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9. Supplemental Figure 2 (RT-PCR analysis of 10 exons in multiple tissues of human, chimpanzee and rhesus macaque). Ce: cerebellum. K: kidney. L: liver. M: muscle. Hs: human. Pt: chimpanzee. Rm: rhesus macaque.

Supplemental Methods

Identification of HJAY array probes perfectly matching exons or exon-exon junctions of orthologous human, chimpanzee and rhesus mRNA transcripts

For every HJAY probe, we obtained the genomic coordinate of its target sequence on the hg18 assembly of the human genome according to Affymetrix's probe annotations. Using the UCSC pairwise genome alignments of the human genome (hg18) to the genomes of chimpanzee (panTro2) and rhesus macaque (rheMac2) (1-2), we identified all HJAY probes that perfectly matched orthologous transcripts from chimpanzees or rhesus macaques. Next, for each HJAY probeset (typically consisting of 8 probes), we removed probes that contained mismatches for their orthologous transcripts. We defined a probeset as having sufficient coverage for chimpanzee or rhesus transcripts, if it had >=3 probes that perfectly matched its orthologous transcripts. Finally, we sought to identify alternative splicing events with sufficient probeset coverage for human-versus-chimpanzee or human-versus-rhesus comparisons of splicing patterns. The HJAY array was designed for a total of 20815 mRNA/EST-supported alternative splicing events in human genes. For each alternative splicing event, every possible mRNA isoform product was targeted by one or multiple HJAY probesets. For example, each exon skipping event was interrogated by four probesets: one “skip” probeset targeting the exon skipping junction of the exon skipping isoform, and three “include” probesets targeting the upstream exon junction, the cassette exon, and the downstream exon junction of the exon inclusion isoform (3). We defined an alternative splicing event as having sufficient probeset coverage for the human-versus-chimpanzee or human-versus-rhesus comparison, if every possible mRNA isoform had at least one probeset containing >=3 perfect-match probes for orthologous chimpanzee or rhesus transcripts. Based on this criterion, we collected 15544 alternative splicing events for the human-versus-chimpanzee comparison (10630 exon skipping events, 3835 alternative splice site selection, and 1079 mutually exclusive exon usage), and 10147 events for the human-versus-rhesus comparison (6842 exon skipping events, 2467 alternative splice site selection, and 838 mutually exclusive exon usage).

Identification of differential splicing events between human, chimpanzee and rhesus cerebellum RNAs

We developed a series of statistical methods for detection of differential splicing events from the Affymetrix HJAY array data (3-8). In this work, these methods were applied to HJAY array data of human, chimpanzee and rhesus tissues after minor modifications (see details below). Specifically, we used microarray signals of HJAY probes perfectly matching orthologous transcripts to identify differential splicing events between humans and chimpanzees or humans and rhesus macaques. An overview of our HJAY array data analysis is provided below.

Background correction: Raw HJAY array CEL files were processed by the ProbeEffects program for background correction and normalization (5). We predicted the background intensities of individual HJAY probes, using a sequence-specific linear model trained from ‘anti-genomic’ background probes on the HJAY array (5). These ‘anti-genomic’ background probes were selected by Affymetrix to avoid a broad range of animal, plant and bacterial genomes (see http://www.affymetrix.com/support/technical/datasheets/exon_arraydesign_datasheet.pdf). For every probe, the predicted background intensity was an estimate for the amount of non-specific hybridization to the probe. This background intensity was subtracted from the observed probe intensity before downstream analysis.

Expression Index Calculation: We calculated gene expression indexes of human, chimpanzee and rhesus tissues, using HJAY exon probes that perfectly matched orthologous transcripts from multiple species as described before (9). For the human-versus-chimpanzee analysis, for each gene we started with all exon probes that uniquely and perfectly matched orthologous transcripts from human and chimpanzee genomes. From these probes, we used a correlation-based iterative probe selection algorithm to select a subset of probes with highly correlated intensities across all samples (7). This probe selection algorithm was developed to remove probes that may not reflect overall gene expression levels, such as probes targeting alternative exons or putative exon predictions, as well as low-affinity or cross-hybridizing probes (7). Our previous studies show that this probe selection algorithm produces robust expression indexes (5-6, 10) . The selected probes were regarded as reliable indicators of overall gene expression levels. In genes with >=6 selected probes, the background-corrected intensities of selected probes were fitted to the Li-Wong model (11) as in (5, 7) to construct robust estimates of gene expression indexes. The same procedure was applied to human and rhesus HJAY array data in the human-versus-rhesus analysis.

Identification of differential splicing events between human and chimpanzee or human and rhesus cerebellums: We used a modified version of the MADS+ algorithm (3, 8) to identify differential splicing events between human and chimpanzee or human and rhesus cerebellums. MADS+ was an algorithm we developed for detecting differential splicing events from the Affymetrix HJAY array data. Briefly, for each probe in a particular sample, MADS+ calculate a "splicing index", represented as the background corrected probe intensity divided by the estimated gene expression index. Two separate one-sided t-tests are performed to test if the splicing index of a probe is substantially higher in one sample group over the other group. Next, the p-values of individual probes of a probeset are summarized using Fisher's method to obtain a probeset-level p-value for differential splicing (8). Finally, MADS+ reads pre-compiled annotation files of alternative splicing events queried by the HJAY array. For each alternative splicing event, MADS+ evaluates the p-values of multiple probesets targeting exons and exon-exon junctions, requiring opposite trends for probesets targeting competing isoforms as evidence of differential splicing. For example, for each exon skipping event, MADS+ requires that the "skip" probeset and at least one of the three "include" probesets have p-values below a pre-defined significance cutoff (0.01 in this study), and that significant "include" and "skip" probesets display opposite directions of change in splicing index between the two sample groups. It should be noted that the MADS+ algorithm has been demonstrated to have a high accuracy in detecting differential splicing events in a series of previous studies (3, 8, 12).

In this work, we modified the original MADS+ algorithm for comparative analysis of splicing patterns between humans and nonhuman primates. We used MADS+ in two separate pairwise comparisons (human-versus-chimpanzee and human-versus-rhesus). In each pairwise comparison, several default filters were applied prior to the MADS+ analysis. Specifically, we removed lowly expressed genes whose average gene expression indexes were below a given cutoff (300 in this study) in any of the two species included in a pairwise comparison. We also removed genes with a substantial fold change (2.0 in this study) in gene expression indexes between species. Finally, individual probes with low intensities (50 in this study) in both species or extremely high intensities (higher than 95% quantile of all exon probes of the same gene) were also removed to ensure robust estimates of splicing indexes. Subsequent to these filtering steps, an alternative splicing event was included in the human-versus-chimpanzee or human-versus-rhesus comparison, if every possible mRNA isoform produced by the alternative splicing event had at least one probeset containing >=3 perfect-match probes for orthologous chimpanzee or rhesus transcripts. For these events, MADS+ was applied to exon probes and exon-exon junction probes that perfectly matched orthologous transcripts to identify candidate differential splicing events between species.

Ranking of cassette exons with HJAY predicted splicing differences between human and chimpanzee or human and rhesus cerebellums

For each cassette exon predicted by the HJAY analysis as having splicing differences between human and chimpanzee cerebellums, we calculated a single combined p-value for the overall statistical significance of splicing differences, by summarizing the individual p-values of all available perfect-match probes targeting orthologous exons and exon-exon junctions of the human and chimpanzee transcripts. The combined p-value was calculated using the Fisher's method as described before (8). The resulting p-values were used to rank all exons. The same approach was used to rank cassette exon predicted by the HJAY analysis as having splicing differences between human and rhesus cerebellums.

References

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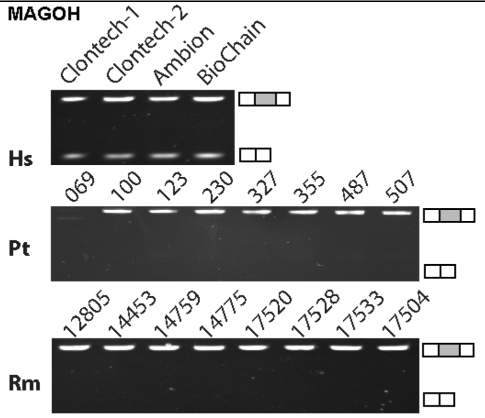
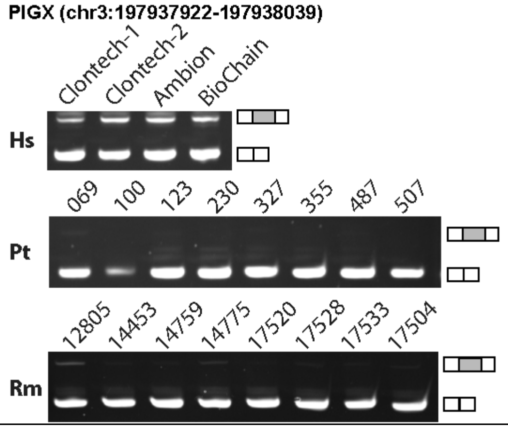
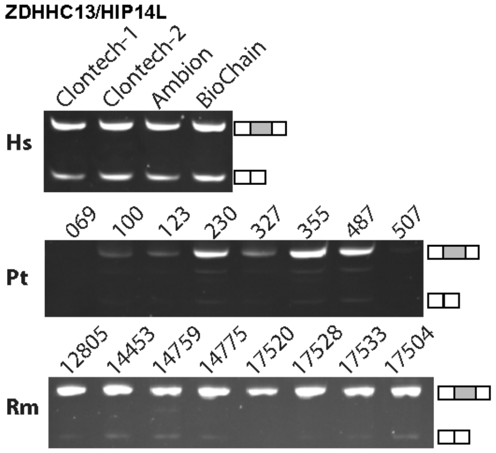
Supplemental Table 1. Description of cerebellum samples.

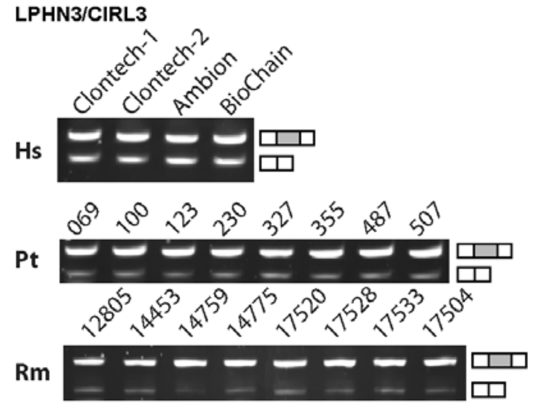
Sample ID	**Species**	**HJAY**	**RT-PCR**	**Description of Donor(s)**
Clontech-1	Human	X	X	Male/Female, 24 donors, age 16-70
Clontech-2	Human	X	X	Male/Female, 10 donors, age 22-68
Ambion	Human		X	Female, single donor, age 59
BioChain	Human		X	Male, single donor, age 26
069	Chimpanzee	X	X	Male, age 30
100	Chimpanzee	X	X	Female, age 27
123	Chimpanzee	X	X	Female, age 28
230	Chimpanzee		X	Female, age 42
327	Chimpanzee	X	X	Male, age 37
355	Chimpanzee	X	X	Female, age 17
487	Chimpanzee	X	X	Male, age 30
507	Chimpanzee		X	Male, age 31
12805	Rhesus Macaque	X	X	Male, age 11
14453	Rhesus Macaque	X	X	Female, age 11
14759	Rhesus Macaque	X	X	Male, age 8
14775	Rhesus Macaque	X	X	Female, age 8
17504	Rhesus Macaque		X	Female, age 24
17520	Rhesus Macaque	X	X	Female, age 18
17528	Rhesus Macaque		X	Female, age 18
17533	Rhesus Macaque	X	X	Female, age 18

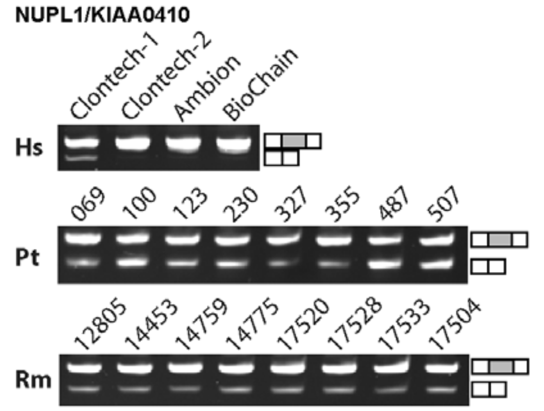
Supplemental Table 2: RT-PCR results of 33 exons with validated splicing differences between human, chimpanzee and rhesus cerebellums.

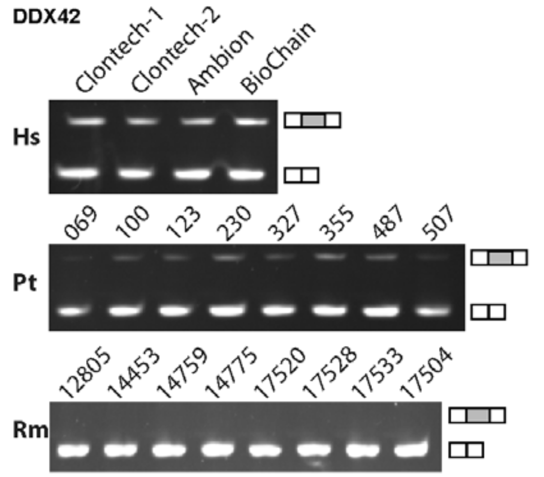
Gene Symbol	MAGOH	
Exon genome coordinate	-chr1:53471801-53471912	
Full Name	Mago-nashi homolog, proliferation-associated (Drosophila)	
Exon inclusion level	Human<<chimpanzee/rhesus	
Notes	Human specific skipping of exon 3 (coding region)	

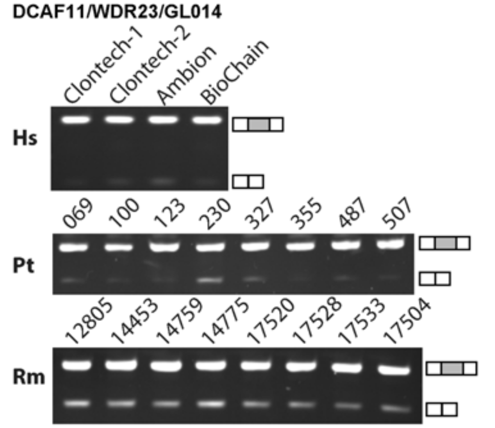
Gene Symbol	PIGX	
Exon genome coordinate	+ chr3:197937922-197938039	
Full Name	Phosphatidylinositol glycan anchor biosynthesis, class X	
Exon inclusion level	Human>>chimpanzee/rhesus	
Notes	Human specific inclusion between exon 3 and 4, introducing premature termination codon and NMD	

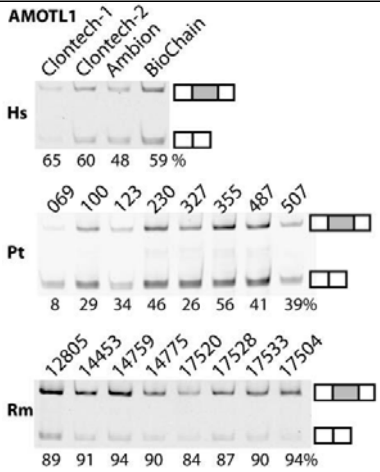
Gene Symbol	ZDHHC13/HIP14L	
Exon genome coordinate	+chr11:19121105-19121246	
Full Name	zinc finger, DHHC-type containing 13, Huntingtin-interacting protein 14 -related protein	
Exon inclusion level	Human<<chimpanzee/rhesus	
Notes	Human specific increase in skipping of exon 2, which causes usage of a downstream translational start site on exon 5	

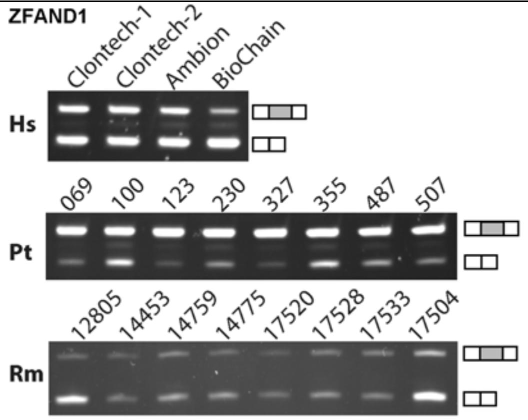
Gene Symbol	LPHN3/CIRL3	
Exon genome coordinate	+chr4:62461031-62461070	
Full Name	LPHN3 latrophilin 3	
Exon inclusion level	Human<<chimpanzee/rhesus	
Notes	Human specific increase in exon 4 skipping (coding region)	

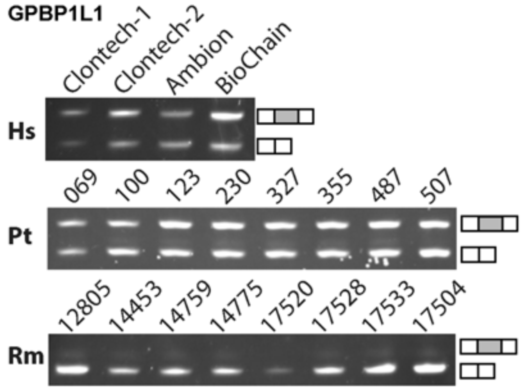
Gene Symbol	NUPL1/KIAA0410	
Exon genome coordinate	+chr13:24781384-24781420	
Full Name	Nucleoporin like 1	
Exon inclusion level	Human>>chimpanzee/rhesus	
Notes	Human specific increase in exon 3 inclusion (coding region)	

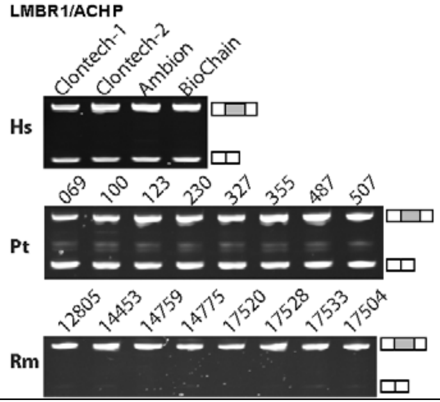
Gene Symbol	DDX42	
Exon genome coordinate	+chr17:59206199-59206270	
Full Name	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	
Exon inclusion level	Human>chimpanzee>rhesus	
Notes	Human specific increase in exon 2 inclusion (5’UTR)	

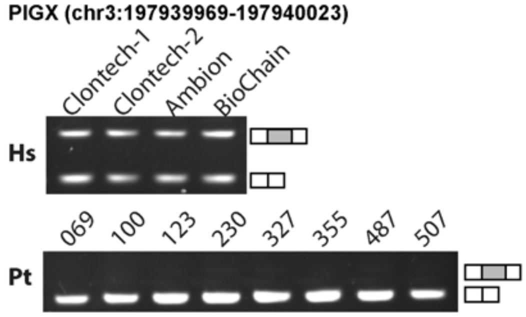
Gene Symbol	DCAF11/WDR23/GL014	
Exon genome coordinate	+chr14:23656716-23656781	
Full Name	DDB1 and CUL4 associated factor 11	
Exon inclusion level	Human/chimpanzee>>rhesus	
Notes	Human and chimpanzee showed increased exon 5 inclusion when compared to rhesus (coding region, alternative N-terminal reading frame)	

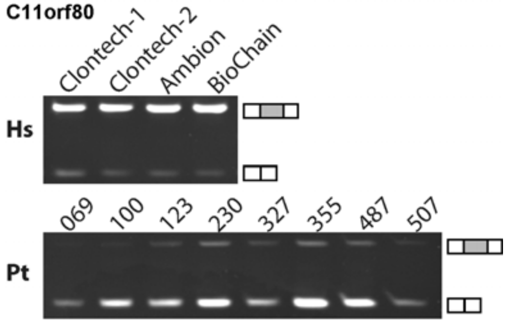
Gene Symbol	AMOTL1	
Exon genome coordinate	+chr11:94167824-94167974	
Full Name	Angiomotin like 1	
Exon inclusion level	Rhesus>>human>chimpanzee	
Notes	Rhesus showed increased exon 2 (coding region) inclusion when compared to human/chimpanzee. Exon 2 skipping results in the absence of three threonine/serine phosphorylation sites.	

