8E-01
ATAGGG	0.80	7.9E-01	0.60	1.0E+00
ACCTGT	0.80	8.9E-01	0.84	9.7E-01
GGCCTA	0.79	7.8E-01	0.87	7.9E-01
GAATGA	0.79	8.7E-01	0.89	9.1E-01
CAGACC	0.79	8.4E-01	1.14	1.8E-01
TACCTC	0.79	8.0E-01	3.87	**1.1E-65**
ATCCTT	0.79	8.8E-01	0.72	1.0E+00
AACTGA	0.79	8.7E-01	0.94	7.8E-01

GGGTTG	0.79	8.6E-01	0.88	8.3E-01
CCATCT	0.79	9.3E-01	0.63	1.0E+00
AAGTAA	0.79	8.8E-01	0.74	1.0E+00
CCTCAG	0.79	9.3E-01	1.04	3.3E-01
ATCCTA	0.79	8.0E-01	0.70	9.9E-01
CAGTGG	0.79	9.0E-01	0.75	1.0E+00
ATTCCA	0.79	8.6E-01	1.34	**1.6E-04**
TTCTCC	0.79	9.5E-01	0.67	1.0E+00
TGTTAG	0.79	8.6E-01	0.85	9.5E-01
GTAGTA	0.79	7.8E-01	1.13	2.0E-01
TCTATT	0.79	8.8E-01	1.15	2.9E-02
ATAAGA	0.79	8.2E-01	0.74	1.0E+00
AGAGTT	0.79	8.8E-01	0.71	1.0E+00
TGATAT	0.79	8.5E-01	0.89	8.8E-01
CCAGTT	0.79	8.6E-01	0.84	9.7E-01
GCAATA	0.79	7.6E-01	4.29	**9.2E-89**
CAAAAC	0.79	8.4E-01	0.67	1.0E+00
CATCTT	0.79	9.2E-01	0.80	1.0E+00
GTTCCC	0.79	8.4E-01	0.68	9.9E-01
AACACA	0.79	8.5E-01	0.70	1.0E+00
AAAATT	0.79	9.5E-01	0.48	1.0E+00
TGACTG	0.79	8.8E-01	1.13	8.5E-02
ATCTTG	0.79	8.8E-01	0.96	6.8E-01
AAGGTG	0.79	8.6E-01	1.19	4.1E-02
TGGTCT	0.79	9.0E-01	0.86	9.5E-01
TCAATG	0.79	8.2E-01	0.98	5.8E-01
ATATAG	0.79	8.2E-01	0.92	8.1E-01
TCTTCT	0.79	9.8E-01	0.64	1.0E+00
CAAGTA	0.79	8.0E-01	0.85	9.4E-01
TAAGTG	0.79	8.8E-01	1.05	3.0E-01
CCCCAC	0.79	9.4E-01	0.52	1.0E+00
GTGTAG	0.79	8.2E-01	1.10	2.5E-01
TTTGGG	0.78	9.5E-01	0.89	9.4E-01
AGGGGA	0.78	9.2E-01	0.40	1.0E+00
CCTGTA	0.78	8.7E-01	0.90	8.9E-01
CCACTG	0.78	9.1E-01	0.92	8.1E-01
ACTTTT	0.78	9.6E-01	0.92	9.6E-01
CCCCTG	0.78	9.2E-01	0.63	1.0E+00
GATAAT	0.78	8.2E-01	0.89	8.8E-01
ATTTAT	0.78	9.5E-01	1.58	**6.5E-38**
CCCATG	0.78	8.8E-01	0.58	1.0E+00
AGAACA	0.78	8.7E-01	0.79	1.0E+00
ACCAAG	0.78	8.3E-01	0.95	6.8E-01
ATCAGT	0.78	8.5E-01	0.83	9.7E-01
CTGAGA	0.78	9.1E-01	0.66	1.0E+00
GTAACA	0.78	8.5E-01	1.64	**8.3E-07**
ACATGC	0.78	8.4E-01	0.79	9.7E-01
GATGAG	0.78	8.6E-01	0.54	1.0E+00
GGCACC	0.78	8.4E-01	0.71	9.7E-01
ATAAAA	0.78	9.4E-01	1.12	**6.0E-04**

AAGATT	0.78	8.7E-01	0.85	9.8E-01
TGCTCT	0.78	9.6E-01	1.10	1.3E-01
TATTTA	0.78	9.5E-01	1.70	**4.6E-56**
CACATC	0.78	8.4E-01	0.62	1.0E+00
TGGGTC	0.78	8.8E-01	1.13	2.0E-01
ATTACT	0.78	8.8E-01	0.88	9.1E-01
GAGTAT	0.78	8.3E-01	0.93	7.2E-01
GTCCAC	0.78	8.0E-01	0.85	8.1E-01
GGTGTT	0.78	8.8E-01	1.08	2.4E-01
GGACCA	0.78	8.0E-01	2.66	**7.7E-19**
CATCAG	0.78	8.6E-01	0.62	1.0E+00
CCACCC	0.78	9.3E-01	0.56	1.0E+00
TTACTT	0.78	9.3E-01	0.81	1.0E+00
TGTCCA	0.78	8.9E-01	0.80	9.8E-01
ACTCAT	0.78	8.6E-01	0.56	1.0E+00
AGGCTG	0.78	9.5E-01	0.75	1.0E+00
GCCTAC	0.78	7.7E-01	0.81	8.5E-01
TGGAGA	0.78	9.2E-01	0.85	9.7E-01
CACTCT	0.78	9.1E-01	0.45	1.0E+00
GTGTTC	0.78	8.9E-01	0.99	5.7E-01
AAGATG	0.78	8.7E-01	0.78	1.0E+00
GTATAT	0.78	8.8E-01	1.51	**1.0E-10**
TCTTAT	0.78	9.2E-01	0.77	1.0E+00
TGGAAC	0.78	8.4E-01	1.26	3.0E-02
CCTGGG	0.77	9.8E-01	0.94	7.4E-01
GGAGGA	0.77	9.3E-01	0.60	1.0E+00
ATGGAA	0.77	9.0E-01	0.86	9.7E-01
GATTTT	0.77	9.6E-01	0.82	1.0E+00
GCTACT	0.77	8.1E-01	0.74	9.9E-01
CCTAGT	0.77	8.0E-01	0.95	6.5E-01
TCAGTG	0.77	9.2E-01	1.09	1.6E-01
ATGCTA	0.77	8.4E-01	1.27	2.1E-02
CACACA	0.77	9.4E-01	0.49	1.0E+00
CCTTCC	0.77	9.6E-01	0.81	9.9E-01
GTCCCT	0.77	9.1E-01	0.74	9.9E-01
ACCCTC	0.77	8.9E-01	0.59	1.0E+00
TCTCAC	0.77	9.2E-01	0.73	1.0E+00
GGGACA	0.77	8.9E-01	1.08	2.9E-01
ACCATT	0.77	8.6E-01	0.94	7.6E-01
CTCAGA	0.77	9.1E-01	0.97	6.6E-01
ATTCTC	0.77	9.1E-01	0.75	1.0E+00
GAAAAT	0.77	9.4E-01	0.80	1.0E+00
CAGTTA	0.77	8.7E-01	0.90	8.8E-01
GACCCC	0.77	8.7E-01	0.33	1.0E+00
GAGGCC	0.77	9.1E-01	0.85	8.8E-01
AATCTG	0.77	8.8E-01	0.80	9.9E-01
GGTCTA	0.77	7.7E-01	1.05	4.1E-01
CAGAAA	0.77	9.4E-01	0.88	9.8E-01
TAATGT	0.77	9.2E-01	1.27	**5.9E-05**
TTGATC	0.77	8.4E-01	1.28	2.4E-02