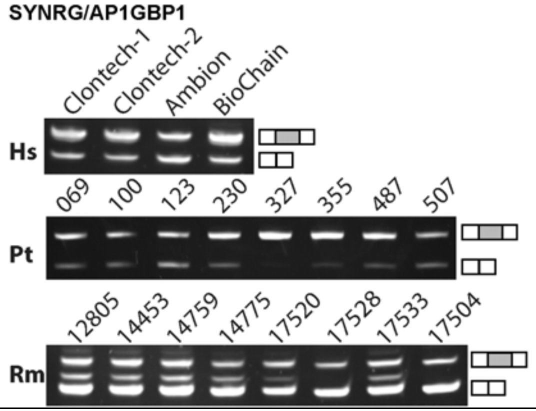
Gene Symbol	ZFAND1	
Exon genome coordinate	-chr8:82792039-82792078	
Full Name	Zinc finger, AN1-type domain 1	
Exon inclusion level	Chimpanzee>>human/rhesus	
Notes	Chimpanzee showed increased inclusion of exon 3 when compared to human/rhesus. Skipping of exon 3 moves the translation start site to exon 5 and produces a truncated protein missing the two zinc finger motifs.	

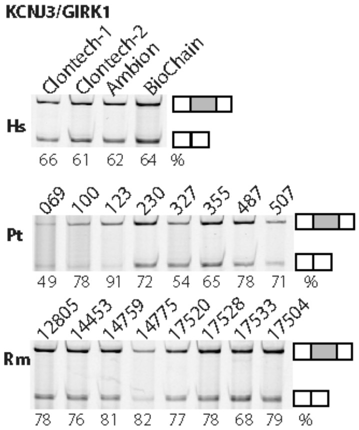
Gene Symbol	GPBP1L1	
Exon genome coordinate	-chr1:45923835-45923879	
Full Name	GC-rich promoter binding protein 1-like 1	
Exon inclusion level	Human/chimpanzee>>rhesus	
Notes	Human/chimpanzee specific inclusion of exon 2 (5'UTR) when compared to rhesus. Rhesus lacks 3' splice site.	

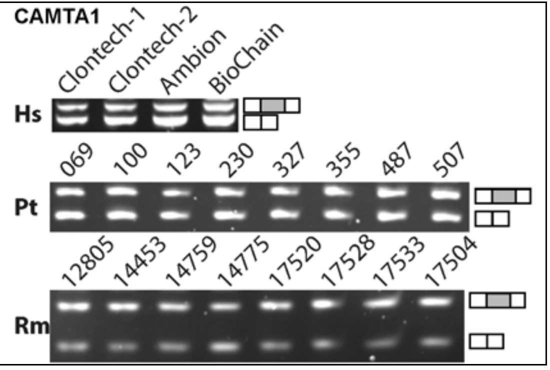
Gene Symbol	LMBR1/ACHP	
Exon genome coordinate	-chr7:156173484-156173646	
Full Name	limb region 1 homolog (mouse)	
Exon inclusion level	Human/chimpanzee<<rhesus	
Notes	Human/chimpanzee specific increase in skipping of exon 16 (coding region) when compared to rhesus	

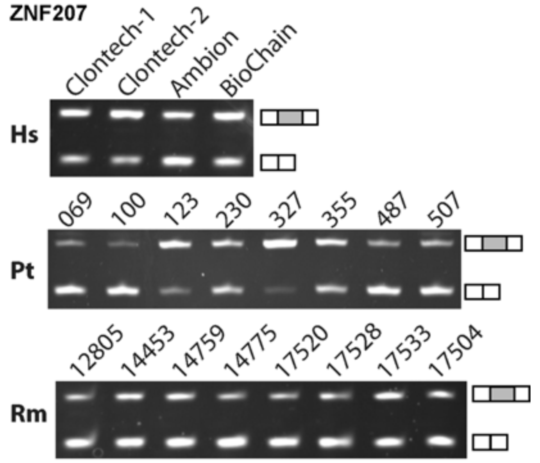
Gene Symbol	PIGX	
Exon genome coordinate	+chr3:197939969-197940023	
Full Name	Phosphatidylinositol glycan anchor biosynthesis, class X	
Exon inclusion level	Human>>chimpanzee	
Notes	Human specific inclusion of exon 5 (coding region) when compared to chimpanzee. Rhesus genomic sequence unavailable for primer design.	

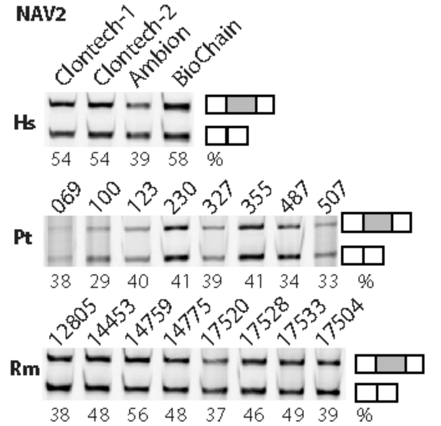
Gene Symbol	C11orf80	
Exon genome coordinate	+chr11:66346610-66346721	
Full Name	Chromosome 11 open reading frame 80	
Exon inclusion level	Human >>chimpanzee	
Notes	Human specific increase in exon 2 (37aa in coding region) inclusion where compared to chimpanzee. Rhesus genomic sequence unavailable for primer design.	

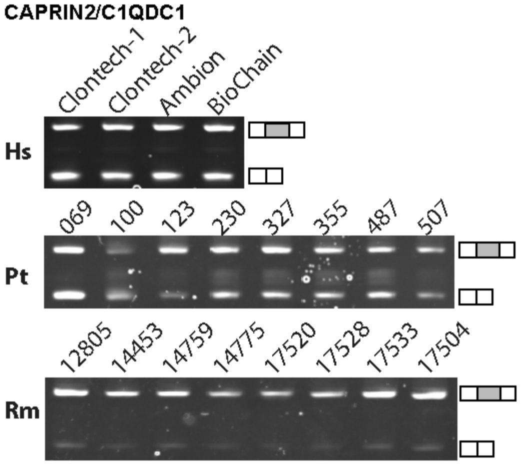
Gene Symbol	SYNRG/AP1GBP1	
Exon genome coordinate	-chr17:32954395-32954430	
Full Name	Synergin, gamma	
Exon inclusion level	Human/chimpanzee>rhesus	
Notes	Human/chimpanzee specific increase in exon 22 (coding region) inclusion when compared to rhesus	

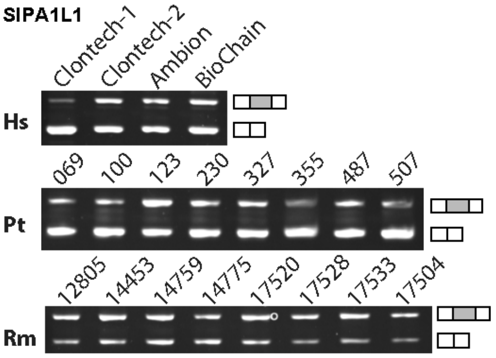
Gene Symbol	KCNJ3/GIRK1	
Exon genome coordinate	+chr2:155274360-155274577	
Full Name	Potassium inwardly-rectifying channel, subfamily J, member 3	
Exon inclusion level	Human<chimpanzee/rhesus	
Notes	Human specific decrease in exon 2 inclusion (coding region) when compared to chimpanzee/rhesus (with several individual outliers in chimpanzees).	

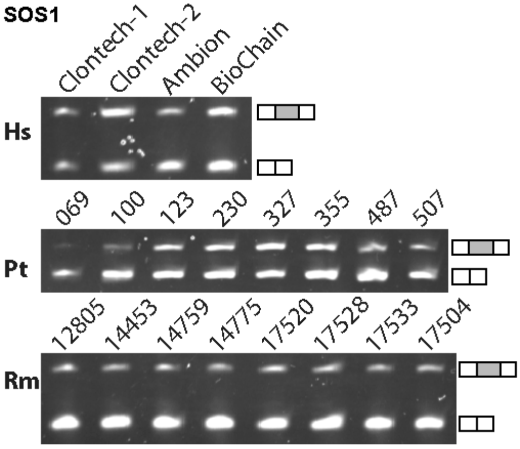
Gene Symbol	CAMTA1	
Exon genome coordinate	+chr1:7738284-7738315	
Full Name	Calmodulin binding transcription activator 1	
Exon inclusion level	Human<chimpanzee <rhesus	
Notes	Skipping of exon 22 (coding region) results in alternative protein C-terminus	

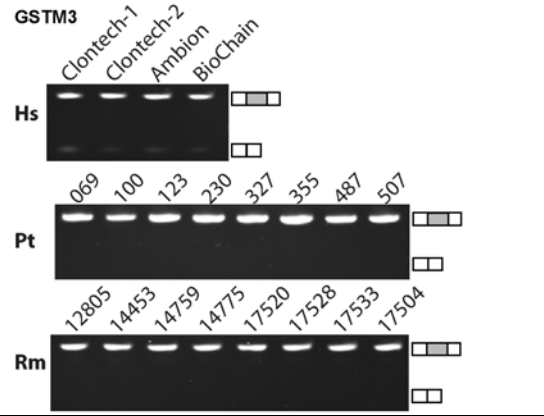
Gene Symbol	ZNF207	
Exon genome coordinate	+chr17:27712599-27712647	
Full Name	Zinc finger protein 207	
Exon inclusion level	Human>rhesus	
Notes	Rhesus specific decrease in exon 6 (coding region) inclusions when compared to human (with individual outliers). Exon 6 inclusion levels in chimpanzees vary among individuals.	

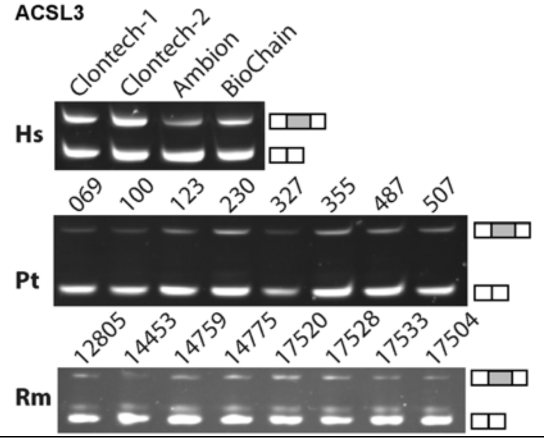
Gene Symbol	NAV2	
Exon genome coordinate	+chr11:19862415-19862484	
Full Name	Neuron navigator 2	
Exon inclusion level	Human>chimpanzee/rhesus	
Notes	Human specific increase in the target exon (23aa insertion between exon 6 and 7) inclusion when compared to chimpanzee and rhesus (with individual outliers).	

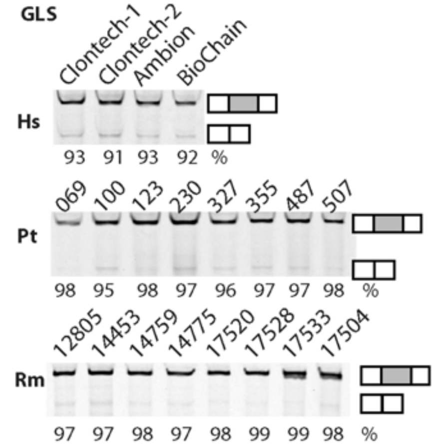
Gene Symbol	CAPRIN2/C1QDC1	
Exon genome coordinate	-chr12:30777829-30777912	
Full Name	Caprin family member 2	
Exon inclusion level	Human/chimpanzee<rhesus	
Notes	Human/chimpanzee show decreased exon 5 inclusion level when compared to rhesus. Transcripts with exon 5 skipping use an alternative translation start on exon 6	

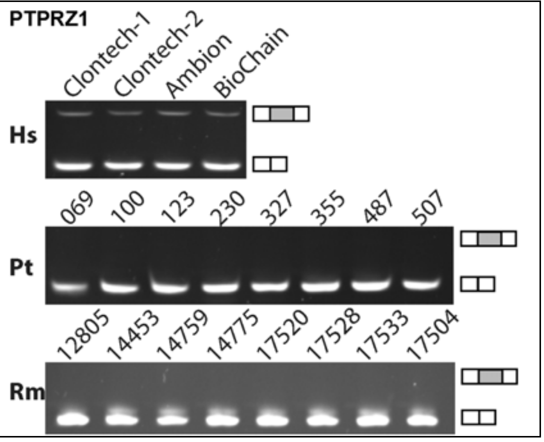
Gene Symbol	SIPA1L1/DKFZp686G1344	
Exon genome coordinate	+chr14:71241190-71241253	
Full Name	Signal-induced proliferation-associated 1 like	
Exon inclusion level	Human/chimpanzee<rhesus	
Notes	Human/chimpanzee show decreased exon 13 (coding region) inclusion level when compared to rhesus.	

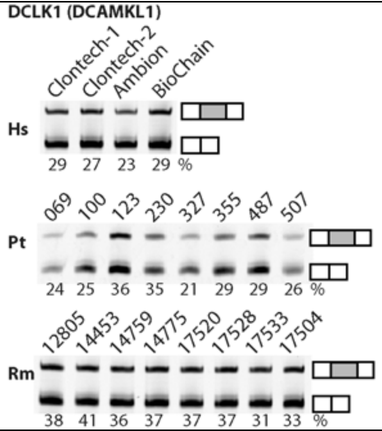
Gene Symbol	SOS1	
Exon genome coordinate	-chr2:39069914-39069959	
Full Name	Son of sevenless homolog 1	
Exon inclusion level	Human/chimpanzee>rhesus	
Notes	Human/chimpanzee show increased exon 21 (coding region) inclusion level when compared to rhesus.	

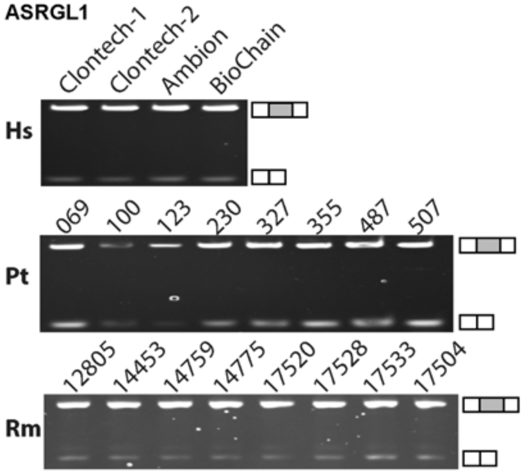
Gene Symbol	GSTM3	
Exon genome coordinate	-chr1:110083977-110084053	
Full Name	Glutathione S-transferase mu 3 (brain)	
Exon inclusion level	Human<chimpanzee/rhesus	
Notes	Human specific skipping of exon 2 results in alternative translational start site and alternative reading frame, thus an alternative N-terminus.	

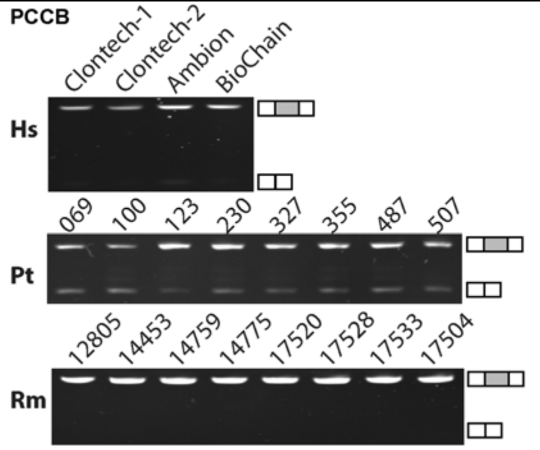
Gene Symbol	ACSL3	
Exon genome coordinate	+chr2:223473635-223473742	
Full Name	Acyl-CoA synthetase long-chain family member 3	
Exon inclusion level	Human>chimpanzee/rhesus	
Notes	Human specific increase in exon 3 (5'UTR) inclusion level	

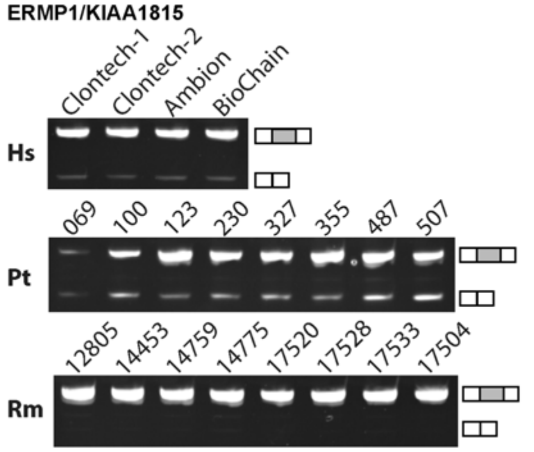
Gene Symbol	GLS	
Exon genome coordinate	+chr2:191527725-191527789	
Full Name	Glutaminase	
Exon inclusion level	Human<chimpanzee/rhesus	
Notes	Human specific decrease in exon 17 inclusion level (coding region, skipping form results in alternative 65aa c-terminus)	

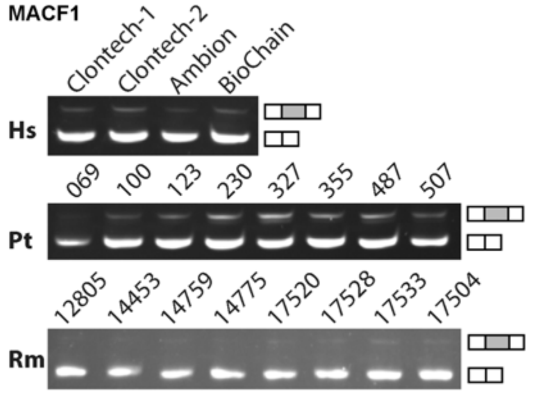
Gene Symbol	PTPRZ1	
Exon genome coordinate	+chr7:121474963-121475080	
Full Name	Protein tyrosine phosphatase, receptor-type, Z polypeptide 1	
Exon inclusion level	Human>chimpanzee/rhesus	
Notes	Human specific 117nt exon inclusion between exon 23 and 24 (coding region, 39aa insertion). Human specific creation of 5’ splice site.	

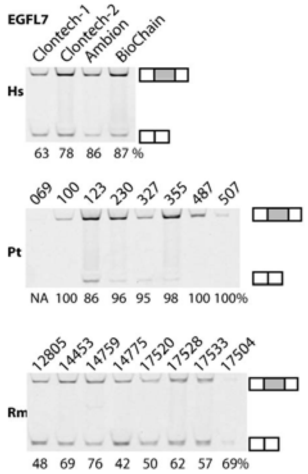
Gene Symbol	DCLK1 (DCAMKL1)	
Exon genome coordinate	-chr13:35260348-35260422	
Full Name	Doublecortin-like kinase 1	
Exon inclusion level	Human<rhesus	
Notes	Human specific decrease in exon 19 inclusion level compared to rhesus (coding, alternative c-terminus).	

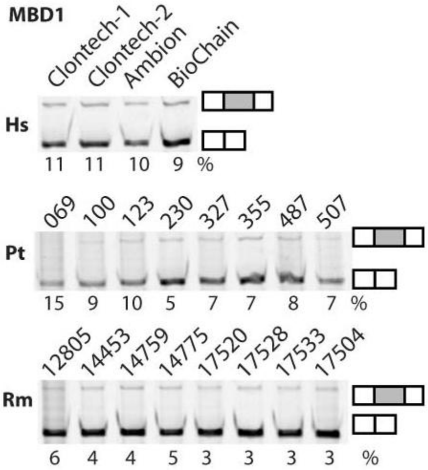
Gene Symbol	ASRGL1	
Exon genome coordinate	+chr11:61880372-61880515	
Full Name	Asparaginase-like 1	
Exon inclusion level	Human/rhesus >chimpanzee	
Notes	Chimpanzee specific decrease of exon 3 inclusion (coding). Exon 3 skipping results in alternative translational start site and N-terminal truncation.	

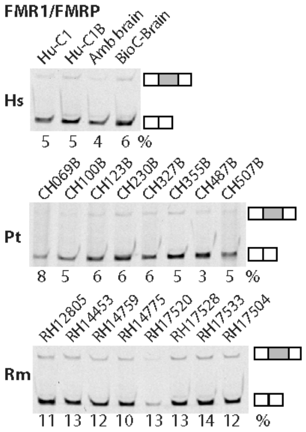
Gene Symbol	PCCB	
Exon genome coordinate	+chr3:137528686-137528787	
Full Name	Propionyl Coenzyme A carboxylase, beta polypeptide	
Exon inclusion level	Human/rhesus>chimpanzee	
Notes	Chimpanzee specific exon 12 (coding region) skipping which results in premature termination and NMD.	

Gene Symbol	ERMP1/KIAA1815	
Exon genome coordinate	-chr9:5815091-5815219	
Full Name	Endoplasmic reticulum metallopeptidase 1	
Exon inclusion level	Rhesus>human>chimpanzee	
Notes	Skipping of exon 3 (coding region) results in alternative translational start site and N-terminal truncation.	

Gene Symbol	MACF1	
Exon genome coordinate	+chr1:39707805-39707874	
Full Name	microtubule-actin crosslinking factor 1	
Exon inclusion level	Human/chimpanzee>rhesus	
Notes	Inclusion of exon (coding region 69nt insertion between exon 98 and 99) results in 23aa insertion into the final protein product.	

Gene Symbol	EGFL7	
Exon genome coordinate	+chr9:138683878-138683994	
Full Name	EGF-like-domain, multiple 7	
Exon inclusion level	Chimpanzee>human>rhesus	
Notes	Skipping of exon 5 (coding region) results in premature termination and NMD. Splicing patterns have individual variations within species.	

Gene Symbol	MBD1	
Exon genome coordinate	-chr18:46055737-46055812	
Full Name	Methyl-CpG binding domain protein 1	
Exon inclusion level	Human/chimpanzee>rhesus	
Notes	Target exon is 75nt between exon 8 and 9, coding for a 25aa peptide insertion in the final protein product	

Gene Symbol	FMR1/FMRP	
Exon genome coordinate	+chrX:146827309-146827372	
Full Name	Fragile X mental retardation 1	
Exon inclusion level	Human/chimpanzee<rhesus	
Notes	Exon 12 inclusion results in the insertion of a 21aa peptide in the final protein product	

Supplemental Table 3: The rankings of RT-PCR confirmed splicing differences between human and chimpanzee or human and rhesus cerebellums among all events predicted by HJAY. Red indicates consistent results between RT-PCR and HJAY predictions. Blue indicates false positive predictions by HJAY. Green indicates false negatives by HJAY. 'NA' indicates an insufficient number of perfect-match probes targeting orthologous transcripts for between-species comparison of splicing.

Gene symbol	Exon location (hg18)	Phylogenetic patterns of exon inclusion levels	Rank in human vs. chimpanzee	Rank in human vs. rhesus
ZFAND1	chr8:82792039-82792078	chimp>>human/rhesus	13	NS
GPBP1L1	chr1:45923834-45923879	human/chimp>>rhesus	NS	44
AMOTL1	chr11:94167824-94167974	rhesus>>human>chimp	NS	76
LPHN3 /CIRL3	chr4:62461031-62461070	human<<chimp/rhesus	206	150
MAGOH	chr1:53471801-53471912	human<<chimp/rhesus	NS	177
ACHP	chr7:156173484-156173646	chimp<human<<rhesus	36	50
PIGX	chr3:197937922-197938039	human>>chimp/rhesus	5	NA
NUPL1	chr13:24781384-24781420	human>>chimp/rhesus	94	NA
ZDHHC13 /HIP14L	chr11:19121105-19121246	human<<chimp/rhesus	172	NA
DDX42	chr17:59206199-59206270	human>>chimp>rhesus	8	NA
PIGX	chr3:197939969-197940023	human>>chimp	1	NA
FACE2	chr11:66346610-66346721	human>>chimp	3	NA
GL014	chr14:23656716-23656781	human/chimp>>rhesus	NS	185
ASRGL1	chr11:61880372-61880515	human/rhesus>chimp	15	NS
AP1GBP1	chr17:32954394-32954430	human/chimp>rhesus	NA	18
NAV2	chr11:19862415-19862484	human>chimp/rhesus	12	NS
ZNF207	chr17:27712599-27712647	human/chimp>rhesus	NS	8
PCCB	chr3:137528686-137528787	rhesus>human>chimp	121	131
GSTM3	chr1:110083977-110084053	human<chimp/rhesus	NA	104
C1QDC1	chr12:30777829-30777912	human/chimp<rhesus	NS	60
KCNJ3 /GIRK1	chr2:155274360-155274577	human<chimp/rhesus	NS	251
SIPA1L1	chr14:71241190-71241253	human/chimp<rhesus	NS	23
ERMP1	chr9:5815091-5815219	rhesus>human>chimp	147	NA
ACSL3	chr2:223473635-223473742	human>chimp/rhesus	2	NA

PTPRZ1	chr7:121474963-121475080	human>chimp/rhesus	150	NA
MACF1	chr1:39707805-39707874	human/chimp>rhesus	153	316
GLS	chr2:191527725-191527789	human<chimp/rhesus	239	NS
DCLK1	chr13:35260348-35260422	human/chimp<rhesus	NS	41
CAMTA1	chr1:7738284-7738315	human<chimp<rhesus	NS	59
EGFL7	chr9:138683878-138683994	human/chimp>rhesus	NS	320
SOS1	chr2:39069914-39069959	human/chimp>rhesus	NS	13
MBD1	chr18:46055737-46055812	human/chimp>rhesus	158	83
FMRP	chrX:146827309-146827372	human/chimp<rhesus	NS	166

Supplemental Table 4: Cassette exons predicted by the HJAY array to have splicing differences between human and chimpanzee cerebellums.
Columns ‘upstream junction’, ‘downstream junction’, ‘exon’ and ‘skip junction’ contain MADS+ p values of differential splicing between human and chimpanzee cerebellums. ‘+’ indicates higher exon inclusion levels in humans. ‘-’ indicates lower exon inclusion levels in humans. ‘NA’ indicates an insufficient number of perfect-match probes targeting orthologous transcripts for between-species comparison of splicing. Exons highlighted in red are true positive HJAY predictions confirmed by RT-PCR. Exons highlighted in blue are false positive HJAY predictions according to RT-PCR analysis. Exons are sorted based on the rankings of statistical significance for splicing differences between species.

Gene symbol	Exon location (hg18)	Strand	Upstream junction	Downstream junction	Exon	Skip junction
PIGX	chr3:197939969-197940023	+	+1.5E-35	+3.8E-17	+4.0E-22	+9.5E-12
ACSL3	chr2:223473635-223473742	+	+3.0E-21	+4.1E-32	+6.9E-14	+3.1E-06
RCE1	chr11:66346610-66346721	+	+9.9E-27	+1.4E-31	+1.1E-10	+2.7E-07
C14ORF159	chr14:90693735-90693787	+	+1.2E-16	+2.2E-17	+2.2E-17	+4.2E-09
PIGX	chr3:197937922-197938039	+	+5.2E-11	+1.9E-32	NA	+1.1E-08
PDE4DIP	chr1:143729237-143729356	-	+3.8E-23	NA	+4.7E-18	+7.9E-03
MFN2	chr1:11965166-11965234	+	+4.4E-13	+8.0E-19	+1.8E-05	+4.4E-14
DDX42	chr17:59206199-59206270	+	+3.2E-12	+1.1E-23	+4.4E-07	+4.2E-07
RHOT1	chr17:27524068-27524192	+	+6.1E-17	NA	+5.7E-22	+7.3E-05
B3GALNT1	chr3:162290425-162290544	-	+5.4E-19	+2.0E-18	NA	+3.2E-03
GRK4	chr4:2956037-2956133	+	NA	+2.5E-11	+4.9E-22	+7.6E-03
NAV2	chr11:19862415-19862484	+	+4.5E-13	+7.0E-04	+3.4E-13	+7.8E-09
ZFAND1	chr8:82792038-82792078	-	-2.3E-09	-1.5E-13	-1.4E-08	-2.1E-08
APLP2	chr11:129498716-129498884	+	+5.5E-09	+4.9E-05	+4.6E-08	+3.7E-15
ASRGL1	chr11:61880372-61880515	+	NA	+3.4E-09	+3.8E-03	+5.2E-14
SNRPN	chr15:22794605-22794726	+	NA	-2.5E-10	NA	-5.8E-10
FIP1L1	chr4:53975538-53975646	+	NA	+1.1E-11	+9.5E-07	+1.6E-05
DMTF1	chr7:86630490-86630584	+	NA	NA	+1.1E-08	+1.1E-07
LMBR1	chr7:156221947-156222070	-	-1.7E-07	NA	-2.1E-09	-1.8E-12
ZNF638	chr2:71514113-71514173	+	NA	NA	+1.9E-14	+8.4E-08
TJP2	chr9:71055770-71056100	+	+1.8E-08	+4.0E-05	+3.6E-03	+5.7E-17
ABCA5	chr17:64833434-64833553	-	NA	+4.8E-11	+3.3E-07	+1.8E-04
FLJ45455	chr17:11395937-11395994	+	NA	+2.2E-15	+2.7E-07	+1.8E-03
TTLL7	chr1:84125447-84125555	-	NA	NA	+9.6E-03	+2.0E-15
SUZ12P	chr17:26110634-26110683	+	+3.6E-05	+1.8E-10	NA	+5.7E-04
RBM12B	chr8:94822032-94822100	-	+2.6E-15	NA	+1.5E-03	+4.7E-06
OGT	chrX:70691764-70691960	+	-2.4E-04	-1.6E-02	-2.4E-04	-9.6E-20
PAK7	chr20:9747327-9747433	-	+2.4E-09	NA	+3.2E-03	+2.2E-09
ANKS1B	chr12:97725752-97725824	-	-1.3E-07	-3.4E-03	-2.0E-07	-5.1E-11
THOC5	chr22:28257066-28257099	-	-7.0E-08	NA	NA	-2.7E-11
NAPB	chr20:23325708-23325819	-	NA	-5.7E-01	-1.9E-09	-3.6E-17
NAV2	chr11:20034651-20034750	+	NA	NA	+5.4E-03	+2.1E-04
SLC4A10	chr2:162438671-162438761	+	-7.2E-02	-2.6E-06	-3.0E-13	-2.8E-08
EIF4ENIF1	chr22:30176274-30176346	-	+1.0E-09	+1.9E-05	+6.0E-07	+2.1E-04
MCF2L	chr13:112793435-112793510	+	-1.1E-02	-2.7E-06	-2.2E-10	-3.5E-03