ATATCA	0.77	8.4E-01	0.80	9.8E-01
AAGGGC	0.76	8.7E-01	1.79	**2.9E-07**
ATTTTT	0.76	1.0E+00	0.97	8.8E-01
CAGTCC	0.76	8.6E-01	0.53	1.0E+00
CCAAAT	0.76	8.9E-01	1.34	**3.4E-05**
GTATGT	0.76	9.4E-01	1.19	1.9E-02
GCCTTT	0.76	9.6E-01	1.75	**1.5E-16**
ACCTTT	0.76	9.4E-01	0.88	9.5E-01
AGCCCT	0.76	9.3E-01	0.89	8.5E-01
AAAATA	0.76	9.8E-01	0.76	1.0E+00
AAACAA	0.76	9.3E-01	0.63	1.0E+00
GTGAAG	0.76	8.8E-01	1.28	**5.3E-03**
AGACTT	0.76	9.0E-01	1.15	5.0E-02
GGCTCA	0.76	9.2E-01	0.72	1.0E+00
CCTAAT	0.76	8.5E-01	0.97	6.0E-01
AGTCCA	0.76	8.6E-01	1.05	3.6E-01
AGAGGT	0.76	8.9E-01	0.69	1.0E+00
ATATAT	0.76	9.5E-01	0.94	9.4E-01
GCTCAC	0.76	9.0E-01	0.60	1.0E+00
GACTGC	0.76	8.3E-01	1.44	**6.6E-03**
TAGGTT	0.76	8.7E-01	0.98	5.7E-01
ACTCAG	0.76	8.9E-01	1.07	2.7E-01
GTCTAG	0.76	8.1E-01	0.93	7.0E-01
TATTAG	0.76	8.8E-01	0.89	8.8E-01
GGGGAA	0.76	9.3E-01	0.52	1.0E+00
GACTCT	0.76	8.9E-01	0.61	1.0E+00
TTACAG	0.76	9.3E-01	0.89	9.4E-01
CACATA	0.75	8.6E-01	0.61	1.0E+00
TAAGTA	0.75	9.2E-01	0.85	9.5E-01
CAAAGT	0.75	9.1E-01	0.87	9.6E-01
AGATTA	0.75	8.6E-01	0.89	8.8E-01
GTATGC	0.75	8.1E-01	1.42	**9.2E-03**
GAAACT	0.75	9.1E-01	0.87	9.4E-01
TCTGTA	0.75	9.4E-01	1.63	**2.1E-16**
ATCCTC	0.75	8.9E-01	0.45	1.0E+00
GTCTTA	0.75	8.8E-01	1.16	8.0E-02
GATATG	0.75	8.4E-01	0.81	9.3E-01
GCTGGT	0.75	9.1E-01	1.17	8.3E-02
CTGGGT	0.75	9.6E-01	0.84	9.5E-01
TCCTTG	0.75	9.7E-01	0.89	8.9E-01
GGATAT	0.75	8.5E-01	0.83	9.3E-01
AGGTCA	0.75	8.9E-01	0.92	7.7E-01
ATCTTC	0.75	9.0E-01	0.80	9.8E-01
AAACAT	0.75	9.4E-01	0.73	1.0E+00
GTGTCT	0.75	9.7E-01	1.29	**1.6E-03**
AGCAAG	0.75	8.9E-01	0.85	9.4E-01
AAGTTA	0.75	9.1E-01	0.97	6.5E-01
AGAGGA	0.75	9.3E-01	0.59	1.0E+00
TTGAGA	0.75	9.5E-01	0.69	1.0E+00
GTCATT	0.75	9.2E-01	0.93	8.1E-01

TCCTAA	0.75	9.0E-01	0.82	9.7E-01
CTCCCC	0.75	9.8E-01	0.67	1.0E+00
GTACAC	0.75	8.2E-01	1.33	4.2E-02
GGGGTA	0.75	8.3E-01	0.77	9.2E-01
CAACCT	0.75	8.7E-01	0.47	1.0E+00
ATCTCC	0.75	8.9E-01	0.53	1.0E+00
GTTCTC	0.75	9.3E-01	0.76	9.9E-01
GGCAGT	0.75	9.1E-01	1.12	1.7E-01
AGGAGT	0.75	9.0E-01	0.47	1.0E+00
GATCTC	0.75	8.5E-01	0.56	1.0E+00
ATCACA	0.75	8.9E-01	0.79	9.9E-01
AGCTAG	0.75	8.4E-01	0.90	7.6E-01
TTTATG	0.75	9.6E-01	1.39	**8.5E-10**
CAACCC	0.75	8.4E-01	0.44	1.0E+00
GGTGAC	0.75	8.8E-01	1.01	5.0E-01
GGAAGA	0.75	9.4E-01	0.84	9.8E-01
GTATTC	0.75	8.6E-01	1.30	**5.0E-03**
TCCCTG	0.74	9.7E-01	0.84	9.7E-01
ACTATA	0.74	8.5E-01	0.79	9.7E-01
CCTTTA	0.74	9.2E-01	1.04	3.4E-01
ACACAG	0.74	9.3E-01	0.60	1.0E+00
GGGGCA	0.74	9.4E-01	0.68	9.9E-01
GCCTGT	0.74	9.5E-01	0.96	6.7E-01
AGTCAG	0.74	9.0E-01	0.84	9.4E-01
AGAAGT	0.74	9.0E-01	0.69	1.0E+00
GTCTCA	0.74	9.1E-01	0.77	9.9E-01
GCTCAT	0.74	8.9E-01	0.58	1.0E+00
GGGCCT	0.74	9.5E-01	1.28	3.1E-02
ACATCT	0.74	9.0E-01	1.08	2.2E-01
TTCTTC	0.74	9.9E-01	0.59	1.0E+00
AGCACT	0.74	9.2E-01	1.46	**1.4E-06**
GGCCCA	0.74	9.1E-01	0.75	9.7E-01
CCCACC	0.74	9.7E-01	0.83	9.3E-01
ACATAG	0.74	8.4E-01	0.73	9.9E-01
AGTTCT	0.74	9.5E-01	0.70	1.0E+00
CCAACA	0.74	8.8E-01	0.65	1.0E+00
AGTCCT	0.74	9.0E-01	0.76	9.9E-01
ATGGGC	0.74	8.9E-01	0.89	7.8E-01
TGATGG	0.74	9.3E-01	0.86	9.3E-01
CTGGTC	0.74	9.0E-01	1.13	1.7E-01
TGGGGC	0.74	9.6E-01	0.72	9.9E-01
ATCTTA	0.74	9.0E-01	0.78	9.9E-01
GGTTTT	0.74	9.8E-01	0.87	9.9E-01
TTTGCC	0.74	9.5E-01	1.42	**1.4E-06**
TGTTAT	0.74	9.4E-01	0.89	9.5E-01
TGTGTA	0.74	9.6E-01	1.38	**5.6E-08**
AGTACC	0.74	8.3E-01	0.91	7.3E-01
CCAGGA	0.74	9.5E-01	0.87	9.2E-01
GTTATG	0.74	8.5E-01	0.93	7.4E-01
TCCTAT	0.74	8.9E-01	0.79	9.8E-01