LMBR1	chr7:156173484-156173646	-	+3.4E-07	+1.7E-05	+1.1E-07	+3.9E-08
TMEM144	chr4:159376039-159376107	+	+4.8E-16	+1.9E-02	+5.4E-02	+3.6E-09
C10ORF76	chr10:103743284-103743350	-	+1.7E-06	+9.4E-06	+7.3E-06	+6.5E-10
SPTLC1	chr9:93881536-93881669	-	+4.2E-08	NA	NA	+2.4E-08
PIGN	chr18:57981743-57981869	-	NA	+2.8E-09	NA	+5.1E-08
AFMID	chr17:73713621-73713726	+	+1.1E-07	-1.8E-16	NA	-1.7E-06
ZNF211	chr19:62843091-62843247	+	NA	-1.5E-07	-6.3E-05	-7.4E-04
FAM49B	chr8:130985926-130986013	-	-6.4E-01	+1.1E-08	+6.7E-12	+1.3E-07
CD74	chr5:149762876-149763068	-	+8.9E-08	+1.4E-05	+9.5E-07	+6.2E-04
RSU1	chr10:16898977-16899089	-	-3.8E-08	-1.0E-05	-1.9E-03	-2.3E-05
SLITRK2	chrX:144711214-144711363	+	+1.6E-09	NA	+2.0E-01	+3.6E-13
SEC24C	chr10:75176393-75176480	+	+1.6E-06	+4.2E-11	+1.6E-02	+5.3E-05
PACRGL	chr4:20335528-20335609	+	NA	-7.7E-04	-2.7E-04	-1.3E-12
ASNS	chr7:97337025-97337061	-	+4.5E-09	NA	+1.1E-05	+6.8E-05
PLA2G4C	chr19:53299656-53299793	-	NA	NA	+3.3E-03	+2.9E-04
HSD17B14	chr19:54008524-54008621	-	-1.2E-06	NA	NA	-1.9E-09
ANK1	chr8:41638550-41638616	-	+3.5E-09	+2.1E-01	+7.7E-07	+6.5E-05
ODF2	chr9:130271282-130271453	+	+7.8E-05	+7.1E-03	+4.3E-03	+4.9E-11
TBC1D9B	chr5:179227050-179227101	-	+1.7E-06	+2.1E-05	+2.5E-03	+2.2E-10
EVL	chr14:99673829-99673892	+	+3.5E-04	+3.0E-04	+6.3E-04	+1.2E-14
RNF146	chr6:127645124-127645233	+	NA	-3.8E-02	-5.8E-17	-4.7E-03
TRPC1	chr3:143937910-143938065	+	-9.8E-02	+1.2E-03	+5.1E-07	+9.6E-12
TRMT11	chr6:126369680-126369793	+	+1.5E-11	+1.9E-02	NA	+4.2E-07
C4ORF30	chr4:17420257-17420413	-	NA	NA	-7.0E-05	-2.8E-08
LZTR1	chr22:19671792-19671872	+	-1.7E-02	-2.9E-08	-5.2E-02	-1.6E-11
UBA2	chr19:39613320-39613404	+	-5.1E-03	-3.3E-13	-2.0E-02	-5.9E-06
DNER	chr2:229991067-229991190	-	+1.0E-05	+1.1E-05	NA	+9.1E-08
PLEKHM2	chr1:15920410-15920470	+	+2.1E-06	+2.6E-06	+5.2E-04	+1.7E-04
PDXK	chr21:43988032-43988116	+	+8.6E-14	+1.3E-01	+1.3E-05	+9.7E-04
BCAS3	chr17:56120162-56120338	+	+5.4E-10	NA	NA	+3.0E-03
ABLIM3	chr5:148600431-148600530	+	+6.1E-04	+6.6E-06	+9.5E-03	+1.3E-11
WNK1	chr12:858999-859458	+	-2.9E-02	-3.4E-08	-1.7E-05	-4.3E-08
PTPRN	chr2:219872665-219872752	-	-8.0E-08	-2.3E-05	-3.9E-04	-3.2E-04
SLC25A32	chr8:104494826-104494935	-	+1.7E-08	+2.7E-04	+5.6E-04	+6.7E-03
GPR155	chr2:175055983-175056132	-	NA	NA	+2.2E-03	+4.4E-08
SRPK2	chr7:104553464-104553557	-	-4.0E-05	-4.7E-10	-4.8E-04	-8.0E-04
MLLT4	chr6:168037390-168037435	+	NA	+1.4E-05	+4.1E-04	+5.6E-06
ATP5H	chr17:70547781-70547853	-	-4.7E-06	+2.6E-01	-2.0E-03	-5.2E-12
DGUOK	chr2:74037759-74037875	+	-1.3E-01	-8.5E-03	-3.4E-06	-2.7E-14
SRI	chr7:87682045-87682187	-	-2.3E-04	NA	-1.1E-07	-4.1E-06
PFKM	chr12:46805374-46805612	+	NA	NA	-1.6E-08	-2.9E-04
CROP	chr17:46170496-46170559	+	-1.8E-07	NA	NA	-5.6E-06
UBQLN1	chr9:85471084-85471168	-	+2.8E-04	+2.3E-07	+1.3E-01	+1.3E-03
SARS	chr1:109580949-109581015	+	-1.5E-01	-1.4E-08	-6.2E-07	-5.4E-06
ZC3H14	chr14:88104135-88104250	+	+9.1E-06	+1.5E-05	+4.5E-04	+2.0E-04
BCAS3	chr17:56120162-56120338	+	+5.4E-10	NA	NA	+3.0E-03
GLMN	chr1:92504844-92504886	-	-1.6E-09	NA	-2.0E-02	-7.0E-05
SAPS2	chr22:49174328-49174406	+	NA	-2.8E-07	-1.2E-02	-1.8E-06
LARP1	chr5:154153552-154153753	+	-8.7E-10	-1.6E-02	-5.4E-04	-5.4E-05
TJP2	chr9:71054110-71054221	+	-7.9E-07	-1.0E-01	-2.1E-05	-1.8E-08

PHF14	chr7:10988523-10989311	+	-1.0E-04	-1.8E-03	-1.1E-07	-9.6E-06
TTC8	chr14:88377521-88377611	+	-1.3E-01	-1.0E-03	-1.0E-01	-5.5E-17
VCAN	chr5:82850923-82853884	+	-6.8E-01	NA	-4.1E-07	-1.5E-10
ELP2	chr18:31973379-31973574	+	+2.7E-01	NA	+8.9E-05	+5.5E-07
XPO6	chr16:28071751-28071786	-	NA	-2.2E-04	-9.5E-09	-1.4E-03
AMPH	chr7:38423949-38424075	-	+4.0E-04	+4.0E-01	+1.2E-02	+6.3E-06
SNAP25	chr20:10172622-10172682	+	+3.0E-04	+1.8E-09	+1.5E-01	+1.2E-03
FAF1	chr1:50690052-50690453	-	NA	NA	+7.1E-07	+1.2E-03
NUPL1	chr13:24781384-24781420	+	+1.1E-04	+5.6E-03	+6.8E-06	+3.8E-06
RHOT1	chr17:27558643-27558695	+	NA	NA	+1.5E-06	+1.4E-03
CADM2	chr3:86111003-86111123	+	+2.5E-15	+1.8E-03	-5.9E-02	+5.3E-03
EXOC7	chr17:71598004-71598073	-	-2.8E-03	NA	-1.2E-04	-7.1E-08
EDC3	chr15:72766484-72766573	-	+4.5E-01	+2.7E-13	NA	+2.7E-03
UGP2	chr2:63935521-63935574	+	NA	NA	-1.1E-07	-5.6E-04
SPOP	chr17:45069119-45069170	-	-1.8E-01	+1.8E-08	NA	+5.2E-08
SNRK	chr3:43306235-43306285	+	-6.3E-01	+3.4E-14	-2.8E-01	+1.4E-05
ATP2B4	chr1:201968973-201969081	+	-7.3E-02	NA	-2.2E-03	-1.1E-09
AHI1	chr6:135860018-135860080	-	+1.8E-03	NA	+1.1E-07	+7.7E-03
SS18	chr18:21916324-21916490	-	NA	NA	+1.5E-05	+1.6E-04
PKM2	chr15:70282416-70282583	-	+7.0E-05	+1.8E-03	+4.9E-04	+6.6E-06
ICA1L	chr2:203442503-203442573	-	NA	-1.0E-07	-8.3E-02	-1.2E-04
SLC38A1	chr12:44934863-44934986	-	NA	NA	+4.0E-05	+2.2E-05
HIVEP2	chr6:143146350-143146445	-	+6.3E-04	+8.2E-04	+7.1E-05	+7.9E-06
UBE3B	chr12:108403824-108403930	+	+9.5E-07	+2.5E-01	-1.1E-01	+1.6E-05
AGFG1	chr2:228105097-228105169	+	NA	NA	-8.6E-06	-2.1E-05
HNRNPD	chr4:83495071-83495178	-	-3.0E-04	-1.7E-06	-7.8E-02	-1.3E-06
AGFG2	chr7:99992152-99992185	+	+1.0E-05	+2.2E-06	NA	+2.2E-03
NDUFV1	chr11:67135943-67136025	+	+4.6E-06	+2.4E-02	+2.3E-06	+9.4E-04
C16ORF61	chr16:79589390-79589457	-	NA	NA	+9.1E-04	+6.0E-07
TSPAN3	chr15:75135185-75135260	-	+6.6E-10	-4.9E-02	+6.7E-02	+4.7E-07
KIAA0802	chr18:8799445-8799559	+	+7.6E-07	NA	-2.0E-04	-1.1E-09
CSDE1	chr1:115085670-115085817	-	+1.3E-05	NA	+3.4E-01	+6.2E-03
ZNF385B	chr2:180095853-180095892	-	NA	-4.1E-08	NA	-9.9E-03
COBL	chr7:51207646-51207721	-	NA	NA	-2.3E-05	-7.9E-04
SRRM1	chr1:24846156-24846286	+	-1.1E-04	NA	-3.0E-02	-2.6E-07
PCCB	chr3:137528686-137528787	+	+2.0E-01	+2.6E-06	+6.5E-06	+2.6E-04
VPS39	chr15:40271555-40271588	-	+3.3E-06	NA	NA	+7.9E-04
HNRPDL	chr4:83565739-83565844	-	+5.2E-01	-2.7E-02	-5.8E-08	-6.6E-09
C11ORF58	chr11:16730907-16731017	+	NA	-3.5E-07	-4.4E-03	-8.9E-03
C11ORF60	chr11:117933662-117933815	-	NA	-4.0E-04	-7.6E-06	-2.6E-04
MFSD11	chr17:72249853-72249950	+	NA	NA	+2.8E-07	+7.7E-03
AP3M2	chr8:42132653-42132714	+	NA	NA	-9.2E-05	-6.9E-05
ERMP1	chr9:5795026-5795217	-	-1.9E-01	+7.2E-01	-5.8E-03	-3.6E-12
ARIH2	chr3:48957572-48957618	+	-5.1E-04	-8.7E-03	-3.8E-05	-7.3E-05
DCUN1D4	chr4:52448045-52448167	+	-7.6E-02	-2.5E-03	-3.8E-07	-2.8E-06
WASF1	chr6:110588530-110588628	-	NA	+1.0E-03	-4.7E-01	+8.4E-06
TBCK	chr4:107378096-107378144	-	-6.9E-03	-7.9E-05	-1.9E-06	-3.4E-04
DTNA	chr18:30563424-30563508	+	-2.8E-05	NA	NA	-3.0E-04
AAAS	chr12:51994801-51994900	-	NA	NA	-4.2E-05	-3.5E-04
ZFYVE16	chr5:79759066-79759120	+	NA	+4.6E-03	NA	+1.0E-04

VPS24	chr2:86622885-86622946	-	-5.4E-05	-3.0E-01	-1.6E-03	-5.2E-08
ENPP2	chr8:120653596-120653671	-	+9.7E-05	NA	+7.9E-02	+5.3E-06
P2RX4	chr12:120139319-120139467	+	-6.7E-01	+3.2E-07	+5.7E-02	+5.0E-03
SAPS2	chr22:49177161-49177310	+	+3.9E-03	+6.4E-03	-6.2E-01	+2.8E-07
SOCS4	chr14:54568330-54568459	+	+2.9E-03	+5.1E-03	+1.6E-02	+3.0E-05
PTPRM	chr18:8112239-8112314	+	+1.4E-10	-3.4E-03	+1.5E-09	-1.9E-04
SNX6	chr14:34143091-34143225	-	-2.4E-05	-3.5E-05	-3.2E-02	-1.8E-03
LRP8	chr1:53513890-53514013	-	+4.2E-03	+2.2E-01	-4.7E-02	+1.3E-07
NDRG3	chr20:34716617-34716656	-	-7.5E-03	-2.5E-05	-1.7E-02	-1.4E-04
GUCY1A2	chr11:106122486-106122579	-	-1.8E-04	NA	NA	-4.3E-04
ABLIM1	chr10:116223627-116223705	-	NA	+6.0E-05	NA	+6.2E-03
ERMP1	chr9:5815091-5815219	-	+1.6E-03	+1.3E-03	+4.5E-02	+6.5E-07
PDP1	chr8:94999314-94999349	+	-1.5E-03	-1.8E-02	-1.4E-06	-4.8E-03
KRIT1	chr7:91712714-91712824	-	NA	NA	-7.4E-04	-7.4E-06
PTPRZ1	chr7:121474963-121475080	+	+6.4E-02	+1.5E-07	+2.5E-03	+1.6E-03
FAM118B	chr11:125604329-125604398	+	+6.4E-02	+1.0E-07	NA	+5.8E-03
TRIP12	chr2:230433365-230433491	-	+8.6E-04	+1.9E-04	+1.7E-03	+7.6E-03
MACF1	chr1:39707805-39707874	+	-6.1E-01	-6.8E-03	-3.8E-05	-1.8E-04
CD59	chr11:33711616-33711732	-	-8.4E-02	-3.6E-03	-1.1E-03	-6.4E-03
PPP2R4	chr9:130944780-130944907	+	-1.8E-04	-1.7E-02	NA	-3.9E-05
ZNF415	chr19:58310768-58310876	-	NA	+1.5E-01	-4.7E-03	-9.4E-12
CCNDBP1	chr15:41273570-41273627	+	NA	+3.4E-07	+3.0E-01	+8.8E-03
MBD1	chr18:46055737-46055812	-	+9.8E-06	+1.6E-02	+1.9E-03	+2.9E-04
EIF2B5	chr3:185339328-185339421	+	-4.1E-03	-2.4E-02	NA	-2.2E-05
ZNF346	chr5:176382766-176382841	+	NA	NA	+7.2E-03	+5.6E-05
PANX2	chr22:48955987-48956038	+	-1.2E-04	NA	-1.6E-01	-3.1E-05
AGTPBP1	chr9:87483069-87483133	-	+8.8E-02	-7.3E-06	NA	-2.6E-06
GSTA4	chr6:52960113-52960165	-	-8.2E-07	-3.9E-03	-4.2E-01	-4.2E-05
SUZ12P	chr17:26094444-26094513	+	-1.8E-04	+3.6E-05	-2.2E-04	-9.2E-09
BBS1	chr11:66035251-66035286	+	NA	-3.6E-04	-1.4E-02	-1.5E-04
KIAA0146	chr8:48369008-48369172	+	+2.4E-04	+2.8E-03	+1.6E-01	+7.3E-06
RAPGEF6	chr5:130792493-130792808	-	+2.9E-02	+2.6E-04	NA	+2.3E-05
NAT15	chr16:3437482-3437621	+	NA	+8.6E-03	NA	+2.2E-03
MYO18A	chr17:24436747-24436792	-	-8.5E-05	NA	-8.7E-03	-2.4E-03
SDR39U1	chr14:23981223-23981306	-	+8.0E-05	+1.7E-03	+1.7E-01	+3.3E-05
ACBD5	chr10:27564026-27564147	-	+3.5E-02	+6.6E-04	+1.6E-03	+5.4E-05
ZDHHC13	chr11:19121105-19121246	+	-6.0E-04	-8.2E-02	-1.7E-02	-2.0E-06
OSBPL1A	chr18:20073181-20073344	-	-1.0E-05	-2.6E-02	-8.9E-04	-1.1E-03
HPS4	chr22:25197178-25197354	-	NA	-4.0E-04	-3.6E-02	-1.7E-05
PHF20	chr20:33950705-33950984	+	+2.0E-03	+3.1E-02	+1.8E-01	+1.1E-03
CD59	chr11:33709545-33709590	-	-3.6E-03	NA	+1.1E-03	+2.4E-05
MFGE8	chr15:87254026-87254158	-	+4.9E-03	+3.8E-02	+2.5E-02	+2.5E-05
SPPL2A	chr15:48805561-48805615	-	NA	NA	-8.1E-05	-5.9E-03
GALK2	chr15:47361475-47361574	+	+6.0E-02	+1.2E-04	+1.1E-02	+2.1E-04
PICALM	chr11:85365313-85365373	-	-3.0E-03	+4.1E-03	-1.1E-01	+9.3E-14
SORBS1	chr10:97144357-97144420	-	-4.5E-04	NA	-6.8E-02	-6.7E-05
SPATS2L	chr2:201012089-201012296	+	NA	+3.1E-02	+1.4E-03	+8.6E-05
ZNF227	chr19:49425725-49425809	+	-1.4E-03	+6.7E-02	+4.5E-01	-8.0E-13
CDC42BPB	chr14:102490287-102490365	-	-1.2E-01	+1.8E-05	+5.0E-02	+2.6E-07
TAPT1	chr4:15807378-15807444	-	NA	-3.4E-03	NA	-2.1E-03

BIN1	chr2:127534641-127534686	-	-5.0E-03	NA	NA	-3.3E-04
C5ORF33	chr5:36244483-36244549	-	NA	-2.1E-01	-2.1E-06	-7.2E-03
MBNL1	chr3:153658608-153658672	+	-8.6E-02	NA	-2.4E-04	-2.1E-04
USP4	chr3:49291250-49291339	-	-5.6E-05	-7.9E-02	-3.3E-02	-1.6E-03
AGPAT3	chr21:44204940-44205088	+	+2.7E-05	NA	+4.1E-01	+2.7E-05
SERGEF	chr11:17988193-17988262	-	-1.4E-01	+2.1E-09	+3.0E-01	+4.0E-04
FZD3	chr8:28413368-28413414	+	-5.4E-02	NA	-8.3E-03	-9.1E-06
TPM1	chr15:61140964-61141040	+	-9.2E-05	+5.5E-05	+6.7E-06	+9.8E-03
KIAA2026	chr9:5934870-5934960	-	-7.0E-01	NA	+4.3E-03	+6.4E-07
G3BP2	chr4:76798190-76798289	-	-2.8E-02	+2.5E-01	-1.1E-03	-1.3E-07
CADM1	chr11:114585503-114585587	-	-5.5E-03	-1.5E-01	NA	-1.4E-05
FN1	chr2:215965898-215966171	-	+2.2E-04	+1.3E-03	+9.6E-02	+4.1E-03
ASPH	chr8:62757551-62757596	-	-8.3E-04	-9.6E-02	-4.5E-02	-8.8E-04
TM2D1	chr1:61925051-61925181	-	+4.7E-03	NA	NA	+7.7E-03
WDR20	chr14:101733844-101733937	+	-1.7E-01	NA	-2.3E-05	-3.8E-04
CLUAP1	chr16:3523099-3523156	+	+7.0E-02	+9.3E-02	+1.7E-05	+7.8E-04
PNPLA6	chr19:7506012-7506088	+	-4.3E-04	+6.1E-01	NA	-3.7E-06
SHF	chr15:43253065-43253206	-	+7.8E-08	-3.1E-02	+4.7E-02	+9.2E-04
DGKG	chr3:187469283-187469400	-	+1.2E-01	+7.8E-04	+1.6E-01	+5.2E-06
CADM1	chr11:114574335-114574368	-	+1.4E-05	+1.3E-01	-1.9E-01	+6.4E-05
LPHN3	chr4:62461031-62461070	+	-7.7E-02	-1.5E-03	NA	-4.5E-04
ZNF706	chr8:102283736-102283851	-	-7.8E-02	+1.5E-05	NA	+1.4E-04
POLB	chr8:42315686-42315744	+	-3.5E-05	-1.4E-01	-4.3E-02	-1.1E-03
CUGBP2	chr10:11402825-11402867	+	-8.8E-02	-1.7E-03	NA	-5.4E-04
PATL1	chr11:59180004-59180094	-	+1.8E-07	+6.3E-01	-5.3E-01	+7.1E-05
NDRG4	chr16:57092392-57092482	+	-2.9E-01	+1.7E-09	-4.2E-02	+2.5E-04
SLC4A7	chr3:27447792-27448164	-	-9.5E-02	NA	-3.7E-04	-2.7E-03
FLRT3	chr20:14257779-14257973	-	-7.8E-02	+9.4E-04	-3.3E-04	-1.7E-04
DMWD	chr19:50979738-50979813	-	+1.4E-01	-5.2E-03	+5.5E-02	-1.0E-04
FAM135A	chr6:71252590-71252668	+	-9.6E-03	NA	-4.2E-01	-9.0E-07
TNIK	chr3:172329196-172329361	-	-1.6E-01	-9.7E-02	-1.4E-03	-5.8E-05
GPD1L	chr3:32144571-32144749	+	+2.2E-01	+8.2E-05	+1.3E-02	+7.1E-04
XPA	chr9:99484302-99484533	-	NA	-2.7E-01	+2.1E-05	+2.6E-03
BAALC	chr8:104294322-104294489	+	NA	NA	-5.9E-03	-4.3E-03
MMS19	chr10:99233849-99233898	-	-1.7E-01	-3.6E-02	+1.7E-08	+3.5E-04
ZNF346	chr5:176401384-176401477	+	+4.5E-03	-3.2E-01	+6.3E-02	+9.1E-03
NPEPPS	chr17:43009409-43009525	+	-6.3E-02	NA	-7.7E-03	-4.4E-04
KIF13A	chr6:17879323-17879428	-	-2.5E-01	NA	-5.0E-04	-7.9E-04
C10ORF76	chr10:103639158-103639237	-	+9.4E-03	-9.8E-02	+1.1E-04	+3.1E-04
C16ORF35	chr16:113505-113544	-	-8.3E-03	-3.4E-01	+5.9E-03	+3.9E-06
INTS12	chr4:106844253-106844415	-	-6.6E-02	NA	+5.1E-06	+1.7E-03
GIGYF2	chr2:233273538-233273608	+	+9.8E-02	+5.0E-02	+2.5E-04	+6.6E-04
TCEB1	chr8:75034553-75034607	-	+2.3E-01	+8.1E-02	+9.0E-03	+7.8E-04
ADCYAP1R1	chr7:31106268-31106349	+	NA	-2.1E-01	+2.6E-03	+4.9E-05
LSM14B	chr20:60137375-60137483	+	-8.5E-03	NA	-1.3E-03	-4.1E-03
SNED1	chr2:241661353-241661452	+	-7.4E-03	-1.1E-04	-1.7E-01	-7.9E-04
RSBN1	chr1:114140330-114140448	-	NA	-4.1E-01	-1.8E-04	-2.4E-03
CAMK2G	chr10:75257852-75257885	-	-2.3E-01	+2.0E-03	-4.9E-04	-5.9E-06
PHF21A	chr11:46068581-46068693	-	+1.7E-01	-6.7E-04	-2.5E-02	-5.1E-05
CPNE3	chr8:87606220-87606341	+	NA	-3.5E-04	-2.1E-01	-6.7E-03

ERLEC1	chr2:53888939-53889101	+	+5.6E-01	NA	-5.8E-05	-9.4E-04
LRRC8A	chr9:130688114-130688221	+	-1.6E-01	+1.5E-04	+3.7E-03	+9.2E-03
TTC8	chr14:88369789-88369819	+	+8.8E-02	+7.6E-02	+7.3E-04	+9.7E-04
GLS	chr2:191527725-191527789	+	-4.4E-03	+4.5E-02	-4.9E-02	-5.0E-05
SLC6A6	chr3:14484599-14484724	+	+7.9E-04	-1.4E-02	+7.4E-04	+9.7E-03
INPP5K	chr17:1365931-1366160	-	-2.8E-01	NA	+2.6E-03	+5.3E-04
RAB11FIP2	chr10:119783482-119783542	-	+1.8E-01	+1.2E-03	-3.3E-01	+3.9E-04
SRGAP2	chr1:204698339-204698378	+	NA	5.8E-04+	2.8E-01-	2.0E-03
NRXN2	chr11:64201040-64201085	-	+3.7E-04	NA	+6.6E-01	+8.5E-03
MADD	chr11:47270669-47270723	+	-3.4E-03	+3.0E-01	-1.0E-02	-2.2E-04
MEIS1	chr2:66592784-66592930	+	+1.8E-01	+1.7E-03	+6.0E-02	+5.1E-03
SAPS2	chr22:49222282-49222363	+	-1.6E-04	+5.1E-06	+4.8E-02	+2.5E-03
SPIRE1	chr18:12475957-12475999	-	-5.9E-01	+1.8E-01	+4.4E-03	+4.1E-05
LAPTM4A	chr2:20100779-20100856	-	+8.1E-03	+1.0E-01	+3.0E-01	+3.2E-04
PUF60	chr8:144974823-144974874	-	+6.0E-03	+4.6E-01	+6.5E-01	+3.0E-06
RNF14	chr5:141334552-141334704	+	+3.8E-05	-5.9E-01	+4.1E-01	+3.0E-03
FUZ	chr19:55004446-55004644	-	+9.9E-03	-3.7E-01	NA	+5.0E-04
CD59	chr11:33709545-33709590	-	-3.6E-03	NA	+1.1E-03	+2.4E-05
USMG5	chr10:105143945-105144141	-	-7.2E-02	NA	+6.3E-03	+3.5E-04
CDC42BPA	chr1:225302250-225302334	-	+6.4E-01	+2.7E-03	-1.5E-01	+5.7E-04
PLCB4	chr20:9333959-9333995	+	+4.3E-01	+2.0E-01	+2.5E-03	+1.3E-03
C18ORF25	chr18:42073968-42074151	+	-3.2E-01	-3.8E-01	-4.2E-03	-1.3E-04
WDFY3	chr4:85867037-85867088	-	-5.0E-01	+6.9E-04	-5.6E-01	+4.1E-05
ZNF227	chr19:49413783-49413845	+	-3.1E-01	-2.9E-03	-1.2E-01	-4.7E-03
DDX19B	chr16:68907372-68907508	+	-2.1E-01	-1.0E-09	+3.4E-04	+5.4E-03
AGAP2	chr12:56408367-56408427	-	+3.4E-01	+3.8E-03	+1.2E-01	+5.9E-03
EXOC7	chr17:71598818-71598911	-	+5.1E-03	-2.8E-03	-3.0E-01	+3.0E-07
KIF1B	chr1:10308755-10309004	+	+3.9E-01	+8.1E-03	+2.2E-01	+9.0E-03
EIF4E2	chr2:233147216-233147295	+	+1.9E-01	+1.7E-03	-5.3E-01	+7.7E-03
GPHN	chr14:66379148-66379187	+	+4.5E-04	+1.3E-04	-1.0E-03	-7.9E-03
RIMS1	chr6:73031398-73031476	+	+8.1E-04	-2.2E-02	-8.1E-03	-1.5E-03
SEC24B	chr4:110622281-110622386	+	+2.0E-09	-3.1E-03	+1.7E-01	-4.3E-03
C10ORF104	chr10:73653651-73653820	+	-2.7E-02	+7.0E-05	-5.5E-01	+1.9E-03
ARHGAP12	chr10:32182999-32183140	-	-5.4E-03	+7.3E-05	+1.8E-01	-7.6E-06
HDDC2	chr6:125661558-125661661	-	+8.5E-07	-2.2E-01	-6.2E-05	-9.1E-03
FGF1	chr5:141960450-141960554	-	-1.3E-02	+4.3E-02	+5.9E-03	+4.6E-03
RNF14	chr5:141338051-141338579	+	-5.9E-01	+5.1E-01	-2.9E-03	-4.5E-04
FBXO44	chr1:11641176-11641272	+	-2.0E-03	-1.3E-01	+8.6E-03	-1.4E-03
SFXN5	chr2:73041767-73041885	-	+1.4E-02	+2.7E-01	-7.1E-05	-5.6E-03
EAPP	chr14:34068314-34068432	-	-2.6E-02	-5.0E-01	+3.8E-03	+3.2E-03
TRAPPC1	chr17:7775548-7775619	-	+9.9E-03	+4.8E-01	-3.6E-02	+7.6E-03
CAMKK2	chr12:120215337-120215460	-	-3.4E-03	-2.3E-02	+1.9E-04	+6.2E-03
MARK3	chr14:103036245-103036290	+	+3.8E-03	-3.7E-03	+2.0E-01	-6.9E-04
PXK	chr3:58381302-58381335	+	+5.4E-01	+4.3E-01	-5.2E-03	-9.8E-03
KEAP1	chr19:10460867-10461044	-	-8.9E-03	+1.8E-03	+2.6E-01	-1.5E-03
FLJ45455	chr17:11223455-11223551	+	+2.1E-01	-1.8E-03	+7.6E-03	+9.8E-03

Supplemental Table 5: Cassette exons predicted by the HJAY array to have splicing differences between human and rhesus cerebellums.
Columns ‘upstream junction’, ‘downstream junction’, ‘exon’ and ‘skip junction’ contain MADS+ p values of differential splicing between human and rhesus cerebellums. ‘+’ indicates higher exon inclusion levels in humans. ‘-’ indicates lower exon inclusion levels in humans. ‘NA’ indicates an insufficient number of perfect-match probes targeting orthologous transcripts for between-species comparison of splicing. Exons highlighted in red are true positive HJAY predictions confirmed by RT-PCR. Exons highlighted in blue are false positive HJAY predictions according to RT-PCR analysis. Exons are sorted based on the rankings of statistical significance for splicing differences between species.

Gene symbol	Exon location (hg18)	Strand	Upstream junction	Downstream junction	Exon	Skip junction
NRCAM	chr7:107827115-107827273	-	+1.00E-18	+4.40E-34	NA	+2.60E-24
NDRG4	chr16:57102049-57102088	+	-1.60E-25	-2.50E-24	-1.10E-30	-2.40E-06
KIAA0652	chr11:46642122-46642221	+	-8.80E-17	-2.10E-28	-2.00E-21	-2.00E-13
ITGB1	chr10:33235398-33235496	-	-3.20E-08	NA	NA	-6.90E-40
ZDHHC16	chr10:99203545-99203593	+	+3.10E-20	+1.30E-16	+5.20E-09	+5.10E-22
R3HDM2	chr12:55968906-55968960	-	+5.20E-24	+3.10E-07	+2.50E-16	+3.80E-12
HNRNPF	chr10:43210083-43210142	-	NA	NA	+5.40E-07	+3.10E-20
ZNF207	chr17:27712599-27712647	+	+2.00E-13	+1.10E-23	+1.10E-06	+1.70E-16
UBAP2	chr9:33953723-33953789	-	+3.50E-09	NA	+1.10E-04	+1.20E-07
FLRT3	chr20:14257779-14257973	-	-3.20E-17	-9.70E-16	NA	-5.50E-16
GPBP1L1	chr1:45923834-45923879	-	+1.20E-02	+8.00E-08	+1.20E-07	+9.60E-06
BEND6	chr6:56987218-56987282	+	+1.60E-25	NA	+2.10E-09	+1.50E-12
SOS1	chr2:39069914-39069959	-	+5.10E-16	+6.00E-20	NA	+1.80E-10
TUBD1	chr17:55313036-55313253	-	-2.40E-14	-9.80E-19	-1.80E-06	-8.50E-13
IP6K2	chr3:48705706-48705775	-	NA	-1.20E-10	-1.10E-10	-2.20E-13
MUDENG	chr14:56810714-56810908	+	+4.30E-08	NA	+1.10E-04	+9.50E-21
MFN2	chr1:11965166-11965234	+	+3.70E-09	+6.20E-20	+3.50E-15	+6.30E-06
AP1GBP1	chr17:32954394-32954430	-	+2.40E-15	NA	+4.10E-09	+9.50E-18
STAU2	chr8:74783820-74783951	-	-1.80E-14	-7.70E-14	-1.50E-10	-2.30E-05
GLMN	chr1:92504844-92504886	-	-4.20E-18	-1.70E-13	NA	-2.70E-06
MORF4L2	chrX:102826264-102826313	-	+3.90E-13	+5.70E-11	NA	+5.60E-09
HNRNPH1	chr5:178975152-178975202	-	+4.20E-02	+6.40E-14	+3.40E-04	+2.90E-25
SIPA1L1	chr14:71241190-71241253	+	-1.30E-12	-3.20E-06	-7.80E-08	-1.50E-18
SNRK	chr3:43316249-43316311	+	-2.40E-22	+1.10E-01	NA	-3.90E-17
DOPEY1	chr6:83863168-83863261	+	NA	+4.20E-13	+3.10E-17	+7.00E-05
UBA2	chr19:39613320-39613404	+	-5.60E-16	-4.60E-03	NA	-6.10E-21
EXD2	chr14:68745299-68745552	+	NA	-6.50E-23	NA	-1.50E-07
KPNA1	chr3:123659262-123659385	-	-2.80E-05	-1.40E-13	-3.60E-12	-1.40E-14
CAMK2D	chr4:114648840-114648873	-	-1.80E-09	NA	-2.50E-27	-8.30E-03
ANK1	chr8:41638104-41638239	-	-2.10E-02	-4.80E-05	+1.10E-13	+5.40E-03
ABLIM3	chr5:148600431-148600530	+	+2.60E-06	+7.80E-14	+4.20E-08	+2.30E-17
KIAA0802	chr18:8799445-8799559	+	+6.00E-09	NA	NA	+2.00E-21
ANUBL1	chr10:45468437-45468513	-	NA	+1.70E-17	NA	+7.10E-12
ZMYND11	chr10:233850-233945	+	-3.00E-10	-7.00E-21	NA	-5.10E-06
PKD1	chr16:2082955-2083095	-	+4.00E-04	+3.60E-17	NA	+3.20E-05
FAM118B	chr11:125604329-125604398	+	+1.20E-09	+2.80E-18	NA	+4.90E-06

MAP2	chr2:210296563-210296656	+	NA	-5.30E-25	-2.40E-06	-4.50E-03
MAP7	chr6:136746501-136746612	-	+7.70E-16	+1.90E-01	NA	+3.50E-07
HNRPDL	chr4:83565739-83565844	-	-2.30E-03	-4.60E-08	-1.90E-14	-1.20E-15
SON	chr21:33866726-33866806	+	NA	-3.60E-13	-3.40E-14	-7.20E-08
DCLK1	chr13:35260348-35260422	-	-3.30E-06	-3.60E-09	-1.40E-05	-3.00E-03
WNK1	chr12:850691-850775	+	-1.60E-07	-8.00E-08	-1.10E-18	-1.10E-05
UBE3A	chr15:23205327-23205447	-	NA	+7.50E-03	+1.20E-09	+1.30E-11
GPBP1L1	chr1:45923834-45923879	-	+1.20E-02	+8.00E-08	+1.20E-07	+9.60E-06
PFKM	chr12:46805374-46805612	+	NA	-6.00E-06	NA	-2.50E-16
CRYZL1	chr21:33935354-33935481	-	NA	+5.20E-11	NA	+7.30E-11
CTNND1	chr11:57318057-57318129	+	NA	-4.80E-06	-1.00E-02	-2.70E-25
KLHL24	chr3:184843961-184844024	+	NA	+2.70E-07	+1.20E-03	+2.60E-08
TRPC1	chr3:143937910-143938065	+	-5.90E-07	+1.40E-06	+1.30E-08	+1.90E-21
ACHP	chr7:156173484-156173646	-	-8.40E-05	+8.70E-02	-1.90E-03	-2.60E-27
G3BP2	chr4:76806138-76806257	-	+9.60E-09	+2.60E-02	+1.80E-01	+1.10E-04
ZNF484	chr9:94677117-94677162	-	NA	-4.80E-09	NA	-1.00E-13
NKTR	chr3:42643695-42643723	+	NA	+6.70E-05	+1.10E-07	+1.90E-14
PELI1	chr2:64185338-64185468	-	+1.10E-05	+9.80E-09	+1.60E-04	+1.70E-07
ABLIM1	chr10:116212793-116212913	-	-2.30E-01	-2.80E-06	-6.90E-06	-1.70E-14
4-Sep	chr17:53959291-53959338	-	-7.10E-03	+2.20E-23	-4.00E-03	+8.30E-18
RIMS1	chr6:73027128-73027191	+	+1.10E-12	+9.00E-02	+1.60E-01	+6.10E-20
ST7	chr7:116649212-116649352	+	+8.50E-02	+6.00E-12	+1.90E-04	+4.70E-17
CAMTA1	chr1:7738284-7738315	+	-6.30E-03	-9.40E-05	-2.80E-09	-1.90E-09
C1QDC1	chr12:30777829-30777912	-	-4.70E-05	-2.80E-07	-2.50E-09	-8.70E-09
PHF14	chr7:10988523-10989311	+	-1.40E-16	-5.80E-09	-1.20E-07	-7.50E-03
DIS3	chr13:72253427-72253495	-	+2.40E-12	NA	-4.10E-02	+2.90E-17
MAP3K4	chr6:161439299-161439449	+	NA	+7.60E-10	NA	+2.90E-04
TXNDC11	chr16:11732001-11732131	-	NA	-8.00E-09	-7.30E-03	-2.20E-06
SNAP25	chr20:10172622-10172682	+	NA	+8.00E-13	+1.30E-03	+5.20E-06
LZTR1	chr22:19671792-19671872	+	-4.30E-07	-1.80E-07	-6.70E-03	-1.50E-08
LRIG1	chr3:66534722-66534794	-	NA	-5.90E-04	-1.20E-16	-4.50E-03
MAPKAP1	chr9:127308409-127308517	-	-9.20E-14	-1.80E-02	-2.20E-06	-2.70E-09
SEZ6L2	chr16:29791526-29791565	-	+2.00E-07	+5.60E-07	+1.90E-09	+4.00E-04
TDP1	chr14:89511877-89511912	+	+1.00E-12	+2.70E-06	NA	+1.80E-06
NUMA1	chr11:71401094-71401136	-	-4.80E-10	NA	-6.80E-08	-7.20E-06
DENND1A	chr9:125571613-125571663	-	-2.80E-07	NA	NA	-8.30E-03
MPZL1	chr1:166011924-166012027	+	+1.10E-13	-8.00E-14	-6.20E-14	-2.00E-07
DIS3	chr13:72252984-72253142	-	-2.90E-17	NA	NA	-4.70E-04
C18ORF1	chr18:32654928-32655090	-	-1.30E-15	NA	NA	-3.00E-03
AMOTL1	chr11:94167824-94167974	+	NA	-1.90E-03	NA	-1.90E-17
MAX	chr14:64613814-64613899	-	NA	NA	+6.00E-06	+1.20E-07
SLC3A2	chr11:62408036-62408160	+	-2.30E-08	NA	NA	-7.10E-09
RDH11	chr14:67226681-67226891	-	+1.50E-11	NA	NA	+1.10E-05
ARHGAP4	chrX:152839743-152839806	-	-8.30E-06	+2.50E-02	-1.10E-03	-1.10E-08
ACAA1	chr3:38145784-38145883	-	NA	+1.20E-05	NA	+2.70E-12
ETFA	chr15:74363152-74363221	-	+3.60E-09	+7.30E-11	NA	+1.30E-04
MBD1	chr18:46055737-46055812	-	+7.20E-12	+6.40E-06	+1.00E-07	+4.20E-04
CEP350	chr1:178226264-178226379	+	+1.50E-06	+3.00E-04	+2.30E-05	+4.50E-08
ANKS1B	chr12:97725752-97725824	-	-1.20E-03	-8.60E-05	-5.30E-12	-3.30E-09
DTNA	chr18:30672055-30672133	+	NA	+3.30E-01	-1.90E-13	-5.00E-12