AAGTTG	0.73	9.2E-01	1.07	2.3E-01
GGACCT	0.73	8.8E-01	0.95	6.6E-01
GCAAGC	0.73	8.3E-01	1.17	1.9E-01
AGTAAG	0.73	8.7E-01	0.61	1.0E+00
GTTATT	0.73	9.4E-01	1.02	3.9E-01
ATATTA	0.73	9.4E-01	0.89	9.7E-01
GTAGGG	0.73	8.9E-01	0.58	1.0E+00
CTGTCA	0.73	9.5E-01	1.12	9.8E-02
AAATAT	0.73	9.8E-01	0.82	1.0E+00
GCCTCT	0.73	9.7E-01	1.17	6.0E-02
CAGATT	0.73	9.2E-01	1.04	3.5E-01
AAAGAC	0.73	8.9E-01	1.01	4.7E-01
GTGGAT	0.73	8.8E-01	0.76	9.9E-01
GTATAG	0.73	8.3E-01	1.75	**1.9E-06**
ATCCAG	0.73	8.8E-01	0.90	8.4E-01
GGGTCT	0.73	9.3E-01	1.00	5.1E-01
TTGGAG	0.73	9.4E-01	0.84	9.7E-01
TGATTC	0.73	9.3E-01	0.87	9.2E-01
CCTATT	0.73	8.7E-01	1.30	**7.9E-03**
GGGATG	0.73	9.3E-01	0.75	9.8E-01
GTCTCT	0.73	9.8E-01	0.69	1.0E+00
GGAAAC	0.73	8.8E-01	0.82	9.7E-01
AGACCT	0.73	9.1E-01	0.89	8.3E-01
CTTCCC	0.73	9.8E-01	0.83	9.8E-01
AGTGGT	0.73	9.2E-01	0.79	9.8E-01
CAATAG	0.73	8.2E-01	1.14	2.0E-01
GGGGTT	0.73	9.2E-01	0.65	1.0E+00
ACAAGG	0.73	8.7E-01	0.86	8.8E-01
ATCAGG	0.73	8.7E-01	1.14	1.6E-01
GTTTTC	0.73	9.9E-01	0.87	9.9E-01
AGGGAA	0.72	9.6E-01	0.87	9.5E-01
ATCTGT	0.72	9.6E-01	1.05	2.5E-01
CTTATT	0.72	9.7E-01	1.00	5.3E-01
GCCCTT	0.72	9.5E-01	0.72	9.9E-01
ATCACT	0.72	9.1E-01	0.73	1.0E+00
GCCCCT	0.72	9.6E-01	0.93	7.1E-01
ATATAA	0.72	9.5E-01	0.77	1.0E+00
ACACCT	0.72	9.0E-01	0.87	8.9E-01
GGGGGT	0.72	9.5E-01	0.68	9.9E-01
GGAGAC	0.72	9.1E-01	0.79	9.5E-01
GTGAAT	0.72	9.3E-01	1.40	**1.5E-05**
AGTAAT	0.72	9.1E-01	0.86	9.5E-01
CTAGAC	0.72	8.1E-01	1.12	2.8E-01
AAATTT	0.72	9.9E-01	0.57	1.0E+00
GCCAAA	0.72	8.7E-01	3.10	**2.1E-54**
AGTCAC	0.72	8.9E-01	0.98	6.0E-01
GAGTGT	0.72	9.3E-01	0.93	7.5E-01
GAGGCA	0.72	9.4E-01	0.84	9.5E-01
GTTGAC	0.72	8.6E-01	1.21	1.0E-01
GTTTTA	0.72	9.9E-01	1.04	2.2E-01

TGAGGA	0.72	9.7E-01	0.70	1.0E+00
AGGCCC	0.72	9.5E-01	0.76	9.6E-01
GGGAAC	0.71	9.0E-01	0.84	8.8E-01
GAGTTG	0.71	9.2E-01	0.84	9.2E-01
CCAGTC	0.71	9.1E-01	0.72	9.8E-01
CCCAAA	0.71	9.4E-01	0.65	1.0E+00
CTCATA	0.71	8.9E-01	0.55	1.0E+00
TATTAT	0.71	9.7E-01	0.88	9.8E-01
TGAGAG	0.71	9.6E-01	0.53	1.0E+00
TATCCC	0.71	8.6E-01	0.76	9.5E-01
CATTGA	0.71	9.1E-01	0.83	9.7E-01
CTCAAA	0.71	9.5E-01	0.53	1.0E+00
ATCCCT	0.71	9.3E-01	0.81	9.6E-01
AACAAC	0.71	8.5E-01	0.77	9.7E-01
CTGTAA	0.71	9.5E-01	1.53	**5.8E-13**
GTCATC	0.71	8.8E-01	0.87	8.4E-01
ATTTAG	0.71	9.5E-01	0.95	7.5E-01
CTTAGA	0.71	9.1E-01	0.91	8.3E-01
ACTTAG	0.71	9.0E-01	0.50	1.0E+00
GCCCTC	0.71	9.6E-01	0.83	9.0E-01
GTTGTT	0.71	9.8E-01	0.55	1.0E+00
CTATTA	0.71	9.0E-01	0.91	8.1E-01
GTTTAT	0.71	9.7E-01	1.11	5.5E-02
AAAGTT	0.71	9.7E-01	0.99	5.8E-01
CCTCTC	0.71	9.9E-01	0.56	1.0E+00
ATATGC	0.71	8.8E-01	1.39	**6.1E-04**
CTAGAG	0.71	9.0E-01	0.74	9.9E-01
TACAGA	0.71	9.2E-01	1.31	**4.1E-04**
ATATGT	0.71	9.5E-01	0.86	9.8E-01
GTTGAT	0.71	9.2E-01	0.95	6.9E-01
ACAATC	0.71	8.2E-01	2.21	**1.0E-11**
ACTTCC	0.71	9.3E-01	0.61	1.0E+00
ACTGTC	0.71	9.3E-01	1.06	3.2E-01
ACTTTC	0.71	9.5E-01	0.93	8.0E-01
TCTACA	0.71	8.9E-01	0.68	1.0E+00
CAGTCA	0.70	9.3E-01	0.72	1.0E+00
AGGGAT	0.70	9.3E-01	0.98	5.7E-01
TACTGG	0.70	8.8E-01	1.12	2.0E-01
ATGGGA	0.70	9.4E-01	0.81	9.8E-01
TCTCCC	0.70	9.9E-01	0.58	1.0E+00
CTGGAG	0.70	9.8E-01	0.82	9.8E-01
AGATCT	0.70	9.2E-01	0.83	9.5E-01
TTTTTC	0.70	1.0E+00	0.71	1.0E+00
AGATAA	0.70	9.3E-01	0.78	1.0E+00
GAACCT	0.70	9.0E-01	0.84	9.1E-01
GTATGA	0.70	9.0E-01	1.31	1.5E-02
GGGTAT	0.70	8.7E-01	0.87	8.2E-01
CTAGTG	0.70	8.7E-01	1.30	2.8E-02
ACACAC	0.70	9.6E-01	0.35	1.0E+00
ACCAGG	0.70	9.2E-01	1.19	9.6E-02