CAMK2G	chr10:75257852-75257885	-	NA	-1.70E-07	-1.50E-11	-9.10E-04
GON4L	chr1:154012809-154012896	-	+3.90E-12	+8.90E-05	NA	+2.20E-07
YIPF3	chr6:43591321-43591417	-	+2.60E-11	-2.60E-06	NA	+1.20E-05
NAPB	chr20:23325708-23325819	-	NA	-1.40E-01	-8.00E-08	-1.00E-16
PMPCB	chr7:102735278-102735391	+	NA	-3.20E-06	NA	-8.40E-12
RAD51C	chr17:54138237-54138382	+	NA	+4.60E-14	NA	+5.80E-03
BCAS1	chr20:52016851-52017019	-	-5.00E-03	-3.90E-10	NA	-7.80E-05
CLIP1	chr12:121401610-121401643	-	+2.30E-06	+5.30E-10	+9.20E-04	+5.10E-06
TTC17	chr11:43414289-43414460	+	+3.30E-02	+3.50E-10	+1.20E-02	+6.20E-05
ASNS	chr7:97337025-97337061	-	+3.30E-06	NA	NA	+7.20E-06
ASNS	chr7:97338966-97339244	-	-8.90E-06	NA	NA	-3.30E-06
SNAP91	chr6:84359619-84359697	-	+3.80E-01	NA	-1.80E-04	-1.70E-19
SF3B3	chr16:69142053-69142082	+	-5.50E-12	-2.50E-05	-6.10E-05	-1.30E-03
HERPUD1	chr16:55526816-55526888	+	+5.00E-04	NA	-4.50E-01	+2.30E-07
ST3GAL6	chr3:99975453-99975517	+	+1.40E-04	+5.00E-03	+4.30E-06	+3.90E-11
SLC20A2	chr8:42447741-42447876	-	-4.50E-01	-3.60E-05	-7.10E-05	-3.40E-19
AGFG1	chr2:228104050-228104170	+	+1.10E-12	+1.90E-05	+2.60E-01	+4.60E-08
GSTM3	chr1:110083977-110084053	-	-4.60E-10	NA	NA	-2.40E-04
DLG1	chr3:198361010-198361064	-	-3.80E-04	+1.70E-26	-2.80E-02	-2.70E-10
MAPT	chr17:41416380-41417133	+	-1.20E-04	-2.60E-12	NA	-1.60E-03
USP37	chr2:219052616-219052682	-	+1.70E-09	+2.50E-03	+3.40E-06	+9.00E-07
SEZ6L	chr22:25099416-25099449	+	-1.20E-04	-2.80E-10	-5.10E-07	-7.90E-04
MGEA5	chr10:103549988-103550147	-	+1.20E-03	NA	NA	+1.70E-12
GRM3	chr7:86232257-86232865	+	NA	+3.40E-05	+1.10E-01	+1.30E-08
MBNL1	chr3:153633195-153633399	+	+2.90E-11	+5.60E-01	+3.00E-04	+8.80E-05
PDXK	chr21:43988032-43988116	+	+1.20E-13	NA	+5.30E-04	+1.40E-03
FAM107A	chr3:58531092-58531190	-	-6.70E-03	NA	NA	-1.20E-10
TRIT1	chr1:40090989-40091135	-	NA	-1.10E-06	-5.60E-02	-3.60E-11
RPP14	chr3:58271075-58271173	+	-9.40E-03	NA	-7.60E-10	-2.70E-09
PHF15	chr5:133940356-133940485	+	-1.50E-05	-1.30E-08	-1.10E-04	-5.10E-05
ANKRD6	chr6:90388361-90388466	+	+8.50E-09	+2.40E-02	+1.10E-03	+5.50E-10
ZNF655	chr7:98998746-98998825	+	NA	+6.60E-11	NA	+4.30E-04
C1ORF12	chr1:53457126-53457183	-	+7.10E-09	+4.60E-11	-2.30E-03	+4.60E-03
ARIH2	chr3:48957572-48957618	+	-1.20E-01	-1.40E-06	-4.00E-06	-3.50E-10
CADM1	chr11:114585503-114585587	-	-1.80E-02	-6.20E-06	-2.70E-04	-2.20E-13
SSBP2	chr5:80947047-80947132	-	-5.00E-01	+1.30E-15	+2.40E-01	+1.30E-09
MLLT10	chr10:21886555-21886759	+	+7.50E-02	+1.10E-16	-3.10E-01	+9.10E-06
PITPNM3	chr17:6369399-6369507	-	+1.20E-10	+6.10E-03	+2.50E-02	+7.00E-04
APC	chr5:112101948-112102056	+	NA	+4.10E-12	+1.30E-01	+3.60E-06
ZNF706	chr8:102283736-102283851	-	NA	+7.90E-11	NA	+5.00E-04
PKP4	chr2:159098195-159098292	+	+1.10E-02	+7.40E-03	-2.10E-01	+3.90E-15
ATP2B4	chr1:201968973-201969081	+	-1.30E-06	NA	-1.60E-03	-1.10E-07
CELSR2	chr1:109609012-109609154	+	-2.70E-05	+1.10E-13	NA	-4.70E-15
TSC22D2	chr3:151638674-151638831	+	NA	NA	-3.60E-03	-5.40E-12
PCCB	chr3:137528686-137528787	+	-1.60E-04	NA	NA	-7.00E-10
ANK3	chr10:61498400-61506212	-	-2.50E-02	-5.10E-07	-1.50E-08	-1.00E-04
PSME4	chr2:53954979-53955135	-	+2.80E-03	NA	-5.50E-01	+2.20E-04
SSX2IP	chr1:84909459-84909579	-	-2.40E-07	NA	-5.00E-02	-3.00E-10
EIF3H	chr8:117815696-117815744	-	-1.10E-03	NA	-1.40E-02	-2.10E-16
ADD1	chr4:2898166-2898200	+	-6.30E-03	+7.80E-02	-1.70E-01	-3.10E-23

CREBBP	chr16:3781982-3782096	-	-3.30E-07	-5.10E-04	-6.40E-06	-8.00E-04
ANK1	chr8:41638104-41638239	-	-2.10E-02	-4.80E-05	+1.10E-13	+5.40E-03
MAP4	chr3:47885707-47885821	-	+8.10E-03	+9.10E-03	-4.50E-01	+1.10E-09
ANUBL1	chr10:45455694-45455875	-	NA	+2.30E-09	NA	+2.10E-04
RBM15	chr1:110689683-110689794	+	NA	-1.40E-12	NA	-2.20E-03
OPA1	chr3:194826574-194826685	+	+2.70E-02	+2.50E-01	-3.30E-12	-4.00E-13
ZMYND11	chr10:257134-257296	+	-1.40E-05	+3.20E-01	-1.20E-09	-2.00E-07
GFPT1	chr2:69434894-69434948	-	-1.60E-05	-1.10E-05	-2.10E-06	-2.40E-03
AGFG1	chr2:228105097-228105169	+	NA	-4.10E-03	-7.60E-10	-1.90E-05
PXMP3	chr8:78063097-78063129	-	NA	+2.20E-09	NA	+6.00E-03
AKAP8L	chr19:15370440-15370577	-	-5.20E-12	-1.10E-02	-3.80E-03	-4.40E-04
FLNB	chr3:58113474-58113544	+	-1.30E-07	NA	-1.30E-06	-1.20E-03
KIAA0226	chr3:198902341-198902416	-	NA	NA	+8.50E-05	+1.60E-03
LPHN3	chr4:62461031-62461070	+	+6.20E-02	-1.30E-07	NA	-2.30E-11
SPP1	chr4:89120568-89120610	+	NA	-3.00E-05	NA	-5.50E-08
DCLK2	chr4:151339629-151339680	+	-8.10E-03	-2.80E-01	-2.30E-14	-1.30E-05
LSM14B	chr20:60136035-60136152	+	+6.20E-10	-2.50E-01	+3.30E-07	+3.50E-05
MAGI1	chr3:65408736-65408772	-	+1.00E-01	+5.90E-10	+9.00E-06	+1.00E-04
GFM1	chr3:159850487-159850544	+	+3.10E-07	+1.40E-03	+3.30E-01	+3.10E-07
PSMB7	chr9:126207416-126207532	-	+5.20E-01	+2.30E-15	NA	+7.30E-03
TIA1	chr2:70305963-70306029	-	-1.70E-01	-2.10E-01	-2.80E-14	-2.50E-05
UBE2D2	chr5:138922012-138922176	+	-6.40E-04	NA	NA	-1.50E-07
ABI2	chr2:203967667-203967814	+	+3.80E-05	+2.10E-03	+2.00E-01	+9.00E-07
ELMO2	chr20:44455574-44455647	-	-4.60E-03	NA	-5.90E-01	-1.70E-13
ARID1B	chr6:157537672-157537831	+	-3.10E-01	-5.50E-09	-3.00E-06	-2.90E-05
MKRN1	chr7:139820649-139820758	-	NA	-9.00E-05	NA	-6.00E-08
HIPK3	chr11:33326287-33326350	+	-1.00E-05	NA	-3.80E-05	-5.60E-06
SORBS1	chr10:97125719-97125803	-	+2.60E-01	+2.40E-05	+2.40E-01	+3.90E-15
PDE6D	chr2:232310140-232310246	-	NA	+3.70E-06	+6.20E-04	+1.30E-04
MAP4K4	chr2:101854387-101854579	+	-3.50E-04	-3.20E-05	-7.10E-04	-2.90E-07
ANK1	chr8:41638550-41638616	-	+8.00E-16	-5.70E-03	NA	+5.40E-03
SLC24A2	chr9:19587226-19587277	-	-1.10E-07	-9.80E-06	NA	-4.10E-03
ZC3H14	chr14:88132830-88132905	+	+4.50E-01	-1.40E-12	-9.20E-04	-6.30E-03
SENP6	chr6:76389186-76389294	+	NA	NA	-2.50E-08	-1.50E-06
NPTN	chr15:71676415-71676763	-	-2.40E-02	-1.80E-02	-1.00E-04	-1.40E-11
PARP6	chr15:70330239-70330349	-	+8.30E-07	+1.50E-02	+1.70E-03	+3.20E-08
C10ORF4	chr10:120443203-120443251	-	NA	NA	-3.30E-06	-9.00E-06
CADM2	chr3:86111003-86111123	+	+5.40E-04	NA	+7.80E-02	+2.80E-07
BRPF1	chr3:9832757-9832886	+	NA	NA	-1.20E-08	-7.60E-03
MLLT6	chr17:34117264-34117319	+	-1.30E-07	-1.70E-05	+1.00E-03	+1.60E-09
MAGOH	chr1:53471801-53471912	-	-6.10E-04	-7.30E-09	-5.10E-02	-7.40E-07
TFIP11	chr22:25236029-25236247	-	+2.00E-10	-9.40E-04	NA	+7.00E-06
RBM23	chr14:22448531-22448644	-	+2.70E-12	-2.30E-02	NA	+1.20E-03
CLK4	chr5:177981999-177982066	-	+1.50E-10	NA	+1.50E-01	+9.90E-05
PTPRK	chr6:128854569-128854687	-	-1.60E-05	NA	NA	-4.10E-06
ACAA1	chr3:38150446-38150504	-	-4.20E-01	+5.00E-08	+2.30E-01	+4.60E-12
C18ORF2	chr18:42073968-42074151	+	+4.40E-01	-6.50E-03	-8.00E-08	-5.40E-09
ANK2	chr4:114513137-114513230	+	-4.50E-01	-2.00E-07	-4.40E-03	-2.70E-05
WDR23	chr14:23656716-23656781	+	+9.10E-02	+2.20E-03	+4.80E-04	+5.70E-04
MORF4L2	chrX:102820082-102820184	-	-5.60E-09	+3.70E-01	-2.50E-03	-2.50E-08

PIK3CB	chr3:139905974-139906025	-	-3.10E-01	NA	-3.20E-05	-4.60E-11
ASB8	chr12:46830136-46830190	-	NA	+1.20E-05	NA	+1.60E-05
ZFYVE9	chr1:52504914-52505091	+	-7.10E-06	+4.00E-18	-1.50E-05	+1.60E-05
SERGEF	chr11:17937592-17937759	-	-3.20E-06	-3.30E-05	NA	-2.70E-05
CPNE1	chr20:33710265-33710318	-	+4.90E-03	+2.30E-02	NA	+6.00E-10
FMR1	chrX:146827309-146827372	+	-1.20E-05	-2.50E-04	-7.90E-05	-7.00E-04
DAZAP1	chr19:1376876-1376959	+	+5.10E-01	+6.60E-06	+5.60E-03	+2.40E-05
AGAP2	chr12:56408367-56408427	-	+2.30E-01	+3.80E-03	+3.10E-03	+1.70E-11
GRIN1	chr9:139162424-139162487	+	-4.00E-02	-1.00E-07	-1.00E-03	-4.40E-04
TTBK2	chr15:40907417-40907522	-	+1.70E-03	+4.20E-05	NA	+1.40E-03
HNRNPD	chr4:83495071-83495178	-	-1.20E-03	-1.40E-04	-2.60E-06	-1.10E-03
C12ORF3	chr12:111009869-111009988	-	-3.90E-08	+1.80E-02	NA	-7.80E-03
KIAA0652	chr11:46596450-46596501	+	+9.20E-08	-2.40E-08	NA	+7.90E-06
KLHL8	chr4:88323378-88323565	-	NA	-2.70E-02	+9.40E-04	+3.00E-09
RAB5A	chr3:19987043-19987213	+	NA	-6.50E-05	-1.90E-03	-7.90E-07
LRSAM1	chr9:129293314-129293395	+	+2.00E-04	NA	+1.90E-03	+7.30E-06
CSDE1	chr1:115085670-115085817	-	+2.70E-04	NA	-3.50E-01	+8.50E-03
TTC8	chr14:88377521-88377611	+	-8.80E-04	-4.80E-02	-2.00E-02	-5.50E-12
SEC24B	chr4:110622281-110622386	+	NA	-8.90E-06	-9.90E-03	-6.10E-06
CAPRIN2	chr12:30755939-30755983	-	NA	NA	-8.30E-06	-5.50E-03
USP10	chr16:83295846-83295967	+	-6.40E-07	NA	NA	-3.40E-03
R3HDM2	chr12:55969058-55969090	-	+1.90E-14	-3.80E-12	+1.00E-06	-1.60E-03
MBNL1	chr3:153658608-153658672	+	+3.00E-01	NA	-1.30E-09	-6.90E-05
DLG1	chr3:198280486-198280528	-	-4.20E-04	+3.80E-01	-3.00E-07	-8.40E-06
PHF20L1	chr8:133880522-133880600	+	-8.20E-02	-3.50E-07	NA	-3.60E-03
WAC	chr10:28924667-28924976	+	NA	+2.20E-03	+1.40E-03	+1.80E-06
CADPS	chr3:62442437-62442584	-	+4.10E-01	-2.20E-04	+3.10E-01	-6.90E-12
PABPC4	chr1:39802094-39802181	-	-3.20E-03	-4.00E-05	-1.20E-02	-7.70E-03
NDRG3	chr20:34716617-34716656	-	+1.70E-10	NA	-1.50E-01	+1.30E-04
PCM1	chr8:17841830-17841947	+	-1.70E-01	-4.20E-07	-4.70E-05	-6.30E-03
RBM9	chr22:34504017-34504071	-	+2.90E-04	NA	+3.70E-02	+2.80E-05
ABCA3	chr16:2298451-2298625	-	+6.40E-05	NA	NA	+1.20E-04
BRSK2	chr11:1425603-1425669	+	+2.10E-02	-2.70E-04	-9.30E-04	-3.20E-07
ARHGAP2	chr5:142566955-142567066	+	NA	+7.40E-04	-2.90E-01	+2.20E-05
ATE1	chr10:123671853-123671916	-	+6.00E-07	+3.30E-05	+3.70E-01	+2.90E-04
EIF4ENIF1	chr22:30176274-30176346	-	+3.80E-02	+1.80E-04	+5.90E-02	+7.60E-05
PLA2G6	chr22:36874445-36874576	-	NA	-5.50E-05	NA	-1.90E-03
USP3	chr15:61616276-61616408	+	-1.20E-04	+8.70E-03	NA	-6.60E-06
ZMYM3	chrX:70389163-70389849	-	+2.80E-01	+4.40E-06	+3.00E-02	+1.70E-03
FAM40A	chr1:110383968-110384082	+	NA	-7.10E-04	NA	-2.70E-05
FAM49B	chr8:130961803-130961886	-	-4.00E-02	+7.40E-09	-1.70E-07	-2.70E-09
VPS53	chr17:511798-511885	-	NA	+1.70E-03	NA	+2.00E-04
DGUOK	chr2:74037759-74037875	+	-7.90E-03	NA	NA	-2.40E-05
DMXL2	chr15:49539086-49539149	-	NA	-3.00E-01	+2.40E-03	+1.60E-05
LONRF1	chr8:12639151-12639240	-	+1.10E-03	+1.00E-04	+4.90E-01	+2.00E-05
SFXN5	chr2:73041767-73041885	-	NA	NA	-2.30E-05	-9.20E-04
RAD1	chr5:34949331-34949440	-	NA	-1.20E-03	NA	-1.10E-05
YWHAE	chr17:1219752-1219785	-	-3.70E-02	-4.40E-01	-6.10E-10	-7.90E-04
HDAC9	chr7:18635497-18635629	+	-4.00E-02	-3.90E-04	-3.00E-03	-3.40E-05
WDR1	chr4:9714617-9714708	-	-3.30E-02	NA	+8.70E-03	+2.60E-06