TTATAG	0.70	9.5E-01	1.01	4.5E-01
GAGACA	0.70	9.3E-01	0.74	1.0E+00
ATTCTT	0.70	9.9E-01	0.84	1.0E+00
GCTAGT	0.70	8.5E-01	1.28	5.2E-02
GAGTCA	0.70	9.0E-01	0.82	9.3E-01
GATAAG	0.70	8.6E-01	0.80	9.3E-01
TAATAT	0.70	9.7E-01	0.92	9.2E-01
ACATAT	0.70	9.4E-01	0.90	8.9E-01
TCAGGA	0.70	9.6E-01	1.35	**9.9E-05**
TGTCCC	0.69	9.8E-01	0.84	9.4E-01
GTGTAT	0.69	9.4E-01	1.39	**1.6E-05**
TCAATC	0.69	8.5E-01	0.74	9.7E-01
AAACTG	0.69	9.6E-01	1.02	4.3E-01
ATACAT	0.69	9.4E-01	0.89	9.3E-01
AAGTGT	0.69	9.6E-01	1.26	**1.8E-03**
ATACCT	0.69	9.1E-01	1.16	9.6E-02
CTCTGA	0.69	9.9E-01	0.92	8.5E-01
CTGTTA	0.69	9.4E-01	1.23	**6.3E-03**
AAAAGA	0.69	9.9E-01	0.61	1.0E+00
TGAGGG	0.69	9.8E-01	0.68	1.0E+00
ATGAGA	0.69	9.5E-01	0.58	1.0E+00
GGATCC	0.69	8.7E-01	1.11	2.9E-01
CCCCAG	0.69	9.9E-01	0.78	9.8E-01
TTCTAC	0.69	9.3E-01	0.95	6.9E-01
TAGAAG	0.69	9.3E-01	0.88	9.1E-01
AGAGTA	0.69	9.1E-01	0.88	8.7E-01
TCTTAC	0.69	9.4E-01	0.77	9.9E-01
GTGACT	0.69	9.5E-01	1.29	**4.3E-03**
TCCAGC	0.69	9.6E-01	0.67	1.0E+00
GCCTCA	0.69	9.5E-01	1.07	2.6E-01
TTGGGG	0.68	9.8E-01	0.75	1.0E+00
GGGAAA	0.68	9.8E-01	0.76	1.0E+00
GTCCCC	0.68	9.7E-01	0.73	9.7E-01
TCTTCC	0.68	1.0E+00	1.00	5.1E-01
TTACAC	0.68	8.8E-01	1.20	8.4E-02
GGTACC	0.68	8.6E-01	1.31	8.9E-02
CTTGGA	0.68	9.7E-01	0.91	8.5E-01
CCCCTT	0.68	9.9E-01	0.48	1.0E+00
TGGGAA	0.68	9.9E-01	0.80	1.0E+00
AGTATA	0.68	9.3E-01	0.73	1.0E+00
ATAGGA	0.68	8.9E-01	0.68	1.0E+00
GATGGA	0.68	9.4E-01	0.81	9.7E-01
GTGGTC	0.68	9.3E-01	1.02	4.6E-01
GTAGAT	0.68	8.9E-01	1.43	**1.6E-03**
GTCAAG	0.68	8.8E-01	1.07	3.4E-01
TACTTC	0.68	9.3E-01	0.83	9.5E-01
ACTTTA	0.68	9.7E-01	1.01	4.6E-01
TACTTA	0.68	9.4E-01	0.91	8.2E-01
GGGAGT	0.68	9.6E-01	0.68	9.9E-01
GCAGTC	0.68	8.9E-01	1.03	4.5E-01

AGAAGG	0.68	9.8E-01	0.77	1.0E+00
GGAAAG	0.68	9.8E-01	0.59	1.0E+00
TGGTAT	0.68	9.4E-01	0.91	8.3E-01
AGGGGG	0.67	9.7E-01	0.50	1.0E+00
TGGGGT	0.67	9.9E-01	0.63	1.0E+00
ATACTT	0.67	9.7E-01	0.73	1.0E+00
GGGGAT	0.67	9.6E-01	0.55	1.0E+00
CCTATG	0.67	9.0E-01	0.81	9.1E-01
GAACAG	0.67	9.4E-01	0.79	9.8E-01
GGCCCT	0.67	9.8E-01	0.64	1.0E+00
TATGCA	0.67	9.4E-01	2.26	**2.9E-29**
GTGAGC	0.67	9.8E-01	0.83	9.4E-01
TCCTTA	0.67	9.7E-01	0.87	9.3E-01
ACAGAG	0.67	9.8E-01	0.57	1.0E+00
GCTAGA	0.67	8.9E-01	1.19	1.3E-01
CAAAAG	0.67	9.6E-01	0.75	1.0E+00
GTAAAA	0.67	9.7E-01	0.97	7.0E-01
GGAGAG	0.67	9.9E-01	0.75	1.0E+00
CTACTT	0.67	9.5E-01	0.79	9.9E-01
TATCAC	0.67	8.7E-01	1.02	4.8E-01
GACAGA	0.67	9.7E-01	0.71	1.0E+00
GCACCT	0.67	9.4E-01	1.10	2.5E-01
AGTCAT	0.67	9.6E-01	0.66	1.0E+00
GATCAC	0.67	9.0E-01	0.72	9.8E-01
TACTGT	0.67	9.7E-01	1.75	**2.6E-19**
AATGGG	0.67	9.5E-01	0.80	9.8E-01
GGTACA	0.66	8.7E-01	1.33	2.7E-02
GATGTA	0.66	8.9E-01	1.36	**1.2E-03**
TAGGGC	0.66	8.9E-01	0.95	6.3E-01
TCCACA	0.66	9.6E-01	0.91	8.2E-01
GTAGGA	0.66	9.4E-01	0.90	7.7E-01
TTGAGC	0.66	9.4E-01	0.83	9.6E-01
TAAAGA	0.66	9.7E-01	1.04	2.4E-01
CCCTTG	0.66	9.8E-01	0.74	9.9E-01
AAAGAG	0.66	9.7E-01	0.69	1.0E+00
CTTAGG	0.66	9.3E-01	0.97	6.2E-01
CTATAG	0.66	8.9E-01	0.75	9.7E-01
TCCCCA	0.66	9.9E-01	0.67	1.0E+00
AACATA	0.66	9.5E-01	0.75	1.0E+00
AATATG	0.66	9.6E-01	0.84	9.9E-01
CTATTG	0.66	8.9E-01	1.21	6.6E-02
AAAGTA	0.66	9.7E-01	0.63	1.0E+00
GTCAGT	0.66	9.5E-01	0.92	7.8E-01
TATATC	0.66	9.2E-01	1.01	4.7E-01
GTCTTT	0.66	1.0E+00	0.96	7.0E-01
ACCAGT	0.66	9.4E-01	1.11	1.9E-01
GATTCT	0.66	9.7E-01	0.83	9.8E-01
TGTTCC	0.66	9.8E-01	0.68	1.0E+00
ATAGAG	0.66	9.2E-01	0.80	9.7E-01
ACCTTA	0.66	9.2E-01	0.97	6.0E-01

GTTACC	0.66	8.6E-01	1.27	5.6E-02
GAACAA	0.66	9.3E-01	1.29	**5.9E-03**
GCACTC	0.66	9.1E-01	0.69	9.9E-01
GATCAG	0.66	9.1E-01	0.72	9.8E-01
AAAATC	0.66	9.8E-01	0.49	1.0E+00
TTTTCC	0.66	1.0E+00	0.67	1.0E+00
GAAGAT	0.66	9.5E-01	0.77	9.9E-01
CTTGTG	0.66	9.8E-01	1.09	1.6E-01
CTCAGT	0.65	9.8E-01	0.79	9.9E-01
TCACAC	0.65	9.6E-01	0.64	1.0E+00
TTGAGG	0.65	9.7E-01	0.69	1.0E+00
AACTGG	0.65	9.3E-01	1.46	**3.9E-05**
AGGATT	0.65	9.6E-01	0.58	1.0E+00
GACATG	0.65	9.4E-01	0.75	9.9E-01
TCTGAG	0.65	9.9E-01	0.66	1.0E+00
GAATCT	0.65	9.5E-01	0.79	9.8E-01
GATGTT	0.65	9.7E-01	0.96	7.0E-01
GTAAGC	0.65	9.4E-01	1.12	2.3E-01
CCTCTT	0.65	1.0E+00	0.82	9.9E-01
AAAACC	0.65	9.6E-01	0.62	1.0E+00
ACTTGC	0.65	9.4E-01	1.11	2.1E-01
GTTCAA	0.65	9.3E-01	0.63	1.0E+00
ATAGAT	0.65	9.4E-01	0.85	9.5E-01
TTTCCC	0.65	1.0E+00	0.45	1.0E+00
TCATGT	0.65	9.8E-01	0.83	9.9E-01
GACAAG	0.65	9.3E-01	0.94	7.0E-01
CCTCTA	0.65	9.5E-01	0.53	1.0E+00
GAGACT	0.65	9.6E-01	0.86	9.2E-01
GAGCAA	0.65	9.4E-01	0.90	8.2E-01
TCCCTC	0.65	1.0E+00	0.55	1.0E+00
TTCCCA	0.65	1.0E+00	0.72	1.0E+00
TAGGGG	0.65	9.5E-01	0.51	1.0E+00
GAACTG	0.65	9.6E-01	0.91	8.3E-01
GTATTT	0.65	1.0E+00	1.51	**2.2E-21**
TCTAAG	0.65	9.4E-01	0.89	8.4E-01
AGGACA	0.65	9.6E-01	0.85	9.3E-01
GTACAG	0.64	9.3E-01	2.26	**6.6E-19**
ATAGTG	0.64	9.3E-01	1.07	3.0E-01
ACCCTG	0.64	9.9E-01	0.68	1.0E+00
AGTGAG	0.64	9.9E-01	0.45	1.0E+00
TCCCAC	0.64	9.8E-01	0.54	1.0E+00
CCACTC	0.64	9.7E-01	0.69	9.9E-01
GTCAGC	0.64	9.5E-01	0.95	6.7E-01
TCCTCT	0.64	1.0E+00	0.53	1.0E+00
CTTATA	0.64	9.4E-01	0.87	9.0E-01
GAAGAG	0.64	9.8E-01	0.75	1.0E+00
CCTTGT	0.64	9.9E-01	1.11	1.3E-01
GTACTC	0.64	9.0E-01	1.14	2.5E-01
GGGACT	0.64	9.7E-01	0.81	9.5E-01
CAATGT	0.64	9.5E-01	1.21	2.8E-02

GGAGAT	0.64	9.5E-01	0.74	9.9E-01
CCCTCA	0.64	9.9E-01	0.71	1.0E+00
ATCCCC	0.63	9.6E-01	0.46	1.0E+00
ACTAGA	0.63	9.3E-01	1.00	5.3E-01
GAGGTT	0.63	9.6E-01	0.73	1.0E+00
CCTGTT	0.63	1.0E+00	1.03	3.8E-01
CCTAGG	0.63	9.4E-01	0.50	1.0E+00
AGATGC	0.63	9.5E-01	1.12	1.4E-01
GATGCT	0.63	9.7E-01	1.33	**2.6E-03**
AGTGGC	0.63	9.8E-01	0.91	7.8E-01
TTGGGA	0.63	9.9E-01	0.73	1.0E+00
GTAGGT	0.63	9.6E-01	1.22	9.4E-02
TATATA	0.63	9.9E-01	0.95	8.7E-01
CTATGC	0.63	9.0E-01	2.15	**4.4E-10**
GATCTT	0.63	9.6E-01	0.89	8.6E-01
ACTTGG	0.63	9.7E-01	0.72	1.0E+00
AAAAAC	0.63	9.9E-01	0.43	1.0E+00
TCTACT	0.63	9.6E-01	0.73	1.0E+00
TTATCT	0.63	9.9E-01	0.90	9.2E-01
ACTTAT	0.63	9.5E-01	0.91	8.2E-01
TAAAAA	0.62	1.0E+00	0.52	1.0E+00
ACCCAT	0.62	9.4E-01	0.63	1.0E+00
ATATTC	0.62	9.8E-01	0.91	8.7E-01
ACCCAG	0.62	9.9E-01	0.47	1.0E+00
TACACA	0.62	9.5E-01	0.64	1.0E+00
ATGTAG	0.62	9.6E-01	1.45	**1.5E-05**
ATCACC	0.62	9.2E-01	0.83	9.0E-01
AGCTAC	0.62	9.1E-01	0.82	9.3E-01
ATTATC	0.62	9.5E-01	0.99	5.6E-01
ATTGTA	0.62	9.9E-01	1.45	**1.2E-10**
GTATGG	0.62	9.2E-01	0.82	9.0E-01
AACTAT	0.62	9.6E-01	0.83	9.6E-01
CAAATC	0.62	9.4E-01	0.82	9.7E-01
CAATCT	0.62	9.3E-01	1.05	3.7E-01
GGCTAT	0.61	9.1E-01	0.86	8.2E-01
GCAACC	0.61	8.9E-01	0.90	7.4E-01
TGAGAC	0.61	9.8E-01	0.65	1.0E+00
AAGAGA	0.61	9.9E-01	0.58	1.0E+00
TCAAAT	0.61	9.8E-01	0.65	1.0E+00
GAAGAC	0.61	9.3E-01	1.06	3.5E-01
TAAGTT	0.61	9.9E-01	1.18	2.4E-02
GAGTAA	0.61	9.3E-01	0.85	8.8E-01
AGTTGT	0.61	9.8E-01	1.09	1.6E-01
TGTAAT	0.61	1.0E+00	1.51	**2.6E-15**
CATACA	0.61	9.5E-01	0.76	9.9E-01
TACTCT	0.61	9.8E-01	0.67	1.0E+00
CTACTG	0.61	9.5E-01	1.57	**6.5E-06**
CCCAAC	0.61	9.7E-01	0.48	1.0E+00
AGGCAC	0.61	9.7E-01	0.87	8.4E-01
AAAGTC	0.61	9.7E-01	0.85	9.5E-01