SRPK2	chr7:104553464-104553557	-	-4.80E-01	-2.20E-04	-7.80E-09	-5.00E-04
ITSN1	chr21:34120991-34121037	+	-7.00E-05	+4.80E-01	-2.50E-01	-3.20E-09
FLJ45455	chr17:11223455-11223551	+	+1.20E-02	-4.00E-04	+2.10E-03	+1.70E-13
FAM13B	chr5:137320064-137320130	-	-3.50E-02	-4.70E-04	NA	-6.10E-06
MEGF11	chr15:63986016-63986062	-	NA	-7.80E-05	-3.40E-02	-8.70E-04
C5ORF33	chr5:36244483-36244549	-	NA	-1.80E-05	-1.40E-03	-4.00E-03
AUTS2	chr7:69876949-69877021	+	-1.60E-02	-3.80E-01	-8.40E-03	-2.10E-11
TMEM50	chr1:25539551-25539657	+	-3.40E-03	-1.10E-15	+5.80E-04	+1.70E-03
ARRB2	chr17:4566190-4566235	+	-1.10E-03	-8.40E-02	-1.60E-03	-8.30E-05
MAP7D2	chrX:19983772-19983838	-	NA	+1.50E-01	+6.70E-03	+9.40E-07
MBD1	chr18:46056202-46056349	-	-4.90E-02	NA	+6.20E-03	+2.70E-09
TMEM85	chr15:32307921-32308082	+	+2.90E-11	-2.10E-03	+1.30E-01	-2.40E-09
FLJ45455	chr17:11395937-11395994	+	NA	+2.70E-03	NA	+4.00E-04
ARMC8	chr3:139430449-139430542	+	+2.20E-05	NA	+1.70E-03	+6.80E-03
KCNJ3	chr2:155274360-155274577	+	+9.50E-06	+2.30E-01	-7.80E-03	-4.30E-17
NASP	chr1:45838643-45838716	+	NA	NA	-3.30E-03	-1.30E-05
SEC24C	chr10:75189385-75189558	+	-1.30E-01	NA	+4.30E-04	+5.00E-03
MAP4	chr3:47885707-47885821	-	+8.10E-03	+9.10E-03	-4.50E-01	+1.10E-09
GPM6B	chrX:13735689-13735809	-	-1.20E-01	-2.40E-06	-1.00E-01	-2.20E-04
XPA	chr9:99484302-99484533	-	NA	-3.60E-03	NA	-1.10E-04
TMEM10	chr7:12220351-12220545	+	NA	-1.10E-03	NA	-1.30E-04
TRIP12	chr2:230433365-230433491	-	+4.50E-02	+1.20E-03	+6.10E-03	+1.40E-05
CTNNB1	chr3:41240684-41240816	+	-4.40E-01	-8.10E-02	-1.40E-08	-6.20E-04
HMGXB4	chr22:33988315-33988414	+	NA	NA	-7.90E-04	-8.50E-04
VPS24	chr2:86622885-86622946	-	-9.70E-05	+3.10E-02	NA	-1.80E-06
OSBPL6	chr2:178945098-178945206	+	-4.20E-04	-8.90E-02	-2.90E-04	-1.20E-04
MDM2	chr12:67493600-67493675	+	+1.10E-03	NA	+4.30E-01	+3.70E-07
ASAP1	chr8:131443097-131443199	-	NA	+4.40E-03	NA	+1.90E-04
PABPC4	chr1:39802094-39802181	-	-3.20E-03	-4.00E-05	-1.20E-02	-7.70E-03
SLC4A7	chr3:27447792-27448164	-	-3.40E-03	NA	NA	-4.50E-04
FAM126B	chr2:201618463-201618561	-	-3.90E-13	NA	+4.00E-05	+1.60E-03
HNRNPL	chr19:44024092-44024162	-	-4.40E-02	-8.80E-02	-5.70E-06	-3.70E-04
CPEB2	chr4:14619059-14619149	+	NA	+4.40E-01	-7.00E-07	-1.30E-03
RUNX1T1	chr8:93143949-93144113	-	-4.40E-02	+1.80E-03	-6.10E-09	-2.30E-04
NCOR1	chr17:15931210-15931384	-	-9.20E-03	-2.20E-01	-2.30E-03	-3.60E-06
SFRS2	chr17:72243448-72243552	-	+6.50E-04	+1.40E-08	-6.40E-07	+7.30E-03
RNF38	chr9:36380463-36380613	-	-2.80E-06	+8.90E-05	+7.90E-02	+4.10E-06
FBXW11	chr5:171317205-171317307	-	-1.60E-04	+7.60E-03	-8.50E-07	-8.30E-03
DNAJC16	chr1:15728169-15728354	+	NA	NA	-7.40E-04	-7.90E-03
RIMS1	chr6:73040772-73040856	+	+4.30E-04	-3.10E-01	-6.80E-05	-1.80E-11
MYEF2	chr15:46231722-46231773	-	-5.70E-04	-1.70E-03	-2.20E-01	-3.40E-04
RPS6KC1	chr1:211312834-211312951	+	-4.40E-03	NA	-1.70E-02	-2.00E-04
CLTA	chr9:36199263-36199317	+	+1.90E-04	NA	-2.90E-01	+1.70E-05
UHRF1BP	chr12:99046488-99046634	-	+3.00E-01	+4.50E-03	+1.80E-02	+2.70E-05
UNQ1887	chr12:119713654-119713743	-	+2.90E-05	-1.50E-01	+4.00E-01	+9.70E-08
AFF4	chr5:132301239-132301331	-	NA	NA	-1.70E-04	-3.30E-03
PKIB	chr6:123037921-123037988	+	NA	+3.60E-03	NA	+7.10E-04
SLC26A10	chr12:56294565-56294655	+	-2.50E-04	+2.20E-01	NA	-3.50E-04
HACL1	chr3:15591487-15591593	-	-2.50E-02	-1.80E-04	-4.40E-02	-2.70E-05
XRN2	chr20:21254916-21255044	+	-3.80E-01	+1.80E-03	+1.10E-01	+2.50E-07

FAM120A	chr9:95360683-95360818	+	+1.10E-04	+4.90E-02	+2.80E-01	+9.00E-05
MYO9A	chr15:69972359-69972572	-	-2.30E-04	+6.00E-01	-1.40E-05	-2.20E-03
HNRNPA2	chr7:26197200-26197273	-	NA	+2.00E-04	-1.70E-03	+4.50E-05
FSD1L	chr9:107263621-107263717	+	NA	-2.60E-03	NA	-9.90E-03
VEZT	chr12:94176151-94176189	+	-2.40E-01	NA	-9.40E-03	-1.10E-04
BCAS3	chr17:56820760-56820851	+	NA	-1.20E-03	-7.80E-02	-6.40E-04
SRPX	chrX:37898658-37898780	-	+6.40E-01	-1.70E-01	+8.50E-03	+8.20E-03
HECW1	chr7:43120280-43120515	+	+2.50E-01	NA	-2.80E-04	-2.40E-05
ARFIP2	chr11:6458128-6458229	-	+3.10E-05	-5.50E-07	-6.20E-03	+6.80E-05
FBXW11	chr5:171273951-171274014	-	+7.60E-03	+3.70E-04	+2.90E-01	+3.20E-03
SPATS2L	chr2:201012089-201012296	+	NA	+1.00E-02	+6.40E-03	+8.80E-03
EI24	chr11:124956316-124956428	+	+4.00E-01	-2.80E-07	-3.40E-01	-8.20E-04
MSRA	chr8:9991163-9991238	+	+3.70E-06	+3.00E-01	-9.60E-02	+5.60E-05
FAM179B	chr14:44547865-44548098	+	-1.20E-04	NA	+1.70E-07	-3.40E-03
C18ORF1	chr18:13633357-13633411	+	-1.80E-10	+3.90E-05	-2.70E-04	+4.10E-04
RELA	chr11:65185983-65186135	-	NA	+4.10E-03	-1.80E-03	+2.90E-05
ITPR2	chr12:26834356-26834427	-	+6.60E-04	NA	-5.30E-01	+4.40E-05
NFIA	chr1:61621496-61621625	+	-6.70E-06	-1.10E-04	+4.10E-03	+3.70E-06
WDFY3	chr4:85867037-85867088	-	-4.40E-02	+1.50E-03	-8.60E-06	-6.10E-04
CADM1	chr11:114574335-114574368	-	-6.20E-06	-8.80E-07	+5.50E-04	+7.50E-08
SFRS7	chr2:38826789-38826825	-	NA	+5.00E-05	+2.20E-01	+6.90E-03
ARRB2	chr17:4566016-4566077	+	-1.60E-01	-1.10E-03	+9.20E-06	+8.40E-04
FBXW11	chr5:171273951-171274014	-	+7.60E-03	+3.70E-04	+2.90E-01	+3.20E-03
ITSN1	chr21:34117660-34117827	+	+4.40E-03	+4.40E-01	-5.40E-01	+7.00E-05
FOXN3	chr14:88726483-88726546	-	+2.60E-03	+1.30E-03	-2.00E-05	-4.30E-06
GBA2	chr9:35728228-35728371	-	-1.50E-01	+9.50E-03	NA	+3.90E-05
RAPGEF2	chr4:160491660-160491735	+	-4.00E-05	+2.30E-01	-4.00E-02	-6.20E-04
8-Sep	chr5:132137513-132137803	-	-1.70E-01	-2.50E-03	NA	-5.80E-03
GSTM4	chr1:110015617-110015728	+	+2.00E-03	-2.00E-04	+1.10E-02	+1.70E-04
MACF1	chr1:39707805-39707874	+	+2.50E-12	+8.10E-02	-9.00E-09	-7.20E-03
USP28	chr11:113182420-113182516	-	+1.60E-04	+5.80E-02	+3.00E-01	+2.00E-03
PAN3	chr13:27669321-27669483	+	+5.80E-02	+8.90E-02	-2.10E-03	-3.80E-08
EPB41L3	chr18:5388019-5388142	-	+9.10E-03	+1.90E-01	-4.10E-01	+5.40E-05
EGFL7	chr9:138683878-138683994	+	-3.30E-05	+2.80E-03	NA	+6.20E-05
HR	chr8:22030332-22030497	-	-2.40E-04	+3.80E-01	NA	-9.90E-03
KIF1A	chr2:241345408-241345684	-	-9.80E-05	+1.90E-01	NA	-2.80E-03
ZNF326	chr1:90245758-90245897	+	-9.80E-03	-4.20E-01	-9.80E-02	-1.50E-04
SNX15	chr11:64556215-64556251	+	+1.90E-03	-3.30E-03	+3.50E-01	+1.10E-06
SCAMP5	chr15:73095986-73096143	+	+9.60E-03	-3.40E-01	-2.30E-03	+1.40E-08
BPTF	chr17:63355536-63355698	+	-4.20E-03	+6.60E-03	-2.70E-07	+7.40E-05
SLC6A6	chr3:14484599-14484724	+	+1.70E-04	-2.50E-06	+2.00E-01	+5.00E-04
NCAM1	chr11:112597227-112597257	+	-3.70E-01	+2.30E-03	-3.40E-04	-2.90E-05
WDR7	chr18:52595010-52595109	+	-6.40E-06	+5.40E-12	-1.20E-01	-9.70E-03
RBM26	chr13:78825288-78825360	-	+3.70E-01	+2.50E-01	-7.20E-06	-5.30E-04
RBM12B	chr8:94822032-94822100	-	+7.20E-03	NA	+1.50E-01	+3.00E-03
CAMTA2	chr17:4830210-4830305	-	-7.10E-04	NA	+8.80E-02	-3.40E-03
COPS7A	chr12:6707352-6707428	+	-1.30E-01	-1.70E-02	-7.80E-03	-4.90E-03
FAM126B	chr2:201560332-201560500	-	-1.10E-02	+7.30E-04	-1.70E-03	+9.10E-06
MXRA7	chr17:72191523-72191604	-	-1.70E-05	+2.90E-04	+1.30E-02	+1.80E-05
BFAR	chr16:14656423-14656568	+	+8.90E-05	-2.40E-04	-3.70E-03	-7.20E-03

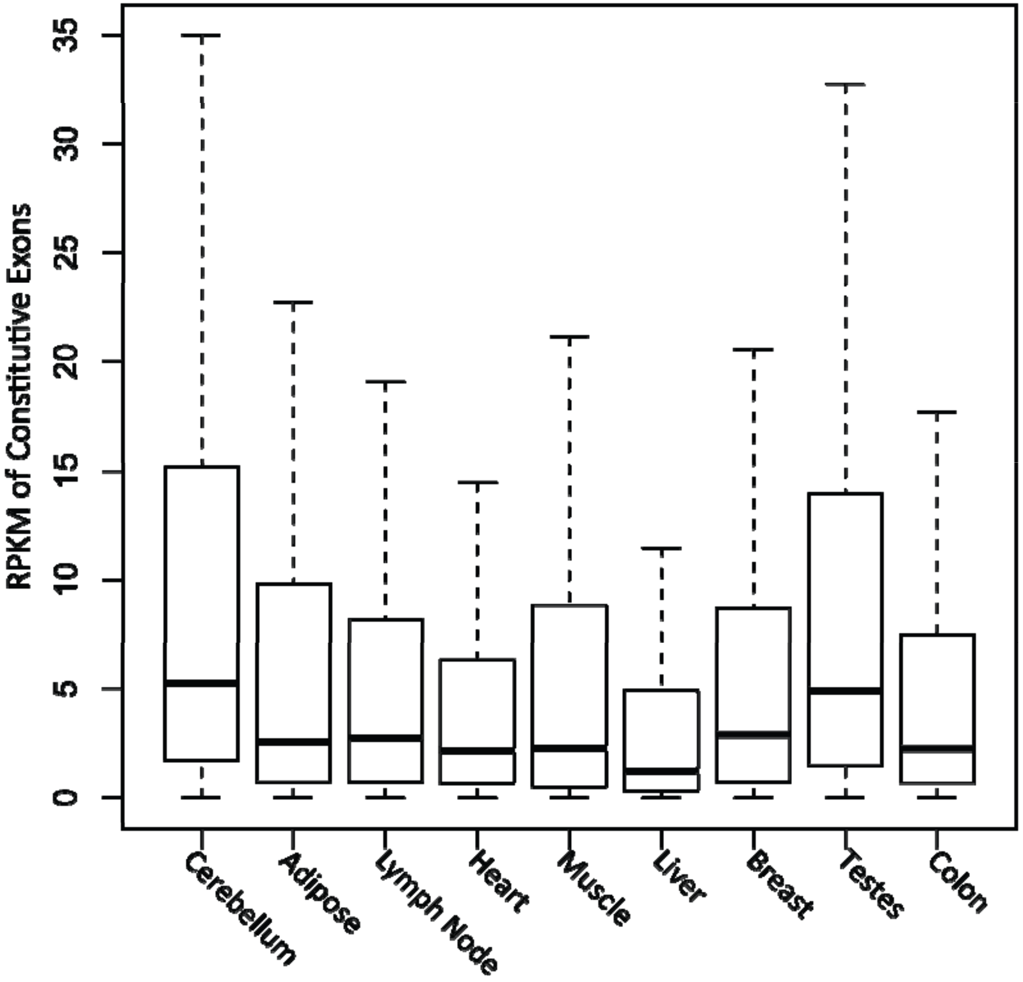
NAE1	chr16:65418080-65418184	-	-5.20E-07	+2.60E-04	NA	+3.70E-03
CACNA1B	chr9:140031411-140031474	+	NA	-3.40E-04	+4.90E-03	+1.50E-03
TNRC4	chr1:149946244-149946394	-	+7.50E-03	-3.60E-03	-4.30E-03	+2.00E-04
RCOR3	chr1:209544047-209544105	+	+7.80E-03	+7.10E-04	-2.20E-03	-1.60E-03

Supplemental Table 6: List of RT-PCR primers.