TGGAGT	0.61	9.9E-01	0.68	1.0E+00
TAGGAG	0.61	9.6E-01	0.56	1.0E+00
GTAAGA	0.61	9.9E-01	0.86	8.8E-01
TAGTGA	0.61	9.7E-01	0.98	6.0E-01
GTATAA	0.61	9.6E-01	1.65	**6.6E-10**
GAGAGT	0.61	9.7E-01	0.47	1.0E+00
ATGGGT	0.60	9.7E-01	0.86	8.7E-01
CACCCT	0.60	9.9E-01	0.55	1.0E+00
TTGCAG	0.60	1.0E+00	1.01	4.7E-01
ACAGGG	0.60	9.8E-01	0.85	9.1E-01
GCCCCA	0.60	9.9E-01	0.69	9.9E-01
CCTGAG	0.60	1.0E+00	0.70	1.0E+00
AGGAGA	0.60	1.0E+00	0.69	1.0E+00
GTACTG	0.60	9.6E-01	2.14	**6.7E-15**
ATCTAT	0.60	9.5E-01	1.00	5.2E-01
GGATAG	0.60	9.2E-01	0.60	1.0E+00
GATATT	0.60	9.8E-01	0.95	7.4E-01
GAAATA	0.60	9.9E-01	0.94	8.4E-01
GAGGTA	0.60	9.2E-01	0.53	1.0E+00
ACTCCA	0.60	9.8E-01	0.60	1.0E+00
AAATAC	0.60	9.9E-01	0.67	1.0E+00
AGTGCC	0.60	9.7E-01	3.19	**3.1E-42**
CCCCAT	0.60	9.9E-01	0.43	1.0E+00
CCCAGT	0.59	9.9E-01	0.73	9.9E-01
GGACAG	0.59	9.9E-01	1.00	5.0E-01
GCCCTA	0.59	9.3E-01	0.99	5.4E-01
ACCTAG	0.59	9.4E-01	0.99	5.6E-01
GAGGAA	0.59	9.9E-01	0.68	1.0E+00
CAGAGT	0.59	9.9E-01	0.58	1.0E+00
GTCCAG	0.59	9.8E-01	1.30	1.9E-02
GAGTCT	0.59	9.9E-01	0.58	1.0E+00
ACAGTG	0.59	9.9E-01	1.08	2.0E-01
GAAACC	0.59	9.5E-01	0.79	9.8E-01
GTCATG	0.59	9.6E-01	0.97	6.2E-01
GTAATA	0.59	9.6E-01	1.55	**7.1E-08**
ATACTG	0.59	9.8E-01	1.15	7.4E-02
GTTACT	0.59	9.6E-01	1.07	2.9E-01
GATGGG	0.59	9.9E-01	0.73	9.9E-01
AAAAGT	0.59	1.0E+00	0.60	1.0E+00
AACATC	0.58	9.6E-01	0.99	5.5E-01
CTAGTA	0.58	9.1E-01	0.77	9.5E-01
ATATCT	0.58	9.8E-01	0.78	9.9E-01
GACAGT	0.58	9.7E-01	1.06	3.1E-01
TATAGC	0.58	9.1E-01	0.95	6.6E-01
CTTACC	0.58	9.7E-01	0.99	5.6E-01
TACTTG	0.58	9.8E-01	1.32	**4.1E-04**
GAGTGA	0.58	9.9E-01	0.63	1.0E+00
CAAAAA	0.58	1.0E+00	0.50	1.0E+00
TGTAGG	0.58	9.7E-01	1.03	4.4E-01
AACCTA	0.58	9.3E-01	0.74	9.8E-01

GAGCTA	0.58	9.5E-01	0.63	1.0E+00
CTTAAT	0.58	9.9E-01	1.05	2.8E-01
CAAGAT	0.58	9.6E-01	0.76	9.9E-01
ATGAGG	0.58	9.8E-01	0.61	1.0E+00
GGTCTC	0.58	9.8E-01	0.68	9.9E-01
GCCCAC	0.58	9.8E-01	0.90	7.6E-01
TACCTT	0.58	9.9E-01	0.93	8.0E-01
CTATGT	0.57	9.7E-01	0.97	6.2E-01
CCCACA	0.57	1.0E+00	0.68	1.0E+00
GGAAAA	0.57	1.0E+00	0.64	1.0E+00
GTCAAT	0.57	9.2E-01	1.46	**3.3E-03**
CCCTAC	0.57	9.5E-01	0.44	1.0E+00
CTTCCA	0.57	1.0E+00	0.94	7.7E-01
AATATC	0.57	9.7E-01	0.75	1.0E+00
ACAATT	0.57	9.7E-01	1.04	3.4E-01
CTGAGG	0.57	1.0E+00	0.64	1.0E+00
GCACCC	0.57	9.7E-01	0.61	9.9E-01
CCCCCA	0.57	1.0E+00	0.24	1.0E+00
ACAGAT	0.57	9.8E-01	0.87	9.4E-01
GATGCC	0.57	9.6E-01	1.08	3.1E-01
CTCCCA	0.56	1.0E+00	0.49	1.0E+00
AAGGCC	0.56	9.8E-01	1.49	**5.7E-04**
TCATAT	0.56	9.8E-01	0.85	9.6E-01
TTGCCC	0.56	9.9E-01	0.69	1.0E+00
GAGTCC	0.56	9.8E-01	1.03	4.6E-01
ACCCTA	0.56	9.5E-01	0.46	1.0E+00
GAGATT	0.56	9.9E-01	0.63	1.0E+00
GATTCC	0.56	9.7E-01	0.55	1.0E+00
GTACCT	0.56	9.7E-01	1.62	**6.2E-05**
GTACAT	0.56	9.7E-01	1.93	**6.0E-15**
GAAAGT	0.56	9.9E-01	0.82	9.9E-01
TATACT	0.56	9.8E-01	1.00	5.2E-01
TTAGGG	0.56	9.8E-01	1.15	1.4E-01
AGACAT	0.56	9.8E-01	0.87	9.2E-01
AGTAGG	0.56	9.8E-01	0.97	6.1E-01
TAAGGG	0.55	9.8E-01	1.15	1.7E-01
AGGTTG	0.55	9.9E-01	0.58	1.0E+00
TCCCCT	0.55	1.0E+00	0.34	1.0E+00
AGTACA	0.55	9.7E-01	0.87	8.7E-01
TCCCCC	0.55	1.0E+00	0.34	1.0E+00
GCCTTA	0.55	9.6E-01	4.91	**5.7E-116**
GTATTA	0.55	9.8E-01	1.49	**6.6E-07**
TGAGCA	0.55	1.0E+00	0.82	9.8E-01
AGTATT	0.55	1.0E+00	1.44	**5.9E-10**
TCTACC	0.55	9.6E-01	1.13	2.1E-01
TACATA	0.55	9.9E-01	1.27	**1.3E-03**
TAGTCT	0.55	9.7E-01	1.01	5.0E-01
TGAGGC	0.55	1.0E+00	0.64	1.0E+00
ACTCCC	0.55	9.8E-01	0.48	1.0E+00
CCCCTC	0.55	1.0E+00	0.57	1.0E+00

GGAGTT	0.55	9.9E-01	0.60	1.0E+00
TGGGAC	0.55	9.9E-01	0.93	7.3E-01
ACTCTC	0.55	9.9E-01	0.34	1.0E+00
GGATGT	0.54	9.9E-01	0.92	7.8E-01
TGAGGT	0.54	1.0E+00	0.76	9.9E-01
ATCTCT	0.54	1.0E+00	0.56	1.0E+00
CTCATG	0.54	1.0E+00	0.38	1.0E+00
TAGGGA	0.54	9.9E-01	0.88	8.4E-01
AAAAAT	0.54	1.0E+00	0.38	1.0E+00
TATGAG	0.54	9.8E-01	0.63	1.0E+00
GAGTGC	0.54	9.9E-01	0.93	7.2E-01
TCCTAG	0.54	9.9E-01	0.70	1.0E+00
AGTATG	0.54	9.8E-01	0.82	9.5E-01
GGATTC	0.54	9.7E-01	0.74	9.9E-01
AGTCTC	0.53	9.9E-01	0.58	1.0E+00
GATGTG	0.53	9.9E-01	1.04	3.7E-01
CTCCAC	0.53	9.9E-01	0.59	1.0E+00
AAGGAC	0.53	9.7E-01	1.05	3.7E-01
TACTAC	0.53	9.3E-01	1.21	1.0E-01
GATTAT	0.53	9.9E-01	0.71	1.0E+00
AAGAGT	0.53	9.9E-01	0.75	1.0E+00
CACCCA	0.53	1.0E+00	0.44	1.0E+00
CCCTGT	0.53	1.0E+00	0.91	8.4E-01
GAAAAC	0.53	9.9E-01	0.70	1.0E+00
GACCTA	0.53	9.3E-01	1.73	**2.5E-04**
TATCTG	0.52	9.9E-01	0.92	8.3E-01
ACACTC	0.52	9.7E-01	0.85	8.7E-01
GAGAGG	0.52	1.0E+00	0.63	1.0E+00
CTGATG	0.52	1.0E+00	0.81	9.8E-01
CTGAGT	0.52	1.0E+00	0.55	1.0E+00
CAGCAC	0.52	1.0E+00	0.93	7.5E-01
TCTCAG	0.52	1.0E+00	1.17	2.6E-02
TAGAGT	0.52	9.9E-01	0.78	9.8E-01
TTCCAG	0.52	1.0E+00	1.01	4.8E-01
GGATAC	0.52	9.0E-01	0.82	8.6E-01
GGATTA	0.52	9.9E-01	0.53	1.0E+00
ATAGGC	0.52	9.5E-01	0.62	1.0E+00
CCCTTC	0.52	1.0E+00	0.73	1.0E+00
TCCCAG	0.52	1.0E+00	0.73	1.0E+00
CCTTAC	0.52	9.8E-01	1.20	1.0E-01
TATTCC	0.51	9.9E-01	0.86	9.2E-01
AGTAGT	0.51	9.8E-01	1.07	3.0E-01
ACTTAC	0.51	9.8E-01	0.59	1.0E+00
AGTCTT	0.51	1.0E+00	0.96	6.9E-01
CAGTAC	0.51	9.7E-01	1.21	1.0E-01
AAACAC	0.51	9.9E-01	0.95	7.5E-01
GGCCAA	0.51	9.8E-01	1.03	4.3E-01
TTGGGT	0.51	1.0E+00	1.06	3.1E-01
TGAGCC	0.50	1.0E+00	0.96	6.8E-01
AAAAAG	0.50	1.0E+00	0.47	1.0E+00

CTACCT	0.50	9.9E-01	2.29	**3.5E-20**
CAGATA	0.50	9.9E-01	0.69	1.0E+00
AGGACC	0.50	9.8E-01	1.32	2.8E-02
AAGACT	0.50	9.9E-01	0.88	9.3E-01
TAATAC	0.50	9.8E-01	1.03	4.3E-01
TAGATG	0.50	9.9E-01	1.10	1.8E-01
CACTAG	0.50	9.6E-01	1.31	3.8E-02
AGGCTA	0.50	9.6E-01	0.78	9.4E-01
TAATAG	0.50	9.9E-01	0.84	9.4E-01
CCTAAG	0.50	9.7E-01	0.64	1.0E+00
ACCCCT	0.49	1.0E+00	0.38	1.0E+00
GGAGTG	0.49	1.0E+00	0.73	1.0E+00
ATAGCC	0.49	9.6E-01	0.98	5.8E-01
CATATA	0.49	9.8E-01	0.93	7.7E-01
CCTTAG	0.49	9.9E-01	1.01	4.9E-01
AGATAT	0.49	9.9E-01	0.81	9.8E-01
GGTTCC	0.49	9.8E-01	1.04	4.2E-01
ACTCTG	0.49	1.0E+00	0.66	1.0E+00
GAAAAA	0.49	1.0E+00	0.37	1.0E+00
TAAGGT	0.49	9.9E-01	1.22	5.5E-02
GCATAG	0.49	9.6E-01	1.12	2.3E-01
GACACA	0.49	9.9E-01	0.68	1.0E+00
GTAATC	0.49	9.8E-01	0.66	1.0E+00
AGCCAT	0.49	1.0E+00	1.87	**1.3E-14**
CCTATC	0.49	9.7E-01	0.60	9.9E-01
TCTCTA	0.49	1.0E+00	0.51	1.0E+00
TAAGGC	0.48	9.8E-01	0.81	9.2E-01
CATACC	0.48	9.7E-01	0.60	1.0E+00
GACCAA	0.48	9.7E-01	2.69	**1.5E-24**
GGTCAA	0.48	9.7E-01	1.04	4.1E-01
AAACAG	0.48	1.0E+00	0.72	1.0E+00
GTGAGG	0.48	1.0E+00	0.74	9.9E-01
TATGGG	0.48	9.9E-01	0.61	1.0E+00
AAAACA	0.48	1.0E+00	0.61	1.0E+00
GGAACT	0.48	9.9E-01	0.79	9.7E-01
CTTGGG	0.48	1.0E+00	1.03	4.1E-01
AAGTAG	0.47	9.9E-01	0.98	6.1E-01
TGAGAT	0.47	1.0E+00	0.67	1.0E+00
ACACCC	0.47	9.9E-01	0.63	1.0E+00
AGATAC	0.47	9.8E-01	0.63	1.0E+00
AAGAGG	0.47	1.0E+00	0.74	1.0E+00
CATAGA	0.47	9.7E-01	0.80	9.7E-01
CAGTAT	0.47	1.0E+00	1.51	**4.3E-08**
ACTGGG	0.47	1.0E+00	0.77	9.8E-01
TACCAC	0.47	9.7E-01	0.98	5.9E-01
AGATGG	0.47	1.0E+00	0.81	9.9E-01
AGAGTG	0.46	1.0E+00	0.64	1.0E+00
CTAAGA	0.46	9.9E-01	0.63	1.0E+00
AGATTG	0.46	1.0E+00	0.87	9.2E-01
CCCCCC	0.46	1.0E+00	0.06	1.0E+00