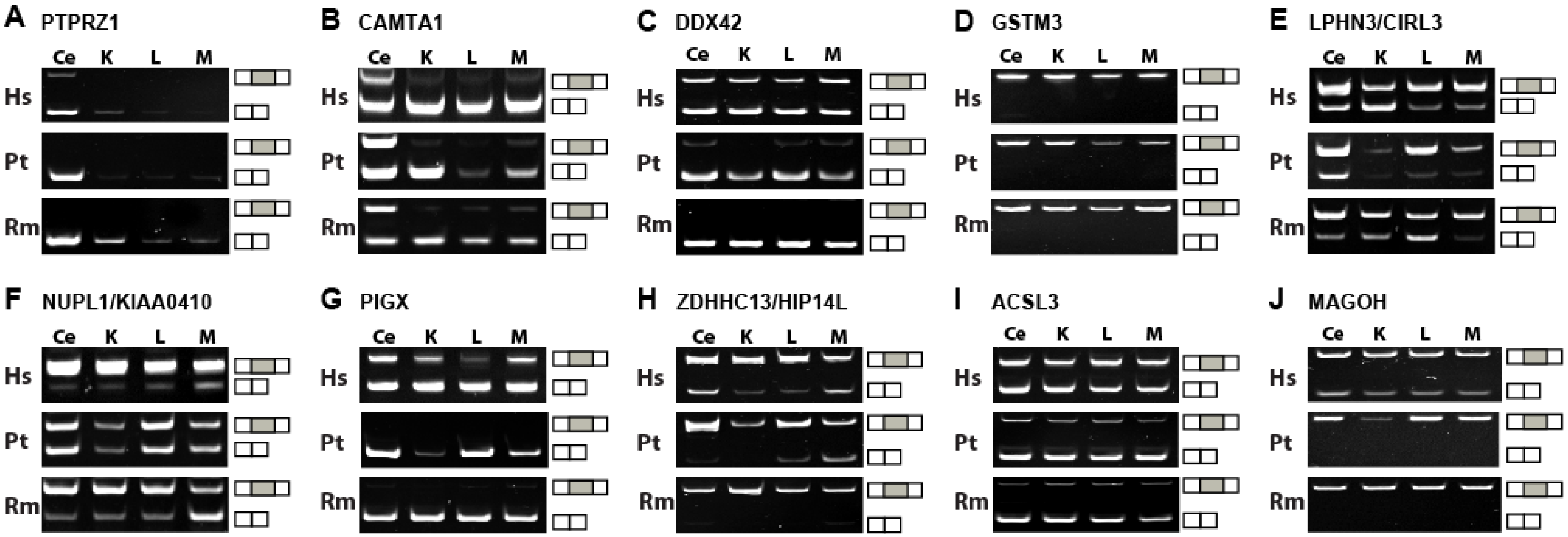
Gene symbol	**Species**	**Forward Primer**	**Reverse Primer**	**Skipping (bp)**	**Inclusion (bp)**
LMBR1/ACHP	Human	TCTGCTCTGCCTGTGATGTC	GTGCTTTCTGATGCCCATTT	112	274
LMBR1/ACHP	Chimpanzee	TCTGCTCTGCCTGTGATGTC	CGGTTGAAATGGAAATGCTT	210	372
LMBR1/ACHP	Rhesus	TCTGCTCTGCCTGTGATGTC	GAGCCAAGGTTGAAATGGAA	216	378
ACSL3	Human	GACACAAGGGCGCATATCTT	CAGGCTTTGCTTTAATTCGG	272	379
ACSL3	Chimpanzee	GACACAAGGGCGCATATCTT	GCTTCATGGTAGATGGTTTTGA	134	241
ACSL3	Rhesus	CACAAGGGCGCGTATCTTTA	GCTTCATGGTAGATGGTTTTGA	129	236
SYNRG/AP1GBP1	Human	CTGTGGAGTGTGCCTCTTGA	ATTCAGGGAAGCGAACTGTG	277	313
SYNRG/AP1GBP1	Chimpanzee	GGCCTGGGATTAAAAATGCT	GGCTTTGGTTCGACACAGTT	172	208
SYNRG/AP1GBP1	Rhesus	CTGTGGAGTGTGCCTCTTGA	ACTGATTGGTCCCTGTCACC	241	277
ASRGL1	Human	GAAGACGATCCCGAGTTCAA	GCCTTGGTCAGTCAGAAAGC	55	198
ASRGL1	Chimpanzee	GAAGACGATCCCGAGTTCAA	GCCTTGGTCAGTCAGAAAGC	55	198
ASRGL1	Rhesus	GAAGACGATCCCGAGTTCAA	TTCTGAGCACCTTTTTCGTG	168	311
C11orf80	Human	GCAAGGTTCCATCCAATTCA	TGTGCAGTTTGGTCCTGAAC	98	209
C11orf80	Chimpanzee	GCAAGGTTCCATCCAATTCA	CACATGAGCAGTGGTGAAGAA	149	260
CAPRIN2/C1QDC1	Human	ACTGACCTGCCCTGAAAGAA	CTTTTCCTTGGCATTTTTGG	119	202
CAPRIN2/C1QDC1	Chimpanzee	GGGTTTGAATGGTGCAGTGT	CTTTTCCTTGGCATTTTTGG	182	265
CAPRIN2/C1QDC1	Rhesus	ACTGACCTGCCCTGAAAGAA	CTTGGCATTTTTGGGAACTG	113	196
CAMTA1	Human	ATAATGAGGTTTCTTCGCCG	TCCTGGGTGTCTTGATTTCC	352	383
CAMTA1	Chimpanzee	AGGTTTCTACGCCGCTGTC	TGTGTGCGTGTGTTGTTGTT	157	188
CAMTA1	Rhesus	AGGTTTCTACGCCGCTGTC	ATTGCTAAGGGATGCTGCTG	86	117
LPHN3/CIRL3	Human	ATCACTTGAATGCTGGGGAC	TGTGGCTGAAGGAGGTTGTT	166	205
LPHN3/CIRL3	Chimpanzee	ACTTGAATGCTGGGGACATC	TGTGGCTGAAGGAGGTTGTT	163	202
LPHN3/CIRL3	Rhesus	ACTTGAATGCTGGGGACATC	TGTGGCTGAAGGAGGTTGTT	163	202
DDX42	Human	GACAGCGCGTACTTTGGG	TGCCAGGACCACCTTTATTC	121	192
DDX42	Chimpanzee	GGACAGCGCGTACTTTGG	TGCCAGGACCACCTTTATTC	122	193
DDX42	Rhesus	CTGGGACAGCGCGTACTT	AACCTCCAAAGCCAAATCCT	152	223
DCAF11/WDR23/GL014	Human	GCACAGCTTTCCTCGAATGT	CAGTGAAGCCCAGATCATTG	57	122
DCAF11/WDR23/GL014	Chimpanzee	GGATGCTACCCCTGACACC	CAGTGAAGCCCAGATCATTG	156	221
DCAF11/WDR23/GL014	Rhesus	GGATGCTACCCCTGACACC	CAGTGAAGCCCAGATCATTG	156	221
GPBP1L1	Human	CCATTTTGGGAAGAGCTTTG	TTGAAAGGCCACACGAATCT	144	189
GPBP1L1	Chimpanzee	CCATTTTGGGAAGAGCTTTG	GATCCATTTCCACCACTTCA	171	216
GPBP1L1	Rhesus	CCATTTTGGGAAGAGCTTTG	TCCATTTCCACCATTTCACA	169	214
GSTM3	Human	TATGGTTCTCGGGTACTGGG	AATTTCACATCCAGCCATTG	71	147
GSTM3	Chimpanzee	GGAAGACCGTTACCATGTCG	AATTTCACATCCAGCCATTG	102	178
GSTM3	Rhesus	TTGGGGTACTGGGATATTCG	GGAAAGTCCAGGTCCAGCTT	85	161

NUPL1/KIAA0410	Human	CTTCTGTGGGGCTCAATTTT	TAGAGCAAATGGTGTGGCAG	224	260
NUPL1/KIAA0410	Chimpanzee	CTTCTGTGGGGCTCAATTTT	AGATGTAGTGGCTGGCGTTC	158	194
NUPL1/KIAA0410	Rhesus	CTTCTGTGGGGCTCAATTTT	AGATGTAGTGGCTGGCGTTC	158	194
ERMP1/KIAA1815	Human	TTGTGGTAAAGCTGGAACCC	TTTCCCTCCTACACCTGCTG	171	299
ERMP1/KIAA1815	Chimpanzee	CCCACAGGCTCTTTTAGCAT	TTTCCCTCCTACACCTGCTG	238	366
ERMP1/KIAA1815	Rhesus	CCCACAGGCTCTTTTAGCAT	TTTCCCTCCTACACCTGCTG	238	366
MACF1	Human	TTTGGGGATTCTCAGCAGTT	GGGAAGATGGTTTGGACCTT	229	298
MACF1	Chimpanzee	TTTGGGGATTCTCAGCAGTT	GGGAAGATGGTTTGGACCTT	229	298
MACF1	Rhesus	TTTGGGGATTCTCAGCAGTT	CCCCCTCTGGTAGGATGAAT	172	241
MAGOH	Human	TGCCAACAACAGCAATTACA	TGTGTTCATCTCCAATGACGA	77	188
MAGOH	Chimpanzee	GCCAACAACAGCAATTACAAG	TGACATCAATAAGGGAACCA	118	229
MAGOH	Rhesus	TGCCAACAACAGCAATTACA	TGTGTTCATCTCCAATGACGA	77	188
PCCB	Human	TGTCCCTGGCTTTCTACCTG	TCATAGGCACCTCCATAGGC	40	141
PCCB	Chimpanzee	GGGCTCGTTTTGTCAGATTC	CTTTGCTCCCATGACTGC	177	278
PCCB	Rhesus	GGGCTCGTTTTGTCAGATTC	TCATAGGCACCTCCATAGGC	98	199
PIGX-chr3[197937922:197938039]	Human	AGTGAAGTTTGGGGAAAGCA	GACCACAATCGAGGCTTCTC	307	424
PIGX-chr3[197937922:197938039]	Chimpanzee	GATCCGTATGAGTTGGCTTCA	CGAGGCTTCTCCATCTTCAC	216	333
PIGX-chr3[197937922:197938039]	Rhesus	TGAGTTGGCTTCATTACGAGAG	ATCGAGGTTTCTCCATCGTG	210	327
PIGX-chr3[197939969:197940023]	Human	GTGAAGATGGAGAAGCCTCG	TCTGAGTGAGCCCAGCATTT	97	151
PIGX-chr3[197939969:197940023]	Chimpanzee	TGCCAGACGAGATTCACAGT	CTTCTGAGTGAGCCCAGCAT	175	229
PTPRZ1	Human	AATGCACTCCTCATTCCTGG	TCGATTCTTTTCCCTGTTGC	132	249
PTPRZ1	Chimpanzee	GAAACTGAGGTGCTGGACAGT	TCGATTCTTTTCCCTGTTGC	171	288
PTPRZ1	Rhesus	GAAACTGAGGTGCTGGACAGT	TCGATTCTTTTCCCTGTTGC	171	288
SIPA1L1/DKFZp686G1344	Human	GGCAGAACACCCAGTCAGAT	ATGCCCTTGTTTGTTTGGAG	206	269
SIPA1L1/DKFZp686G1344	Chimpanzee	GGCAGAACACCCAGTCAGAT	ATGCCCTTGTTTGTTTGGAG	206	269
SIPA1L1/DKFZp686G1344	Rhesus	TTGGAGTGAGCCGTAGATCC	ATGCCCTTGTTTGTTTGGAG	242	305
SOS1	Human	GATCATTCGAGCCCTTTTCA	GGGACAGGCACTTCATCAGT	83	128
SOS1	Chimpanzee	CATCTGCACCAAATTCTCCA	GGGACAGGCACTTCATCAGT	175	220
SOS1	Rhesus	GATCATTCGAGCCCTTTTCA	GGGACAGGCACTTCATCAGT	83	128
ZDHHC13/HIP14L	Human	CAGCAGGAAGTGGGAGAAGA	TAGCAGCCCAATGAAGAAGC	224	370
ZDHHC13/HIP14L	Chimpanzee	CAGCAGGAAGTGGGAGAAGA	TAGCAGCCCAATGAAGAAGC	224	370
ZDHHC13/HIP14L	Rhesus	CAGCAGGAAGTGGGAGAAGA	AGCAGCCCAATGAAGAAGTG	223	369
ZFAND1	Human	TGTGTGTGATGATTGTTCAGGA	GCCACAAGTTCTCTCTCAGCA	119	159
ZFAND1	Chimpanzee	TGTGTGTGATGATTGTTCAGGA	GCCACAAGTTCTCTCTCAGCA	119	159

ZFAND1	Rhesus	TCTTCCGTTTGTGTGTGATGA	TTGAATGAGCATGGGTAAGATG	101	141
ZNF207	Human	CCAGGTGTTCCTCCTCTGAT	GGTCCAGGTGGCATCATT	95	143
ZNF207	Chimpanzee	TGCCAGGTGTTCCTCCT	CAGGCATCAGAGGTGGTATT	120	168
ZNF207	Rhesus	CCAGGTGTTCCTCCTCTGAT	GGTCCAGGTGGCATCATT	95	143
Fluorescent labeling RT-PCR	**GFPN tag sequence: 5’-CGTCGCCGTCCAGCTCGACCAG-3’**				
Gene symbol	**Species**	**Forward Primer**	**Reverse Primer**	**Skipping (bp)**	**Inclusion (bp)**
AMOTL1	Human	GFPN-GTGAATGGGGTTGATTGTCC	AGTTCATGTTCTCGGTTGGG	293	443
AMOTL1	Chimpanzee	GFPN-GTGAATGGGGTTGATTGTCC	CTCAGGAAGTTTGGGGAGTG	207	357
AMOTL1	Rhesus	GFPN-GTGAATGGGGTTGATTGTCC	CTCAGGAAGTTTGGGGAGTG	207	357
DCLK1 (DCAMKL1)	Human	GFPN-ATGATGGCCTCCCAGAAAAT	CTTGTACCGGCTCCTCACAT	185	259
DCLK1 (DCAMKL1)	Chimpanzee	GFPN-ATGATGGCCTCCCAGAAAAT	CTTGTACCGGCTCCTCACAT	185	259
DCLK1 (DCAMKL1)	Rhesus	GFPN-ATGATGGCCTCCCAGAAAAT	CTTGTACCGGCTCCTCACAT	185	259
EGFL7	Human	GFPN-GTGTACCAGCCCTTCCTCAC	GACACAGCTCCCTCCGTTC	97	213
EGFL7	Chimpanzee	GFPN-TGCTGTCCGGGCTCA	TGTCACCCTGCCATCCT	189	305
EGFL7	Rhesus	GFPN-GTGTACCAGCCCTTCCTCAC	ATGCAGCTTCCTCCGTTC	96	212
FMR1/FMRP	Human	GFPN-TCAAGGGTTGGACCTAATGC	AGCGATGCTGTCCTTTGTTC	171	234
FMR1/FMRP	Chimpanzee	GFPN-TCAAGGGTTGGACCTAATGC	AGCGATGCTGTCCTTTGTTC	144	207
FMR1/FMRP	Rhesus	GFPN-TCAAGGGTTGGACCTAATGC	AGCGATGCTGTCCTTTGTTC	144	207
KCNJ3/GIRK1	Human	GFPN-GGACGGAAAACTCACGCTTA	TGGTGCTATTAAAGGGGACG	291	508
KCNJ3/GIRK1	Chimpanzee	GFPN-GGACGGAAAACTCACGCTTA	GGGGACTTCAAATGTTGCAT	225	442
KCNJ3/GIRK1	Rhesus	GFPN-GGACGGAAAACTCACGCTTA	GGGGACTTCAAATGTTGCAT	225	442
GLS	Human	GFPN-ATGGAACAGCGGGACTATGA	ACGGTTTGATTTTCCTTCCC	184	248
GLS	Chimpanzee	GFPN-ATGGAACAGCGGGACTATGA	ATGGTGTCCAAAGTGCAGTG	101	165
GLS	Rhesus	GFPN-ATGGAACAGCGGGACTATGA	TGGACGGTTTGATTTTCCTT	187	251
MBD1	Human	GAAATGTGTCCAGCGACGTT	GFPN-CCATCTTGGAGTCACAGCCT	71	146
MBD1	Chimpanzee	AGCCGAGGGTGTGGAGTAT	GFPN-AGCCATCTTGGAGTCACAGC	174	249
MBD1	Rhesus	AGCCGAGGGTGTGGAGTAT	GFPN-AGCCATCTTGGAGTCACAGC	174	249
NAV2	Human	TTCTTCAGCCTCTCCCGATA	GFPN-TGCGTCGGTTGTTAGCAGTA	307	376
NAV2	Chimpanzee	GAAGCAGCACCTCTCCTCAC	GFPN-GATACCCTCGCGGTAGGAC	204	273
NAV2	Rhesus	GAAGCAGCACCTCTCCTCAC	GFPN-GATACCCTCGCGGTAGGAC	204	273



Supplemental Figure 1



Supplemental Figure 2