GTGTAC	0.46	9.8E-01	1.94	**2.5E-08**
GTAATT	0.46	1.0E+00	1.26	**3.7E-04**
AGGTGT	0.45	1.0E+00	0.83	9.7E-01
ACTCCT	0.45	1.0E+00	0.48	1.0E+00
TACCTA	0.45	9.8E-01	0.89	8.1E-01
GAGTGG	0.45	1.0E+00	0.76	9.8E-01
AATACC	0.45	9.8E-01	0.93	7.1E-01
CACTCC	0.45	1.0E+00	0.79	9.6E-01
GGTTAT	0.45	9.9E-01	0.99	5.4E-01
GTATCT	0.45	1.0E+00	1.10	1.8E-01
AAGAAG	0.45	1.0E+00	0.58	1.0E+00
TTCCCC	0.45	1.0E+00	0.48	1.0E+00
GGGTTC	0.44	1.0E+00	0.72	9.8E-01
ACAGTC	0.44	9.9E-01	0.95	6.8E-01
CTTACT	0.44	1.0E+00	0.53	1.0E+00
CTCTAC	0.44	9.9E-01	0.47	1.0E+00
TAGCCC	0.43	9.8E-01	0.87	7.8E-01
TAAAAG	0.43	1.0E+00	0.85	1.0E+00
GATAGT	0.43	9.7E-01	0.83	8.8E-01
CTACAG	0.43	9.9E-01	0.80	9.7E-01
GGTCAT	0.43	9.9E-01	1.14	1.8E-01
CCTACT	0.43	9.9E-01	0.77	9.5E-01
TCCCTA	0.43	1.0E+00	0.53	1.0E+00
TACAAT	0.42	9.9E-01	1.04	3.5E-01
CTATTC	0.42	9.9E-01	0.76	9.7E-01
TATCTT	0.42	1.0E+00	0.97	6.7E-01
CATATC	0.42	9.8E-01	0.75	9.7E-01
TTCCAC	0.42	1.0E+00	0.71	1.0E+00
CCCCCT	0.41	1.0E+00	0.36	1.0E+00
GGGGGA	0.41	1.0E+00	0.45	1.0E+00
GAGATC	0.41	9.9E-01	0.71	9.8E-01
TGAGTG	0.41	1.0E+00	0.62	1.0E+00
CCCTTA	0.41	1.0E+00	0.59	1.0E+00
GTAAGT	0.41	1.0E+00	1.09	2.4E-01
TTACCC	0.41	9.9E-01	0.62	1.0E+00
ATCATC	0.40	9.9E-01	0.65	1.0E+00
CCTATA	0.40	9.8E-01	0.95	6.5E-01
CACCCC	0.40	1.0E+00	0.55	1.0E+00
CTACCC	0.40	9.9E-01	0.48	1.0E+00
TACTCA	0.40	1.0E+00	0.79	9.7E-01
TGAGTA	0.39	1.0E+00	0.68	1.0E+00
GATACC	0.39	9.6E-01	0.66	9.7E-01
ACTATT	0.39	1.0E+00	0.97	6.5E-01
GCTATC	0.39	9.7E-01	1.04	4.5E-01
TAAGAG	0.39	1.0E+00	0.65	1.0E+00
AAAAAA	0.39	1.0E+00	0.26	1.0E+00
AGCTAT	0.39	9.9E-01	1.07	2.9E-01
TACTCC	0.38	9.9E-01	0.67	9.9E-01
GGGTGC	0.38	1.0E+00	1.33	3.5E-02
CTCCTA	0.38	1.0E+00	0.67	1.0E+00

AGTTAC	0.38	1.0E+00	0.91	7.9E-01
AGTGTA	0.38	1.0E+00	1.44	**3.7E-05**
TACTAG	0.38	9.9E-01	0.91	7.5E-01
GGTATA	0.37	9.9E-01	0.73	9.7E-01
CTAGGG	0.37	1.0E+00	0.52	1.0E+00
GACTCC	0.37	1.0E+00	0.50	1.0E+00
AAGATA	0.37	1.0E+00	0.71	1.0E+00
ATACCC	0.37	9.7E-01	0.60	1.0E+00
ACATAC	0.36	1.0E+00	0.58	1.0E+00
CACTTG	0.36	1.0E+00	1.06	2.8E-01
TCACCC	0.36	1.0E+00	0.70	9.9E-01
GGAGTC	0.36	1.0E+00	0.70	9.9E-01
GTGAGA	0.36	1.0E+00	0.65	1.0E+00
GTATCC	0.36	9.9E-01	1.06	4.0E-01
ATACCA	0.36	9.9E-01	1.03	4.3E-01
ACCTAT	0.36	9.9E-01	1.17	1.4E-01
ATACAC	0.35	9.9E-01	0.74	9.8E-01
CACTAT	0.35	9.9E-01	1.07	3.3E-01
CAATGA	0.35	9.9E-01	1.08	2.8E-01
ACTGAG	0.35	1.0E+00	0.79	9.9E-01
GAGCAT	0.34	1.0E+00	1.11	2.0E-01
AGTATC	0.34	9.9E-01	0.65	1.0E+00
TCCACC	0.34	1.0E+00	0.53	1.0E+00
ATATAC	0.33	1.0E+00	0.87	9.2E-01
TACCCC	0.33	1.0E+00	0.44	1.0E+00
TATCTA	0.33	1.0E+00	0.97	6.2E-01
AACTAC	0.33	9.9E-01	1.28	2.7E-02
GTATAC	0.32	9.9E-01	1.15	1.7E-01
TATACC	0.32	9.9E-01	1.13	2.1E-01
GTCCTC	0.31	1.0E+00	0.80	9.4E-01
AGACTC	0.31	1.0E+00	0.62	1.0E+00
ATAATA	0.31	1.0E+00	0.76	1.0E+00
AAGTAT	0.31	1.0E+00	0.77	1.0E+00
GATTAC	0.31	1.0E+00	0.32	1.0E+00
GGTATC	0.30	9.9E-01	1.08	3.7E-01
GTGAGT	0.30	1.0E+00	0.65	1.0E+00
CTCTAT	0.29	1.0E+00	0.78	9.6E-01
AGAGTC	0.29	1.0E+00	0.44	1.0E+00
CCCTAG	0.29	1.0E+00	0.55	1.0E+00
GGACAA	0.29	1.0E+00	1.08	2.9E-01
CAAGAC	0.28	1.0E+00	0.66	1.0E+00
GACTAT	0.28	9.9E-01	0.84	8.8E-01
GTAAGG	0.27	1.0E+00	1.02	4.8E-01
ACCCAA	0.27	1.0E+00	0.65	1.0E+00
AATACA	0.26	1.0E+00	0.67	1.0E+00
CCCTAT	0.25	1.0E+00	0.67	9.9E-01
ATTGAG	0.25	1.0E+00	0.58	1.0E+00
CCCCTA	0.25	1.0E+00	0.42	1.0E+00
TACTAT	0.24	1.0E+00	0.78	9.8E-01
AATAGG	0.23	1.0E+00	0.70	1.0E+00

GATACT	0.23	1.0E+00	1.06	3.5E-01
TCTATG	0.23	1.0E+00	1.42	**7.9E-04**
CTATGA	0.23	1.0E+00	1.28	2.3E-02
ACTATG	0.22	1.0E+00	1.01	5.0E-01
CTATCT	0.22	1.0E+00	0.73	9.9E-01
GTACCC	0.22	1.0E+00	0.59	9.8E-01
TCTATC	0.20	1.0E+00	0.73	9.8E-01
TACCCT	0.20	1.0E+00	0.52	1.0E+00
ACAACC	0.19	1.0E+00	0.57	1.0E+00
TACCCA	0.18	1.0E+00	0.58	1.0E+00
ACCCCC	0.13	1.0E+00	0.24	1.0E+00
GTCTAT	0.13	1.0E+00	1.07	3.4E-01
GAGATA	0.08	1.0E+00	0.69	1.0E+00
GAGTAC	0.00	1.0E+00	1.05	4.3E-01
CTACTC	0.00	1.0E+00	0.47	1.0E+00
ACTACC	0.00	1.0E+00	1.82	**2.1E-05**

[1] S:B values are provided for hexamers in the upstream and downstream introns of skipped exons (-150 to -30, +10 to +150) and in the extension region of tandem UTRs. P values for the S:B values as assessed by binomial test are also provided.